

UNIVERSITY OF ZULULAND



***In silico* genome-wide analysis of P450s, their redox partners and secondary metabolite
gene-clusters in the bacterial class *Alphaproteobacteria***

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requirement for the degree of Master of Science

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DECLARATION

I, Nomfundo Nzuza, declare that this dissertation is entirely my own work and has not been taken from the work of others, except where I have appropriately acknowledged and referenced the original source. This dissertation has never been submitted for any degree for examination at any university. Considering the quality is more important than the quantity (Gould, 2016), care has been taken to present the dissertation in a publication format to enable presentation of data in a concise manner and for easy understanding of the work. I state that the ferredoxin work was carried out in collaboration with my colleague, Ms Tiara Padayachee, and the work presented in this dissertation has been published as indicated in the research outputs section.



Signed on the day of 17 September 2021

Reference: Gould, J., 2016. Future of the thesis. *Nature*, 535(7610), pp.26-29.

ABSTRACT

Cytochrome P450 monooxygenases (CYPs/P450s), heme-thiolate proteins, are well-known players in the generation of secondary metabolites that are valuable to humans. With the exception of self-sufficient P450s, all P450s need electrons to perform their enzymatic reactions and these electrons are supplied by redox proteins such as ferredoxins, iron-sulfur (Fe-S) cluster proteins. However, to date, comprehensive comparative analysis of P450s, their redox proteins and secondary metabolite gene clusters in the ancient group of bacterial class *Alphaproteobacteria* has not been reported. Thus, this study aimed to address this research gap. In this study, comprehensive analysis of P450s, ferredoxins and P450s' role in generation of secondary metabolites in *Alphaproteobacteria* has been carried out. This study also proposes a subtype classification and nomenclature for ferredoxins based on the characteristic spacing between the cysteine amino acids of the Fe-S binding motif as a subtype signature to assess diversity and lateral gene transfer (LGT) of ferredoxins across the living organisms.

Genome data-mining and annotation of P450s in 599 alphaproteobacterial species belonging to 164 genera revealed the presence of P450s in only 241 species belonging to 82 genera that are grouped into 143 P450 families and 214 P450 subfamilies, including 77 new P450 families. Alphaproteobacterial species have the highest average number of P450s compared to *Firmicutes* species and cyanobacterial species. The lowest percentage of alphaproteobacterial species in P450s (2.4%) was found to be part of secondary metabolite biosynthetic gene clusters (BGCs) compared with other bacterial species, indicating that during evolution large numbers of P450s became part of BGCs in other bacterial species. The study revealed that some of the P450 families found in alphaproteobacterial species were passed on to other bacterial species. This is the first study to report on the identification of CYP125 P450, cholesterol and cholest-4-en-3-one hydroxylase in alphaproteobacterial species (*Phenylobacterium zucineum*) and to predict cholesterol side-chain oxidation capability (based on homolog proteins) by *P. zucineum*.

Genome wide analysis of ferredoxins revealed presence of 1306 ferredoxins in 241 alphaproteobacterial species. The 2[4Fe-4S] cluster type was found to be the most abundant with 711 ferredoxins followed by 2Fe-2S with 490 ferredoxins, 3Fe-4S with 60 ferredoxins, 2[4Fe-4S]Alv with 31 ferredoxins, 7Fe-8S with 12 ferredoxins and 4Fe-4S with two ferredoxins. To assess the diversity and LGT of ferredoxins, ferredoxins collected from *Alphaproteobacteria* and from species of different domains of life that are reported in the literature were grouped into different subtypes based on the cysteine binding motif. A large number of alphaproteobacterial species ferredoxin subtypes were found across the species of

Bacteria, Archaea and Eukarya, suggesting common evolutionary origin of ferredoxins between Archaea and Bacteria and LGT of ferredoxins between prokaryotes (Archaea/Bacteria) and eukaryotes.

DEDICATION

I would like to dedicate this work to my mother Nikeziwe Nzuza, my late aunt Busisiwe Nzuza, my dad and siblings.

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Firstly, I give thanks and praises to the Lord Almighty for being by my side throughout the whole process. I also highly appreciate my supervisor, Prof Khajamohiddin Syed, who saw a potential in me and made me grow in the research field. I thank him for his support and guidance. I also acknowledge Prof David R Nelson (University of Tennessee, Memphis USA), Dr Wanping Chen (University of Göttingen, Germany) and Dr Dominik Gront (University of Warsaw, Poland) for their collaboration. I will not leave aside all my P450 group members for their support. Lastly, I would like to thank my family and friends for always having my back and keeping me motivated at all times.

RESEARCH OUTPUTS

- **Articles**

Nomfundo Nzuza[@], Tiara Padayachee[@], Wanping Chen, Dominik Gront, David R Nelson, Khajamohiddin Syed. Diversification of ferredoxins across living organisms (2021) *Current Issues in Molecular Biology* 43(3), 1374-1390. [@] Equally contributed to the study.

Nomfundo Nzuza, Tiara Padayachee, Puleng Rosinah Syed, Justyna Dorota Kryś, Wanping Chen, Dominik Gront, David R Nelson, Khajamohiddin Syed. Ancient bacterial class *Alphaproteobacteria* cytochrome P450 monooxygenases can be found in other bacterial species (2021) *International journal of molecular sciences*, 22(11), p.5542.

Nomfundo Nzuza (co-author) Comprehensive analyses of cytochrome P450 monooxygenases and secondary metabolite biosynthetic gene clusters in *Cyanobacteria* (2020) *International journal of molecular sciences*, 21(2), p.656.

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- **IN NEWS**

1. National Research Foundation facebook posts on 29 October, 2021 : <https://www.facebook.com/pg/NRFSouthAfrica/posts/>
2. YIBA news, 11 October 2021 : <https://yiba.co.za/unizulu-researchers-solved-the-six-decades-old-mystery-of-the-evolution-of-electron-transfer-proteins/>
3. Zululand observer on 15 October, 2021: <https://www.pressreader.com/south-africa/zululand-observer/textview>
4. UNIZULU website on 6 October 2021: <http://www.unizulu.ac.za/unizulu-researchers-solved-the-six-decades-old-mystery-of-the-evolution-of-electron-transfer-proteins/>

ABBREVIATIONS

Anti-SMASH	Antibiotics & Secondary Metabolite Analysis Shell
BGC	Biosynthetic Gene Cluster
BLAST	Basic Local Alignment Search Tool
CDPS	tRNA-dependent cyclodipeptide synthases
CYP/P450	Cytochrome P450 monooxygenase
iTOL	Interactive Tree of Life
MAFFT	Multiple alignment using fast Fourier transform
NCBI	National Center for Biotechnology Information
NRPS	Non-ribosomal peptide synthases
T1PKS	Type I Polyketide synthase
KEGG	Kyoto Encyclopedia of Genes and Genomes
Trex	Tree and Reticulogram Reconstruction
Fd	Ferredoxin
Fe-S	Iron-sulfur

TABLE OF CONTENTS

DECLARATION	1
ABSTRACT.....	2
DEDICATION.....	4
ACKNOWLEDGEMENTS.....	5
RESEARCH OUTPUTS.....	6
ABBREVIATIONS	8
TABLE OF CONTENTS.....	9
LIST OF FIGURES	11
LIST OF TABLES.....	13
CHAPTER 1: INTRODUCTION	14
1.1 Introduction	14
1.2. Problem statement.....	16
1.3 Value to the body of knowledge	16
1.4. Aim and objectives.....	17
1.4.1. Study aim	17
1.4.2. Study objectives.....	17
1.5. Dissertation overview.....	17
CHAPTER 2: LITERATURE REVIEW	18
2.1 Proteobacteria.....	18
2.2 <i>Alphaproteobacteria</i>	18
2.2.1 Nitrogen fixing <i>Alphaproteobacteria</i>	19
2.2.2. One-carbon (C1) metabolising <i>Alphaproteobacteria</i>	19
2.2.3. Pathogenic <i>Alphaproteobacteria</i>	20
2.3 Alphaproteobacterial secondary metabolites	21
2.4 Cytochrome P450 monooxygenases	24
2.5 P450s and their role in the biosynthesis secondary metabolites	25
2.6 Nomenclature of P450s	26
2.7 P450s and redox proteins	27
CHAPTER 3: ANCIENT BACTERIAL CLASS <i>ALPHAPROTEOBACTERIA</i> CYTOCHROME P450 MONOOXYGENASES CAN BE FOUND IN OTHER BACTERIAL SPECIES.....	29
3.1. Introduction	29

3.2. Results and Discussion.....	31
3.2.1. Only 40% of alphaproteobacterial species have P450s	31
3.2.2. Alphaproteobacterial species have the highest number of P450 families only next to <i>Streptomyces</i>	34
3.2.3. Only a few P450s are involved in secondary metabolism in alphaproteobacterial species	46
3.2.4. Alphaproteobacterial P450 families can be found in other bacterial species	50
3.2.5. Functional analysis of alphaproteobacterial P450s.....	57
3.3. Materials and Methods	58
3.3.1. Species and satabase	58
3.3.2. Genome data mining and annotation of P450s	58
3.3.3. Phylogenetic analysis of P450s.....	58
3.3.4. Generation of P450 profile heat-maps	59
3.3.5. Secondary metabolite BGC analysis and identification of P450s that are part of BGCs.....	59
3.3.6. Identification of cholesterol side-chain oxidizing genes/proteins	59
CHAPTER 4: GENOME WIDE-ANALYSIS OF FERREDOXINS, P450 REDOX PROTEINS, IN ALPHAPROTEOBACTERIAL SPECIES	61
4.1 Introduction	61
4.2 Materials and Methods	65
4.2.1. Species and database.....	65
4.2.2. Genome data mining and annotation of ferredoxins.....	65
4.2.3. Ferredoxins subtype classification and nomenclature	68
4.2.4. Assigning Fe-S cluster subtypes to the ferredoxins retrieved from literature	69
4.2.5. Phylogenetic analysis of ferredoxins	69
4.2.6. Generation of ferredoxin subtype profile heat maps.....	70
4.3. Results and Discussion.....	70
4.3.1. Alphaproteobacterial-species have different Fe-S cluster type ferredoxins in their genomes	70
4.3.2. Diversity analysis of ferredoxins among alphaproteobacterial species	71
4.3.4. Evolutionary linkage of ferredoxins subtype classification.....	79
4.3.5. LGT of ferredoxins among <i>Alphaproteobacteria</i> and other living organisms	79
CHAPTER 5: CONCLUSIONS AND FUTURE PERSPECTIVES.....	81
REFERENCES	83
Annexure A.....	94
Annexure B	157

LIST OF FIGURES

Figure 1.1. Applications of P450s and the various reactions they catalyse (Kelly and Kelly, 2013)	14
Figure 1.2. Different classes under the phylum <i>Proteobacteria</i> (https://alchetron.com/Proteobacteria).....	15
Figure 2. 1. The use of <i>Methylobacterium extorquens</i> in biotechnological applications (Ochsner et al., 2015)	20
Figure 2. 2. Representation of some examples or reactions catalysed by P450s (Cederbaum, 2015)	25
Figure 2. 3. Carotenoid biosynthesis by CYP175A1 (Greule et al., 2018).....	26
Figure 2. 4. Diagrammatic representation of P450 nomenclature (Brixius-Anderko et al., 2017)	27
Figure 2. 5. Various types of P450 systems (a) Class 1 bacterial P450 system, (b) Class II, eukaryotic membrane-bound system, (c) P450 and reductase P450 system and (d) P450RhF-type fusion system (Erdogan, 2019)	28
Figure 3. 1. Comparative analysis of P450 statistics in the bacterial class <i>Alphaproteobacteria</i> . Detailed information is presented in Annexure A-Table S1.....	32
Figure 3.2. Phylogenetic analysis of Alphaproteobacterial P450s. P450 families that are expanded in these species were highlighted in different colors and indicated in the figure. Alphaproteobacterial P450 protein sequences used to construct the phylogenetic tree	34
Figure 3. 3. Heat map figure representing the presence or absence of cytochrome P450 families in 599 Alphaproteobacterial species. The data have been represented as -3 for family absence (green) and 3 for family presence (red). One hundred and forty-three Alphaproteobacterial species form the vertical axis and 214 P450 families form the horizontal axis. The respective data used in the generation of this figure are presented in Supplementary Dataset 2 that is available at https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/	46
Figure 3. 4. Comparative analysis of types of secondary metabolite BGCs in Alphaproteobacterial species. BGCs that are populated in Alphaproteobacterial species were presented in the figure. The number at the top of each bar represents the total number of clusters. Detailed information is presented in Supplementary Dataset 3, available at https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/	47
Figure 3. 5. Comparative analysis of P450 families among different bacterial species. The number of P450 families indicated with number (bold case) and P450 families that are common between Alphaproteobacterial species and other bacterial species were listed in the figure...	51
Figure 4. 1. Basic structures of the common iron-sulfur clusters the 2Fe-2S, 3Fe-4S and 4Fe-4S clusters (Fontecave, 2006).....	61
Figure 4. 2. Ferredoxins nomenclature based on the spacing between the cysteine amino acids of Fe-S cluster binding motif. Ferredoxins start with their Fe-S cluster type, followed by ST indicating subtype and then numeric indicating its subtype number in that type. Proteins grouped into different subtypes have the same characteristic spacing between the cysteine amino acids of the Fe-S cluster binding motif.	69

Figure 4. 3. Comparative analysis of ferredoxins iron-sulfur (Fe-S) cluster features in alphaproteobacterial species. The number next to the bar indicate the count for that category. Detailed information on species and their ferredoxins is presented in Tables S1 in Annexure B.	70
Figure 4. 4. Phylogenetic analysis of ferredoxins. Ferredoxins belonging to different Fe-S cluster types were highlighted in different colors and indicated in the figure. Ferredoxin protein sequences used to construct the phylogenetic tree are presented in Tables S2.	79
Figure 4. 5. Heat map figure representing the presence (red) and absence (green) of ferredoxin subtypes in Archaea, Bacteria and Eukarya. Ferredoxin subtypes form the vertical axis and domains of life forms the horizontal axis	80

LIST OF TABLES

Table 2. 1. Some of the secondary metabolites produced by alphaproteobacterial species and their biological functions	23
Table 3. 1. Comparative analysis of main characteristics of P450s in different bacterial species	33
Table 3. 2. Comparative analysis of P450 families and subfamilies in alphaproteobacterial species	35
Table 3. 3. Identification of P450s that are part of the secondary metabolite BGCs in alphaproteobacterial species. Reference cluster information was obtained by performing BLAST at the anti-SMASH database (Blin et al., 2019), as indicated in the materials and methods section. The cluster type and most similar known cluster names available at anti-SMASH database (Blin et al., 2019) were listed in the table	48
Table 3. 4. Identification of homolog proteins involved in cholesterol side-chain oxidation in <i>Phenylobacterium zucineum</i> . <i>Mycobacterium tuberculosis</i> H37Rv cholesterol side-chain degrading proteins from the published literature (van Wyk et al., 2019) were used to identify homolog proteins in <i>P. zucineum</i> . Gene and protein IDs and enzyme annotations were from KEGG (Kanehisa et al., 2019b)	53
Table 3. 5. Functional analysis of alphaproteobacterial P450s.....	57
Table 4. 1. Information on ferredoxins that are used as reference proteins in the study	66
Table 4. 2. Subtype classification of ferredoxin across the domains of life. Ferredoxins collected from species belonging to different biological kingdoms that are reported in the literature and data mined at PDB also presented in the table as per their subtypes under the domains: Archaea, Bacteria and Eukarya. Ferredoxin protein sequences as per their nomenclature are presented in Tables S2 and S3 in Annexure B	72

CHAPTER 1: INTRODUCTION

1.1 Introduction

Cytochrome P450 monooxygenases (CYPs/P450s) are heme thiolate-proteins that are the centre of attention due to their stereo- and regio-specific enzymatic reactions. P450s got their title from a characteristic spectral maximum at 450 nm as the heme pigment absorb at 450 nm wavelength on binding of carbon monoxide to its ferrous iron (Klingenberg, 1958). P450s were found in species in all kingdoms of life (Nelson, 2018), including viruses that are classified as non-living entities (Lamb et al., 2019). P450s plays a significant role in the oxidation of different compounds in both biosynthetic and biodegradation pathways as well as the oxidation of foreign chemical compounds such as drugs and environmental contaminants as indicated in Figure 1.1. They are also involved in a wide range of catalytic reactions as shown in Figure 1.1. P450s serving as drug targets against human pathogenic microbes and protozoans also play a key role in drug development (Kelly and Kelly, 2013). P450s are found to play a key role in the biosynthesis of secondary metabolites that are beneficial to humans as antibacterial, antifungal, antiparasitic, anti-cancer and immune suppressors.

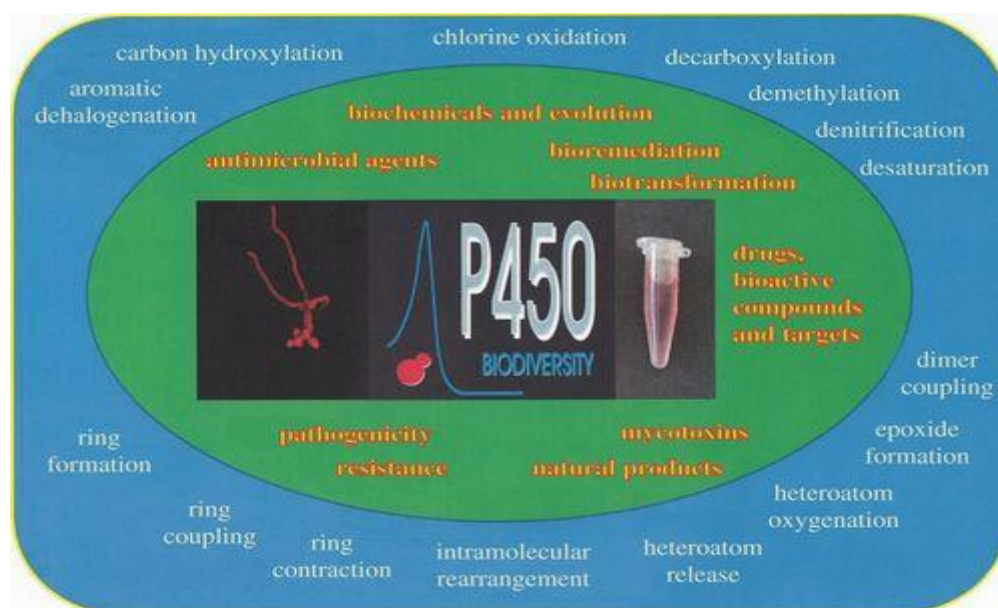


Figure 1.1. Applications of P450s and the various reactions they catalyze (Kelly and Kelly, 2013)

The phylum *Proteobacteria* is currently the largest and most diverse phylum within the bacterial domain (Gupta, 2005). It consists of a wide range of bacteria which are gram-negative with different metabolic characteristics including chemolithoautotrophy (obtains the energy from the oxidation of inorganic compounds), chemoorganotrophy (acquire energy from the

oxidation of organic compounds) and phototrophy (acquire energy from light) (Bryant and Frigaard, 2006; Swan et al., 2011). *Proteobacteria* are connected to processes such as nitrogen fixation and oxidation of iron, sulfur, and methane (Itavaara et al., 2016). The 16S rRNA gene phylogenetic analysis showed that the *Proteobacteria* phylum is categorized into six classes: *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria* and *Zetaproteobacteria* (Rizzatti et al., 2017; Mukhopadhy et al., 2012; Swan et al., 2011) (Figure 1.2).

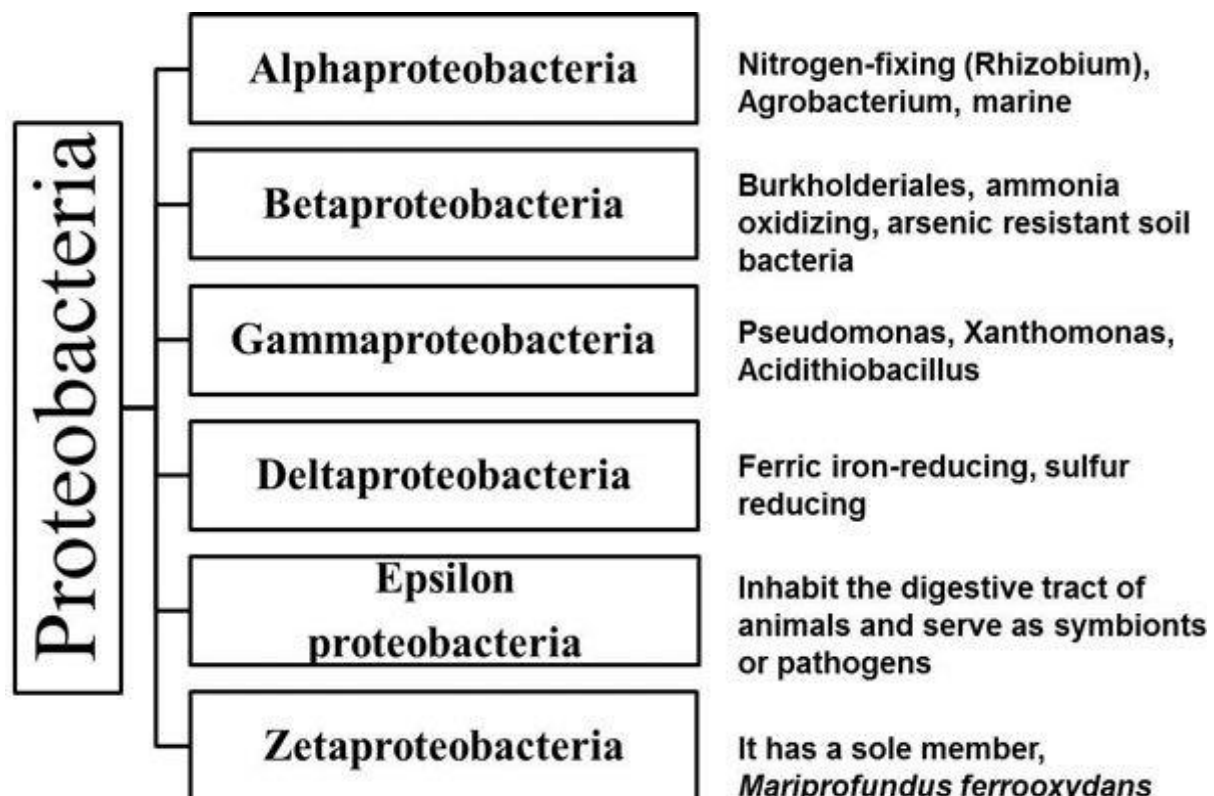


Figure 1.2. Different classes under the phylum *Proteobacteria* (<https://alchetron.com/Proteobacteria>)

In this study, the focus is on the class *Alphaproteobacteria* as it consists of many marine and terrestrial species with a diversity of lifestyles (Timmermans et al., 2017). They inhabit diverse ecological niches, from water to soil, and from both extra and intracellular associations with eukaryotes, including unicellular organisms (nematodes, arthropods), and multicellular plants and mammals (Batut et al., 2004). Some of the species are in symbiotic relationships with plants such as species belonging to the genus *Agrobacterium* whereas species belonging to *Rickettsiaceae*, *Brucellaceae* and *Bartonellaceae* are human pathogens (Mukhopadhy et

al., 2012) and a few are of ecological importance and play a huge role in carbon, nitrogen and sulphur cycles (Kerstens et al., 2006). These bacteria are found in large amounts in the upper layer of the ocean (Gupta, 2005). In spite of their differences, all alphaproteobacterial species are oligotrophs and therefore can survive in an environment with a deficiency of nutrients (Phung et al., 2004).

Secondary metabolites from a few alphaproteobacterial species have been isolated and their biological properties have been evaluated. Both in greenhouse and in field trials, *Azospirillum* species secondary metabolites were shown to exert beneficial effects on plant growth and crop yields (Steenhoudt and Vanderleyden, 2000). *Phaeobacter gallaeciensis* produces the antibacterial compound tropodithietic acid which is an inhibitor of *Vibrio anguillarum* (D'Alvise et al., 2012) and the fish-pathogenic bacteria (D'Alvise et al., 2013). *Phaeobacter* spp. can be used as a biological pest-control against *V. anguillarum* (D'Alvise et al., 2012). In the mid-1970s, the plant growth-promoting effects of *Azospirillum* were well recognized, and this bacterium has been recommended for using as a bio-fertilizer to increase plant growth and reduce the use of chemical fertilizers (Alexandre, 2017).

1.2. Problem statement

Alphaproteobacterial species produce different secondary metabolites of biotechnological value. It is well-known fact that a cluster of genes known as biosynthetic gene-clusters produce secondary metabolites in bacterial species. Among the genes, P450s were found to play a key role in the production of secondary metabolites as these enzymes contribute to the diversity of secondary metabolites. These enzymes require electrons to perform their activity and these electrons were supplied by the redox proteins. However, to date, comprehensive comparative analysis of P450s, their redox proteins and secondary metabolite gene clusters in alphaproteobacterial species has not been reported. Thus, this study aimed to address this research gap.

1.3 Value to the body of knowledge

This study generated fundamental knowledge about the profile of P450s in different strains belonging to the bacterial class *Alphaproteobacteria*. For the first time, this study reports identification of CYP125 P450s and cholesterol oxidation pathways in alphaproteobacterial species. Also, in this study, for the first time subtype classification and nomenclature for ferredoxins have been proposed.

1.4. Aim and objectives

1.4.1. Study aim

This study aimed to perform a comprehensive analysis of P450s, their redox proteins and secondary metabolite gene clusters present in alphaproteobacterial species.

1.4.2. Study objectives

- To perform genome data mining and annotation of P450s and their redox protein in the class *Alphaproteobacteria*.
- To perform phylogenetic analysis of P450s and redox proteins in *Alphaproteobacteria*.
- To perform genome data mining and identification of secondary metabolites.
- To identify P450s involved in the biosynthesis of secondary metabolites.

1.5. Dissertation overview

This thesis is divided into five chapters. Chapter 1 provides a brief overview of the work, with introduction, problem statement, value to the body of knowledge, study aim and objectives. Chapter 2 consists of a literature review. Chapter 3 consists of P450s data-mining, annotation, phylogenetic analysis and their role in secondary metabolism. This chapter is presented in the format of a research article that has been published in the International Journal of Molecular Sciences. Chapter 4 consists of ferredoxin analysis and this chapter is presented in the format of a research article that was submitted to Current Issues in Molecular Biology. Chapter 5 consists of overall conclusions and future perspectives. Supplementary data is presented in Annexures A and B.

CHAPTER 2: LITERATURE REVIEW

2.1 Proteobacteria

Phylum *Proteobacteria* is currently the largest and most diverse phylum within the bacterial domain (Gupta, 2005). *Proteobacteria* got its name after the Greek God “Petrus” who was able to presumed diverse forms, in reflection of the variation of physiology and morphology of bacteria of which it consists (Ettema and Andersson, 2009). As such, proteobacterial species differ in their morphology, motility and metabolism. They have been described as rods, cocci, curved, spiral, ring-shaped, filamentous and sheathed (Mukhopadhyaya et al., 2012). This phylum is of great biological importance, as it includes species of veterinary, industrial, medical, and agricultural interest (Kersters et al., 2006). It consist of species with an extensive phylogenetic, ecological and pathogenic significance (Woese et al., 1984). *Proteobacteria* have been located in different environmental places as free living bacteria (*Pseudomonas*), as symbiotic bacteria (*Betaproteobacteria*), as endosymbionts (*P. endosymbionts*), and as obligate intracellular parasites (*Rickettsia*). Proteobacterial species have also been found in extremes of temperatures as thermophiles in hot-springs and psychrophiles in glacier ice (Moreno, 1998). Phylogenetically, according to the 16S rRNA gene analysis, this phylum has six classes, 460 genera and more than 1600 species (Kersters et al., 2006).

2.2 Alphaproteobacteria

Species of the class *Alphaproteobacteria* are exceptionally diverse in their morphological and physiological characteristics even though they share a common ancestor. Several species of the *Alphaproteobacteria* are of ecological importance for the huge role they play in the carbon, nitrogen and sulfur cycles. Without these species (especially nitrogen-fixing rhizobia) life on earth, more especially in the agricultural sector, would be different (Kersters et al., 2006).

Studies on the evolution or emergence of the mitochondria, which allows the eukaryotic cells to produce energy through oxidative phosphorylation, have established that mitochondria are a result of endosymbiotic capture of the *Alphaproteobacteria* (*Rickettsia*) by the primitive eukaryotic cell (Falah and Gupta, 1994; Gupta and Malhotra, 1994; Lake and Rivera, 1994; Karlin and Brocchieri, 2000; Esser et al., 2004). In addition, numerous alphaproteobacterial species have been documented as obligate intracellular organisms (*Rickettsiales*, *Brucella*, *Bartonella*) that are human and animal pathogens (Moreno and Moriyon, 2002). *Bartonella* species were known to cause Carrion’s disease (*B. bacilliformis*), trench fever (*B. quintana*), and cat scratch disease (*B. henselae*) (Rolain et al., 2004).

2.2.1 Nitrogen fixing *Alphaproteobacteria*

Rhizobia are among other important bacterial symbionts that play a significant role in the atmospheric nitrogen fixation through a process called biological nitrogen fixation in plants (Laranjo et al., 2014). Most of these bacterial groups are part of the *Rhizobiaceae* family found in the *Alphaproteobacteria* within the genera *Rhizobium*, *Mesorhizobium*, *Ensifer* and *Bradyrhizobium* (Berrada and Fikri-Benbrahim, 2014). However, not only *Alphaproteobacteria* genera contain species with nitrogen fixing characteristics but also the genus *Burkholderia*, *Cupriavidus* from *Betaproteobacteria* and some *Gammaproteobacteria* form part of species that are plant symbionts, specifically legumes (Berrada and Fikri-Benbrahim, 2014). The use of these micro-organisms in agriculture is beneficial as they are less expensive and are environmentally friendly biofertilizers which promote significant plant growth in return for organic compounds (Afzal and Bano, 2008).

2.2.2. One-carbon (C1) metabolising *Alphaproteobacteria*

The genus *Methylobacterium* contains bacterial species that are able to metabolize one-carbon (C1) compound as a single source of carbon and therefore plays an important role in global carbon cycling (Anthony, 1982). C1 compounds including methane, methanol, methylated amines, methylated glycines and halomethanes are used by methylotherophs as carbon sources (Anthony, 1982; Lidstrom, 1992; Kelly and Murrell, 1999). *Methylobacterium extorquens* as the most studied species of this genus have gained an interest in biotechnological applications for use as a host in the production of methanol-based products (Senior and Windass, 1980; Anthony and Williams, 2003). Some of the *M. extorquens* applications in biotechnology are indicated in Figure 2.1.

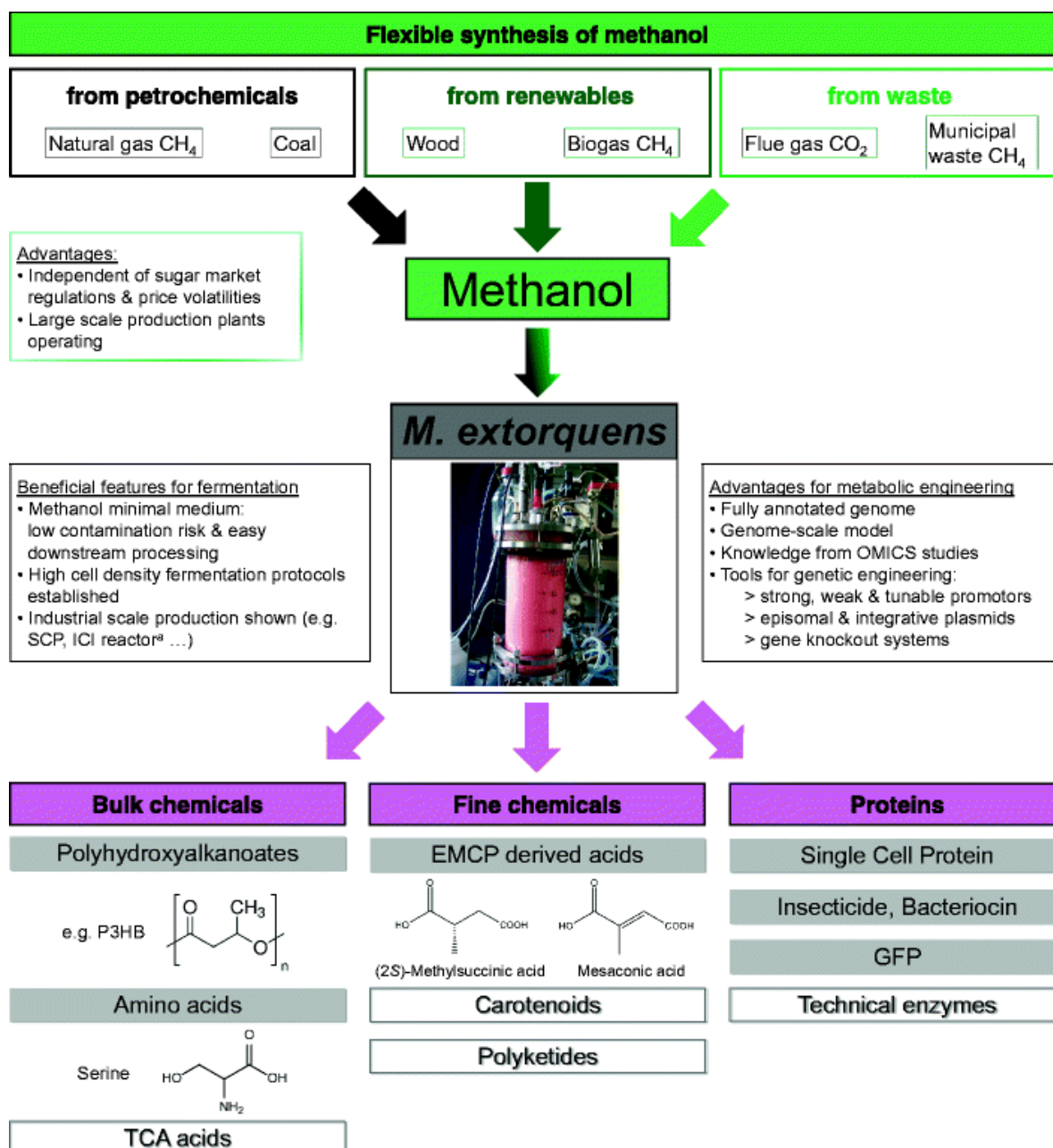


Figure 2. 1. The use of *Methylobacterium extorquens* in biotechnological applications (Ochsner et al., 2015)

2.2.3. Pathogenic Alphaproteobacteria

2.2.3.1. *Brucella*

Brucellosis is an infectious disease caused by species from the genus *Brucella*. The zoonotic is transmitted to humans either by consumption of contaminated animal products, direct contact with infected animals or by working in a medical laboratory (Dadar et al., 2019b; Dadar et al., 2019a). Species including *B. abortus*, *B. suis*, and *B. melitensis* are the most pathogenic species

for humans and animals (Kolo et al., 2018). Brucellosis infections have critical economic impacts on animal farming due to abortions, poor weight gains and animal product production (McLeod, 2011; Franc et al., 2018). It is still a major public health concern globally with over 500 000 reported cases yearly by the World Health Organization (WHO) (Ezama et al., 2018).

2.2.3.2. *Bartonella*

Bartonella species are highly adapted facultative intracellular pathogens that cause acute and chronic infections worldwide in numerous mammals including humans (Wagner and Dehio, 2019). They infect the endothelial cells and erythrocytes of both the incident and natural reservoir host (Diniz et al., 2016). Incidental transmission to humans as a non-reservoir host by bloodsucking arthropod vectors can lead to zoonotic disease with clinical manifestations such as trench fever, lymphadenopathy, neuroretinitis, endocarditis, encephalitis, and myocarditis (Wagner and Dehio, 2019).

2.2.3.3. *Rickettsia*

Rickettsiosis are common arthropod-borne illnesses with clinical complications that range from mild to severe with threatening fatalities (La Scola and Raoult, 1997). These illnesses are classified into three major groups: the scrub typhus which results from *Orientia tsutsugamushi*, spotted fever caused by *Rickettsia rickettsii*, *R. conorii*, *R. africae*, and *R. japonica* and epidemic typhus that results from infection by *Rickettsia typhi* and *R. prowazekii* (La Scola and Raoult, 1997).

2.3 Alphaproteobacterial secondary metabolites

Secondary metabolites are different types of natural compounds produced by specific groups of bacteria, plants, fungi and animals (Cragg and Newman, 2013; Cummings et al., 2014). However, they are not part of the growth factors. Astaxanthin, a marine carotenoid, has biological functions as a vitamin A precursor, anticancer agent and an enhancer of immune response. It has been found to be synthesized by *Agrobacterium aurantiacum* (Misawa et al., 1995). *Alphaproteobacteria* isolated from marine tunicate was found to produce heptyl prodigioson, a compound that has antimalarial, immunosuppressive and apoptosis-inducing activities (Lazaro et al., 2002; Soliev et al., 2011). Some species belonging to the genus *Roseobacter* produce sodium-channel blocking toxins that are found to have biotechnological value in marine ecosystems (Wagner-Döbler et al., 2004). Secondary metabolites produced by endophytic alphaproteobacterial species (*Azospirillum* sp. B510) were found to promote plant

growth and also help plants to produce different secondary metabolites that help in fighting against pathogens (Maheshwari, 2010). The endophyte, *Azospirillum* sp. B510, was found to increase the resistance of its host plant, *Oryza sativa*, against pathogenic fungi by inducing the biosynthesis of phenolic compounds: flavonoids, alkylresorcinols and hydroxycinnamic acid derivatives (Chamam et al., 2013). Some alphaproteobacterial secondary metabolites and their biological functions are shown in Table 2.1.

Table 2. 1. Some of the secondary metabolites produced by alphaproteobacterial species and their biological functions

Secondary metabolite	Species (source)	Biological function	Reference
Didemnin	<i>Tistrella mobilis</i>	Biological effects	(Rinehart et al., 1983, Timmermans et al., 2017)
Thalassospiramide	<i>Thalassospira</i> sp. CNJ-328	Inhibitor of calpain 1 protein, have neuroprotective properties	(Oh et al., 2007, Timmermans et al., 2017)
Tropodithietic Acid	<i>Phaeobacter gallaeciensis</i> and <i>P. porticola</i>	Antibiotic, biocontrol and anti-cancer	(Timmermans et al., 2017)
Phytohormone	<i>Methylobacterium</i> sp. NC4	Improve plant growth	(Meena et al., 2012)
6-gingerol and curcumin	<i>Bradyrhizobium japonicum</i> CPAC 15 and <i>Bradyrhizobium diazoefficiens</i> CPAC 7	antitumor activity	(Siqueira et al., 2014)
Gibberellins, salicylic acid (SA), indole-3-acetic acid (IAA), zeatin, and abscisic acid	<i>Sphingomonas</i> species	Promote plant germination and growth	(Khan et al., 2014)
Cyclodipeptides	<i>Sulfitobacter</i> species	Bioactive agents	(McMurry, 2014)

2.4 Cytochrome P450 monooxygenases

In 1958, Klingenberg first reported the existence of an unknown carbon monoxide-binding pigment protein in rat liver microsome preparations which were later named as “cytochrome P450s” (Klingenberg, 1958). The protein when reduced with carbon monoxide absorbed 450 nm wavelength (Omura, 1999). This molecule was highly unstable to solubilisation treatments with detergents and the nature of the pigment was not clarified. Years later, heme protein nature of the microsomal carbon monoxide-binding protein was made clear by Omura and Sato and they also coined the term “Cytochrome P450” (Omura and Sato, 1962; Omura and Sato, 1964b; Omura and Sato, 1964a).

Initially P450s were found to perform monooxygenation reaction as represented below where the substrate is represented as RH and the hydroxylated product as ROH:



Later, P450s were found to perform different types of reactions (Isin and Guengerich, 2007; Denisov et al., 2005) (Figure 2.2). The reactions of P450s include oxidative dehalogenation, peroxidation, oxidative C–C bond cleavage, N-dealkylation, O-dealkylation, hydroxylation, and alcohol and aldehyde oxidation (Sakaki, 2012). Some examples of the oxidation reactions are shown in Figure 2.2.

Example of the general type of oxidation reactions catalyzed by the cytochrome P450-containing monooxygenation	
REACTION	EXAMPLE
Aliphatic hydroxylation	$R-CH_2-CH_2-CH_3 \rightarrow R-CH_2-CHOH-CH_3$
Aromatic hydroxylation	$R-\text{C}_6\text{H}_5 \rightarrow R-\text{C}_6\text{H}_4\text{-OH}$
Epoxidation	$R-CH=CH-R^I \rightarrow R-\text{CH}(\text{O})-\text{CH}-R^I$
N-, O-, or S-dealkylation	$R-(\overset{\text{H}}{\text{N}}, \text{O}, \text{S})-CH_3 \rightarrow R-(\text{NH}_2, \text{OH}, \text{SH}) + \text{CH}_2\text{O}$
Deamination	$R-CH_2-NH_2 \rightarrow R-\overset{\text{O}}{\parallel}{C}-H + NH_3$
N-hydroxylation	$R-NH-\overset{\text{O}}{\parallel}{C}-CH_3 \rightarrow R-NOH-\overset{\text{O}}{\parallel}{C}-CH_3$
Sulfoxidation	$R-S-R \rightarrow R-\overset{\text{O}}{\parallel}{S}-R^I$
Desulfuration	$R_1R_2\overset{\text{S}}{\parallel}{P}-X \rightarrow R_1R_2\overset{\text{O}}{\parallel}{P}-X + S$
Oxidative Dehalogenation	$R-\overset{\text{X}}{\underset{\text{H}}{\text{C}}}-H \rightarrow R-\overset{\text{X}}{\underset{\text{H}}{\text{C}}}-OH \rightarrow R-\overset{\text{O}}{\parallel}{C}-H + HX$

* X=halogen

Figure 2. 2. Representation of some examples or reactions catalysed by P450s (Cederbaum, 2015)

2.5 P450s and their role in the biosynthesis secondary metabolites

P450s are frequently found to be part of the major secondary metabolite pathways in bacteria: polyketide synthesis, non-ribosomal peptide synthesis, ribosomally synthesised and post-translationally modified peptides as well as traditional pathways that produce alkaloids, terpenes, steroids, fatty acids and enzyme cofactors (Greule et al., 2018). Secondary metabolites include a wide range of antibacterial, antifungal, antiparasitic, anti-cancer and immunosuppressor compounds that can be exploited for use in human therapy. All these compounds show structural diversity and different P450 enzymes play a role in the oxidation of a number of these compounds. Thus, P450s play a key role in the production of secondary metabolites (Podust and Sherman, 2012; Greule et al., 2018). Genes for biosynthesis of secondary metabolites are typically positioned close to each other on a chromosome and thus these genes are collectively known as secondary metabolite gene clusters (Medema et al., 2015). Therefore, programmed alteration of genes encoding these enzymes provides the

potential of redesigning antibiotic structures to make molecules with new biological activities (Podust and Sherman, 2012). Here I present one example of a critical reaction catalysed by CYP175A1 from the *Thermus thermophilus* HB27 that performs carotene hydroxylation (Greule et al., 2018) (Figure 2.3).

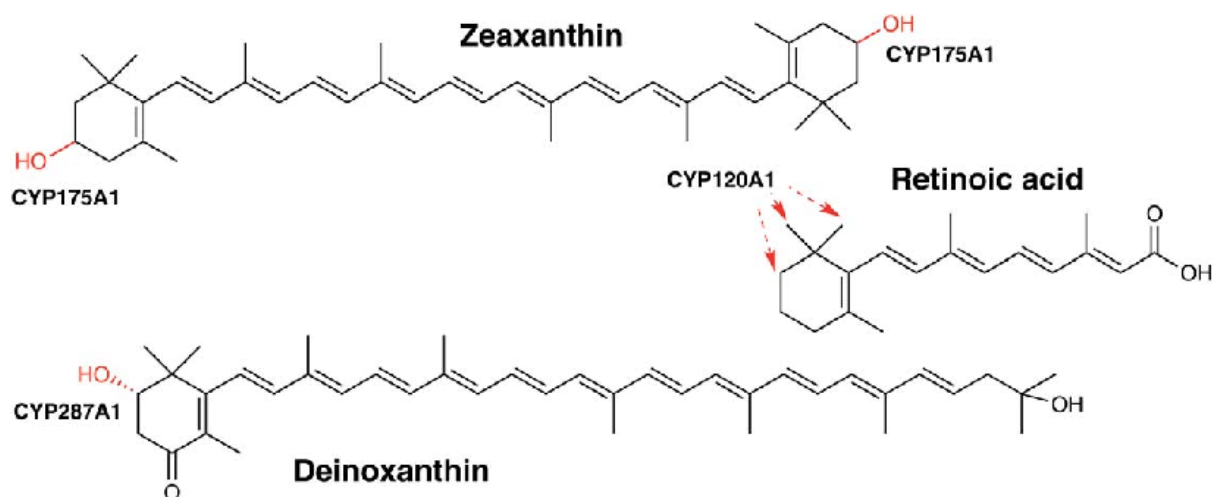


Figure 2. 3. Carotenoid biosynthesis by CYP175A1 (Greule et al., 2018)

2.6 Nomenclature of P450s

P450s are named based on the established nomenclature rule by the International P450 Nomenclature committee (Nelson et al., 1993; Nelson, 2006; Nelson, 2009b) (Figure 2.4): The recommendations for naming a P450 gene include:

- Italicized root symbol P450 symbolising cytochrome P450.
- Arabic number entitling a P450 family.
- A letter indicating a subfamily when there is more than one subfamily known to be within that family.
- Arabic numeral representing the single gene.

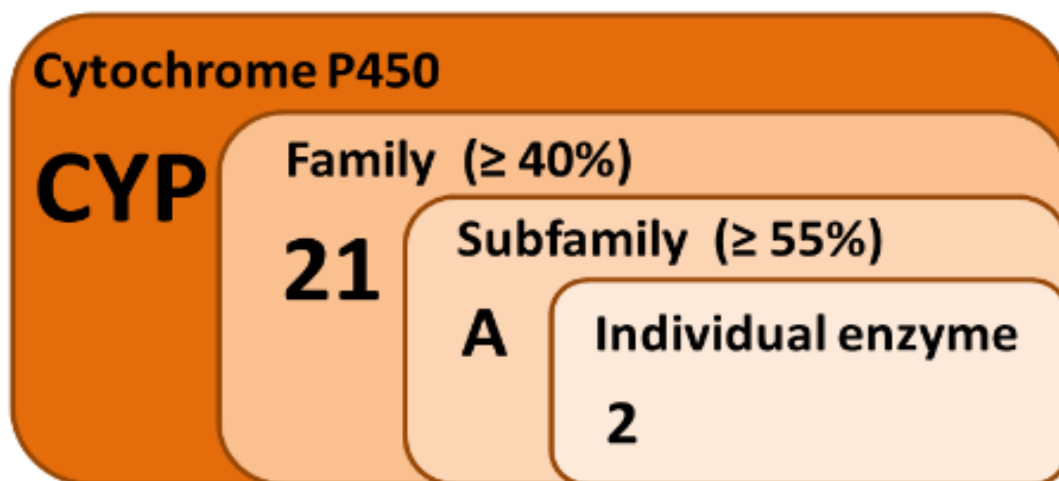


Figure 2. 4. Diagrammatic representation of P450 nomenclature (Brixius-Anderko et al., 2017)

2.7 P450s and redox proteins

P450s, except self-sufficient P450s, need two electrons to perform their enzymatic reactions. Thus, P450s must be associated with redox partner proteins to obtain these electrons (Hannemann et al., 2007; Kelly and Kelly, 2013). P450s and their redox partners are classified into three-, two-, or one-system(s) (Hannemann et al., 2007). Most prokaryotic P450s are three component systems (Figure 2.5a), which consist of NADH/NADPH-dependent FAD-containing reductase and a ferredoxin or FMN-dependent flavodoxin. Eukaryotic P450s are classified as two-component systems, containing a membrane bound P450 that depends on another integral membrane protein known as NADH/NADPH diflavin (FMN/FAD) reductase (CPR) which provides electrons for the reaction (Figure 2.5b) (Fasan, 2012). Self-sufficient P450s, even though they occasionally occur, are classified as a one-component system (Figure 2.5c-d). Single enzymes (P450 B_{M3}) offer great advantages compared to multi-proteins (Fasan, 2012) (Figure 2.5).

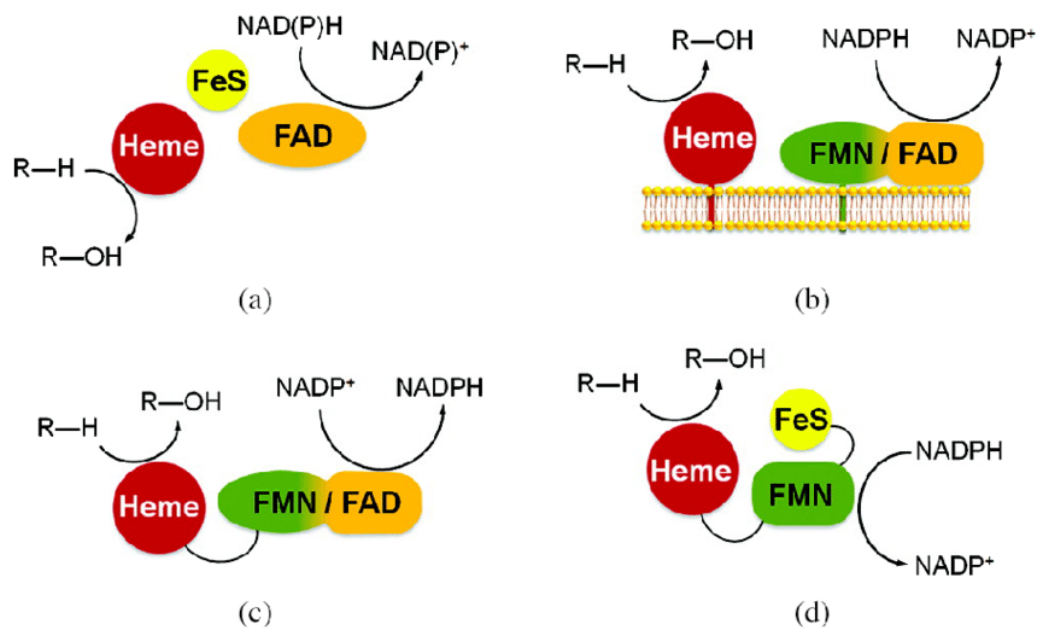


Figure 2. 5. Various types of P450 systems (a) Class 1 bacterial P450 system, (b) Class II, eukaryotic membrane-bound system, (c) P450 and reductase P450 system and (d) P450RhF-type fusion system (Erdogan, 2019)

CHAPTER 3: ANCIENT BACTERIAL CLASS *ALPHAPROTEOBACTERIA* CYTOCHROME P450 MONOOXYGENASES CAN BE FOUND IN OTHER BACTERIAL SPECIES

3.1. Introduction

Cytochrome P450 monooxygenases (CYPs/P450s) are heme thiolate-proteins known to humans for more than five and a half decades (Yamazaki, 2014). P450s perform enzymatic reactions with stereo- and regio-specific oxidation and because of this capability these enzymes are subjected to various applications in all forms of biology (Urlacher and Girhard, 2019b, Li et al., 2020). Most living organisms and some non-living entities such as viruses have been found to have P450s in their genomes (Nelson, 2018b, Lamb et al., 2019), indicating their important role in primary and secondary metabolism.

P450 reactions are critical in determining the drug toxicity of prodrugs and xenobiotic compounds (Guengerich, 2020). P450s are well-known drug targets for some of the microbial pathogens (Lepesheva et al., 2018, Jawallapersand et al., 2014). Some of the P450s from microbes have been characterized and their application in the production of chemicals that are valuable to humans, such as secondary metabolites (compounds produced by the organisms that have no role in their growth, development or reproduction) has been explored (Girvan and Munro, 2016, McLean et al., 2015, Kelly and Kelly, 2013, Girhard et al., 2015, Urlacher and Girhard, 2019a, Di Nardo and Gilardi, 2020). Well-known examples of P450s' involvement are antibiotic production, such as in the biosynthesis of the macrolide antibiotic erythromycin and glycopeptide antibiotics (Andersen et al., 1993, Bischoff et al., 2005), the production of the anticancer drugs taxol and perillyl alcohol (Jennewein et al., 2005, van Beilen et al., 2005) and the production of pharmaceutical compounds such as pravastatin (Di Nardo and Gilardi, 2020).

P450s' critical role in the synthesis of secondary metabolites has been thoroughly reviewed (Podust and Sherman, 2012, Greule et al., 2018, Di Nardo and Gilardi, 2020). It was found that the coding sequences (genes) of enzymes involved in the synthesis of different secondary metabolites, including P450s, were part of gene clusters named biosynthetic gene clusters (BGCs) (Cimermancic et al., 2014), where P450s were found to be critical in contributing to the diversity of the secondary metabolites (Podust and Sherman, 2012, Greule et al., 2018, Di Nardo and Gilardi, 2020). In the pre-genome sequencing era, identification of

such gene clusters and P450s that formed part of the clusters required tedious and laborious work. The current genome sequencing era has revolutionized the process and bioinformatics programs are available for the identification of BGCs in organisms (Cimermancic et al., 2014). However, to date, identification and annotation of P450s still involve manual sorting and naming as per the International P450 Nomenclature Committee rule, i.e. sequences with >40% identity are assigned to the same family as the named homolog P450 and sequences with >55% identity are assigned to the same subfamily as the named homolog P450 (Nelson, 1998a, Nelson, 2006, Nelson, 2009a). Proteins with <40% identity are assigned to a new P450 family. The current genome sequencing era has offered the opportunity to understand P450s' profiles and thus evolution patterns, particularly in bacterial species where the impact of lifestyle has been found to affect the P450 profiles in an organism (Padayachee et al., 2020) profoundly.

The bacterial class *Alphaproteobacteria* contains the most abundant, extraordinarily diverse and ancient group of bacteria (Muñoz-Gómez et al., 2019, Ettema and Andersson, 2009). *Alphaproteobacteria* consist of species with a diversity of lifestyles, geographical distribution and genome size (Ettema and Andersson, 2009). They inhabit diverse ecological niches, from water to soil, and form both extra- and intracellular associations with eukaryotes, including unicellular organisms, and multicellular plants and mammals (Muñoz-Gómez et al., 2019, Ettema and Andersson, 2009). Some species are in symbiotic relationships with plants such as species belonging to the genus *Agrobacterium*; species belonging to *Rickettsiaceae*, *Brucellaceae* and *Bartonellaceae* are human pathogens (Mukhopadhyaya et al., 2012), of which a few are of ecological importance, playing a huge role in carbon, nitrogen and sulfur cycles (Kerstens et al., 2006). These bacteria are found in large amounts in the upper layer of the ocean (Gupta, 2005). In spite of their differences, all alphaproteobacterial species are oligotrophs, therefore they can survive in an environment with low nutrients (Phung et al., 2004). *Alphaproteobacteria* contain species that have biotechnological significance, especially some of the species found to produce secondary metabolites, compounds that play no role in the growth or reproduction of organisms, but gives the organism a selective advantage (Timmermans et al., 2017, O'Brien and Wright, 2011). The biological properties of these secondary metabolites in the field of drug discovery are invaluable and strenuous efforts to find new secondary metabolites with biotechnological potentials are being made around the world. Some of the secondary metabolites produced by alphaproteobacterial species and their biological function are presented in Table 2.1.

It is a well-known fact that P450s are involved in the production of secondary metabolites per se; they contribute to the diversity of secondary metabolites produced by an organism (Greule et al., 2018, Podust and Sherman, 2012, Di Nardo and Gilardi, 2020). Recent genome data mining, annotation of P450s and analysis of P450s' association with secondary metabolism in some bacterial species such as mycobacterial species (Senate et al., 2019), *Streptomyces* species (Mnguni et al., 2020), cyanobacterial species (Khumalo et al., 2020b) and Firmicutes species (Padayachee et al., 2020) revealed that quite a large number of P450s are involved in the production of secondary metabolites. Apart from these bacterial species, none of the other bacterial species' P450 repertoire has been analyzed. In addition to this, to date, the P450 repertoire of Alphaproteobacterial species and their association with secondary metabolism has not been reported despite the fact that P450s, in general, are involved in the production of secondary metabolites and these species do produce secondary metabolites. Thus, in this study, we address these research gaps by performing genome-wide data mining, annotation and phylogenetic analysis of P450s and identification of P450s involved in secondary metabolism in the bacterial class *Alphaproteobacteria*.

3.2. Results and Discussion

3.2.1. Only 40% of alphaproteobacterial species have P450s

Genome data mining and annotation of P450s in 599 alphaproteobacterial species belonging to 164 genera (Table S1 in Annexure A) revealed the presence of P450s in only 241 species belonging to 82 genera (Figure 3.1). This indicates that only 40% of alphaproteobacterial species and 50% of *Alphaproteobacteria* genera have P450s (Figure 3.1). All the species analyzed in the study belonging to genera such as *Agrobacterium*, *Rhodopseudomonas*, *Hyphomicrobium*, *Ketogulonicigenium*, *Filomicrobium*, *Phenylobacterium*, *Roseobacter*, *Gluconacetobacter* and *Nitrobacter* and most of the species belonging to genera such as *Sinorhizobium*, *Rhizobium*, *Bradyrhizobium* and *Sphingobium* have P450s in their genomes (Table S1 in Annexure A). A significant number of species belonging to genera such as *Rickettsia*, *Bartonella*, *Ehrlichia*, *Wolbachia* and *Anaplasma* were analyzed in this study; no P450s were found in these species, suggesting that species in these genera probably do not have P450s (Table S1 in Annexure A). Detailed information on genera, species and P450 information is presented in Table S1. In total 874 P450s apart from 52 short-P450s were identified in 241 alphaproteobacterial species (Table S2 in Annexure A). On average four P450s were found in 241 alphaproteobacterial species; 65 species had a single P450 in their genome (Table S1 in Annexure A). Of these 65 species, 30 were from the genus *Brucella* alone

(Table S1 in Annexure A). Comparative analysis of P450s in alphaproteobacterial species revealed that *Bradyrhizobium oligotrophicum* has the highest number of P450s (17 P450s) in its genome, followed by 16 P450s in the species *Bradyrhizobium japonicum* E109, *Novosphingobium aromaticivorans* and *Sphingomonas wittichii* and 15 P450s in *Bradyrhizobium diazoefficiens* USDA 110 (Table S2 in Annexure A). Comparative analysis with other bacterial species revealed Alphaproteobacterial species have the highest average number of P450s compared to Firmicutes species (Padayachee et al., 2020) and cyanobacterial species (Khumalo et al., 2020b), but the lowest number compared to *Streptomyces* species (Mnguni et al., 2020, Senate et al., 2019) and mycobacterial species (Parvez et al., 2016) (Table 3.1). A list of P450s and their sequences along with short-P450s is presented in Supplementary Dataset 1 that is available at <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/>.

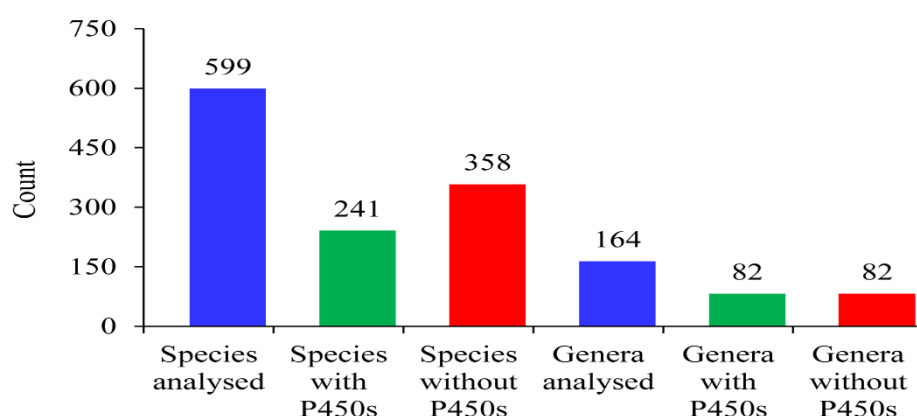


Figure 3. 1. Comparative analysis of P450 statistics in the bacterial class *Alphaproteobacteria*. Detailed information is presented in Annexure A-Table S1

Table 3. 1. Comparative analysis of main characteristics of P450s in different bacterial species

	Alphaproteo-bacterial species	<i>Firmicutes</i> species	<i>Streptomyces</i> species	Mycobacterial species	Cyanobacterial species
Total no. of species analyzed	599	972	203	60	114
No of species that have P450s	241	229	203	60	114
No. of P450s	874	712	5460	1784	341
No. of families	143	14	253	77	36
No. of subfamilies	214	53	698	132	79
Dominant P450 family	CYP202	CYP107	CYP107	CYP125	CYP110
Average no. of P450s	4	1	27	30	3
P450 diversity percentage	0.07	0.008	0.02	0.07	0.09
No. of P450s part of BGCs	21	126	1231	204	27
Percentage of P450s part of BGCs	2.4	18	23	11	8
Reference(s)	This work	(Mthethwa et al., 2018, Padayachee et al., 2020)	(Senate et al., 2019, Mnguni et al., 2020)	(Parvez et al., 2016, Senate et al., 2019)	(Khumalo et al., 2020b)

3.2.2. Alphaproteobacterial species have the highest number of P450 families only next to *Streptomyces*

Following the International P450 Nomenclature Committee rules, 874 alphaproteobacterial species P450s were grouped into 143 P450 families and 214 P450 subfamilies (grouped in the same family when they share >40% and same subfamily when they share >55%; less than 40% identity assigned to a new P450 family) (Nelson, 1998a, Nelson, 2006), based on the phylogenetic analysis of P450s (Figure 3.2) (Nelson et al., 1993, Nelson, 1998b, Nelson, 2006). A list of P450 families and subfamilies, their count and percentage contribution to the total number of P450s is presented in Table 3.2.

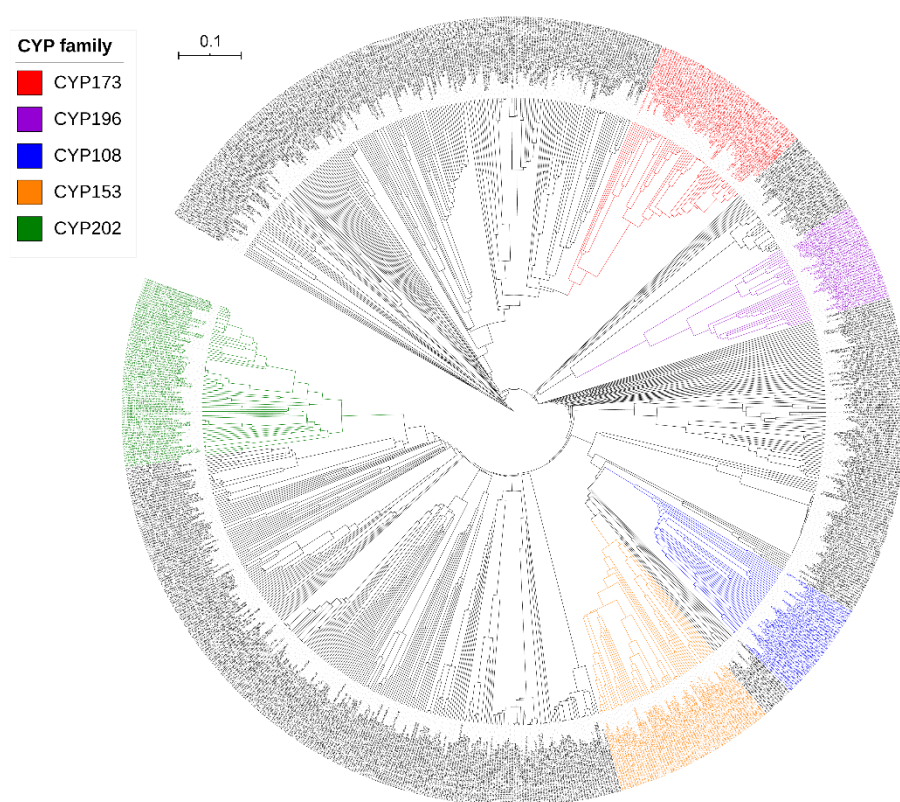


Figure 3.2. Phylogenetic analysis of Alphaproteobacterial P450s. P450 families that are expanded in these species were highlighted in different colors and indicated in the figure. Alphaproteobacterial P450 protein sequences used to construct the phylogenetic tree

Table 3. 2. Comparative analysis of P450 families and subfamilies in alphaproteobacterial species

P450 family		P450 count	Percentage count	Subfamily	P450 count
CYP1010		1	0.11%	A	1
CYP1017		1	0.11%	A	1
CYP101		10	1.14%	B	1
				C	3
				D	2
				E	2
				Q	1
				R	1
CYP102		12	1.37%	A	10
				K	1
				AC	1
CYP1036		2	0.23%	B	1
				C	1
CYP103		4	0.46%	A	4
CYP104		13	1.49%	A	13
CYP105		4	0.46%	BF	3
				CX	1
CYP1061		2	0.23%	B	2
CYP1068		4	0.46%	A	4
CYP1075		1	0.11%	A	1
CYP1076		1	0.11%	A	1

CYP1077		1	0.11%	A	1
CYP1078		8	0.92%	A	7
				C	1
CYP107		10	1.14%	AN	8
				–	1
				JE	1
CYP1081		2	0.23%	B	2
CYP1082		1	0.11%	A	1
CYP1083		5	0.57%	A	3
				C	2
CYP1086		1	0.11%	B	1
CYP1088		2	0.23%	B	2
CYP1089		1	0.11%	A	1
CYP108		37	4.23%	A	2
				D	6
				G	18
				L	1
				P	2
				U	1
				V	1
				W	1
				X	5
CYP1090		2	0.23%	C	2

CYP1091		3	0.34%	A	3
CYP1094		4	0.46%	A	3
				B	1
CYP1098		6	0.69%	A	6
CYP1101		29	3.32%	A	29
CYP1104		10	1.14%	A	4
				C	3
				E	3
CYP1107		16	1.83%	A	12
				B	3
				C	1
CYP1111		7	0.80%	A	5
				B	1
				C	1
CYP1116		3	0.34%	B	3
CYP1118		1	0.11%	B	1
CYP111		2	0.23%	A	1
				B	1
CYP112		23	2.63%	A	23
CYP1135		1	0.11%	A	1
CYP1137		1	0.11%	A	1
CYP1138		2	0.23%	B	2
CYP1141		1	0.11%	A	1

CYP1145		1	0.11%	A	1
CYP114		22	2.52%	A	22
CYP1155		1	0.11%	B	1
CYP115		1	0.11%	A	1
CYP116		1	0.11%	B	1
CYP1170		7	0.80%	A	7
CYP1171		1	0.11%	A	1
CYP1173		1	0.11%	A	1
CYP1174		2	0.23%	A	2
CYP1175		1	0.11%	A	1
CYP117		22	2.52%	A	22
CYP1181		1	0.11%	A	1
CYP1182		1	0.11%	A	1
CYP1186		2	0.23%	A	2
CYP1187		1	0.11%	A	1
CYP1204		2	0.23%	A	2
CYP1206		1	0.11%	B	1
CYP1221		2	0.23%	B	2
CYP1229		4	0.46%	A	1
				B	2
				C	1
CYP1246		2	0.23%	A	2
CYP1250		1	0.11%	A	1

CYP1258		1	0.11%	A	1
CYP125		1	0.11%	P	1
CYP1275		1	0.11%	B	1
CYP127		19	2.17%	A	18
				C	1
CYP1281		1	0.11%	A	1
CYP1291		5	0.57%	B	3
				C	2
CYP1302		2	0.23%	A	2
CYP1311		2	0.23%	A	2
CYP1312		1	0.11%	A	1
CYP1326		2	0.23%	B	2
CYP1330		1	0.11%	A	1
CYP1337		1	0.11%	A	1
CYP133		1	0.11%	F	1
CYP1349		1	0.11%	A	1
CYP1350		1	0.11%	A	1
CYP1371		1	0.11%	B	1
CYP1376		2	0.23%	B	1
				C	1
CYP1384		1	0.11%	A	1
CYP1396		1	0.11%	A	1
CYP1405		1	0.11%	B	1

CYP1406		3	0.34%	B	2
				C	1
CYP1460		1	0.11%	C	1
CYP147		16	1.83%	D	16
CYP1515		2	0.23%	A	2
CYP151		2	0.23%	C	2
CYP152		13	1.49%	B	4
				C	3
				E	2
				P	1
				AA	1
				AB	2
CYP153		60	6.86%	A	44
				C	2
				D	14
CYP155		4	0.46%	J	3
				K	1
CYP1591		1	0.11%	A	1
CYP1597		1	0.11%	A	1
CYP1732		3	0.34%	A	3
CYP1733		2	0.23%	A	1
				B	1
CYP1734		1	0.11%	A	1

CYP1735		1	0.11%	A	1
CYP1736		1	0.11%	A	1
CYP1737		2	0.23%	A	2
CYP1738		1	0.11%	A	1
CYP1739		2	0.23%	A	2
CYP173		60	6.86%	A	45
				B	8
				C	3
				G	1
				H	1
				J	2
CYP1740		1	0.11%	A	1
CYP1741		1	0.11%	A	1
CYP1742		1	0.11%	A	1
CYP1743		1	0.11%	A	1
CYP1744		1	0.11%	A	1
CYP1745		1	0.11%	A	1
CYP1746		1	0.11%	A	1
CYP1747		1	0.11%	A	1
CYP1748		1	0.11%	A	1
CYP1749		2	0.23%	A	1
				B	1
CYP1750		1	0.11%	A	1

CYP1751		1	0.11%	A	1
CYP1752		4		A	4
CYP1753		1	0.11%	A	1
CYP1754		1	0.11%	A	1
CYP1755		1	0.11%	A	1
CYP180		1	0.11%	D	1
CYP186		7	0.80%	K	7
CYP191		1	0.11%	B	1
CYP192		3	0.34%	A	3
CYP193		17	1.95%	A	17
CYP194		10	1.14%	A	10
CYP195		21	2.40%	A	18
				D	1
				E	2
CYP196		37	4.23%	A	34
				B	2
				C	1
CYP197		2	0.23%	R	2
CYP199		16	1.83%	A	11
				B	1
				J	1
				K	1
				L	1

				M	1
CYP200		8	0.92%	A	5
				B	2
				C	1
CYP201		31	3.55%	A	25
				B	3
				C	3
CYP202		70	8.01%	A	46
				B	24
CYP203		13	1.49%	A	12
				B	1
CYP204		2	0.23%	A	2
CYP206		19	2.17%	A	9
				B	1
				C	3
				D	6
CYP219		2	0.23%	A	2
CYP223		3	0.34%	A	2
				E	1
CYP224		1	0.11%	A	1
CYP225		7	0.80%	A	7
CYP226		2	0.23%	C	1
				D	1

CYP278		2	0.23%	A	1
				C	1
CYP286		1	0.11%	C	1
CYP288		2	0.23%	B	2
CYP289		33	3.78%	A	33
CYP290		6	0.69%	A	5
				B	1
CYP2140		1	0.11%	A	1
CYP1236		1	0.11%	A	1
CYP2334		2	0.23%	A	2

P450 family and subfamily-level comparative analysis with other bacterial species revealed that alphaproteobacterial species have the highest number of P450 families and subfamilies compared to *Firmicutes* species, mycobacterial species and cyanobacterial species and the lowest compared to *Streptomyces* species (Table 3.1). The highest diversity of P450 families and subfamilies observed in alphaproteobacterial species is possibly due to their diverse lifestyle that led to the generation of diverse P450 families and subfamilies, as the lifestyle of an organism is known to have an impact the P450 repertoire in their genomes (Padayachee et al., 2020). Thus, for this reason, 77 new P450 families were observed in these species, contributing to the P450 family diversity (Table S3 in Annexure A). In aligning with high P450 family and subfamily diversity, alphaproteobacterial species also showed the highest P450 diversity percentage compared to *Firmicutes* species and *Streptomyces* species; the same as mycobacterial species but lower than cyanobacterial species (Table 3.1). A point to be noted is that the number of cyanobacterial species analyzed is almost half of alphaproteobacterial species and thus cyanobacterial species have a slightly higher P450 diversity percentage (Table 3.1). P450 family-level analysis revealed that some P450 families are expanded in alphaproteobacterial species (Table 3.2). Among the P450 families, the CYP202 family has the highest number of P450s (70 P450s), followed by CYP153 and CYP173 (each 60 P450s), CYP108 and CYP196 (each 37 P450s) (Table 3.2). Sixty-five P450 families have a single

member and 29 P450 families have two members, indicating the diversity of P450 families in alphaproteobacterial species (Table 3.2). Analysis of P450 families and subfamilies in alphaproteobacterial species revealed that the P450 family with the highest number of subfamilies was CYP108 (9 subfamilies) followed by CYP101, CYP152, CYP199, CYP173 (each with 6 subfamilies) and CYP206 (5 subfamilies). Interestingly, some of the subfamilies are expanded in the dominant P450 families such as CYP202, CYP173, CYP153, CYP196, CYP289, CYP201, CYP1101, CYP112, CYP114 and CYP117, where subfamily “A” is dominant (Table 3.2). A detailed analysis of the subfamilies and their member count are presented in Table 3.2. Heat-map analysis of the presence and absence of P450 families in different alphaproteobacterial species revealed that none of the P450 family is conserved in these species (Figure 3.3). Non-conservation of P450 families in bacterial species is not common; it was also observed in cyanobacterial species (Khumalo et al., 2020b). However, the co-presence of quite a number of P450 families was found in a large number of species, such as CYP173 and CYP202 in 32 species, CYP196 and CYP201 in 16 species, CYP195 and CYP199 in 10 species, CYP195 and CYP196 in 11 species, CYP173, CYP117, CYP127, CYP112 and CYP114 in 10 species and CYP173, CYP147, CYP201 and CYP206 in nine species (Figure 3.3). A point to be noted is that the co-presence of some P450 families was also observed in other bacterial species (Padayachee et al., 2020). When compared to other bacterial species, the CYP202 family is dominant in Alphaproteobacterial species, while CYP110 in cyanobacterial species, CYP125 in mycobacterial species and CYP107 in both the *Firmicutes* species and *Streptomyces* species dominant (Table 3.1).



Figure 3. 3. Heat map figure representing the presence or absence of cytochrome P450 families in 599 Alphaproteobacterial species. The data have been represented as -3 for family absence (green) and 3 for family presence (red). One hundred and forty-three Alphaproteobacterial species form the vertical axis and 214 P450 families form the horizontal axis. The respective data used in the generation of this figure are presented in Supplementary Dataset 2 that is available at <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/>

3.2.3. Only a few P450s are involved in secondary metabolism in alphaproteobacterial species

Analysis of metabolite biosynthetic gene clusters (BGCs) revealed that 504 species of 599 alphaproteobacterial species have secondary metabolite BGCs in their genomes (Supplementary Dataset 3; available at <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/>). In total 2262 secondary

metabolite BGCs belonging to 93 types were found in 504 species (Supplementary Dataset 3). Among the 93 cluster types, terpene was the dominant cluster (270 clusters), followed by Homoserine lactone (hserlactone) (180 clusters), bacteriocin (118 clusters), betalactone (82 clusters) and nonribosomal peptides (NRPS) (79 clusters) in these species (Figure 3.4). Most similar known clusters analysis revealed that of 2 262 BGCs, 642 BGCs showed similarity to 132 known clusters and 96 of these clusters showed 100% identity to known clusters, indicating their involvement in the specific secondary metabolite (Supplementary Dataset 3; available at <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/>).

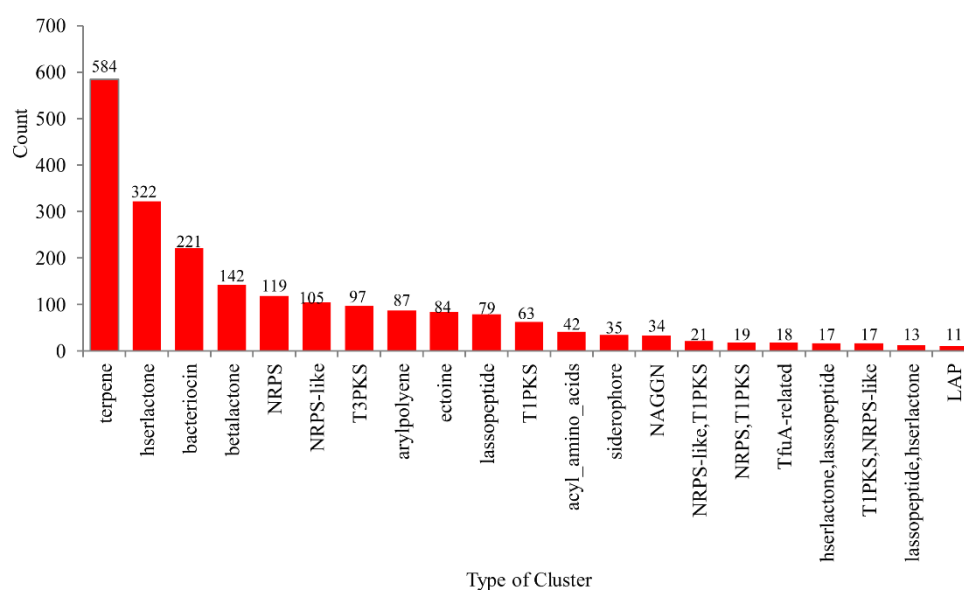


Figure 3. 4. Comparative analysis of types of secondary metabolite BGCs in Alphaproteobacterial species. BGCs that are populated in Alphaproteobacterial species were presented in the figure. The number at the top of each bar represents the total number of clusters. Detailed information is presented in Supplementary Dataset 3, available at <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8197338/>

Analysis of P450s that are part of BGCs revealed that only 2.4% of alphaproteobacterial species P450s are involved in the production of secondary metabolites (Table 3.3). The percentage of P450s involved in the production of secondary metabolites in alphaproteobacterial species was found to be lowest compared to other bacterial species such as *Cyanobacteria* (8%), *Firmicutes* species (18%), mycobacterial species (11%) and *Streptomyces* species (23%) (Table 3.1). Twenty-one P450s from 19 alphaproteobacterial species were found to be part of BGCs (Table 3.3). Of the 16 P450 families that are part of

BGCs, CYP206 is the dominant family (5 P450s-24%), followed by CYP1101 (2 P450s-10%) and the remaining 14 P450 families (CYP195, CYP1101, CYP2334, CYP199, CYP173, CYP153, CYP152, CYP1302, CYP127, CYP1246, CYP1138, CYP1104, CYP108, CYP107, CYP1326) have a single P450 (Table 3.3). Dominant P450 families such as CYP173, CYP153 and CYP108 have only one representative as part of BGCs, indicating no correlation between the dominant P450 family vs BGCs (Table 3.3). A point to be noted is that three P450s, CYP1326A2, CYP2334A1 and CYP195A21 from *Sulfitobacter* sp.AM1-D1, were found to be part of BGCs (Table 3.3). Most similar known cluster analysis revealed that CYP1101A27 from *Celeribacter indicus* certainly involved in the production of Ectoine as the percentage identity with the most similar known cluster was 100% (Table 3.3).

Table 3. 3. Identification of P450s that are part of the secondary metabolite BGCs in alphaproteobacterial species. Reference cluster information was obtained by performing BLAST at the anti-SMASH database (Blin et al., 2019), as indicated in the materials and methods section. The cluster type and most similar known cluster names available at anti-SMASH database (Blin et al., 2019) were listed in the table

Species name	P450	Reference cluster information		
		Cluster type	Most similar known cluster	similarity
<i>Novosphingobium aromaticivorans</i>	CYP153C1	Terpene	Astaxanthin dideoxyglycoside	75%
<i>Mesorhizobium japonicum</i> MAFF 303099	CYP127A3v1	Hserlactone	-	-
<i>Agrobacterium fabrum</i>	CYP206A1	Terpene	-	-
<i>Agrobacterium</i> sp. H13-3	CYP206A4	Terpene	-	-
<i>Agrobacterium tumefaciens</i>	CYP206A4	Terpene	-	-

<i>Agrobacterium rhizogenes</i>	CYP206A2	Terpene	-	-
<i>Rhizobium</i> sp. IRBG74	CYP206A3	Terpene	-	-
<i>Rhizobium</i> sp. NT-26	CYP107JE1	NAGGN	-	-
<i>Bradyrhizobium</i> sp. S23321	CYP199A26	Hserlactone, t2pks	Colabomycin	4%
<i>Bradyrhizobium oligotrophicum</i>	CYP108L2	NRPS	-	-
<i>Bosea vaviloviae</i>	CYP1101A30	T1PKS	S56-p1, NRPS	3%
<i>Beijerinckia indica</i>	CYP173J1	NRPS,T1PKS	-	-
<i>Pseudorhodoplanes sinuspersici</i>	CYP1104E2	T1PKS	Sphingan polysaccharide, saccharide	13%
<i>Rhodobacter sphaeroides</i> ATCC 17025	CYP152C2	Hserlactone	Conglobatin, NRPS	10%
<i>Celeribacter indicus</i>	CYP1101A27	Ectoine	Ectoine, other	100%
<i>Hyphomonadaceae bacterium</i> UKL13-1	CYP1246A4	Terpene	-	-

<i>Sphingopyxis macrogoltabida</i> 203	CYP1302A1	NRPS	-	-
<i>Xanthobacter autotrophicus</i>	CYP1138B1	T1PKS	-	-
<i>Sulfitobacter</i> sp.AM1-D1	CYP1326A2	acyl_amino_acids	-	-
	CYP195A21	Bacteriocin	-	-
	CYP2334A1	NRPS-like	-	-

3.2.4. Alphaproteobacterial P450 families can be found in other bacterial species

It is a well-known fact that bacterial species in *Alphaproteobacteria* are regarded as an ancient group of bacteria (Muñoz-Gómez et al., 2019, Ettema and Andersson, 2009). A comparison of P450 families with other bacterial species will provide important P450 family evolutionary distribution patterns. To understand this aspect, we performed comprehensive comparative analysis of P450 families from different bacterial species (Figure 3.5). As shown in Figure 3.5, four P450 families were commonly found among alphaproteobacterial species, *Firmicutes* species and cyanobacterial species. Quite a large number of P450 families were found to be common among alphaproteobacterial species, *Streptomyces* species (22 P450 families) and mycobacterial species (14 P450 families) (Figure 3.5). Only the CYP107 family was found to be conserved among all bacterial species (Figure 3.5). CYP152 and CYP197 were commonly found in alphaproteobacterial species, *Firmicutes* species and *Streptomyces* species. Neither of these families is present in mycobacterial species. This indicates that the P450 families that are commonly found among alphaproteobacterial species and other bacterial species are indeed passed from alphaproteobacterial species and retained by other bacterial species throughout the speciation, suggesting the important role of these P450 families. One interesting observation is that the CYP125 P450 family, a cholesterol and cholest-4-en-3-one hydroxylase (McLean et al., 2009, Ouellet et al., 2010) and potential drug target against tuberculosis-causing bacteria *Mycobacterium tuberculosis* H37Rv (Ortiz de Montellano, 2018), is commonly found in

Alphaproteobacteria and mycobacterial species and *Streptomyces* species (Figure 3.5), indicating that a cholesterol hydroxylation capability already existed in ancient bacteria as described elsewhere (Holert et al., 2018) and that these bacterial species retained this ability to survive better in the host environment, as mentioned elsewhere (Senate et al., 2019).

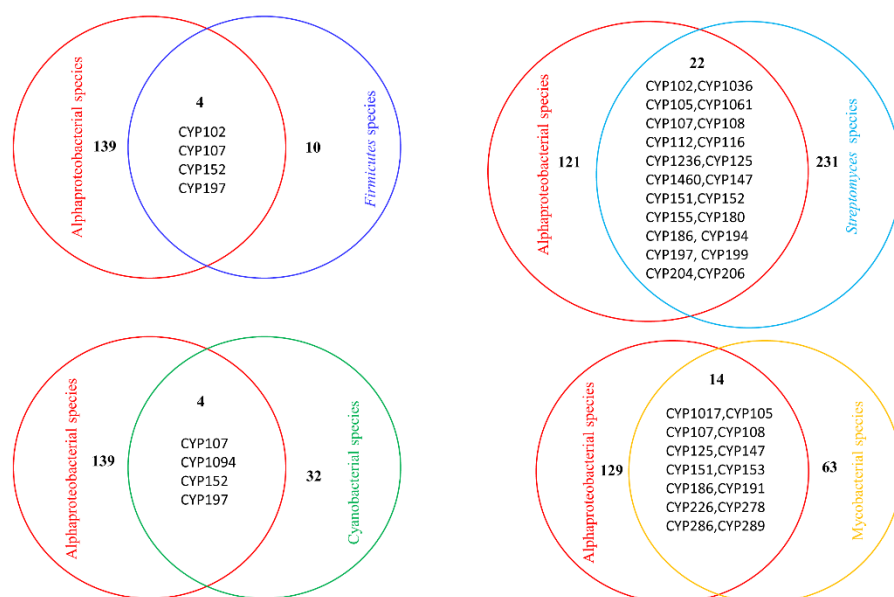


Figure 3. 5. Comparative analysis of P450 families among different bacterial species. The number of P450 families indicated with number (bold case) and P450 families that are common between Alphaproteobacterial species and other bacterial species were listed in the figure

A point to be noted is that only one alphaproteobacterial species, namely *Phenylobacterium zucineum*, was found to have CYP125 P450 among 599 species used in the study, indicating two scenarios, i.e., loss of this P450 in other alphaproteobacterial species or gain by *P. zucineum*. This phenomenon needs further investigation. However, the presence of CYP125 P450 indicates cholesterol side-chain degradation and its subsequent utilization as carbon source *via* the beta-oxidation pathway (van Wyk et al., 2019) in *P. zucineum*. In order to identify the cholesterol side-chain oxidizing enzymes in *P. zucineum*, if any, we used *Mycobacterium tuberculosis* H37Rv cholesterol side-chain oxidizing enzymes as listed in the literature (van Wyk et al., 2019)]. Based on the homology percentage and annotation of enzymes at KEGG, we identify all possible cholesterol side-chain oxidizing enzymes (31 enzymes) in *P. zucineum*, indicating that this alphaproteobacterial species is indeed capable of oxidizing the cholesterol side-chain, where the CYP125 reaction will be critical in removing

the side-chain from cholesterol (Table 3.4). As shown in Table 3.4, two homologs (one named fadD) were found for fadD36 (Rv1193) Acyl-CoA synthetase. Our prediction on cholesterol side-chain degradation by *P. zucineum* is solely based on homolog proteins' functions, including CYP125 and further validation by experimentation is required.

Table 3. 4. Identification of homolog proteins involved in cholesterol side-chain oxidation in *Phenylobacterium zucineum*. *Mycobacterium tuberculosis* H37Rv cholesterol side-chain degrading proteins from the published literature (van Wyk et al., 2019) were used to identify homolog proteins in *P. zucineum*. Gene and protein IDs and enzyme annotations were from KEGG (Kanehisa et al., 2019b)

Proteins involved in cholesterol side-chain oxidation in <i>Mycobacterium tuberculosis</i> H37Rv			Homolog proteins in <i>Phenylobacterium zucineum</i>			
Gene name	Gene ID	Enzyme	Protein ID	% identity	% homolog	Enzyme
fadD36	Rv1193	Acyl-CoA synthetase	PHZ_c1345 (fadD)	29	41	Long-chain acyl-CoA synthetase
			pzu:PHZ_c1155	38	52	Malonyl-CoA/methylmalonyl-CoA synthetase
fadD19	Rv3515c	Probable fatty-acid-CoA ligase	pzu:PHZ_c2065	39	57	Fatty-acid-CoA ligase
fadD3	Rv3561	Acyl-CoA synthetase (AMP forming)	pzu:PHZ_c1909	35	47	Long-chain-fatty-acid--CoA ligase
fadD17	Rv3506	Possible fatty-acid-CoA ligase	pzu:PHZ_c0597	30	46	Fatty-acyl-CoA synthase
fadD19	Rv3515c	Probable fatty-acid-CoA ligase	pzu:PHZ_c2065	39	57	Long-chain fatty acid:CoA ligase
fadD10	Rv0099	Fatty acid-CoA synthase	pzu:PHZ_c2512	29	43	Long-chain-fatty-acid--CoA ligase

fadD9	Rv2590	Fatty acid-CoA synthase	pzu:PHZ_c21 23	25	38	Long-chain acyl-CoA synthetase
fadD18	Rv3513c	Possible fatty-acid-CoA ligase	pzu:PHZ_c20 65	55	73	CoA-synthetase, long-chain fatty acid:CoA ligase
fadE22	Rv3061c	Acyl-CoA dehydrogenase	pzu:PHZ_c26 78	40	54	Dehydrogenase family protein
fadE23	Rv3140	Acyl-CoA dehydrogenase	pzu:PHZ_c08 90	33	51	Acyl-CoA dehydrogenase
fadE24	Rv3139	Acyl-CoA dehydrogenase	pzu:PHZ_c23 65	32	48	Acyl-CoA dehydrogenase
fadE25	Rv3274c	Acyl-CoA dehydrogenase FADE25	pzu:PHZ_c16 80	40	60	Acyl-CoA dehydrogenase
fadE26	Rv3504	Probable acyl-CoA dehydrogenase	pzu:PHZ_c23 36	33	50	Acyl-CoA dehydrogenase
fadE27	Rv3505	Probable acyl-CoA dehydrogenase	pzu:PHZ_c24 06	28	45	Isovaleryl CoA dehydrogenase
fadE28	Rv3544c	Probable acyl-CoA dehydrogenase	pzu:PHZ_c24 98	26	43	Acyl-CoA dehydrogenase
fadE29	Rv3543c	Probable acyl-CoA dehydrogenase	pzu:PHZ_c25 41	32	51	Acyl-CoA dehydrogenase
fadE30	Rv3560c	Probable acyl-CoA dehydrogenase	pzu:PHZ_c25 41	41	57	Acyl-CoA dehydrogenase

fadE31	Rv3562	Probable acyl-CoA dehydrogenase	pzu:PHZ_c26 78	36	53	Dehydrogenase family protein
fadE32	Rv3563	Probable acyl-CoA dehydrogenase	pzu:PHZ_c24 98	32	45	Acyl-CoA dehydrogenase
fadE33	Rv3564	Probable acyl-CoA dehydrogenase	pzu:PHZ_c26 79	33	48	Acyl-CoA dehydrogenase family protein
fadE34	Rv3573c	Probable acyl-CoA dehydrogenase	pzu:PHZ_c26 78	38	56	Dehydrogenase family protein
fadE5	Rv0244c	Acyl-CoA dehydrogenase	pzu:PHZ_c33 54	36	51	Acyl-CoA dehydrogenase
mbtN (fadE14)	Rv1346	Acyl-CoA dehydrogenase	pzu:PHZ_c03 88	30	48	Acyl-CoA dehydrogenase
echA9	Rv1071c	3-Hydroxyisobutyryl-CoA hydrolase	pzu:PHZ_c16 79	39	57	Enoyl-CoA hydratase/isomerase family protein
echA19	Rv3516	Possible enoyl-CoA hydratase	pzu:PHZ_c25 35	38	54	Enoyl-CoA hydratase/carnithine racemase
echA20	Rv3550	Possible enoyl-CoA hydratase	pzu:PHZ_c34 29	33	51	Enoyl-CoA hydratase/isomerase family protein
fadB2	Rv0468	hydroxybutyryl-CoA dehydrogenase	pzu:PHZ_c31 52	43	60	3-Hydroxyacyl-CoA dehydrogenase
fadB3	Rv1715	Hydroxybutyryl-CoA dehydrogenase	pzu:PHZ_c31 52	35	49	3-Hydroxyacyl-CoA dehydrogenase

fadA5	Rv3546	Acetoacetyl-CoA thiolase	pzu:PHZ_c2504	40	60	Acetyl-CoA C-acetyltransferase
hsd4A	Rv3502c	17 β -Hydroxysteroid dehydrogenase (17 β -HSD)	pzu:PHZ_c2008	36	49	Short-chain dehydrogenase/reductase SDR
ltp2	Rv3540c	Probable ketoacyl-CoA thiolase	pzu:PHZ_c3245	36	49	Acetyl-CoA C-acetyltransferase

3.2.5. Functional analysis of alphaproteobacterial P450s

A literature survey on functional analysis of alphaproteobacterial P450s revealed that several P450s are functionally characterized from these species and are involved in oxidation of xenobiotic compounds (Table 3.5). This study results revealed that twenty-one P450s were found to be involved in synthesis so secondary metabolites where CYP1101A27 from *C. indicus* involved in the production of Ectoine (Table 3.5). However, the physiological functional relevance of P450s in these species needs to be investigated.

Table 3. 5. Functional analysis of alphaproteobacterial P450s

P450	Function	Reference
CYP101B1	α -ionone, β -damascone, phenylcyclohexane and <i>p</i> -cymene hydroxylation	(Hall and Bell, 2015)
CYP101C1	Ionone derivative hydroxylation	(Ma et al., 2011)
CYP101D1	Terpenoid (camphor) hydroxylase	(Yang et al., 2010, Batabyal and Poulos, 2013)
CYP101D2	Camphor 5-exo hydroxylase	(Yang et al., 2011)
CYP108D1	Aromatic hydrocarbon hydroxylase	(Yang et al., 2010, Bell et al., 2012b)
CYP153C1 , CYP153D1	Alkane hydroxylase	(Zhou et al., 2011)
CYP111A2	Oxidizes linalool to 8-hydroxylinalool	(Yang et al., 2010)
CYP111B1	β -Ionone hydroxylation	(Krings and Berger, 2010)
CYP112A2	Oxidation of Rapamycin	(Cho et al., 2019)
CYP127A3	Hydroxylation of testosterone	(Agematu et al., 2006)

CYP195A2	Degradation of 4-fluoro-, 4-chloro- and 4-methylsalicylic acid, and 3-chloro- and 3-methylsalicylic acid	(Guo et al., 2008)
CYP199A1	Hydroxylation of 2-naphthoic acid	(Furuya and Kino, 2009)
CYP199A2	Hydroxylation of 2-naphthoic acid, para-substituted benzoic acids and involved in the degradation of ligninolic compounds	(Furuya and Kino, 2009, Bell et al., 2012a)
CYP199A4	Catalyzes heteroatom dealkylations, sulfoxidation, and amide and cyclic hemiacetal formation	(Coleman et al., 2018)
CYP200A1	Hydroxylation of testosterone	(Agematu et al., 2006)
CYP201A2	Involved in the biodegradation of tributyl phosphate	(Berne et al., 2007)

3.3. Materials and Methods

3.3.1. Species and satabase

In this study, 599 alphaproteobacterial species genomes that are available for public use at Kyoto Encyclopedia of Genes and Genomes (KEGG) data base (Kanehisa et al., 2019b) were used (Table S1 in Annexure A). Detailed information on species, species codes, genera and genbank accession codes is presented in Table S1 in Annexure A.

3.3.2. Genome data mining and annotation of P450s

P450 mining in alphaproteobacterial species was carried out using the methods recently described by our laboratory (Khumalo et al., 2020b, Padayachee et al., 2020). Briefly, the whole proteome of alphaproteobacterial species was downloaded from KEGG and subjected to the NCBI Batch Web CD-Search Tool (Lu et al., 2020). Proteins that belong to the P450 superfamily were selected and annotated, based on the International P450 Nomenclature Committee rule, i.e., proteins with > 40% identity and > 55% identity are grouped under the same family and subfamily, respectively (Nelson, 2006, Nelson et al., 1993, Nelson, 1998a). Proteins with less than 40% identity are assigned to a new P450 family.

3.3.3. Phylogenetic analysis of P450s

Phylogenetic analysis of P450s was carried out following the procedure described recently by our laboratory (Khumalo et al., 2020b, Padayachee et al., 2020). The phylogenetic tree of P450s

was constructed using alphaproteobacterial species P450 protein sequences. Firstly, the MAFFT v6.864 (Katoh et al., 2005) was used to align the protein sequences that are part of the Trex web server (Boc et al., 2012). The alignments were then be subjected to interpret the best tree by the Trex web server (Boc et al., 2012). Lastly, a web-based tool, iTol, was used to create, visualize and colour the tree (Letunic and Bork, 2016).

3.3.4. Generation of P450 profile heat-maps

P450 profile heat-maps were generated following the procedure described recently by our laboratory (Khumalo et al., 2020b, Padayachee et al., 2020). The heat-map was generated using the P450 family data to show the presence or absence of P450s in alphaproteobacterial species. The data were represented as (3) for family presence (red) and (-3) for family absence (green). A tab-delimited file was imported into Mev (Multi-experiment viewer) (Howe et al., 2011). Hierarchical clustering using a Euclidean distance metric was used to cluster the data. Alphaproteobacterial species with P450s in their genome formed the vertical axis and P450 families formed the horizontal axis.

3.3.5. Secondary metabolite BGC analysis and identification of P450s that are part of BGCs

Secondary metabolite BGC analysis and identification of P450s that are part of BGCs in alphaproteobacterial species was carried out following the procedure described recently by our laboratory (Khumalo et al., 2020b, Padayachee et al., 2020). Briefly, alphaproteobacterial species individual genome ID (Table S1) was submitted to antiSMASH (Blin et al., 2019) for identification of secondary metabolite BGCs. Results were downloaded both in the form of gene cluster sequences and Excel spreadsheets representing species-wise cluster information, and finally P450s that are part of a specific gene cluster were identified. Standard gene cluster abbreviation terminology available at the anti-SMASH database (Blin et al., 2019) was sustained in this study.

3.3.6. Identification of cholesterol side-chain oxidizing genes/proteins

Thirty-one cholesterol side-chain oxidizing genes/proteins from *M. tuberculosis* H37Rv (van Wyk et al., 2019) were used in the study to identify homologs in *P. zucineum*. Reference proteins were blasted individually against the *P. zucineum* genome and based on the percentage identity, homology, coverage and annotation at KEGG, the homolog proteins were identified in *P. zucineum*. A point to be noted is that *M. tuberculosis* and *P. zucineum* are distantly related

and thus the lowest percentage identity between these two organisms' proteins is expected, as previously observed (Holert et al., 2018).

CHAPTER 4: GENOME-WIDE ANALYSIS OF FERREDOXINS IN ALPHAPROTEOBACTERIAL SPECIES

4.1 Introduction

Wharton of DuPont Group first coined the term ‘ferredoxin’ (Fd) referring to the brownish protein (iron-sulfur protein) initially found in *Clostridium pasteurianum* (Reference). Since then, these proteins are found to be ubiquitously present in all biological kingdoms. Ferredoxins can be defined as an ancient ubiquitous group of proteins with non-heme iron in the active center that is non-covalently linked with acid-labile sulfide and cysteinyl sulfur (Bruschi and Guerlesquin, 1988; Fontecave, 2006). Some of their characteristics include the presence of iron and sulfide atoms, lower oxidation reduction potentials, size range of about 6kDa to over 500kDa and capable of transferring electrons in biological reactions (Bruschi and Guerlesquin, 1988).

Major ferredoxin iron-sulfur groups have been categorized on the basis of their iron and acid labile contents (Figure 4.1) (Fontecave, 2006), reduction potential, amino acid sequence relationships, biological resources and their spectral properties (Beinert et al., 1983). Common types of ferredoxin iron-sulfur clusters include [4Fe-4S], 2Fe-2S, 3Fe-4S (Fontecave, 2006) (Figure 4.1) and 7Fe-8S, the combination of 3Fe-4S & 4Fe-4S and 2[4Fe-4S] also known as 8Fe-8S (Tong and Rouault, 2006; Hannemann et al., 2007). In these Fe-S clusters, each iron atom is tetrahedrally coordinated by thiolate ligands of cysteines side chains and consists of bridging inorganic sulfur resulting in unique spectroscopic properties (Fontecave, 2006).

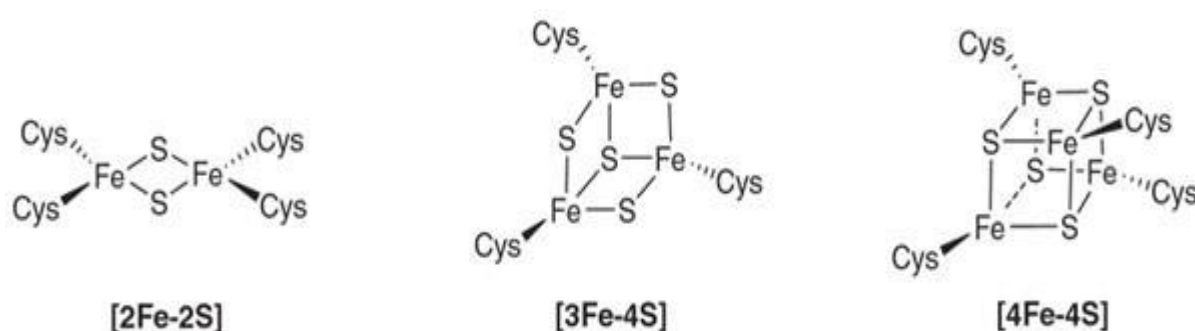


Figure 4. 1. Basic structures of the common iron-sulfur clusters the 2Fe-2S, 3Fe-4S and 4Fe-4S clusters (Fontecave, 2006)

Being electron transport systems, they are involved in the metabolism of carbon, nitrogen, hydrogen, oxygen and sulfur, photosynthesis, gene regulation, steroid synthesis and other biological processes (Orme-Johnson and Orme-Johnson, 1978a; Orme-Johnson and Orme-Johnson, 1978b).

According to the classification of the Fe-S cluster proteins into different types, each of the Fe-S cluster types have their own characteristic Fe-S binding motif where Fe-atom binding cysteine amino acids reside. The characteristic Fe-S binding motif includes four cysteines for 2Fe-2S, three cysteines and a proline that follows after the third cysteine for 3Fe-4S, four cysteines and a proline that follows after the fourth cysteine for 4Fe-4S and the 7Fe-8S ferredoxins having both 3Fe-4S and 4Fe-4S cluster features. The 2[4Fe-4S] ferredoxins have two 4Fe-4S motifs but the spacing between Fe-atom binding cysteines are different compared to the 4Fe-4S cluster type motif. 2[4Fe-4S] proteins are divided into two subfamilies with small proteins (approximately 55 amino acids) having isopotential Fe-S clusters and larger proteins, known as Alvin (Alv) ferredoxins, having clusters with different potentials (Saridakis et al., 2009). Sequence analysis revealed the presence of an extra cysteine in 2[4Fe-4S]Alv ferredoxins exactly after three amino acids following the last cysteine of the second 4Fe-4S binding cluster (Saridakis et al., 2009). Based on the arrangement of cysteines in the Fe-S binding motif, 2Fe-2S cluster proteins were also classified as plant-type, mitochondrial-type, bacterial-type and thioredoxin-type (Zanetti and Pandini, 2013).

The 4Fe-4S clusters are regarded as the most versatile type of clusters as they can occur in three distinct oxidation reduction states as $3^+ 2^+$ and 1^+ . However, they can only operate in two redox states either as low potential $[4Fe-4S]^{3+/+}$ with reduction potentials from -250mV to -650mV (Armstrong et al., 1988; Yoch and Carithers, 1979) or as the high potential iron-sulfur proteins (HiPIPs) $[4Fe-4S]^{3+/2+}$ with positive potentials between +50mV to +500mV.

The in vitro oxidative damage of the 4Fe-4S cluster where one Fe is lost leads to the conversion to the 3Fe-4S cluster. However, in the case of the 3Fe-4S cluster that forms part of the 7Fe-8S cluster type (3Fe-4S & 4Fe-4S) in ferredoxins from *Azotobacter vinelandii* (Langen et al., 1992) and *Thermus thermophilus*, the presence of 3Fe-4S type is not as a result of oxidative damage but is found to be part of catalytic functions (Beinert et al., 1983). This implies that not all 3Fe-S clusters occur due to oxidative damage. The Fe-S clusters can undergo thorough interconversions (4Fe-4S to 2Fe-2S) as an effective mechanism in a number

of organisms as a way of dealing with oxidative stress and a change in intracellular iron concentrations (Jones et al., 2002).

It is believed that among Fe-S cluster types 4Fe-4S clusters are the first to be evolved as the conditions that mimic the primitive Earth resulted in the formation of 4Fe-4S clusters (Beinert et al., 1997; Meyer, 2008; Venkateswara Rao and Holm, 2004). Studies indicated that the 4Fe-4S cluster is sensitive to oxygen compared to the 2Fe-2S cluster (Imlay, 2006; Jagannathan and Golbeck, 2009; Hsueh et al., 2013) and thus it is predicted that after the Great Oxidation Event organisms preferred 2Fe-2S clusters due their oxygen tolerance. This phenomenon is also observed in a study where comparative analysis of 2Fe-2S and 4Fe-4S cluster proteins and flavodoxin proteins across the domains of life were carried out and it was found that 4Fe-4S cluster type proteins are abundantly present in anaerobic organisms whereas 2Fe-2S cluster type proteins are abundant in aerobic organisms (Campbell et al., 2019). A study dating back to 1966 on observing the symmetrical origin of 2[4Fe-4S] ferredoxin from *C. pasteurianum* by Eck and Dayhoff led to the proposal that all proteins emerged through the duplication of even shorter and simpler ancestral peptides (Eck and Dayhoff, 1966). Recently, it has been shown that indeed 2[4Fe-4S] ferredoxins have drifted from their symmetric roots via gene duplication followed by mutations (Mutter et al., 2019). Numerous studies reporting the gene duplication events as the source of the growth and diversification of Fe-S proteins have been listed in a recent article (Campbell et al., 2019).

The Fe-S proteins act as electron donors for the catalytic activities of cytochrome P450 monooxygenases (CYPs/P450s) (Hannemann et al., 2007). P450s are a remarkable part of a superfamily of enzymes consisting of heme as a cofactor. Over the last five decades, these enzymes have gained a lot of attention for their special versatility (Kelly and Kelly, 2013). The CYP gene is set to have evolved from a common ancestor about 3.2 billion years ago (Lewis et al., 1998). Therefore, this explains the ubiquitous existence of P450s across the species from all biological kingdoms (Nelson, 2018a). Despite sharing P450s' common functional characteristic as monooxygenases, there are differences in the P450 electron transport systems in both eukaryotic and prokaryotic organisms (Degtyarenko and Archakov, 1993; Bernhardt, 1995).

The majority of P450s, depending on the type of P450 system, require redox partners - either NADH or NADPH - to donate the two reducing equivalents for the catalytic reactions of P450s, except self-sufficient P450s (Hannemann et al., 2007; Munro et al., 2013). The co-

factors FAD, FMN/2Fe-2S and Cytochrome b5 (in the case of a microsomal system) shuttle electrons one at a time (Lewis and Hlavica, 2000). The electron flow from reductant to oxidant by the redox partners is presented as follows:

Bacterial system: $\text{NADH} \rightarrow \text{FAD} \rightarrow \text{redoxin} \rightarrow \text{P450}$

Microsomal system: $\text{NADPH} \rightarrow \text{FAD} \rightarrow \text{FMN} \rightarrow \text{P450}$

whereby the arrow represents the flow of a single electron (Degtyarenko and Archakov, 1993).

P450s and their redox partners can be classified into three, two and one component systems (Fasan, 2012). The electron transport systems by redox proteins in P450s have been classified into a number of novel classes (Hannemann et al., 2007).

Studies on the evolution of ferredoxins are rare and from the available data one can understand that ferredoxins originated from a common ancestor but divergent evolution played a critical role in their diversity (Yasunobu and Tanaka, 1973; Harayama et al., 1991; Cammack, 1983; Bruschi and Guerlesquin, 1988). In addition to this, ferredoxins are believed to be evolved from different ancestral genes that are diversified from a common ancestor (Yasunobu and Tanaka, 1973; Harayama et al., 1991; Cammack, 1983; Bruschi and Guerlesquin, 1988). Only a handful of studies reported lateral (or horizontal) gene transfer (LGT) of ferredoxins (Petitjean et al., 2012; Nixon et al., 2002; Pfeifer et al., 1993). The ferredoxin domain of cyanobacterial origin was found to be acquired by photosynthetic eukaryotes thorough HGT in chloroplast DnaJ-like proteins (Petitjean et al., 2012). Eukaryotic protists such as *Giardia lamblia* and *Entamoeba histolytica* ferredoxins were predicted to be acquired from anaerobic bacteria by HGT (Nixon et al., 2002). Based on the percentage similarity, *Halobacterium salinarium* ferredoxin is predicted to be acquired by LGT from cyanobacterial species (Pfeifer et al., 1993).

Apart from the above handful of studies that are confined to a small number of ferredoxins and a few species, to our knowledge, no information is presented on the diversity of ferredoxins within a cluster type and lateral gene transfer ((LGT) of ferredoxins across different living organisms. The current genome sequencing era has resulted in the availability of a large number of organisms' genomes that have been sequenced. This gives us an opportunity to look into ferredoxin protein sequences and better understand their diversity across the domains of life. Thus, this study aimed to address this research gap by performing genome data mining, annotation and comparative analysis of ferredoxins between the ancient bacterial group

Alphaproteobacteria and ferredoxins from the species belonging to different domains of life that are reported in the literature. In order to understand the diversity of ferredoxins within Fe-S cluster types in organisms, we here propose a subtype classification of the Fe-S cluster types based on the characteristic spacing between the cysteine amino acids of Fe-S binding motif as a subtype signature, considering the fact that this motif is conserved in ferredoxins per se in Fe-S cluster proteins. Furthermore, we also propose a nomenclature system for easy identification of cluster type and subtype for a ferredoxin.

4.2 Materials and Methods

4.2.1. Species and database

In this study, 241 alphaproteobacterial species genomes that are available for public use at Kyoto Encyclopedia of Genes and Genomes (KEGG) database (Kanehisa et al., 2019a) were used (Table S1 in Annexure B). These species are known to have P450s in their genome (Nzuza et al., 2021) and thus selected for ferredoxins analysis considering P450s need ferredoxins for their function and so as one can expect presence of a higher number of ferredoxins in these species. List of species used in the study along with their species codes are presented in Table S1 in Annexure B.

4.2.2. Genome data mining and annotation of ferredoxins

Ferredoxins belonging to different Fe-S cluster types reported in the literature (Table 4.1) used as reference proteins. Protein BLAST (Altschul et al., 1990) were performed using these reference proteins against each of the bacterial species' genomes at KEGG (Kanehisa et al., 2019a). The hit proteins were manually checked for the presence of ferredoxin Fe-S cluster type canonical motif and the proteins that have the Fe-S binding motif were selected. The selected proteins were then subjected to protein BLAST (Altschul et al., 1990) at National Center for Biotechnology and Information (NCBI) (Sayers et al., 2021) against Protein Data Bank (PDB) database (2019) and analyzed for the presence of ferredoxins characteristic motif at Pfam database (El-Gebali et al., 2019), InterPro database (Mitchell et al., 2019) and NCBI Conserved Domains Database (CDD) (Lu et al., 2020). Proteins that had a hit against ferredoxins at PDB database and have ferredoxin motifs as indicated by different databases were selected for further analysis. The rationale for using the PDB database as the first priority to sort hit proteins is that the BLAST against this database not only helped in identifying ferredoxin proteins but also helped in accurately identifying Fe-atom binding cysteine amino acids based on the alignment of hit protein sequence with crystallized ferredoxin sequence. In addition to this, in some cases, BLAST against PDB database also helped to sort proteins

accurately whether they are 3Fe-4S or 4Fe-4S cluster proteins and 7Fe-8S or 2[4Fe-4S] cluster proteins. Hit proteins that are found to be dehydrogenases, oxidases or reductases with Fe-S binding motif is not considered as ferredoxins as the Fe-S clusters in these proteins exceeded more than two and also, they belong to a different protein family. Furthermore, sequences that had hits to ferredoxins but not in full-length also not considered for further analysis. We also noted that manual sorting of Fe-S cluster proteins into different types by consulting as many as possible databases such as PDB database (2019), Pfam database (El-Gebali et al., 2019), InterPro database (Mitchell et al., 2019) and NCBI CDD (Lu et al., 2020) is an important for accurate assigning of Fe-S proteins to different types and also accurately identifying the Fe-atom binding cysteine amino acids. In this study, at most care has been taken to select only ferredoxins for further analysis.

Table 4. 1. Information on ferredoxins that are used as reference proteins in the study

2Fe-2S		
GenBank accession number or PDB code	Species name	Reference
NP_004100.1 (Adrenodoxin)	<i>Homo sapiens</i>	(Cai et al., 2017)
1PDX (Putidaredoxin)	<i>Pseudomonas putida</i>	(Pochapsky et al., 1999)
ABB56370.1	<i>Synechococcus elongatus</i> PCC 7942 = FACHB-805	(Koksharova et al., 2006)
ABB56928.1	<i>Synechococcus elongatus</i> PCC 7942 = FACHB-805	(Koksharova et al., 2006)
WP_013424358.1 (FraEuI1c_3227)	<i>Frankia</i> sp. EuI1c (<i>Frankia inefficax</i> sp.)	(Lau et al., 2019)
WP_012394830.1 (mmi:MMAR_3155)	<i>Mycobacterium marinum</i>	(Child et al., 2018)
3Fe-4S/4Fe-4S		
CAB59502.1	<i>Streptomyces coelicolor</i> A3(2)	(Bentley et al., 2002)
WP_013425251.1 (FraEuI1c_4132)	<i>Frankia</i> sp. EuI1c (<i>Frankia inefficax</i> sp.)	(Lau et al., 2019)
WP_013426476.1 (FraEuI1c_5370)	<i>Frankia</i> sp. EuI1c (<i>Frankia inefficax</i> sp.)	(Lau et al., 2019)

WP_011740769.1 (Mmar_2879)	<i>Mycobacterium marinum</i>	(Child et al., 2018)
WP_012395565.1 (Mmar_3973)	<i>Mycobacterium marinum</i>	(Child et al., 2018)
WP_012396301.1 (Mmar_4763)	<i>Mycobacterium marinum</i>	(Child et al., 2018)
NP_215277.1 (FdX-Rv0763c)	<i>Mycobacterium tuberculosis</i> H37Rv	(Ortega Ugalde et al., 2018, McLean et al., 2006)
NP_216302.1 (FdxE-Rv1786)	<i>Mycobacterium tuberculosis</i> H37Rv	(Ortega Ugalde et al., 2018, McLean et al., 2006)
ABB57779.1	<i>Synechococcus elongatus</i> PCC 7942 = FACHB-805	(Koksharova et al., 2006)
7Fe-8S		
NP_215693 (FdxC-Rv1177),	<i>Mycobacterium tuberculosis</i> H37Rv	(Ortega Ugalde et al., 2018)
NP_216523.1 (FdxA-Rv2007c)	<i>Mycobacterium tuberculosis</i> H37Rv	(Ortega Ugalde et al., 2018)
2VKR	<i>Acidianus ambivalens</i>	(Frazão et al., 2008)
1H98	<i>Thermus thermophilus</i>	(Macedo-Ribeiro et al., 2001)
ABB56846.1	<i>Synechococcus elongatus</i> PCC 7942 = FACHB-805	(Koksharova et al., 2006)
2[4Fe-4S]		
2ZVS	<i>Escherichia coli</i> K-12	(Saridakis et al., 2009)
2FDN	<i>Clostridium acidurici</i>	(Dauter et al., 1997)
WP_013068980.1 (FDI)	<i>Rhodobacter capsulatus</i>	(Saeki et al., 1991)
2[4Fe-4S]Alv		

1BLU	<i>Allochromatium vinosum</i>	(Moulis et al., 1996)
2FGO	<i>Pseudomonas aeruginosa</i>	(Dauter et al., 1997)
WP_023923722.1 (FDIII)	<i>Rhodobacter capsulatus</i>	(Saeki et al., 1991)
1RGV	<i>Thauera aromatica</i> K172	(Unciuleac et al., 2004)

Note: For easy identification purpose for some ferredoxins their most popular literary names were included in parenthesis right after their GenBank accession number or PDB code.

4.2.3. Ferredoxins subtype classification and nomenclature

Ferredoxins selected under different Fe-S cluster types were then subjected to multiple sequence alignment (MSA) at Clustal Omega database (Madeira et al., 2019). Based on the MSA patterns proteins were separated into different groups to such an extent where there will be no amino acid gaps between the cysteine amino acids of the Fe-S cluster binding motif. Ferredoxins that are not aligned with other proteins were then subjected to analysis of spacing between cysteine amino acids of the Fe-S cluster binding motif individually. Then the spacing patterns between cysteine amino acids of the Fe-S cluster binding motif is presented as the characteristic signature of a subtype. Analysis of ferredoxins revealed that proline amino acid is not always conserved in 2[4Fe-4S] ferredoxins and thus is not included in the Fe-S binding motif signature for this type ferredoxins. Although proline included for 7Fe-8S cluster proteins, only cysteine residues and the amino acid spacing between these residues can be taken as a signature as non-conservation of proline will be expected when more number of ferredoxins analyzed. In order to represent different sub-types in a type, a nomenclature system developed such that each protein start with its Fe-S cluster type followed by abbreviation “ST” for “subtype” and then numeric indicating its subtype number in a type (Figure 4.2). Subtype numbers are assigned following the occurrence of new ferredoxins along the study. Ferredoxins identified in the bacterial species of *Alphaproteobacteria* and retrieved from literature is presented along with their nomenclature in Table S2 in Annexure B.

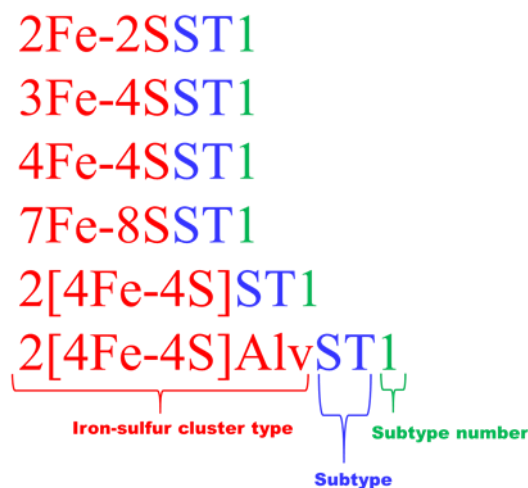


Figure 4. 2. Ferredoxins nomenclature based on the spacing between the cysteine amino acids of Fe-S cluster binding motif. Ferredoxins start with their Fe-S cluster type, followed by ST indicating subtype and then numeric indicating its subtype number in that type. Proteins grouped into different subtypes have the same characteristic spacing between the cysteine amino acids of the Fe-S cluster binding motif.

4.2.4. Assigning Fe-S cluster subtypes to the ferredoxins retrieved from literature

Ferredoxins that are reported in the literature were collected by going through the published articles and also data mining at PDB database (2019). Most of the ferredoxins belonging to the species of Archaea and some Eukarya is retrieved from article published by Campbell and co-workers (Campbell et al., 2019). Search at PDB database was carried out using Fe-S cluster type name and collected the ferredoxin sequences after manually looking at the Fe-S clusters of the ferredoxin. These ferredoxins were then subjected to subtype nomenclature as described in the section 4.2.3. Ferredoxins retrieved from literature and data mined at PDB database were presented along with their nomenclature in Table S3 in Annexure B.

4.2.5. Phylogenetic analysis of ferredoxins

Phylogenetic analysis of ferredoxins was carried out following the procedure described recently by our laboratory (Padayachee et al., 2020, Khumalo et al., 2020a). The phylogenetic tree of ferredoxins was constructed using protein sequences. Firstly, the MAFFT v6.864 (Kato et al., 2005) was used to align the protein sequences that are part of the Trex web server (Boc et al., 2012). The alignments were then be subjected to interpret the best tree by the Trex web server (Boc et al., 2012). Lastly, a web-based tool, iTol, was used to create, visualize and color the tree (Letunic and Bork, 2016).

4.2.6. Generation of ferredoxin subtype profile heat maps

Ferredoxin subtype profile heat maps were generated following the procedure described recently by our laboratory (Padayachee et al., 2020, Khumalo et al., 2020a). The heat map was generated using the ferredoxin subtype data to show the presence or absence of ferredoxin subtypes in three domains of life, Archaea, Bacteria and Eukarya. The data were represented as (−3) for sub-type absence (green) and (3) for subtype presence (red). A tab-delimited file was imported into Mev (Multi-experiment viewer) (Howe et al., 2011). Hierarchical clustering using a Euclidean distance metric was used to cluster the data. Ferredoxin subtypes formed the vertical axis and three domains of life formed the horizontal axis.

4.3. Results and Discussion

4.3.1. Alphaproteobacterial-species have different Fe-S cluster type ferredoxins in their genomes

Genome data mining of 241 alphaproteobacterial species revealed presence of 1306 ferredoxins in their genomes (Figure 4.3 and Table S1 in Annexure B). This suggests that alphaproteobacterial species have an average of approximately 5 ferredoxins in their genomes (Figure 4.3). Among alphaproteobacterial species *Sphingomonas wittichii* have the highest number of twelve ferredoxins (Table S1 in Annexure B). Six different Fe-S cluster type ferredoxins were found in alphaproteobacterial species (Figure 4.3).

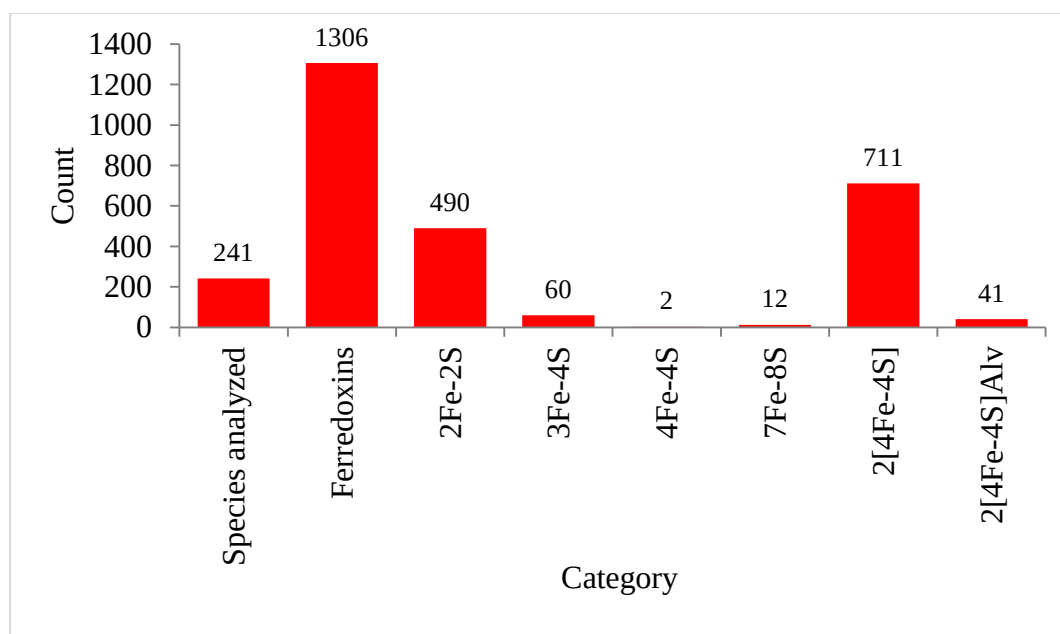


Figure 4. 3. Comparative analysis of ferredoxins iron-sulfur (Fe-S) cluster features in alphaproteobacterial species. The number next to the bar indicate the count for that category. Detailed information on species and their ferredoxins is presented in Tables S1 in Annexure B.

Analysis of ferredoxins Fe-S cluster types in alphaproteobacterial species revealed that 2[4Fe-4S] cluster type ferredoxins was found to be most abundant with 711 ferredoxins followed by 2Fe-2S with 490 ferredoxins, 3Fe-4S with 60 ferredoxins, 2[4Fe-4S]Alv with 31 ferredoxins, 7Fe-8S with 12 ferredoxins and 4Fe-4S cluster with 2 ferredoxins (Figure 4.3). Based on the analysis it shows that alphaproteobacterial species have more ferredoxins belonging to the 2[4Fe-4S] cluster. Therefore, this suggests that this Fe-S cluster type is most preferable by the *Alphaproteobacteria*.

4.3.2. Diversity analysis of ferredoxins among alphaproteobacterial species

In this study, we tested amino acid spacing pattern between the cysteine amino acids of Fe-S cluster binding motif as a signature for ferredoxins subtype classification which therefore developed to understand the diversity of ferredoxins within a cluster type and LGT of ferredoxins types using alphaproteobacterial species as a model organisms considering the fact that alphaproteobacterial species are ancient species and thus serves as the best models for understanding these aspects. A detailed analysis on ferredoxin Fe-S cluster subtypes in alphaproteobacterial species is presented below:

Based on the amino acid spacing pattern between the cysteine amino acids of the Fe S cluster binding motif, 490 2Fe-2S ferredoxins of alphaproteobacterial species can be grouped into 29 subtypes (Table 4.2). Among alphaproteobacterial 2Fe-2S ferredoxin sub-types, subtype 1 has a greater number of ferredoxins followed by subtype 2 (Table 4.2) indicating subtype 1 ferredoxins are highly preferable by these species. Sixty 3Fe-4S ferredoxins found in alphaproteobacterial species can be grouped into 5 different subtypes (Table 4.2). Among the 5 subtypes, subtype 1 ferredoxins present in more numbers followed by subtypes 2 and 3 (Table 4.2) indicating ferredoxins with subtype 1 are preferred by alphaproteobacterial species. The two 4Fe-4S ferredoxins found in alphaproteobacterial species can be grouped into the same subtype (Table 4.2). Twelve 7Fe-8S ferredoxins found in alphaproteobacterial species grouped into four different subtypes. Seven hundred and eleven 2[4Fe-4S] ferredoxin found in alphaproteobacterial species can be grouped into 16 subtypes whereas (Table 4.2). Subtype 1 ferredoxins are more in number in alphaproteobacterial species followed by subtypes 2 and 3 (Table 4.2). The 31 2[4Fe-4S]Alv ferredoxins of alphaproteobacterial species were grouped into 8 different subtypes (Table 4.2). Of the eight subtypes, subtypes 1 and 2 have almost a greater number of ferredoxins compared to rest of the subtypes (Table 4.2).

Table 4. 2. Subtype classification of ferredoxin across the domains of life. Ferredoxins collected from species belonging to different biological kingdoms that are reported in the literature and data mined at PDB also presented in the table as per their subtypes under the domains: Archaea, Bacteria and Eukarya. Ferredoxin protein sequences as per their nomenclature are presented in Tables S2 and S3 in Annexure B

Subtypes	Cysteine spacing signature	No. AA	No of ferredoxins			
			<i>Alphaproteobacteria</i>	From Literature		
				Archaea	Bacteria	Eukarya
2Fe-2S						
Subtype 1	CX ₅ CX ₂ CX ₃₆ C	47	296		2	64
Subtype 2	CX ₅ CX ₂ CX ₃₇ C	48	81		4	22
Subtype 3	CX ₄ CX ₂ CX ₂₉ C	39	11	7	11	55
Subtype 4	CX ₅ CX ₂ CX ₃₅ C	46	12		2	
Subtype 5	CX ₅ CX ₂ CX ₃₈ C	49	12			
Subtype 6	CX ₄ CX ₂ CX ₃₄ C	44	11	7	1	
Subtype 7	CX ₄ CX ₂ CX ₅₁ C	61	8		1	
Subtype 8	CX ₄ CX ₂ CX ₃₁ C	41	7	1	1	
Subtype 9	CX ₄ CX ₂ CX ₃₃ C	43	2	19		2
Subtype 10	CX ₅ CX ₂ CX ₃₉ C	50	2		1	
Subtype 11	CX ₄ CX ₂ CX ₃₅ C	46	1			
Subtype 12	CX ₄ CX ₂ CX ₂₅ C	35	1			

Subtype 13	$CX_7CX_{34}CX_3C$	48	1			
Subtype 14	$CX_4CX_{29}C$	36	1			
Subtype 15	$CX_7CX_{29}C$	39	1			
Subtype 16	$CX_7CX_{35}C$	45	1			
Subtype 17	$CX_5CX_2CX_{33}C$	44	1			
Subtype 18	$CX_5CX_2CX_{34}C$	45	2	2	1	1
Subtype 19	$CX_5CX_2CX_{35}C$	46	1			
Subtype 20	$CX_5CX_2CX_{32}C$	43			1	5
Subtype 23	$CX_7CX_{38}CX_3C$	52			1	
Subtype 24	$CX_4CX_2CX_{30}C$	40		70		1
Subtype 25	$CX_5CX_2CX_{30}C$	41				1
Subtype 26	$CX_{12}CX_{30}CX_3C$	49	21			
Subtype 27	$CX_{12}CX_{31}CX_3C$	50	4			
Subtype 28	$CX_8CX_{44}CX_3C$	59	3			
Subtype 29	$CX_8CX_{33}CX_3C$	48	3			
Subtype 30	$CX_8CX_{32}CX_3C$	47	2			
Subtype 31	$CX_4CX_{36}CX_3C$	47	1	1		
Subtype 32	$CX_8CX_{38}CX_3C$	53	1			
Subtype 33	$CX_8CX_{39}CX_3C$	54	1			
Subtype 34	$CX_9CX_{33}CX_3C$	49	1			

Subtype 35	$CX_{12}CX_{33}CX_3C$	52	1			
Subtype 36	$CX_3CX_1CX_{38}C$	46			1	
Subtype 37	$CX_{12}CX_{32}CX_3C$	51			1	
Subtype 38	$CX_4CX_2CX_{28}C$	38		40		3
Subtype 39	$CX_4CX_2CX_{46}C$	56		2		
Subtype 40	$CX_4CX_2CX_{49}C$	59		3		
Subtype 41	$CX_4CX_2CX_{45}C$	55		2		
Subtype 42	$CX_4CX_2CX_{65}C$	75		1		
Subtype 43	$CX_4CX_2CX_{50}C$	60		2		
Subtype 44	$CX_4CX_2CX_{47}C$	57		2		
Subtype 45	$CX_4CX_2CX_{48}C$	58		1		
Subtype 46	$CX_5CX_2CX_{52}C$	63		2		
Subtype 47	$CX_5CX_2CX_{31}C$	42		1		
Subtype 48	$CX_5CX_2CX_{28}C$	39		2		
Subtype 49	$CX_5CX_2CX_{27}C$	38		10		
Subtype 50	$CX_5CX_2CX_{82}C$	93		2		
Subtype 51	$CX_5CX_2CX_{29}C$	40		1		
Subtype 52	$CX_4CX_2CX_{32}C$	42		1		
Subtype 53	$CX_5CX_2CX_{42}C$	53				1
Subtype 54	$CX_4CX_2CX_{22}C$	32				2

Subtype 55	CX ₄ CX ₂ CX ₂₉ C	39		2		
3Fe-4S						
Subtype 1	CX ₅ CX ₃₈ CP	47	26	2	7	
Subtype 2	CX ₅ CX ₃₇ CP	46	16		13	
Subtype 3	CX ₅ CX ₃₆ CP	45	14		2	
Subtype 4	CX ₅ CX ₄₀ CP	49	3			
Subtype 5	CX ₅ CX ₃₆ CP	45	1			
Subtype 6	CX ₅ CX ₃₅ CP	44			5	
Subtype 7	CX ₅ CX ₄₉ CP	58			2	
4Fe-4S						
Subtype 1	CX ₅ CX ₃ CX ₃₃ CP	46	2			
Subtype 3	CX ₂ CX ₂ CX ₄₅ CP	54			1	
Subtype 7	CX ₂ CX ₂ CX ₃₆ CP	45			2	
Subtype 8	CX ₂ CX ₂ CX ₃₄ CP	43			1	
Subtype 9	CX ₂ CX ₂ CX ₃₈ CP	46		1		1
Subtype 10	CX ₅ CX ₃ CX ₃₂ CP	45		1		
Subtype 11	CX ₅ CX ₃ CX ₃₀ CP	43		12		
Subtype 12	CX ₅ CX ₃ CX ₃₁ CP	44		2		
7Fe-8S						
Subtype 1	CX ₇ CX ₃ CPX ₁₇ CX ₂ CX ₂ CX ₃ CP*	43	6		13	

Subtype 2	CX ₅ CX ₃ CPX ₄₀ CX ₂ CX ₂ CX ₃ CP	64	4			
Subtype 3	CX ₅ CX ₃ CPX ₂₀ CX ₂ CX ₂ CX ₃ CP	44	1			
Subtype 4	CX ₁₀ CX ₃ CPX ₂₂ CX ₂ CX ₂ CX ₃ CP	51	1			
Subtype 5	CX ₅ CX ₃ CPX ₂₆ CX ₂ CX ₂ CX ₃ CP	50		1		
Subtype 6	CX ₅ CX ₃ CPX ₂₄ CX ₂ CX ₂ CX ₃ CP	48			1	1
Subtype 7	CX ₁₀ CX ₃ CPX ₁₇ CX ₂ CX ₂ CX ₃ CP	46			1	
Subtype 8	CX ₅ CX ₃ CPX ₂₂ CX ₂ CX ₂ CX ₃ CP	46		9		
Subtype 9	CX ₅ CX ₃ CPX ₁₈ CX ₂ CX ₂ CX ₃ C	42		1		
Subtype 10	CX ₃ CX ₃ CPX ₂₂ CX ₂ CX ₂ CX ₃ CP	44		2		
2[4Fe-4S]						
Subtype 1	CX ₂ CX ₄ CX ₃ CX ₁₈ CX ₂ CX ₂ CX ₃ C	42	267			
Subtype 2	CX ₂ CX ₂ CX ₃ CX ₁₈ CX ₂ CX ₈ CX ₃ C	46	90		4	
Subtype 3	CX ₂ CX ₂ CX ₃ CX ₂₀ CX ₂ CX ₂ CX ₃ C	42	32	52	1	
Subtype 4	CX ₇ CX ₂ CX ₃ CX ₂₃ CX ₂ CX ₂ CX ₃ C	50	5			
Subtype 5	CX ₂ CX ₂ CX ₃ CX ₄₂ CX ₂ CX ₂ CX ₃ C	64	3			
Subtype 6	CX ₂ CX ₂ CX ₃ CX ₁₈ CX ₂ CX ₇ CX ₃ C	45	2			
Subtype 7	CX ₂ CX ₂ CX ₃ CX ₁₈ CX ₂ CX ₆ CX ₃ C	44	2			
Subtype 8	CX ₂ CX ₂ CX ₃ CX ₂₄ CX ₂ CX ₂ CX ₃ C	46	2	2		
Subtype 9	CX ₂ CX ₂ CX ₃ CX ₁₈ CX ₂ CX ₂ CX ₃ C	40	1	78	3	1

Subtype 10	$CX_2CX_2CX_3CX_{21}CX_2CX_2CX_3C$	43	6	2		
Subtype 11	$CX_2CX_2CX_3CX_{18}CX_3CX_2CX_3C$	41		2		
Subtype 12	$CX_2CX_2CX_3CX_{28}CX_2CX_2CX_3C$	50	132	1		2
Subtype 13	$CX_2CX_2CX_3CX_{27}CX_2CX_2CX_3C$	49	2			
Subtype 14	$CX_5CX_2CX_3CX_{20}CX_2CX_2CX_3C$	45	21			
Subtype 15	$CX_2CX_2CX_3CX_{19}CX_2CX_2CX_3C$	41	1	58		
Subtype 16	$CX_2CX_2CX_3CX_{40}CX_2CX_2CX_3C$	50	1			
Subtype 17	$CX_2CX_2CX_3CX_{29}CX_2CX_2CX_3C$	51	144			2
Subtype 18	$CX_4CX_2CX_3CX_{18}CX_2CX_2CX_3C$	42		1	1	
Subtype 19	$CX_3CX_2CX_3CX_{20}CX_2CX_2CX_3C$	43			2	
Subtype 20	$CX_2CX_2CX_3CX_{17}CX_2CX_2CX_3C$	39		24	1	
Subtype 21	$CX_3CX_3CX_3CX_{37}CX_1CX_3CX_3C$	61			1	
Subtype 22	$CX_2CX_2CX_3CX_{26}CX_2CX_2CX_3C$	48				6
Subtype 23	$CX_2CX_2CX_3CX_{30}CX_2CX_2CX_3C$	52				1
Subtype 24	$CX_2CX_2CX_3CX_{33}CX_2CX_2CX_3C$	55		22		
Subtype 25	$CX_2CX_2CX_3CX_{32}CX_2CX_2CX_3C$	54		23		
Subtype 26	$CX_2CX_2CX_3CX_{23}CX_2CX_2CX_3C$	45		2		
Subtype 27	$CX_2CX_2CX_3CX_{34}CX_2CX_2CX_3C$	56		1		
Subtype 28	$CX_2CX_2CX_3CX_{14}CX_2CX_2CX_3C$	36		2		
Subtype 29	$CX_2CX_2CX_3CX_{22}CX_2CX_2CX_3C$	44		2		

Subtype 30	CX ₂ CX ₂ CX ₂ CX ₃₈ CX ₂ CX ₂ CX ₃ C	59		1		
Subtype 31	CX ₄ CX ₂ CX ₃ CX ₁₉ CX ₂ CX ₂ CX ₃ C	43		24		
Subtype 32	CX ₅ CX ₂ CX ₃ CX ₁₉ CX ₂ CX ₂ CX ₃ C	44		3		
Subtype 33	CX ₂ CX ₂ CX ₃ CX ₁₆ CX ₂ CX ₂ CX ₃ C	38		16		
2[4Fe-4S]Alv						
Subtype 1	CX ₂ CX ₂ CX ₃ CX ₁₈ CX ₂ CX ₈ CX ₃ CX ₃ C	50	10		5	
Subtype 2	CX ₂ CX ₂ CX ₃ CX ₃₉ CX ₂ CX ₂ CX ₃ CX ₃ C	65	9			
Subtype 3	CX ₂ CX ₂ CX ₃ CX ₄₃ CX ₂ CX ₂ CX ₃ CX ₃ C	69	5		1	
Subtype 4	CX ₂ CX ₂ CX ₃ CX ₄₂ CX ₂ CX ₂ CX ₃ CX ₃ C	68	1			
Subtype 5	CX ₂ CX ₂ CX ₃ CX ₄₀ CX ₂ CX ₂ CX ₃ CX ₃ C	66	2			
Subtype 6	CX ₂ CX ₂ CX ₃ CX ₃₈ CX ₂ CX ₂ CX ₃ CX ₃ C	64	1			
Subtype 7	CX ₂ CX ₂ CX ₃ CX ₄₆ CX ₂ CX ₂ CX ₃ CX ₃ C	72	2			
Subtype 8	CX ₂ CX ₂ CX ₃ CX ₄₄ CX ₂ CX ₂ CX ₃ CX ₃ C	70	1			
Subtype 9	CX ₂ CX ₂ CX ₃ CX ₃₀ CX ₂ CX ₂ CX ₃ CX ₃ C	56		2		
Subtype 10	CX ₂ CX ₂ CX ₃ CX ₁₉ CX ₂ CX ₂ CX ₃ CX ₃ C	45		8		

Note: *, Only 7Fe-8S ferredoxins from *M. tuberculosis* H37Rv (Rv2007c) was found to have “arginine (R)” instead of “proline (P)”. Proline is not conserved in 2[4Fe-4S] cluster ferredoxins and thus not included in the signature. Although proline included for 7Fe-8S cluster ferredoxins, only cysteine residues and the amino acid spacing between these residues can be taken as a signature. No AA indicates, number of amino acids in cysteine spacing signature motif.

4.3.4. Evolutionary linkage of ferredoxins subtype classification

The phylogenetic evolution of the collected and annotated ferredoxin sequences shown in Figure 4.4 revealed that most of the ferredoxin types and subtypes were aligned to the tree according to the classification and nomenclature we have proposed in 4.2.3. This shows that the binding motif of the cysteine amino acids in the Fe-S protein sequence is evolutionarily conserved and passed across the species respectively. The 2Fe-2S ferredoxin subtypes are all aligned together except for a few. It is the similar case for the other types. However, the way branches are closely aligned indicates the strong ancestral link between the classified ferredoxin types in *Alphaproteobacteria* and ferredoxins from other domains of life.

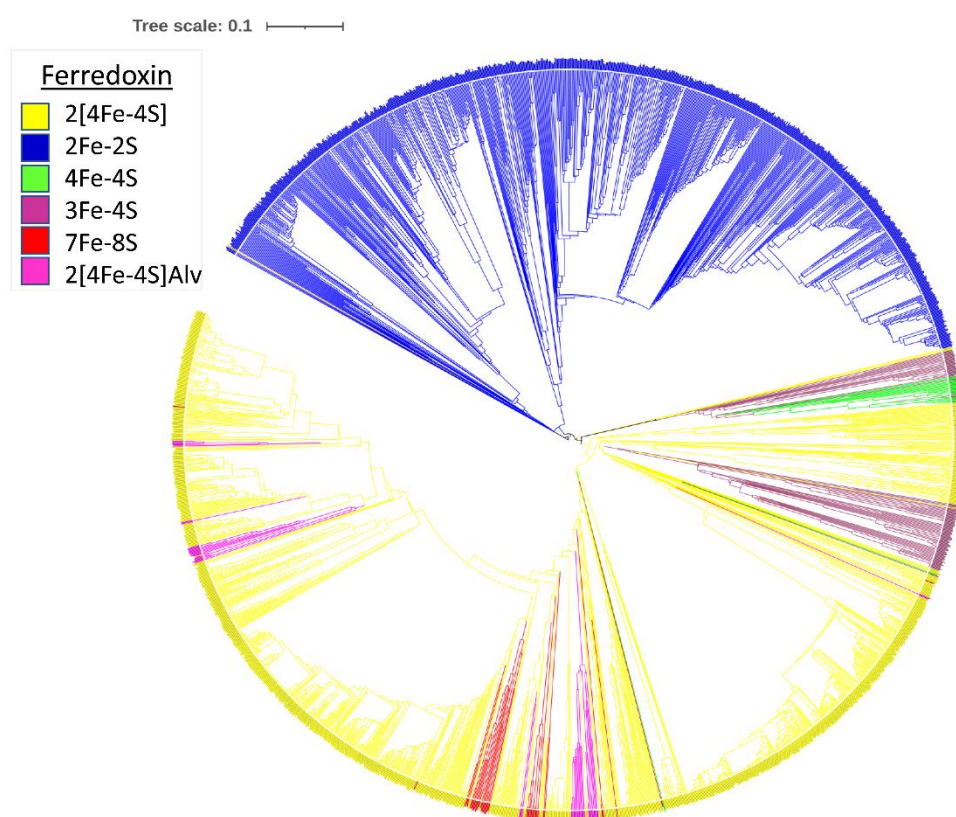


Figure 4. 4. Phylogenetic analysis of ferredoxins. Ferredoxins belonging to different Fe-S cluster types were highlighted in different colors and indicated in the figure. Ferredoxin protein sequences used to construct the phylogenetic tree are presented in Table S2.

4.3.5. LGT of ferredoxins among *Alphaproteobacteria* and other living organisms

The modern genomic era has led to genome sequencing of numerous organisms and therefore the availability of ferredoxin sequences from all biological domains. This has given us an opportunity to look for the common ancestral link and LGT of ferredoxins. Ferredoxins that

are common to alphaproteobacterial species and other bacterial species will serve as an indication of common ancestral origin and as ferredoxins that are common among prokaryotes and eukaryotes. The proposed subtype classification of ferredoxins in this study has definitely helped to better understand the discussed aspects on ferredoxins. To better understand the ancestral linkage and LGT of ferredoxins across the living organisms we have collected and annotated 538,95 and 171 ferredoxins from Archaea, Bacteria (excluding ferredoxins from *Alphaproteobacteria*) and Eukarya respectively) (Tables 4.2 and S3 in Annexure B).

The comparative analysis of ferredoxin subtypes has revealed common ferredoxin subtypes among *Alphaproteobacteria* and other biological domains (Figure 4.5). In 2Fe-2S type, subtype 3 and 18, and in 2[4Fe-4S], subtype 9 was found to be present in all domains indicating their ancestral link (between Archaea and Bacteria) and LGT from prokaryotes to eukaryotes (Figure 4.5). The 2Fe-2S subtype 31 and 2[4Fe-4S] subtype 8, 10 and 15 were found common between *Alphaproteobacteria* and Archaea and 2[4Fe-4S] subtype 17 was found common between *Alphaproteobacteria* and Eukaryota indicating the LGT.

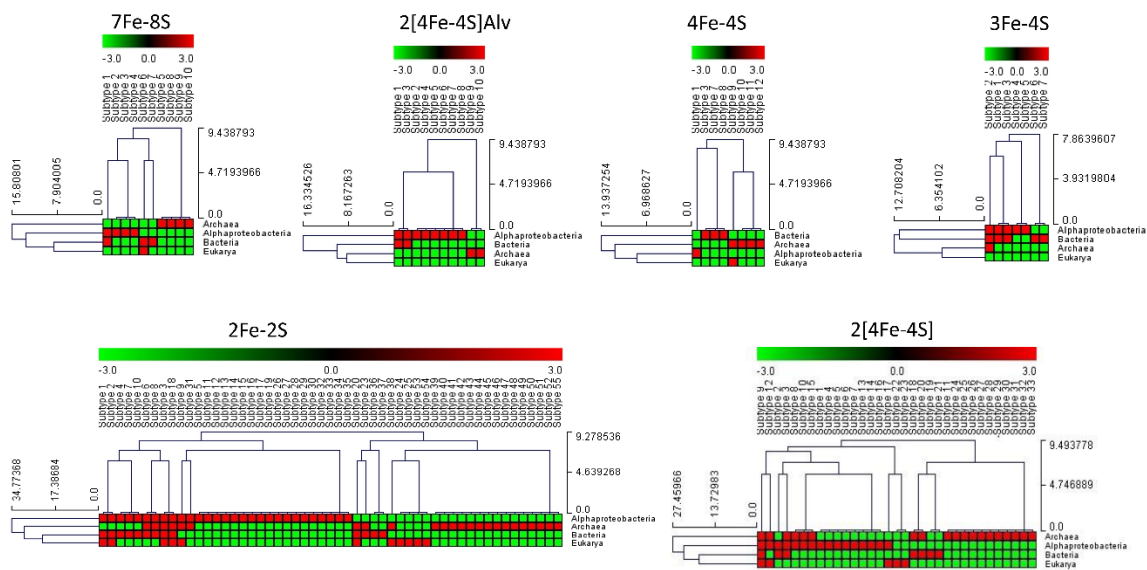


Figure 4. 5. Heat map figure representing the presence (red) and absence (green) of ferredoxin subtypes in Archaea, Bacteria and Eukarya. Ferredoxin subtypes form the vertical axis and domains of life form the horizontal axis

CHAPTER 5: CONCLUSIONS AND FUTURE PERSPECTIVES

Cytochrome P450 monooxygenases (CYPs/P450s) have been well-known proteins for the last six decades. The stereo- and regio-specific oxidation of a variety of compounds by these enzymes led to their applications in quite large areas of biological research. Understanding the evolution of P450s in the bacterial population is now gaining momentum owing to the availability of a large number of bacterial genomes. This study is the first of its kind on the analysis of P450s in an ancient group of bacteria belonging to the class *Alphaproteobacteria*. Comparative analysis of P450s between different bacterial species revealed that, during speciation, a large number of P450s became part of secondary metabolite gene clusters (as observed in *Streptomyces* species and mycobacterial species) and some P450s were passed all the way from *Alphaproteobacteria* to other bacterial species. This study also reports the first identification of CYP125 P450 in alphaproteobacterial species and predicts that *P. zucineum* is capable of utilizing the cholesterol side-chain as carbon source. Future studies should include thorough profiling of cholesterol-degrading genes/proteins and experimental validation of cholesterol degrading ability. Furthermore, comparative analysis of alphaproteobacterial species and more bacterial species should be carried out to deduce the evolution pattern of P450 families and to identify the loss/gain of new P450 families compared to *Alphaproteobacteria* with respect to habitat or geographical distribution. The results of this study will serve as reference for future genome data mining and annotation of P450s in species of *Alphaproteobacteria*.

Ferredoxins, iron-sulfur (Fe-S) cluster proteins are ubiquitously present in all domains of life due to their involvement in fundamental metabolic processes. It is well-known that ferredoxins transfer electrons to P450s. However, to date, genome wide-analysis of ferredoxins in alphaproteobacterial species is not reported. Thus, this study aimed to address this research gap. The study revealed the presence of all six different Fe-S cluster type ferredoxins in alphaproteobacterial species. In order to understand the diversity of ferredoxins within a cluster type and lateral gene transfer (LGT) of ferredoxins among different domains of life for the first time, subtype classification of ferredoxins is proposed based on the amino acid spacing pattern between the cysteine amino acids of the Fe-S cluster binding motif as a subtype signature. The study revealed a high diversity of ferredoxins within a cluster in alphaproteobacterial species. Some ferredoxins were found to have a common ancestral origin as they are found in Archaea and LGT of ferredoxins from prokaryotes (Archaea/Bacteria) to eukaryotes. Work is in progress on comprehensive analysis of ferredoxins from other bacterial, archaeal and

eukaryotic species for better understanding of the evolution of ferredoxins across the domains of life and also to deduce the definitive characteristic signatures for ferredoxin subtypes.

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Annexure A

Table S1. Information on Alphaproteobacterial species and their respective genera used in the study. Species abbreviations, their genome IDs (GenBank) and presence or absence of P450s in different species were also presented in the table.

Genus	Total no. of species	Species have P450s	Species don't have P450s	Species code	Species name	Genome IDs
<i>Rickettsia</i>	47	0	47	rpr	<i>Rickettsia prowazekii</i> Madrid E	AJ235269
				rpo	<i>Rickettsia prowazekii</i> BuV67-CWPP	CP003393
				rpw	<i>Rickettsia prowazekii</i> Chernikova	CP003391
				rpz	<i>Rickettsia prowazekii</i> Dachau	CP003394
				rpg	<i>Rickettsia prowazekii</i> GvV257	CP003395
				rps	<i>Rickettsia prowazekii</i> Katsinyian	CP003392
				rpv	<i>Rickettsia prowazekii</i> RpGvF24	CP003396
				rpq	<i>Rickettsia prowazekii</i> Rp22	CP001584
				rpl	<i>Rickettsia prowazekii</i> Breinl	CP004889
				rpn	<i>Rickettsia prowazekii</i> NMRC Madrid E	CP004888
				rty	<i>Rickettsia typhi</i> Wilmington	AE017197
				rtt	<i>Rickettsia typhi</i> TH1527	CP003397
				rtb	<i>Rickettsia typhi</i> B9991CWPP	CP003398
				rcm	<i>Rickettsia canadensis</i> McKiel	CP000409
				rcc	<i>Rickettsia canadensis</i> CA410	CP003304
				rbe	<i>Rickettsia bellii</i> RML369-C	CP000087

				rbo	<i>Rickettsia bellii</i> OSU 85-389	CP000849
				rco	<i>Rickettsia conorii</i>	AE006914
				rfe	<i>Rickettsia felis</i>	CP000054
				rak	<i>Rickettsia akari</i>	CP000847
				rri	<i>Rickettsia rickettsii</i> Sheila Smith	CP000848
				rrj	<i>Rickettsia rickettsii</i> Iowa	CP000766
				rra	<i>Rickettsia rickettsii</i> Arizona	CP003307
				rrc	<i>Rickettsia rickettsii</i> Colombia	CP003306
				rrh	<i>Rickettsia rickettsii</i> Hauke	CP003318
				rrb	<i>Rickettsia rickettsii</i> Brazil	CP003305
				rrn	<i>Rickettsia rickettsii</i> Hino	CP003309
				rrp	<i>Rickettsia rickettsii</i> Hlp#2	CP003311
				rrm	<i>Rickettsia rickettsii</i> Morgan	CP006010
				rrr	<i>Rickettsia rickettsii</i> R	CP006009
				rms	<i>Rickettsia massiliae</i> MTU5	CP000684
				rmi	<i>Rickettsia massiliae</i> AZT80	CP003319
				rpk	<i>Rickettsia peacockii</i>	CP001227
				raf	<i>Rickettsia africae</i>	CP001612
				rhe	<i>Rickettsia heilongjiangensis</i>	CP002912
				rja	<i>Rickettsia japonica</i>	AP011533
				rsv	<i>Rickettsia slovaca</i> 13-B	CP002428
				rsw	<i>Rickettsia slovaca</i> D-CWPP	CP003375
				rph	<i>Rickettsia philipii</i>	CP003308
				rau	<i>Rickettsia australis</i>	CP003338
				rmo	<i>Rickettsia montanensis</i>	CP003340

				rpp	<i>Rickettsia parkeri</i>	CP003341
				rre	<i>Rickettsia rhipicephali</i>	CP003342
				ram	<i>Rickettsia amblyommatis</i> GAT-30V	CP003334
				rab	<i>Rickettsia amblyommatis</i> Ac37	CP012420
				rmc	<i>Rickettsia monacensis</i>	LN794217
				ric	<i>Rickettsia</i> sp. MEAM1 (<i>Bemisia tabaci</i>)	CP016305
<i>Orientia</i>	2	0	2	ots	<i>Orientia tsutsugamushi</i> Boryong	AM494475
				ott	<i>Orientia tsutsugamushi</i> Ikeda	AP008981
<i>Phycorickettsia</i>	1	0	1	ptc	<i>Candidatus Phycorickettsia trachydisci</i>	CP027845
<i>Wolbachia</i>	10	0	10	wol	<i>Wolbachia</i> wMel (<i>Drosophila melanogaster</i>)	AE017196
				wri	<i>Wolbachia</i> wRi (<i>Drosophila simulans</i>)	CP001391
				wen	<i>Wolbachia</i> wHa (<i>Drosophila simulans</i>)	CP003884
				wed	<i>Wolbachia</i> wNo (<i>Drosophila simulans</i>)	CP003883
				wpi	<i>Wolbachia</i> wPip (<i>Culex quinquefasciatus</i>)	AM999887
				wbm	<i>Wolbachia</i> wBm (<i>Brugia malayi</i>)	AE017321
				woo	<i>Wolbachia</i> wOo (<i>Onchocerca ochengi</i>)	HE660029
				wcl	<i>Wolbachia</i> wCle (<i>Cimex lectularius</i>)	AP013028

				weo	<i>Wolbachia wFol (Folsomia candida)</i>	CP015510
				wpp	<i>Wolbachia pipientis</i>	CP031221
<i>Anaplasma</i>	10	0	10	ama	<i>Anaplasma marginale St. Maries</i>	CP000030
				amf	<i>Anaplasma marginale Florida</i>	CP001079
				amw	<i>Anaplasma marginale Dawn</i>	CP006847
				amp	<i>Anaplasma marginale Gypsy Plains</i>	CP006846
				acn	<i>Anaplasma centrale</i>	CP001759
				aph	<i>Anaplasma phagocytophilum HZ</i>	CP000235
				apy	<i>Anaplasma phagocytophilum HZ2</i>	CP006616
				apd	<i>Anaplasma phagocytophilum Dog2</i>	CP006618
				apha	<i>Anaplasma phagocytophilum JM</i>	CP006617
				aoh	<i>Anaplasma ovis</i>	CP015994
<i>Ehrlichia</i>	14	0	14	eru	<i>Ehrlichia ruminantium</i> <i>Welgevonden (South Africa)</i>	CR767821
				erw	<i>Ehrlichia ruminantium</i> <i>Welgevonden (France)</i>	CR925678
				erg	<i>Ehrlichia ruminantium Gardel</i>	CR925677
				ecn	<i>Ehrlichia canis</i>	CP000107
				ech	<i>Ehrlichia chaffeensis Arkansas</i>	CP000236
				echa	<i>Ehrlichia chaffeensis Heartland</i>	CP007473
				echj	<i>Ehrlichia chaffeensis Jax</i>	CP007475
				echl	<i>Ehrlichia chaffeensis Liberty</i>	CP007476
				echs	<i>Ehrlichia chaffeensis Osceola</i>	CP007477
				echv	<i>Ehrlichia chaffeensis Saint Vincent</i>	CP007478
				echw	<i>Ehrlichia chaffeensis Wakulla</i>	CP007479

				echp	<i>Ehrlichia chaffeensis</i> West Paces	CP007480
				emr	<i>Ehrlichia muris</i>	CP006917
				ehh	<i>Ehrlichia</i> sp. HF	CP007474
<i>Neorickettsia</i>	3	0	3	nse	<i>Neorickettsia sennetsu</i>	CP000237
				nri	<i>Neorickettsia risticii</i>	CP001431
				nhm	<i>Neorickettsia helminthoeca</i>	CP007481
<i>Midichloria</i>	1	0	1	mmn	<i>Candidatus Midichloria mitochondrii</i>	CP002130
<i>Fokinia</i>	1	0	1	fso	<i>Candidatus Fokinia solitaria</i>	CP025989
<i>Unclassified rickettiales</i>	2	0	2	rbt	<i>Rickettsiales bacterium</i> Ac37b	CP009217
				ren	<i>Rickettsiales endosymbiont of Stachyamoeba lipophora</i>	CP033611
<i>Paracaedibacter</i>	1	0	1	paca	<i>Candidatus Paracaedibacter acanthamoebae</i>	CP008941
<i>Paracaedimonas</i>	1	0	1	caq	<i>Candidatus Paracaedimonas acanthamoebae</i>	CP008936
<i>Nucleicultrix</i>	1	0	1	naf	<i>Candidatus Nucleicultrix amoebiphila</i>	CP008743
<i>Unclassified Holosporaceae</i>	1	0	1	ea	<i>Endosymbiont of Acanthamoeba</i> sp. UWC8	CP004403
<i>Mesorhizobium</i>	8	7	1	mlo	<i>Mesorhizobium japonicum</i> MAFF 303099	BA000012
				mln	<i>Mesorhizobium loti</i> NZP2037	CP016079

				mci	<i>Mesorhizobium ciceri</i> (biovar <i>Biserrulae</i>)	CP002447
				mop	<i>Mesorhizobium opportunistum</i>	CP002279
				mam	<i>Mesorhizobium australicum</i>	CP003358
				mamo	<i>Mesorhizobium amorphae</i>	CP015318
				meso	<i>Mesorhizobium sp. B7</i>	CP018171
				mesw	<i>Mesorhizobium sp. WSM1497</i>	CP021070
<i>Chelativorans</i>	1	1	0	mes	<i>Chelativorans sp. BNC1</i>	CP000390
<i>Hoeflea</i>	1	1	0	hoe	<i>Hoeflea sp. IMCC20628</i>	CP011479
<i>Aminobacter</i>	2	1	1	aak	<i>Aminobacter aminovorans</i>	CP015005
				amih	<i>Aminobacter sp. MSH1</i>	CP026265
<i>Phyllobacterium</i>	1	0	1	pht	<i>Phyllobacterium zundukense</i>	CP017940
<i>Parvibaculum</i>	1	1	0	pla	<i>Parvibaculum lavamentivorans</i>	CP000774
<i>Unclassified Rhodobiaceae</i>	1	0	1	rbs	<i>Rhodobiaceae bacterium SMS8</i>	CP030277
<i>Sinorhizobium</i>	15	14	1	sme	<i>Sinorhizobium meliloti 1021</i>	AL591688
				smk	<i>Sinorhizobium meliloti AK83</i>	CP002781, CP002782, CP002783
				smq	<i>Sinorhizobium meliloti BL225C</i>	CP002740
				smx	<i>Sinorhizobium meliloti SM11</i>	CP001830
				smi	<i>Sinorhizobium meliloti Rm41</i>	HE995405
				smeg	<i>Sinorhizobium meliloti GR4</i>	CP003933
				smel	<i>Sinorhizobium meliloti 2011</i>	CP004140
				smer	<i>Sinorhizobium meliloti RMO17</i>	CP009144
				smd	<i>Sinorhizobium medicae</i>	CP000738

				rhi	<i>Sinorhizobium fredii</i> NGR234	CP001389
				sfh	<i>Sinorhizobium fredii</i> HH103	HE616890
				sfd	<i>Sinorhizobium fredii</i> USDA 257	CP003563
				six	<i>Sinorhizobium</i> sp. RAC02	CP016450
				same	<i>Sinorhizobium americanum</i>	CP013107
				sino	<i>Sinorhizobium</i> sp. CCBAU 05631	CP023063
<i>Ensifer</i>	3	2	1	ead	<i>Ensifer adhaerens</i> OV14	CP007236, CP007237
				eah	<i>Ensifer adhaerens</i> Casida A	CP015880
				esj	<i>Ensifer sojae</i>	CP023067
<i>Agrobacterium</i>	8	8	0	atu	<i>Agrobacterium fabrum</i>	AE007869 (circ), AE007870 (lin)
				ara	<i>Agrobacterium radiobacter</i>	CP000628, CP000629
				atf	<i>Agrobacterium tumefaciens</i> Ach5	CP011246 (circ), CP011247 (lin)
				ata	<i>Agrobacterium tumefaciens</i> S33	CP014259 (circ), CP014260 (lin)
				avi	<i>Agrobacterium vitis</i>	CP000633, CP000634
				agr	<i>Agrobacterium</i> sp. H13-3	CP002248 (circ), CP002249 (lin)
				agc	<i>Agrobacterium</i> sp. RAC06	CP016499
				aro	<i>Agrobacterium rhizogenes</i>	CP019701, CP019702
<i>Rhizobium</i>	21	18	3	ret	<i>Rhizobium etli</i> CFN 42	CP000133
				rec	<i>Rhizobium etli</i> CIAT 652	CP001074
				rel	<i>Rhizobium etli</i> bv. <i>mimosae</i> Mim1	CP005950
				rep	<i>Rhizobium etli</i> bv. <i>phaseoli</i> IE4803	CP007641

				rei	<i>Rhizobium</i> sp. IE4771	CP006986
				rle	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841	AM236080
				rlt	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304	CP001191
				rlg	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325	CP001622
				rlb	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1689	CP007045
				rlu	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> CB782	CP007067
				rtr	<i>Rhizobium tropici</i>	CP004015
				rir	<i>Rhizobium</i> sp. IRBG74	HG518322
				rhl	<i>Rhizobium favelukesii</i>	HG916852
				rga	<i>Rhizobium gallicum</i>	CP006877
				rhn	<i>Rhizobium</i> sp. N1341	CP013505
				rpha	<i>Rhizobium phaseoli</i>	CP013580
				rht	<i>Rhizobium</i> sp. NT-26	FO082820
				rhx	<i>Rhizobium</i> sp. N731	CP013601
				rhv	<i>Rhizobium</i> sp. S41	CP016320, CP016433
				rhk	<i>Rhizobium</i> sp. Kim5	CP021124
				rez	<i>Rhizobium esperanzae</i>	CP013500
<i>Neorhizobium</i>	4	2	2	ngl	<i>Neorhizobium galegae</i> bv. <i>officinalis</i> bv. <i>officinalis</i> HAMBI 1141	HG938355

				ngg	<i>Neorhizobium galegae</i> bv. <i>orientalis</i> HAMBI 540	HG938353
				neo	<i>Neorhizobium</i> sp. SOG26	CP025512
				nen	<i>Neorhizobium</i> sp. NCHU2750	CP030827
<i>Liberibacter</i>	7	1	6	las	<i>Candidatus Liberibacter asiaticus</i> psy62	CP001677
				laa	<i>Candidatus Liberibacter asiaticus</i> gxpsy	CP004005
				lat	<i>Candidatus Liberibacter asiaticus</i> Ishi-1	AP014595
				lso	<i>Candidatus Liberibacter</i> <i>solanacearum</i>	CP002371
				lcc	<i>Liberibacter crescens</i>	CP003789
				lar	<i>Candidatus Liberibacter americanus</i>	CP006604
				lau	<i>Candidatus Liberibacter africanus</i>	CP004021
<i>Shinella</i>	1	1	0	shz	<i>Shinella</i> sp. HZN7	CP015736
<i>Brucella</i>	43	30	13	bme	<i>Brucella melitensis</i> bv. 1 16M	AE008917, AE008918
				bmel	<i>Brucella melitensis</i> bv. 1 16M	CP007763, CP007762
				bmi	<i>Brucella melitensis</i> ATCC 23457	CP001488, CP001489
				bmz	<i>Brucella melitensis</i> M28	CP002459, CP002460
				bmj	<i>Brucella melitensis</i> M5-90	CP001851, CP001852
				bmw	<i>Brucella melitensis</i> NI	CP002931, CP002932
				bmee	<i>Brucella melitensis</i> bv. 3 Ether	CP007760, CP007761
				bmf	<i>Brucella abortus</i> 2308	AM040264, AM040265
				bmb	<i>Brucella abortus</i> bv. 1 9-941	AE017223, AE017224

				bmc	<i>Brucella abortus</i> S19	CP000887, CP000888
				baa	<i>Brucella abortus</i> A13334	CP003176, CP003177
				babo	<i>Brucella abortus</i> bv. 2 86/8/59	CP007765, CP007764
				babr	<i>Brucella abortus</i> bv. 6 870	CP007709, CP007710
				babt	<i>Brucella abortus</i> 63 75	CP007663, CP007662
				babb	<i>Brucella abortus</i> BDW	CP007681, CP007680
				babu	<i>Brucella abortus</i> bv. 9 C68	CP007705, CP007706
				babs	<i>Brucella abortus</i> BER	CP007682, CP007683
				babc	<i>Brucella abortus</i> NCTC 10505	CP007700, CP007701
				bms	<i>Brucella suis</i> 1330	AE014291, AE014292
				bsi	<i>Brucella suis</i> 1330	CP002997, CP002998
				bsf	<i>Brucella suis</i> bv. 1	CP006961, CP006962
				bsui	<i>Brucella suis</i> bv. 2 Bs143CITA	CP007695, CP007696
				bsup	<i>Brucella suis</i> bv. 2 PT09143	CP007691, CP007692
				bsuv	<i>Brucella suis</i> bv. 2 PT09172	CP007693, CP007694
				bsuc	<i>Brucella suis</i> bv. 2 Bs364CITA	CP007697, CP007698
				bmt	<i>Brucella suis</i> ATCC 23445	CP000911, CP000912
				bsz	<i>Brucella suis</i> bv. 3	CP007719, CP007718
				bsv	<i>Brucella suis</i> VBI22	CP003128, CP003129
				bsw	<i>Brucella suis</i> ZW043	CP009094, CP009095
				bsg	<i>Brucella suis</i> ZW046	CP009096, CP009097
				bov	<i>Brucella ovis</i>	CP000708, CP000709
				bcs	<i>Brucella canis</i> ATCC 23365	CP000872, CP000873
				bsk	<i>Brucella canis</i> HSK A52141	CP003174, CP003175
				bol	<i>Brucella canis</i> Oliveri	HG803175, HG803176

				bcar	<i>Brucella canis</i> RM6/66	CP007758, CP007759
				bcas	<i>Brucella canis</i> SVA13	CP007629, CP007630
				bmr	<i>Brucella microti</i>	CP001578, CP001579
				bpp	<i>Brucella pinnipedialis</i> B2/94	CP002078, CP002079
				bpv	<i>Brucella pinnipedialis</i> 6/566	CP007743, CP007742
				bcet	<i>Brucella ceti</i> TE10759-12	CP006896, CP006897
				bcee	<i>Brucella ceti</i> TE28753-12	CP006898, CP006899
				bvl	<i>Brucella vulpis</i>	LN997863, LN997864
				bru	<i>Brucella</i> sp. 2002734562	CP016979, CP016980
<i>Ochrobactrum</i>	4	3	1	oan	<i>Ochrobactrum anthropi</i> ATCC 49188	CP000758, CP000759
				oah	<i>Ochrobactrum anthropi</i> OAB	CP008820, CP008819
				ops	<i>Ochrobactrum pseudogrignonense</i>	CP015775, CP015776
				och	<i>Ochrobactrum</i> sp. A44	CP022604, CP022603
<i>Bradyrhizobium</i>	14	10	4	bja	<i>Bradyrhizobium diazoefficiens</i> USDA 110	BA000040
				bju	<i>Bradyrhizobium japonicum</i> USDA 6	AP012206
				bjp	<i>Bradyrhizobium japonicum</i> E109	CP010313
				bra	<i>Bradyrhizobium</i> sp. ORS 278	CU234118
				bbt	<i>Bradyrhizobium</i> sp. BTAi1	CP000494
				brs	<i>Bradyrhizobium</i> sp. S23321	AP012279
				aol	<i>Bradyrhizobium oligotrophicum</i>	AP012603
				brc	<i>Bradyrhizobium</i> sp. CCGE-LA001	CP013949
				brad	<i>Bradyrhizobium</i> sp. BF49	LN901633

				bic	<i>Bradyrhizobium icense</i>	CP016428
				bro	<i>Bradyrhizobium</i> sp. ORS 285	LT859959
				brk	<i>Bradyrhizobium</i> sp. SK17	CP025113
				bot	<i>Bradyrhizobium ottawaense</i>	CP029425
				brq	<i>Bradyrhizobium</i> sp. 2 39S1MB	CP029426
<i>Rhodopseudomonas</i>	7	7	0	rpa	<i>Rhodopseudomonas palustris</i> CGA009	BX571963
				rpb	<i>Rhodopseudomonas palustris</i> HaA2	CP000250
				rpc	<i>Rhodopseudomonas palustris</i> BisB18	CP000301
				rpd	<i>Rhodopseudomonas palustris</i> BisB5	CP000283
				rpe	<i>Rhodopseudomonas palustris</i> BisA53	CP000463
				rpt	<i>Rhodopseudomonas palustris</i> TIE-1	CP001096
				rpx	<i>Rhodopseudomonas palustris</i> DX-1	CP002418
<i>Nitrobacter</i>	2	2	0	nwi	<i>Nitrobacter winogradskyi</i>	CP000115
				nha	<i>Nitrobacter hamburgensis</i>	CP000319
<i>Oligotropha</i>	3	0	3	oca	<i>Oligotropha carboxidovorans</i> OM5 (Mississippi)	CP001196
				ocg	<i>Oligotropha carboxidovorans</i> OM5 (Goettingen)	CP002826
				oco	<i>Oligotropha carboxidovorans</i> OM4	CP002821
<i>Bosea</i>	4	2	2	bop	<i>Bosea</i> sp. PAMC 26642	CP014301
				bos	<i>Bosea</i> sp. RAC05	CP016464
				bvv	<i>Bosea vaviloviae</i>	CP017147

				boi	<i>Bosea sp. Tri-49</i>	CP017946
<i>Variibacter</i>	1	0	1	vgo	<i>Variibacter gotjawalensis</i>	AP014946
<i>Bartonella</i>	20	0	20	bhe	<i>Bartonella henselae</i> Houston-1	BX897699
				bhn	<i>Bartonella henselae</i> BM1374163	HG965802
				bhs	<i>Bartonella henselae</i> BM1374165	HG969191
				bqu	<i>Bartonella quintana</i> Toulouse	BX897700
				bqr	<i>Bartonella quintana</i> RM-11	CP003784
				bbk	<i>Bartonella bacilliformis</i>	CP000524
				btr	<i>Bartonella tribocorum</i> CIP 105476	AM260525
				btx	<i>Bartonella tribocorum</i> BM1374166	HG969192
				bgr	<i>Bartonella grahamii</i>	CP001562
				bcd	<i>Bartonella clarridgeiae</i>	FN645454
				baus	<i>Bartonella australis</i>	CP003123
				bvn	<i>Bartonella vinsonii</i>	CP003124
				banc	<i>Bartonella ancashensis</i>	CP010401
				bapi	<i>Bartonella apis</i>	CP015625
				bart	<i>Bartonella sp.</i> JB15	CP019787
				bara	<i>Bartonella sp.</i> A1379B	CP019780
				barw	<i>Bartonella sp.</i> WD16.2	CP019781
				barr	<i>Bartonella sp.</i> Raccoon60	CP019786
				baro	<i>Bartonella sp.</i> 1-1C	CP019489
				barj	<i>Bartonella sp.</i> JB63	CP019788
<i>Xanthobacter</i>	1	1	0	xau	<i>Xanthobacter autotrophicus</i>	CP000781
<i>Azorhizobium</i>	1	1	0	azc	<i>Azorhizobium caulinodans</i>	AP009384
<i>Starkeya</i>	1	0	1	sno	<i>Starkeya novella</i>	CP002026

<i>Methylobacterium</i>	6	5	1	mex	<i>Methylobacterium extorquens</i> PA1	CP000908
				mea	<i>Methylobacterium extorquens</i> AM1	CP001510
				mdi	<i>Methylobacterium extorquens</i> DM4	FP103042
				mch	<i>Methylobacterium extorquens</i> CM4	CP001298
				mpo	<i>Methylobacterium populi</i>	CP001029
				mza	<i>Methylobacterium zatmanii</i>	CP021054
<i>Methylobacterium</i>	11	6	5	mrd	<i>Methylobacterium radiotolerans</i>	CP001001
				met	<i>Methylobacterium</i> sp. 4-46	CP000943
				mno	<i>Methylobacterium nodulans</i>	CP001349
				mor	<i>Methylobacterium oryzae</i>	CP003811
				meta	<i>Methylobacterium</i> sp. AMS5	CP006992
				maqu	<i>Methylobacterium aquaticum</i>	AP014704
				mphy	<i>Methylobacterium phyllosphaerae</i>	CP015367
				mee	<i>Methylobacterium currus</i>	CP028843, CP028844
				metd	<i>Methylobacterium</i> sp. DM1	CP029173
				metx	<i>Methylobacterium</i> sp. XJLW	CP016429
				mets	<i>Methylobacterium</i> sp. 17SD2-17	CP029550
<i>Microvirga</i>	2	0	2	moc	<i>Microvirga ossetica</i>	CP016616
				miv	<i>Microvirga</i> sp. 17 mud 1-3	CP029481
<i>Beijerinckia</i>	1	1	0	bid	<i>Beijerinckia indica</i>	CP001016
<i>Methylocella</i>	1	1	0	msl	<i>Methylocella silvestris</i>	CP001280
<i>Chelatococcus</i>	2	0	2	chel	<i>Chelatococcus</i> sp. CO-6	CP012398
				cdq	<i>Chelatococcus daeguensis</i>	CP018095
<i>Hyphomicrobium</i>	4	4	0	hdn	<i>Hyphomicrobium denitrificans</i> ATCC 51888	CP002083

				hdt	<i>Hyphomicrobium denitrificans</i> 1NES1	CP005587
				hmc	<i>Hyphomicrobium</i> sp. MC1	FQ859181
				hni	<i>Hyphomicrobium nitrativorans</i>	CP006912
<i>Rhodomicrobium</i>	1	0	1	rva	<i>Rhodomicrobium vannielii</i>	CP002292
<i>Pelagibacterium</i>	1	1	0	phl	<i>Pelagibacterium halotolerans</i>	CP003075
<i>Filomicrobium</i>	2	2	0	fil	<i>Candidatus Filomicrobium</i> <i>marinum</i> W	LN829118
				fiy	<i>Candidatus Filomicrobium</i> <i>marinum</i> Y	LN829119
<i>Devosia</i>	2	1	1	deq	<i>Devosia</i> sp. H5989	CP011300
				dei	<i>Devosia</i> sp. I507	CP026747
<i>Blastochloris</i>	2	0	2	bvr	<i>Blastochloris viridis</i>	CP012946
				blag	<i>Blastochloris</i> sp. GI	AP018907
<i>Rhodoplanes</i>	1	1	0	rhz	<i>Rhodoplanes</i> sp. Z2-YC6860	CP007440
<i>Maritalea</i>	1	0	1	mmyr	<i>Maritalea myrionectae</i>	CP021330
<i>Methylocystis</i>	3	2	1	msc	<i>Methylocystis</i> sp. SC2	HE956757
				mbry	<i>Methylocystis bryophila</i>	CP019948
				mros	<i>Methylocystis rosea</i>	CP034086
<i>Methylosinus</i>	1	0	1	mtw	<i>Methylosinus trichosporium</i>	CP023737
<i>Pleomorphomonas</i>	1	0	1	pleo	<i>Pleomorphomonas</i> sp. SM30	AP017626
<i>Martelella</i>	3	1	2	mey	<i>Martelella endophytica</i>	CP010803
				maad	<i>Martelella</i> sp. AD-3	CP014275
				mmed	<i>Martelella mediterranea</i>	CP020330
<i>Aureimonas</i>	1	0	1	aua	<i>Aureimonas</i> sp. AU20	CP006367

<i>Breoghanian</i>	1	0	1	brn	<i>Breoghanian</i> sp. L-A4	CP031841
<i>Hodgkinia</i>	4	0	4	hci	<i>Candidatus Hodgkinia cicadicola</i> <i>Dsem</i>	CP001226
				hct	<i>Candidatus Hodgkinia cicadicola</i> <i>TETULN</i>	CP008699
				hcc	<i>Candidatus Hodgkinia cicadicola</i> <i>TETUND1</i>	CP007232
				hcd	<i>Candidatus Hodgkinia cicadicola</i> <i>TETUND2</i>	CP007233
<i>Methyloceanibacter</i>	1	1	0	mcg	<i>Methyloceanibacter caenitepidi</i>	AP014648
<i>Tokpelaia</i>	1	0	1	thd	<i>Candidatus Tokpelaia hoelldoblerii</i>	CP017315
<i>Pseudorhodoplane</i> <i>s</i>	1	1	0	psin	<i>Pseudorhodoplanes sinuspersici</i>	CP021112
<i>Hartmannibacter</i>	1	0	1	hdi	<i>Hartmannibacter diazotrophicus</i>	LT960614
<i>Unclassified</i> <i>Rhizobiales</i>	1	0	1	rbm	<i>Rhizobiales bacterium</i> NRL2	CP016093
<i>Caulobacter</i>	7	4	3	ccr	<i>Caulobacter vibrioides</i> CB15	AE005673
				ccs	<i>Caulobacter vibrioides</i> NA1000	CP001340
				cak	<i>Caulobacter</i> sp. K31	CP000927
				cse	<i>Caulobacter segnis</i>	CP002008
				chq	<i>Caulobacter henricii</i>	CP013002
				cmb	<i>Caulobacter mirabilis</i>	CP024201
				cfh	<i>Caulobacter flavus</i>	CP026100
<i>Phenylobacterium</i>	2	1	1	pzu	<i>Phenylobacterium zucineum</i>	CP000747

				phb	<i>Phenylobacterium</i> sp. HYN0004	CP029479
<i>Brevundimonas</i>	7	0	7	bsb	<i>Brevundimonas subvibrioides</i>	CP002102
				brd	<i>Brevundimonas</i> sp. DS20	CP012897
				bne	<i>Brevundimonas naejangsanensis</i>	CP015614
				brg	<i>Brevundimonas</i> sp. GW460-12-10-14-LB2	CP015511
				brl	<i>Brevundimonas</i> sp. LM2	CP019508
				bvc	<i>Brevundimonas vesicularis</i>	CP022048
				bdm	<i>Brevundimonas diminuta</i>	CP035093
<i>Asticcacaulis</i>	1	1	0	aex	<i>Asticcacaulis excentricus</i>	CP002395, CP002396
Unclassified <i>Caulobacteraceae</i>	1	0	1	cbot	<i>Caulobacteraceae</i> bacterium OTSz_A_272	CP013244
<i>Ruegeria</i>	4	2	2	sil	<i>Ruegeria pomeroyi</i>	CP000031
				sit	<i>Ruegeria</i> sp. TM1040	CP000377
				rue	<i>Ruegeria</i> sp. NKC1-1	CP031092
				rua	<i>Ruegeria</i> sp. AD91A	CP031946
<i>Epibacterium</i>	1	0	1	rmb	<i>Epibacterium mobile</i>	CP015230
<i>Rhodobacter</i>	7	5	2	rsp	<i>Rhodobacter sphaeroides</i> 2.4.1	CP000143, CP000144
				rsh	<i>Rhodobacter sphaeroides</i> ATCC 17029	CP000577, CP000578
				rsq	<i>Rhodobacter sphaeroides</i> ATCC 17025	CP000661
				rsk	<i>Rhodobacter sphaeroides</i> KD131	CP001150, CP001151
				rcp	<i>Rhodobacter capsulatus</i>	CP001312
				rhp	<i>Rhodobacter</i> sp. LPB0142	CP017781

				rbl	<i>Rhodobacter blasticus</i>	CP020470
<i>Jannaschia</i>	1	1	0	jan	<i>Jannaschia</i> sp. CCS1	CP000264
<i>Roseobacter</i>	2	2	0	rde	<i>Roseobacter denitrificans</i>	CP000362
				rli	<i>Roseobacter litoralis</i>	CP002623
<i>Paracoccus</i>	10	3	7	pde	<i>Paracoccus denitrificans</i>	CP000489, CP000490
				pami	<i>Paracoccus aminophilus</i>	CP006650
				pye	<i>Paracoccus yeei</i>	CP020442
				pcon	<i>Paracoccus contaminans</i>	CP020612
				pzh	<i>Paracoccus zhejiangensis</i>	CP025430
				paro	<i>Paracoccus</i> sp. BM15	CP025408
				paru	<i>Paracoccus</i> sp. CBA4604	CP025583
				pamn	<i>Paracoccus aminovorans</i>	LN832559
				pmut	<i>Paracoccus mutanoliticus</i>	CP030239
				pars	<i>Paracoccus</i> sp. SC2-6	CP030918
<i>Dinoroseobacter</i>	1	1	0	dsh	<i>Dinoroseobacter shibae</i>	CP000830
<i>Ketogulonicigenium</i>	3	3	0	kvu	<i>Ketogulonicigenium vulgare</i> Y25	CP002224
<i>m</i>				kvl	<i>Ketogulonicigenium vulgare</i> WSH-001	CP002018
				kro	<i>Ketogulonicigenium robustum</i>	CP019937
<i>Pseudovibrio</i>	1	1	0	psf	<i>Pseudovibrio</i> sp. FO-BEG1	CP003147
<i>Phaeobacter</i>	6	4	2	pga	<i>Phaeobacter inhibens</i> DSM 17395	CP002976
				pgl	<i>Phaeobacter inhibens</i> 2.10	CP002972
				pgd	<i>Phaeobacter gallaeciensis</i> DSM 26640	CP006966

				php	<i>Phaeobacter porticola</i>	CP016364
				ppic	<i>Phaeobacter piscinae</i>	CP010681
				phq	<i>Phaeobacter</i> sp. LSS9	CP031956
<i>Octadecabacter</i>	3	2	1	oat	<i>Octadecabacter antarcticus</i>	CP003740
				oar	<i>Octadecabacter arcticus</i>	CP003742
				otm	<i>Octadecabacter temperatus</i>	CP012160
<i>Leisingera</i>	2	1	1	lmd	<i>Leisingera methylohalidivorans</i>	CP006773
				lej	<i>Leisingera</i> sp. NJS204	CP035417
<i>Roseibacterium</i>	1	1	0	red	<i>Roseibacterium elongatum</i>	CP004372
<i>Planktomarina</i>	1	1	0	ptp	<i>Planktomarina temperata</i>	CP003984
<i>Celeribacter</i>	4	2	2	cid	<i>Celeribacter indicus</i>	CP004393
				cmar	<i>Celeribacter marinus</i>	CP012023
				ceh	<i>Celeribacter ethanolicus</i>	CP022196
				cmag	<i>Celeribacter manganoxidans</i>	CP021404
<i>Marinovum</i>	1	1	0	malg	<i>Marinovum algicola</i>	CP010855
<i>Confluentimicrobi um</i>	1	1	0	con	<i>Confluentimicrobium</i> sp. EMB200- NS6	CP010869
<i>Rhodovulum</i>	3	2	1	rsu	<i>Rhodovulum sulfidophilum</i>	AP014800
				rhv	<i>Rhodovulum</i> sp. MB263	CP020384
				rhc	<i>Rhodovulum</i> sp. P5	CP015039
<i>Pannonibacter</i>	1	1	0	pphr	<i>Pannonibacter phragmitetus</i>	CP013068
<i>Halocynthiibacter</i>	1	0	1	hat	<i>Halocynthiibacter arcticus</i>	CP014327
<i>Labrenzia</i>	3	2	1	lap	<i>Labrenzia</i> sp. CP4	CP011927
				lagg	<i>Labrenzia aggregata</i>	CP019630
				labr	<i>Labrenzia</i> sp. VG12	CP022529

<i>Defluviimonas</i>	1	1	0	daa	<i>Defluviimonas alba</i>	CP012661
<i>Yangia</i>	2	1	1	yan	<i>Yangia</i> sp. CCB-MM3	CP014595, CP014596
				ypac	<i>Yangia pacifica</i>	CP022189, CP022190
<i>Sulfitobacter</i>	5	1	4	suam	<i>Sulfitobacter</i> sp. AM1-D1	CP018076
				spse	<i>Sulfitobacter pseudonitzschiae</i>	CP022415
				sulz	<i>Sulfitobacter</i> sp. SK012	CP025804
				suli	<i>Sulfitobacter</i> sp. JL08	CP025815
				suld	<i>Sulfitobacter</i> sp. D7	CP020694
<i>Donghicola</i>	1	0	1	don	<i>Donghicola</i> sp. JLT3646	CP018572
<i>Salipiger</i>	1	1	0	tpro	<i>Salipiger profundus</i>	CP014796
<i>Tateyamaria</i>	1	1	0	tom	<i>Tateyamaria omphalii</i>	CP019312
<i>Pelagibaca</i>	1	1	0	paby	<i>Pelagibaca abyssi</i>	CP015093
<i>Thioclava</i>	1	1	0	thw	<i>Thioclava nitratreducens</i>	CP019437
<i>Roseovarius</i>	2	1	1	rmm	<i>Roseovarius mucosus</i>	CP020474
				rok	<i>Roseovarius</i> sp. AK1035	CP030099
<i>Roseitalea</i>	1	0	1	rpod	<i>Roseitalea porphyridii</i>	CP036532
<i>Yoonia</i>	1	1	0	lvs	<i>Yoonia vestfoldensis</i>	CP021431
<i>Antarctobacter</i>	1	0	1	aht	<i>Antarctobacter heliothermus</i>	CP022540
<i>Rhodobaca</i>	1	0	1	rbg	<i>Rhodobaca barguzinensis</i>	CP024899
<i>Sagittula</i>	1	0	1	sagu	<i>Sagittula</i> sp. P11	CP021913
<i>Thalassococcus</i>	2	0	2	thas	<i>Thalassococcus</i> sp. SH-1	CP027665
				thaa	<i>Thalassococcus</i> sp. S3	CP022303
<i>Gemmobacter</i>	1	0	1	geh	<i>Gemmobacter</i> sp. HYN0069	CP028918
<i>Tabrizicola</i>	1	0	1	taw	<i>Tabrizicola</i> sp. K13M18	CP034328
<i>Silicimonas</i>	1	0	1	salo	<i>Silicimonas algicola</i>	CP034588

<i>Sedimentitalea</i>	1	0	1	sedi	<i>Sedimentitalea</i> sp. W43	CP033219
<i>Unclassified Rhodobacteraceae</i>	1	0	1	rbz	<i>Rhodobacteraceae</i> bacterium G7	CP021114
<i>Maricaulis</i>	1	1	0	mmr	<i>Maricaulis maris</i>	CP000449
<i>Hyphomonas</i>	1	1	0	hne	<i>Hyphomonas neptunium</i>	CP000158
<i>Hirschia</i>	1	1	0	hba	<i>Hirschia baltica</i>	CP001678
<i>Glycocalis</i>	1	0	1	gak	<i>Glycocalis alkaliphilus</i>	CP018911
<i>Hyphomonadaceae</i> <i>e</i>	1	1	0	hbc	<i>Hyphomonadaceae</i> bacterium UKL13-1	CP012156
<i>Zymomonas</i>	8	0	8	zmo	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4	AE008692
				zmn	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> NCIMB 11163	CP001722
				zmm	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 10988	CP002850
				zmb	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 29191	CP003704
				zmi	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> CP4 = NRRL B-14023	CP006818
				zmc	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> CP4 = NRRL B-14023	CP003715
				zmr	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> NRRL B-12526	CP003709
				zmp	<i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> ATCC 29192	CP002865

<i>Novosphingobium</i>	7	3	4	nar	<i>Novosphingobium aromaticivorans</i>	CP000248
				npp	<i>Novosphingobium</i> sp. PP1Y	FR856862
				npn	<i>Novosphingobium pentaromativorans</i>	CP009291
				nre	<i>Novosphingobium resinovorum</i>	CP017075
				nov	<i>Novosphingobium</i> sp. P6W	CP030352, CP030353
				not	<i>Novosphingobium</i> sp. THN1	CP028347
				ntd	<i>Novosphingobium tardaugens</i>	CP034179
<i>Sphingopyxis</i>	11	7	4	sal	<i>Sphingopyxis alaskensis</i>	CP000356
				sphk	<i>Sphingopyxis fribergensis</i>	CP009122
				sphp	<i>Sphingopyxis</i> sp. 113P3	CP009453
				smag	<i>Sphingopyxis macrogoltabida</i> EY-1	CP012700
				smaz	<i>Sphingopyxis macrogoltabida</i> 203	CP009429
				ster	<i>Sphingopyxis terrae</i>	CP013342
				sgi	<i>Sphingopyxis granuli</i>	CP012199
				sphl	<i>Sphingopyxis</i> sp. LPB0140	CP018154
				sphq	<i>Sphingopyxis</i> sp. QXT-31	CP019449
				spho	<i>Sphingopyxis</i> sp. MG	CP026381
				sphu	Uncultured <i>Sphingopyxis</i> sp. UC10	LT598653
<i>Sphingomonas</i>	17	3	14	swi	<i>Sphingomonas wittichii</i>	CP000699
				sphd	<i>Sphingomonas wittichii</i> DC-6	CP021181
				sphm	<i>Sphingomonas</i> sp. MM-1	CP004036
				stax	<i>Sphingomonas taxi</i>	CP009571
				sphi	<i>Sphingomonas</i> sp. WHSC-8	CP010836
				ssan	<i>Sphingomonas sanxanigenens</i>	CP006644

				snj	<i>Sphingomonas sp. NIC1</i>	CP015521
				smy	<i>Sphingomonas melonis</i>	CP017578
				span	<i>Sphingomonas panacis</i>	CP014168
				skr	<i>Sphingomonas koreensis</i>	CP018820
				splm	<i>Sphingomonas sp. LM7</i>	CP019511
				splk	<i>Sphingomonas sp. LK11</i>	CP013916
				sphj	<i>Sphingomonas sp. JJ-A5</i>	CP018221
				spkc	<i>Sphingomonas sp. KC8</i>	CP016306
				sphc	<i>Sphingomonas sp. Cra20</i>	CP024923
				sphf	<i>Sphingomonas sp. FARSPH</i>	CP029985
				spha	<i>Sphingomonas sp. YZ-8</i>	CP032829
<i>Sphingobium</i>	14	9	5	sjp	<i>Sphingobium japonicum</i>	AP010803, AP010804
				sch	<i>Sphingobium chlorophenolicum</i>	CP002798, CP002799
				ssy	<i>Sphingobium sp. SYK-6</i>	AP012222, AP012223
				syb	<i>Sphingobium sp. YBL2</i>	CP010954
				sbd	<i>Sphingobium baderi</i>	CP013264
				spmi	<i>Sphingobium sp. MI1205</i>	CP005188, CP005189
				sphb	<i>Sphingobium sp. EP60837</i>	CP015986, CP015987
				sphr	<i>Sphingobium sp. RAC03</i>	CP016456
				sinb	<i>Sphingobium indicum</i>	CP013070
				spht	<i>Sphingobium sp. TKS</i>	CP005083, CP005084
				shyd	<i>Sphingobium hydrophobicum</i>	CP022745, CP022746
				sya	<i>Sphingobium yanoikuyae</i>	CP023741
				sclo	<i>Sphingobium cloacae</i>	AP017655
				spyg	<i>Sphingobium sp. YG1</i>	AP018518, AP018519

<i>Citromicrobium</i>	1	1	0	cij	<i>Citromicrobium</i> sp. JL477	CP011344
<i>Sphingorhabdus</i>	3	1	2	sphg	<i>Sphingorhabdus</i> sp. M41	CP014545
				sfla	<i>Sphingorhabdus flavimaris</i>	CP022336
				sphy	<i>Sphingorhabdus</i> sp. YGSMI21	CP022548
<i>Blastomonas</i>	2	1	1	blas	<i>Blastomonas</i> sp. RAC04	CP016460
				bfw	<i>Blastomonas fulva</i>	CP020083
<i>Rhizorhabdus</i>	1	0	1	rdi	<i>Rhizorhabdus dicambivorans</i>	CP023449
<i>Sphingosinicella</i>	2	0	2	smic	<i>Sphingosinicella microcystinivorans</i>	AP018711
				sphs	<i>Sphingosinicella</i> sp. BN140058	CP035501
<i>Erythrobacter</i>	7	2	5	eli	<i>Erythrobacter litoralis</i> HTCC2594	CP000157
				elq	<i>Erythrobacter litoralis</i> DSM 8509	CP017057
				ery	<i>Erythrobacter</i> sp. s21-N3	CP011310
				egn	<i>Erythrobacter gangjinensis</i>	CP018097, CP018098
				efv	<i>Erythrobacter flavus</i>	CP022528
				erk	<i>Erythrobacter</i> sp. KY5	CP021912
				err	<i>Erythrobacter</i> sp. YH-07	CP031357
<i>Altererythrobacter</i>	6	5	1	aay	<i>Altererythrobacter atlanticus</i>	CP011452
				amx	<i>Altererythrobacter marensis</i>	CP011805
				aep	<i>Altererythrobacter epoxidivorans</i>	CP012669
				anh	<i>Altererythrobacter namhicola</i>	CP016545
				ado	<i>Altererythrobacter dongtanensis</i>	CP016591
				alb	<i>Altererythrobacter</i> sp. B11	AP018498
<i>Croceicoccus</i>	2	1	1	cna	<i>Croceicoccus naphthovorans</i>	CP011770
				cman	<i>Croceicoccus marinus</i>	CP019602
<i>Porphyrobacter</i>	3	2	1	pns	<i>Porphyrobacter neustonensis</i>	CP016033

				porl	<i>Porphyrobacter</i> sp. LM 6	CP017113
				phz	<i>Porphyrobacter</i> HT-58-2	CP022600
<i>Gluconobacter</i>	4	0	4	gox	<i>Gluconobacter oxydans</i> 621H	CP000009
				goh	<i>Gluconobacter oxydans</i> H24	CP003926
				goy	<i>Gluconobacter oxydans</i> DSM 3504	CP004373
				gal	<i>Gluconobacter albidus</i>	CP014689
<i>Granulibacter</i>	4	0	4	gbe	<i>Granulibacter</i> <i>bethesdensis</i> CGDNIH1	CP000394
				gbh	<i>Granulibacter</i> <i>bethesdensis</i> CGDNIH2	CP003183
				gbc	<i>Granulibacter</i> <i>bethesdensis</i> CGDNIH3	CP003181
				gbs	<i>Granulibacter</i> <i>bethesdensis</i> CGDNIH4	CP003182
<i>Acidiphilium</i>	2	0	2	acr	<i>Acidiphilium cryptum</i>	CP000697
				amv	<i>Acidiphilium multivorum</i>	AP012035
<i>Gluconacetobacter</i>	2	2	0	gdi	<i>Gluconacetobacter diazotrophicus</i> PA1 5 (Brazil)	AM889285
				gdj	<i>Gluconacetobacter diazotrophicus</i> PA1 5 (JGI)	CP001189
<i>Komagataeibacter</i>	5	0	5	gxy	<i>Komagataeibacter medellinensis</i>	AP012159
				gxl	<i>Komagataeibacter xylinus</i>	CP004360
				kna	<i>Komagataeibacter nataicola</i>	CP019875
				keu	<i>Komagataeibacter europaeus</i>	CP021467
				ksc	<i>Komagataeibacter saccharivorans</i>	CP023036

<i>Acetobacter</i>	17	1	16	apt	<i>Acetobacter pasteurianus</i> IFO 3283-01	AP011121
				apw	<i>Acetobacter pasteurianus</i> IFO 3283-01-42C	AP011163
				apf	<i>Acetobacter pasteurianus</i> IFO 3283-03	AP011128
				apu	<i>Acetobacter pasteurianus</i> IFO 3283-07	AP011135
				apg	<i>Acetobacter pasteurianus</i> IFO 3283-12	AP011170
				apq	<i>Acetobacter pasteurianus</i> IFO 3283-22	AP011142
				apx	<i>Acetobacter pasteurianus</i> IFO 3283-26	AP011149
				apz	<i>Acetobacter pasteurianus</i> IFO 3283-32	AP011156
				apk	<i>Acetobacter pasteurianus</i> 386B	HF677570
				asz	<i>Acetobacter senegalensis</i>	LN606600
				asv	<i>Acetobacter oryzafermentans</i>	CP011120
				aace	<i>Acetobacter aceti</i>	CP014692
				aper	<i>Acetobacter persici</i>	CP014687
				apom	<i>Acetobacter pomorum</i>	CP023657
				ato	<i>Acetobacter tropicalis</i>	CP022699
				aasc	<i>Acetobacter ascendens</i>	CP015164
				acet	<i>Acetobacter</i> sp. JWB	CP030871

<i>Asaia</i>	1	0	1	abg	<i>Asaia bogorensis</i>	AP014690
<i>Kozakia</i>	1	0	1	kba	<i>Kozakia baliensis</i>	CP014674
<i>Roseomonas</i>	2	0	2	rgi	<i>Roseomonas gilardii</i>	CP015583, CP015584
				ros	<i>Roseomonas</i> sp. FDAARGOS_362	CP024588
<i>Neoasaia</i>	1	0	1	nch	<i>Neoasaia chiangmaiensis</i>	CP014691
<i>Commensalibacter</i>	1	0	1	coq	<i>Commensalibacter</i> sp. AMU001	CP033087
<i>Rhodospirillum</i>	3	0	3	rru	<i>Rhodospirillum rubrum</i> ATCC 11170	CP000230
				rrf	<i>Rhodospirillum rubrum</i> F11	CP003046
				rce	<i>Rhodospirillum centenum</i>	CP000613
<i>Pararhodospirillum</i>	1	0	1	rpm	<i>Pararhodospirillum photometricum</i>	HE663493
<i>Magnetospirillum</i>	5	1	4	mag	<i>Magnetospirillum magneticum</i>	AP007255
				mgy	<i>Magnetospirillum gryphiswaldense</i> MSR-1 v2	HG794546
				mgry	<i>Magnetospirillum gryphiswaldense</i> MSR-1	CP027526
				magx	<i>Magnetospirillum</i> sp. XM-1	LN997848
				magn	<i>Magnetospirillum</i> sp. ME-1	CP015848
<i>Azospirillum</i>	9	3	6	azl	<i>Azospirillum</i> sp. B510	AP010946
				ali	<i>Azospirillum lipoferum</i>	FQ311868
				abs	<i>Azospirillum brasilense</i> Sp245	HE577327
				abq	<i>Azospirillum brasilense</i> Az39	CP007793
				abf	<i>Azospirillum brasilense</i> Sp7	CP012914

				ati	<i>Azospirillum thiophilum</i>	CP012401, CP012402, CP012403, CP012404
				ahu	<i>Azospirillum humicireducens</i>	CP015285
				azt	<i>Azospirillum</i> sp. TSH58	CP022364
				azm	<i>Azospirillum</i> sp. M2T2B2	CP029829
<i>Tistrella</i>	1	1	0	tmo	<i>Tistrella mobilis</i>	CP003236
<i>Endolissoclinum</i>	2	0	2	thal	<i>Candidatus Endolissoclinum faulkneri</i> L2	CP003539
				efk	<i>Candidatus Endolissoclinum faulkneri</i> L5	CP006745
<i>Thalassospira</i>	3	0	3	txi	<i>Thalassospira xiamenensis</i>	CP004388
				thac	<i>Thalassospira marina</i>	CP024199
				tii	<i>Thalassospira indica</i>	CP031555
<i>Magnetospira</i>	1	1	0	magq	<i>Magnetospira</i> sp. QH-2	FO538765
<i>Haematospirillum</i>	1	0	1	hjo	<i>Haematospirillum jordaniae</i>	CP014525
<i>Nitrospirillum</i>	1	0	1	nao	<i>Nitrospirillum amazonense</i>	CP022110, CP022111, CP022112, CP022113
<i>Niveispirillum</i>	1	0	1	ncb	<i>Niveispirillum cyanobacteriorum</i>	CP025611, CP025612
<i>Parvularcula</i>	1	0	1	pbr	<i>Parvularcula bermudensis</i>	CP002156
<i>Magnetococcus</i>	1	0	1	mgm	<i>Magnetococcus marinus</i>	CP000471
<i>Pelagibacter</i>	2	0	2	pub	<i>Candidatus Pelagibacter ubique</i>	CP000084
				pel	<i>Candidatus Pelagibacter</i> sp. IMCC9063	CP002511
<i>Unclassified Pelagibacteraceae</i>	2	0	2	apc	<i>Alpha proteobacterium HIMB59</i>	CP003801

				apm	<i>Alpha proteobacterium HIMB5</i>	CP003809
<i>Micavibrio</i>	2	0	2	mai	<i>Micavibrio aeruginosavorus</i> ARL-13	CP002382
				man	<i>Micavibrio aeruginosavorus</i> EPB	CP003538
<i>Polymorphum</i>	1	1	0	pgv	<i>Polymorphum gilvum</i>	CP002568
<i>Phreatobacter</i>	1	0	1	phr	<i>Phreatobacter</i> sp. S-12	CP027668
<i>Puniceispirillum</i>	1	1	0	apb	<i>Candidatus Puniceispirillum marinum</i>	CP001751
<i>Unclassified Alphaproteobacteria</i>	1	0	1	abaw	<i>Alphaproteobacteria bacterium</i> WS11	CP032509
<i>Methylovirgula</i>	1	0	1	mlg	<i>Methylovirgula ligni</i>	CP025086
<i>Haematobacter</i>	1	0	1	hml	<i>Haematobacter massiliensis</i>	CP035510

Table S2. Comparative analysis of P450s and those associated with secondary metabolite biosynthetic gene clusters in the bacterial class *Alphaproteobacteria*. Standard abbreviations representing type of clusters as indicated in anti-SMASH [39] were used in the Table.

Species name	Species code	No. of P450s	No. of P450 families	No. of P450 subfamilies	No. of BG Cs	No. of BG Cs have P450s	BGC type	No. of P450s in BG Cs	P450 name
<i>Bradyrhizobium oligotrophicum</i>	aol	17	12	14	14	1	NRPS	1	CYP108L2
<i>Bradyrhizobium japonicum</i> E109	bjp	16	13	14	8				
<i>Novosphingobium aromaticivorans</i>	nar	16	11	14	2	1	terpene	1	CYP153C1
<i>Sphingomonas wittichii</i>	swi	16	16	16	4				
<i>Bradyrhizobium diazoefficiens</i> USDA 110	bja	15	13	13					
<i>Bradyrhizobium japonicum</i> USDA 6	bju	12	10	10	9				
<i>Bradyrhizobium</i> sp. BF49	brad	12	10	11	3				
<i>Blastomonas</i> sp. RAC04	blas	12	10	12	4				

<i>Bradyrhizobium</i> sp. ORS 278	bra	11	10	11	8				
<i>Sphingopyxis macrogoltabida</i> 203	smaz	11	8	9	10	1	NRPS	1	CYP1302 A1
<i>Sphingobium</i> sp. MI1205 Chromosome 1	spmi	11	10	10	6				
<i>Bradyrhizobium</i> sp. BTAi1	bbt	10	10	10	15				
<i>Bradyrhizobium</i> sp. S23321	brs	10	9	9	7	1	hserlactone	1	CYP199A 26
<i>Rhodopseudomonas palustris</i> HaA2	rpb	10	10	10	6				
<i>Parvibaculum lavamentivorans</i>	pla	9	5	5	3				
<i>Sinorhizobium fredii</i> NGR234	rhi	9	9	9	5				
<i>Rhizobium</i> sp. IE4771	rei	9	9	9	5				
<i>Rhodopseudomonas palustris</i> BisB5	rpd	9	9	9	6				
<i>Sphingopyxis granuli</i>	sgi	9	6	9	6				
<i>Mesorhizobium opportunistum</i>	mop	8	8	8	7				
<i>Rhizobium etli</i> bv. <i>mimosae</i> Mim1	rel	8	8	8	6				
<i>Jannaschia</i> sp. CCS1	jan	8	8	8	5				
<i>Hyphomonas neptunium</i>	hne	8	6	6	3				
<i>Sinorhizobium americanum</i>	same	7	7	7	6				

<i>Ensifer adhaerens</i> OV14 (Chromosome 1)	ead	7	6	6	8				
<i>Rhizobium etli</i> bv. <i>phaseoli</i> IE4803	rep	7	7	7	4				
<i>Rhizobium tropici</i>	rtr	7	7	7					
<i>Rhizobium gallicum</i>	rga	7			6				
<i>Rhizobium</i> sp. N1341	rhn	7	6	6	6				
<i>Rhizobium phaseoli</i>	rpha	7	7	7	5				
<i>Rhizobium</i> sp. N731	rhx	7	7	7	6				
<i>Bradyrhizobium icense</i>	bic	7	7	7	9				
<i>Rhodopseudomonas palustris</i> TIE-1	rpt	7	7	7	6				
<i>Methylobacterium radiotolerans</i>	mrđ	7	6	6	9				
<i>Methylobacterium</i> sp. 4-46	met	7	7	7	15				
<i>Methylobacterium aquaticum</i>	maqu	7	6	6	7				
<i>Erythrobacter litoralis</i> DSM 8509	elq	7	7	7	2				
<i>Porphyrobacter</i> sp. LM 6	porl	7	7	7	1				
<i>Mesorhizobium japonicum</i> MAFF 303099	mlo	6	6	6	8	1	hserlactone	1	CYP206A 1
<i>Mesorhizobium ciceri</i> (biovar <i>Biserrulae</i>)	mci	6	6	6	6				

<i>Mesorhizobium amorphae</i>	mamo	6	6	6	7				
<i>Rhizobium etli</i> CIAT 652	rec	6	6	6	5				
<i>Rhodopseudomonas palustris</i> CGA009	rpa	6	6	6	7				
<i>Rhodopseudomonas palustris</i> DX-1	rpx	6	6	6	8				
<i>Methylobacterium nodulans</i>	mno	6	6	6	11				
<i>Methylobacterium oryzae</i>	mor	6	4	4	10				
<i>Sphingobium</i> sp. YBL2	syb	6	5	6	5				
<i>Erythrobacter litoralis</i> HTCC2594	eli	6	4	6	1				
<i>Sulfitobacter</i> sp. AM1-D1	suam	6	6	6	6	1	acyl_amino_acids, bacteriocin, NRPS-like	3	CYP1326 A2, CYP195A 21, CYP2334 A1
<i>Mesorhizobium australicum</i>	mam	5	5	5	7				
<i>Sinorhizobium meliloti</i> GR4	smeg	5	4	4	4				
<i>Rhizobium etli</i> CFN 42	ret	5	5	5					
<i>Methylobacterium extorquens</i> PA1	mex	5	5	5	7				

<i>Methylobacterium extorquens</i> AM1	mea	5	5	5	7				
<i>Methylobacterium extorquens</i> DM4	mdi	5	5	5	7				
<i>Hyphomicrobium denitrificans</i> 1NES1	hdt	5	5	5	3				
<i>Caulobacter</i> sp. K31	cak	5	4	4	4				
<i>Caulobacter segnis</i>	cse	5	5	5	2				
<i>Celeribacter indicus</i>	cid	5	4	4	6	1	ectoine	1	CYP1101 A27
<i>Novosphingobium</i> sp. PP1Y	npp	5	5	5	3				
<i>Novosphingobium pentaromativorans</i>	npp	5	4	5	5				
<i>Sphingopyxis alaskensis</i>	sal	5	5	5	6				
<i>Sphingopyxis fribergensis</i>	sphk	5	4	4	12				
<i>Sphingopyxis</i> sp. 113P3	sphp	5	4	4					
<i>Agrobacterium fabrum</i>	atu	4	4	4	1	1	terpene	1	CYP206A 1
<i>Agrobacterium tumefaciens</i> Ach5	atf	4	4	4	1	1	terpene	1	CYP206A 4
<i>Agrobacterium vitis</i> Chromosome 1	avi	4	4	4	8				

<i>Rhizobium</i> sp. NT-26	rht	4	4	4	6	1	NAGGN	1	CYP107JE 1
<i>Bradyrhizobium</i> sp. CCGE-LA001	brc	4	4	4	11				
<i>Rhodopseudomonas palustris</i> BisA53	rpe	4	4	4	6				
<i>Methylobacterium extorquens</i> CM4	mch	4	4	4	7				
<i>Methylobacterium populi</i>	mpo	4	3	3	7				
<i>Hyphomicrobium denitrificans</i> ATCC 51888	hdn	4	4	4	4				
<i>Caulobacter vibrioides</i> CB15	ccr	4	4	4	4				
<i>Caulobacter vibrioides</i> NA1000	ccs	4	4	4	4				
<i>Ruegeria pomeroyi</i>	sil	4	4	4	6				
<i>Leisingera methylohalidivorans</i>	lmd	4	4	4	9				
<i>Marinovum algicola</i>	malg	4	4	4	5				
<i>Confluentimicrobium</i> sp. EMB200-NS6	con	4	4	4	5				
<i>Salipiger profundus</i>	tpro	4	3	3	5				
<i>Pelagibaca abyssi</i>	paby	4	4	4	6				
<i>Sphingomonas</i> sp. MM-1	sphm	4	3	3	4				
<i>Sphingobium chlorophenolicum</i>	sch	4	4	4	6				

<i>Sphingobium</i> sp. RAC03	sphr	4	3	3	5				
<i>Citromicrobium</i> sp. JL477	cij	4	4	4	2				
<i>Altererythrobacter epoxidivorans</i>	aep	4	4	4	1				
<i>Azospirillum</i> sp. B510	azl	4	4	4	2				
<i>Tistrella mobilis</i>	tmo	4	4	4	11				
<i>Hirschia baltica</i>	hba	3	3	3	3				
<i>Mesorhizobium</i> sp. B7	meso	3	3	3	5				
<i>Hoeflea</i> sp. IMCC20628	hoe	3	3	3	5				
<i>Sinorhizobium meliloti</i> SM11	smx	3	3	3	5				
<i>Sinorhizobium fredii</i> USDA 257	sfd	3	3	3	8				
<i>Agrobacterium radiobacter</i>	ara	3	3	3	3				
<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304	rlt	3	3	3	4				
<i>Rhizobium leguminosarum</i> bv. trifolii WSM1689	rlb	3	3	3	5				
<i>Rhizobium</i> sp. IRBG74	rir	3	3	3	1	1	terpene	1	CYP206A 3
<i>Rhodopseudomonas palustris</i> BisB18	rpc	3	3	3	8				
<i>Methylobacterium</i> sp. AMS5	meta	3	3	3	7				

<i>Hyphomicrobium</i> sp. MC1	hmc	3	3	3	4				
<i>Candidatus Filomicrobium marinum</i> W	fil	3	3	3	3				
<i>Candidatus Filomicrobium marinum</i> Y	fiy	3	3	3	3				
<i>Rhodoplanes</i> sp. Z2-YC6860	rhz	3	3	3	7				
<i>Phenylobacterium zucineum</i>	pzu	3	3	3	3				
<i>Ruegeria</i> sp. TM1040	sit	3	3	3	5				
<i>Rhodobacter capsulatus</i>	rcp	3	2	2	3				
<i>Roseobacter denitrificans</i>	rde	3	3	3	6				
<i>Roseobacter litoralis</i>	rli	3	3	3	7				
<i>Pseudovibrio</i> sp. FO-BEG1	psf	3	3	3	6				
<i>Phaeobacter inhibens</i> DSM 17395	pga	3	3	3	6				
<i>Phaeobacter inhibens</i> 2.10	pgl	3	3	3	6				
<i>Phaeobacter gallaeciensis</i> DSM 26640	pgd	3	3	3	5				
<i>Phaeobacter porticola</i>	php	3	3	3	4				
<i>Planktomarina temperata</i>	ptp	3	3	3	1				
<i>Labrenzia</i> sp. CP4	lap	3	3	3	7				
<i>Defluviimonas alba</i>	daa	3	3	3	3				

<i>Hyphomonadaceae bacterium UKL13-1</i>	hbc	3	3	3	2	1	terpene	1	CYP1246 A4
<i>Sphingobium japonicum</i>	sjp	3	3	3	7				
<i>Altererythrobacter atlanticus</i>	aay	3	3	3	2				
<i>Polymorphum gilvum</i>	pgv	3	3	3	8				
<i>Agrobacterium rhizogenes</i>	aro	3	3	3	3	1	terpene	1	CYP206A 2
<i>Neorhizobium galegae</i> bv. <i>officinalis</i> bv. <i>officinalis</i> HAMBI 1141	ngl	3	3	3	3				
<i>Paracoccus yeei</i>	pye	3	3	3	5				
<i>Mesorhizobium loti</i> NZP2037	mln	2	2	2	8				
<i>Chelativorans</i> sp. BNC1	mes	2	2	2	4				
<i>Sinorhizobium meliloti</i> 1021	sme	2	2	2	4				
<i>Sinorhizobium meliloti</i> AK83	smk	2	2	2	9				
<i>Sinorhizobium meliloti</i> BL225C	smq	2	2	2	4				
<i>Sinorhizobium meliloti</i> Rm41	smi	2	2	2	4				
<i>Sinorhizobium meliloti</i> 2011	smel	2	2	2	4				
<i>Sinorhizobium meliloti</i> RMO17	smer	2	2	2	4				

<i>Sinorhizobium medicae</i>	smd	2	2	2	5				
<i>Sinorhizobium fredii</i> HH103	sfh	2	2	2	7				
<i>Sinorhizobium</i> sp. RAC02	six	2	2	2	1				
<i>Ensifer adhaerens</i> Casida A	eah	2	2	2					
<i>Agrobacterium</i> sp. H13-3	agr	2	2	2	1	1	terpene	1	CYP206A 4
<i>Agrobacterium</i> sp. RAC06	agc	2	2	2	8				
<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841	rle	2	2	2	5				
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325	rlg	2	2	2	5				
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> CB782	rlu	2	2	2	4				
<i>Neorhizobium galegae</i> bv. <i>orientalis</i> HAMBI 540	ngg	2	2	2	2				
<i>Bosea</i> sp. RAC05	bos	2	2	2	3				
<i>Bosea vaviloviae</i>	bvv	2	2	2	6	1	T1PKS	1	CYP1101 A30
<i>Azorhizobium caulinodans</i>	azc	2	2	2	6				
<i>Beijerinckia indica</i>	bid	2	2	2	10	1	NRPS,T1PKS	1	CYP173J1
<i>Methylocella silvestris</i>	msl	2	2	2	12				
<i>Hyphomicrobium nitrativorans</i>	hni	2	2	2	4				

<i>Methylocystis</i> sp. SC2	msc	2	2	2	13				
<i>Methyloceanibacter caenitepidi</i>	mcg	2	2	2	6				
<i>Rhodobacter sphaeroides</i> 2.4.1	rsp	2	2	2	5				
<i>Rhodobacter sphaeroides</i> ATCC 17029	rsh	2	2	2	6				
<i>Rhodobacter sphaeroides</i> ATCC 17025	rsq	2	2	2	5	1	hserlactone	1	CYP152C 2
<i>Paracoccus denitrificans</i>	pde	2	2	2	7				
<i>Paracoccus aminophilus</i>	pami	2	2	2	7				
<i>Dinoroseobacter shibae</i>	dsh	2	2	2					
<i>Ketogulonicigenium robustum</i>	kro	2	2	2	3				
<i>Octadecabacter arcticus</i>	oar	2	2	2	5				
<i>Octadecabacter temperatus</i>	otm	2	2	2	2				
<i>Roseibacterium elongatum</i>	red	2	2	2	7				
<i>Celeribacter marinus</i>	cmar	2	2	2	2				
<i>Rhodovulum</i> sp. P5	rhc	2	2	2	7				
<i>Labrenzia aggregata</i>	lagg	2	2	2	7				
<i>Tateyamaria omphalii</i>	tom	2	2	2	5				

<i>Thioclava nitratreducens</i>	thw	2	2	2	5				
<i>Roseovarius mucosus</i>	rmm	2	2	2	8				
<i>Yoonia vestfoldensis</i>	lvs	2	2	2	5				
<i>Maricaulis maris</i>	mmr	2	2	2	1				
<i>Sphingobium</i> sp. EP60837 Chromosome 1	sphb	2	2	2	3				
<i>Altererythrobacter marensis</i>	amx	2	2	2	2				
<i>Altererythrobacter dongtanensis</i>	ado	2	2	2	4				
<i>Porphyrobacter neustonensis</i>	pns	2	2	2	2				
<i>Gluconacetobacter diazotrophicus</i> PA1 5 (Brazil)	gdi	2	2	2	5				
<i>Gluconacetobacter diazotrophicus</i> PA1 5 (JGI)	gdj	2	2	2	4				
<i>Azospirillum brasilense</i> Sp245	abs	2	2	2	4				
<i>Magnetospira</i> sp. QH-2	magq	2	2	2					
<i>Sphingobium baderi</i>	sbd	2	2	2					
<i>Aminobacter aminovorans</i>	aak	1	1	1	5				
<i>Agrobacterium tumefaciens</i> S33	ata	1	1	1	3				
<i>Rhizobium favelukesii</i>	rhl	1	1	1	3				
<i>Liberibacter crescens</i>	lcc	1	1	1					

<i>Shinella</i> sp. HZN7	shz	1	1	1	2				
<i>Brucella melitensis</i> bv. 1 16M	bme	1	1	1	4				
<i>Brucella melitensis</i> bv. 1 16M	bmel	1	1	1	4				
<i>Brucella melitensis</i> ATCC 23457	bmi	1	1	1	3				
<i>Brucella melitensis</i> M28	bmz	1	1	1	4				
<i>Brucella melitensis</i> M5-90	bmj	1	1	1	3				
<i>Brucella melitensis</i> NI	bmw	1	1	1	4				
<i>Brucella melitensis</i> bv. 3 Ether	bmee	1	1	1	3				
<i>Brucella abortus</i> 2308	bmf	1	1	1	4				
<i>Brucella abortus</i> S19	bmc	1	1	1	5				
<i>Brucella abortus</i> A13334	baa	1	1	1	5				
<i>Brucella abortus</i> bv. 2 86/8/59	babo	1	1	1	5				
<i>Brucella abortus</i> bv. 6 870	babr	1	1	1	5				
<i>Brucella abortus</i> 63 75	babt	1	1	1	6				
<i>Brucella abortus</i> BDW	babb	1	1	1	5				
<i>Brucella abortus</i> bv. 9 C68	babu	1	1	1	5				
<i>Brucella abortus</i> BER	babs	1	1	1	5				

<i>Brucella abortus</i> NCTC 10505	babc	1	1	1	5				
<i>Brucella suis</i> bv. 2 Bs143CITA	bsui	1	1	1	5				
<i>Brucella suis</i> bv. 2 PT09143	bsup	1	1	1	5				
<i>Brucella suis</i> bv. 2 PT09172	bsuv	1	1	1	5				
<i>Brucella suis</i> bv. 2 Bs364CITA	bsuc	1	1	1	5				
<i>Brucella suis</i> bv. 3	bsz	1	1	1	5				
<i>Brucella suis</i> ZW043	bsw	1	1	1	6				
<i>Brucella suis</i> ZW046	bsg	1	1	1	6				
<i>Brucella canis</i> ATCC 23365	bcs	1	1	1	4				
<i>Brucella canis</i> HSK A52141	bsk	1	1	1	5				
<i>Brucella canis</i> RM6/66	bcar	1	1	1	5				
<i>Brucella canis</i> SVA13	bcas	1	1	1	5				
<i>Brucella pinnipedialis</i> 6/566	bpv	1	1	1	5				
<i>Brucella ceti</i> TE10759-12	bcet	1	1	1	5				
<i>Ochrobactrum anthropi</i> ATCC 49188	oan	1	1	1	7				
<i>Ochrobactrum anthropi</i> OAB	oah	1	1	1	7				
<i>Ochrobactrum pseudogrignonense</i>	ops	1	1	1	6				

<i>Nitrobacter winogradskyi</i>	nwi	1	1	1	4				
<i>Nitrobacter hamburgensis</i>	nha	1	1	1	3				
<i>Xanthobacter autotrophicus</i>	xau	1	1	1	9	1	T1PKS	1	CYP1138 B1
<i>Pelagibacterium halotolerans</i>	phl	1	1	1	4				
<i>Devosia</i> sp. H5989	deq	1	1	1	2				
<i>Methylocystis bryophila</i>	mbry	1	1	1	9				
<i>Martelella endophytica</i>	mey	1	1	1	4				
<i>Pseudorhodoplanes sinuspersici</i>	psin	1	1	1	9	1	T1PKS	1	CYP1104 E2
<i>Asticcacaulis excentricus</i>	aex	1	1	1	5				
<i>Rhodobacter sphaeroides</i> KD131	rsk	1	1	1	5				
<i>Ketogulonicigenium vulgare</i> Y25	kvu	1	1	1	3				
<i>Ketogulonicigenium vulgare</i> WSH-001	kvl	1	1	1	3				
<i>Rhodovulum sulfidophilum</i>	rsu	1	1	1					
<i>Pannonibacter phragmitetus</i>	pphr	1	1	1	9				
<i>Yangia</i> sp. CCB-MM3	yan	1	1	1	5				
<i>Sphingopyxis terrae</i>	ster	1	1	1	6				

<i>Sphingopyxis</i> sp. LPB0140	sphl	1	1	1	2				
<i>Sphingomonas</i> sp. WHSC-8	sphi	1	1	1					
<i>Sphingobium</i> sp. SYK-6	ssy	1	1	1	7				
<i>Sphingobium indicum</i>	sinb	1	1	1	2				
<i>Sphingorhabdus</i> sp. M41	sphg	1	1	1	3				
<i>Altererythrobacter namhicola</i>	anh	1	1	1	2				
<i>Croceicoccus naphthovorans</i>	cna	1	1	1					
<i>Acetobacter aceti</i>	aace	1	1		2				
<i>Magnetospirillum gryphiswaldense</i> MSR-1 v2	mgry	1	1	1					
<i>Azospirillum brasilense</i> Az39	abq	1	1	1	3				
<i>Candidatus Puniceispirillum marinum</i>	apb	1	1	1	2				
<i>Rickettsiales bacterium</i> Ac37b	rbt				1				
<i>Rickettsiales endosymbiont of Stachyamoeba lipophora</i>	ren				1				
<i>Candidatus Paracaedibacter acanthamoebae</i>	paca				2				
<i>Candidatus Paracaedimonas acanthamoebae</i>	caq				1				
<i>Candidatus Nucleicultrix amoebiphila</i>	naf				2				

<i>Endosymbiont of Acanthamoeba sp. UWC8</i>	eaa				1				
<i>Mesorhizobium sp. WSM1497</i>	mesw				7				
<i>Aminobacter sp. MSH1</i>	amih				5				
<i>Phyllobacterium zundukense</i>	pht				2				
<i>Roseitalea porphyridii</i>	rpod				7				
<i>Rhodobiaceae bacterium SMS8</i>	rbs				2				
<i>Sinorhizobium sp. CCBAU 05631</i>	sino				7				
<i>Ensifer sojae</i>	esj				5				
<i>Rhizobium sp. S41</i>	rhv				1				
<i>Rhizobium sp. Kim5</i>	rhk				4				
<i>Rhizobium esperanzae</i>	rez				7				
<i>Neorhizobium sp. SOG26</i>	neo				3				
<i>Neorhizobium sp. NCHU2750</i>	nen				3				
<i>Candidatus Liberibacter asiaticus psy62</i>	las				2				
<i>Candidatus Liberibacter asiaticus gxpsy</i>	laa				2				
<i>Candidatus Liberibacter asiaticus Ishi-1</i>	lat				2				
<i>Candidatus Liberibacter solanacearum</i>	lso				2				

<i>Candidatus Liberibacter americanus</i>	lar				2				
<i>Candidatus Liberibacter africanus</i>	lau				2				
<i>Brucella abortus</i> bv. 1 9-941	bmb				2				
<i>Brucella suis</i> 1330	bms				2				
<i>Brucella suis</i> 1330	bsi				2				
<i>Brucella suis</i> bv. 1	bsf				2				
<i>Brucella suis</i> ATCC 23445	bmt				2				
<i>Brucella suis</i> VBI22	bsv				2				
<i>Brucella ovis</i>	bov				3				
<i>Brucella canis</i> Oliveri	bol				2				
<i>Brucella microti</i>	bmr				3				
<i>Brucella pinnipedialis</i> B2/94	bpp				3				
<i>Brucella ceti</i> TE28753-12	bcee				3				
<i>Brucella vulpis</i>	bvl				3				
<i>Brucella</i> sp. 2002734562	bru				2				
<i>Ochrobactrum</i> sp. A44	och				4				
<i>Bradyrhizobium</i> sp. ORS 285	bro				12				

<i>Bradyrhizobium</i> sp. SK17	brk				12				
<i>Bradyrhizobium ottawaense</i>	bot				7				
<i>Bradyrhizobium</i> sp. 2 39S1MB	brq				7				
<i>Oligotropha carboxidovorans</i> OM5 (Mississippi)	oca				4				
<i>Oligotropha carboxidovorans</i> OM5 (Goettingen)	ocg				3				
<i>Oligotropha carboxidovorans</i> OM4	oco				3				
<i>Bosea</i> sp. PAMC 26642	bop				2				
<i>Bosea</i> sp. Tri-49	boi				5				
<i>Variibacter gotjawalensis</i>	vgo				4				
<i>Bartonella henselae</i> Houston-1	bhe				1				
<i>Bartonella henselae</i> BM1374163	bhn				1				
<i>Bartonella henselae</i> BM1374165	bhs				1				
<i>Bartonella quintana</i> Toulouse	bqu				2				
<i>Bartonella quintana</i> RM-11	bqr				2				
<i>Bartonella bacilliformis</i>	bbk				1				
<i>Bartonella tribocorum</i> CIP 105476	btr				2				
<i>Bartonella tribocorum</i> BM1374166	btx				2				

<i>Bartonella grahamii</i>	bgr				2				
<i>Bartonella clarridgeiae</i>	bcd				2				
<i>Bartonella australis</i>	baus				2				
<i>Bartonella vinsonii</i>	bvn				2				
<i>Bartonella ancashensis</i>	banc				2				
<i>Bartonella apis</i>	bapi				2				
<i>Bartonella sp. JB15</i>	bart				1				
<i>Bartonella sp. A1379B</i>	bara				2				
<i>Bartonella sp. WD16.2</i>	barw				1				
<i>Bartonella sp. Raccoon60</i>	barr				2				
<i>Bartonella sp. 1-1C</i>	baro				2				
<i>Bartonella sp. JB63</i>	barj				1				
<i>Starkeya novella</i>	sno				4				
<i>Methylobacterium zatmanii</i>	mza				7				
<i>Methylobacterium phyllosphaerae</i>	mphy				10				
<i>Methylobacterium currus</i>	mee				7				
<i>Methylobacterium sp. DM1</i>	metd				8				

<i>Methylobacterium</i> sp. XJLW	metx				9				
<i>Methylobacterium</i> sp. 17SD2-17	mets				6				
<i>Microvirga ossetica</i>	moc				4				
<i>Microvirga</i> sp. 17 mud 1-3	miv				7				
<i>Methylovirgula ligni</i>	mlg				6				
<i>Chelatococcus</i> sp. CO-6	chel				6				
<i>Chelatococcus daeguensis</i>	cdq				5				
<i>Rhodomicrobium vannielii</i>	rva				7				
<i>Devosia</i> sp. I507	dei				6				
<i>Blastochloris viridis</i>	bvr				6				
<i>Blastochloris</i> sp. GI	blag				3				
<i>Maritalea myrionectae</i>	mmy r				4				
<i>Methylocystis rosea</i>	mros				14				
<i>Methylosinus trichosporium</i>	mtw				9				
<i>Pleomorphomonas</i> sp. SM30	pleo				4				
<i>Martelella</i> sp. AD-3	maad				5				

<i>Martelella mediterranea</i>	mmed				5				
<i>Aureimonas</i> sp. AU20	aua				4				
<i>Breoghanian</i> sp. L-A4	brn				7				
<i>Candidatus Tokpelaia hoelldoblerii</i>	thd				3				
<i>Hartmannibacter diazotrophicus</i>	hdi				8				
<i>Rhizobiales bacterium</i> NRL2	rbm				8				
<i>Caulobacter henricii</i>	chq				4				
<i>Caulobacter mirabilis</i>	cmb				5				
<i>Caulobacter flavus</i>	cfh				5				
<i>Phenylobacterium</i> sp. HYN0004	phb				1				
<i>Brevundimonas subvibrioides</i>	bsb				3				
<i>Brevundimonas</i> sp. DS20	brd				5				
<i>Brevundimonas naejangsensis</i>	bne				3				
<i>Brevundimonas</i> sp. GW460-12-10-14-LB2	brg				2				
<i>Brevundimonas</i> sp. LM2	brl				5				
<i>Brevundimonas vesicularis</i>	bvc				2				

<i>Brevundimonas diminuta</i>	bdm				7				
<i>Caulobacteraceae bacterium OTSz_A_272</i>	cbot				3				
<i>Ruegeria sp. AD91A</i>	rua				7				
<i>Epibacterium mobile</i>	rmb				5				
<i>Rhodobacter sp. LPB0142</i>	rhp				4				
<i>Rhodobacter blasticus</i>	rbl				3				
<i>Paracoccus contaminans</i>	pcon				3				
<i>Paracoccus zhejiangensis</i>	pzh				6				
<i>Paracoccus sp. BM15</i>	paro				8				
<i>Paracoccus sp. CBA4604</i>	paru				4				
<i>Paracoccus aminovorans</i>	pamn				5				
<i>Paracoccus mutanoliticus</i>	pmut				2				
<i>Paracoccus sp. SC2-6</i>	pars				3				
<i>Phaeobacter piscinae</i>	ppic				5				
<i>Phaeobacter sp. LSS9</i>	phq				7				
<i>Octadecabacter antarcticus</i>	oat				8				
<i>Leisingera sp. NJS204</i>	lej				8				

<i>Celeribacter ethanolicus</i>	ceh				4				
<i>Celeribacter manganoxidans</i>	cmag				3				
<i>Rhodovulum</i> sp. MB263	rhm				5				
<i>Halocynthiibacter arcticus</i>	hat				5				
<i>Labrenzia</i> sp. VG12	labr				6				
<i>Yangia pacifica</i>	ypac				3				
<i>Sulfitobacter pseudonitzschiae</i>	spse				9				
<i>Sulfitobacter</i> sp. SK012	sulz				8				
<i>Sulfitobacter</i> sp. JL08	suli				5				
<i>Sulfitobacter</i> sp. D7	suld				5				
<i>Donghicola</i> sp. JLT3646	don				5				
<i>Roseovarius</i> sp. AK1035	rok				8				
<i>Antarctobacter heliothermus</i>	aht				9				
<i>Rhodobaca barguzinensis</i>	rbg				3				
<i>Sagittula</i> sp. P11	sagu				3				
<i>Thalassococcus</i> sp. SH-1	thas				3				
<i>Thalassococcus</i> sp. S3	thaa				9				

<i>Gemmobacter</i> sp. HYN0069	geh				6				
<i>Tabrizicola</i> sp. K13M18	taw				5				
<i>Silicimonas algicola</i>	sal				6				
<i>Sedimentitalea</i> sp. W43	sedi				5				
<i>Haematobacter massiliensis</i>	hml				3				
<i>Rhodobacteraceae</i> bacterium G7	rbz				5				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4	zmo				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> NCIMB 11163	zmn				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 10988	zmm				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 29191	zmb				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> CP4 = NRRL B-14023	zmi				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> CP4 = NRRL B-14023	zmc				2				
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> NRRL B-12526	zmr				2				
<i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> ATCC 29192	zmp				1				

<i>Novosphingobium resinovorum</i>	nre				4				
<i>Novosphingobium</i> sp. P6W	nov				4				
<i>Novosphingobium</i> sp. THN1	not				2				
<i>Novosphingobium tardaugens</i>	ntd				1				
<i>Sphingopyxis macrogoltabida</i> EY-1	smag				8				
<i>Sphingopyxis</i> sp. QXT-31	sphq				8				
<i>Sphingopyxis</i> sp. MG	spho				4				
Uncultured <i>Sphingopyxis</i> sp. UC10	sphu				6				
<i>Sphingomonas wittichii</i> DC-6	sphd				6				
<i>Sphingomonas taxi</i>	stax				3				
<i>Sphingomonas sanxanigenens</i>	ssan				5				
<i>Sphingomonas</i> sp. NIC1	snj				3				
<i>Sphingomonas melonis</i>	smy				5				
<i>Sphingomonas panacis</i>	span				4				
<i>Sphingomonas koreensis</i>	skr				6				
<i>Sphingomonas</i> sp. LM7	splm				1				
<i>Sphingomonas</i> sp. LK11	splk				3				

<i>Sphingomonas</i> sp. JJ-A5	sphj				4				
<i>Sphingomonas</i> sp. KC8	spkc				5				
<i>Sphingomonas</i> sp. Cra20	sphc				3				
<i>Sphingomonas</i> sp. FARSPH	sphf				4				
<i>Sphingomonas</i> sp. YZ-8	spha				4				
<i>Sphingobium</i> sp. TKS	spht				4				
<i>Sphingobium hydrophobicum</i>	shyd				4				
<i>Sphingobium yanoikuyae</i>	sya				10				
<i>Sphingobium cloacae</i>	sclo				1				
<i>Sphingobium</i> sp. YG1	spyg				4				
<i>Sphingorhabdus flavimaris</i>	sfla				5				
<i>Sphingorhabdus</i> sp. YGSMI21	sphy				4				
<i>Blastomonas fulva</i>	bfw				5				
<i>Rhizorhabdus dicambivorans</i>	rdi				7				
<i>Sphingosinicella microcystinivorans</i>	smic				9				
<i>Sphingosinicella</i> sp. BN140058	sphs				6				
<i>Erythrobacter</i> sp. s21-N3	ery				4				

<i>Erythrobacter gangjinensis</i>	egn				3				
<i>Erythrobacter flavus</i>	efv				2				
<i>Erythrobacter</i> sp. KY5	erk				3				
<i>Erythrobacter</i> sp. YH-07	err				4				
<i>Altererythrobacter</i> sp. B11	alb				4				
<i>Croceicoccus marinus</i>	cman				4				
<i>Porphyrobacter</i> sp. HT-58-2	phz				2				
<i>Gluconobacter oxydans</i> 621H	gox				2				
<i>Gluconobacter oxydans</i> H24	goh				4				
<i>Gluconobacter oxydans</i> DSM 3504	goy				1				
<i>Gluconobacter albidus</i>	gal				1				
<i>Granulibacter bethesdensis</i> CGDNIH1	gbe				6				
<i>Granulibacter bethesdensis</i> CGDNIH2	gbh				6				
<i>Granulibacter bethesdensis</i> CGDNIH3	gbc				6				
<i>Granulibacter bethesdensis</i> CGDNIH4	gbs				6				
<i>Acidiphilium cryptum</i>	acr				4				
<i>Acidiphilium multivorum</i>	amv				6				

<i>Komagataeibacter medellinensis</i>	gxy				3				
<i>Komagataeibacter xylinus</i>	gxl				3				
<i>Komagataeibacter nataicola</i>	kna				6				
<i>Komagataeibacter europaeus</i>	keu				6				
<i>Komagataeibacter saccharivorans</i>	ksc				4				
<i>Acetobacter pasteurianus</i> IFO 3283-01	apt				3				
<i>Acetobacter pasteurianus</i> IFO 3283-01-42C	apw				3				
<i>Acetobacter pasteurianus</i> IFO 3283-03	apf				3				
<i>Acetobacter pasteurianus</i> IFO 3283-07	apu				3				
<i>Acetobacter pasteurianus</i> IFO 3283-12	apg				3				
<i>Acetobacter pasteurianus</i> IFO 3283-22	apq				3				
<i>Acetobacter pasteurianus</i> IFO 3283-26	apx				3				
<i>Acetobacter pasteurianus</i> IFO 3283-32	apz				3				
<i>Acetobacter pasteurianus</i> 386B	apk				3				
<i>Acetobacter senegalensis</i>	asz				4				
<i>Acetobacter oryzafermentans</i>	asv				4				
<i>Acetobacter persici</i>	aper				7				

<i>Acetobacter pomorum</i>	apom				4				
<i>Acetobacter tropicalis</i>	ato				4				
<i>Acetobacter ascendens</i>	aasc				3				
<i>Acetobacter sp. JWB</i>	acet				4				
<i>Asaia bogorensis</i>	abg				2				
<i>Kozakia baliensis</i>	kba				3				
<i>Roseomonas gilardii</i>	rgi				6				
<i>Roseomonas sp. FDAARGOS_362</i>	ros				6				
<i>Neoasaia chiangmaiensis</i>	nch				4				
<i>Commensalibacter sp. AMU001</i>	coq				2				
<i>Rhodospirillum rubrum ATCC 11170</i>	rru				9				
<i>Rhodospirillum rubrum F11</i>	rrf				11				
<i>Rhodospirillum centenum</i>	rce				5				
<i>Pararhodospirillum photometricum</i>	rpm				3				
<i>Magnetospirillum magneticum</i>	mag				4				
<i>Magnetospirillum gryphiswaldense MSR-1</i>	mgry				4				
<i>Magnetospirillum sp. XM-1</i>	magx				6				

<i>Magnetospirillum</i> sp. ME-1	magn				4				
<i>Azospirillum lipoferum</i>	ali				2				
<i>Azospirillum brasilense</i> Sp7	abf				3				
<i>Azospirillum thiophilum</i>	ati				2				
<i>Azospirillum humicireducens</i>	ahu				2				
<i>Azospirillum</i> sp. TSH58	azt				2				
<i>Azospirillum</i> sp. M2T2B2	azm				2				
<i>Candidatus Endolissoclinum faulkneri</i> L2	thal				4				
<i>Candidatus Endolissoclinum faulkneri</i> L5	efk				4				
<i>Thalassospira xiamenensis</i>	txi				6				
<i>Thalassospira marina</i>	thac				5				
<i>Thalassospira indica</i>	tii				5				
<i>Haematospirillum jordaniae</i>	hjo				2				
<i>Nitrospirillum amazonense</i>	nao				2				
<i>Niveispirillum cyanobacteriorum</i>	ncb				3				
<i>Parvularcula bermudensis</i>	pbr				4				
<i>Magnetococcus marinus</i>	mgm				2				

<i>Candidatus Pelagibacter ubique</i>	pub				1				
<i>Candidatus Pelagibacter sp. IMCC9063</i>	pel				1				
<i>Alpha proteobacterium HIMB59</i>	apc				1				
<i>Alpha proteobacterium HIMB5</i>	apm				1				
<i>Micavibrio aeruginosavorus ARL-13</i>	mai				3				
<i>Micavibrio aeruginosavorus EPB</i>	man				2				
<i>Phreatobacter sp. S-12</i>	phr				2				
<i>Alphaproteobacteria bacterium WS11</i>	abaw				5				

Table S3: List of new P450 families identified in Alphaproteobacterial species.

CYP1010A1
CYP1017A1
CYP103A1
CYP104A1
CYP1075A1
CYP1076A1
CYP1077A1
CYP1078A1
CYP112A1
CYP1135A1
CYP1137A1
CYP1141A1
CYP1145A1
CYP1170A1
CYP1171A1
CYP1173A1
CYP1174A1
CYP1175A1
CYP1181A1
CYP1182A1
CYP1186A1
CYP1187A1
CYP1258A1
CYP127A1
CYP1281A1
CYP1302A1
CYP1311A1
CYP1312A1
CYP1384A1
CYP1396A1
CYP1515A1
CYP152AA1
CYP1732A1
CYP1733A1
CYP1734A1
CYP1735A1
CYP1736A1
CYP1737A1

CYP1738A1
CYP1739A1
CYP173A1
CYP1740A1
CYP1741A1
CYP1742A1
CYP1743A1
CYP1744A1
CYP1745A1
CYP1746A1
CYP1747A1
CYP1748A1
CYP1749A1
CYP1750A1
CYP1751A1
CYP1752A1
CYP1753A1
CYP1754A1
CYP1755A1
CYP192A1
CYP193A1
CYP194A1
CYP195A1
CYP196A1
CYP199A1
CYP200A1
CYP201A1
CYP202A1
CYP203A1
CYP204A1
CYP206A1
CYP2140A1
CYP219A1
CYP223A1
CYP224A1
CYP225A1
CYP2334A1
CYP289A1
CYP290A1

Annexure B

Table S1. Comparative analysis of ferredoxins between the bacterial groups Alphaproteobacteria.

Alphaproteobacteria

Species name	Species code	Ferredoxin types					
		2Fe-2S	3Fe-4S	4Fe-4S	7Fe-8S	2[4Fe-4S]	2[4Fe-4S]Alv
<i>Rhizobium favelukesii</i>	rhl	1				3	
<i>Mesorhizobium japonicum</i> MAFF 303099	mlo	1				4	
<i>Mesorhizobium loti</i> NZP2037	mln	2				4	
<i>Mesorhizobium ciceri</i> (biovar Biserrulae)	mci	1				4	
<i>Mesorhizobium opportunistum</i>	mop	1	1			3	
<i>Mesorhizobium australicum</i>	mam	1	1			4	
<i>Mesorhizobium amorphae</i>	mamo	4	1			3	
<i>Mesorhizobium</i> sp. B7	meso	1				2	
<i>Chelativorans</i> sp. BNC1	mes	1				2	
<i>Hoeflea</i> sp. IMCC20628	hoe	2				2	
<i>Aminobacter aminovorans</i>	aak	7				4	
<i>Parvibaculum lavamentivorans</i>	pla	5				2	
<i>Sinorhizobium meliloti</i> 1021	sme					3	
<i>Sinorhizobium meliloti</i> AK83	smk	1				5	1
<i>Sinorhizobium meliloti</i> BL225C	smq	1				5	
<i>Sinorhizobium meliloti</i> SM11	smx					5	1
<i>Sinorhizobium meliloti</i> Rm41	smi	1				5	
<i>Sinorhizobium meliloti</i> GR4	smeg	1				5	
<i>Sinorhizobium meliloti</i> 2011	smel	1				5	
<i>Sinorhizobium meliloti</i> RMO17	smer	1				5	

<i>Sinorhizobium medicae</i>	smd	1				4	
<i>Sinorhizobium fredii</i> NGR234	rhi	4	1			4	
<i>Sinorhizobium fredii</i> HH103	sfh	2				3	
<i>Sinorhizobium fredii</i> USDA 257	sfd	2				3	
<i>Sinorhizobium</i> sp. RAC02	six	1				6	
<i>Sinorhizobium americanum</i>	same	2	1			7	
<i>Ensifer adhaerens</i> OV14	ead	2				3	
<i>Ensifer adhaerens</i> Casida A	eah	2			1	6	
<i>Agrobacterium fabrum</i>	atu	1				3	
<i>Agrobacterium radiobacter</i>	ara	1				3	
<i>Agrobacterium tumefaciens</i> Ach5	atf	1				3	
<i>Agrobacterium tumefaciens</i> S33	ata	2				3	
<i>Agrobacterium vitis</i>	avi	1				3	
<i>Agrobacterium</i> sp. H13-3	agr	1				5	
<i>Agrobacterium</i> sp. RAC06	agc	1				1	
<i>Agrobacterium rhizogenes</i>	aro	1				3	
<i>Rhizobium etli</i> CFN 42	ret	1	1			4	
<i>Rhizobium etli</i> CIAT 652	rec	1	1			4	
<i>Rhizobium etli</i> bv. <i>mimosae</i> Mim1	rel	1	1			5	
<i>Rhizobium etli</i> bv. <i>phaseoli</i> IE4803	rep	2				4	
<i>Rhizobium</i> sp. IE4771	rei	2	1			5	
<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841	rle	2			1	2	1
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM2304	rlt	1				4	
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1325	rlg	1				3	
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> WSM1689	rlb	1				2	
<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> CB782	rlu	1				3	
<i>Rhizobium tropici</i>	rtr	2	2			3	
<i>Rhizobium</i> sp. IRBG74	rir	1				4	
<i>Rhizobium gallicum</i>	rga	2	2			4	

<i>Rhizobium</i> sp. N1341	rhn	1	1		1	4	
<i>Rhizobium phaseoli</i>	rpha	1	1			4	
<i>Rhizobium</i> sp. NT-26	rht	1				2	
<i>Rhizobium</i> sp. N731	rhx	1	1		1	4	
<i>Neorhizobium galegae</i> bv. <i>officinalis</i> bv. <i>officinalis</i> HAMBI 1141	ngl	2			1	3	1
<i>Neorhizobium galegae</i> bv. <i>orientalis</i> HAMBI 540	ngg	2			1	3	
<i>Liberibacter crescens</i>	lcc					1	
<i>Shinella</i> sp. HZN7	shz	2				3	
<i>Brucella melitensis</i> bv. 1 16M	bme	1				2	
<i>Brucella melitensis</i> bv. 1 16M	bmel	1				2	
<i>Brucella melitensis</i> ATCC 23457	bmi	1				2	
<i>Brucella melitensis</i> M28	bmz	1				2	
<i>Brucella melitensis</i> M5-90	bmj	1				2	
<i>Brucella melitensis</i> NI	bmw	1				2	
<i>Brucella melitensis</i> bv. 3 Ether	bmee	1				2	
<i>Brucella abortus</i> 2308	bmf					2	
<i>Brucella abortus</i> S19	bmc	1				2	
<i>Brucella abortus</i> A13334	baa	1				2	
<i>Brucella abortus</i> bv. 2 86/8/59	babo	1				2	
<i>Brucella abortus</i> bv. 6 870	babr	1				2	
<i>Brucella abortus</i> 63 75	babt	1				2	
<i>Brucella abortus</i> BDW	babb	1				2	
<i>Brucella abortus</i> bv. 9 C68	babu	1				2	
<i>Brucella abortus</i> BER	babs					2	
<i>Brucella abortus</i> NCTC 10505	babc	1				2	
<i>Brucella suis</i> bv. 2 Bs143CITA	bsui					2	
<i>Brucella suis</i> bv. 2 PT09143	bsup					2	
<i>Brucella suis</i> bv. 2 PT09172	bsuv					2	

<i>Brucella suis</i> bv. 2 Bs364CITA	bsuc	1				2	
<i>Brucella suis</i> bv. 3	bsz	1				2	
<i>Brucella suis</i> ZW043	bsw	1				2	
<i>Brucella suis</i> ZW046	bsg	1				3	
<i>Brucella canis</i> ATCC 23365	bcs	1				2	
<i>Brucella canis</i> HSK A52141	bsk	1				2	
<i>Brucella canis</i> RM6/66	bcar	1				2	
<i>Brucella canis</i> SVA13	bcas	1				2	
<i>Brucella pinnipedialis</i> 6/566	bpv	1				2	
<i>Brucella ceti</i> TE10759-12	bcet	1				2	
<i>Ochrobactrum anthropi</i> ATCC 49188	oan	1				2	
<i>Ochrobactrum anthropi</i> OAB	oah	1				2	
<i>Ochrobactrum pseudogrignonense</i>	ops	1				2	
<i>Bradyrhizobium diazoefficiens</i> USDA 110	bja	3	1			5	1
<i>Bradyrhizobium japonicum</i> USDA 6	bju	2	2			4	
<i>Bradyrhizobium japonicum</i> E109	bjp	4	2			5	
<i>Bradyrhizobium</i> sp. ORS 278	bra	4				4	1
<i>Bradyrhizobium</i> sp. BTAi1	bbt	6			1	7	1
<i>Bradyrhizobium</i> sp. S23321	brs	3	1			4	1
<i>Bradyrhizobium oligotrophicum</i>	aol	6			1	5	1
<i>Bradyrhizobium</i> sp. CCGE-LA001	brc	3	1			2	1
<i>Bradyrhizobium</i> sp. BF49	brad	1	1			3	
<i>Bradyrhizobium icense</i>	bic	3	2		1	6	1
<i>Rhodopseudomonas palustris</i> CGA009	rpa	2	1			5	1
<i>Rhodopseudomonas palustris</i> HaA2	rpb	2	1			6	1
<i>Rhodopseudomonas palustris</i> BisB18	rpc	1				5	1
<i>Rhodopseudomonas palustris</i> BisB5	rpd	1	1			6	1
<i>Rhodopseudomonas palustris</i> BisA53	rpe	1				5	1
<i>Rhodopseudomonas palustris</i> TIE-1	rpt	2	1			6	1

<i>Rhodopseudomonas palustris</i> DX-1	rpx	2				6	1
<i>Nitrobacter winogradskyi</i>	nwi	1				4	
<i>Nitrobacter hamburgensis</i>	nha	1	1			3	
<i>Bosea</i> sp. RAC05	bos	1				2	
<i>Bosea vaviloviae</i>	bvv	3				2	
<i>Xanthobacter autotrophicus</i>	xau	3				7	1
<i>Azorhizobium caulinodans</i>	azc	4				5	1
<i>Methylobacterium extorquens</i> PA1	mex	1	1			3	
<i>Methylobacterium extorquens</i> AM1	mea	1	1			3	
<i>Methylobacterium extorquens</i> DM4	mdi	1	1			3	
<i>Methylobacterium extorquens</i> CM4	mch	1	1			5	
<i>Methylobacterium populi</i>	mpo	1	1			3	
<i>Methylobacterium radiotolerans</i>	mrd	1	2			3	
<i>Methylobacterium</i> sp. 4-46	met	1	1			3	
<i>Methylobacterium nodulans</i>	mno	2	1			3	
<i>Methylobacterium oryzae</i>	mor	1	2			2	
<i>Methylobacterium</i> sp. AMS5	meta	1	1			2	
<i>Methylobacterium aquaticum</i>	maqu	1	2			2	
<i>Beijerinckia indica</i>	bid	7				5	
<i>Methylocella silvestris</i>	msl	6				3	1
<i>Hyphomicrobium denitrificans</i> ATCC 51888	hdn	1				3	
<i>Hyphomicrobium denitrificans</i> 1NES1	hdt	1				3	
<i>Hyphomicrobium</i> sp. MC1	hmc	4				3	
<i>Hyphomicrobium nitrativorans</i>	hni	1				3	
<i>Pelagibacterium halotolerans</i>	phl	2				2	
<i>Candidatus Filomicrobium marinum</i> W	fil	1				3	
<i>Candidatus Filomicrobium marinum</i> Y	fiy	1				3	
<i>Devosia</i> sp. H5989	deq	2				2	
<i>Rhodoplanes</i> sp. Z2-YC6860	rhz	2				3	

<i>Methylocystis</i> sp. SC2	msc	6				3	1
<i>Methylocystis bryophila</i>	mbry	6				5	1
<i>Martelella endophytica</i>	mey	1				5	
<i>Methyloceanibacter caenitepidi</i>	mcg	2				2	
<i>Pseudorhodoplanes sinuspersici</i>	psin	6				3	
<i>Caulobacter vibrioides</i> CB15	ccr	1				2	
<i>Caulobacter vibrioides</i> NA1000	ccs	1				2	
<i>Caulobacter</i> sp. K31	cak	1	1			2	
<i>Caulobacter segnis</i>	cse	2				3	
<i>Phenylobacterium zucineum</i>	pzu	1				2	
<i>Asticcacaulis excentricus</i>	aex	2				2	
<i>Ruegeria pomeroyi</i>	sil	3				2	
<i>Ruegeria</i> sp. TM1040	sit	1				2	
<i>Rhodobacter sphaeroides</i> 2.4.1	rsp	2				6	
<i>Rhodobacter sphaeroides</i> ATCC 17029	rsh	2				4	
<i>Rhodobacter sphaeroides</i> ATCC 17025	rsq	1				4	
<i>Rhodobacter sphaeroides</i> KD131	rsk	2				5	
<i>Rhodobacter capsulatus</i>	rcp	3				3	1
<i>Jannaschia</i> sp. CCS1	jan	1			1	2	
<i>Roseobacter denitrificans</i>	rde	2				2	
<i>Roseobacter litoralis</i>	rli	2				2	
<i>Paracoccus denitrificans</i>	pde	2				2	
<i>Paracoccus aminophilus</i>	pami	1				4	
<i>Paracoccus yeei</i>	pye	1				2	
<i>Dinoroseobacter shibae</i>	dsh	1				2	
<i>Ketogulonicigenium vulgare</i> Y25	kvu	1				2	
<i>Ketogulonicigenium vulgare</i> WSH-001	kvl	1				2	
<i>Ketogulonicigenium robustum</i>	kro	1				2	
<i>Pseudovibrio</i> sp. FO-BEG1	psf	1				2	

<i>Phaeobacter inhibens</i> DSM 17395	pga	1				2	
<i>Phaeobacter inhibens</i> 2.10	pgl	1				2	
<i>Phaeobacter gallaeciensis</i> DSM 26640	pgd	1				2	
<i>Phaeobacter porticola</i>	php	1				2	
<i>Octadecabacter arcticus</i>	oar	2				3	
<i>Octadecabacter temperatus</i>	otm	1			1	5	
<i>Leisingera methylohalidivorans</i>	lmd	2				2	
<i>Roseibacterium elongatum</i>	red	1				3	
<i>Planktomarina temperata</i>	ptp	2				2	
<i>Celeribacter indicus</i>	cid	4				5	
<i>Celeribacter marinus</i>	cmar	1				2	
<i>Marinovum algicola</i>	malg	1				2	
<i>Confluentimicrobium</i> sp. EMB200-NS6	con	7				4	
<i>Rhodovulum sulfidophilum</i>	rsu	2				3	1
<i>Rhodovulum</i> sp. P5	rhc	2				4	1
<i>Pannonibacter phragmitetus</i>	pphr	4				2	
<i>Labrenzia</i> sp. CP4	lap	2				2	
<i>Labrenzia aggregata</i>	lagg	2			1	2	
<i>Defluviimonas alba</i>	daa	3				2	1
<i>Yangia</i> sp. CCB-MM3	yan	3				3	
<i>Sulfitobacter</i> sp. AM1-D1	suam	1				2	
<i>Salipiger profundus</i>	tpro	1				2	
<i>Tateyamaria omphalii</i>	tom	1				2	
<i>Pelagibaca abyssi</i>	paby	1				3	
<i>Thioclava nitratreducens</i>	thw	2				2	
<i>Roseovarius mucosus</i>	rmm	1				3	
<i>Yoonia vestfoldensis</i>	lvs	2				2	
<i>Maricaulis maris</i>	mmr	1				2	
<i>Hyphomonas neptunium</i>	hne	1				2	

<i>Hirschia baltica</i>	hba	2				2	
<i>Hyphomonadaceae bacterium</i> UKL13-1	hbc	1				2	
<i>Novosphingobium aromaticivorans</i>	nar	7	1			2	
<i>Novosphingobium</i> sp. PP1Y	npp	4				3	
<i>Novosphingobium pentaromativorans</i>	npr	3				2	
<i>Sphingopyxis alaskensis</i>	sal	2				2	
<i>Sphingopyxis fribergensis</i>	sphk	6				2	
<i>Sphingopyxis</i> sp. 113P3	sphp	2				2	
<i>Sphingopyxis macrogoltabida</i> 203	smaz	3	2			2	
<i>Sphingopyxis terrae</i>	ster	4				2	
<i>Sphingopyxis granuli</i>	sgi	4	1			2	
<i>Sphingopyxis</i> sp. LPB0140	sphl	2				2	
<i>Sphingomonas wittichii</i>	swi	8	2			2	
<i>Sphingomonas</i> sp. MM-1	sphm	3	1			2	
<i>Sphingomonas</i> sp. WHSC-8	sphi	5				4	
<i>Sphingobium japonicum</i>	sjp	2	1			2	
<i>Sphingobium chlorophenolicum</i>	sch	5	2			2	
<i>Sphingobium</i> sp. SYK-6	ssy	3				2	
<i>Sphingobium</i> sp. YBL2	syb	6	1	1		3	
<i>Sphingobium baderi</i>	sbd	6				2	
<i>Sphingobium</i> sp. MI1205	spmi	4				2	
<i>Sphingobium</i> sp. EP60837	sphb	3	2			2	
<i>Sphingobium</i> sp. RAC03	sphr	3	1			2	
<i>Sphingobium indicum</i>	sinb	2				2	
<i>Citromicrobium</i> sp. JL477	cij	3				2	
<i>Sphingorhabdus</i> sp. M41	sphg	3				2	
<i>Blastomonas</i> sp. RAC04	blas	5		1		2	
<i>Erythrobacter litoralis</i> HTCC2594	eli	4				2	
<i>Erythrobacter litoralis</i> DSM 8509	elq	3				2	

<i>Altererythrobacter atlanticus</i>	aay	3				2	
<i>Altererythrobacter marensis</i>	amx	3				2	
<i>Altererythrobacter epoxidivorans</i>	aep	4				2	
<i>Altererythrobacter namhicola</i>	anh	4				2	
<i>Altererythrobacter dongtanensis</i>	ado	3				2	
<i>Croceicoccus naphthovorans</i>	cna	4				2	
<i>Porphyrobacter neustonensis</i>	pns	3				2	
<i>Porphyrobacter</i> sp. LM 6	porl	3				2	
<i>Gluconacetobacter diazotrophicus</i> PA1 5 (Brazil)	gdi	1				4	
<i>Gluconacetobacter diazotrophicus</i> PA1 5 (JGI)	gdj	1				4	
<i>Acetobacter aceti</i>	aace	1				3	
<i>Magnetospirillum gryphiswaldense</i> MSR-1 v2	mgv	4				4	1
<i>Azospirillum</i> sp. B510	azl	4				2	
<i>Azospirillum brasilense</i> Sp245	abs	4				4	1
<i>Azospirillum brasilense</i> Az39	abq	4				4	1
<i>Tistrella mobilis</i>	tmo	1				2	
<i>Magnetospira</i> sp. QH-2	magq	5				3	1
<i>Polymorphum gilvum</i>	pgv	4				2	
<i>Candidatus Puniceispirillum marinum</i>	apb	2				2	
241		490	60	2	12	712	31

Table S2. Ferredoxin protein sequences identified in 241 alphaproteobacterial species. Ferredoxins were sorted as per their Fe-S cluster type and subtypes. Name of the ferredoxins were followed as mentioned in methodology. Name of the ferredoxins includes their nomenclature name followed by protein ID from KEGG database and species name.

Alphaproteobacteria

2Fe-2S

Subtype 1

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>2Fe-2SST1 (rhl:LPU83_2264) Rhizobium favelukesii
MPKLTIVAFDGTFRFDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDDEWTER
VGPPEAMEEDMLDFAFDVRPTSRLSCQIRMKAALDGLTVHVPERQA

>2Fe-2SST1 (mlo:msl0793) Mesorhizobium japonicum MAFF 303099
MTKLTFIAHDGTQFDVDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYDVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (mln:A9174_21805) Mesorhizobium loti NZP2037
MTKLTFIAHDGTQFDVDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYDVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (mci:Mesci_4101) Mesorhizobium ciceri (biovar
Biserrulae)
MTKLTFIAHDGTHFDMDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYDVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (mop:Mesop_4144) Mesorhizobium opportunistum
MTKLTFIAHDGTHFDVDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYEVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (mam:Mesau_03907) Mesorhizobium australicum
MTKLTFIAHDGTHFDVDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYDVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (mamo:A6B35_18150) Mesorhizobium amorphae
MTKLTFIAHDGTQFDVDAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWTAE
VGEPEAMEEDMLDFAYEVQPNSRLSCQIKVRDALDGLVVRVPERQG

>2Fe-2SST1 (meso:BSQ44_12710) Mesorhizobium sp. B7
MTKITYIAHDGSKFEVEAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDEAWSAA
VGEPEAMEEDMLDFAYDVRPTSRLSCQIRVSDEL DGLVVRVPERQA

>2Fe-2SST1 (mes:Meso_1410) Chelativorans sp. BNC1
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MPRLKFIAFDGTEFDIQADNGSTLMQNAVRNGVPGIEAECGGACACATCHVYVDEAWAEI
VGPPEPMEEDMLDFAYDVRPTSRLSCQVRVREELDGLTVRIPERQG
>2Fe-2SST1(hoe:IMCC20628_01555)*Hoeflea* sp. IMCC20628
MTKITLVAYDGRFEVAAENGSTVMENAIRNSVPGIEAECGGACACATCHVYVDEQWVDA
VGAPAPMEEDMLDFAFDVRPTSRLSCQIKVRSELDGLVVHVPERQA
>2Fe-2SST1(aak:AA2016_0623)*Aminobacter aminovorans*
MYRVTFVDADGQATELTANEGQSVMSVAVANGIDQILAECGGSCACGTCHCYVDESWTEK
LPAADDSEQGMIECLMNPTERSRLTCQLKMSAALDGLVVHLPREQY
>2Fe-2SST1(aak:AA2016_3872)*Aminobacter aminovorans*
MTKLTYIAHDGTRFEVEAENGSTVMENAIRNAVPGIEAECGGACACATCHVYVDDAWTAI
VGEPEAMEEDMLDFAYEVRPSSRLSCQIKVRDELGLVVSIPERQG
>2Fe-2SST1(aak:AA2016_5379)*Aminobacter aminovorans*
MIEINFTEADGNTRILSADPGSTLLNAILGAGIKGIVAECGGGCSCGTCHVHVALDWTGR
LPAPADDETDMLSLAEDVTEKSRLACQIRLAPELNGLSVTIPGAA
>2Fe-2SST1(pla:Plav_2520)*Parvibaculum lavamentivorans*
MAKITYIEHNGTEHTIDVENGMTVMGAIKNSIPGIDADCGGACACATCHVYVAEGWTEK
VGPAESMEEDMLDFAFDVRENSRLSCQIKVTDELGLKVNLPKQF
>2Fe-2SST1(pla:Plav_0126)*Parvibaculum lavamentivorans*
MAKITYIEHDGTEHTIEVANGITLMEA AVKASIPGIDGDCGGACACATCMVYVPDEWKPK
LPEVETMEETMLDFCEHTEANSRLSCQLVASDELGDGIRLQMPESQH
>2Fe-2SST1(sm:Sinme_1719)*Sinorhizobium meliloti* AK83
MTKLTI VAFD GARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQA
>2Fe-2SST1(sm:SinmeB_1564)*Sinorhizobium meliloti* BL225C
MTKLTI VAFD GARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQA
>2Fe-2SST1(smi:BN406_01547)*Sinorhizobium meliloti* Rm41
MTKLTI VAFD GARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQA
>2Fe-2SST1(smeg:C770_GR4Chr1864)*Sinorhizobium meliloti* GR4
MTKLTI VAFD GARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQA
>2Fe-2SST1(sm:SM2011_c00192)*Sinorhizobium meliloti* 2011
MTKLTI VAFD GARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ

VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQ
 >2Fe-2SST1(smer:DU99_09905) *Sinorhizobium meliloti* RMO17
 MTKLTIVAFDGDARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
 VGTPEAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLVVHVPERQA
 >2Fe-2SST1(smd:Smed_1536) *Sinorhizobium medicae*
 MTKLTIVAFDGDARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAQ
 VGAPEAMEEDMLDFAYDVRPTSRLSCQIKVSEALDGLIVHVPERQA
 >2Fe-2SST1(rhi:NGR_c16660) *Sinorhizobium fredii* NGR234
 MTKLTIVAFDGDTRHDLVDENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAA
 VGAPEAMEEDMLDFAYDVRPTSRLSCQIKIGEALDGLVVHVPERQA
 >2Fe-2SST1(sfh:SFHH103_01547) *Sinorhizobium fredii* HH103
 MTKLTIVAFDGDTRHDLVDENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAA
 VGAPEAMEEDMLDFAYDVRPTSRLSCQIKIGEALDGLVVHVPERQA
 >2Fe-2SST1(sfd:USDA257_c40890) *Sinorhizobium fredii* USDA 257
 MTKLTIVAFDGDTRHDLVDENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAAA
 VGAPEAMEEDMLDFAYDLRATSRLSCQIKMSEALDGLVVHVPERQA
 >2Fe-2SST1(six:BSY16_912) *Sinorhizobium* sp. RAC02
 MSKLTIVAFDGDTRHELDVAKGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWSAI
 VGPPEAMEEDMLDFAYDVRPTSRLSCQIKMSDAFDGLVVHVPERQA
 >2Fe-2SST1(ead:OV14_a0405) *Ensifer adhaerens* OV14
 MDAEGKSTEVEAEIGQSVMSAAVQNGIDAIAAECGGSCACGTCHCYIDGTWAGRLPSPDY
 QEQDMLDCVVNPDESRSLSCQITVSDALDGLVVHLPAGQY
 >2Fe-2SST1(ead:OV14_2992) *Ensifer adhaerens* OV14
 MTKLTIVAFDGDTRHELDVENGSTVMENAVRNSVPGVEAECGGACACATCHVYVDDAWTAV
 VGAPEAMEEDMLDFAYDVRPTSRLSCQIKVSDALDGLVVHVPERQA
 >2Fe-2SST1(eah:FA04_22110) *Ensifer adhaerens* Casida A
 MPKIVFIDADGTTKEIHAEIGQSLMSAAVQNGIDAIAAECGGSCACGTCHCYIDGEWSDR
 LPAPEFQEQDMIECVVNPNEISRSLSCQITVSAELDGLVVHLPAGQY
 >2Fe-2SST1(eah:FA04_07845) *Ensifer adhaerens* Casida A
 MTKLTIVAFDGDARHELDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAQT
 VGAPEAMEEDMLDFAYDVRPTSRLSCQIKMSDALDGLVVHVPERQA
 >2Fe-2SST1(atu:Atu1350) *Agrobacterium fabrum*
 MTKLTIVAFDGDTPHELDVSNGSTVMENAVRNSVPGIDAECGGACACATCHVYVDDAWAER
 VGGPEPMEEDMLDFAFEVRPTSRLSCQIKMNDELGLVVHVPERQG

>2Fe-2SST1(ara:Arad_2639)*Agrobacterium radiobacter*
MTKLTIVAFDGTFRFDLNADDGSTVMENAVRNSVPGVDAECGGACACATCHVYVDDNWVEK
VGGPAPMEEDMLDFAFDVRPSSRLSCQIKMTQALDGLVVHVPERQA

>2Fe-2SST1(atf:Ach5_12480)*Agrobacterium tumefaciens* Ach5
MTKLTIVAFDGTTPHELDVSNGSTVMENAVRNSIPGIDAECGGACACATCHVYVDDAWAER
VGGPEPMEEDMLDFAFEVRPTSRLSCQIKMKDELDGLVVHVPERQG

>2Fe-2SST1(ata:AWN88_12060)*Agrobacterium tumefaciens* S33
MTKLTIVAFDGTTPHELDVSNGSTVMENAVRNSIPGIDAECGGACACATCHVYVDDAWSER
VGGPEPMEEDMLDFAFDVRPTSRLSCQIKMSDDLGLVVHVPERQG

>2Fe-2SST1(avi:Avi_2243)*Agrobacterium vitis*
MTQLTIVAFDGTFRFDLDAADGSTVMENAVRNSVPGIDAECGGACACATCHVYVDEAWVEK
TGGPAPMEEDMLDFATDVRPNSRLSCQIKIAPALAGLVVHVPERQG

>2Fe-2SST1(agr:AGROH133_05800)*Agrobacterium* sp. H13-3
MTKLTIVAFDGTTPHELDVSNGSTVMENAVRNSIPGIDAECGGACACATCHVYVDDAWAER
VGGPEPMEEDMLDFAFEVRPTSRLSCQIKMKDELDGLVVHVPERQG

>2Fe-2SST1(agc:BSY240_360)*Agrobacterium* sp. RAC06
MANISIIAFDGTFRFDIAAADGSTVMENAVRNSVPGIDAECGGACACATCHVYVDDSWSEK
VGQPSAMEEDMLDFAVDVRPTSRLSCQIKVTAALEGLVVHVPERQG

>2Fe-2SST1(aro:B0909_06650)*Agrobacterium rhizogenes*
MTKLTIVAFDGTTPHELDVSNGSTVMENAVRNSIPGIDAECGGACACATCHVYVDDAWTER
VGGPEPMEEDMLDFAFDVRPTSRLSCQIKMNDELGLVVHVPERQG

>2Fe-2SST1(ret:RHE_CH02338A)*Rhizobium etli* CFN 42
MPKLTIVAFDGTFRFDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rec:RHECIAT_CH0002436)*Rhizobium etli* CIAT 652
MPKLTIVAFDGTTHFDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rel:REMIM1_CH02350)*Rhizobium etli* bv. *mimosae* Mim1
MPKLTIVAFDGTFRFDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rep:IE4803_CH02381)*Rhizobium etli* bv. *phaseoli*
IE4803
MPKLTIVAFDGTFRFDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLIVHVPERQA

>2Fe-2SST1(rei:IE4771_CH02468)*Rhizobium* sp. IE4771
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLIVHVPERQA

>2Fe-2SST1(rle:RL2652)*Rhizobium leguminosarum* bv. *viciae* 3841
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rlt:Rleg2_1973)*Rhizobium leguminosarum* bv. *trifolii*
WSM2304
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEAWTEQ
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rlg:Rleg_2185)*Rhizobium leguminosarum* bv. *trifolii*
WSM1325
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rlb:RLEG3_21580)*Rhizobium leguminosarum* bv. *trifolii*
WSM1689
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rlu:RLEG12_21290)*Rhizobium leguminosarum* bv.
trifolii CB782
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEAWTEQ
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1(rtr:RTCIAT899_CH10015)*Rhizobium tropici*
MTKLTIVAFDGTFRDLNVDEGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGGPEAMEEDMLDFAFDVRPNSRLSCQIKMKSALDGLVVHVPERQA

>2Fe-2SST1(rir:BN877_I1333)*Rhizobium* sp. IRBG74
MTKLTIVAFDGTTPHELDVSNGSTVMENAVRNSIPGIDAECGGACACATCHVYVDDAWSER
VGGPEPMEEDMLDFAFDVRPTSRLSCQIKMSDDLGLVVHVPERQG

>2Fe-2SST1(rga:RGR602_CH02127)*Rhizobium gallicum*
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTER
VGPPEAMEEDMLDFAFDVRPTSRLSCQIRMKAALDGLIVQVPERQA

>2Fe-2SST1(rhn:AMJ98_CH02396)*Rhizobium* sp. N1341
MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1 (rpha:AMC79_CH02467) *Rhizobium phaseoli*
 MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
 VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1 (rht:NT26_1928) *Rhizobium* sp. NT-26
 MTKLTIVAFDGTFRDIDASNGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWAEA
 VGAPSAMEEDMLDFAHDVRPTSRLSCQIKMTDALEGLVVQVPERQG

>2Fe-2SST1 (rhx:AMK02_CH02411) *Rhizobium* sp. N731
 MPKLTIVAFDGTFRDLDVDQGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEEWTEK
 VGQPEAMEEDMLDFAFDVRPTSRLSCQIRMKAAYDGLVVHVPERQA

>2Fe-2SST1 (ngl:RG1141_CH16740) *Neorhizobium galegae* bv.
officinalis bv. *officinalis* HAMBI 1141
 MTKLTIVAFDGTFRDIEAEPGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEAWTEK
 VGPPAPMEEDMLDFAFEVKPNSRLSCQIKVKADLDGLVVNVPERQA

>2Fe-2SST1 (ngl:RG1141_PB00350) *Neorhizobium galegae* bv.
officinalis bv. *officinalis* HAMBI 1141
 MTTIHFQSPSGEVTTLKGVVGQSIMELATSNGVSAIEADCGGACACATCHVIVDQSWTER
 LPAPGVMERDMLDFVAEPTSTSRLSCQLHITDDHDGLLLHLPSKQS

>2Fe-2SST1 (ngg:RG540_CH17130) *Neorhizobium galegae* bv.
orientalis HAMBI 540
 MTKLTIVAFDGTFRDIEAEPGSTVMENAVRNSVPGIEAECGGACACATCHVYVDEAWTEK
 VGPPAPMEEDMLDFAFEVKPNSRLSCQIKVKADLDGLVVNVPERQA

>2Fe-2SST1 (shz:shn_09835) *Shinella* sp. HZN7
 MSKLTIVAFDGTREHLDVANGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWSAI
 VGPPEAMEEDMLDFAYEVRPTSRLSCQIKMSDALDGLVVHVPERQA

>2Fe-2SST1 (bme:BMEI0959) *Brucella melitensis* bv. 1 16M
 MSQGIKMTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYV
 DDDWADTVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bmel:DK63_462) *Brucella melitensis* bv. 1 16M
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bmi:BMEA_A1066) *Brucella melitensis* ATCC 23457
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bmz:BM28_A1035) *Brucella melitensis* M28

MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (bmw:BMNI_I1000) *Brucella melitensis* NI
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (bmee:DK62_399) *Brucella melitensis* bv. 3 Ether
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (bmc:BAbS19_I09700) *Brucella abortus* S19
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (baa:BAA13334_I02338) *Brucella abortus* A13334
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babo:DK55_1030) *Brucella abortus* bv. 2 86/8/59
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babr:DO74_860) *Brucella abortus* bv. 6 870
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babt:DK49_786) *Brucella abortus* 63 75
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babb:DK48_1089) *Brucella abortus* BDW
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babu:DK53_1012) *Brucella abortus* bv. 9 C68
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (babc:DO78_935) *Brucella abortus* NCTC 10505
 MTKIVFVSADGATRTEVEADSGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD
 TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN
 >2Fe-2SST1 (bsuc:BSSP2_I1041) *Brucella suis* bv. 2 Bs364CITA
 MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECGGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bsz:DK67_1919)*Brucella suis* bv. 3

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bsw:IY71_05090)*Brucella suis* ZW043

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bsg:IY72_04830)*Brucella suis* ZW046

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bcs:BCAN_A1040)*Brucella canis* ATCC 23365

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bsk:BCA52141_I0089)*Brucella canis* HSK A52141

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bcar:DK60_1077)*Brucella canis* RM6/66

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bcas:DA85_04885)*Brucella canis* SVA13

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bpv:DK65_352)*Brucella pinnipedialis* 6/566

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (bcet:V910_100966)*Brucella ceti* TE10759-12

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDDDWAD

TVGGPDPMEEDMLDFAYEVRPTSRLSCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (oan:Oant_2112)*Ochrobactrum anthropi* ATCC 49188

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDEDWTD

TVGGPDAMEEDMLDFAYEVRPTSRLSCQIRVSDDIDGLVVQVPERQN

>2Fe-2SST1 (oah:DR92_1606)*Ochrobactrum anthropi* OAB

MTKIVFVSADGATRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDEDWTD

TVGGPDAMEEDMLDFAYEVRPTSRLSCQIRVSDDIDGLVVQVPERQN

>2Fe-2SST1 (ops:A8A54_04740) *Ochrobactrum pseudogrignonense*
MTKIIIFVSADGASRTEVEADNGSSVMEAAIRNGIPGIDAECEGACACATCHVYVDEEDWTE
TVGGPDAMEEDMLDFAYEVQPN SRLSCQIRVSDEIDGLVVKVPERQN

>2Fe-2SST1 (bja:bl15885) *Bradyrhizobium diazoefficiens* USDA 110
MAKIHFDVHKGETRTVEIENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKVSDELDGLVVSTPERQA

>2Fe-2SST1 (bjj:BJ6T_38260) *Bradyrhizobium japonicum* USDA 6
MAKINFVDHKGETRTVEIENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKVSDELDGLVVATPERQA

>2Fe-2SST1 (bjp:RN69_18555) *Bradyrhizobium japonicum* E109
MAKINFVDHKGETRTVEIENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKVSDELDGLVVATPERQA

>2Fe-2SST1 (bra:BRADO5081) *Bradyrhizobium* sp. ORS 278
MAKITFVDHTGESRTVDIENGATVMEAAIRNAIPGIEAECEGACACATCHVYVDEAWREK
VGPPTPMEEDMLDFGYDVRPNSRLACQIKVSDELDGLVVATPERQA

>2Fe-2SST1 (bbt:BBta_5552) *Bradyrhizobium* sp. BTAi1
MAKITFVDHTGESRTVEIENGATVMEAAIRNAIPGIEAECEGACACATCHVYVDEAWREK
VGPPTPMEEDMLDFGYEVRPNSRLSCQIKVSDELDGLVVATPERQA

>2Fe-2SST1 (brs:S23_23680) *Bradyrhizobium* sp. S23321
MAKIHFDVHKGETRTVEIENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKVSDELDGLVVATPERQA

>2Fe-2SST1 (aol:S58_26040) *Bradyrhizobium oligotrophicum*
MAKITFVDHTGESRTVDVENGATVMEAAIRNAIPGIEAECEGACACATCHVYVDEAWREK
VGPPTPMEEDMLDFGYDVRPNSRLSCQIKVSDELNGLVVSTPERQA

>2Fe-2SST1 (brc:BCCGELA001_25050) *Bradyrhizobium* sp. CCGE-LA001
MAKIHFDVHKGETRTVEIENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKISDELDGLVVATPERQA

>2Fe-2SST1 (brad:BF49_5756) *Bradyrhizobium* sp. BF49
MAKIHFDVHKGETRTVDVENGATVMEAAIRNSIPGIEAECEGACACATCHVYVDEAWREK
VGSPTPMEEDMLDFGFDVRPNSRLSCQIKVSDDLGLVVATPERQA

>2Fe-2SST1 (bic:LMTR13_28045) *Bradyrhizobium icense*
MAKIHFDVHNKEKRTIEVENGATVMEAAIRNAIPGIEAECEGACACATCHVYVDEAWREK
VGAPTPMEEDMLDFGFDVRPNSRLSCQIKVSDDLGLVVSTPERQA

>2Fe-2SST1 (rpa:RPA3956) *Rhodopseudomonas palustris* CGA009

MAKINFVDHTGETRTVEVEEGATVMEAAIRNAIPGVEAECGGACACATCHVYVDEAWREK
 VGGPSPMEEDMLDFGYDVRPNSRLSCQIKVSNELDGLIVTTPERQA
 >2Fe-2SST1 (rpb:RPB_3843) *Rhodopseudomonas palustris* HaA2
 MAKIHFVDHSGETRIVDVENGATVMEAAIRNAIPGIEAECGGACACATCHVYVDEAWREK
 VGGPSPMEEDMLDFGYDVRPNSRLSCQIKVSELDGLVISTPDRQA
 >2Fe-2SST1 (rpc:RPC_1457) *Rhodopseudomonas palustris* BisB18
 MAKINFVDHSGETRSVEVEEGATVMEAAIRNAVPGIEAECGGACACATCHVYVDEAWRDK
 TGAPTMEEDMLDFGFDVRPNSRLSCQIKVTEELDGLVVTVPERQA
 >2Fe-2SST1 (rpd:RPD_1643) *Rhodopseudomonas palustris* BisB5
 MAKIHFVDHSGETRIVDVENGATVMEAAIRNAIPGIEAECGGACACATCHVYVDEAWREK
 VGGPSPMEEDMLDFGYDVRPSSRLSCQIKVSELDGLVISTPDRQA
 >2Fe-2SST1 (rpe:RPE_1476) *Rhodopseudomonas palustris* BisA53
 MAKINFVDHKGETRTVEVEEGATVMEAAIRNAVPGIEAECGGACACATCHVYVDEAWRDK
 TGAPTMEEDMLDFGYDVRPNSRLSCQIKVTDALDGLVVSIPERQA
 >2Fe-2SST1 (rpt:Rpal_4477) *Rhodopseudomonas palustris* TIE-1
 MAKINFVDHTGETRTVEVEEGATVMEAAIRNAIPGVEAECGGACACATCHVYVDEAWREK
 VGGPSPMEEDMLDFGYDVRPNSRLSCQIKVSNELDGLIVTTPERQA
 >2Fe-2SST1 (rpx:Rpx1_1396) *Rhodopseudomonas palustris* DX-1
 MAKIHFVDHTGETRTVEVEEGATVMEAAIRNAIPGVEAECGGACACATCHVYVDEAWREK
 VGGPSPMEEDMLDFGYDVRPNSRLSCQIKVSNELDGLIVTTPERQA
 >2Fe-2SST1 (nwi:Nwi_1088) *Nitrobacter winogradskyi*
 MTKINFVDHSGETRITVDVENGATVMEAAIRNAVPGIEAECGGACACATCHVYIDDAWTEK
 VGKPTMEEDMLDFGYDVRPNSRLSCQIKVSELEGLVVTVPERQA
 >2Fe-2SST1 (nha:Nham_1320) *Nitrobacter hamburgensis*
 MTKINFVDHSGETRITVDVENGATVMEAAIRNAVPGIEAECGGACACATCHVYIDEAWSK
 VGKPTMEEDMLDFGYDVRPNSRLSCQIKVSELDGLVVSTPERQA
 >2Fe-2SST1 (bos:BSY19_1779) *Bosea* sp. RAC05
 MPQVTFIDAHGESRTVEGEAGATVMEVAIRNGVPGIEAECGGACACATCHVYVDEAWTAK
 TGRPEPMEEDMLDFAFEVKPTSRLSCQIKLRDDLGLVVRTPSRQG
 >2Fe-2SST1 (bvv:BHK69_12405) *Bosea vaviloviae*
 MPKITYIDAQGESRTVEGETGSTVMEVAVRNAIPGIEAECGGACACATCHVYVDDAWAAK
 TGHPEPMEEDMLDFAFDVRPTSRLSCQIRVKDDLGLIVRTPARQG
 >2Fe-2SST1 (xau:Xaut_4124) *Xanthobacter autotrophicus*
 MVAITFIEYNGTAHQVEGPEGATAMETAVRNGVPGIVAECGGACACATCHVYVDEAWADK

VGEPSEMEEGMLDFATDVRPSSRLSCQIKLTAALDGLVLNIPETQG
 >2Fe-2SST1(xau:Xaut_2914)*Xanthobacter autotrophicus*
 MARFTVQTRNGDQMEVTGRDGATLLKAMRKAGVEEVVAQCGGGCACATCHVYVTPPEGGA
 LPPVGPAEARMLATSRYRTLNSRLSCQLKLEPGLEQMLVVIAPDDGGDF
 >2Fe-2SST1(azc:AZC_2219)*Azorhizobium caulinodans*
 MPAITFVVSFEGASRTVQAPVGATAMEVAVRNGVPGIDADCGGACACATCHVYVDEAWRAA
 VGEPEGMEEDMLDFATDVRPSSRLSCQIKITEALDGLVLHTPERQG
 >2Fe-2SST1(mex:Mext_4466)*Methylobacterium extorquens* PA1
 MPKITFVDHAGTARTIDGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDGEWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTPELDGLIVTTTPARQG
 >2Fe-2SST1(mea:Mex_1p4911)*Methylobacterium extorquens* AM1
 MPKITFVDHAGTARTIDGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDGEWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTPELDGLIVTTTPARQG
 >2Fe-2SST1(mdi:METDI5502)*Methylobacterium extorquens* DM4
 MPKITFVDHAGTARTIDGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDGEWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTPELDGLIVTTTPARQG
 >2Fe-2SST1(mch:Mchl_4930)*Methylobacterium extorquens* CM4
 MPKITFVDHAGAARTIDGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDGEWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTAELDGLIVTTTPARQG
 >2Fe-2SST1(mpo:Mpop_4980)*Methylobacterium populi*
 MPKITFVDHAGTARTIDGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDEAWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTPELDGLVVTTPARQG
 >2Fe-2SST1(mrd:Mrad2831_1946)*Methylobacterium radiotolerans*
 MPKITVVDHAGTERTVEGSGATVMETAMRNNVPGIDAECGGACACATCHVYVADAWIDT
 VGKAQDMEQDMLDFASDVRENSRLSCQIKITPALDGLVVTTPPQQG
 >2Fe-2SST1(met:M446_6065)*Methylobacterium* sp. 4-46
 MVQITYVDAAGTPRTVAGEVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDPEWEAA
 VGPAEPMEQDMLDFASDVRPNSRLSCQIRVRPELDGLKVTTTPARQG
 >2Fe-2SST1(mno:Mnod_6602)*Methylobacterium nodulans*
 MVQITYVDAAGTPRTVEGAVGSTVMETAIRNNVPGIDAECGGACACATCHVYVDPEWAEA
 VGPAEPMEQDMLDFASDVRPNSRLSCQIRLKPELDGLTVTTTPTRQG
 >2Fe-2SST1(mor:MOC_2358)*Methylobacterium oryzae*
 MPKITVVDHAGTERTVEGSGATVMETALRNNVPGIDAECGGACACATCHVYVADAWIEV
 VGKAQDMEQDMLDFASDVRENSRLSCQIKITPALDGLVVTTPSQQG

>2Fe-2SST1 (meta:Y590_22775) *Methylobacterium* sp. AMS5
 MPKITFVDHAGTARTIDGEGVSTVMETAIRNNVPGIDAECGGACACATCHVYVDGEWADK
 VGPAEPMEQDMLDFASDVRATSRLCCQIRVTPELDGLIVTTPARQG

>2Fe-2SST1 (maqu:Maq22A_c09135) *Methylobacterium aquaticum*
 MVQITYVDAAGTARSVKGEVSTVMETAIRNNVPGIDAECGGACACATCHVYVGEDWAEA
 VGPAEPMEQDMLDFASDVRPTSRLSCQIRLKPELDGLTVTTPARQG

>2Fe-2SST1 (bid:Bind_0539) *Beijerinckia indica*
 MTKMTFITFDGTSIPVEAENGEILMRVGQRCEIPGILGECGGTCSCGSCHVYIDESWRDR
 VPPVKELEQMMIDSLMTKQDNSRLTCMILVAPELDGLILHLPNPNL

>2Fe-2SST1 (bid:Bind_2346) *Beijerinckia indica*
 MVKITFIDSFGQHRTVEAEEGTTVMENAIRNGIPEIVAECGGGCACATCHVYVDEAFLEK
 TGKPSEKEEDMLDFAYKVQPN SRLSCQIKVRPELDGMTVTTPDRQG

>2Fe-2SST1 (msl:Msil_3549) *Methylocella silvestris*
 MPKITFVDSLGEARTVDAEVGSTVMEAAIRNAIPEIAAECGGGCACATCHVYVDDPWGKL
 TGKASDQEEDMLDFAYAVQPN SRLSCQITVTEELDGLHVTTTPDRQG

>2Fe-2SST1 (hdn:Hden_1632) *Hyphomicrobium denitrificans* ATCC
 51888
 MTKITFIQPDGEGQTVEVENGLTVMEAAKLNDVAGIEAECGGACACATCHVYVDKAWREK
 AGKPSEMEEDMLDFAFDVREESRLSCQIKISDALDGLIVRVPEKQF

>2Fe-2SST1 (hdt:HYPDE_30043) *Hyphomicrobium denitrificans* 1NES1
 MTKITFIQPDGESQTVEAENGLTVMEAAKLNDIAGIEAECGGACACATCHVYVDEAWREK
 TGKPSEMEEDMLDFAFDVREESRLSCQIKISDALDGLVVRVPEKQF

>2Fe-2SST1 (hmc:HYPMC_1912) *Hyphomicrobium* sp. MC1
 MTKITFIQPDGESQTVEAENGLTVMEAAKLNDIAGIEAECGGACACATCHVYVDDAWRDK
 VGKASDMEEDMLDFAFDVREGSRLSCQIKISDAIDGLVVRVPAKQF

>2Fe-2SST1 (hni:W911_11090) *Hyphomicrobium nitrativorans*
 MVKLTFIQPDGASQTVEADAGATVMEAAKQNDVPGIDAECGGACACATCHVYVDAAWVDK
 VGTPDPMEEDMLDFAFDVRKESRLSCQIKITDALDGITFRVPEKQF

>2Fe-2SST1 (phl:KKY_1900) *Pelagibacterium halotolerans*
 MITFVEPDGARREVEAENGATLMETAIRNGVRGIVAECGGACTCATCHVYVEEEWFGVTG
 GPSSMEEDMLDFAFDVKDTSRLSCQIKIRDDLDGLVVNVPSRQG

>2Fe-2SST1 (fil:BN1229_v1_2936) *Candidatus Filomicrobium marinum*
 W
 MAKITFIQPDGSTQVVEATPGTTVMEAAKLNGVPGIEAECGGACACATCHVYVSDDWREQ

VGAPSEMEEDMLDFAFDVRESSRLSCQIKVTDALDGLVLSVPAKQF
 >2Fe-2SST1 (fiy:BN1229_v1_2981) *Candidatus Filomicrobium marinum*
 Y
 MAKITFIQPDGSTQVVEATPGTTVMEAAKLNQVPGIEAECGGACACATCHVYVSDDWREQ
 VGAPSEMEEDMLDFAFDVRESSRLSCQIKVTDALDGLVLSVPAKQF
 >2Fe-2SST1 (deq:XM25_10565) *Devosia* sp. H5989
 MTKITYVEPDGSRIEVEAENGSTVMENAIMNGVPGIVAECGGACTCATCHVYVDDAWTET
 VGGPSVMEEDMLDFAFDVRENSRLSCQIKVRDELGLVNVNPTREQ
 >2Fe-2SST1 (rhz:RHPLAN_49350) *Rhodoplanes* sp. Z2-YC6860
 MPKITFIDFAGSSRTIDADVGATVMETAIKNDVPGIEAECGGACACATCHVYVDEAWREK
 VGGPTPMEEDMLDFGYDVKNPNSRLSCQIKVTDALDGLVVRTPERQA
 >2Fe-2SST1 (rhz:RHPLAN_48480) *Rhodoplanes* sp. Z2-YC6860
 MPKITYIEQDGTERTVEAEAGSTVMETAINDIPGILATCGGSCSCATCHVYVDEDWVDK
 LPPPELDENDMLDTAHDLQENSRLSCQIKVTDELGLIVTTTPARQI
 >2Fe-2SST1 (msc:BN69_2605) *Methylocystis* sp. SC2
 MAKFTLET RDGARQDIAGKNGVSLMKLIRRGVEELVAQCGGSCACATCHVYLTLPQGIE
 MASSGPGESRMLATASHRKFNRLACQIRFDDILDGMEIRIAPEDATGF
 >2Fe-2SST1 (mbry:B1812_15995) *Methylocystis bryophila*
 MTFVDSKGQARTVEGEVGSTVMETARRNDIPEIAAECGGACACATCHVYVDAAWLEKTGA
 RSQMEEDMLDFAFAVEQNSRLCCQIVVKPELEGLILRTPAQGG
 >2Fe-2SST1 (mbry:B1812_21155) *Methylocystis bryophila*
 MASFTLETREGARSEVKAKDGVTLMKLIRRSGAEELVAQCGGSCACATCHVYVSPREGVT
 LPPMRPDESRLATAGERRMTRSLACQIKFDAALDGMHVTIAPENLDDI
 >2Fe-2SST1 (mey:TM49_15150) *Martelella endophytica*
 MLKLKFIGNDETVDLEVPSSVMENAVRNSVPGIEAECGGACACATCHVYVDPDWMMAK
 VGEPEPMEEDMLDFAIDVRANSRLSCQIEMRDELGLTVRIPERQG
 >2Fe-2SST1 (mcg:GL4_1666) *Methyloceanibacter caenitepidi*
 MLKVTFIQPDGIENTVEAEPGMTLMEEAVKNSVRGIAAECGGACSCATCHVYVEEAWREA
 TGEPEAMEEDMLDFAFDVRPSSRLSCQIRLTEELDGLTVRIPEKQF
 >2Fe-2SST1 (psin:CAK95_17970) *Pseudorhodoplanes sinuspersici*
 MSKITFIEHDGTVHEVEAETGETVMEAA MRGGVSGIVAECGGSCATCHVYVDEAWLDK
 TGERSPDEEDQLDNAYDVRANSRLSCQIKISEELDGLLVRTPSYQGR
 >2Fe-2SST1 (psin:CAK95_17965) *Pseudorhodoplanes sinuspersici*
 MAKITFIDHGGESRTVDAENGATVMETAIKNGIPGIEAECGGACACATCHVYVDEAWTEV

VGAPSPMEEDMLDFGFDVKPNSRLSCQIKVTDQLDGLVLRTPERQA
 >2Fe-2SST1(ccr:CC_3524) *Caulobacter vibrioides* CB15
 MAKITYIQHDGAEQVIDVKPGLTVMGAVKNNVPGIDADCGGACACATCHVYVDEAWLDK
 TGDKSAMEESMLDFAENVEPNSRLSCQIKVSDALDGLVVRLPESQH
 >2Fe-2SST1(ccs:CCNA_03639) *Caulobacter vibrioides* NA1000
 MAKITYIQHDGAEQVIDVKPGLTVMGAVKNNVPGIDADCGGACACATCHVYVDEAWLDK
 TGDKSAMEESMLDFAENVEPNSRLSCQIKVSDALDGLVVRLPESQH
 >2Fe-2SST1(cak:Caul_4835) *Caulobacter* sp. K31
 MAKITYIEHDGTDHVIDVKPGLTVMGAVKNNVPGIDADCGGACACATCHVYVDEAWLPK
 TGEKSAMEESMLDFAENVEPNSRLSCQIKVSDALDGLVVRLPESQH
 >2Fe-2SST1(cse:Cseg_0160) *Caulobacter segnis*
 MAKITYIEHDGTEHALDVKPGLTVMGAVKNNVPGIDADCGGACACATCHVYVDEAWLDK
 TGDKSAMEESMLDFAENVEPNSRLSCQIKVTDALDGLVVRLPESQH
 >2Fe-2SST1(cse:Cseg_3028) *Caulobacter segnis*
 MPKITFIQHDGATLVVEGRPGQSLMEAAVQNNVPGIDADCGGACACGTCQVHVQAPWQEA
 LTLPSAMEAEMLSFTSDPQPSSRLACQIILEERHEGLMVRVPAHQH
 >2Fe-2SST1(aex:Astex_0212) *Asticcacaulis excentricus*
 MPKITYIESNGKTHEIEVKTGNSVMEGAIKHNIPGIDADCGGACACATCHVYVDAEWFDK
 TGGPSVMEESMLDFAQDVEPTSRLSCQIRVTEALDGLIVRLPESQH
 >2Fe-2SST1(psf:PSE_4116) *Pseudovibrio* sp. FO-BEG1
 MPKITFITSSGESHEVDAAAGSTVMENAIKNMVPGIEAECGGACACATCHVYVDPANNDK
 TGEPEPMEEDMLDFAQDVRDTSRLSCQIRVTDEMDGLVVHIPESQS
 >2Fe-2SST1(con:TQ29_05630) *Confluentimicrobium* sp. EMB200-NS6
 MAKIIFVDHDGTHKEVEASVGSNVMQAAVDNNIEGIDGDCGGMCAATCHVTVDPEWFAK
 TGARSENEESMLTFLPEIAETARLGCQIEITDELDGLVVHLPIEQF
 >2Fe-2SST1(con:TQ29_19120) *Confluentimicrobium* sp. EMB200-NS6
 MSIQVVFIDSMGERREVSSREGQSLMEAAATMAGVPGIDADCGGACACATCQVYVDPKWLS
 LLPPTSEGEASMLEFAANRQDSSRLACQIRLTADLDGLTVTTPEFQF
 >2Fe-2SST1(pphr:APZ00_14900) *Pannonibacter phragmitetus*
 MPKITFITADGARHDVEAASGATVMESAIAKHMVPGIEAECGGACACATCHVYVDEEWSAR
 AGSPDPMEEEDMLDFAYDVKNPNSRLSCQIKMSDELGDGIVVHVPERQA
 >2Fe-2SST1(pphr:APZ00_07260) *Pannonibacter phragmitetus*
 MPRIIFQSADGTRTEVEAASGQSLMSAAVAHGIEEIAAECGGACACGTCHCYIPEGQGIT
 LPEAEEMELAMIECVIDPRPQSRLTCQVTVSEAMDGLVVVELPASQH

>2Fe-2SST1(lap:ACP90_10170)*Labrenzia* sp. CP4
MPKITFVTADGTRTDVDAEAGSTVMENAIKNMVQGIEAECGGACACATCHVYVDDAWSGK
TGSPEPMEEDMLDFAYDVKPTSRLSCQIKVTSDDLGLVVHVPERQA

>2Fe-2SST1(lagg:B0E33_22090)*Labrenzia aggregata*
MPKITFVTADGTRTDVDAEAGSTVMENAIKNMVQGIEAECGGACACATCHVYVDDAWSGK
TGSPEPMEEDMLDFAYDVKPTSRLSCQIKVTSDDLGLVVHVPERQA

>2Fe-2SST1(mmr:Mmar10_0081)*Maricaulis maris*
MPKITIYIEHNGTEHVIDVATGLTVMGAVRNLPVGIDADCGGACACATCHVYVDPAWADK
TGSREAMEDSMLDFAEEVQETSRLSCQIKVSDGLDGLVVRMPQNQG

>2Fe-2SST1(hne:HNE_1889)*Hyphomonas neptunium*
MAKITVYVSHDGTERTVEAKNGESVMEAAIKNSIPGIDADCGGACACATCHVYVDEAFLDK
AGTQEEMEKSMLDFAENVKPNLSRLSCQIKVSDALDGLRVSTPESQH

>2Fe-2SST1(ba:Hbal_2335)*Hirschia baltica*
MAKITIYIEHDGTEHSVDAKNGSSVMEAAIRENVPGIDADCGGACACATCHVYVDASFMDK
VGAPNDMEQSMLDFAEGVESNSRLSCQITVKDDLGLIVRMPESQT

>2Fe-2SST1(hbc:AEM38_00300)*Hyphomonadaceae bacterium* UKL13-1
MAKVITYIEHSGTEHVIEVPVGTTIMEGAVKNRVPGIDADCGGACACATCHVFVDAAWIEK
TGKPGSMEESSMLDFAEGVTPLSRLSCQISMTSDLDGIVVRLPAAQH

>2Fe-2SST1(smaz:LH19_03020)*Sphingopyxis macrogoltabida* 203
MPSVNFHAADGSVETIEIEVGDSVMRGARDNMVEGIEADCGGVCACATCHIYIAPDWLER
VGPAGADESEMLDCVNDPRPNSRLSCQIAMTDDLEGLTVFLPESQR

>2Fe-2SST1(swi:Swit_0285)*Sphingomonas wittichii*
MMTEIRFIDADGAVTIARGDNGFSLMEVAKRHGVSGIVAECGGSCACATCHVHVDAAWLE
AVGEPNPGEADMLDFARGRRPDSRLSCQIRITPALDGLIVHVPESQG

>2Fe-2SST1(sch:Sphch_3064)*Sphingobium chlorophenolicum*
MANLIVVDRSGQEHVIEAANGWSVMEAIRDNGIDELLALCGGCCSCATCHVYVDETQNAR
FAAMTDDENDLLDSSDYRKTNLSRLSCQLIVDGTPEIIRLSIAPED

>2Fe-2SST1(aep:AMC99_00144)*Altererythrobacter epoxidivorans*
MVLVSIVADNGTVHEVAASVGLSMEAAAMNDVPGIEGDCGGFCACGTCHCYVDESDAAI
LPDMHELERATLDFAYDVTERSRLACQIPITEQMDGIRVRLPARQY

>2Fe-2SST1(azl:AZL_b01710)*Azospirillum* sp. B510
MPTITFIQANGTEHTVTFDPGKTLMQAAVDNLVPGIQADCGGYCNCATCHCFVEPPWEAT
LPAPEQPEQDMLTCAIDPQPNSRLSCQIVLTEAMSGLVVRLPVSQT

>2Fe-2SST1(pgv:SL003B_1500)*Polymorphum gilvum*

MPHITYITADGSRHEVDAAEGTTVMENAIKMNVPGIEAECGGACACATCHVYVDEAWAER
 VGHPEPMEEDMLDFAYDVRPTSRLSCQIKVTAALDGLVVHVPERQA
 >2Fe-2SST1 (pgv:SL003B_4084) *Polymorphum gilvum*
 MTINLVFIDSSGARREITSPEGQSLMETATMAGIPGIDADCGGACACATCQVYVAEEWVG
 KLPPIAEAEANMLEFAANRQANSRLACQIRLTPELDGLTVTTPEFQF
 >2Fe-2SST1 (pgv:SL003B_4103) *Polymorphum gilvum*
 MAINLVFIDSTGERREISAAEGRTLMEAACLAGIPGIDADCGGACACATCQVYVDAEWQS
 RLPPVGNPEANMLNFAANRRENSRLACQIRLTAEMDGLIVSTPEFQF
 >2Fe-2SST1 (gdi:GDI2370) *Gluconacetobacter diazotrophicus* PA1 5
 (Brazil)
 MIFIESDGTREVDAPVGLSVLEIAHKHGVLDLEGACEGSLACATCHVVVDPDWAPKLAAP
 TEDEEDMLDLAFGLEKTSRLGCQIVMTEALDGLVVRLPHKA
 >2Fe-2SST1 (aace:A0U92_16090) *Acetobacter aceti*
 MPHMI FVEPDGTERKVDAPVGLSVLEIAHKHGVLDLEGACEGSLACATCHVIVDPSWAPKL
 SEATEDEEDMLDLAFGLEATSRLGCQIIMNDEL DGLTVRLPRKS

 >2Fe-2SST1 (apb:SAR116_1022) *Candidatus Puniceispirillum marinum*
 MPNIIFVKPDGTELVNVNNEGVSVMEAGRDANLGIEGTCCGGCLSCATCHVIVDADWFAKT
 GAPSEDEEDMLDLAFGLTETSRLGCQLTMSAELDGIRLTIPDDM
 >2Fe-2SST1 (rtr:RTCIAT899_PC02805) *Rhizobium tropici*
 MCEIVFIDSAGRETRVEAQEGETLMVAVRSGIDGIVAQCGGALACGTCHCYIEQPHLDR
 LPPPSEEEAMMIEFVMEPMPNSRLSCQILASSVVDGMRVIVPDSQH
 >2Fe-2SST1 (gdj:Gdia_0615) *Gluconacetobacter diazotrophicus* PA1 5
 (JGI)
 MPHMI FIESDGTREVDAPVGLSVLEIAHKHGVLDLEGACEGSLACATCHVVVDPDWAPKL
 AAPTEDEEDMLDLAFGLEKTSRLGCQIVMTEALDGLVVRLPHKA
 >2Fe-2SST1 (mgy:MGMSRv2__1381) *Magnetospirillum gryphiswaldense*
 MSR-1 v2
 MPKMTFITADGSRNEVEAPEGLSVLEIAHRNKIDLEGACEGSLACSTCHIVVDPDWYERL
 AAAEEDEEDMLDLAFGLTSTSR LGCQIIMKQELDGLVVTVPAATRNM SVDDK
 >2Fe-2SST1 (magq:MGMAQ_2629) *Magnetospira* sp. QH-2
 MPKMTFIEPNGTRREVDAPLGQSVLEIAH HNKIDLEGACEGSLACSTCHVIVDQEWYDKL
 EEASEDEEDMLDLAFALHTSR LGCQIVISEELDGLVVNLPAATRNVAVDDK
 >2Fe-2SST1 (azl:AZL_020110) *Azospirillum* sp. B510

MPKMTFIETDGTREVDAPLGLSVLEIAHKNSLDLEGACEGSLACSTCHVVIEPEWFDVL
PEAQEDEEDMLDLAFGLTKTSRLGCQIIMTEELDGLVVRLPGGSNNAMK
>2Fe-2SST1(abq:ABAZ39_09740)*Azospirillum brasilense* Az39
MPKMTFIEPNGTRHEVDAPLGLSVLEVAHKHGLDLEGACEGSLACSTCHVIVEPEWFDVL
NEASEDEEDMLDLAFGLTKTSRLGCQIIISEELDGLAVRLPGGTNNAMR
>2Fe-2SST1(sph1:LPB140_08735)*Sphingopyxis* sp. LPB0140
MVKVIFTNISGSVIQVEGNEGDCLLDVGQAAGQPLEGTCEGQMACSTCHVIVKDAWFDK
LPPASENEEDMLDLAAGARRTSRLSCQILLTKDL DGLTVAIPSES SRNMQGL
>2Fe-2SST1(sphg:AZE99_06970)*Sphingorhabdus* sp. M41
MKKITVHFVSSDGEKTVTAEESEGDNLLTVAQIHDQPLEGTCEGQMACSTCHVIVESADF
DRLPEATEMEEDMLDLAAGARRTSRLACQITLTADLDGLTVHMPVESHNMQIV
>2Fe-2SST1(blas:BSY18_949)*Blastomonas* sp. RAC04
MIEVTFISADGKSRQTVQAQDGDRLLDVAQAHGLPLEGTCEGQMACSTCHLIIDAADFAK
LPEPVEMEEDMLDLAVAVTRTSRLSCQIFLRDEWQSLTCRVP AESYDMQGM
>2Fe-2SST1(sphi:TS85_09595)*Sphingomonas* sp. WHSC-8
MIRVRFVSADGARLREVEGGEGDRLLELAQNDGQPLEGTCEGQMSCSTCHVIVADEDFER
LPRASEEEEEEDMLDLAVGATRTRSLACQILLTPDL DGLTVRMP PGHRDMQGR
>2Fe-2SST1(sgi:SGRAN_2433)*Sphingopyxis granuli*
MRVTFIHADGKGRTAEAEVPGDILLDVAQAHLMPLEGTCEGQMACSTCHVIVAREDFDRL
PPASEEEEEEDMLDLAAGARRTSRLSCQVVLTEALDGLTVHIPGES SRNMQGAR
>2Fe-2SST1(sal:Sala_0795)*Sphingopyxis alaskensis*
MRVTFIHADGKGRTAEAEAPGSTLLDVAQAHLI PLEGTCEGQMACSTCHVVVESQDFDRL
PPASEMEEDMLDLAAGARRTSRLSCQIVLTEDMDGLTVRI PAES SRNMQGVR
>2Fe-2SST1(sphk:SKP52_07080)*Sphingopyxis fribergensis*
MRVTFIHADGKARTEAEAEPGSILLDIAQAHMMPLEGTCEGQMACSTCHVIVAKEDFDRL
PPASEMEEDMLDLAAGVRRTSRLSCQIVLTEALAGLTVHIPAES SRNMQGPR
>2Fe-2SST1(sphp:LH20_07565)*Sphingopyxis* sp. 113P3
MRVTFIHADGKRRTAEAEAPGDILLDVAQAHMMPLEGTCEGQMACSTCHVIVAKEDFGRL
PPASEEEEEEDMLDLAAGVRRTSRLSCQIVLTEDLDGLTVHIPAES SRNMQGPR
>2Fe-2SST1(smaz:LH19_10545)*Sphingopyxis macrogoltabida* 203
MRVTFIHADGKQRTEAEAEPGSILLDVAQAHMMPLEGTCEGQMACSTCHVIVAKEDFDRL
PEASEMEEDMLDLAAGVRRTSRLACQIVLTDALDGLTVHIPAES SRNMQGPR
>2Fe-2SST1(ster:AOA14_14170)*Sphingopyxis terrae*
MRVTFIHADGKGRT EVVAEPGSILLDVAQAHMMPLEGTCEGQMACSTCHVIVAKEDFGRL

PPASEMEEDMLDLAAGVRRTSRLSCQIVLTEDLDGLTVHIPSESRNMQGR

>2Fe-2SST1(sphm:G432_03420) *Sphingomonas* sp. MM-1

MGGMTTVRFVSADGSHIDEVEAPAGARLLDVAQANGQPLEGTCEGQMACSTCHVIVDRED

FPKLDEATEMEEDLLDLAASVTRWSRLACQVYLPEGLESLTVRIPGESRNMQGR

>2Fe-2SST1(swi:Swit_0053) *Sphingomonas wittichii*

MTRVVFISADGEHRSEVEASPGQHLLDVAQADGQPLEGTCEGQMACSTCHVIVDAADFAR

LPRASEMEEDLLDLASHVTRTSRLACQIVLTDALDGLTVRMPVGARNMQGR

>2Fe-2SST1(ssy:SLG_13390) *Sphingobium* sp. SYK-6

MTRITFISANGADVMEVEAAPGDTLLDIAQAAGQPLEGTCEGQMACSTCHVIIDPADFPK

LPRASEEEEEEDMLDLAAATTRTSRLACQIVLSEAMESLTVRIPPESRNMQGL

>2Fe-2SST1(sbd:ATN00_13340) *Sphingobium baderi*

MTRVTFISADGESRQEVDAPAGSVLLNVAQAAGQPLEGTCEGQMACSTCHVIVDAADFSR

LPRATEEEEEEDMLDLAASATRTSRLSCQIVLDAALESLTVRIPPETYNMQGM

>2Fe-2SST1(spmi:K663_07205) *Sphingobium* sp. MI1205

MIRVTFISADGENRQEVDADVGSVLLDVAQAAGQPLEGTCEGQMACSTCHVIVEAQDFPR

LKAASEAEEDMLDLAAAATRTSRLSCQIVLDDKLDGLTVRIPSESCNMQGM

>2Fe-2SST1(sphb:EP837_00295) *Sphingobium* sp. EP60837

MIRVTFISADGENRQEVDAAAGSVLLDVAQAAGQPLEGTCEGQMACSTCHVIVEAGDFSK

LKAASEAEEDMLDLAAAATRTSRLSCQIVLEEKLDGLTVRIPGESHNMQGM

>2Fe-2SST1(sphr:BSY17_609) *Sphingobium* sp. RAC03

MTRVTFISADGERRQEVDAPAGSVLLDIAQAAGQPLEGTCEGQMACSTCHVIVEATDFPR

LGRASEDEEDMLDLAASATRTSRLSCQIILADGLDQLTVRIPPESYNMQGM

>2Fe-2SST1(sjp:SJA_C1-21730) *Sphingobium japonicum*

MTRVVFISADGEHKQEVEAPPGAVLLDVAQAAGQPLEGTCEGQMACSTCHVIVDAADFSK

LGKASEDEEDMLDLAAAATRTSRLSCQIVLDEQLDSLTVRIPGESYNMQGM

>2Fe-2SST1(sch:Sphch_0633) *Sphingobium chlorophenolicum*

MTRVIFISADGENKQEVEAPAGSVLLNIAQAAGQPLEGTCEGQMACSTCHVIVDAADFPK

LKKASEDEEDMLDLAAAATRTSRLSCQIVLDEKLESLTVRIPGESYNMQGM

>2Fe-2SST1(sinb:SIDU_04495) *Sphingobium indicum*

MTRVVFISADGEHKQEVEAPPGAVLLDVAQAAGQPLEGTCEGQMACSTCHVIVDAADFSK

LGKASEDEEDMLDLAAAATRTSRLSCQIVLDEQLDSLTVRIPGESYNMQGM

>2Fe-2SST1(syb:TZ53_17235) *Sphingobium* sp. YBL2

MTRVVFISADGEHKQEVEAPTGAVLLEVAQAAGQPLEGTCEGQMACSTCHVIVDAADFPK

LKRASEDEEDMLDLAAAATRTSRLSCQIVLDEKLDLTVRIPGESYNMQGM

>2Fe-2SST1 (aep:AMC99_01768) *Altererythrobacter epoxidivorans*
MTITVRFIDARGGVTEATAEAGDNLRLVAQAAGMPLEGTCEGQIACSTCHVIVADDWFGK
LPDASEEEEEEDMLDFAAGVKRCSRLSCQIELTPEMDGLTVTIPIESYDMRRK

>2Fe-2SST1 (anh:A6F65_01188) *Altererythrobacter namhicola*
MSITVHFTSRDGRHTAIAEPGDNLRLVAQAAGMPLEGTCEGQMACSTCHVVVAAEWFDR
LAEPSEEEEEEDMLDLAANVRRTSRLSCQVDLTPELDGLEVEIPAESH DARLF

>2Fe-2SST1 (ado:A6F68_01585) *Altererythrobacter dongtanensis*
MIKVTFTTEPRGGVIEAEAE PGDNLLRLGQAKGLPLEGTCEGQMACSTCHVIVAAEWFDR
PPASEEEEEEDMLDLAAGACRTSRLACQIELTPDL DGLAVRVPADSHDARRL

>2Fe-2SST1 (nnp:JI59_02495) *Novosphingobium pentaromativorans*
MLSVRFVTTDGNKLTVEAEAGACLLVAQAAGMPLEGTCEGQMACSTCHVIVSPEWFDKL
KPASADEEDMLDLAAGVTRTSRLSCQIELTEALDGI ELRIPGVSHDMQID

>2Fe-2SST1 (nar:Saro_2796) *Novosphingobium aromaticivorans*
MVRVTFVKPDGEKVS AE GEEGQRLLEVGNVGM PLEGTCEGQMACSTCHVVIDAAWFDRL
PPAVDDEEDMLDLAAGVTRTSRLSCQIELTEALDGLV VHPSEVQDMQGR

>2Fe-2SST1 (eli:ELI_02205) *Erythrobacter litoralis* HTCC2594
MKIVFETAEGA AVEAE AAPGDTLLAIAQAAGLPLEGTCEGQMACSTCHVIVAKEWFAQLP
EASEEEEEEDMLDLAYGVSATSRLSCQIELTEKMDGLTVRIPSDSRDMSGV

>2Fe-2SST1 (cij:WG74_08040) *Citromicrobium* sp. JL477
MKVIFHKADGQ RVEAE AQAGDVLLRVAQAAGMPLEGTCEGQMACSTCHVLVAKWFAQLP
EASEDEEDMLDLAYGVRPTSRLSCQITLTDALDGM EVTIPADAHDMGR

>2Fe-2SST1 (amx:AM2010_1166) *Altererythrobacter marensis*
MSVRVRFVSARGAVTEAEGAEGTPLLELAQAAGMPLEGTCEGQMACSTCHVIVAAEWFAR
LPASEEEEEEDMLDLAAGVQRTSRLSCQILLSAELDGLVQIPSES RDMSVL

>2Fe-2SST1 (cna:AB433_09775) *Croceicoccus naphthovorans*
MVHVNFVTAKGEKVEAEAAEGD SLLKVAQAAGMPLEGTCEGQMACSTCHVVVAPAWFGKL
PISSEDEEDMLDLAADVQGTSRLSCQIVLDAPLDGLEVRIPSQVHDVQRG

>2Fe-2SST1 (pns:A9D12_09360) *Porphyrobacter neustonensis*
MSITITFIDPRGKPV EVAADSGDNLRLRVGQAAGLPLEGTCEGQMACSTCHVIVAPEWFDR
LLPAAEEEEEDMLDFAAGARRTSRLSCQIELTAEMDGLTVTIPAASTDARRM

>2Fe-2SST1 (por1:BG023_111367) *Porphyrobacter* sp. LM 6
MSITITFLDPHGKAIETKAKPGDNLRLRVGQAAGLPLEGTCEGQMACSTCHVIVAAEWFDR
LPHASEEEEEEDMLDFAAGARRTSRLSCQIELTAELDGLTVSVPKESNDLRRM

>2Fe-2SST1 (elq:Ga0102493_1175) *Erythrobacter litoralis* DSM 8509

MGIKVRFIDPQGRAVEAEGEPGDSLLRVGQAAGLPLEGTCEGQMACSTCHVIVAPEWFDR
 LAQASEEEEEEDMLDFAAGVRRSRLSCQIELTDEMDGLTVSVPSESIDARRM
 >2Fe-2SST1 (sphr:BSY17_1914) *Sphingobium* sp. RAC03
 MPKLIVVNRAGEEQAVEGDNGLSVMEVIRDNGFDELLALCGGCCSCATCHVYVDPDFADV
 LPAMTEDENDLLDSSDHRNDTSRLSCQVVLSDALDGLRVTIAPED
 >2Fe-2SST1 (nar:Saro_1115) *Novosphingobium aromaticivorans*
 MPKIVVVNRAGEEKTVDADAGLSVMEAIRDNGFDELLALCGGCCSCATCHVYVDPAFADK
 IPAMSEDENDLLDSSDHRNESSRLSCQVQITGDL DGLRVTIAPED
 >2Fe-2SST1 (sinb:SIDU_09805) *Sphingobium indicum*
 MAKLIVVNRSGEEQAVEAQSGLSVMEIIRDNGFDELLALCGGCCSCATCHVFVDPAFADS
 LPAISEDENDLLDSSDHRNETSRLSCQLQFSDSLDGLRVTIAPED
 >2Fe-2SST1 (sjp:SJA_C1-08030) *Sphingobium japonicum*
 MAKLIVVNRSGEEQAVEAQSGLSVMEIIRDNGFDELLALCGGCCSCATCHVFVDPAFADS
 LPAISEDENDLLDSSDHRNETSRLSCQLQFSDSLDGLRVTIAPED
 >2Fe-2SST1 (sch:Sphch_1567) *Sphingobium chlorophenolicum*
 MAKLIVVNRSGEEQAVEAQSGLSVMEIIRDNGFDELLALCGGCCSCATCHVFVDPAFADS
 LPPVSEDENDLLDSSDHRNETSRLSCQLTFSDSLDGLRVTIAPED
 >2Fe-2SST1 (syb:TZ53_13050) *Sphingobium* sp. YBL2
 MAKLIVVNRSGEEQAVEAENGLSVMEIIRDNGFDELLALCGGCCSCATCHVFVDPAFADN
 LPPISDDENDLLDSSDHRNETSRLSCQLTFSDSLDGLRVTIAPED
 >2Fe-2SST1 (sbd:ATN00_00140) *Sphingobium baderi*
 MPKLIVVNRGEERAVIDGDNGLSVMEIVRDNGFDELLALCGGCCSCATCHVYIDPAFADK
 LPAMSEDENDLLDSSDHRNEQSRLSCQIMISDDL DGLRVTIAPED
 >2Fe-2SST1 (spmi:K663_03095) *Sphingobium* sp. MI1205
 MPKLIVVNRSGEEQAVEGDNGLSVMEVIRDNGFDELLALCGGCCSCATCHVYVDPAFADK
 LPAISEDENDLLDSSDHRNDSSRLSCQLVMNAELDGLRVTIAPED
 >2Fe-2SST1 (spmi:K663_17356) *Sphingobium* sp. MI1205
 MAKLTVVNRSGEEQTIEAQDGLSVMEILLRDNGFDELLALCGGCCSCATCHVYVDPFADS
 LPTISDDENDLLDSSDHRNEHSRLSCQLPFSDSL DGLRVTIAPED
 >2Fe-2SST1 (sphb:EP837_01905) *Sphingobium* sp. EP60837
 MAKLIVVNRSGEEQAVEGDNGLSVMEVIRDNGFDELLALCGGCCSCATCHVYVDPAFADK
 LPALSEDENDLLDSSDHRNDSSRLSCQLVLNDDL DGLRVTIAPED
 >2Fe-2SST1 (sphi:TS85_16420) *Sphingomonas* sp. WHSC-8
 MPKLIVVTREGEERTVDGDTGLSVMEVIRDNGFDELLALCGGCCSCATCHVHVDPFEFAAK

LPPMSEDENDLLDSASDRNDQSRLSCQIPFTDALDGLKVTIAAED
 >2Fe-2SST1 (cna:AB433_13620) *Croceicoccus naphthovorans*
 MPNIIIVDREGNEKTVEADDGLTVMEAIRDNGFDELLALCGGCCSCATCHVYVDPFAFAAK
 LPELSEDEDDLLDSSDHRNETSRLSCQIPLNADLDGIKVTIAPED
 >2Fe-2SST1 (npn:JI59_08680) *Novosphingobium pentaromativorans*
 MPKLTIVTREGEEREIAAEEGRSVMEVIRDAGFDELLALCGGCCSCATCHVMVAPEFADR
 LPPISEDENDLLDSSEHRTELSRLSCQLPVTESIDGLRITIAPED
 >2Fe-2SST1 (sgi:SGRAN_3239) *Sphingopyxis granuli*
 MPSLTVVDREGTAHTLEADAGLTLMEVIRDNGFDELLALCGGCCSCATCHIHVDPAFAAK
 LPAMSDDENDLLDSSSEDRNETSRLSCQIPFDDALDGIKVTIARED
 >2Fe-2SST1 (sph1:LPB140_05125) *Sphingopyxis* sp. LPB0140
 MPTINVIDRSGAKREVEAEMGLSVMEVIRDNGFDELLALCGGCCSCATCHVYIDA EYADK
 IPAMQEDDDLLLESTDHRNATSRLSCQIEVSDAIDGMTVTIAPED
 >2Fe-2SST1 (blas:BSY18_2454) *Blastomonas* sp. RAC04
 MPKINLVTRDGTASII EAGDTLTLMEAIRDNGCDELLALCGGCCSCATCHVHIDDAFLAR
 IPAMSEDENDLLDSSSEHRNANSRLSCQIALTEALDGITVTLAKED
 >2Fe-2SST1 (syb:TZ53_18515) *Sphingobium* sp. YBL2
 MPELNVITRDGAQQQTINASADTSVMEAIRDSGFDELLALCGGCCSCATCHVYVDPFAFAQS
 LPPVSDDESDLLDGSPHRNDYSRLSCQVMMTEALSGLTITIAPED
 >2Fe-2SST1 (sbd:ATN00_17430) *Sphingobium baderi*
 MPELNVITRDGAQQIINATADVSVMEAIRDAGFDELLALCGGCCSCATCHVYVDPFAFAAS
 LPPVSDDESDLLDGSPHRNDYSRLSCQVVMTDALSGLTVTIAPED
 >2Fe-2SST1 (sphi:TS85_13360) *Sphingomonas* sp. WHSC-8
 MAEIRITTRDGVVERPVAMTPGYSLMEAIRDAGIDELMALCGGSCSCATCHVFIDPEFADR
 LPPISEDDEDDLLDSSDHRGPTSRLSCQIPLSDALDGLAATIAPED
 >2Fe-2SST1 (sbd:ATN00_07550) *Sphingobium baderi*
 MSTLNIVTRDGS AVRVTPEPGLSVMEIIRENGIDELMALCGGCCSCATCHVFIAEDSFQ
 LPAMSADEDDLLDSSSEHRRHVSRLSCQIPWSDVLDGLTITIAPED
 >2Fe-2SST1 (rhi:NGR_b14760) *Sinorhizobium fredii* NGR234
 MEEDMSNFTVISRNGQVVPPIEGREGISVMEHIRDAGVDELLALCGGCCSCATCHVYVDDD
 FQEHLPALTVDEDDLLDSSDHRRSQSRLSCQIRFAPELKGMIIVTLAPED
 >2Fe-2SST1 (rhi:NGR_b16340) *Sinorhizobium fredii* NGR234
 MSNFTVISRNGQIVPVEGRDGISIMEHIRDAGVDELLALCGGCCSCATCHVYVDDDFQEH
 LPSLSVDEDDLLDSSDHRRPQSRLSCQVRFTAELAGMIIVTLAPED

>2Fe-2SST1 (eli:ELI_01725) *Erythrobacter litoralis* HTCC2594
 MPKLVVTTREGETSEVQVDDGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDES FVEK
 LPRMSEDEDDLLESSDHRESNSRLSCQIPFTPDL DGLKVTIAPED

>2Fe-2SST1 (elq:Ga0102493_11208) *Erythrobacter litoralis* DSM 8509
 MPKLVVTNREGETSEIDVEDGLTVMEAIRDNGFDELLALCGGCCSCATCHIHVDPAAMDK
 LPAMSEDEDDLLESSDHRTETSRLSCQIPFTDAL DGLKVTIAPED

>2Fe-2SST1 (aep:AMC99_01878) *Altererythrobacter epoxidivorans*
 MPKLIVTTREGETSEIQVDDGLTVMEAIRDNGFDELLALCGGCCSCATCHIHVDPSFKDK
 LPAMSEDEDDLLESSDHRNENSRLSCQIPFTSDLDGLKVTIADED

>2Fe-2SST1 (anh:A6F65_02274) *Altererythrobacter namhicola*
 MPKLIVTTREGETTEVDVESGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDAQYKDK
 LPAMSEDEDDLLDSSDHRDDTSRLSCQIPFTDELDGLKVTIAQED

>2Fe-2SST1 (pns:A9D12_08835) *Porphyrobacter neustonensis*
 MPRLVVTNREGATSEIEVG DGLTVMEAIRDNGFDELLALCGGCCSCATCHVVVDPAFADK
 LPKISEDEDDLLESSDHRVATSRLSCQIPLTADLDGLHVTIAPED

>2Fe-2SST1 (por1:BG023_111277) *Porphyrobacter* sp. LM 6
 MPRLVVTNREGTTSEIEVSDGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDPAFADK
 LPKMSEDEDDLLESSDHR AAGSRLSCQIPFTADLDGLHVTIAPED

>2Fe-2SST1 (aay:WYH_01357) *Altererythrobacter atlanticus*
 MPKLLVVTRDGEERTVEADSG LTVMEVVRDNGFDELLALCGGCCSCATCHVHVDPAFKDK
 LPAMSEDEDDLLDSSEHRDENSRLSCQIPFTDELDGMKVRIAEED

>2Fe-2SST1 (ado:A6F68_01490) *Altererythrobacter dongtanensis*
 MPKLIVVNRAGEEKAVDVADGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDPAFKER
 LPAMSEDEDDLLESTDHRDENSRLGCQVPFTADLDGMRVTIAQED

>2Fe-2SST1 (amx:AM2010_425) *Altererythrobacter marensis*
 MPKLIVVNRSGEESSIDVEDGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDPAFRDK
 LPAISEDEDDLLESSDHRDENSRLGCQIPFTGDL DGLKVSIAQED

>2Fe-2SST1 (sphm:G432_02590) *Sphingomonas* sp. MM-1
 MPKLFVVTREGEKVV DGGQIGLTVMENIRDNGFDELLALCGGCCSCATCHVHVDAADF DK
 LKPMGDDENDLLDSSDHRVATSRLSCQIPFTEELDGLRV TIAPED

>2Fe-2SST1 (cij:WG74_07555) *Citromicrobium* sp. JL477
 MPKLTVVDRSGTERTIEVG DGLTVMEAIRDNGFDELLALCGGCCSCATCHVHVDPAFGDK
 LPAMSEDEDDLLESSDHRNETSRLSCQIEFTSDLDGLKVQIAPED

>2Fe-2SST1 (blas:BSY18_1559) *Blastomonas* sp. RAC04

MPKLIVVNRAGEESTIEADTGLSVMEAIRDNGFDELLALCGGCCSCATCHVHVDAEWTDK
LPPVSADEDDLLDSSDHRNATSRLSCQIQMTAALDGLKVAIAPED
>2Fe-2SST1 (sphr:BSY17_102) *Sphingobium* sp. RAC03
MPKLIVVNRAGDETSVDARDGVSVMEAIRDNGFDELLALCGGCCSCATCHVYVDEEWTRA
VGTPGEDENDLLDSSDHRGDRSRLSCQIMMTAGLDGLRVIAIAPED
>2Fe-2SST1 (smaz:LH19_14855) *Sphingopyxis macrogoltabida* 203
MAKLIVVTRDGTETEHEIEGDTSLTVMENIRDAGFDELLALCGGCCSCATCHVHVEAGDKAA
MPAMSEDENDLLDSTTDRDDNSRLSCQLPFSDALDGLRVIAAED
>2Fe-2SST1 (sphk:SKP52_11840) *Sphingopyxis fribergensis*
MAKLIVVTRDGTETEHEIEGDTSLTVMENIRDAGFDELLALCGGCCSCATCHVHVEAGDKGA
MPAMSEDENDLLDSTTDRDDASRLSCQIPFSDALDGLKVRIAAED
>2Fe-2SST1 (sphp:LH20_08015) *Sphingopyxis* sp. 113P3
MAKLIVVTRDGTETEHEIEGDASLTVMENIRDAGFDELLALCGGCCSCATCHVHVEAGNKDA
LPAMSEDENDLLDSTSDRDENSRLSCQIPFSDALDGLKVRIAEED
>2Fe-2SST1 (ster:AOA14_16445) *Sphingopyxis terrae*
MAKLIVVTRDGTETEHEIEGDTSLTVMENIRDAGFDELLALCGGCCSCATCHVHVEAGDAAA
LPAMSEDENDLLDSTSDRDDTSRLSCQIPFSDALDGLKVRIAAED
>2Fe-2SST1 (sgi:SGRAN_2600) *Sphingopyxis granuli*
MAKLIVVTRDGTETEHEIEGDTSLTVMENIRDAGFDELLALCGGCCSCATCHVHVEEGNRDA
IPAMSEDENDLLDSTSDRDGNSRLSCQIPFTAELDGLRVRIAEED
>2Fe-2SST1 (nnp:JI59_14295) *Novosphingobium pentaromativorans*
MPQITVVNQSGEESSEVEASEGRTLMEVIRDNGFDELLALCGGCCSCATCHVHIDPAFVDEK
LPAMSEDENDLLDSSSEHRNEYSRLSCQIPVTGALEGCKVTIAQED
>2Fe-2SST1 (sal:Sala_0845) *Sphingopyxis alaskensis*
MAKLIVVTRDGTETEHEIEGDTSLTVMENIRDAGFDELLALCGGCCSCATCHVHVEAGDRDA
LPAMSEDENDLLDSTTDRDETSRLSCQIPFSDALDGLKVRIAAED
>2Fe-2SST1 (npp:PP1Y_AT7331) *Novosphingobium* sp. PP1Y
MPQITVVNQSGEESSEVEASEGRTLMEVIRDSGFDELLALCGGCCSCATCHVHIDPAFMEK
LPAMSEDENDLLDSSDHRNEYSRLSCQIPVTGALEGLKVVTIAQED
>2Fe-2SST1 (sphg:AZE99_03245) *Sphingorhabdus* sp. M41
MPTIHVTGRDGEEKAVSVDSGISVMEAIRDNGFDELLALCGGCCSCATCHVHIDADWKAK
LPPMSEDEDDLLDSSDHRDEF SRLSCQIELSDDLEGLKVRIAEED
>2Fe-2SST1 (spmi:K663_20183) *Sphingobium* sp. MI1205
MPRLIVTTRSGETLIVESREVSVMIAIRDAGIDEVLALCGGCCSCATCHVHVDEEDWFEK

LPPMTDDEGDLLDSSDHRTATSRLSCQLPFSEALDGLRVTIAPED
 >2Fe-2SST1 (sphb:EP837_03874) *Sphingobium* sp. EP60837
 MPQLIVTTRKGAEINIVESREVSVMEDIAIRDAGIDEVLALCGGCCSCATCHVHVDEDEDWIEK
 LPPMTDDEGDLLDSSDHRTATSRLSCQLPFSQALDGLRVTIAPED
 >2Fe-2SST1 (cij:WG74_12065) *Citromicrobium* sp. JL477
 MINVLATLRDGSTKTISTTPDGSLMEAIRDSGIDELLALCGGCCSCATCHVHVDESWLAK
 LPDISEDEDDLLDSSDHRDDQSRLSCQIPLTEDLDGLKVTIAQED
 >2Fe-2SST1 (nar:Saro_0509) *Novosphingobium aromaticivorans*
 MSKHAMIDLKVVKRDGTKLTLQASPGMSVMEALRDNGLDELLALCGGCCSCATCHIYVEA
 GPDGVDEVGGADEDDLLDSSDHRHNSRLSCQITLGSAMSGLVVRVAPED
 >2Fe-2SST1 (ssy:SLG_08500) *Sphingobium* sp. SYK-6
 MAQLKVVTRDGSLEHFEAPDGYTVMEAIRDQGIDELLAICGGGCCSCATCHVFVEEAFLDK
 LPPLKGDEDDLLDSSDHRQANSRLSCQLPIGPGLGMTVVTIAPED
 >2Fe-2SST1 (ssy:SLG_18840) *Sphingobium* sp. SYK-6
 MVQIVVTDRGGAQQSIEAKSGLSLMEVIRDHGIDELLALCGGCLSCATCHVYVELAYLPK
 LPAMSADEDDLLDSSSHRTAASRLSCQIVIGDELDGLEATIAPED
 >2Fe-2SST1 (swi:Swit_0363) *Sphingomonas wittichii*
 MPTIIVTTRDGQELSLEADTGLSLMEVIRDGGADELLALCGGCCSCATCHVKVDPAFLAA
 LPPMSEDESDLLDSSDHRDATSRLSCQISVDDGLAGLRVAIAPED
 >2Fe-2SST1 (sch:Sphch_3575) *Sphingobium chlorophenolicum*
 MPNIIVTARDGAEREIAAETGLSLMEAIRDAGIDEMLLALCGGCCSCATCHVKVDPAFTAL
 LPTVSEDESDLLDSSSEHRDAYSRLSCQIPLTAELDGLRIAIAPED
 >2Fe-2SST1 (syb:TZ53_05355) *Sphingobium* sp. YBL2
 MPNVIVTTRDGAEREIAAETGLSLMEAIRDAGIDEMLLALCGGCCSCATCHVKVDPAFFRL
 LPTVSEDESDLLDSSSEHRDEYSRLSCQIPLTAELDGLRIAIAPED
 >2Fe-2SST1 (hba:Hbal_2471) *Hirschia baltica*
 MIRIVATTRDGTRSELSADSGLSLMEVLRDRDLDEGVCGGAVSCASCHVYVADEWVDKL
 SAPDEMEEALVGDLVHAKPNSRLCCQIVLSKFDGLEVTVPSEM
 >2Fe-2SST1 (con:TQ29_17605) *Confluentimicrobium* sp. EMB200-NS6
 MPILNVTDRDGSEKQVDVTMTESLMHVLRDAGYHIAAECGGAAACGTCHVYVDEAWLSKL
 PEAGEIEAEMVDLLEETKPTSRLSCQVQMDDSLGLKVTLAPEE
 >2Fe-2SST1 (magq:MGMAQ_3127) *Magnetospora* sp. QH-2
 MPTLTVTDAQGVTKELDADTGLSVMEILREAGYPVAGECNGSLACATCHVIIDPNWFGKL
 EDQAEEEEEDILDTVFNLEETSRLACQIMMSDDLGLAVSLPS

>2Fe-2SST1 (aex:Astex_1069) *Asticcacaulis excentricus*
MSDELHILCTDRDGVQHTLPAIEGWRIMEIIRDNGLPIKAECGGALECATCHVYVGADWL
PKLIGKSDEEEEEKLDEAFVLKRNRLSCQILMRDDLNGLEVTLAPEG

>2Fe-2SST1 (bvv:BHK69_21665) *Bosea vaviloviae*
MHVRVTDREGEQRELEALEGWRRLMEIIRDWGLPIKAECGGACACATCHVYVAADWVDKLH
PPREEELERLDEAFDVRPNSRLACQILFSPELDGLTVVLAPELD

>2Fe-2SST1 (hoe:IMCC20628_01988) *Hoeflea* sp. IMCC20628
MHIHVTDQTGTRHTLEALEGFRVMEIIRDWGLDIKAECGGACACATCHVHVSDDWTDRLY
PIEAEEDMLDQAFDVRDNSRLSCQLLMSEELDGLVTLAPGTETGDRAAA

>2Fe-2SST1 (psin:CAK95_03715) *Pseudorhodoplanes sinuspersici*
MKISVTDHAGTEHELEALPGWRVMEIIRDWDLPIKAECGGACACATCHVYVDAAWFGRLP
GESEEEIDQLEILADRMPSRLACQVLMSEELDGLKVTLPAGSRP

>2Fe-2SST1 (phl:KKY_1892) *Pelagibacterium halotolerans*
MRIFVTDQDGTEHELEALEGWRVMEVIRDWGLNIKAECGGSCACATCHVFVDAEWQDKLN
PPTDEEEDMLD TVADYEANSRLSCQILMSEELDGLKVTLPADSARQDEAA

>2Fe-2SST1 (deq:XM25_10530) *Devosia* sp. H5989
MKIHVTDQAGVEHELEGLEGWRVMEVIRDWGLNIKAECGGACSCATCHVYVAPEWFDKVG
TRSDDEEDLLD TVGDVKPTSRLSCQILMSDEL DGLKVTLPAAASAAQ

>2Fe-2SST1 (bvv:BHK69_19925) *Bosea vaviloviae*
MAILNVIDRDGRAHELEAVEGWRVMEILRDYKVGIEGVC GGSCDCATCHV VVAPDWAKRL
PEPREDEIDALDTLPLIEATSRLSCQIIWSDDL DGLTLTLAEAA

>2Fe-2SST1 (mbry:B1812_19095) *Methylocystis bryophila*
MQDAAARAPQQHVVVLVEDREGKLHELETLEGWRRLMEILRDHGVGMDTNC GGS LACAECH
VLIDPAWMGRLPAPSQEELDKLDELPLIHENSRLSCQILWTD D YDGMKVTVAQAT

>2Fe-2SST1 (msl:Msil_1812) *Methylocella silvestris*
MDEPAIEPAEPEGPPRTPLAVTLSEGGLSRRIDGFDGERLLDALLRAKAAVMPLCNGRAC
CGGCRIRIEKSWRDRVTPSGRGERSVLRYIDDPHEDDR LSCQIALSAEVEGLVVRTLERQ
PAPAQAGADAEEINAGK

>2Fe-2SST1 (pzu:PHZ_c0215) *Phenylobacterium zucineum*
MHDGQAAHREPQAGGPRKACRPHDFHERGRRLSERLTRSAMA KITYIEHDGTEHVIDVKP
GLSVMGAVKNNIPGIDADCGGACACATCHVYVDEAF LAKTGTRSAMEESMLDFAEGVEE
NSRLSCQIKVTDDL DGLVVRMPESQH

>2Fe-2SST1 (msc:BN69_2451) *Methylocystis* sp. SC2

MAKMSFEDAATRYGAEPGGGAPTKVKITFIDSQQQARSVEGEVGSTVMETARRNDIPEIT
AECGGACACATCHVYVDEKWAECTGKASQMEEDMLDFAFDVKPNSRLCCQITVRPELDGL
VLTPAQGG

>2Fe-2SST1 (same:SAMCFNEI73_Ch2044) *Sinorhizobium americanum*
MRDHCRFSGRSRNRASARVDWPVDLLEETALNSGWPRLPRRLVLAGGSHPFIPEREMTKL
TIVAFDGTRHDLDVENGSTVMENAVRNSVPGIEAECGGACACATCHVYVDDAWSAAVGAP
EAMEEDMLDFAYDVRPTSRLSCQIKMSEALDGLIVHVPERQA

>2Fe-2SST1 (abs:AZOBR_70188) *Azospirillum brasilense* Sp245
MPKMTFIEPNGTRHEVDAPLGLSVLEVAHKHGLDLEGACEGSLACSTCHVIVEPEWFDVL
NEASEDEEDMLDLAFGLTKTSRLGCQIIISEELDGLAVRLPGGTNSGHALTYRRGALRGR
RGPHPPPGRNRASPLAGAAPPVLRW

>2Fe-2SST1 (npp:PP1Y_AT28162) *Novosphingobium* sp. PP1Y
MPQRRRRESELLSVQFVTADGNKLTVQAEAGARLLEVAQAAGMPLEGTCEGQMACSTCHV
IVAPEWFERLKPASNDEEDMLDLAAGVTRTSRLSCQIELTEALDGIELRIPGVSHDMQIG

>2Fe-2SST1 (nar:Saro_1477) *Novosphingobium aromaticivorans*
MRADCIPLHSKQDPPLTAILVTTRDGTRTEIQAEPGLSLMEALRDAGIDELLALCGGCCS
CATCHVLVAPAFADRLPALSGDENDLLDSSDHRTPHSRLSCQITINDKLEGLEVEIAPED

>2Fe-2SST1 (msc:BN69_0738) *Methylocystis* sp. SC2
MSNIDNIVARRPAESSQQSLPTLHVEDRDGVVHELEAVEGWRLMEILRDHGVGMDNTCGG
ALACAECHVVLDAESARRVPPPREEEVEKLDELPLYENSRLSCQIIWSDEMSEGLRLKLT
QET

>2Fe-2SST1 (bmg:BM590_A1025) *Brucella melitensis* M5-90
MEAAIRNGIPGIDAECGGACACATCHVYVDDDDWADTVGGPDPMEEDMLDFAYEVRPTSRL
SCQIRVTDDLEGLVVQVPERQN

>2Fe-2SST1 (aay:WYH_00986) *Altererythrobacter atlanticus*
MAEAQPGDNLLLEVQACGMPLEGTCEGQMACSTCHVIIAPEWFARLPEASEEEEEEDMLDLA
ADVARTSRLSCQIDLTDDLDGMEVRMPSASHDMQGR

>2Fe-2SST1 (sbd:ATN00_08840) *Sphingobium baderi*
MLALRDEAGFEIAGECGGFCICGTCHVYIARSEQAASFPPSEEESELA AFLQHYGPDSRL
ACQIPLASVPEGLTIHIAPEE

>2Fe-2SST1 (swi:Swit_5088) *Sphingomonas wittichii*
MPKVVFVAADGREIETNVDIGTDLMHAGLYNSVPGLLGECSGGLACATCRVHVPAEWQGV
LPAALPAEAEELLGFCEESPPEARLSCQIKMTQELDGLRLLPEDQD

>2Fe-2SST1 (swi:Swit_4893) *Sphingomonas wittichii*

MPKVIYVSEDGSELETTVDVGVDLMHAGLYNSIPGILGECSSGGLACATCRVRVPVEWQSI
LPPAFPSEAEELGFCDEAPPEARLSCQIKMTQEELDGIRLLVSNNLD
>2Fe-2SST1 (sch:Sphch_3593) *Sphingobium chlorophenolicum*
MVHVTFITPSGVATTLDGDVGQSVMDIGKRAGVENIIGECGSAACATCHVHVDPAWIDL
VGPPSDDEWDMLDFAHGKRADSRLSCQIRLRPALEGLIVHTPERQG
>2Fe-2SST1 (syb:TZ53_05790) *Sphingobium* sp. YBL2
MVHVTFITPAGIATTLDGDVGQSVMDIGKRAGVENIIGECGSAACATCHVHVDPAWIDR
VGPPSADEWDMLDFAHGKRADSRLSCQIRLRAALDGLIVHTPERQG
>2Fe-2SST1 (aak:AA2016_1168) *Aminobacter aminovorans*
MKVEVHFRLPDNSVRKVEATCGLSLMEAGKQAGVPGIIGDCGGGAMCATCHVYVDLDWQD
RAGEPEATESLMLQLTEEQRDNSRLSCQITVEEELDGLVVEVPKEHI
>2Fe-2SST1 (swi:Swit_1759) *Sphingomonas wittichii*
MVRVRFQRPDGSETACDVAAGLSLMEAAALNNGVDEIIADCGGALSCATCHVYVDDGWMMDR
TGAPSEVEEEMLEFAVDRRPNSRLSCQIKLGEGLDGLSVALPQRQQ
>2Fe-2SST1 (aak:AA2016_1195) *Aminobacter aminovorans*
MSLITVHFIIHPDERVESVQTDGTGLTVMEVAREAGVSGILAECGGGAICSTCHVHVAQDWY
HRLTPPEATEGMLLELAPGHDAYSRLSCQIELDATHDGISVRVPECQSDY
>2Fe-2SST1 (rpx:Rpx1_3651) *Rhodopseudomonas palustris* DX-1
MPSITFILPDGERRTTEAAVGDTAMYAALSLGLDGVVAECGGNAVCATCHVYVEHGLEKL
PAVAGDEDDLLDGTAAERLPNSRLSCQIKLSSDLGLILRIPDRQV
>2Fe-2SST1 (rpa:RPA1872) *Rhodopseudomonas palustris* CGA009
MPSITFILPDGERRTTEAAVGDTAMYAALSLGLDGVVAECGGNAVCATCHVYVEHGLEKL
PAVAADEDDLLDGTAAERLPNSRLSCQIKLSSDLGLILRIPDRQV
>2Fe-2SST1 (rpt:Rpal_2078) *Rhodopseudomonas palustris* TIE-1
MPSITFILPDGERRTTEAAVGDTAMYAALSLGLDGVVAECGGNAVCATCHVYVEHGLEKL
PAVAGDEDDLLDGTAAERLPNSRLSCQIKLSSDLGLILRIPDRQV
>2Fe-2SST1 (swi:Swit_0998) *Sphingomonas wittichii*
MKISYLDQDGTRTDLDAGEGTNLMELAVRGGVTTIEGECGGALACATCHVHIPDEWRGVT
GEPSSDEREMLEFGVGVDERSRLCCQIRVTAAMDGLVVLTPASQR
>2Fe-2SST1 (swi:Swit_1843) *Sphingomonas wittichii*
MPMITFVAPDGAEYVVDARGLHSVMEAAARNHMPGIDADCGSGSCATCHVHVDAAWAQA
TGAADEMEQAMLDCVEEPSATSRLSCQIRVSDALDGLVVRLPARQG
>2Fe-2SST1 (tmo:TMO_c0588) *Tistrella mobilis*
MPKITFIERDGNRREVEAPVGLSILEIAHRNSIDIEGACEGSLACSTCHVIVAPEDFERL
PDAAEEEEEDMLDLAWGLTKTSRLGCQIIITEELDGLTVSLPTEVHNALID

Subtype 2

>2Fe-2SST2 (rep:IE4803_PC00148) *Rhizobium etli* bv. phaseoli
IE4803

MAEITFILPDGGHKACPAASEGLSLMELALQNSVPGIVAECNGAAACGTCHVIMDDALIDV
LDPISDHENDMLDFTNAPREPGSRLSCQIRVDGRLNGAVVRVASEM

>2Fe-2SST2 (rei:IE4771_PD00148) *Rhizobium* sp. IE4771

MAEITFILPDGGHKACPAASEGLSLMELALQNSVPGIVAECNGAAACGTCHVIMDDALIEV
LDPISDHENDMLDFTNAPREPGSRLSCQIRVDGRLNGAVVRVASEM

>2Fe-2SST2 (mamo:A6B35_25070) *Mesorhizobium amorphae*

MPTIRFLLADGAELAVEAQNGRTLMEALESSVPGIIAECNGSAACATCHVVLPEEIMVA
LGPISEHENDMLDFAEAPRESGSRLSCQVRVSDMLDNVSVRIPSA

>2Fe-2SST2 (sfd:USDA257_c26490) *Sinorhizobium fredii* USDA 257

MPTITFITAEKGKEHAVTAEIGRSVMEIALEKSIPGVVAECNGSAACATCHCYFDPAFVEA
IGPIGEHESDMLDFTASPRRPESRLSCQIRVADALHGMTVRIPAVQ

>2Fe-2SST2 (same:SAMCFNEI73_pC1878) *Sinorhizobium americanum*

MPTITFITAEKGQHAVTAEIGRSVMEIALEKNIPGVVAECNGSAACATCHCYFDPAFAAA
IGPIGEHESDMLDFTASPRRPESRLSCQVRVADALDGMTVHIPAVQ

>2Fe-2SST2 (rhi:NGR_b07650) *Sinorhizobium fredii* NGR234

MPTITFITAEKGQHAVTAEIGRSVMEIALEKSIPGVVAECNGSAACATCHCYFDPAFTEA
IGPVGEHESDMLDFTAAPRRPESRLSCQVRVVDTLTGMTVRIPAMQ

>2Fe-2SST2 (sfh:SFHH103_06381) *Sinorhizobium fredii* HH103

MPTITFITAEKGKEHAVTAEIGRSVMEIALEKSIPGVVAECNGSAACATCHCYFDPAYADM
IGAIGEHEHESDMLDFTASPRRPESRLSCQVRVVDTLTGMTVRIPAMQ

>2Fe-2SST2 (pde:Pden_3464) *Paracoccus denitrificans*

MGAPRRTTERNTVPFITWRDADGTEISANVAAGTNLMRAAVDAGVQGIHGDCGGALACAT
CHVATDTAWAERLGPPGALEDEMLDMVEGERTPTSRLSCQILARDELEGLVLIVPACG

>2Fe-2SST2 (sil:SPO0766) *Ruegeria pomeroyi*

MRVTWKLADGREIAAEVAPGLSLMEAAALANNVPGVIGECGGCLSCATCHVVVDAAWSERT
GAPGEFEDAMLDITAAERQPRSRSLSCQIEAHPDLGLVLHVPEA

>2Fe-2SST2 (lvs:LOKVESSMR4R_00421) *Yoonia vestfoldensis*

MKVTWTLQDGGTRTADVAPGTNMMEA AVANGINGVVGECGGCLSCATCHVYVADDWADKT
 GGPEDFEDAMLDATAERKATSRLSCQIVADDSLDGLHLIVPTP
 >2Fe-2SST2 (cid:P73_4762) *Celeribacter indicus*
 MVNIVFIALDGEKHEVSATPGASVMQAAMGASVDGILAECCGAGACATCRCGVVSAPDGS
 IEAPTDMELEMLEFVAEDLSNNDRLTCQLTVTPSLEGAVFQVRDNDV
 >2Fe-2SST2 (bra:BRADO6809) *Bradyrhizobium* sp. ORS 278
 MTTITFIHADNRSQTVEASDGDLSLMAALTHGVDGIVAECGGNAVCATCHVYIDEAWTAR
 LDPVSDDEDALLDGTAAERLPNSRLSCQIKVQPALAGLVVRIPDKQS
 >2Fe-2SST2 (bbt:BBta_0730) *Bradyrhizobium* sp. BTAi1
 MTTITFIHPDNRSETVEAEDGATVMLAALTHGVDGIVAECGGNAVCATCHVYVDDAWTSK
 LEPVSDDEDALLDGTAAERRPNSRLSCQIKVQPALAGLVVRIPDRQS
 >2Fe-2SST2 (aol:S58_06530) *Bradyrhizobium oligotrophicum*
 MTTITFIHADNRSERVEAVDGDLSLMAALTHGVDGIVAECGGNAVCATCHVYVDEAWASK
 LDPVSDDEDALLDGTAAERRPNSRLSCQIKVQPGLAGLVIRIPDRQS
 >2Fe-2SST2 (rpb:RPB_3614) *Rhodopseudomonas palustris* HaA2
 MPSITFIHPDGRSEIVDAAIGDSAMFAALNHGIDSIVAECGGNAVCATCHVYVDDLWLAK
 LPPVDANEDDLLDGTASDRLPNSRLSCQIKIAPELDGLVLRRLPERQT
 >2Fe-2SST2 (brc:BCCGELA001_34410) *Bradyrhizobium* sp. CCGE-LA001
 MPAITFIHPGGKSDRVEAIDGESAMQAATRHGLDGILAECCGNAMCATCHVYVDDAWLAR
 LPDIADDEDALLDGTASERLPNSRLSCQIHLTPALDGLVLQLPERQV
 >2Fe-2SST2 (bic:LMTR13_36455) *Bradyrhizobium icense*
 MPSITFVHPDGRAQRIDGGDGESAMQAATRHVDNGILAECGGNAMCATCHVYVDEDWLAR
 LPAMGDDEDALLDGAAAERRANSRLSCQIKLAADLDGLVLNLPDRQL
 >2Fe-2SST2 (bja:blr1049) *Bradyrhizobium diazoefficiens* USDA 110
 MPAITFIHADGKSDRVETSGGESAMQAATRHGLDGILAECCGNAMCATCHVYVDEAWLAR
 LPAMADDEDALLDGTATERLPNSRLSCQIMITPALDGLVLRRLPERQV
 >2Fe-2SST2 (bju:BJ6T_10740) *Bradyrhizobium japonicum* USDA 6
 MPAITFIHADGKSDRVETSGGESAMQAATRHGLDGILAECCGNAMCATCHVYIDA AWLGR
 LPAMADDEDALLDGTAAERLPNSRLACQIMITPVLDGLVLRRLPERQV
 >2Fe-2SST2 (bjp:RN69_10165) *Bradyrhizobium japonicum* E109
 MRIRFVQPDGTEKCVNEDPGVSVMVA AIRHGVAGINGDCGGSMDCATCHVYLDEAQSKLV
 PPPTSHEIDL SAVVAERRPTSRLSCQLRPFDRSDELIVHVPDAQ
 >2Fe-2SST2 (bjp:RN69_05240) *Bradyrhizobium japonicum* E109
 MPAITFIHADGKSDRVETSGGESAMQAATRHGLDGILAECCGNAMCATCHVYIDA AWLGR

LPAMADDEDALLDGTAAERLPNSRLACQIMITPVLDGLVLRRLPERQV
 >2Fe-2SST2 (mno:Mnod_8461) *Methylobacterium nodulans*
 MPRIVFVGRDGAEHGVEVPAGISAMAAAIRSNVRGIEAECGGSLLDCATCHVYVDNRFVGL
 LPEPSELEREMLACVAADRRETSRLSCQIVLTPELEGLTLHLPEVQS
 >2Fe-2SST2 (ngg:RG540_PA03930) *Neorhizobium galegae* bv.
orientalis HAMBI 540
 MTKVIFISPDGAETAVIDAIDGDNVMRTALANDIDGIVAECGGSMMMCATCHCYVDAAWKER
 VGPRSDGEDDMLESASSEVRPTSRLSCQIRILPDLDGLVIHLPEST
 >2Fe-2SST2 (pphr:APZ00_12860) *Pannonibacter phragmitetus*
 MVKVITYVHHDGTRTEVDGKEGDTVMHTAVAQDVEGIVGECGGAMMCATCHCYVDDEWLDA
 AGERRDGEEDMLDCGAAEVKPNLSRLSCQIRLSPALDGLVVHLPEEQM
 >2Fe-2SST2 (pphr:APZ00_24835) *Pannonibacter phragmitetus*
 MTKIHFISATGIETVIDARDGDSVMHAAIINDVEGILAECGGSMMMCATCHCYVDPAWQDR
 VTPPSEPEAGMLASAASAVRATSRLSCQITVGPELEGLVIHLPEAQL
 >2Fe-2SST2 (lap:ACP90_00235) *Labrenzia* sp. CP4
 MVQITFVQPNGSRKTIDASEGASVMETAVSHGVDGIFAECGGAMMCATCHCYVDEAWSDK
 TGARTDGEEIMLECAAADLRETSRLSCQIRLTGALDGLVVHLPEQA
 >2Fe-2SST2 (lagg:B0E33_11745) *Labrenzia aggregata*
 MVQITFVQPNGSRKTIDASEGASVMETAVSHGVDGIFAECGGAMMCATCHCYVDEAWSDK
 TGARTDGEEIMLECAAADLRETSRLSCQIRLTGALDGLVVHLPEQA
 >2Fe-2SST2 (thw:BMG03_04540) *Thioclava nitratireducens*
 MIKVITYVAQDGTRTNIDADEGDSVMHAAVSNDVDGIVGECGGSMMMCATCHCYVDDAWAEK
 VGPRSAGEDDMLEGAASEVTERSRLSCQIKLTPELDGLVVHLPEEQF
 >2Fe-2SST2 (sphm:G432_04860) *Sphingomonas* sp. MM-1
 MITINVTTTRDGRQQIDGQEGSALMEMLRDAGLGVDGTGCGMCSGCSCHVYIASSETTLPK
 PSEDEADMLEGMSIVEVRPSSRLSCQIILKPELDGLEVEIAPQF
 >2Fe-2SST2 (rhc:RGUI_1200) *Rhodovulum* sp. P5
 MSAPTTGHPNEARMAKITYIEHNGTEHVVEVANGLTVMEGARDNSIPGIDADCGGACACS
 TCHAYIHPDWVDRLLPAIEDMEADMLDFAYATDPKRSRLTCQVKVTDALDGLIVQMPEKQI
 >2Fe-2SST2 (sit:TM1040_1949) *Ruegeria* sp. TM1040
 MGLARCRRQRYTRYRVPKKGRIMAKITYIEHNGTEHVVDVANGLTVMEGARDNNIPGIE
 ADCGGACACSTCHVYIAPDWVEKLPAKDDMEEDMLDFAFEPDAARSRLTCQIKVTDALDGLV
 VHMPEKQI
 >2Fe-2SST2 (mcg:GL4_0882) *Methyloceanibacter caenitepidi*

MMEVIRDWGLPIKAECGGACACATCHVWVAEEWVDKLPPTDEETEMLDGAFSVDDRRSR
 LSCQLLMTPELDGLVVELAPESLTDIVDSTAATGTSG
 >2Fe-2SST2 (bbt:BBta_1599) *Bradyrhizobium* sp. BTAi1
 MRTVEAAHDESAMQAAKRNGIDGIIGECGGSCICATCHCHVDQAWLTRVGPAGDIEADVL
 EFEATDVRPESRLACQIPITDALAGLVLVHVVGRSR
 >2Fe-2SST2 (cid:P73_3499) *Celeribacter indicus*
 MVKITYIEFGGTEHVVDVPVVGSTVMEGARDNGIPGIDADCGGACACSTCHVYVAPDWVDK
 LPERDPMEEEDMLDFAFEPDPVRSRLTCQIKVTEALDGLVVMPEKQI
 >2Fe-2SST2 (rga:RGR602_PC02299) *Rhizobium gallicum*
 MATISVRTRDGELHSFEGRVGASLMENIRNGGFDELLAMCGGCLSCATCHVFVEELPASA
 SLPIPSIDETELIEGSDYRQENSRLSCQIPFDETLSGIVIGIAPED
 >2Fe-2SST2 (pla:Plav_2127) *Parvibaculum lavamentivorans*
 MPRVKYVEANGREYLVEADTGISAMEAAVKNGVPGIDGDCGAAACATCHVYVDPDWIGK
 TGPAAEGLKSMLEFAEDVNENSRLACQITLSDTLGLVLKLPEKQH
 >2Fe-2SST2 (sil:SPO1348) *Ruegeria pomeroyi*
 MAKITYIEHNGTQHTVEVANGLTVMGARDNNIPGIEADCGGACACSTCHVYIHPDWVEK
 LPAKDDMEEDMLDFAFEPDPPARSRLTCQLKVTDALDGLVVMPEKQI
 >2Fe-2SST2 (dsh:Dshi_2731) *Dinoroseobacter shibae*
 MAKITYVEHNGTEHVVDVANGLTVMGARDNNIPGIEADCGGACACSTCHVYVHPDWVGK
 LPGKEAMEEDMLDFAYQPDPPARSRLTCQIKVSEALDGLVVMPEKQI
 >2Fe-2SST2 (lmd:METH_05610) *Leisingera methylohalidivorans*
 MAKITYIEHNGTSHVVDVANGLTVMGARDNNIPGIEADCGGACACSTCHVYIAPDWVEK
 LPAKDDMEEDMLDFAFEPDPPARSRLTCQIKVSDALDGLVVMPEKQI
 >2Fe-2SST2 (red:roselon_00079) *Roseibacterium elongatum*
 MAKITYIEHNGTEHVVDVPNGLTVMGARDNGIPGIEADCGGACACSTCHVYVHPDWVSK
 LPAVDPMEEEDMLEFAFQPDTERSRLTCQLKVTDALDGLVVMPEKQI
 >2Fe-2SST2 (paby:Ga0080574_TMP4710) *Pelagibaca abyssi*
 MAKITYIEHNGTEHVVDVPTGLTVMGARDNGIPGIEADCGGACACSTCHVYVHPDWVGK
 LPGKEEMEEDMLDFAFEPDPERSRLTCQLKVSDALDGLVVMPEKQI
 >2Fe-2SST2 (rsh:Rsph17029_1996) *Rhodobacter sphaeroides* ATCC
 17029
 MAKITYVEFNGTEHVIDVAAGLTVMGARDNGVPGIEADCGGACACSTCHVYVDPAWTDK
 LPKKEAMEEDMLDFAWQPDPPARSRLTCQIKVSDALDGLKVFIPEKQI

>2Fe-2SST2 (rsq:Rsph17025_0944) *Rhodobacter sphaeroides* ATCC 17025
 MAKITYVEHNGTEHVIDVANGLTVMEGARDNGVPGIEADCGGACACSTCHVYVDPAAVVGK
 LPRKEAMEEDMLDFAWEPDPVRSRLTCQIKVTESLDGLKVFIPEKQI

>2Fe-2SST2 (rsk:RSKD131_1681) *Rhodobacter sphaeroides* KD131
 MAKITYVEFNGTEHVIDVAAGLTVMEGARDNGVPGIEADCGGACACSTCHVYVDPAAWTDK
 LPKKEAMEEDMLDFAWQPDPARSRLTCQIKVSDALDGLKVFIPEKQI

>2Fe-2SST2 (jan:Jann_3168) *Jannaschia* sp. CCS1
 MAKITYIEHNGTKHDVEVANGLTVMEGARDNSIPGIEADCGGACACSTCHVYVDPAAVVEK
 LPAIDPMEEDMLEFAYEPDSARSRLTCQLKVTDELGLVVMPEKQI

>2Fe-2SST2 (pga:PGA1_c23660) *Phaeobacter inhibens* DSM 17395
 MAKITYVEHNGAEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDAGWVEK
 LPAKDDMEEDMLDFAWEPDPARSRLTCQIKVTDDLNGLVVHMPEKQI

>2Fe-2SST2 (pgl:PGA2_c21620) *Phaeobacter inhibens* 2.10
 MAKITYVEHNGAEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDAGWVEK
 LPAKDDMEEDMLDFAWEPDPARSRLTCQIKVTDDLNGLVVHMPEKQI

>2Fe-2SST2 (pgd:Gal_01024) *Phaeobacter gallaeciensis* DSM 26640
 MAKITYVEHNGAEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDAGWVEK
 LPAKDDMEEDMLDFAWEPDPARSRLTCQIKVTDDLNGLVVHMPEKQI

>2Fe-2SST2 (php:PhaeoP97_02237) *Phaeobacter porticola*
 MAKITYVEHNGAEHVVDVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDAAWVEK
 LPAKDDMEEDMLDFAWEPDPARSRLTCQIKVSDDLNGLVVHMPEKQI

>2Fe-2SST2 (con:TQ29_11980) *Confluentimicrobium* sp. EMB200-NS6
 MAKITYIEHDGTEHTVDVPTGMTVMEGARDNNIPGIDADCGGACACSTCHAYIAPDWVEK
 LPKMEAMEEDMLDFAWAPDPARSRLTCQIKVSDDLGLVVNLPEKQI

>2Fe-2SST2 (yan:AYJ57_11300) *Yangia* sp. CCB-MM3
 MAKITYIEFGGTEHVVEVATGMTVMEGARDNGIPGIEADCGGACACSTCHVYVHPDWVEK
 LPAKDDMEEDMLDFAFEPDPSRSRLTCQLKVTDALDGLVVMPEKQI

>2Fe-2SST2 (tom:BWR18_04810) *Tateyamaria omphalii*
 MAKITYIEHGGTEHVVDVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVHPDWVEK
 LPAKDDMETDMLDFAWEPDETRSRLTCQLKITDALDGLVVMPEKQI

>2Fe-2SST2 (rsp:RSP_0352) *Rhodobacter sphaeroides* 2.4.1
 MAKITYVEFNGTEHVIDVAAGLTVMEGARDNGVPGIEADCGGACACSTCHVYVDPAAWTDK
 LPKKEAMEEDMLDFAWQPDPARSRLTCQIKVSDALDGLKVFIPEKQI

>2Fe-2SST2 (rmm:ROSMUCSMR3_00986) *Roseovarius mucosus*
 MAKITYIEHNGTRHEVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDPWVVGK
 LPAKDDMEEDMLDFAYQPDPARSRLTCQLKVTEALDGLVVMPEKQI

>2Fe-2SST2 (rde:RD1_1925) *Roseobacter denitrificans*
 MAKITYIEHGGTEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDPWVVEK
 LPGKDDMEEDMLDFAYEPDPARSRLTCQLKVTDALDGLIVQMPEKQI

>2Fe-2SST2 (rli:RLO149_c010230) *Roseobacter litoralis*
 MAKITYIEHGGTEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDPWVIEK
 LPGKDDMEEDMLDFAYQPDPARSRLTCQLKVTDALDGLIVQMPEKQI

>2Fe-2SST2 (oar:OA238_c07330) *Octadecabacter arcticus*
 MAKITYIEHGGKEHIVEVANGLTVMEGARDNGIPGIEADCGGACACSTCHVYIDAADWADK
 VPAKDAMEEDMLDFAYEPDPARSRLTCQLKVTDALDGLIVQMPEKQI

>2Fe-2SST2 (otm:OSB_10470) *Octadecabacter temperatus*
 MAKITYIEHGGKEHIVDVANGLTVMEGARDNGIPGIEADCGGACACSTCHVYVDAAWVEK
 IPAKDAMEEDMLDFAYEPDAEKSRLTCQLKVTDGLDGLVVRMPEKQI

>2Fe-2SST2 (ptp:RCA23_c27570) *Planktomarina temperata*
 MAKITYIEHGGAEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDSAWVEK
 LPAMDGMEEDMLDFAFEPKPGQSRLTCQLRVSDALDGLVVRMPERQI

>2Fe-2SST2 (rsu:NHU_00961) *Rhodovulum sulfidophilum*
 MAKITYIEHNGTEHVIDVANGLTVMEGARDNGVPGIDADCGGACACSTCHAYVHPDWVDR
 LPPVEDMEADMLDFAYATDPKRSRLTCQIKVAEALDGLIVQLPEKQI

>2Fe-2SST2 (suam:BO069_05855) *Sulfitobacter* sp. AM1-D1
 MAKITYVEHGGKEHVVEVANGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDPWVVDK
 LPARDDMEEDMLDFAYEPDAERSRLTCQLKVTDALDGLRVQMPEKQI

>2Fe-2SST2 (tpro:Ga0080559_TMP592) *Salipiger profundus*
 MAKITYIEHNGTEHVVEVANGLTVMEGARDNNIPGIDADCGGACACSTCHVYVHPDWVAK
 LPERDDMEEDMLDFAYEPDPERSLTCQLKVSDALDGLIVQMPQM

>2Fe-2SST2 (lvs:LOKVESSMR4R_00927) *Yoonia vestfoldensis*
 MAKITYVEHGGKEHVVDVANGLTVMEGARDNGIPGIEADCGGACACSTCHVYVDDAWVVDK
 LPAKDAMEDMLDFAYQPDVKSRLTCQLKVSDALDGLRVQMPEKQI

>2Fe-2SST2 (pde:Pden_4027) *Paracoccus denitrificans*
 MAKITYIEHNGTVHEIDVKPGMTVMEGARDNGVPGIDADCGGACACSTCHVYVAPEWVDR
 LPTRDPMEEDMLDFAWQPDVRSRLTCQIKVTPELDGLVVNLPERQI

>2Fe-2SST2 (pami:JCM7686_1496) *Paracoccus aminophilus*

MAKITYIEHNGTTHEVDVKPGMTVMEGARDNGIPGIDADCGGACACSTCHVYVAEDWVER
LPEKDPMEEDMLDFAYQPDAKRSRLTCQIKVTPELDGLVVQLPERQI
>2Fe-2SST2 (pye:A6J80_18515) *Paracoccus yeei*
MAKITYIEHNGTAHEIDVKPGMTVMEGARDNGVPGIDADCGGACACSTCHVYVAPEWVDR
LPPKDPMEEDMLDFAWQPDPARSRLTCQIKVTPDLGLVVQLPERQI
>2Fe-2SST2 (kvu:EIO_0828) *Ketogulonicigenium vulgare* Y25
MARITYVEFNGTEHVVDVPTGLTVMEGARDNGIPGIEADCGGACSCSTCHVYVDPWVVDQ
LPQRDPMEEDMLDFALAPDPVRSRLSCQLRVNDSLGLRVDMPERQI
>2Fe-2SST2 (kvl:KVU_0361) *Ketogulonicigenium vulgare* WSH-001
MARITYVEFNGTEHVVDVPTGLTVMEGARDNGIPGIEADCGGACSCSTCHVYVDPWVVDQ
LPQRDPMEEDMLDFALAPDPVRSRLSCQLRVNDSLGLRVDMPERQI
>2Fe-2SST2 (kro:BVG79_00616) *Ketogulonicigenium robustum*
MARITYVEFNGTEHVVDVPTGLTVMEGARDNGIPGIEADCGGACSCSTCHVYVDPWVVAQ
LPERDPMEEDMLDFALEPDPVRSRLSCQLRVTDALDGLRVNMPERQI
>2Fe-2SST2 (rcp:RCAP_rcc02404) *Rhodobacter capsulatus*
MAKIIIFIEHNGTRHEVEAKPGLTVMEEAARDNGVPGIDADCGGACACSTCHAYVDPWVVDK
LPKALPTETDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI
>2Fe-2SST2 (cmar:IMCC12053_2492) *Celeribacter marinus*
MAKITYIEFNGTEHVVDVPNGRTVMEGARDNGVPGIDADCGGACACSTCHVYVSPWVEK
LTPKDAMEEDMLDFAYQPDAARSRLTCQIKVTDAIDGLVVNLPEKQI
>2Fe-2SST2 (daa:AKL17_2730) *Defluviimonas alba*
MAKITYVEHSGTRHEIEVAPGLTVMEGARDNGVPGIEADCGGACACSTCHVYVDAAWLDR
VPPKDAMEEDMLDFAWQPDPARSRLTCQIKVTPDLGLVVHLPERQI
>2Fe-2SST2 (thw:BMG03_07110) *Thioclava nitratreducens*
MAKITYVEFNGTRHEIDVKPGMTVMEGARDNGVPGIDADCGGACACSTCHVYVDKDWIEK
LPPRDPMEEDMLDFAYEPDPVTSRLTCQIKVTDELDGLIVNLPEKQI
>2Fe-2SST2 (10mamo:A6B35_31415) *Mesorhizobium amorphae*
MIKITYVEHNGREHTVGVPQGGTLMEGARDNGIPGIEADCGGACSCATCHAYIDSAWIEK
LPAKQPMEDMLDFAYEPDATRSRLTCQVRVTEALNGLVLHMPERQA
>2Fe-2SST2 (shz:shn_17160) *Shinella* sp. HZN7
MVQITFVEHDGSRHVVEAAAGMTLMEAARDDDVRGILAECCGACSCSTCHVYVAPEWVDR
LPAISALEQDMLDFAHDPDPARSRLSCQIKLTDGLLVLDLPERQG
>2Fe-2SST2 (abs:AZOBR_p330135) *Azospirillum brasilense* Sp245
MAKVTFIEHDGLEQVVDIPTGWTLMQGAVQSGVAGIEGECGGSCACATCHCYVDEALVDS

LPPPSETEEEMLDCTASERRSNSRLSCQIRVSDALDGMVVRLPEAQS
>2Fe-2SST2 (abq:ABAZ39_27950) *Azospirillum brasilense* Az39
MAKVTFIEHDGLEQVVDIPTGWTLMQGAVQSGVAGIEGECGGSCACATCHCYVDEALVDS
LPPPSETEEEMLDCTASERRSNSRLSCQIRVSDALDGIVVRLPEAQS
>2Fe-2SST2 (magq:MGMAQ_2658) *Magnetospira* sp. QH-2
MPKVITYIEHDGAEEHHVELPAGWTLMQGATLNGIDGIEGECGGSCGCATCHCYVDEPWLKG
LEPASETEEEEMLECTESPRESNSRLSCQIKATPALDGIVVRLPEAQS
>2Fe-2SST2 (aol:S58_10680) *Bradyrhizobium oligotrophicum*
MPRITFIEPDGTVRLVDAEPHESAMQAAKRNGVDGIIGECGGSCICATCHCHVDEAWLDR
VGPAGDIEADLLEFEAADVRPESRLACQIQITEALDGLVLHVAGRSR
>2Fe-2SST2 (pgv:SL003B_3177) *Polymorphum gilvum*
MPKIIIFMEPDGSRRLDLEVPVGTSLMQAAVQNGVEGIVGECGGSCMCATCHVLVDEAGLAR
LPPKSDSEDEMLEFSVGERHPGSRLGCQITVTAEALDGLTVRVPG
>2Fe-2SST2 (malg:MALG_02188) *Marinovum algicola*
MAKITYIEHNGTRHEVDVATGLTVMEGARDNNIPGIEADCGGACACSTCHVYVDKAWTEK
LPPMDAMEEDMLDFAYEPDPERSRLTCQLKVSDDLGLVVMPEKQI

Subtype 3

>2Fe-2SST3 (bbt:BBta_1591) *Bradyrhizobium* sp. BTAi1
MTELSAMIDEGGARRFRIRLERPDGTFTFDAASDEYLLYSMIDAGIESPYICEQGWCLAC
AARLVSGKVDRSDALTVYAEDAEGFLLLCSTKPCSDLILTLDERQTRRDMVQHRIEHNQ
LARAYPPGARLRFRRGRATPRMSSGD
>2Fe-2SST3 (aol:S58_10600) *Bradyrhizobium oligotrophicum*
MTDLSTSTDEGDARRFRVRLERPDGTFTFDAASDEYLLYSMIDAGIDTPYICEQGWCLAC
AARLVSGKVDRSDALTVYPEDAEGFLLLCSTKPCSDLVLMMLDERQTRRDMVQHRIEHNQ
LARAYPPGARLHFRRGRAAPRIDPCTLSKR
>2Fe-2SST3 (rde:RD1_2377) *Roseobacter denitrificans*
MRKHKVTLRNRDNLTFDVGEDAEI IDIVEAAGHVLPACRYGGCISCAARMISGSVRQPK
GTALNKRQSEAGYVLLCVARPTADCVFDVGVESHTTLYQNPFAAAAASQLARASKE
>2Fe-2SST3 (rli:RLO149_c020910) *Roseobacter litoralis*
MRKHKVTLRNRDNLSEFVGEDAEI IDIVEAAGHVLPACRYGGCITCAARMISGSVRQPK

GTALNKRQSEAGYVLLCVARPTADCVFDVGVESHTTLYQNPFASAAAASQLARANTE
>2Fe-2SST3 (11mamo:A6B35_14570) *Mesorhizobium amorphae*
MTSFTITLANQGGATFDVDRRKPLLQSLREQGVDLPYGCKYGGCITCAAKMISGNVDQKA
QRALNNRQINNGYIILCVARPLSDCTLEVGVESHDKLYRNPFLDPLAAHELKADIATPLE
DKK
>2Fe-2SST3 (apb:SAR116_0299) *Candidatus Puniceispirillum marinum*
MSMITIANRENATYQVKGRKPLLDELRDQGVDLPYGCKYGGCITCAAKLIDGEIDQRAQV
ALNNWQLNNGYVILCVARAKTDCTLEIGVESHDLYRNPFLDPLQPHELKADIATPLDAE
K
>2Fe-2SST3 (oar:OA238_c13340) *Octadecabacter arcticus*
MNATRTITIANCGGATYQVEARRPLLDCLREQGVDLPYGCKYGGCITCAAKLTAGEVDQR
RQVALNNRQINNGYVLLCVARAVTDCTLEVGVESHDKLYRNPFLDPLEPHELKADIATPK
ER
>2Fe-2SST3 (sil:SPO2377) *Ruegeria pomeroyi*
MTTHTVTIANREGASFQVNARRPLLEQLRDQGVDLPYGCEYGGCITCAAKLTAGEVDQRR
QVALNNRQIANGYVILCVARATSDITLEIGVESHDLYRNPFLDPLQPHELKADIATPRP
SIGDALEQTKES
>2Fe-2SST3 (ptp:RCA23_c25280) *Planktomarina temperata*
MIVTLSNRDGAQYKVDPRRPLLDCLRQDQGVDPYGCKYGGCITCAAKLTAGEVDQRRQVA
LNNRQINQGYVILCVARPMSDITLEIGVESHDLYRNPFLDPLQSHELKADIAPKEV
>2Fe-2SST3 (rle:pRL100075) *Rhizobium leguminosarum* bv. *viciae*
3841
MTGEAVLAPFKVEFAKQGRITDVTSDQTVLSCAKKAGIKIPSSCSNGLCGTCKSKLVSGT
INMHHNGGIRQREIDAGFFLPCCSKPLTDLIER
>2Fe-2SST3 (lmd:METH_03515) *Leisingera methylohalidivorans*
MLDAALENAMDAPYACKAGVCSTCRCKVLEGEVEMVANHALEDYEVEKGYVLSCQAYPVT
DNVVVDYDQ

Subtype 4

>2Fe-2SST4 (azc:AZC_3424) *Azorhizobium caulinodans* azc
MKEVSMTTIVTISPGGEVLEAAEGMSLLEVLLKGDIKIPHKCDGKASCGSCHIFVQEGRKG
LTKIAREENEKLDSIVGVGSKSRLACQAKVLGTENIKIELLGFGSGL
>2Fe-2SST4 (msc:BN69_2649) *Methylocystis* sp. SC2
MPTVTIMPSGKTVDAAEGATLLQIIMSSGEEINHKCEGKAQCGSCHIIYVHEGRKGISKIA

REENERLDTIVGIGSKSRLACQAKILGTENIKVELLGFASGL
 >2Fe-2SST4 (mbry:B1812_07990) *Methylocystis bryophila*
 MATVTIMPSGKSVEAAEGATLLEIILSAGEGINHKCEGKAQCGSCHIFVQEGRKGVSKIG
 REENEKLDITIVGVGSKSRLACQTKVLGTENIKLELLGFSSGL
 >2Fe-2SST4 (brs:S23_46150) *Bradyrhizobium* sp. S23321
 MTTLTVLPEGKTIEVSEGTTLAALLGAEIAVPHKCEGQAKCGSCHIIYVQEGRKGLSKIA
 RLENEKLDSIVGVGSKSRLACQATVLGTEDVKIELLLGFGSGL
 >2Fe-2SST4 (bbt:BBta_5894) *Bradyrhizobium* sp. BTAi1
 MATLTVMPGKTIEVGEGTTILAALLGAEVEIPHKCEGQAKCGSCHIFLQEGRKGVSKVT
 RLENEKLDITIVGVGSKSRLACQATILGTENVKIELLLGFGSGL
 >2Fe-2SST4 (bra:BRADO5410) *Bradyrhizobium* sp. ORS 278
 MATLTVMPGKTIEVGEGTTILAALLAADVEIPHKCEGQAKCGSCHIFLQEGRKGVSKVS
 KLENEKLDSIVGVGSKSRLACQATILGTENVKIELLLGFGSGL
 >2Fe-2SST4 (aol:S58_22960) *Bradyrhizobium oligotrophicum*
 MATLTVMPGKTIEVGEGTTILAALLGAEVEIPHKCEGQAKCGSCHIFLQEGRKGVSKVS
 KLENEKLDSIVGVGSKSRLACQATILGTENVKIELLLGFGSGL
 >2Fe-2SST4 (bid:Bind_1905) *Beijerinckia indica*
 MPTVTIKPSGKTQVAAEGSILIDAIIAAGEPIEVKCNRDACESCHVFILEGKKSLAKMG
 RPESEKLD SMVGVASKSRLACQCVLGTENVTVELLGALSG
 >2Fe-2SST4 (mbry:B1812_10000) *Methylocystis bryophila*
 MPTLTLLPSGKTDDAEPGTRLLDAILATGEKIVSKCGGEAKCGECHVFIQEGRKSLSKMQ
 RAENEKLDITIPGVGSKSRLACQTLFGTENVTVELLGFGSGL
 >2Fe-2SST4 (sphi:TS85_14400) *Sphingomonas* sp. WHSC-8
 MTTVTIMPSGKTVDVVGSTLLAAILAADSKIQHNC DGKATCGTCHIFVLEGRKGVSKIG
 REENEKLDSIVGVGSKSRLACQATLLGTEDVMLEVL SFR
 >2Fe-2SST4 (msl:Msil_3636) *Methylocella silvestris*
 MPLLLTIQPSGKTIEAAEGTSLLDALLAAGEKIVSKCGGNAKCGQCHVFVQEGRKTISKMT
 RVENEMLDITIIIGVGSKSRLACQAMFGTEPVTVEVLSFV
 >2Fe-2SST4 (ster:AOA14_03605) *Sphingopyxis terrae*
 MPEIIIVLRDGSYRIIDTDPEYSLMEAIRDAGVDEMLAMCGGCCSCATCHVYIEESGGDL
 SEPSADEDDLDDSTGCRTSQSRLACQVRLAESTIKRARIAPED

Subtype 5

>2Fe-2SST5 (pla:Plav_1783) *Parvibaculum lavamentivorans*
MPTIIFIEPDGVEYPIAVKSGTTARDAAVNNSVPGIDGDCGGECACATCHVHVDAAWMAR
TGMAEPGGMEANLLQFAEGSTENSRLACQITMTDDLDGLMLRIPDGQH

>2Fe-2SST5 (npp:PP1Y_AT31173) *Novosphingobium* sp. PP1Y
MIKVTFVAHDGHRFPVEIGEGLTAREAALFNDVPGIDGDCGGQCACATCHVQVDPAWIER
VGRLADDSMEADLLQFAEGTTAESRLACQIRLDAGLDGLVLHVPEQQY

>2Fe-2SST5 (sphk:SKP52_24465) *Sphingopyxis fribergensis*
MIKVTFVSADGTRRTVEIDEGLSAREAALFNSVPGIDGDCGGVCACATCHVHVLDLAWMDR
VGPPEEGGMESDLIQFAEGTTETSRLACQISMVPELDGLVLHLPELQH

>2Fe-2SST5 (sphk:SKP52_13375) *Sphingopyxis fribergensis*
MVKVTFVSSDGTREVEIAEGETAREAALFNDVPGIDGDCGGVCACATCHVHVDPAWIDR
VGRLVEGAAEAELLQFAEGANEYSRLACQIPMVEGVEGLILHVPEQQY

>2Fe-2SST5 (ster:AOA14_00650) *Sphingopyxis terrae*
MVKVTFVSSDGTREVEIAEGETAREAALFNDVPGIDGDCGGVCACATCHVHVDPAWIDR
VGRLVEGAAEAELLQFAEGANEYSRLACQIPMVEGVEGLILHVPEQQY

>2Fe-2SST5 (sgi:SGRAN_1596) *Sphingopyxis granuli*
MIKITFVASDGERREVEIEEGETAREAALYNDVPGIDGDCGGVCACATCHVHVDPWIDK
VGRLMHDGMEADLLQFAEGTTEYSRLACQIPMKPMLDGLVLHLPEQQY

>2Fe-2SST5 (blas:BSY18_3827) *Blastomonas* sp. RAC04
MVKVTFVAHDGRRFPVEIGSGMTAREAALFNDVPGIDGDCGGQCACATCHVHVDPWIGR
VGCLVDGSMEADLLQFVEGRTEESRLACQIKLDERLDGLVLYVPEQQY

>2Fe-2SST5 (eli:ELI_14940) *Erythrobacter litoralis* HTCC2594
MIKITFVASDGERREVEIEEGETAREAALYNDVPGIDGDCGGVCACATCHVHVDPWIDK
VGRLMHDGMEADLLQFAEGTTEYSRLACQIPMKPMLDGLVLHLPEQQY

>2Fe-2SST5 (nar:Saro_3658) *Novosphingobium aromaticivorans*
MAKVTFVQPDGSQRTCVNFEGMTLMQLAVGNLVDGIDALCGGMMQCATCHCWIDPEWIGR
TGMAGPDERAMLEAIEGVEIRPESRLSCQVQLGEELDGLVVRIPPEQPGV

>2Fe-2SST5 (npp:PP1Y_Mpl3486) *Novosphingobium* sp. PP1Y
MAKVTFIQPDGTPRECVNFEGMTLMQLGVANLVEGIDALCGGMMQCATCHCWIDPAWIEI
TGRAGEDERAMLESIEGVEIRPESRLTCQIQLGEELDGLVVRVPPEQPGV

>2Fe-2SST5 (sphg:AZE99_00825) *Sphingorhabdus* sp. M41
MPKVITYISSDGESRTLDVAVGETVMRGALDNDVDGIVAECGGGLACATCHCYVDAAWAAQ
VGTPTSQDEIDMLEMAAAEIRDTSRLSCQIEISAEELDGLVVHLPEEQY

>2Fe-2SST5 (blas:BSY18_806) *Blastomonas* sp. RAC04

MPAVTYVEFDGAEHAIDLALGENVMRGALHNDLPGIVGECGGGLACATCHCYVDDAWTER
VGGPASREESEMLESTAAPIKSSRLSCQIVMSAELDGLIVHLPEAQY

Subtype 6

>2Fe-2SST6(yan:AYJ57_00160) *Yangia* sp. CCB-MM3
MTKGS�TFTDVLTVTVPAQTRIIEISEKVGAGIVFGCREGDCGTCITHVLEGSEHLSDP
SALELRVLRENLAGQSDRLACQCQVLGGAVKVKPG
>2Fe-2SST6(rhc:RGUI_2054) *Rhodovulum* sp. P5
MATAKLTFADVALTVNVPSGTRIIEISEKIGSGITYGCREGECGTCITRIVEGMENLSQP
SALEERVLLKDNMAGHDDRLACQCQVLGGTVKVRPG
>2Fe-2SST6(daa:AKL17_1542) *Defluviimonas alba*
MEKATLTFTDVATTVTVPAGTRIIEMSEKVGSGITYGCREGECGTCLTHVIEGAENLSEP
SVLELRVLAENMAGRKDRLACQCRILGGAACKVRPG
>2Fe-2SST6(rsp:RSP_3190) *Rhodobacter sphaeroides* 2.4.1
MEKATLTFTDVAITVNVPPGSRIIEMSEKVGSGITYGCREGECGTCVTHIIEGSENLSDP
SALELRVLSEN MAGKDDRLACQCRVL SGAVKVRPG
>2Fe-2SST6(rsh:Rsp17029_3929) *Rhodobacter sphaeroides* ATCC
17029
MEKATLTFTDVAITVNVPPGSRIIEMSEKVGSGITYGCREGECGTCVTHIIEGSENLSDP
SALELRVLSEN MAGKDDRLACQCRVL SGAVKVRPG
>2Fe-2SST6(rsk:RSKD131_3366) *Rhodobacter sphaeroides* KD131
MEKATLTFTDVAITVNVPPGSRIIEMSEKVGSGITYGCREGECGTCVTHIIEGSENLSDP
SALELRVLSEN MAGKDDRLACQCRVL SGAVKVRPG
>2Fe-2SST6(cid:P73_2169) *Celeribacter indicus*
MDKISITFIPNGNKTVSVDPGSNLLRASLREKGGIPFRCGGGFCGTCRCRIVEGREHADD
VKAKERHRLSEEDVANGFRMACQTFVNGDVKISWG
>2Fe-2SST6(rcp:RCAP_rcc03285) *Rhodobacter capsulatus*
MDKATLTFTDVSITVNVPTGTRIIEMSEKVGSGITYGCREGECGTCMTHILEGSENLSEP
TALEMRVLEENLGGKDDRLACQCRVLGGAVKVRPA
>2Fe-2SST6(aak:AA2016_0331) *Aminobacter aminovorans*

MINITFITNDNKQVSAPENSNLLRVSLREKGGIPFKCGGGLCGTCKCRIETGIENTDAVK
 PKERNHLTSDDLAAGFRMACQTFVLGDVAVSWVPKGR
 >2Fe-2SST6 (psin:CAK95_12430) *Pseudorhodoplanes sinuspersici*
 MLVSAPGNSNLLRVSLREKGGIPFKCGGGLCGTCKCRIEKGLEHTDTVKAKERKHLTEEQ
 IKEGYRMACQTFVNGDVSVSW
 >2Fe-2SST6 (psin:CAK95_12440) *Pseudorhodoplanes sinuspersici*
 MPKVVLHRDGQVYQDEVKDNTNLVVRAGIKQFPYPNLRYGCGMGKCAKACRILKGGEHL
 PAPNWKEKKQLGAVRLEQGYRLICQLWLNHDIELAQDLQPLEPAAPASA

Subtype 7

>2Fe-2SST7 (bid:Bind_3149) *Beijerinckia indica*
 MADITFASPLLPKNKTVYGIAGDTHLLAVARDHRIPVPFNCEGDGCGSCLIKVTVLDGK
 QPMGSTLSEKEKFTLAAHGKLSKEAKELAEIADIPPQYRLACQYIVRDEPILVEFSGEPG
 VEIDPARHKHERAALNDIETTGAEDREYAESVKA
 >2Fe-2SST7 (mgy:MGMSRv2__0351) *Magnetospirillum gryphiswaldense*
 MSR-1 v2
 MANVTFSGPTLEKNVTVYAVAGANGTLLAVAKANNIKIPFECQDGECEGSCCLIKVTHLGDN
 APKAIHLTDKEKLTLSVNGKLTKELLAKTEVEDMPPPYRLACQYIVRDEDILVEFSGEAG
 VEIDLRR
 >2Fe-2SST7 (msl:Msil_3778) *Methylocella silvestris*
 MPVVTFTSETLHRDVRAYATAGDTSTVLSVALAQGVKIPHDCRDGECGSCCLIEVKYVEGK
 PKMAIALTEKEKIKLRELKGKITAQQIQDAETNDIAPPYRLACQFIVREEEIIIHFTGEPA
 GA
 >2Fe-2SST7 (rsu:NHU_03481) *Rhodovulum sulfidophilum*
 MAIITFTSPQM HKDKTVYGVAGDTKTILALAEDNRIPFDCRDGNCGSCCLIEVSYDNPA
 DKKAIMLTEKEKQKLKELGKLTQQEIDDAEVRDMPPRYRLACQFIARDEDVTVSFSGMPV
 GSD
 >2Fe-2SST7 (con:TQ29_02130) *Confluentimicrobium* sp. EMB200-NS6
 MATITFSSPIMKRDKTVYAVAGNTDTILGLAEHGIPIPFECRDGNCGSCCLIEVTYLEDK

PKMAVALTEKEKARLKEKVKVTQKEITEAEVNDLPPHYRLACQYIARHEDIRITFTGEPG
GA

>2Fe-2SST7(rcp:RCAP_rcc00573)*Rhodobacter capsulatus*
MPNITFTSPIMKKDKTIYAVAGNTATILALAKEHAIPFECGDGDCASCLIEVTHLDNK
PAMAMMLTEKEKARLKELOMITAEIEAAEVSDLPPRFRLACQFI PRDEDVMVHFTGTPG
GSV

>2Fe-2SST7(daa:AKL17_1546)*Defluviimonas alba*
MPNITFHSSIMKKDKTIYAVAGNTATLLALARAHDIPFECGDGICGSCCLIEVTLLADK
PLMGMALTEKEKARLKELOKITPAELEQAEVNDIPPRFRMACQFVPRDEDVLVSFTGTPG
GSA

>2Fe-2SST7(yan:AYJ57_00175)*Yangia* sp. CCB-MM3
MANITFQSPIMQRDKTVYAVAGNTATILALAKEHEIPFDCGDGDCGSCCLIEVTSLEDK
PAMGLALTEKEKARLKELSKLTAEIENAEVNDMPPRYRLACQFIARNEDVLVRFSGAPG
GSD

Subtype 8

>2Fe-2SST8(nar:Saro_3849)*Novosphingobium aromaticivorans*
MRTETHQIRIVGGGQFACPEGERVLIAMERSGGNDIGVGCRGGGCGFCVVRVVEGEYRTG
KMSTAKVSVADQAKGYVLACRLYPLNDLVIEIG

>2Fe-2SST8(cna:AB433_18105)*Croceicoccus naphthovorans*
MARTVTGLYQIRVVGGEFTCGGDERVLLAMERCGAGDIGVGCRGGGCGICRVKVVEGDY
RTGKMSAAKVSDSDLQAGYALACRLFPAGNLVIAVE

>2Fe-2SST8(syb:TZ53_09045)*Sphingobium* sp. YBL2
MDDRDVEGLTQAAPFQIEIGGVRFPCRADQSLAAMIASGRKALAVGCRSGGCGVCRIRI
QAGRCSTGHMNRVVSAADEQAGIVLACRAYPSSDIRAVPLPRASFGAAPVGRAA

>2Fe-2SST8(msl:Msil_1473)*Methylocella silvestris*
MASERFTLTLEGHGASSGYADERVLVALERAQGFGQIKNMPCRLPVGCRGGGCGICRVRV
LAGAYRRDPMSRTHVSVEDEGAGLVLACCIYPLSDLSLRLEPPAAVKGMGQKAIQQG

>2Fe-2SST8(magq:MGMAQ_0645)*Magnetospira* sp. QH-2
MAHSRHSGKFAIRVEGDPRTYFCAADQKVIAALEECGQIGIRVGCREGGCGVCRVRVVS
EYETGKMSRAHVSEEQESQGFALSCRLFPRSNLHLEAAGIRTGSGDRET

>2Fe-2SST8(ata:AWN88_11340)*Agrobacterium tumefaciens* S33

MALPRSIHLPQIDRSIAVAEGETVLQAALAAGIAYPHGCRMGRGCGACKSRLVSGEVDLLK
HTPFSLTEEEKADGLTLACRAIPLSDVVIGWLNADALSDSDADLLSTPER
>2Fe-2SST8 (sphk:SKP52_20385) *Sphingopyxis fribergensis*
MTRTVDIHQAGRAIAVGDGQTILEAALDAGIAYPHGCRSGRCGTCKSRLVAGEVDMLPHT
CFALTPEEKAQGLILACRAQPLTNIEVAWLKKEDEAVAHPARRVKTDVAAPDDATRANTE
PPFQYAARQAGGKTAS

Subtype 9

>2Fe-2SST9 (aak:AA2016_0333) *Aminobacter aminovorans*
MPTVVIHSGEAFSGEVKEDTNLVVRAGIKQFPYPHLAYKCGMGKCGTCASRILAGAEHL
PPPNWKEKKQLGDKIDEGFRLVCQLWIKNDIELRQEKVTEQA
>2Fe-2SST9 (cid:P73_2167) *Celeribacter indicus*
MPQEGGAASASSEAGNLMPKVILHKGGEVFEGEVDNTNLVVRAGIKKFFPNLAYKCGM
GKCSTCTCRILRGGDHLEAPNWKEKRQLGEKLEEGYRLACQLWVSEDIELTQDL

Subtype 10

>2Fe-2SST10 (sbd:ATN00_07810) *Sphingobium baderi*
MQIIIFRNAEAGERIVMASEGDTLMHVALANDIIGIPGDCGGQCACGTCHVYVDPWVERV
GRVEPGSTEETMIFGAPVDARPN SRLACQVNLI AIHDGLIVEIPEGQ
>2Fe-2SST10 (anh:A6F65_02151) *Altererythrobacter namhicola*
MPTVTVLPADIAMETQPGETLLGAAQRLGYTWPTVCGGEGQCRTCYAVIEQGEDALSPVT
ALEEEASPALAIVARRAGKPVRLACQAVPTGDITVQRSGVRKS

Subtype 11

>2Fe-2SST11 (hmc:HYPMC_3657) *Hyphomicrobium* sp. MC1
MATLTIMPADKSIEVADGTTLLAAILSSGIDFPHNCEDQGCRGGCHVFVQEGRKGLSKIA
REENEKLDSIVGVGSKSRLACQAKVLGTENIKVELLGFSGSL

Subtype 12

>2Fe-2SST12 (psin:CAK95_14295) *Pseudorhodoplanes sinuspersici*
MKWACEIDREKIAFAAVDPQSACRIHTAGRWSFRLQEPSPGVLAIAQKSVSVPDNCSRNS
NGPFVVKLARSQRELLWNSDERDLLSLSEKNGVELLNGCRTGQCESCLVKVLSGQVAHLA
PVELEEPGTCLTCCAVPLSDLVLDA

Subtype 13

>2Fe-2SST13 (nar:Saro_0183) *Novosphingobium aromaticivorans*
MIASREEIAQAERALELLGGFAPKRHILLCAGPEKDKCAPRAVGDEAWNYLKKRLGELKL
GGAQGVLRNKVGCLRVCIAGPVAVVYPDNVWYHSCTPPVLERIIQEHVIGGVPVEDYRLR
QPAASLAE

Subtype 14

>2Fe-2SST14 (azc:AZC_1282) *Azorhizobium caulinodans*
MDAVKAALHQLGVPNSQVKTEGFGTDRRDPSKKAQKLGKVIATVSFRESHLSAAAREGMT
LLDVADESGVFIIDSACRSGTCGVKLTSGKVRLGTDDALSDEERAQGYILACQAQPDGDVA
LDV

Subtype 15

>2Fe-2SST15 (mln:A9174_10550) *Mesorhizobium loti* NZP2037
MPEEAIFTETFTSLPSDQGPGADEPVTITFARSGRTVMAKRGEGMIRAAEANGIAVDYSC
RTGERGSCRCKLLAGEVEMPEGTALTSKERKAGLILACVARPISDAVTIDL

Subtype 16

>2Fe-2SST16 (bid:Bind_0407) *Beijerinckia indica*
MPIVTIKPQDKTQEGAEGTTLREVIIAAGIPLNECTCAKGYFDNCHAFITEGKKSLGKAT
REENERLDQIVGVGSKSRLICEAKLGPENVTVELLGALSG

Subtype 17

>2Fe-2SST17 (con:TQ29_00555) *Confluentimicrobium* sp. EMB200-NS6
MPEITFVTTAGEEITKEIPVGLSLMRGAVEAGINDILAECCGVASCGTCKIILDEANAGR
IPPADAFEGSMLEDDPEGWRLSCQIIIVDDTLEGLVVRLAPTEY

Subtype 18

>2Fe-2SST18 (con:TQ29_17640) *Confluentimicrobium* sp. EMB200-NS6
MPKITYEQPDGTRAELEVEEGMSVMRGAVDNGIDGIVAECGGACACATCQVVIGAWEWDK
LPAPGVLEEAMLEDVEGDDRRLSCQIEVTAELDGMVVKIPATQY
>2Fe-2SST18 (sphk:SKP52_00895) *Sphingopyxis fribergensis*
MPTLTVINRAGNAQQLEAGSGLSVMEVIRDAGYDELLALCGGCCSCATCHVYVEGDVDPG
VPGNDENDLLDSSDHRTERSRLACQIRFADDLAGLTIRIAPED

Subtype 19

>2Fe-2SST19 (pla:Plav_2523) *Parvibaculum lavamentivorans*
MRIILIDTEGVEHTLEAAEGWRVMEIIRDYGFPIVAECGGACACGTCQVEVDPDWAAKLH
EPREEELDMLDQNYGGEWSRLSCQLLMNAKLDGLRVRLADIAIRKAA

Subtype 26

>2Fe-2SST26 (bja:blr1765) *Bradyrhizobium diazoefficiens* USDA 110
MNSEKEFHLPQLYRHHVFACNTQRPPNHPHGSCGASGAQALWDRMGKAIEAQGLDDIGFATA
GCLGFCNSGPLLVVYPDGVWYRATTPEDVDEIVISHLKHGQRVDRLVIVLKRS

>2Fe-2SST26 (bjp:RN69_39120) *Bradyrhizobium japonicum* E109
MNSEKEFHLPQLYRHHVFACNTQRPPNHPHGSCGASGAQALWDRMGKAIEAQGLDDIGFATA
GCLGFCNSGPLLVVYPDGVWYRATTPEDVDEIVISHLKHGQRVDRLVIVLKRS

>2Fe-2SST26 (bra:BRADO5398) *Bradyrhizobium* sp. ORS 278
MSDGGVAEAEDEFEIIPQLYKYHAFVCLTQRPPGHPRGSCGALGVQPLWDRLTKTIEAQRLTD
VGVTAAGCFGFCSAGPMMVVYPDGIWYRPTKPEDIDEIVESHFKQGKRVDRLVMVLKR

>2Fe-2SST26 (bbt:BBta_5882) *Bradyrhizobium* sp. BTai1
MSETDVAEADDAFELPQLYKYHAFVCLTQRPPGHPRGSCGALGVQPLWDRLTKTIEAQRLTD
IGVTAAGCFGFCSAGPMMVVYPDGIWYRPTKPEDIDEIVESHFKQGKRVDRLVMVLKR

>2Fe-2SST26 (brs:S23_46050) *Bradyrhizobium* sp. S23321

MSDGVNEEEFQLPQLYRHHVFACHTQRPPGHPRGSCGAAGGAALWERFGKAIEAQRLTDIGF
TASGCLGFCAAGPLMVIYPDGVWYRPTTPEDVDEIVESHLKQGKRVDRLVMVLARS

>2Fe-2SST26 (aol:S58_23070) *Bradyrhizobium oligotrophicum*

MSDSEVAEADDEFVFPQLYKYHAFVCLTQRPPGHPRGSCGALGVQPLWDRLTKTIESQRLTD
IGVTAAGCFGFCSAGPMMVVYPDGIWYRPTKPEDIDEIVESHFKQGKRVDRLVMVLKR

>2Fe-2SST26 (brC:BCCGELA001_31070) *Bradyrhizobium* sp. CCGE-LA001

MNAEDELELPQLYRHHVFACHTERPPTHPHGSCAASGALALWDRMGKAIEAQALSDVALTPA
GCLGFCNTGPLMVVYPDGVWYRPTTAEDIDEIVESHLRKGRVDRLVIVLKRS

>2Fe-2SST26 (biC:LMTR13_26520) *Bradyrhizobium iCense*

MNAETEFQLPQLYRHHVFACHVQRPPTHPHGSCGAAGAQLWDRMSKAIEAQGLTDIGFTAA
GCLGFCNAGPLMVVYPDGVWYRPTTADDIDEIIESHLKEGKRVDRLVMVLKRS

>2Fe-2SST26 (xau:Xaut_2332) *XanthobaCter autotrophicus*

MSEAAESEVLDIPQVYTHHVFCCFTQRPPQHPRGSCGANGAAPLWDRLAKKLEASGRDIAM
TSAGCLSFCQAGPIMVVYPQGIWYTPKSPEDIDEIVTSHLLGGKPVERLIIVPRI

>2Fe-2SST26 (azC:AZC_0303) *Azorhizobium Caulinodans*

MTETATLSLTDVPQVYKRHHVFACFQQRPPTHPRGSCGAAGAQLWERLGKQIEATGQRDIVM
TATGCMGFQAGPIMVVYPEGVWYQPRTPEDVDEIVTTHLVGGTLVERLVIVPRI

>2Fe-2SST26 (bid:Bind_3574) *BeijerinCkia indica*

MTLEVPQVFKYHIFTCTKRPAGHPRGSCMERGAQPLWERLGQKLEAKQLPGVSMTMTGCLS
FCQAGPLMVVYPEGIWYHPEKPEDIDEIVQSHFVEGNPVERLIIVPQR

>2Fe-2SST26(msl:Msil_1738) *MethyloCella silvestris*

MSSVAELDLPVVFKEYHVIACFTKRPPGHPRGSCMESGAQPLWEHLQKKVEAQRLTDVCVTAS
GCLSFCRAGPLMVVYPEGVWYHPETVDDIDEIVDRHFGAGEPVERLIIVPKV

>2Fe-2SST26(hmC:HYPMC_3647) *Hyphomicrobium* sp. MC1

MTTTLDDDVVDVPQVYKHHIFACFTQRPPNHPRGSCGAVGAQPLWDYLSKALEAEHLSDVGF
TAAGCLGFCRTGPLMVVYPEGIWYRPSTAEDIDEIVQSHFKQGKRVDRLVMVLSKN

>2Fe-2SST26(hmC:HYPMC_3564) *Hyphomicrobium* sp. MC1

MEVVSGNGGKSATAQSSAANDSEPVYRIHVFCVNERPPTHRRGSCGGKGSRLCDYMCRLG
MATGVRRIRINHAGCMNVCEHGPVLVIYPEGVWYRFETQEDVEEILRSHIVAGRKVER
LALSIDPTTLHG

>2Fe-2SST26(msC:BN69_2661) *MethyloCystis* sp. SC2 msC

MSDTPEEEFELPQLYKRHVFACTQRPPNHPRGSCGSLGAQPLWERLGKRVEADGGGEIGFT
SAGCMGFCSAGPLMVVYPEGVWYRPTTAEDIDEIYDShLKGKRVDRMLVILSR

>2Fe-2SST26(mbry:B1812_07930) *MethyloCystis bryophila*

MSDASEEEFEVPQLYKRHVFACTQRPPTHPRGSCGANGAQPLWDRLGKLVEADGSGEIGFT
AAGCMGFCSAGPLMVVYPEGIWYRPTTPEDVDEIYSSHLKGKRVDRMLVILTR

>2Fe-2SST26(mgy:MGMSRv2__3321) *Magnetospirillum gryphiswaldense*
MSR-1 v2

MSVSTDPELFYRIHAFICTNRRADDHPRGSCAARGSEPLRDYLKAAAKKKGVGGVRVNAAGC
LDRCELGPVLVIYPEGIWYGFNSREDIDEIIDTHLLGGGRVTRLMLTPDQK

>2Fe-2SST26(magq:MGMAQ_3806) *Magnetospira* sp. QH-2

MSEAPYYRSHVFCVSNQRVEGHPRGCCADKDSASLRTYLKVKTKQLELNDVRINNAGCLDRC
ENGPVMVIYPEGVWYKVATRADMDEILESHIQGGRVEHLMLSNED

>2Fe-2SST26(azl:AZL_a04200) *Azospirillum* sp. B510

MPLDIPQTFRHHVFCCAQQRPPGHPRGSCAAKGAHPLWQRLDQKIQQQGLTDIGMAMTGCLG
FCSAGPLMVVYPEGIWYRPETPEDIDEIVDSHLVNNDTPVERLVMVLTR

>2Fe-2SST26(abs:AZOBR_140175) *Azospirillum brasilense* Sp245

MSLDLPQVFRHHVFCCAQQRPPGHPRGSCAAKNAHPLWEQLGQRIQAKGLLDVGMMAWTGCLG
FCSAGPLMVVYPEGLWYRPETPEDIDEIVDSHLVNNTTPVERLVMVLTR

>2Fe-2SST26(abq:ABAZ39_05635) *Azospirillum brasilense* Az39

MSLDLPQVFRHHVFCCAQQRPPGHPRGSCAAKNAHPLWEQLGQRIQAKGLLDVGMMAWTGCLG
FCSAGPLMVVYPEGLWYRPETPADIDEIVDSHLVNNTTPVERLVMVLTR

Subtype 27

>2Fe-2SST27(sphi:TS85_14385) *Sphingomonas* sp. WHSC-8

MELPEELPQLYKRHIFACHTQRPPQHPRGSCGAAGAGPLWERLGKRIEALDLTGVEVGFTASG
CLGFCSAGPLIVYIYPEGVWYKPQSEADIDLIVEHHLQQDRLEDLVVLSR

>2Fe-2SST27(azl:AZL_000100) *Azospirillum* sp. B510

MTDPNPYFEAHVFCCTNRRPDGHKRGSCAAQGSEKLRDYMKAARELGFDGKVRINSAGCLD
RCELGP TLVIYPEGVWYSYHSTADIDDLQTHLVEGRRVERLMLTTEQREL RPDQRG

>2Fe-2SST27(abs:AZOBR_10399) *Azospirillum brasilense* Sp245

MTDPKPYFEAHVFSCNRRPDGHRGSCAARGSEKLRDYMKAARELGLDGRVRINAAGCLD
RCELGPVLVVYPEGVWYTYRSFADVDAILETHVIGGGRVERLMLKPEQKELLPEQVG

>2Fe-2SST27(abq:ABAZ39_14075) *Azospirillum brasilense* Az39

MTDPKPYFEAHVFSCNRRPDGNKRGSCAARGSEKLRDYMKAARELGLDGRVRINAAGCLD
RCELGPVLVVYPEGVWYTYHSFADVDAILETHVIGGGRVERLMLKPEQKELLPEQVG

Subtype 28

>2Fe-2SST28(elq:Ga0102493_11923) *ErythrobaCter litoralis* DSM
8509

MSDNELLSARSSLARHYESAPARPD SAPVERHIFLCALSDKAKCCSREEGEAAWAFKTRLK
ERGLVGPRRTADHPKGAGGGVQRTKADCLQICGKGPIAVVWPDGVWYHSCMPQALERIIDEH
LVGGVPVEEYRLSPLGED

>2Fe-2SST28(pns:A9D12_04600) *PorphyrobaCter neustonensis*

MLCARTNLARHFGDPQKGTAIARHIMLCAISEKQKCCSREAGEEAWGFLKSRLKELGLVGPO
RREDSKRGAGGGVQRTKADCLQLCAAGPIAVVWPDGVWYHSCSPAVLERVIQEHLIGGVPVE
DFRLKPAV

>2Fe-2SST28(por1:BG023_11413) *PorphyrobaCter* sp. LM 6

MNREELLCAQNSLAKHYGDAAGTAIQRHIMLCALSEKQKCCSREAGEESWGFLKTRLKELG
LVGPLRDANSPRGAGGGVQRTKADCLQICAAGPVAVVWPDGVWYHSCSPQVLERIIQEHLIG
GEPVEDFRLTPA

Subtype 29

>2Fe-2SST29(eli:ELI_12930) *ErythrobaCter litoralis* HTCC2594

MTSEKKLDKARRALRSIAGERVERHIFLCALSEKQKCKLDEGERAWKYLKSRMKELGLPKA
GVAQRTKADCLQVCAAGPVAVVYPDQVWYHSCNEDVLERIIQQHLIGGEPVEEFRLRSPV

>2Fe-2SST29 (aay:WYH_02285) *AltererythrobaCter atlantiCus*

MNKDSPEQPDLGKAQRALGKIGGEAIDRHIFLCGLSEKQECCRREVGERSWKYLRRLKELG
LAGKGGIQRSKADCLQICEAGPIAVIWPDRVWYHSCTEEVLERIIQEHLIGGRPVEDYRLRS
SESSSGSITASS

>2Fe-2SST29 (Cna:AB433_16560) *CroCeiCoCCus naphthovorans* Can

MGGGAEFTRHIFLCADQTKPKCCPKKVGLESWDHLKKRLAELGLDRSGGVMRTKANCLRLCV
AGPLAVVYPDGVWYHSCKPEVLDRIIDEHLIGGVPVEEYRLTVEGES

Subtype 30

>2Fe-2SST30 (amx:AM2010_2385) *AltererythrobaCter marensis*

MTSPRDLARAQRALGAIGGETVARHIFLCVSEKQKCCRREEGERAWKYLKKRLKDLRLAGT
TVQRTKADCLQVCETGPIAVVWPDQVWYHSCTEDVLERIIQQHLIGGVPVEDYRLHSAPGG

>2Fe-2SST30 (ado:A6F68_00497) *AltererythrobaCter dongtanensis*

MTPEPDIAKARAALAKIGGERVERQIFLCAMSEKQKCCSREEGERAWKFLKRRLKELGLVGR
TVQRAKADCLQVCEAGPVAVVWPDQVWYHSCNEAALERIIQEHLIGGVPVEDLRLREL

Subtype 31

>2Fe-2SST31 (bid:Bind_1539) *BeijerinCkia indiCa* (Thioredoxin-
like)

MALKDIFGQPAEARRLVVCVGPCCNKTGEAEVFLEELRQTMLAEGLDAMVGTASCMRRACL
GKCTGEPLAYIHPEEVWYHQLSPANLLRILREHLLGLRPVAELILPEE

Subtype 32

>2Fe-2SST32 (aep:AMC99_02527) *AltererythrobaCter epoxidivorans*
(Thioredoxin-like)

MSRSGKLEEAQKALTKIGGETIERHIFLCGISDKQKCCRREEGERAWKYLKKRLKQLKLAGP
LREDGGGIQRTKADCLQICAAGPIALVWPDRVWYHSADEEVLERIIQDHLIGGKVVEEYRLK
TPPAGD

Subtype 33

>2Fe-2SST33 (anh:A6F65_00445) *AltererythrobaCter namhiCola*
(Thioredoxin-like)

MSEKKLGKAEKAFAKIGGGAMSRHIFLCAISDKQKCCKKRAEGEAAWKFLKRRMKELGLTSPA
KAPDGMVVQRTKADCLQVCEAGPIAVVWPDGVWYHSCDPDALERIIQQHLIGGEPVEDLRLR
PPREA

Subtype 34

>2Fe-2SST34 (msC:BN69_0624) *MethyloCystis* sp. SC2

MTETAIKPFRLHVFVCVNTRDGRSACCEDHGAKEALAKVKEALKALPFAKRDGVRLTQSGCLG
QCEHGPVAVVYPGGKWISYASADELIRFVLEAIEAPD

Subtype 35

>2Fe-2SST35 (mgy:MGMSRv2__1348) *Magnetospirillum gryphiswaldense*
MSR-1 v2

MSHKYHVFVCTTSRPAGHPRGCCTSKGGGTAMFDQMMAFQKGMLWEKGVSLAQASCLGFCG
NGPLMVVYPEGVWYQPVAAADYDEIVDSHFKKGQVVERLRVNPQH

3Fe-4S

Subtype 1

>3Fe-4SST1 (bju:BJ6T_68600) *Bradyrhizobium japonicum* USDA 6
MTERLRVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVP PGLEDKAWLAKSNCP
EIAIDVIEE

>3Fe-4SST1 (bjp:RN69_33285) *Bradyrhizobium japonicum* E109
MTERLRVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVP PGLEDKAWLAKSNCP
EIAIDVIEE

>3Fe-4SST1 (brs:S23_51090) *Bradyrhizobium* sp. S23321
MTERLRVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVP PGLEDKAWLAKSNCP
EIAIDVIEE

>3Fe-4SST1 (brc:BCCGELA001_13030) *Bradyrhizobium* sp. CCGE-LA001
MTERLKVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVP PGLEDKAWLAKSNCP
EIAIDVIEE

>3Fe-4SST1 (brad:BF49_1786) *Bradyrhizobium* sp. BF49
MTERLRVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVP PGLEDKAWLAKSNCP
EIAIDVIEE

>3Fe-4SST1 (bic:LMTR13_32160) *Bradyrhizobium icense*
MAGKLIKIRVDQDKCQGHARCKSLAPELFELDEFNGAHEVGDGSPAGLEDKAWLAQSNCP
EIAIEVTEE

>3Fe-4SST1 (bic:LMTR13_32125) *Bradyrhizobium icense*
MSENRLVIVKIDPEKCQGHARCHALATELFELDEFNGARVRGSGQIPPSLEDQAWIARAN
CP ELAVEIVEQAKAPD

>3Fe-4SST1 (rpa:RPA1733) *Rhodopseudomonas palustris* CGA009
MSDHLNASETLKIHVDQDKCQGHARCKALAPELFELDDYGNAHETGDGTVP TALIDQAWL
AKSNCP ENAIVIDEA

>3Fe-4SST1 (rpb:RPB_3630) *Rhodopseudomonas palustris* HaA2
MSEMLTIHVDQDKCQGHARCKALAPELFDLDDYGNAHEKGDGVVPADLIDKAWLAKSNCP
ENAIDITED

>3Fe-4SST1 (rpd:RPD_1837) *Rhodopseudomonas palustris* BisB5

MSETLKIHVDDQDKCQGHARCKALAPELFDLDEYGNAHEKGDGSPASLIDKAWLAKSNCP
EVAIDITED

>3Fe-4SST1 (rpt:Rpal_1933) *Rhodopseudomonas palustris* TIE-1
MSDHLNASETLKIHVDDQDKCQGHARCKALAPELFELDDYGNAHETGDGTVPTALIDQAWL
AKSNCPENAIVIDEA

>3Fe-4SST1 (nha:Nham_2692) *Nitrobacter hamburgensis*
MSGTLRIHVDPDKCQGHARCKSLAPELFELDALGNAHEIGDGTVPAGLEDKAWLAQANCP
EFAIAIKEE

>3Fe-4SST1 (nar:Saro_3681) *Novosphingobium aromaticivorans*
MRVIANHALCQGHARCEDLCPEVFATDAVEGKVVLRMEEVPEALEAKVRLAVRNCPEGAL
RVVRSEGAEA

>3Fe-4SST1 (smaz:LH19_26275) *Sphingopyxis macrogoltabida* 203
MKIKVDQHNCIGAGNCAQLAPKVFSQREEDGVVILLDETTPGDSEAEDVAKAVKICPAQAI
SVSEG

>3Fe-4SST1 (smaz:LH19_26370) *Sphingopyxis macrogoltabida* 203
MKVKIDFKRCAGHARCMEEAPDVFQYNNNTNFTFVHRGADLEANRAAIDLAIMACPEQAI
SWVDDNAMSVEDAAEGLD

>3Fe-4SST1 (swi:Swit_1965) *Sphingomonas wittichii*
MRVKVDEDRQCQGHAMCTLACPELFLNDDDGHAYVEAELVPAGFEENVQRQAQRGCPEAAI
IVIED

>3Fe-4SST1 (sphb:EP837_03353) *Sphingobium* sp. EP60837
MRVIANMNVCQGHARCEDLCPEVFSTDAIEGKVVEIQPEFPPELEEKVRMAVRNCPEGAL
RIAKGTGV

>3Fe-4SST1 (rga:RGR602_PB00448) *Rhizobium gallicum*
MRVVIDQDLCGTTGQCVLTLPGTFRQREPDGVAEVCLATVPEALHAAVRLAASQCPVAAI
RVIESDAGYGEPAIVDPAPSPAIEVGRHAAKDHHNPGGHDGTV

>3Fe-4SST1 (mop:Mesop_6229) *Mesorhizobium opportunistum*
MRVVVDQDLCGTTGQCVLTLPGTFRQREPDGVAEVCAATVPQALLAAVRLAASQCPVAAI
RVISDAGDDERASADAAPSPAIEPERHAAKDQRNPEGHDGTV

>3Fe-4SST1 (mam:Mesau_05698) *Mesorhizobium australicum*
MRVVVDQDLCGTTGQCVLTLPGTFRQREPDGVAEVCAATVPQALLAAVRLAASQCPVAAI
RVISDAGDDERASADAAPSPAIEPERHAAKDQRNPEGHDGTV

>3Fe-4SST1 (mamo:A6B35_33020) *Mesorhizobium amorphae*
MRVVVDQDLCGTTGQCVLTLPGTFRQREPDGVAEVCVATVPQALHAAVRLAASQCPVAAI

RVIESNAGDDERASADPAPSPAERHAAKDQRNPGGHDGTV
>3Fe-4SST1 (rhi:NGR_a02720) *Sinorhizobium fredii* NGR234
MRVVIDQDLCGTTGQCVLTLPGTFRQREPDGVAEVCVATVPQALHAAVRLAASQCPVAAI
RVIESDAGDDERASADPARSPAERHAAKDQRIPGGHDGTV
>3Fe-4SST1 (rtr:RTCIAT899_PB00445) *Rhizobium tropici*
MRVVVDQDLCGTTGQCVLTLPGVFRQRELDGVAEVCVVTVPQALHAAVRLAASQCPVAAI
WVVEESAAGDGEPARADPTPSLAEERHATKDCNPGGHDGTV
>3Fe-4SST1 (bjp:RN69_37410) *Bradyrhizobium japonicum* E109
MRVMVDQDLCGTSGQCVLTLPGTFRQREPDGVAEVCVATVPHALHAAVRLAASQCPVAAI
RVIESDAGDGERASADPAPSPAERHAAKDQHNLG
>3Fe-4SST1 (bju:BJ6T_77040) *Bradyrhizobium japonicum* USDA 6
MRVMVDQDLCGTSGQCVLTLPGTFRQREPDGVAEVCVATVPHALHAAVRLAASQCPVAAI
RVIESDAGDGERASADPAPSPAERHAAKDQHNLG
>3Fe-4SST1 (bja:bsl2906) *Bradyrhizobium diazoefficiens* USDA 110
MAERLKVHVDPKCQGHARCKALAPELFELDEYGNAHEAGDGTVPVPGLEEKAWLAKSNCP
EIAIDVIEE

Subtype 2

>3Fe-4SST2 (sphr:BSY17_3857) *Sphingobium* sp. RAC03
MKIRIEKAGCVGNARCAAVSVTLYPLDDDGYYIQTEGFTVPEGMEKAAARNGARACPERIIV
VEEEDGRISWPPAAKA
>3Fe-4SST2 (rtr:RTCIAT899_PB00990) *Rhizobium tropici*
MHIIIVHTAKCQGHARCWFQAPEIFKLDEDEGYILPGNIDVAAGNEFRASRGARSCPERALE
ITRSFDTVGVTA
>3Fe-4SST2 (sch:Sphch_0987) *Sphingobium chlorophenolicum*
MKIIIVHNDKCQGHARCWAMAPHIFDLDEGYIKPGDIEVAEAEDEKLAWKGAKSCPERALE
IEK
>3Fe-4SST2 (syb:TZ53_19620) *Sphingobium* sp. YBL2
MKIIIVHNDKCQGHARCWAMAPNIFELDDEGYIKPGDIDVAEAEDEKLAWKGAKSCPERALE
IGK
>3Fe-4SST2 (sphb:EP837_00047) *Sphingobium* sp. EP60837

MKIIVHNDKCQGHARCWAMAPNIFQLDDEGYIKPGDIEVAETDEKLAWKGAKSCPERALE
IGK

>3Fe-4SST2 (same:SAMCFNEI73_pB0104) *Sinorhizobium americanum*
MRIIVHKNKCQGHARCWAQAPDIFNLDDEGYILPGDIEVAERDELLASRGARSCPERALE
IDATADALLTRLNLFNQACGGVK

>3Fe-4SST2 (ret:RHE_PD00214) *Rhizobium etli* CFN 42
MEYRMRVIVHTSKCQGHARCWAQAPEIFNLDDEGYILPGAIDVEERDELFASRGARSCPE
RALEIDCVSDALLDRLLFNQHCGG

>3Fe-4SST2 (rec:RHECIAT_PB0000258) *Rhizobium etli* CIAT 652
MEYRMRVIVHTSKCQGHARCWAQAPEIFNLDDEGYILPGAIDVEERDELFASRGARSCPE
RALEIDCVSDALLDRLLFNQHCGG

>3Fe-4SST2 (rel:REMIM1_PE00311) *Rhizobium etli* bv. *mimosae* Mim1
MRIIVHSAKCQGHARCWAQAPDIFKLNDEGYILPGEISVEERDELLASRGARSCPERALE
VDCPSDALLDRLLFNQHCRG

>3Fe-4SST2 (rei:IE4771_PB00207) *Rhizobium* sp. IE4771
MRITVHSAKCQGHARCWAQAPDIFNLDDEGYILPGAIDVEERDELLASRGARSCPERALE
IDCASDALLDRLLFNQYCGG

>3Fe-4SST2 (rga:RGR602_PB00272) *Rhizobium gallicum*
MRIIVHNAKCQGHARCWAQAPDIFDLNDEGYILPGDIDVEEKDELLASRGARSCPERALE
IDRTSDALLDRLLFNQHCGG

>3Fe-4SST2 (rh:AMJ98_PC00265) *Rhizobium* sp. N1341
MEYRMRVIVHTSKCQGHARCWAQAPEIFNLDDEGYILPGAIDVEERDELFASRGARSCPE
RALEIDCVSDALLDRLLFNQHCGG

>3Fe-4SST2 (sgi:SGRAN_1060) *Sphingopyxis granuli*
MKAIVDVGKCSGHARCVAVAPHVFLNSDGYNERAINPVPAGHEVEGRRGARACPERAIR
IVEDGEESEAGR

>3Fe-4SST2 (swi:Swit_1742) *Sphingomonas wittichii*
MKVIVDHARCQGHALCMLKAPQVYQLNDDGYNSMPPTTEVPPELEEQARLGAINCPEGAIR
LDKRAVD

>3Fe-4SST2 (rh:AMK02_PC00260) *Rhizobium* sp. N731
MEYRMRVIVHTSKCQGHARCWAQAPEIFNLDDEGYILPGAIDVEERDELFASRGARSCPE
RALEIDCVSDALLDRLLFNQHCGG

>3Fe-4SST2 (rpha:AMC79_PC00242) *Rhizobium phaseoli*
MEYRMRVIVHTSKCQGHARCWAQAPEIFNLDDEGYILPGAIDVEERDELFASRGARSCPE

RALEIDCVSDALLDRLLFNQHCGG

Subtype 3

>3Fe-4SST3 (mex:Mext_4002) *Methylobacterium extorquens* PA1
MKVVVDLNRCQAYAQCIIYAAPGHFALHGREALVYDPSPDETARGEIERAIHACPVRITA
YPDAADAAAGEAR

>3Fe-4SST3 (mea:Mex_1p4390) *Methylobacterium extorquens* AM1
MKVVVDLNRCQAYAQCIIYAAPGHFALHGREALVYDPSPDETARGEIERAIHACPVRITA
YPDAADAAAGEAR

>3Fe-4SST3 (mdi:METDI4996) *Methylobacterium extorquens* DM4
MKVVVDLNRCQAYAQCIIYAAPGHFALHGREALVYDPSPDETARGEIERAIHACPVRITA
YPDAADAAAGEAR

>3Fe-4SST3 (mch:Mchl_4371) *Methylobacterium extorquens* CM4
MKVVVDLNRCQAYAQCIIYAAPGHFALHGREALVYDPSPDETARGEIERAIHACPVRITA
YPDAADAAAGEAR

>3Fe-4SST3 (mpo:Mpop_4483) *Methylobacterium populi*
MKVVVDLNRCQAYAQCIIYAAPGHFVLHGKEALVYDPSPDEAARGEIERAVHACPVRITA
YSDDTTAGEAA

>3Fe-4SST3 (mrd:Mrad2831_3878) *Methylobacterium radiotolerans*
MKPASDTAALRVVVDLNRCQGYAQCCYAAPDAFALRGHEILFYDPAPPAERRGAIERALQ
ACPVRISLQAGPDDGGAP

>3Fe-4SST3 (mrd:Mrad2831_1825) *Methylobacterium radiotolerans*
MSAPADASSGHPGLRVSVDLNLCQAYAQCIIYAAPRHFRIEGHEALFYDPAPPAARDRDI
ERARVACPQAIRVEDPERGA

>3Fe-4SST3 (met:M446_4601) *Methylobacterium* sp. 4-46
MRVVVDLNRCQAYAQCIIYAAPESFALHGPEVLVYDAAPPPERRREIERAVQACPVRILL
EVEPEEAGSHG

>3Fe-4SST3 (mno:Mnod_0158) *Methylobacterium nodulans*

MRVVVDLNRQCQAYAQCCFAAPDSFALHGIEVLVYDPAPPPERRREIERAVQACPVRIML
EVEPEAERHD

>3Fe-4SST3 (mor:MOC_4428) *Methylobacterium oryzae*

MKPAAGAGALRVVVDLNRQGYAQCCYAAPEAFAIRGHEILFYDPAPPADRRGAVERAVE
ACPVR AISLQAGPDDGDAP

>3Fe-4SST3 (mor:MOC_2233) *Methylobacterium oryzae*

MSVDLNLQCQAYAQCCYAAPRHFRIEGHEALFYDPAPAAQDRDDIERARVACPVQAIRVED
PERGA

>3Fe-4SST3 (meta:Y590_19925) *Methylobacterium* sp. AMS5

MKVVDLNRQCQAYAQCIYAAPGHFALHGREALVYDPSPDETARGEIERAIHACPVRITA
YPDAADAAAGEAR

>3Fe-4SST3 (maqu:Maq22A_1p34665) *Methylobacterium aquaticum*

MKVVDLNRQCQAYAQCIYAAPDHFALHGAEALVYDTAPDEAARAEIERAVQACPVRITA
TSDVPAPMPHKVGER

>3Fe-4SST3 (maqu:Maq22A_c00725) *Methylobacterium aquaticum*

MRVVVDLNRQCQAYAQCCYAAPERFVLQGDEILAYDPAPPAAERAAIDRAVQACPVRIRV
EHDETAERAA

Subtype 4

>3Fe-4SST4 (sphm:G432_19810) *Sphingomonas* sp. MM-1

MMQVKTLPERCVSSGQCVMLAPGVFDQDDDGVVLLLRDTVDDGDEASVAAVRSSANVCPAAA
IRLSATPKA

>3Fe-4SST4 (sjp:SJA_C2-04950) *Sphingobium japonicum*

MMQVKTLPERCVSSGQCVMLAPGVFDQDDDGVVLLLRDTVDDGDEASVAAVRSSANVCPAAA
IRLSATPKA

>3Fe-4SST4 (sch:Sphch_3796) *Sphingobium chlorophenolicum*

MQVKTLPERCVSSGQCVMLAPGVFDQDDDGVVLLQDSVDDGDEASVAAVRSSANVCPAAAI
RLSANPKA

Subtype 5

>3Fe-4SST5 (cak:Caul_1918) *Caulobacter* sp. K31

MSSEATPHRATADRSACCGYGTCVAICPEIYQLEGGLVVLTTDIVPAELLERAIEGADSC
PQSAIVIEAVAG

4Fe-4S

Subtype 1

>4Fe-4SST1 (blas:BSY18_2505) *Blastomonas* sp. RAC04
MSGEVTLKVVINKPACCGYGVCADICPEVFKLDENGIVFVESDLVPPELEETAREAADAC
PQSALALVAA
>4Fe-4SST1 (syb:TZ53_18285) *Sphingobium* sp. YBL2
MSQKLKVVIDKAACCGYGVC AEICPQVYKLDANGIVYVDDEIVPEGLEEQAREGAEACPQ
SALAVGAA

7Fe-8S

Subtype 1

>7Fe-8SST1 (ngl:RG1141_CH23220) *Neorhizobium* *galegae* bv.
officinalis bv. *officinalis* HAMBI 1141
MAYIITEPCIDVKD GACTAACPVDCIYEGGRMFYIHPDECINCG LCLSICPVDAIAYDEE
ATEAQMAFIPVNRDYFGAEVTGLGSPGGWDKSRTRNIDHPVVTSTPAREVAH
>7Fe-8SST1 (rle:pRL110029) *Rhizobium* *leguminosarum* bv. *viciae*
3841
MAYVITDPCIDVKDGDCTVACPVDCIYEGGRMFYIHPGECINCG LCLSVCPVDAISWDEE
IPQSRVQFKAVNQDFFGPDVTNWGSPGGWDKNHTTNRDHPLVAAYERA
>7Fe-8SST1 (ngg:RG540_CH24080) *Neorhizobium* *galegae* bv.
orientalis HAMBI 540
MAYIITEPCIDVKD GACTAACPVDCIYEGGRMFYIHPDECINCG LCLSICPVDAIAYDEE
ANEAQMAFIPVNRDYFGADV TGLGSPGGWDKSRTRNIDHPVVT SAPVREAAH
>7Fe-8SST1 (eah:FA04_32640) *Ensifer adhaerens* *Casida* A
MAYVITEPCIDVKDGDCTAACPVDCIYEGGRTFYIHPDECINCG LCLSICPVDAIAWDQE
IPNNQRHFIAVNKEFFGSDVTGMGSPGGWSKECSTTQDHPFVAAFEKAAAIA
>7Fe-8SST1 (lagg:B0E33_29700) *Labrenzia aggregata*

MALIIKSECIDVKGICTTSCPVDICIYEGERMFYIHPEECIECGMCESICPVDAIRYYDE
VTGADRAFIEINKDVFQGPDGGLVSPGGWTRGDTPF RDHPAVRDFFKRDFEEQTT
>7Fe-8SST1 (jan:Jann_3749) *Jannaschia* sp. CCS1
MALVILSACVDVKGICTTSCPVDICIYEGERMFYIHPTIECGMCESICPVDAIRYDDE
VPAEEQPFADLNTSVFQSADGGVQEPGGWAKGMDPLRDPTVLADMAAKTELKREEN

Subtype 2

>7Fe-8SST2 (rhn:AMJ98_CH02815) *Rhizobium* sp. N1341
MEKQPNISRRAPDIVRPTVDPARCEGKAACVAVCPVDVFEIVRIPDETYRDLPLLAKFKI
WAHGMKTAATPNAAACEGCGLCVSACPEHAIRLQ RAG
>7Fe-8SST2 (rhx:AMK02_CH02746) *Rhizobium* sp. N731
MEKQPNISRRAPDIVRPMVDPARCEGKAACVAVCPVDVFEIVRIPDETYRDLPLLAKFKI
WAHGMKTAATPNAAACEGCGLCVSACPEHAIRLQ RAG
>7Fe-8SST2 (bbt:BBta_3785) *Bradyrhizobium* sp. BTAi1
MTDHTEPTPSKRTNAAKVRKAAQHPKRPGAGCKAEPGAFVPVVDHNRCEAKGDCVEVCPY
DVFDVAPIRDADFRTLSFLGRMRVRFHGMKTAYTPNSQLCLACGLCVVACPERAIDLVA A
AAREDHPLSR
>7Fe-8SST2 (aol:S58_42030) *Bradyrhizobium oligotrophicum*
MTDLTKPTLSKRTNPDKVRKAAQHPKRPGLGCKAEPGTFVPVVDNRKCEAKGDCVEVCPY
DVFDVAPISEPDFRAMSFLGRMRVRFHGMKTAYTPNSDRCLACGLCVVACPERAINLVEV
AAGSNMTTRR

Subtype 3

>7Fe-8SST3 (otm:OSB_13110) *Octadecabacter temperatus*
MSKKLPPKPDQTQKPAASVVNIDYDLCINCAICIRSCPVDVLRINRETRWLEATYWEDCML
CKLCELDCEPFGAITISADKPLGFAMSG

Subtype 4

>7Fe-8SST4 (bic:LMTR13_00130) *Bradyrhizobium icense*

MEPQGPSRRALFRGQLLSRPVALIGDACLAEGIVCRSCGDACPASAIRFRPRIGLPPQA
IVNEAVCTGCGECVDACPGATITLGAAHGGDAA

2[4Fe-4S]

Subtype 1

>2[4Fe-4S]ST1 (rhl:LPU83_4061) *Rhizobium favelukesii*
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLRINAEYASVWPNTITVKKDAMPEAKELDGESGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1 (mlo:mlr3855) *Mesorhizobium japonicum* MAFF 303099
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
PGLDKWLQINTEYAEKWPNITAKKEPPADAKTFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (mln:A9174_06575) *Mesorhizobium loti* NZP2037
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
PGLDKWLQINTEYAEKWPNITAKKEPPADAKTFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (mci:Mesci_1325) *Mesorhizobium ciceri* (biovar
Biserrulae)
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
PGLDKWLQVNTEYAEKWPNITAKKEPPADAKSFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (mop:Mesop_1348) *Mesorhizobium opportunistum*
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
SGLDKWLQINTEYAEKWPNITAKKEPPADAKTFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (mam:Mesau_01363) *Mesorhizobium australicum*
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
SGLDKWLQINTEYADKWPNITAKKEPPADAKSFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (mamo:A6B35_01755) *Mesorhizobium amorphae*
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
PGLDKWLQVNTEYAEKWPNITAKKEPPADAKTFDGEAGKFEKYFSAEPGEGD

>2[4Fe-4S]ST1 (meso:BSQ44_00295) *Mesorhizobium* sp. B7
MTYVVTDNCIKCKYMDCI EVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADA IKPDTE
PGLDKWLQVNTEYADKWPNITAKKEPPADAKEFDGVEGKFEKYFSAEAGEGD

>2[4Fe-4S]ST1 (mes:Meso_3378) *Chelativorans* sp. BNC1
MAHLAIALQRGYLTRRKMRPERREPVMTYVVTDNCIKCKYMDCIEVCPVDCFYEGENMLV
IHPDECIDCGVCEPECPAEAIKPDTEPGLEKWLQVNADYAEKWPNITAKKEPPADAKDWD
GIEEKFEKYFSPEPGTGD

>2[4Fe-4S]ST1 (hoe:IMCC20628_04489) *Hoeflea* sp. IMCC20628
MTYVVTDNCIRCKYMDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLEKWLEVNTEYADKWPNITIKREAPEDAKKFDGEAGKFEKYFSEAPGEGD

>2[4Fe-4S]ST1 (aak:AA2016_1364) *Aminobacter aminovorans*
MTYVVTDNCIKCKYMDCIEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAKPDTE
SGLDKWLQINTEYAEKWPNITAKKEPPADAKEFDGVEGKFEKFFSAEPGEGN

>2[4Fe-4S]ST1 (aak:AA2016_5900) *Aminobacter aminovorans*
MTYVVTDACVRCKFTDCVAVCPVDCFHEGENMLVIDPEVCIDCGVCEPECPADAILADTD
PLAAKWLA VNRQYSAHWPVISAQLPPPQDAHAFKGLDGKFEAHFSPAAAAR

>2[4Fe-4S]ST1 (pla:Plav_1695) *Parvibaculum lavamentivorans*
MTYIVTDACIRCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLEKWLELNTEYASKWPNITIKRDPPADADDWQGVSGKFEEHFSAPGEGD

>2[4Fe-4S]ST1 (sme:SMc03875) *Sinorhizobium meliloti* 1021
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smk:Sinme_3255) *Sinorhizobium meliloti* AK83
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smq:SinmeB_3030) *Sinorhizobium meliloti* BL225C
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smx:SM11_chr3386) *Sinorhizobium meliloti* SM11
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smi:BN406_03059) *Sinorhizobium meliloti* Rm41
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smeg:C770_GR4Chr3353) *Sinorhizobium meliloti* GR4
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smel:SM2011_c03875) *Sinorhizobium meliloti* 2011
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smer:DU99_17585) *Sinorhizobium meliloti* RMO17
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNAEFSTQWPNITVKRDPLPEAKEMDGVEEKYEKYFSSEPGQGD

>2[4Fe-4S]ST1 (smd:Smed_3113) *Sinorhizobium medicae*
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNADFSTQWPNITVKRDPLPEATEMDGLEGKYEKYFSPEPGQGD

>2[4Fe-4S]ST1 (rhi:NGR_c32680) *Sinorhizobium fredii* NGR234
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNADFATQWPNITVKRDPLPEAKEMDGVGKYEQYFSEKPGQGD

>2[4Fe-4S]ST1 (sfh:SFHH103_03286) *Sinorhizobium fredii* HH103
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNADFATQWPNITVKRDPLPEAKEMDGVGKYEQYFSEKPGQGD

>2[4Fe-4S]ST1 (sfd:USDA257_c57280) *Sinorhizobium fredii* USDA 257
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAGAIKPDTE
PGLDMWLKLNADFATQWPNITVKRDPLPEAKEMDGVGKYEQYFSEKPGQGD

>2[4Fe-4S]ST1 (six:BSY16_3356) *Sinorhizobium* sp. RAC02
MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKINTEFASIWPNTVTKRDAMPEAKEMDGVGKYEQFFSPNPGQGD

>2[4Fe-4S]ST1 (ead:OV14_0780) *Ensifer adhaerens* OV14
MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDMWLKVNADFATKWPNTIKRDAMPEAKEMDGVGKYEKYFSAEPGQGD

>2[4Fe-4S]ST1 (eah:FA04_17280) *Ensifer adhaerens* Casida A
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDMWLKLNADFASKWPNTVTKRDPMPPEAKEMDGVGKYEKFFSTEPGQGD

>2[4Fe-4S]ST1 (atu:Atu2751) *Agrobacterium fabrum*
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKINTEYAAIWPNTIKRDPMPPEAKEMDGVGKLELYFSAEPGKGD

>2[4Fe-4S]ST1 (atu:Atu4582) *Agrobacterium fabrum*
MPYVVTENCIACKYMDCVEVCPVECFYEGENMLVIHPDQCIDCGICERECPAAAIRPDTE
AGLHVWLDLNRHYSIGIWPRVHQKRTPPDNADTMNGAAAKFSILSKNPGAGG

>2[4Fe-4S]ST1 (ara:Arad_4672) *Agrobacterium radiobacter*

MECFMTYVVTDNVCVRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIK
PDTEPGLDKWLKINADYAAIWPNITVKRDALPEAKELDGEEGKFEKYFSANPGAGD
>2[4Fe-4S]ST1(atf:Ach5_26350)*Agrobacterium tumefaciens* Ach5
MTYVVTDNCCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKLNTEYAAIWPNITIKRDPLPEAKEMDGVGTGKLELYFSAEPGKGD
>2[4Fe-4S]ST1(atf:Ach5_42740)*Agrobacterium tumefaciens* Ach5
MPYVVTENCIACKYMDCVEVCPVECFYEGENMLVIHPDQCIDCGICERECPAAAIRPDTE
AGLHVWLDLNRHYSIGIWPVRVHQKRTPPEDADIMNGAAAKFSIFSKNPGAGG
>2[4Fe-4S]ST1(ata:AWN88_18615)*Agrobacterium tumefaciens* S33
MTYVVTDNCCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKLNAEYAAIWPNITIKRDPMPPEAKEMDGVGKLELYFSAEPGKGD
>2[4Fe-4S]ST1(ata:AWN88_02865)*Agrobacterium tumefaciens* S33
MPYVVTENCIACKYMDCVDVCPVECFYEGENMLVIHPDQCIDCGICESECPAAAIRPDTE
PGLHVWLDLNRHYSIGIWPVRVHQKRAPPDNADIMNGAAAKFSIFSKNPGAGG
>2[4Fe-4S]ST1(avi:Avi_4350)*Agrobacterium vitis*
MEYRMTYIVTDNCCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIK
PDTEPGLDKWLKINAEFAQVWPNITTKRDALPEAKEMDGVGKFEKYFSEKPGTGD
>2[4Fe-4S]ST1(agr:AGROH133_14003)*Agrobacterium* sp. H13-3
MSYVVTENCIACKYMDCVEVCPVECFYAGENMLVIHPDQCIDCGICERECPAAAIRPDTE
AGLHVWLDLNRHYSIGIWPVRVHQKRTPPDDADIMNGAAAKFSIFSKNPGAGD
>2[4Fe-4S]ST1(agr:AGROH133_09162)*Agrobacterium* sp. H13-3
MTYVVTDNCCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKLNTEYAAIWPNITIKRDPLPEAKEMDGVGTGKLELYFSAEPGKGD
>2[4Fe-4S]ST1(agc:BSY240_3071)*Agrobacterium* sp. RAC06
MTYIVTDNCCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKINAEYAKIWPNITVKKEPMPEAKEMDGVGKFEQFFSDKPGSGD
>2[4Fe-4S]ST1(aro:B0909_25795)*Agrobacterium rhizogenes*
MTYVVTDNCCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLKLNAEYAAIWPNITIKRDPMPPEAKEMDGVAGKLELYFSAEPGQGD
>2[4Fe-4S]ST1(aro:B0909_14630)*Agrobacterium rhizogenes*
MPYVVTENCIACKYMDCVEVCPVECFYEGENMLVIHPDQCIDCGICERECPAAAIRPDTE
AGLHVWLDLNRHYSIGIWPVRVHQKRTPPDNADIMNGAAAKFSIFSKNPGAGG
>2[4Fe-4S]ST1(ret:RHE_CH04024)*Rhizobium etli* CFN 42
MTYVVTDNCCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE

PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rec:RHECIAT_CH0004312)*Rhizobium etli* CIAT 652
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rel:REMIM1_CH04122)*Rhizobium etli* bv. *mimosae*
 Mim1
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rep:IE4803_CH04410)*Rhizobium etli* bv. *phaseoli*
 IE4803
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rei:IE4771_CH04360)*Rhizobium* sp. IE4771
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rle:RL4616)*Rhizobium leguminosarum* bv. *viciae*
 3841
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKMDGETGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rlt:Rleg2_3815)*Rhizobium leguminosarum* bv.
trifolii WSM2304
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKEMDGETGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rlg:Rleg_4144)*Rhizobium leguminosarum* bv.
trifolii WSM1325
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKMDGETGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rlb:RLEG3_31680)*Rhizobium leguminosarum* bv.
trifolii WSM1689
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYATIWPNITVKKDPLPEAKMDGETGKFEKYFSEKPGSGD
 >2[4Fe-4S]ST1(rlu:RLEG12_30675)*Rhizobium leguminosarum* bv.
trifolii CB782
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE

PGLDKWLKINTEYATIWPNITVKKDPLPEAKEMDGETGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1(rtr:RTCIAT899_CH17975) *Rhizobium tropici*
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKVNAEYAAIWPNITVKKRDPMPPEAKEMDGEQGKFEKYFSANPGTGD

>2[4Fe-4S]ST1(rir:BN877_I2835) *Rhizobium* sp. IRBG74
 MCSEAQRPGHLHILEFIMTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLAINPDECIDCG
 VCEPECPAEAIKPDTEPGLDKWLKLNAEYAAIWPNITIKRDPMPPEAKEMDGVGKLELYF
 SAEPGKGD

>2[4Fe-4S]ST1(rir:BN877_II1665) *Rhizobium* sp. IRBG74
 MPYVVTENCIACKYMDCVDVCPVECFYEGENMLVIHPDQCIDCGICERECPAAAIRPDTE
 PGLHVWLDLNRHYSIGIWPVRVHQKRAPPDNADIMNGAAAKFSIFSKNPGAGG

>2[4Fe-4S]ST1(rga:RGR602_CH03938) *Rhizobium gallicum*
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINAEYASSWPNITVKKPEMAEAKEMDGEAGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1(rhn:AMJ98_CH04252) *Rhizobium* sp. N1341
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1(rpha:AMC79_CH04245) *Rhizobium phaseoli*
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1(rht:NT26_3598) *Rhizobium* sp. NT-26
 MTYVVTDNCVRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKVNAEYAQIWPNITVKREPMPEAKEMDGVPGKFDQYFSPEPGKGD

>2[4Fe-4S]ST1(rhx:AMK02_CH04150) *Rhizobium* sp. N731
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEYASIWPNITVKKDPLPEAKEMDGQTGKFEKYFSEKPGSGD

>2[4Fe-4S]ST1(ngl:RG1141_CH37300) *Neorhizobium galegae* bv.
officinalis bv. *officinalis* HAMBI 1141
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEFAQMWPNITVKKRDALPEAKEMDGVANKYEQYFSAEPGKGD

>2[4Fe-4S]ST1(ngg:RG540_CH37920) *Neorhizobium galegae* bv.
orientalis HAMBI 540
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLDKWLKINTEFAQMWPNITVKKRDALPEAKEMDGVPNKYEQYFSAEPGKGD

>2[4Fe-4S]ST1(shz:shn_19290) *Shinella* sp. HZN7
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLQINTEFAAIWPNITVKRDAMPEAKEMDGVGKYEKYFSPNPGQGD

>2[4Fe-4S]ST1(bme:BMEI0278) *Brucella melitensis* bv. 1 16M
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmel:DK63_1155) *Brucella melitensis* bv. 1 16M
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmi:BMEA_A1819) *Brucella melitensis* ATCC 23457
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmz:BM28_A1763) *Brucella melitensis* M28
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmg:BM590_A1762) *Brucella melitensis* M5-90
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmw:BMNI_I1693) *Brucella melitensis* NI
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmee:DK62_1791) *Brucella melitensis* bv. 3 Ether
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmf:BAB1_1778) *Brucella abortus* 2308
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(bmc:BAbs19_I16610) *Brucella abortus* S19
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(baa:BAA13334_I01157) *Brucella abortus* A13334
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD

>2[4Fe-4S]ST1(babo:DK55_1723) *Brucella abortus* bv. 2 86/8/59

MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babr:DO74_165) *Brucella abortus* bv. 6 870
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babt:DK49_1480) *Brucella abortus* 63 75
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babb:DK48_396) *Brucella abortus* BDW
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babu:DK53_1706) *Brucella abortus* bv. 9 C68
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babs:DK51_1836) *Brucella abortus* BER
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (babc:DO78_1627) *Brucella abortus* NCTC 10505
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsui:BSSP1_II1207) *Brucella suis* bv. 2 Bs143CITA
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsup:BSPT1_II1200) *Brucella suis* bv. 2 PT09143
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsuv:BSPT2_II1202) *Brucella suis* bv. 2 PT09172
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsuc:BSSP2_II1211) *Brucella suis* bv. 2 Bs364CITA
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsz:DK67_575) *Brucella suis* bv. 3
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE

PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsw:IY71_08675) *Brucella suis* ZW043
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsg:IY72_14080) *Brucella suis* ZW046
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsg:IY72_08440) *Brucella suis* ZW046
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bcs:BCAN_A1805) *Brucella canis* ATCC 23365
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bsk:BCA52141_I2374) *Brucella canis* HSK A52141
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bcar:DK60_1764) *Brucella canis* RM6/66
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bcas:DA85_08480) *Brucella canis* SVA13
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bpv:DK65_1741) *Brucella pinnipedialis* 6/566
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALPEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (bcet:V910_100266) *Brucella ceti* TE10759-12
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNAEYAAKWPINITAKKDALLEAKEMDGVAGKLEQYFSPEAGSGD
 >2[4Fe-4S]ST1 (oan:Oant_1133) *Ochrobactrum anthropi* ATCC 49188
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNTHEYAAKWPINITAKKDALPEAKEMDGVAGKLEKYFSAEPGSGD
 >2[4Fe-4S]ST1 (oah:DR92_684) *Ochrobactrum anthropi* OAB
 MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAISPDTE
 PGLDKWLELNTHEYAAKWPINITAKKDALPEAKEMDGVAGKLEKYFSAEPGSGD

>2[4Fe-4S]ST1(ops:A8A54_09000) *Ochrobactrum pseudogrignonense*
MTYVVTDNCIRCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAIKPDTE
PGLDKWLELNAEYAAKWPNLTAKKDELPEAKEMDGVTGKLEQFFSAEPGSGD

>2[4Fe-4S]ST1(bja:bl10157) *Bradyrhizobium diazoefficiens* USDA
110
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWL SVNADYAKSWPNITQKKESPADAKEFDGMEGKFEKYFSPNPGSGD

>2[4Fe-4S]ST1(bju:BJ6T_01730) *Bradyrhizobium japonicum* USDA 6
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLQVNADYAKSWPNITQKKESPPDAKEFDGQEGKFEKYFSPNPGSGD

>2[4Fe-4S]ST1(bjp:RN69_00815) *Bradyrhizobium japonicum* E109
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLQVNADYAKSWPNITQKKESPPDAKEFDGQEGKFEKYFSPNPGSGD

>2[4Fe-4S]ST1(bbt:BBta_7544 K05524 *Bradyrhizobium* sp. BTAi1
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLGVNAEYAKAWPNITQKKDPPGDAKEHDGEAGKFEKYFSPKPGAGD

>2[4Fe-4S]ST1(aol:S58_70010) *Bradyrhizobium oligotrophicum*
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLGVNAEYAKSWPNITQKKDSPADAKEHDGEDGKFEKYFSSKPGAGD

>2[4Fe-4S]ST1(brc:BCCGELA001_03065) *Bradyrhizobium* sp. CCGE-
LA001
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLGVNADYAKSWPNITQKKESPADAKEFDGMEGKFEKYFSPNPGSGD

>2[4Fe-4S]ST1(brad:BF49_0621) *Bradyrhizobium* sp. BF49
MTYVVTEACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLTVNADYAKSWPNITQKKESPADAKDFDGMGKFDKYFSSNPGSGD

>2[4Fe-4S]ST1(bic:LMTR13_01825) *Bradyrhizobium icense*
MTYVVTEACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWL EVNTEYAKSWPNITQKKDAPPDAKEFEGVEGKFEKYFSKEPGAGD

>2[4Fe-4S]ST1(bic:LMTR13_09220) *Bradyrhizobium icense*
MTYVVTEACIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIAIKPDTE
PGLKWLALNARFAAVPNISDKKAPPADAEFFQGAEEKFDKFFSEAPGLGS

>2[4Fe-4S]ST1(rpa:RPA0489) *Rhodopseudomonas palustris* CGA009
MTYVVTENCIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPAEAIKPDTE

PGLEKWLELNSEYAKTWPNLTQKKDAPADAKEFDGQAGKFEKYFSSEPGSGD

>2[4Fe-4S]ST1(rpc:RPC_0547)*Rhodopseudomonas palustris* BisB18
 MTYVVTEACIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIKPDTE
 PGLEKWLEVNAEYSKTWPNLITQKKDAPADAKEFESVEGKFDKYFSAEPTGD

>2[4Fe-4S]ST1(rpd:RPD_0279)*Rhodopseudomonas palustris* BisB5
 MTYVVTEACIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPADAIKPDTE
 PGLEKWLELNTEYAKSWPNLTQKKEAPGDAKQYEGMEGKFEKFFSPEPTGD

>2[4Fe-4S]ST1(rpe:RPE_0125)*Rhodopseudomonas palustris* BisA53
 MTYVVTEACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKPDTE
 PGLEQWLSLNAEHAWSWPNLITQKKDAPADAKSFDGAEGKFDKYFSAEPTGD

>2[4Fe-4S]ST1(rpt:Rpal_0490)*Rhodopseudomonas palustris* TIE-1
 MTYVVTEACIKCKYTDCVEVCPVDCFYEGDNMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLEKWLELNSEYAKTWPNLTQKKDAPADAKEFDGQAGKFEKYFSSEPGSGD

>2[4Fe-4S]ST1(rpx:Rpx1_0135)*Rhodopseudomonas palustris* DX-1
 MTYVVTEACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLEKWLELNAEHAKTWPNLITQKKDAPADAKEFDGQAGKFDKYFSSEPGSGD

>2[4Fe-4S]ST1(nwi:Nwi_2810)*Nitrobacter winogradskyi*
 MTFVVTENCIKCKYMDCVEVCPVDCFYEGDNMLVINPDECIDCGVCEPECPAEAIKPDSE
 PDLENWLKLNAEYSAVWPNLITIKRDAPADAKTFDGVAGKLEQYFSANPGQGD

>2[4Fe-4S]ST1(nwi:Nwi_0411)*Nitrobacter winogradskyi*
 MTYVVNDACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDSE
 PGVEKWLEVNAEYAGRWPNLITQKKETPPDAKDFEGQEGKFEKYFSPDPTGD

>2[4Fe-4S]ST1(nha:Nham_3630)*Nitrobacter hamburgensis*
 MRLRQGSRRSSSCSPRGVFEMTFVVTENCIKCKYMDCVEVCPVDCFYEGDNMLVINPDE
 CIDCGVCEPECPAEAI FADSEPGLENWLKLNAEYAAVWPNLITIKRDAPADAKAFDGVADK
 LEQYFSANPGTGD

>2[4Fe-4S]ST1(nha:Nham_0506)*Nitrobacter hamburgensis*
 MTYVVNDACIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDSE
 PGLEKWLELNADYAKSWPNLTQKKDAPPDAKEFEGQEGKFEKYFSPNPTGD

>2[4Fe-4S]ST1(bos:BSY19_153)*Bosea* sp. RAC05
 MTYVVTEACIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLESWLQLNSKYASSWPNLITQKKDAPADAKAFDGVAGKLEAHFSANPGECD

>2[4Fe-4S]ST1(bvv:BHK69_02370)*Bosea vaviloviae*
 MTYVVTEACIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE

PGLESWLQLNSKYASSWPNITQKKDAPDAKAFDGVAGKLDEHFSPEPGEGD
 >2[4Fe-4S]ST1(xau:Xaut_4208)*Xanthobacter autotrophicus*
 MAYVVTENCIRCTYMDCVSVCPVDCFYAGENMLVIHPDECIDCGVCEPECPAAAIFPDSD
 PRAGDWAALNAQYAAQWPNITEKGAPPDDADAWKDAADKRALLSAAPAAI
 >2[4Fe-4S]ST1(xau:Xaut_2641)*Xanthobacter autotrophicus*
 MTYVVTENCIRCKYMDCVSVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPD AE
 LGLEKWLALNAEYAKAWPNITLKRDPADAKEWDGKPGKEELFSPEPGQGD
 >2[4Fe-4S]ST1(xau:Xaut_2087)*Xanthobacter autotrophicus*
 MAYVVTDN CIRCKFMDCVAVCPVDCFYEGENMLVINPDECIDCGVCEPECPAAAIAADTA
 PEAGPWIALNAQY AALWPNI AEKKEPPADAAQWMDVADKFESAFSPAPGQADGSSASGAA
 >2[4Fe-4S]ST1(azc:AZC_0232)*Azorhizobium caulinodans*
 MAYVVTENCILCKYTDCVAVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLEKWL SLNAEYAKTWP NITLKR DALPDAKEWDGKPGKEDKFS AEPTGD
 >2[4Fe-4S]ST1(azc:AZC_2802)*Azorhizobium caulinodans*
 MAYVVT DGCIRCKYMDCVSVCPVDCFYAGENMLVIHPDECIDCGVCEPECPAEAIVPD TD
 PRAGEWLALNAEYAATWP NITEKGEPPADADDWKGKAGKLALLDPAPAA
 >2[4Fe-4S]ST1(mex:Mext_3879)*Methylobacterium extorquens* PA1
 MTYVVTDN CIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GDLESWLKL NADYAKTWP NITQKKDAPSDAKQWDGVSGKLEAHFSPNPGSGD
 >2[4Fe-4S]ST1(mea:Mex_1p4253)*Methylobacterium extorquens* AM1
 MTYVVTDN CIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GDLESWLKL NADYAKTWP NITQKKDAPSDAKQWDGVSGKLEAHFSPNPGSGD
 >2[4Fe-4S]ST1(mdi:METDI4865)*Methylobacterium extorquens* DM4
 MTYVVTDN CIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GDLESWLKL NADYAKTWP NITQKKDAPSDAKQWDGVSGKLEAHFSPNPGSGD
 >2[4Fe-4S]ST1(mch:Mchl_4189)*Methylobacterium extorquens* CM4
 MTYVVTDN CIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GDLESWLKL NADYAKTWP NITQKKDAPSDAKQWDGVSGKLEAHFSPNPGSGD
 >2[4Fe-4S]ST1(mpo:Mpop_4336)*Methylobacterium populi*
 MTYVVTDN CIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GNLESWLKL NADYAKTWP NITQKKDAP TDAKQWDGVGGKLEAHFSPNPGSGD
 >2[4Fe-4S]ST1(mrd:Mrad2831_3707)*Methylobacterium radiotolerans*
 MTYVVTDN CIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 SNLDTWLKL NADYAKSWPNITQKKEAPADAKEWDGKTGKLEAHFSPNPGSGD

>2[4Fe-4S]ST1 (met:M446_4804) *Methylobacterium* sp. 4-46
 MTYVVVTENCIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLERWLKLNADFAKNWPNITQKKTAPSDAKEWDGVAGKFDAHFSSNPGTGD

>2[4Fe-4S]ST1 (mno:Mnod_1719) *Methylobacterium nodulans*
 MTYVVVTENCIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLEKWLKLNADLAKSWPNITQKKPAPADAKEWDGVAGKYEAHFSPNPGSGD

>2[4Fe-4S]ST1 (mor:MOC_4232) *Methylobacterium oryzae*
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 SNLDTWLKLNADYAKTWPNTQKKEAPADAKEWDGKAGKLEAHFSPNPGSGD

>2[4Fe-4S]ST1 (meta:Y590_19115) *Methylobacterium* sp. AMS5
 MTYVVTDNCIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 GDLESWLKLNADYAKTWPNTQKKDAPSDAKQWDGVSGKLEAHFSPNPGSGD

>2[4Fe-4S]ST1 (maqu:Maq22A_c25615) *Methylobacterium aquaticum*
 MTYVVTDNCIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGLESWLKLNADMAKGWPNITQKKPAPADAKEWDGKTGKFEAHFSTNPGSGD

>2[4Fe-4S]ST1 (msl:Msil_1370) *Methylocella silvestris*
 MTYVVLENCIKCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 PGIEQWITLNADMAQSWPNITMKREAAPDAKQFDGRPGKFKEFFSPEPGKGD

>2[4Fe-4S]ST1 (hdn:Hden_3159) *Hyphomicrobium denitrificans* ATCC 51888
 MTYVVNEKCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKPDTE
 PGMERWLELNQRQYADNWPNTAKKAALPDADDIKDEPGKFKEYFSPNAGSGD

>2[4Fe-4S]ST1 (hdt:HYPDE_38973) *Hyphomicrobium denitrificans* 1NES1
 MTYVVNDKCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKPDTE
 PGMERWLELNQRQYSESWPNTSKKPALPGADDVKDEPGKFKEYFSANSGSGD

>2[4Fe-4S]ST1 (hdt:HYPDE_41033) *Hyphomicrobium denitrificans* 1NES1
 MTYVVDERCIKCKTTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCRPECVPDAIKPDSE
 PGMEKWLKLNSEYALKWPNITIKKDMPKDARDHWDETGKFKEYFSPNPGAGD

>2[4Fe-4S]ST1 (hmc:HYPMC_0243) *Hyphomicrobium* sp. MC1
 MTFVVTESCIRCKFQDCLQSCPATCFYEGKNMLVINPAECIDCGACEPECPAEAIVRDTA
 PGAEKWVEFNRYAALWPNTIRKPTVVPDDAEDWIEVENKLETEFDPDPAAP

>2[4Fe-4S]ST1 (hmc:HYPMC_4406) *Hyphomicrobium* sp. MC1

MTYVVNEKCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAKPDTE
 PDMEKWMELNRQYADAWPNITAKKAALPDADAVKDEPNKFKEYFSPNPGSGD
 >2[4Fe-4S]ST1 (hni:W911_01685) *Hyphomicrobium nitrativorans*
 MTYVVNEKCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAKPDTE
 PGIERWLEVNREFADKWPNLTAKKAAYADADKYRDEEDKFDKYFSSEPFGSGD
 >2[4Fe-4S]ST1 (phl:KKY_2936A) *Pelagibacterium halotolerans*
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIAKPDTE
 PGLEKWLEVNNTKYASIWPNLTEKRDELPEAKEMDGVGKFEKFFSEEPGEGD
 >2[4Fe-4S]ST1 (fil:BN1229_v1_0756) *Candidatus Filomicrobium*
marinum W
 MTYVVNESCIKCKFTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPVDAIAKPDTE
 PHLEKWLEVNREYADKWPNITSKKDALPEAEHRDEDGKFEKYFSSEPFGDGD
 >2[4Fe-4S]ST1 (fiy:BN1229_v1_0761) *Candidatus Filomicrobium*
marinum Y
 MTYVVNESCIKCKFTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPVDAIAKPDTE
 PHLEKWLEVNREYADKWPNITSKKDALPEAEHRDEDGKFEKYFSSEPFGDGD
 >2[4Fe-4S]ST1 (deq:XM25_15710) *Devosia* sp. H5989
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEIAKPDTE
 SGLDKWLEINTKYANVWPNI TEKREAPADAKEMDGVADKFEKYFSEAPGEGD
 >2[4Fe-4S]ST1 (rhz:RHPLAN_40190) *Rhodoplanes* sp. Z2-YC6860
 MIHVVNESCIKCKYTDCVQVCPVDCFHGENMLVINPDDCIGCGVCVPECPLDAIKTELD
 PGMERWLAVNALYAKQWPNIAMKREAPPDAKAWEDTPDKFEKYFSPNPGTGG
 >2[4Fe-4S]ST1 (rhz:RHPLAN_07640) *Rhodoplanes* sp. Z2-YC6860
 MTYVVNDNCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEIAKPDTE
 PGLEKWLGLNAEYAKTWPNITVKKEAPADAKDWEVAGKFEKFFSAEPGQGD
 >2[4Fe-4S]ST1 (mbry:B1812_01945) *Methylocystis bryophila*
 MTYVVTENCIKCKYMDCVEVCPVDCFYEGANMLVIHPDECIDCGVCEPECPALAIKPDTE
 PELEAWLTLNLEYAQVWPNVITIKREAPADAKEWDGKPGKLEAHFSPEPGQGD
 >2[4Fe-4S]ST1 (mey:TM49_01980) *Martelella endophytica*
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIRPDTE
 PGLDKWLKLNADYADVWPNITIKKEPLEGAEEMDGVGKFEKFFSEKPGAGD
 >2[4Fe-4S]ST1 (psin:CAK95_03725) *Pseudorhodoplanes sinuspersici*
 MTFAVTEACIRCKYTDCVAVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIADTA
 EGAVRWVELNAKYAALWPNISDAKDPDPDAEDFNGKPKDFENHFSPPQPAIEPAN

>2[4Fe-4S]ST1 (psin:CAK95_10545) *Pseudorhodoplanes sinuspersici*
MTYVVNDSCIRCKFMDCEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPVEAIKPD
PGLEKWLSLNAEYAKVWPNI TAKKEPPADHKEWEGVEGKEQYFSPEPGTGN

>2[4Fe-4S]ST1 (oar:OA238_160p0450) *Octadecabacter arcticus*
MTYVVTESCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAILADTD
QGAETWLELNSKFAAKWPNI IQQSEALANAEEYDGMENKFDKYFSSKPR

>2[4Fe-4S]ST1 (otm:OSB_05850) *Octadecabacter temperatus*
MTYVVTDACINCKYQDCIEVCPVDCFYEGENTIVINTEECIDCGVCEPECPVDAIKPDTI
PNSAFWVELNQKHAESWPNI SEKGTTPADADDWANKPDKLSLMSEKPAA

>2[4Fe-4S]ST1 (pphr:APZ00_08695) *Pannonibacter phragmitetus*
MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAILPDTE
PGLEKWIELNAEYAAKWPNI TEKKDALPEAPEFDGIKNKLETHFSPNGPDGA

>2[4Fe-4S]ST1 (lap:ACP90_01635) *Labrenzia* sp. CP4
MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVINPDECIDCGVCEPECPAEAILPDTE
PGLEKWIEVNAEYSEKWPNI TEKKEPLPDAEEFDGKENKFEKYFSPNPAS

>2[4Fe-4S]ST1 (lagg:B0E33_13150) *Labrenzia aggregata*
MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENFLVINPDECIDCGVCEPECPAEAILPDTE
PGLEKWIEVNAEYSEKWPNI TEKKEPLPDAEEFDGKENKFEKYFSPNPAS

>2[4Fe-4S]ST1 (nar:Saro_0123) *Novosphingobium aromaticivorans*
MTYVVTDACIRCKFMDCEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
SGLEQWLELNAKYSAEWPNI TAKKDAPADADEHKGEEGKFDKYFSAEPGEGD

>2[4Fe-4S]ST1 (npp:PP1Y_AT208) *Novosphingobium* sp. PP1Y
MTYVVTDACIKCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
SGLEQWMELNTKYSAEWPNLTSKKDSPEDADEYKGVEGKFEKFFSPEPGEGD

>2[4Fe-4S]ST1 (nnp:JI59_11515) *Novosphingobium pentaromativorans*
MTYVVTDACIKCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
SGLEQWMELNTKYSAEWPNLTSKKDSPEDADEYKGVEGKFEKFFSPEPGEGD

>2[4Fe-4S]ST1 (sal:Sala_2741) *Sphingopyxis alaskensis*
MTYVVTDACVRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
SGLEKWLEVNSKFSAEWPNI TVKKETPADADEYKGVEGKFEKFFSPEPGEGD

>2[4Fe-4S]ST1 (sphk:SKP52_18275) *Sphingopyxis fribergensis*
MTYVVTDACVRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
SGLEKWLEVNSKFSAEWPNI TVKKETPADADEYKGVENKFETLFSPEPGAGD

>2[4Fe-4S]ST1 (sphp:LH20_16645) *Sphingopyxis* sp. 113P3

MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 SGLEKWLEVNSKFSAEWPNITTKKDSPADADEYKGVGDKFEKFFSPEPGEGD
 >2[4Fe-4S]ST1 (smaz:LH19_18985) *Sphingopyxis macrogoltabida* 203
 MTYVVTDACVRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 SGLEKWLEVNTKFSAEWPNITVKKDSPADADEFKGVDDKFDKYFSPEPGEGD
 >2[4Fe-4S]ST1 (ster:AOA14_05595) *Sphingopyxis terrae*
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 SGLEKWLEVNSKFSAEWPNITTKKDSPADADEYKGVDDKYEKFFSPEPGEGD
 >2[4Fe-4S]ST1 (sgi:SGRAN_3575) *Sphingopyxis granuli*
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEQWLELNAKFSADWPNITTKKESPADADEWKGVGDKFDKFFSPEPGEGD
 >2[4Fe-4S]ST1 (sph1:LPB140_05885) *Sphingopyxis* sp. LPB0140
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTVYSAEWPNIITTSKEPPADADEFKNVEDKFDKYFSSEPGECD
 >2[4Fe-4S]ST1 (swi:Swit_3538) *Sphingomonas wittichii*
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGDNMLVINPSECIDCGVCEPECPAEAILPDTE
 SGLEQWLELNNTFAAQWPNITRKREAPADADEWKNVEGKYEKHFSPEPGQGD
 >2[4Fe-4S]ST1 (sphm:G432_14530) *Sphingomonas* sp. MM-1
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 SGLEKWLEVNATFSAQWPNLTRKGEPADADEHKGEEGKYEKYFSPEPGQGD
 >2[4Fe-4S]ST1 (sphi:TS85_18695) *Sphingomonas* sp. WHSC-8
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAIIFPDTE
 NGLEKWLELNRITYSEQWPNITQKGDVPDDADSFKGVEGKEAEFSPEPGTGS
 >2[4Fe-4S]ST1 (sjp:SJA_C1-27340) *Sphingobium japonicum*
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGEAPADADDMKGIENKFEQFFSPEPGAGS
 >2[4Fe-4S]ST1 (sch:Sphch_1458) *Sphingobium chlorophenolicum*
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGDAPADADDMKGVENKFEQFFSPEPGAGS
 >2[4Fe-4S]ST1 (ssy:SLG_34020) *Sphingobium* sp. SYK-6
 MTYVVTDACIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 SGLEQWLELNTRYSAEWPNITAKGEPPADADAMKGETGKFEKYFSPEPGEGS
 >2[4Fe-4S]ST1 (syb:TZ53_13880) *Sphingobium* sp. YBL2
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE

NGLEKWLELNTKFSAEWPNITVKGEAPADADEMKGIENKLEKFFSPEPGAGS
 >2[4Fe-4S]ST1(sbd:ATN00_19100)*Sphingobium baderi*
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGEAPADADDMRGVENKLEQFFSPEPGSGD
 >2[4Fe-4S]ST1(spmi:K663_05250)*Sphingobium* sp. MI1205
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGDAPADADEMKGIENKLEKFFSPEPGSGS
 >2[4Fe-4S]ST1(sphb:EP837_00701)*Sphingobium* sp. EP60837
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGEAPADADDMKGVENKLEKFFSPEPGSGS
 >2[4Fe-4S]ST1(sphr:BSY17_2248)*Sphingobium* sp. RAC03
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKYSAEWPNITVKGDAPADADAMKGVENKLEQYFSPEPGTGS
 >2[4Fe-4S]ST1(sinb:SIDU_01160)*Sphingobium indicum*
 MTYVVTDNCIRCKYMDCVEVCPVDCFYEGENMLVINPNECIDCGVCEPECPAEAILPDTE
 NGLEKWLELNTKFSAEWPNITVKGDAPADADDMKGVENKFEQFFSPEPGAGS
 >2[4Fe-4S]ST1(cij:WG74_02790)*Citromicrobium* sp. JL477
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DNLEKWLELNTKFSNEWPNITQKKDPEDADEHKGEEGKFEEKFFNPEPGEGD
 >2[4Fe-4S]ST1(sphg:AZE99_01690)*Sphingorhabdus* sp. M41
 MTYVVTDACIKCKYMDCVEVCPVDCFYEGDNMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLEINTKYSEEWPNITVSRDPPADAEFEKGMGKFEAFFSPKPGAGD
 >2[4Fe-4S]ST1(blas:BSY18_2670)*Blastomonas* sp. RAC04
 MTYVVTDACIKCKYMDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTKFSAEWPNITVKRESPADADEYKGKDGYEAFFSPEPGEGD
 >2[4Fe-4S]ST1(eli:ELI_13125)*Erythrobacter litoralis* HTCC2594
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGDNMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLEINTKFSADWPNTQKKEPPADADEHKGEEDKYEKYFSAEPGEGD
 >2[4Fe-4S]ST1(elq:Ga0102493_11964)*Erythrobacter litoralis* DSM
 8509
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTKYSAEWPNITSQKEPPEDADDHKGETGKFEKYFSADPGEGD
 >2[4Fe-4S]ST1(aay:WYH_02318)*Altererythrobacter atlanticus*
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE

GGLEKWLELNTKFSAEWPNITEKKDPPADADDDHKGEDGKFDKYFSEEPGEGD

>2[4Fe-4S]ST1 (amx:AM2010_2224) *Altererythrobacter marensis*
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTKYSAEWPNITTQKEPPADADDDHKGEDGKFDKFFSPEPGEGD

>2[4Fe-4S]ST1 (aep:AMC99_02566) *Altererythrobacter epoxidivorans*
 MTYVVTDACIRCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTKFSAEWPNITSQKEPPADADEHKGEEGKFEKYFTPEPGEGD

>2[4Fe-4S]ST1 (ado:A6F68_00457) *Altererythrobacter dongtanensis*
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGETMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTKFSAEWPNITQKKDPPEDADEHKGEEGKFEKFFTPEPGEGD

>2[4Fe-4S]ST1 (pns:A9D12_04415) *Porphyrobacter neustonensis*
 MTYVVTTEDCIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTQYSAIWPNITSQKAPPEDADAHKGEGKGFELYFSAEPGEGD

>2[4Fe-4S]ST1 (gdi:GDI2031) *Gluconacetobacter diazotrophicus* PA1
 5 (Brazil)
 MTYVVVTENCIRCKFMDCVEVCPVDCFYAGENFLVINPDECIDCGVCEPECPAEAIVPDSD
 DRAAAWAEINASYSAKWPNITRKGTPADAEWWDKPGKKDLLSPEPHKD

>2[4Fe-4S]ST1 (gdj:Gdia_0255) *Gluconacetobacter diazotrophicus*
 PA1 5 (JGI)
 MTYVVVTENCIRCKFMDCVEVCPVDCFYAGENFLVINPDECIDCGVCEPECPAEAIVPDSD
 DRAAAWAEINASYSAKWPNITRKGTPADAEWWDKPGKKDLLSPEPHKD

>2[4Fe-4S]ST1 (aace:A0U92_12060) *Acetobacter aceti*
 MTYVVVTENCIRCKFMDCVEVCPVDCFYAGENFLVINPDECIDCGVCEPECPAEAIVPDSD
 DRATAWAEINTKYSALWPNITRKGTPADAEWWDKPNKAELLSPEPHKD

>2[4Fe-4S]ST1 (mgy:MGMSRv2__3124) *Magnetospirillum*
gryphiswaldense MSR-1 v2
 MAYVVVTENCIKCKYQDCVEVCPVDCFYEGENFLVINPDECIDCGVCEPECPAEAIVPDSD
 DKAAAWAQLNRDYSQWPNITRKGDPADADAWKNKPKADLLSPNPGKGT

>2[4Fe-4S]ST1 (azl:AZL_002430) *Azospirillum* sp. B510
 MPYVVTDGCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIVPDTE
 DRATKWLELNRDYSQWPNITRKKDAPADADTFKGVDGKFEKFFSPKAGG

>2[4Fe-4S]ST1 (abs:AZOBR_10204) *Azospirillum brasilense* Sp245
 MPYVVTTEDCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIVPDTE
 GRAEKWMELNRDYAAQWPNLTRKKDALPDADAMKGVDGKFDKFFSPKAGG

>2[4Fe-4S]ST1(abq:ABAZ39_00315) *Azospirillum brasilense* Az39
 MPYVVTEDCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIVPDTE
 GRAEKWMELNRDYAAQWPNLTRKKDALPDADAMKGVGDKFDKFFSPKAGG

>2[4Fe-4S]ST1(magq:MGMAQ_3732) *Magnetospira* sp. QH-2
 MTYIVIENCIKCKYQDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPAEAIVPDTE
 DGVEEWLEINTKYAEIWPNITRKGDAADAADWDGKPKDKALLSTKPGAGTGEG

>2[4Fe-4S]ST1(pgv:SL003B_0397) *Polymorphum gilvum*
 MTYVVTDNCIKCKYTDCVEVCPVDCFYEGENMLVINPDECIDCGVCEPECPAEAILPDTE
 PGLEKWIEINAEYAAKWPNITVKKDPLPEAAEFDGKAGKFEQYFSPNGPDGK

>2[4Fe-4S]ST1(rcp:RCAP_rcc02791) *Rhodobacter capsulatus*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKRPDTE
 PGMEDWVEFNRTYASQWPVITIKKDPMPDHKKYDGETGKREKYFSPNPGTGD

>2[4Fe-4S]ST1(kvu:EIO_0821) *Ketogulonicigenium vulgare* Y25
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKRPDTE
 PDMEKWVEFNRYSEMWPVITSRRDPLPGYEEMDGKPGKLALLSENPGLG

>2[4Fe-4S]ST1(kvl:KVU_0354) *Ketogulonicigenium vulgare* WSH-001
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKRPDTE
 PDMEKWVEFNRYSEMWPVITSRRDPLPGYEEMDGKPGKLALLSENPGLG

>2[4Fe-4S]ST1(kro:BVG79_00609) *Ketogulonicigenium robustum*
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKRPDTE
 PGMEKWVEFNRYAEMWPVITSRRDPLPGYQEMDGKPGKLDLLSENPGEG

>2[4Fe-4S]ST1(otm:OSB_13120) *Octadecabacter temperatus*
 MTYVVTDACIQCKFTDCVEVCPVDCFYEGENTLVIAPDECIDCGVCEPECPADAIIPDTE
 SAAEKWIAFNKGKYAALWPVIIIEKKEPLENADDFVGVEGKLEKYFSEAPAE

>2[4Fe-4S]ST1(red:roselon_02010) *Roseibacterium elongatum*
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENCLVIHPDECIDCGVCEPECPADAIKRPDTE
 PEMEKWVEINRKYAEMWPVIIITRKDPLPTAEEMDGKPGKMELLSENPGEG

>2[4Fe-4S]ST1(cid:P73_4318) *Celeribacter indicus*
 MTYVVTENCIACKFMDCEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKRPDTE
 PDMDKWVAFNRRYAENVWPVILERGEPPANADEMDGVNPKLETLFSPKPGNS

>2[4Fe-4S]ST1(con:TQ29_14735) *Confluentimicrobium* sp. EMB200-NS6
 MTYAVTDNCIGCKYTDCVSVCPVDCFYEGVNMLVINPEECIDCGVCEPECPADAIKADTD
 EEGAKWVAFNARYASLWPVIAAAKEPLPGAEANDGLPGKRDTIFSPDPDPQTA

>2[4Fe-4S]ST1(paby:Ga0080574_TMP5033) *Pelagibaca abyssi*

MTYVVTENCIACKYMDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPAEAISPDTE
 PDMDRWVEFNRYSEIWPVILERGEPPENADAMDGVPDKLKTMFSPNPGNGS
 >2[4Fe-4S]ST1 (apb:SAR116_1071) *Candidatus Puniceispirillum*
marinum
 MTYIVNENCINCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPPEAILPDSE
 PEATKWLDLNRDMSEIWPNIQKIDEMPNAKAAESETGKFDKYFTKAPGKGN
 >2[4Fe-4S]ST1 (rsp:RSP_2424) *Rhodobacter sphaeroides* 2.4.1
 MTYVVTDNCCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMESWVELNRKYAEVWPVIVTKKDPLPEATDLGQPGKLATHFSEKPGEGG
 >2[4Fe-4S]ST1 (rsh:Rsph17029_1088) *Rhodobacter sphaeroides* ATCC
 17029
 MTYVVTDNCCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMESWVELNRKYAEVWPVIVTKKDPLPEATDLGQPGKLATHFSEKPGEGG
 >2[4Fe-4S]ST1 (rsq:Rsph17025_1558) *Rhodobacter sphaeroides* ATCC
 17025
 MAYVVTDNCCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMESWLELNRKYAEIWPVIVTKKDPLPEAADLDGQTGKLATHFSEKPGEGG
 >2[4Fe-4S]ST1 (rsk:RSKD131_0739) *Rhodobacter sphaeroides* KD131
 MTYVVTDNCCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMESWVELNRKYAEVWPVIVTKKDPLPEATDLGQPGKLATHFSEKPGEGG
 >2[4Fe-4S]ST1 (pde:Pden_1826) *Paracoccus denitrificans*
 MTYVVTENCIMCKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRYAESWPVITRKKDPM PGYQEMDGAPGKLEKYFSEAPGEGD
 >2[4Fe-4S]ST1 (pami:JCM7686_1338) *Paracoccus aminophilus*
 MTYVVTENCIMCKFTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRYSELWPVITRKKDPM PGYDDMDGKPGKLEQYFSEAPGEGD
 >2[4Fe-4S]ST1 (pye:A6J80_19220) *Paracoccus yeei*
 MTYVVTDNCIMCKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEQWVEFNRYSELWPVITRKKDPM PGYQEMDGQPGKLEKYFSPNPGEGD
 >2[4Fe-4S]ST1 (tom:BWR18_09485) *Tateyamaria omphalii*
 MTYIVNDSCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRYSEMWPVITRKKDPLPTAEEMDGKEGKMELFSENPGEGG
 >2[4Fe-4S]ST1 (thw:BMG03_16520) *Thioclava nitratireducens*
 MTYVVIDNCINCKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE

PGMESWVELNRKYSELWPVITQKKDPMPEAEKYDGESGKLEKYFSEAPGEGD

>2[4Fe-4S]ST1(lvs:LOKVESSMR4R_02048) *Yoonia vestfoldensis*
 MTYIVNDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEMWPVIIITKKDPLPGAEDMDGKPGKLDLDFSEAPGEGG

>2[4Fe-4S]ST1(jan:Jann_3309) *Jannaschia* sp. CCS1
 MTYIVNDACIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRRKYSEMWPVIIITKKDPLPTADDMDGKPGKMELFSEAAGEGG

>2[4Fe-4S]ST1(oar:OA238_c27270) *Octadecabacter arcticus*
 MTYIVNDSCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEMWPVIIITKKDQLPNAEEMDGKEDKMELFSEAPGEGG

>2[4Fe-4S]ST1(otm:OSB_09470) *Octadecabacter temperatus*
 MTYIVNDACIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEKWPVIIITKKDQLPTAEEMDGKEGKMDLDFSEAPGEGG

>2[4Fe-4S]ST1(cid:P73_3279) *Celeribacter indicus*
 MTYVVIENCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEQWPVILAKKDPLPGYEEKDGEDGKLEKYFSEAAGEGS

>2[4Fe-4S]ST1(cmar:IMCC12053_867) *Celeribacter marinus*
 MTYVVIENCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEAWPVILSKKDPMPGYEEKDGETGKMEKYFSEAAGEGDA

>2[4Fe-4S]ST1(rsu:NHU_00572) *Rhodovulum sulfidophilum*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDEWVEFNRRKYAETWPCIIITRKDPLPEAEERDGEEGKRAKYFSETPGAGG

>2[4Fe-4S]ST1(rhc:RGUI_1920) *Rhodovulum* sp. P5
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDEWVEFNRRKYAEQWPCIIITRKDPLPEAEAKDGETGKREKYFSETPGEGG

>2[4Fe-4S]ST1(daa:AKL17_2861) *Defluviimonas alba*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGVNTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRRKYSEQWPVITQKRDPLPEAAERDGESGKLDKYFIAEPGQGD

>2[4Fe-4S]ST1(yan:AYJ57_12605) *Yangia* sp. CCB-MM3
 MTYVVVTENCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYAELWPVIIITKKDPLPEAEERDGEAGKMTKYFSEAPGEGD

>2[4Fe-4S]ST1(suam:BO069_12095) *Sulfitobacter* sp. AM1-D1
 MTYIVNDSCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSELWPVIIITKKDPLPEAEERDGESGKLEKYFSERPGE

>2[4Fe-4S]ST1 (tpro:Ga0080559_TMP3271) *Salipiger profundus*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENALVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEMWPVVIITKKDPLPEAEERDGE PGKLDKYFSEAPGEGG

>2[4Fe-4S]ST1 (paby:Ga0080574_TMP3586) *Pelagibaca abyssi*
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEMWPVVIISKKDPMPDADERDGE EGKMEKYFSEAPGEGG

>2[4Fe-4S]ST1 (rmm:ROSMUCSMR3_01126) *Roseovarius mucosus*
 MTYIVNDACIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYAEMWPVVIITKKDPLPEAEERDGE AGKLEKYFSEAPGLGG

>2[4Fe-4S]ST1 (sil:SPO1419) *Ruegeria pomeroyi*
 MTYVVTENCIACKYTDCVEVCPVDCFYEGENALVIHPDECIDCGVCEPECPADAIRPDTE
 PGMEQWVEFNRRKYSEMWPVIVTKKDPLPEAEERDGE SGKMEKYFSEAPGEGG

>2[4Fe-4S]ST1 (sit:TM1040_0575) *Ruegeria* sp. TM1040
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDQWVEFNRRKYAELWPVIVSKKDPMPGHEERDGE EGKLEKYFSEAPGEGG

>2[4Fe-4S]ST1 (rde:RD1_1824) *Roseobacter denitrificans*
 MTYIVNDSCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSELWPVVIITKKDPLPTAEERDGE TGKLEKYFSENPGE GG

>2[4Fe-4S]ST1 (rli:RLO149_c028960) *Roseobacter litoralis*
 MTYIVNDSCISCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSELWPVVIITKKDPLPTAEERDGE TGKLEKYFSENPGE GG

>2[4Fe-4S]ST1 (dsh:Dshi_0785) *Dinoroseobacter shibae*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMEKWVEFNRRKYSEAWPVVIITKKDQLPDAEERDGE QGKLEKYFSEAPGEGG

>2[4Fe-4S]ST1 (pga:PGA1_c07530) *Phaeobacter inhibens* DSM 17395
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRRKYSEMWPVIVSKKDPLPEAEERDGE EGKLEKYFSEAPGEGG

>2[4Fe-4S]ST1 (pgl:PGA2_c07040) *Phaeobacter inhibens* 2.10
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRRKYSEMWPVIVSKKDPLPEAEERDGE EGKLEKYFSEAPGEGG

>2[4Fe-4S]ST1 (pgd:Gal_02738) *Phaeobacter gallaeciensis* DSM 26640
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTE
 PDMDKWVEFNRRKYSEMWPVIVSKKDPLPEAEERDGE EGKLEKYFSEAPGEGG

>2[4Fe-4S]ST1 (php:PhaeoP97_02438) *Phaeobacter porticola*

MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKADTE
 PDMDKWVEFNRYSEMWPVIVSKKDPLPDAEERDGEKGKLEKYFSEAPGEGG
 >2[4Fe-4S]ST1(lmd:METH_12915)*Leisingera methylohalidivorans*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIKADTE
 PDMDKWVEFNRYSELWPVIVSKKDPMPGYEERDGEKGKLEKYFSEAPGEGG
 >2[4Fe-4S]ST1(ftp:RCA23_c10050)*Planktomarina temperata*
 MTYVVTDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKADTE
 PDMEKWVDFNRKYSEAWPVIIITTKDELPEAEARDGEKGKLEKYFSEAAGTGG
 >2[4Fe-4S]ST1(malg:MALG_01115)*Marinovum algicola*
 MTYIVNDACIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKADTE
 PDMEKWVEFNRYSEMWPVIIITTKDPLPKAEHHDGEKGKLEKYFSEAPGEGG
 >2[4Fe-4S]ST1(con:TQ29_13275)*Confluentimicrobium* sp. EMB200-
 NS6
 MTYVVVDNCIACKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPADAIKADTE
 PDMEKWVEFNRYSEAWPVIIISKKDPLPEAEERDGETDKLNKYFSEAPGEGG
 >2[4Fe-4S]ST1(mch:Mchl_4203)*Methylospirillum extorquens* CM4
 MTYVVTDNCIRCKYTDCVEVCPVDCFYVGDMLVINPDECIDCGVCEPECPADAIKADTE
 PGLDGWIALNAKYAALWPNISEKRDPLHDAAWDGRPGKLESVFGVSDPATA
 >2[4Fe-4S]ST1(mrd:Mrad2831_6156)*Methylobacterium radiotolerans*
 MTYVVTDNCIRCKYTDCVEVCPVDCFYVGETMLVIDPDECIDCGVCEPECPADAIKADTE
 PGLEGWKAFNAKYAALWPNIAEKVDPAADAAEWDGRDGKLIIVFGAADPAAA
 >2[4Fe-4S]ST1(bid:Bind_3136)*Beijerinckia indica*
 MSYVVLNCKICKYMDCEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPAEAIKPDTE
 SGLEKWQALNRKMAQYWPNTVKREAPPEAKQFDGRPGKFDAFFTTETPGQGD
 >2[4Fe-4S]ST1(mcg:GL4_1145)*Methyloceanibacter caenitepidi*
 MTYVVTDNCIRCKYMDCEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDTE
 ANLESWLDLNAKYAELWPNIAVKREPPVDAAAFVGVPNKLEPFFSPNPGLGDHADHEAIE
 LELRTNPNERRGHP
 >2[4Fe-4S]ST1(ccr:CC_0654)*Caulobacter vibrioides* CB15
 MTYIVTDACVRCKFMDCVEVCPVDCFYEGENFLVINPDECIDCGVCEPECPVDAIKPDTE
 DEADGKWLKINADYAKVWPNTVKGEPPADREDFERETGKFEKYFSEKPGKGS
 >2[4Fe-4S]ST1(ccs:CCNA_00691)*Caulobacter vibrioides* NA1000
 MTYIVTDACVRCKFMDCVEVCPVDCFYEGENFLVINPDECIDCGVCEPECPVDAIKPDTE
 DEADGKWLKINADYAKVWPNTVKGEPPADREDFERETGKFEKYFSEKPGKGS

>2[4Fe-4S]ST1 (cak:Caul_4113) *Caulobacter* sp. K31
 MTYIVTDACIKCKFMDCEVCPVDCFYEGENFLAINPDECIDCGVCEPECPIDAIAIKPDTE
 DEPDGKWLRLINSEYAKIWPNITVKGVPVPPADREAFERETGKFEKYFSEKPGKGS

>2[4Fe-4S]ST1 (cse:Cseg_3714) *Caulobacter* *segnis*
 MTYIVTDACVRCKFMDCEVCPVDCFYEGENFLVINPDECIDCGVCEPECPVDAIAIKPDTE
 DEPDGKWLRLVNADYAKVWPNITVKGVPVPPEDREQFERETGKFEKYFSEKPGKGS

>2[4Fe-4S]ST1 (pzu:PHZ_c0708) *Phenylobacterium* *zucineum*
 MTYIVMDPCIKCKFMDCEVCPVDCFYEGENFLVINPDECIDCGVCEPECPVDAIAIKPDTE
 DDPDGKWLKVNSEYSRVWPNITVKGTPPADAEQFERESGKFEKYFSEKPGGRGS

>2[4Fe-4S]ST1 (aex:Astex_1096) *Asticcacaulis* *excentricus*
 MTYIVTDPCVKCKFMDCEVCPVDCFYEGENFLVINPDECIDCGVCEPECPVDAIAIKPDTE
 DEPDGKWLEVNISKYARVWPNISVKGTPPADREDFERETGKFEKYFSEKPGDGK

>2[4Fe-4S]ST1 (mmr:Mmar10_2295) *Maricaulis* *maris*
 MTYIVTDACVRCKYTDCVEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPVEAIAIKPDTE
 DDKDGKWLAINSKFAETWPNITLRKDAPADADAMADETGKYEKYFSEKPGSGD

>2[4Fe-4S]ST1 (hne:HNE_3418) *Hyphomonas* *neptunium*
 MTYIVVDACIRCKYMDCEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPVEAIAIKPDTE
 DDPDGKWLKLNSDYAKVWPNITRMKEPPADREEFAQETGKLEKYFTANPGAGD

>2[4Fe-4S]ST1 (hba:Hbal_0771) *Hirschia* *baltica*
 MTYIVIDACIKCKYTDCVEVCPVDCFYEGENMLVIDPEECIDCGVCEPECPAEAIIVPDTE
 DDKDGKWLKLNTEYAAKWPNITVRKDPPEDADEWSQVKDKLGPHFSEKPGTGD

>2[4Fe-4S]ST1 (hbc:AEM38_11180) *Hyphomonadaceae* *bacterium* UKL13-1
 MTYIVTDACVKCKYMDCEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPVDAIAIKPDTE
 DEPDGKWLKVNSDYAKIWPNITVKGEPVADRDDFAKEDGKFEKYFSPNPGEGN

>2[4Fe-4S]ST1 (hdn:Hden_0076) *Hyphomicrobium* *denitrificans* ATCC
 51888
 MTFVVTENCIKCKYTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCVPECPAEAIIFSDAE
 PQATAHWLDLNRKHADQWPNIIVAKKAAMPDADAENGRAGKAAEFSPAEATEDAK

>2[4Fe-4S]ST1 (hni:W911_04350) *Hyphomicrobium* *nitrativorans*
 MTFVVTENCIKCKFTDCVEVCPVDCFYEGENMLVIHPDECIDCGVCVPECPADAIFSDAE
 PQATAHWLEVNRYADLWPNLTKKKPPLPNADAENGRQGKANELSPLPASEDVA

>2[4Fe-4S]ST1 (ara:Arad_12331) *Agrobacterium* *radiobacter*
 MTFVVTENCIKCKFQDCVEACPVNCFHEGPNFLVINPSECIDCGVCPECPAEAIYPLEE
 LPVEQAFAALNSELAAEWPFVITIKGPPPADASIWDGKRGKLSLLER

>2[4Fe-4S]ST1 (mln:A9174_34320) *Mesorhizobium loti* NZP2037
 MTYVVTDNCKICKYMDCEVCPVDCFYEGENMLVIHPDECIDCGVCVPECPAEAIKPDTE
 PSATPAWLDLNREYASSWPNI TRKKIPPADANVWDGVPKGKFDHFGSGKPGEGD

>2[4Fe-4S]ST1 (mey:TM49_09940) *Martelella endophytica*
 MTYVVTENCIACKHMDCEVCPVDCFYEGENFLVIHPDECIDCGVCEPECPADAIVPDIG
 DPNLGFWLEINRKYAELWPNIIVKGTTPDNAEAMQDVPNKYRDLFSEKPGDGS

>2[4Fe-4S]ST1 (anh:A6F65_00405) *Altererythrobacter namhicola*
 MTYVVTDACIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGQEKWLEINTKFSAEWPNI TEKKDPPADADEHKGEEGKYEKFFSPEPGEGD

>2[4Fe-4S]ST1 (cna:AB433_16445) *Croceicoccus naphthovorans*
 MTYVVTDACIKCKYMDCEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 SDLEKWLELNTKYSAEWPNI TVKKDSPADADEHKGEEDKFDKYFSAEPGEGD

>2[4Fe-4S]ST1 (por1:BG023_11449) *Porphyrobacter* sp. LM 6
 MTYVVTEDCIKCKYTDCVEVCPVDCFYEGENMLVINPSECIDCGVCEPECPAEAILPDTE
 DGLEKWLELNTQYS AVWPNI TSQKAPPEDADAHKGEKGKFEKYFSTEPGEGD

>2[4Fe-4S]ST1 (rpb:RPB_3415) *Rhodopseudomonas palustris* HaA2
 MTYVVTDNCKGCRYTECVTVCPVECFHVDAAMTYIDPENCIDCGGCAPACPVGAIAPDYR
 LPAHQKFWIDVNRKRAAETPVLTARLPPLPGADRRQALGR

>2[4Fe-4S]ST1 (avi:Avi_7631) *Agrobacterium vitis*
 MTYVVTDQCSGCRYTECVTVCPVECFHIDEEMTYIDPDNCIDCGGCAPVCPVGAIHASYP
 ADKQEWIEINRRRAAETPVVASRLPPLPGAEEERRQALTS

>2[4Fe-4S]ST1 (tmo:TMO_3055) *Tistrella mobilis*
 MAYVVVDNCKICKYQDCVEVCPVDCFYEGENMLVIHPDECIDCGVCEPECPAEAIKPDSD
 DGLEQWAE LN RKYAELWPNI SRKGDAPADADEWNGVPDKLANHFS DKPGQQG

Subtype 2

>2[4Fe-4S]ST2 (mci:Mesci_5841) *Mesorhizobium ciceri* (biovar
 Biserrulae)
 MAFKIIASQCTQCGACEFECPSGAIKFKGESYVVEPQKCTECQGEFDTQQCASVCPVPKT
 CVPA

>2[4Fe-4S]ST2 (mop:Mesop_6415) *Mesorhizobium opportunistum*
 MAFKIIASQCTQCGACEFECPSGAIKFKGESYVVEPQKCTECQGEFDTQQCASVCPVPKT

CVPA

>2[4Fe-4S]ST2(mam:Mesau_05888)*Mesorhizobium australicum*
MAFKIIASQCTQCGACEFECPSGAIKFKGESYVVEPQKCTECQGEFDTQQCASVCPVPKT

CVPA

>2[4Fe-4S]ST2(mamo:A6B35_32325)*Mesorhizobium amorphae*
MAFKILASQCTQCGACEFECPSGAIKFKGEAYVIDPKECTECKEAFDTQQCASVCPVPKT

CVPA

>2[4Fe-4S]ST2(sme:SMA0811)*Sinorhizobium meliloti* 1021
MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(smi:BN406_04228)*Sinorhizobium meliloti* Rm41
MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(smeg:C770_GR4pC1047)*Sinorhizobium meliloti* GR4
MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(smel:SM2011_a0811)*Sinorhizobium meliloti* 2011
MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(smd:Smed_6234)*Sinorhizobium medicae*
MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(same:SAMCFNEI73_pB0086)*Sinorhizobium americanum*
MAFRIIASQCTQCGACEFECPSGAIKFKGEAYVIDPNKCTECKGAFELQQCAYVCPVPKT

CVPVPA

>2[4Fe-4S]ST2(rel:REMIM1_PE00335)*Rhizobium etli* bv. *mimosae*
Mim1

MAFRIIASQCTQCGACEFECPSGAIGFKGEAYVIDPEKCTECKGSFETQQCAEVCPVPKT
CVAAAAAI

>2[4Fe-4S]ST2(rep:IE4803_PB00377)*Rhizobium etli* bv. *phaseoli*
IE4803

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCPVPKT
CVPAAPAI

>2[4Fe-4S]ST2(rei:IE4771_PB00178)*Rhizobium* sp. IE4771

MAFRIIASQCTQCGACEFECPSGAIGFKGEAYVIDPEKCTECKGAFETQQCAEVCPVPKT
CVAAAP

>2[4Fe-4S]ST2(rlt:Rleg2_5042)*Rhizobium leguminosarum* bv.
trifolii WSM2304

MAFKIIASQCTQCGACEFECPSGAISFKIDKFVVDPNVCTECREEFDAPKCRAICPMQNT
CVPA

>2[4Fe-4S]ST2(rlg:Rleg_4923)*Rhizobium leguminosarum* bv.
trifolii WSM1325

MAFKIIASQCTQCGACEFECPSGAISFKTDRFVVDPKICTECRIEFDAPKCRAICPMPNT
CVPA

>2[4Fe-4S]ST2(rhn:AMJ98_PC00281)*Rhizobium* sp. N1341

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCPVPKT
CVLAAPAI

>2[4Fe-4S]ST2(rpha:AMC79_PC00258)*Rhizobium phaseoli*

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCPVPKT
CVLAAPAI

>2[4Fe-4S]ST2(rhx:AMK02_PC00276)*Rhizobium* sp. N731

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCPVPKT
CVLAAPAI

>2[4Fe-4S]ST2(rsp:RSP_7561)*Rhodobacter sphaeroides* 2.4.1

MPYRIVTALCTACGACEIECPSSAIGPAGAAFRIDPLLCTECAGRFETPQCASVCPVPKT
CVPA

>2[4Fe-4S]ST2(rsk:RSKD131_1881)*Rhodobacter sphaeroides* KD131

MPYRIEPARCTACGACEIECPSSAIGPAGAAFRIDPLLCTECAGRFETPQCASVCPVPKT
CVPA

>2[4Fe-4S]ST2(rhc:RGUI_2354)*Rhodovulum* sp. P5

MAYKIVTETCTACGACEFECPNAAIRMVKDTFVVDPNLCSECEGHFENPQCAEVCPVPNT
CIPA

>2[4Fe-4S]ST2(mlo:msl8750)*Mesorhizobium japonicum* MAFF 303099

MAFKIIASQCTQCGACEFECPSGAIKFKGETYVIDPKKCTECEGTFETQQCASVCPVSKT
CVPA

>2[4Fe-4S]ST2(mln:A9174_326)*Mesorhizobium loti* NZP2037

MAFKIIASQCTQCGACEFECPSGAIKFKGETYVIDPKKCTECEGTFETQQCASVCPVSKT
CVPA

>2[4Fe-4S]ST2(rhi:NGR_a01280)*Sinorhizobium fredii* NGR234
MAFKIIASQCTQCGACEFECPSNAIELKGKEYVIDPKKCTECKGVFEIQQCASVCPMPKT
CVPA

>2[4Fe-4S]ST2(rtr:RTCIAT899_PB01415)*Rhizobium tropici*
MAFKIIASQCTQCGACEFECPSGAIELKGGENYVIDPKKCTECEGAFETQQCASVCPVPKT
CVPA

>2[4Fe-4S]ST2(bja:bsr1739) *Bradyrhizobium diazoefficiens* USDA
110
MAYKIIASQCTVCGACEFECPNAAISLKNDIYVINPSQCTQCEGHSDAPKCAVVCPVPDT
CVPA

>2[4Fe-4S]ST2(bju:BJ6T_80810)*Bradyrhizobium japonicum* USDA 6
MAYKIIASQCTVCGACEFECPNAAISLKNDIYVINPSQCTQCEGHSDAPKCAVVCPVPDT
CVPA

>2[4Fe-4S]ST2(bjp:RN69_39250)*Bradyrhizobium japonicum* E109
MAYKIIASQCTVCGACEFECPNAAISLKNDIYVINPSQCTQCEGHSDAPKCAVVCPVPDT
CVPA

>2[4Fe-4S]ST2(bra:BRADO5448)*Bradyrhizobium* sp. ORS 278
MTYKIIASQCTVCGACEFECPNAAIRLKNDDMYIIDPKKCTECEGHFDAPQCAAVCPVPDT
CVPA

>2[4Fe-4S]ST2(brs:S23_46530)*Bradyrhizobium* sp. S23321
MAYKIIASQCTVCGACEFECPNAAISLKRDYVIDPKKCTECEGHFDTAQCAVVCPVPDT
CVPA

>2[4Fe-4S]ST2(aol:S58_22590)*Bradyrhizobium oligotrophicum*
MTSSDVAGIGELHMTYKIIASQCTVCGACEFECPNAAIRLKNDDMYIIDPKKCTECEGHFD
APQCAAVCPVPDTCVPA

>2[4Fe-4S]ST2(bic:LMTR13_26885)*Bradyrhizobium icense*
MAYKIIASQCTVCGACEFECPNAAISLKNDIYVIDPKKCTECEGQCDTPQCAVICPVPGT
CVQA

>2[4Fe-4S]ST2(xau:Xaut_0083)*Xanthobacter autotrophicus*
MAYKIIITSQCTVCGACEFECPNAAISLKNDTYVINPKKCTECEGSFETPQCAVVCPVENT
CVPA

>2[4Fe-4S]ST2(gdi:GDI0431)*Gluconacetobacter diazotrophicus* PA1
5 (Brazil)
MAYRIVTSQCTVCGACEFECPNGAISLKNDLYVINAKKCTECEGQFDTPQCVSVCPVPNT

CVPA

>2[4Fe-4S]ST2(sphi:TS85_14470)*Sphingomonas* sp. WHSC-8
MAYKIIVSQCTGCSACEFECPNAAISMKGDTFIIDPKKCTECEGIFDHAQCDTVCPVPKT
CVPA

>2[4Fe-4S]ST2(rsu:NHU_01471)*Rhodovulum sulfidophilum*
MALKIVKSQCTVCGACEFECPNAAIKFKGEGYIIDAEEKCTECEGQFDTPQCAAVCPVPNT
CVPA

>2[4Fe-4S]ST2(con:TQ29_04770)*Confluentimicrobium* sp. EMB200-NS6
MSLKIIVSQCTVCGACEFECPNAAIKFKNDTYVIDPALCTECEGSYDSPQCAEVCPVPDT
CVPA

>2[4Fe-4S]ST2(mbry:B1812_08155)*Methylocystis bryophila*
MAYKIVASQCTVCGACEFECPNAAIRLKNDMYIIDPKKCTECEGHFDTPKCAEVCPVENT
CVPV

>2[4Fe-4S]ST2(msc:BN69_2612)*Methylocystis* sp. SC2
MAYKIIASQCTVCGACEFECPNAAIRLKNDMYIIDPKKCTECEGHFDTPQCAVVCVENT
CVPA

>2[4Fe-4S]ST2(mno:Mnod_4006)*Methylobacterium nodulans*
MALKIIASQCTMCGACEFECPNNAIRAKGDIYIIDPKECTECEGQFDKPQCATVCPVPNT
CVKAAPVH

>2[4Fe-4S]ST2(met:M446_3601)*Methylobacterium* sp. 4-46
MALKIIASQCTVCGACEFECPNGAIRMKGDIYIVDPKKCTECDGQFDEPQCAAVCPVPNT
CVKAAPAA

>2[4Fe-4S]ST2(rpa:RPA4629)*Rhodopseudomonas palustris* CGA009
MAYKIVASQCTGCSACEPQCPNVAIFEKAGTFVIDPSKCSECIGHYDEPQCVAVCPVDGT
CVIDNSVPRYQAA

>2[4Fe-4S]ST2(azc:AZC_1043)*Azorhizobium caulinodans*
MAYKIIASQCTVCGACEFECPNAAIRLKNDMYIIDPKKCTECEGSFSDSPQCDAVCPVPGT
CVPAG

>2[4Fe-4S]ST2(bbt:BBta_5903) *Bradyrhizobium* sp. BTAi1
MTLKIIASQCTSCSACEPECPNVAISEKNGTFVIDPKKCTECIGHFDEPQCAAVCPVDNT
CVIDNSFPRYQPPA

>2[4Fe-4S]ST2(bjp:RN69_39145) *Bradyrhizobium japonicum* E109
MPFKIIASQCTSCSACEPLCPNVAISEKGGNFVIEAAKCSECVGHFDEPQCAAACPVDNT
CVVDRALPRYQAPV

>2[4Fe-4S]ST2(bju:BJ6T_80600) *Bradyrhizobium japonicum* USDA 6
MCSAACPRVGL EIGSLRRKEEYVPFKIIASQCTSCSACEPLCPNVAISEKGGNFVIEAAK
CSECVGHFDEPQCAAACPVDNTCVVDRALPRYQAPV

>2[4Fe-4S]ST2(bra:BRADO5419) *Bradyrhizobium* sp. ORS 278
MTLKIIASQCTSCSACEPECPNVAISEKNGTFVIDPKKCTECIGHFDEPQCAAVCPVDNT
CVIDNSFPRYQPPA

>2[4Fe-4S]ST2(azc:AZC_3415) *Azorhizobium caulinodans*
MALKIVSSQCTSCSACEPECPNVAISEKNGTFVIDPKKCTECIGHYDVPQCAAVCPVDDT
CIIDTSYPRYQGAA

>2[4Fe-4S]ST2(xau:Xaut_0112) *Xanthobacter autotrophicus*
MTLKIVASQCTSCSACEPECPNVAISEKNGTFVIDPKKCTECIGHFDVPQCAAVCPVDDT
CVIDNAYPRYQPTA

>2[4Fe-4S]ST2(bja:bsr1760) *Bradyrhizobium diazoefficiens* USDA
110
MPFKIIASQCTSCSACEPLCPNVAISEKGGNFVIEAAKCSECVGHFDEPQCAAACPVDNT
CVVDRALPRYQAPV

>2[4Fe-4S]ST2(aol:S58_22870) *Bradyrhizobium oligotrophicum*
MTLKIIASQCTSCSACEPECPNVAISEKNGTFVIDPKKCTECLGHFDEPQCAAVCPVDNT
CVIDNSFPRYQPPA

>2[4Fe-4S]ST2(bic:LMTR13_26645) *Bradyrhizobium icense*
MPFKIIASQCTSCSACEQECPNVAISEKGGTFVIDPKKCTECIGHFEFPQCVAVCPVDNT
CVIDTSLPRY

>2[4Fe-4S]ST2(bid:Bind_0397) *Beijerinckia indica*
MSLKIAVSCVNC SACEAECPNEAISAGEGIYVIDPAKCTECIGFHDDPQCALVCPVEETC
VIDDNYPRYQAA

>2[4Fe-4S]ST2(msc:BN69_2618) *Methylocystis* sp. SC2
MTLKIIASQCTSCSACEPECPNVAITEKNGTFVIDPKKCTECIGHFDAPQCAAVCPVDNT
CVIDNAYPRYQAPA

>2[4Fe-4S]ST2(mbry:B1812_08145) *Methylocystis bryophila*
MTLKIIASQCTSCSACEPECPNVAITEKNGTFVIDPKKCTECIGHFDAPQCAAVCPVDDT
CVIDNAYPRYQPPA

>2[4Fe-4S]ST2(mey:TM49_15610) *Martelella endophytica*
MAMKILADMCTACGDCEPNCPTDAISP KGVYAIDPDVCTECEGVSDTPKCMQACMDDCI
EPA

>2[4Fe-4S]ST2(rsp:RSP_3189)*Rhodobacter sphaeroides* 2.4.1
MSMTISADLCTACGDCEPVCPTHAIIVPRKGIYFIKSEVCTECEGAFDMPQCMSVCTSDSI
APLEA

>2[4Fe-4S]ST2(rsh:Rsph17029_3928)*Rhodobacter sphaeroides* ATCC
17029
MSMTISADLCTACGDCEPVCPTHAIIVPRKGIYFIKSEVCTECEGAFDMPQCMSVCTSDSI
APLEA

>2[4Fe-4S]ST2(rsq:Rsph17025_3189)*Rhodobacter sphaeroides* ATCC
17025
MSMSISADLCTACGDCEPVCPTNAIIPRKGIYFIKADVCTECDGEFDMPQCMNVCTADSI
VPLEA

>2[4Fe-4S]ST2(rcp:RCAP_rcc03284)*Rhodobacter capsulatus*
MAMKIDPELCTSCGDCEPVCPTNAIAPKKG VYVINADTCTECEGEHDL PQCVNACMTDNC
INPAA

>2[4Fe-4S]ST2(rpa:RPA4631)*Rhodopseudomonas palustris* CGA009
MAYKIVTSQCTVCGACEFECPNAAISMKRGT YVIDATKCTECEGQFDKPQCVSVCPVDNT
CVPA

>2[4Fe-4S]ST2(rsk:RSKD131_3365)*Rhodobacter sphaeroides* KD131
MSMTISADLCTACGDCEPVCPTHAIIVPRKGIYFIKSEVCTECEGEFDMPQCMSVCTSDSI
APLEA

>2[4Fe-4S]ST2(rhc:RGUI_2053)*Rhodovulum* sp. P5
MAMMINADMCTACGDCE SVCPTGAIIPSKGVFTIVADKCTECEPDHDMPQCLNSCMEDGC
IVPAE

>2[4Fe-4S]ST2(gdj:Gdia_1575) *Gluconacetobacter diazotrophicus*
PA1 5 (JGI)
MAYRIVTSQCTVCGACEFECPNGAISLKNDLYVINAKKCTECEGQFDTPQCVSVCPVPNT
CVPA

>2[4Fe-4S]ST2(brs:S23_46240)*Bradyrhizobium* sp. S23321
MPFKIISSQCTSCSACEPECPNVAIREKGGTFVIDPKKCTECLGHFDEPQCVAVCPVDNT
CVIDTSLPRYQAPA

>2[4Fe-4S]ST2(rpc:RPC_4471)*Rhodopseudomonas palustris* BisB18
MAYKIISSQCTSCSACEPECPNVAIFEKGGTFHINPKKCTECLGHFDMAQCVAVCPVEGT
CVIDNSVPRYQAPA

>2[4Fe-4S]ST2(rpe:RPE_4540)*Rhodopseudomonas palustris* BisA53

MAYKIVASQCTGCTACEVECPNAAIFEKGGAFIDPAKCSECIGHFDVAQCAAVCPVENT
CVIDKSVPRYVLP

>2[4Fe-4S]ST2(bbt:BBta_5932)*Bradyrhizobium* sp. BTAi1

MAYKIIASQCTVCGACEFECPNAAIRLKNEMYIIDPKKCTECEGHFDAPQCAAVCPVPDT
CVPA

>2[4Fe-4S]ST2(rpb:RPB_0960)*Rhodopseudomonas palustris* HaA2

MAYKIVASQCTSCSACEPECPNEAISERRGVFMIDPSKCTECIGHFDVPQCVAVCPVDGT
CVIDNSVPRASAA

>2[4Fe-4S]ST2(rpt:Rpal_5110)*Rhodopseudomonas palustris* TIE-1

MAYKIVASQCTGCSACEPQCPNVAIFEKAGTFVIDPSKCSECIGHYDEPQCVAVCPVDGT
CVIDNSVPRYQAA

>2[4Fe-4S]ST2(rpt:Rpal_5112)*Rhodopseudomonas palustris* TIE-1

MAYKIVTSQCTVCGACEFECPNAAISMKRGTVIDATKCTECEGQFDKPQCVSVCPVDNT
CVPA

>2[4Fe-4S]ST2(rpx:Rpx1_4807)*Rhodopseudomonas palustris* DX-1

MAYKIVASQCTGCSACEPQCPNVAIFEKAGTFAIDPSKCSECTGHYDEPQCVAVCPVDGT
CVIDNSVPRYQAA

>2[4Fe-4S]ST2(yan:AYJ57_00320)*Yangia* sp. CCB-MM3

MALTIVQSNCTVCGACEFECPNAAIRFEDDTYIIDADLCTECKGHYDIPQCAEICPVPET
CVPA

>2[4Fe-4S]ST2(rpd:RPD_1064)*Rhodopseudomonas palustris* BisB5

MAYKIVASQCTSCSACEPECPNVAITEKRGVFTIDPSTCTECLGHFDVPQCVAVCPVDGT
CVIDNSVPRARAA

>2[4Fe-4S]ST2(sm:Sinme_6360)*Sinorhizobium meliloti* AK83

MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT
CVPA

>2[4Fe-4S]ST2(sm:SinmeB_6022)*Sinorhizobium meliloti* BL225C

MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT
CVPA

>2[4Fe-4S]ST2(sm:SM11_pC1133)*Sinorhizobium meliloti* SM11

MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT
CVPA

>2[4Fe-4S]ST2(smer:DU99_23505)*Sinorhizobium meliloti* RMO17

MAFKIIASQCTQCGACEFECPRGAVNFKGEKYVIDPTKCNECKGGFDTQQCASVCPVSNT

CVPA

>2[4Fe-4S]ST2(ret:RHE_PD00230)*Rhizobium etli* CFN 42

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCVPVKT
CVPAAPAI

>2[4Fe-4S]ST2(rec:RHECIAT_PB0000274)*Rhizobium etli* CIAT 652

MAFRIIASQCTQCGACEFECPSGAIRFKGEIYVIDPEKCTECKGTFETQQCAEVCVPVKT
CVLAAPAI

>2[4Fe-4S]ST2(rir:BN877_p0303)*Rhizobium* sp. IRBG74

MVFKIIASQCTQCGACEFECPSGAIEFKGEKYVIDDPKCTECEGVFEVQQCASVCPTPKT
CVPA

>2[4Fe-4S]ST2(rga:RGR602_PB00242)*Rhizobium gallicum*

MAFRIIASQCTQCGACEFECPSDAIDFKGETYVIDDPKCTECKKTFETQQCAEVCVPVKT
CVPAAPSI

>2[4Fe-4S]ST2(rpb:RPB_0958)*Rhodopseudomonas palustris* HaA2

MAYKIVTSQCTVCGACEFECPNAAISMKRGTYVIDAVKCTECEGHFDKPQCVAVCPVDNT
CVPA

>2[4Fe-4S]ST2(rpc:RPC_4473)*Rhodopseudomonas palustris* BisB18

MAYKIVASQCSVCGACEFECPNAAIVLKRDMYIIIEAAKCTECEGQFDKPQCASVCPVENT
CVPA

>2[4Fe-4S]ST2(rpd:RPD_1062)*Rhodopseudomonas palustris* BisB5

MAYKIIITSQCTVCGACEFECPNAAIAMKRGTYVIDAVKCTECEGHFDKPQCVAVCPVDNT
CVPA

>2[4Fe-4S]ST2(rpx:Rpx1_4809)*Rhodopseudomonas palustris* DX-1

MAYKIVTSQCTVCGACEFECPNAAISMKRGTYVIDATKCTECEGQFDKPQCVSVCPVDNT
CVPA

>2[4Fe-4S]ST2(rpe:RPE_4542)*Rhodopseudomonas palustris* BisA53

MAYKIVASQCSVCGACEFECPNAAISLKREMYVIDASKCTECEGQFDKPQCAVVCPEKT
CIPA

>2[4Fe-4S]ST2(sphi:TS85_14445)*Sphingomonas* sp. WHSC-8

MAYKIIIGSQCTNCSGCEAECPNLAISERGGTFVIDPALCTECIGHFDTPQCVAICPVDNTCV
IDTSVPRYHES

>2[4Fe-4S]ST2(msl:Msil_3645)*Methylocella silvestris*

MTYKIVASQCTSCSACEAECPNVAISEKGGTFVINPKKCTECIGYFDIPQCVAVCPVDNTCV
IDNSLPRYQGNA

>2[4Fe-4S]ST2(mey:TM49_15560)*Martelella endophytica*
MTYSITEHCVSCFACVDVCPGAIQETSPVFTIAEKKCTHCEGAHAVSQCASICPVEGAILD
PLGEMANPPGSLTGIPPEKRLAAGLLV

Subtype 3

>2[4Fe-4S]ST3(syb:TZ53_09145) *Sphingobium* sp. YBL2
MIAHIFEDRCTACQACVSACPTHVLDAAGPDGAPRIARLDQCQTCFLCELHCEADAIYVGP
DQRQAEAISPEAILASGHLGRLRHDHGWDREPEPGSTGHLHDFWQLGPLLREGAEIAARR
YAERHASDRA

>2[4Fe-4S]ST3(shz:shn_23395) *Shinella* sp. HZN7
MIEVISEDRCITGCNICVNVCPNTVFAPVADGIPVIARQDDCQTCFMCEVYCPDDALYVAP
HATEITHVTVAELEARDLFGSYRKSIGWIRGGRPRPAPEIMQRLEHR

>2[4Fe-4S]ST3(bra:BRADO4282) *Bradyrhizobium* sp. ORS 278
MIELILADRCTDCGACVDVCPNTVLDRAVSGPPLLARVEDCQTCFMCELYCRADAIYVAP
DCDRRVATTPDEALASGRLGQYRKHSGWDEWAGQFPNEQWLMETVFRRAGEAVRAAETDDKR
TA

>2[4Fe-4S]ST3(sme:SMc02347) *Sinorhizobium meliloti* 1021
MIEVVSTDRICIRCDICERICPAFVFDRDETGLPVIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(smk:Sinme_2626) *Sinorhizobium meliloti* AK83
MIEVVSTDRICIRCDICERICPAFVFDRDETGLPVIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(smq:SinmeB_2405) *Sinorhizobium meliloti* BL225C
MIEVVSTDRICIRCDICERICPAFVFDRDETGLPVIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(smx:SM11_chr2729) *Sinorhizobium meliloti* SM11
MIEVVSTDRICIRCDICERICPAFVFDRDETGLPVIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(mam:Mesau_03271) *Mesorhizobium australicum*
MIEIVSATRCIECDICVKVCPTNVFDATEHGAPVIARQDDCQTCFLCEIYCPTDALYVAE
AAEGPTGITEAEVEARLLFGSYARALGWTRGKAGGSEFDPTHIRVAQ

>2[4Fe-4S]ST3(smeg:C770_GR4Chr2676) *Sinorhizobium meliloti* GR4

MIEVVSTDR CIRCDICERICPAFVFDRDETGLPV IARQDDCQTCFLCEIYCPADALYVAE
 QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV
 >2[4Fe-4S]ST3((smel:SM2011_c02347) *Sinorhizobium meliloti* 2011
 MIEVVSTDR CIRCDICERICPAFVFDRDETGLPV IARQDDCQTCFLCEIYCPADALYVAE
 QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV
 >2[4Fe-4S]ST3(mci:Mesci_3004) *Mesorhizobium ciceri* (biovar
 Biserrulae)
 MIEIVSATRCVECDICVKVCPANVFDATESGVPVIARQEDCQTCFLCEIYCPTDALYVAE
 FAEGPTGITEAQADARQLFGSYARALGWKRGKAGGSEFDPTHRIRVAQ
 >2[4Fe-4S]ST3((abs:AZOBR_180293) *Azospirillum brasilense* Sp245
 MIELILSERCIACGTCAKVCPPDDVLRTDAAGEPVIAHKEDCQTCYLCELFCEPVDALYVSP
 RTAPDPTVDAAALIAAGLIGSYRRELGWTRGRPGGTETDLSYRMHEAFAEPFGEIWKRSKI
 >2[4Fe-4S]ST3(six:BSY16_5978) *Sinorhizobium* sp. RAC02
 MIEVLADTCTDCNLCVQVCPTNVFEAVPDGPPLILRQDSCQTCFMCELYCPVDALYVDP
 DAEAVHKLTVEGVVRAGNLFGSYRKAIGWHKETRDRRYIDDHFRLLPQ
 >2[4Fe-4S]ST3(bid:Bind_0547) *Beijerinckia indica*
 MIEIIDPTRCTSCNICVKVCPTNVFGSVKNSIPVIARQSDCQTCFMCELYCPADALYVAP
 FTDELQIDDIHASHNNIDFGSYRRAIGWTKETNALRASDQSFELLKP
 >2[4Fe-4S]ST3(cid:P73_2118) *Celeribacter indicus*
 MIEVVSASRCIRCDICVRVCPADVFGKDGEGLPVILRQDDCQTCFLCEIYCPTDALFVAE
 VADEVTGITESVVEASGLFGAYARSLGWAKGRAGGSQFDTTQHLRAAQV
 >2[4Fe-4S]ST3(pami:JCM7686_pAMI6p032) *Paracoccus aminophilus*
 MIEVISAARCTGCNICVQVCPTNVFAAVKGGIPVIARQDDCQTCYMCEVWCPDDALYVAP
 NADGTEGITEPELEAQGRFGSYRRSVGWAKGGRVAPAPQIMSRLRG
 >2[4Fe-4S]ST3(pami:JCM7686_pAMI5p125) *Paracoccus aminophilus*
 MIELVSATRCVTCDVCIKACPMNVFDRAEDGLPV IARQEDCQTCFLCEAHCPTDALFVAA
 ERAPLPAPARLPDEAALIASGIMGSYRARLGWGKGRKPPRDFAAALTLQAQAAAPGRVPP
 GQPRAAQFGRVDANGSELQP
 >2[4Fe-4S]ST3(cid:P73_2383) *Celeribacter indicus*
 MIELVSASRCVTCDLCIAVCPMNVFDRAEDGLPV IARQEDCQTCYLCEAHCPTDALYVAA
 ERTPLSDRLRPREAELAGTDLMGSYRARLGWGRGLRPPGTLNAAVELSHAPAAAAGVAPP
 RQPAPAAAFHEECPDV

>2[4Fe-4S]ST3(same:SAMCFNEI73_pC1420) *Sinorhizobium Americanum*

MIEVIDTETCTDCNLCVKVCPTNVFDAIADGPPVIARQGDQTCFMCEVYCPVDSLYVDP
DPANSYGLTVENVKQANLFGSYRRSIGWAKETRHLRRVDDHFRLPQ

>2[4Fe-4S]ST3(eah:FA04_28520) *Ensifer adhaerens Casida A*

MIEVLDTNTCTDCNLCVQVCPTNVFQAQREGPPLIKRQDACQTCFMCELYCPVDALYVEP
DAEAVHGLTVEGVHERQLFGSYRKAIGWHKDTRHRRLLIDDHFRLLPQ

>2[4Fe-4S]ST3(rel:REMIM1_Pf00314) *Rhizobium etli* bv. *mimosae*
Mim1

MIEVLDPQTCTDCNLCVKVCPTNVFEAVGDGPPVILRQENCQTCFMCELYCPVDALYVDP
DPEATHGLILETVRESGLFGSYRKAIGWHKDTRDRRHIDDHFRLPQ

>2[4Fe-4S]ST3(rei:IE4771_PE00132) *Rhizobium* sp. IE4771

MIEVLDPQTCTDCNLCVKVCPTNVFEAVLDGPPVILRQNNCQTCFMCELYCPVDALYVDP
DPEITHDLTLETVRESSLFGSYRKAIGWHKDTRDRRHIDDHFRLPQ

>2[4Fe-4S]ST3(bbt:BBta_3288) *Bradyrhizobium* sp. BTAi1

MIELIVADRCTDCGACVEVCPTNVLERAPSGPPQLARVEDCQTCFMCELYCRADAIYVAP
DCDRRVAITQETALDSGRLGQYRKHSGWDEWAGQFPNEQWLMETVFRRAGEAAAGAAGAD
DKRTA

>2[4Fe-4S]ST3(cse:Cseg_2020) *Caulobacter segnis*

MIEVVVEDRCTGCGDCVQACPSDVLRVGEGGKAVIAHQVDCQTCLLCELYCPADALFVWP
EVDRVIGVGADQALASGQLGAFRRDHGWGEHAATHTNQHWRMGAIFERARLLAIETAAAK
TARTEDVR

>2[4Fe-4S]ST3(bbt:BBta_4871) *Bradyrhizobium* sp. BTAi1

MIEIIDPERCTACNICVTACPTNVFDKTEGLPVIARQADCQTCFLCELYCPEDALFVSPF
AEQPQGIDVVAARQSGLLGSYRRVAVGWTKDSEHLREADRSFRLFGQ

>2[4Fe-4S]ST3(eah:FA04_29555) *Ensifer adhaerens* Casida A

MIEVISVDRRCIRCDICERICPAFVFDRDETGLPIIARQDDCQTCFLCEIYCPTDALYVAE
AAHGPTGIAEAEVLERDLFGAYARSLGWNRRGRAGGAQDDPTRHIRVAQV

>2[4Fe-4S]ST3(smi:BN406_02424) *Sinorhizobium meliloti* Rm41

MIEVVSTDRRCIRCDICERICPAFVFDRDETGLPVIIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGVYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(smer:DU99_14280) *Sinorhizobium meliloti* RMO17

MIEVVSTDRRCIRCDICERICPAFVFDRDETGLPVIIARQDDCQTCFLCEIYCPADALYVAE
QAHGPIGITEAEVLERDLFGLYARSLGWSRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(six:BSY16_4036) *Sinorhizobium* sp. RAC02

MIEVISEDRCITGCNICVNVCPNTVFDVPVGGNPTIARQDDCQTCFMCEVYCPEDALYVAP
LTTAVTGVTSVELEAKDIFGSYRKSIGWIRGGRPRPTPEIMKRLDHH

>2[4Fe-4S]ST3(six:BSY16_5015) *Sinorhizobium* sp. RAC02

MIEVISTDRRCIRCDICERICPAFVFDRDETGLPVIIARQDDCQTCFLCEIYCPTDALYVAE
NAHGPIGISEADVLERDLFGTYARSLGWNRRGRAGGAQNDPTRHIRVAQV

>2[4Fe-4S]ST3(npp:PP1Y_AT22995) *Novosphingobium* sp. PP1Y

MLIAAGLYPRNTPEPGRLRSSEAQRPLAARTTFDEVVQGLSEPEARFEAGRCLSCGNCFECD
NCFAACPEQAILRLGRGHGYRVEPDLCTGCGICFEQCPCHAIEMQPEPVPTDAPLGPT
DEPLAPHRFRLRV

>2[4Fe-4S]ST3(psf:PSE_2104) *Pseudovibrio* sp. FO-BEG1

MANLSRRAFFTRLsAKPEVANPFRPPWTSEQRIEDKCTGCFECVKACPEGILFSDDNRPFLK
PGVGECTFCEECAKACCPEDGLFNLSEAPWRLTADLKQEACLLQKGVSCRTCTDCCDPR
ALRFDLRTPPAGQIQLDADQCSGCGACLVACPVDAlSLNDQSNTSQESLANA

Subtype 4

>2[4Fe-4S]ST4(abs:AZOBR_110086) *Azospirillum brasilense* Sp245
MAISRADLFRGRFRSEARPSQPPAAPSQALEARIGAGCLSYTGIDCRMCGDHCDHGAIRF
RPLGRGRWLPIIEEGGCTGCGDCAGVCPVKAVTMEAVAA
>2[4Fe-4S]ST4(mgy:MGMSRv2__2006) *Magnetospirillum*
gryphiswaldense MSR-1 v2
MMSHSLSRRALFGRTPPQSPPEAPVKRVAVLGGTCIATQGVACGTCADPCDPRAIKIRPM
LGGRAIPLIDAACTGCGDCLNVCPVGALV LAPAGSGESKPCA
>2[4Fe-4S]ST4(abq:ABAZ39_06965) *Azospirillum brasilense* Az39
MAISRADLFRGRLRSEPVPSEAPQAMVARIGAACLSYTGTDCRMCGDHCDHAAIRFRPLG
RGRWLPIIEEGGCTGCGDCATVCPVKAVTMEVATA
>2[4Fe-4S]ST4(same:SAMCFNEI73_Ch1327) *Sinorhizobium Americanum*
MIGERCLARNGTDCQACRDACPTEAIRFRPRVGGPFLPELEQEACTGCGACLAVCPVAAl
GVREVRGESVYV
>2[4Fe-4S]ST4(rlt:Rleg2_2940) *Rhizobium leguminosarum* bv.
trifolii WSM2304
MQTKALSRRQLLLGHDPASEPDASTSLPHTAMVTEACLSRRGVACRSCDESCPENAIRF
RPRIGGPFLPEIDETLCTGCDACLAICPVGAIA TRINGLEGRNA

Subtype 5

>2[4Fe-4S]ST5(rpa:RPA4612) *Rhodopseudomonas palustris* CGA009
MAIFSTRDGKPWEPTYLTAIDDKKCIGCGRCHKVCSRDMHLMGVNEDGELVACSLDDDD
DDEEFVRKVMVLDAAGNCIGCSACVRVCPKACQTHVKASELGL
>2[4Fe-4S]ST5(rpt:Rpal_5093) *Rhodopseudomonas palustris* TIE-1
MAIFSTRDGKPWEPTYLTAIDDKKCIGCGRCHKVCSRDMHLMGVNEDGELVACSLDDDD
DDEEFVRKVMVLDAAGNCIGCSACVRVCPKACQTHVKASELGL

>2[4Fe-4S]ST5 (rpx:Rpx1_4790) *Rhodopseudomonas palustris* DX-1
MAIFSTRDGPWEPTYLTAIDDKKICGCRCHKVCSRDMHLMGVNEDGELVGCSLDDDD
DDEEFVRKVMVLDSAGNCIGCSACVRVCPKACQTHVKASELGL

Subtype 6

>2[4Fe-4S]ST6 (ngl:RG1141_PB00800) *Neorhizobium galegae* bv.
officinalis bv. officinalis HAMBI 1141
MAFKIVTSQCSQCGACEFVCPSGAVALKGEHYVIDPRKCTECEGFGTQQCAAACPMKCTC
VPA
>2[4Fe-4S]ST6 (ngg:RG540_PA10570) *Neorhizobium galegae* bv.
orientalis HAMBI 540
MAFKIVTSQCSQCGACEFVCPSGAVALKGENYVIDPRKCTECDEFGTQQCAAACPMKETC
VPA

Subtype 7

>2[4Fe-4S]ST7 (mbry:B1812_06580) *Methylocystis bryophila*
MAYRIIASQCTACGACEFECPNGAIRMKGETYIIDAGKCTECDGDGPRCVCVECPVENTCV
RA
>2[4Fe-4S]ST7 (mgy:MGMSRv2__0355) *Magnetospirillum*
gryphiswaldense MSR-1 v2
MALKITTTSTCSACGACEFECPNAAIAMKGETYVIKASACSECDGDDPKCIAVCPVENCIV
KA

Subtype 8

>2[4Fe-4S]ST8 (abq:ABAZ39_29555) *Azospirillum brasilense* Az39
MIELISPTRCTGCNICVSIKPMDFVQTASGQAKGAAPVIARQSDCQTCFLCEAHCDDAL
YVAPDAETVTGIAEEAVAAAGLFGSYRRAIGWSNGHRDNRSADQTFRLAPH

>2[4Fe-4S]ST8 (aak:AA2016_5898) *Aminobacter aminovorans*

MRQVTRGTLVIDADRCKGCELCIVACPPRVLTMSRTGNATGYLYPELAPGCTGCTACQQVCP
DFVFEVYKYHEPIVSGSDAERMQ

Subtype 9

>2[4Fe-4S]ST9 (rpd:RPD_1511) *Rhodopseudomonas palustris* BisB5
MSSHrayPMFDPGQAGVPDDLCPiATDINPMLPGDWRSMPVVDREKCVKCAVCWLYCPV
QCMVERPAWFDVDLRTCKGCGICANECPHRAIAMVEETAG

Subtype 10

>2[4Fe-4S]ST10 (magq:MGMAQ_3495) *Magnetospira* sp. QH-2

MPTFVYMTRCDGCGHCVDICPSDIMHIDKTYRRAYNIEPNMCWECYSCVKACPQNAIDVRGY
ADFAPLGHSVRVRDEEEKGVIAWRIKFRNGKKDLNLLAPITTKPWGTCIPQLKNAPEPSKEQ
RDSQLLYNEPKYIRMDDGDLHTLESNGLVMKEGVYY

>2[4Fe-4S]ST10 (fil:BN1229_v1_3251) *Candidatus* *Filomicrobium*
marinum W

MPTFVYMTRCDGCGHCVDICPSDIMHIDPTYRRAYNIEPNMCWECYSCVKACPQNAIDVR
GYADFAPLGHSVRVQRDEERGTTIAWKIKYRNGTEKEFLSPITTKPWGKHIPKLADVPAPS
RDMRDSELLYNEPKWIRMDDGLRTLKDAGLVLLKKGvYY

>2[4Fe-4S]ST10 (fiy:BN1229_v1_2672) *Candidatus* *Filomicrobium*
marinum Y

MPTFVYMTRCDGCGHCVDICPSDIMHIDPTYRRAYNIEPNMCWECYSCVKACPQNAIDVR
GYADFAPLGHSVRVQRDEERGTTIAWKIKYRNGTEKEFLSPITTKPWGKHIPKLADVPAPS
RDMRDSELLYNEPKWIRMDDGLRTLKDAGLVLLKKGvYY

>2[4Fe-4S]ST10 (aace:A0U92_03265) *Acetobacter aceti*

MITEILSDRCNSCNACVVVCPDHVLDMAKDGQLPVIARPDQCQTCFLCELYCSEDAIYVAVG
VPRSELKNDPLGNIRRDYGWDGHEEDPLKNFWQLGGLLREGVMISSARYALRPSGDKDTEKK
I

>2[4Fe-4S]ST10(bid:Bind_3084) *Beijerinckia indica*

MIVHIFEDLCTGCNACVAACPTHVLDPAEAGRVPLIARQDQCQTCFMCELYCEKDAIYVGPI
QQGPEPVDPELIRKSGLLGQLRRDYEWDA GPDDPAPLREFWRLGP LLMEGAQTAEKRYEERH
PESAALPPR

>2[4Fe-4S]ST10(otm:OSB_13110) *Octadecabacter temperatus*

MSKKLPKPDTQKPAASVVNIDYDLCINCAICIRSCPVDVLRINRETRWLEATYWEDCMLCK
LCELDCPEPGAITISADKPLGFAMSG

Subtype 11

>2[4Fe-4S]ST11(rmm:ROSMUCSMR3_02763) *Roseovarius mucosus*

MWYELRDRSLPSSEGHAVLPRPPGTVREWRLADMCTGCGDCVAVCPKAIVALDKEVLPVVT
IDACGRCGLCADVCTRGAIELTKETRLGLERILKGDGLGQRAG

Subtype 12

>2[4Fe-4S]ST12(rpa:RPA4257) *Rhodopseudomonas palustris* CGA009

MIGFGWLEALLRVGRKLFVKPETQLYPEQKPKLYPRARGRIVLTRDPDGQERCVACNLCA
TVCPVGCIDLAKAVADDGRWYPEYFRVNFARCIFCGFCEDACPTAAIQLTPDYELSEWRR
DALVYEKHDLLISGEGKVRGYRYWSVAGKAIPGKDKGEAEHEAPPVNLKGLLP

>2[4Fe-4S]ST12(rpb:RPB_1354) *Rhodopseudomonas palustris* HaA2

MIGWLEAMLRVGRKLFVKAETQLYPEEKPKLFPRSRGRIVLTRDPDGQERCVACNLCAAV
CPVGCIDLSKAVADDGRWYPEHFRINFARCIFCGFCEEACPTAAIQLTPDFELGEWRRDA
LVYEKHDLLIAGEGKVRGYRYWSVAGKAIDGKDKGCAENESPPVDLKGLLP

>2[4Fe-4S]ST12(rpd:RPD_1333) *Rhodopseudomonas palustris* BisB5

MIGWLEAMLRVGRKLFVKAETQLYPEEKPPLYPRSRGRIVLTRDPDGQERCVACNLCAVV
CPVGCIDLTAKAVADDGRWYPEHFRINFARCIFCGFCEEACPTSAIQLTPDFELGEWRRDA
LVYEKHDLLISGEGKVRGYRYWSVAGKAIDGKDKGEAEHESPPVDLRGLLP
>2[4Fe-4S]ST12(rpe:RPE_1717) *Rhodopseudomonas palustris* BisA53

MKGFGWLEGLLRVGRKLFVKAETVQYPEVRPYLPFRSRGRIVLTRDPDGQERCVACNLCA
VACPVGICIDLAKAVAEDGRWYPEHFRINFARCIFCGYCEEACPTAAIQLTPDFELSEWRR
DALVYDKHDLLIAGEGKVRGYRYWSVAGKAIQKDKGEADHEAPPVDLKGLLP

>2[4Fe-4S]ST12(rpt:Rpal_4736) *Rhodopseudomonas palustris* TIE-1

MIGFGWLEALLRVGRKLFVKPETQLYPEQPKPLYPRARGRIVLTRDPDGQERCVACNLCA
TVCPVGICIDLAKAVADDGRWYPEHFRVNFARCIFCGFCEDACPTAAIQLTDPDYELSEWRR
DALVYEKHDLLISGEGKVRGYRYWSVAGKAIPGKDKGEAEHEAPPVNLKGLLP

>2[4Fe-4S]ST12(rpx:Rpx1_4476) *Rhodopseudomonas palustris* DX-1

MIGFGWLEALLRVGRKLFVKPETQLYPEEKPPLYPRARGRIVLTRDPDGQERCVACNLCA
TVCPVGICIDLSKAVADDGRWYPEHFRVNFARCIFCGFCEDACPTAAIQLTDPDYELSEWRR
DALVYEKHDLLISGEGKVRGYRYWSVAGKAIPGKDKGEAEHEAPPVNLKGLLP

>2[4Fe-4S]ST12(rpc:RPC_4064) *Rhodopseudomonas palustris* BisB18

MIGWLEALLRVGRKLAAKTVTVQYPEVKPQLPFRSRGRIVLTRDPDGQERCVACNLCAVA
CPVGCIDLSKAVAEDGRWYPEHFRINFARCIFCGYCEEACPTAAIQLTPDFELSEWRRDA
LVYDKKDLLIAGEGKVRGYRYWSVAGKAITGKDKGDAEHEAPPVDLKGLRP

>2[4Fe-4S]ST12(rsp:RSP_0107) *Rhodobacter sphaeroides* 2.4.1

MKGILDSILRVGRMIFAPTKTVQYPEEKLPLAPRTRGRIVLTRDPDGQERCVACNLCAAA
CPVDCIDVVKAEPTDGRWYPEFRINFARCIFCGYCEEACPTSAIQLTDPVELADYRRGF
LQYEKEDLLISGEGKHGPGYRYWDVAGKAIAGKAQDPVDPKDLCP

>2[4Fe-4S]ST12(rsh:Rsph17029_1743) *Rhodobacter sphaeroides* ATCC 17029

MKGILDSILRVGRMIFAPTKTVQYPEEKLPLAPRTRGRIVLTRDPDGQERCVACNLCAAA
CPVDCIDVVKAEPTDGRWYPESFRINFARCIFCGYCEEACPTSAIQLTPDVELADYRRGF
LQYEKEDLLISGEGKHHPGYRYWDVAGKTIAGKAQDPVDPKDLCP

>2[4Fe-4S]ST12(rsk:RSKD131_1424) *Rhodobacter sphaeroides* KD131

MKGILDSILRVGRMIFAPTKTVQYPEEKLPLAPRTRGRIVLTRDPDGQERCVACNLCAAA
CPVDCIDVVKAEPTDGRWYPESFRINFARCIFCGYCEEACPTSAIQLTPDVELADYRRGF
LQYEKEDLLISGEGKHHPGYRYWDVAGKAIAGKAQDPVDPKDLCP

>2[4Fe-4S]ST12(rsq:Rsph17025_1696) *Rhodobacter sphaeroides* ATCC 17025

MKGILDSILRVGRMVFAPTKTVEYPEVKLPLAPRTRGRIVLTRDPDGQERCVACNLCAAA
CPVDCIDVVKAEPTDGRWYPESFRINFARCIFCGYCEEACPTSAIQLTPDVELADYRRGS
LQYEKEDLLISGEGKHHPGYRYWDVAGKAIAGKQSDPVDPKDLCP

>2[4Fe-4S]ST12(rga:RGR602_PC00808) *Rhizobium gallicum*

MSRAQDRIGTWIGWAFFADLAKALALTFGYMFARSVTMQYPDKEKWLPYPRYRGHHFLTRDE
EGEIKCVACELCARICPCDCIEVIPYEDEKGRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSFSSRDLVIGRDDLLAKPGKAATGGGVIAARLNTEKDVIVETKETQGYNWW
RNIRRT

>2[4Fe-4S]ST12(rpha:AMC79_CH03559) *Rhizobium phaseoli*

MSRAQDRIGTWIGWTFADLANALTTLGYMFARPVTMQYPDREKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVYPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSFSSADLVIGRDDLLAKPGKAATGGGVVTARLNTKKDVLVETKEMQGYN
WWRNIRRT

>2[4Fe-4S]ST12(ret:RHE_CH03744) *Rhizobium etli* CFN 42

MSRAQDRIGTWIGWTFADLANALTTLFGYMFSSPVTMQYPDTEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSADLVIGRDDLLAKPGKAATGGGVVSARLNTKKDVLVETKEMQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rec:RHECIAT_CH0003640) *Rhizobium etli* CIAT 652

MSRAQDRIGTWIGWTFADLANALTTLGMYFARPVMTMQYPDREKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSADLVIGRDDLLAKPGKAATGGGVVTAHLNTKKDVLVETKEMQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rel:REMIM1_CH03823) *Rhizobium etli* bv. *mimosae*
Mim1

MSRAQDRIGTWIGWTFADLANALTTLFGYMFSSPVTMQYPDTEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSADLVIGRDDLLAKPGKAATGGGVVSARLNTKKDVLVETKEMQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rep:IE4803_CH03631) *Rhizobium etli* bv. *phaseoli*
IE4803

MSRAQDKVGTWIGWAFFADLASALVLTFGYLFSTRVTMQYPDKEKWLPYSRYRGHHFLKR
DEGGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAATGGGVVTARLTTKKDVLVETKEMQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rei:IE4771_CH03668) *Rhizobium* sp. IE4771

MSRAQDKAGRWIGWAFFADLANGLALTFGYLFSTRVTMQYPDKEKWLPYSRYRGHHFLKR

DEAGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAATGGGVVTARLNTKKDVLVETKEKQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rlu:RLEG12_28990) *Rhizobium leguminosarum* bv.
trifolii CB782

MSRAQDRVGTWIGWAFFADLASALALTFGYLFSRTVTMQYPDKEKWLPYSRYRGHHFLTR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAATGGGVVAARLNTTKDVLVETKDTKGYN
WWRNIRRT

>2[4Fe-4S]ST12(rhn:AMJ98_CH03609) *Rhizobium* sp. N1341

MSRAQDRVGTWIGWAFFADLANALALTFGYLFSRTVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSADLVIGRDDLLVKPSKAATGGGVVAARLNTKKDVLVQTKETQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rhx:AMK02_CH03497) *Rhizobium* sp. N731

MSRAQDRVGTWIGWAFFADLANALALTFGYLFSRTVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSADLVIGRDDLLVKPGKAATGGGVVAARLNTKKDVLVQTKETQGYN
WWRNIRRT

>2[4Fe-4S]ST12(rhl:LPU83_pLPU83d0711) *Rhizobium favelukesii*

MSRARNSIGTWIGWTFADLASGLALTFSYMFSSVMTMQYPDKEKWLPYSRYRGHHFLTR
DEEGEIKCVACELCARICPCDCIEVVPYEDEKGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVVGRDDLLSKPGKAATGGGVIAARLNTKKDVLVETKETQGYN
WWRNIRRT

>2[4Fe-4S]ST12(smx:SM11_pC0823) *Sinorhizobium meliloti* SM11

MPSRKLWARTCKTTLSRSEAAMSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTM
QYPDKEKWLPYSRYRGHHFLKRDDEGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPA
KFEIDTARCLFCGLCEDACPADAIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGV
VAARLNTERDVLVEASEPRGYNWWRNIRRK

>2[4Fe-4S]ST12(smi:BN406_04563) *Sinorhizobium meliloti* Rm41

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDEGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(smeg:C770_GR4pC0549) *Sinorhizobium meliloti* GR4

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDEGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(smel:SM2011_a1519) *Sinorhizobium meliloti* 2011

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDEGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(smer:DU99_21870) *Sinorhizobium meliloti* RM017

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDEGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(sm:Sinme_6021) *Sinorhizobium meliloti* AK83

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDDGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(sm:SinmeB_6340) *Sinorhizobium meliloti* BL225C

MSRALDKAGRWIGWAFFADLANGLALTFGYMF SRPVTMQYPDKEKWLPYSRYRGHHFLKR
DDDGEIKCVACELCARICPCDCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGGVVAARLNTERDVLVEASEPRGYN
WWRNIRRK

>2[4Fe-4S]ST12(sm:Smed_3615) *Sinorhizobium medicae*

MHAAQKLWVRTCKKTLRSRSEAAMSHALDKAGRWIGWAFFADLANGLALTFGYMF SKPVT
MQYPDKEKWLPYSRYRGHHFLKRDAEGEIKCVACELCAQICPCDCIEVVPYEDEKGNRRP
AKFEIDTARCLFCGLCEDACPADAIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAMTGGG
VVAARLSTERDVLVEASEPRGYNWWRNIRRK

>2[4Fe-4S]ST12(sf:SFHH103_02098) *Sinorhizobium fredii* HH103

MSRARDTIGTWIGWTFADLANGLALTFGYMF SKSVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCYCIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLAKPGKAATGGGVVAARLNTQKDVLVETDEQQGYN
WWRNIRRR

>2[4Fe-4S]ST12(ea:FA04_27760) *Ensifer adhaerens* Casida A

MSRVVDRAGTWIGWALFADLASAFTLTFGYMF SKPVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCDCIEVVPYEDENGNRHPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSSFSSRDLVIGRDDLLEKPGKAMAGGVVAARLNTDEDVLVETSEPHGYN
WWRNIRRT

>2[4Fe-4S]ST12(ead:OV14_b1479) *Ensifer adhaerens* OV14

MFFADLAKALALTFGYMFSKSVTMQYPDKEKWLPYSRYRGHHFLKRDDQGEIKCVACELC
ARICPCYCIIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPADAIALGQQYEFSSFS
SRDLVIGRDDLKGKPGKATTGGGVVAAHLNTDGDVLVETSELQGYNWWRNIRRT

>2[4Fe-4S]ST12(same:SAMCFNEI73_Ch2563) *Sinorhizobium Americanum*

MSRAQDMIGTWIGWTTFFADLAKGLGLTFGYMFSKTVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCYCIIEVVPYEDEKGNRRPIKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSFSRDLVIGRDDLAKPGKAATGGGVVAAARLNTENDVLVETNEPQGYN
WWRNIRRR

>2[4Fe-4S]ST12(sfd:USDA257_c45940) *Sinorhizobium fredii* USDA
257

MSRAQDIIGTWIGWTTFFADLANGLALTFGYMFSRTVTMQLPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCYCIIEVVPYEDDKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSFSRDLVIGRDDLAKPGKAATGGGVVAAARLNTTKDVLVESNERQGYN
WWRNIRRR

>2[4Fe-4S]ST12(rhi:NGR_c22040) *Sinorhizobium fredii* NGR234

MSRPRDTIGTWIGWTTFFADLATGLALTFGYMFSKTVTMQYPDKEKWLPYSRYRGHHFLKR
DEEGEIKCVACELCARICPCYCIIEVVPYEDEKGNRRPAKFEIDTARCLFCGLCEDACPAD
AIALGQQYEFSSFSRDLVIGRDDLAKPGKAATGGGVVAAARLNTQKDVLVETDERQGYN
WWRNIRRK

>2[4Fe-4S]ST12(pde:Pden_2238) *Paracoccus denitrificans*
MAFDFARATKYFLMWDFIKGFGGLMRYFVSPKPTLNYPHEKGPLSPRFRGEHALRRYPNG
EERCIACKLCEAVCPAQAITIDAEPRDGSRRRTTRYDIDMTKCIYCGFCQEACPVDAIVE
GPNFEYATETREELFYDKQKLLANGERWEAEIARNLQLDAPYR

>2[4Fe-4S]ST12(ccr:CC_1942) *Caulobacter vibrioides* CB15
MFQRITQAVKGAALLDFAGAFGLAMKYMVAPKKTVIYPNERNPQSPRFRGEHALRRYPNG
EERCIACKLCEAICPAQAITIEAEPRDGSRRRTTRYDIDMVKCIYCGLCQEACPVDAIVE
GPNTFATETREELYDKERLLDNGDRWERLIAKNLELDAPYR

>2[4Fe-4S]ST12(ccs:CCNA_02020) *Caulobacter vibrioides* NA1000
MFQRITQAVKGAALLDFAGAFGLAMKYMVAPKKTVIYPNERNPQSPRFRGEHALRRYPNG
EERCIACKLCEAICPAQAITIEAEPRDGSRRRTTRYDIDMVKCIYCGLCQEACPVDAIVE
GPNTFATETREELYDKERLLDNGDRWERLIAKNLELDAPYR

>2[4Fe-4S]ST12(cak:Caul_2824) *Caulobacter* sp. K31
MMMQRISQAIKGVALLDFAGAFGLGIKYMLAPKKTVIYPNERGPQSPRFRGEHALRRYPS
GEERCIACKLCEAICPAQAITIEAEPRDDGSRRRTTRYDIDMVKCIYCGLCQEACPVDAIV

EGPNIEFAVETREELYDKEKLLDNGDRWERLIAKNLELDAPYR

>2[4Fe-4S]ST12(cse:Cseg_2229) *Caulobacter segnis*
MFQRITQAVKGAALLDFAGAFGLAMKYMVAPKKTIVYPNERNPQSPRFRGEHALRRYPNG
EERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMVKCIYCGLCQEACPVD AIVE
GPNIEFATETREELYDKERLLDNGDRWERLIAKNLELDAPYR

>2[4Fe-4S]ST12(pzu:PHZ_c1796) *Phenylobacterium zucineum*
MLNRIGQAVKGAALLDFAGAFGLAMKHMAPKKTIVQYPHERNPQSPRFRGEHALRRYPNG
EERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMVKCIYCGLCQEACPVD AIVE
GPNLEFAVETREELYDKERLLDNGDRWEREIAKNLELDAPYR

>2[4Fe-4S]ST12(aex:Astex_2812) *Asticcacaulis excentricus*
MIGRLVQAAKGALLLDFVGATGLAVKYMFKPKKTINYPFEKGPISPRFRGEHALRRYPNG
EERCIACKLCEAICPAQAITIEAEPREDGSRRTTRYDIDMVKCIYCGLCQEACPVD AIVE
GPNFEFATDTREELYDYSKLLANGDRWEREIAALELDAPYR

>2[4Fe-4S]ST12(mmr:Mmar10_1363) *Maricaulis maris*
MGRIQQAFRGALLMDFWSAFGLGMRYFFAKKATLNYPFEKGPLSPRFRGQHALRRYANGE
ERCIACKLCEAICPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGYCQEACPVD AIVEG
PNFEFAAETREELFYDKAKLLENGDRWEREIAKNLELDAPYR

>2[4Fe-4S]ST12(hne:HNE_1753) *Hyphomonas neptunium*
MSLAQTLRGALLTDFMGAAWIAVREMFRRKATVNYPFEKNPLSPRFRGEHVLRYPNG
RCIACKLCEAICPAQAITIEAEPREDGARRTTRYDIDMVKCIYCGFCQEACPVD AIVEGP
NFEFATETREELFYDKERLLANGDRWERLIAKNLELDAPYR

>2[4Fe-4S]ST12(hba:Hbal_1732) *Hirschia baltica*
MSRISQAIKGAMLSDIVSALGLALRYMFTRKATVNYPFEKGPLSPRFRGEHALRRYANGE
ERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD AIVEG
PNFEFSTETREELFYDKDRLLSNGDRWERQIAKNLELDARYR

>2[4Fe-4S]ST12(hbc:AEM38_05520) *Hyphomonadaceae bacterium*
UKL13-1
MSIAQALKGALMLDFAGAFGLAMKKFFEPKFTINYPFEKGHISPRFRGEHALRRYANGEE
RCIACKLCEAICPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD AIVEGP
NFEFATETREELFYDKDKLLANGDRWEREIAKNLELDAAAYR

>2[4Fe-4S]ST12(rsp:RSP_2523) *Rhodobacter sphaeroides* 2.4.1
MARTSAIDYGRAAKYFLLLD FIKGFGLGMKYFFAPKHTVNYPHEKGPLSPRFRGEHALRR
YPNGEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD
AIVEGPNFEFSTETREELFYNDRLLENGARWEAEIARNLELDAPYR

>2[4Fe-4S]ST12(rsh:Rsph17029_1185) *Rhodobacter sphaeroides* ATCC
17029
MARTSAIDYGRAAKYFLLLD FIKGFGLGMKYFFAPKHTVNYPHEKGPLSPRFRGEHALRR
YPNGEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD
AIVEGPNFEFSTETREELFYNDRLLENGARWEAEIARNLELDAPYR

>2[4Fe-4S]ST12(rsq:Rsph17025_1997) *Rhodobacter sphaeroides* ATCC
17025
MARTGAIDYGRAVKYFLLLD FIKGFGLGMKYFFAPKHTLNYPHEKGPLSPRFRGEHALRR
YPNGEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD
AIVEGPNFEFSVETREELFYTKKLLQNGDRWEAEIARNLELDAPYR

>2[4Fe-4S]ST12(rsk:RSKD131_0838) *Rhodobacter sphaeroides* KD131
MARTSAIDYGRAAKYFLLLD FIKGFGLGMKYFFAPKHTVNYPHEKGPLSPRFRGEHALRR
YPNGEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD
AIVEGPNFEFSTETREELFYNDRLLENGARWEAEIARNLELDAPYR

>2[4Fe-4S]ST12(pami:JCM7686_2499) *Paracoccus aminophilus*
MALDLARATKYFLMWDFLKGFGGLGMRYFFSPKPTLNYPHEKGPLSPRFRGEHALRRYPNG
EERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVD AIVE

GPNFEYSTETREELFYDKKLLDNGARWEAEIARNLAMDAPYR
 >2[4Fe-4S]ST12(pye:A6J80_15510) *Paracoccus yeei*
 MAFDFARATKYFLMWDFIKGFGLGMRYFVSPKPTLNYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEYATETREELFYDKQKLLDNGARWEAEIARNLQMDAPYR
 >2[4Fe-4S]ST12(cid:P73_3435) *Celeribacter indicus*
 MALDYTRAAKYFLMTDIWTGFKIGLRYFFAPKATINYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEFSTETREELFYDKQKLLDNGARWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(cmar:IMCC12053_2424) *Celeribacter marinus*
 MAMDYTRAAKYFLMTDIIAGFRIGLRYFFSPKVTINYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRDDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEFATESREELFYDKDKLLDNGARWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(con:TQ29_06380) *Confluentimicrobium* sp. EMB200-
 NS6
 MAIDYTRATRYFLLADDFINGFRLGFKYFFAPKATINYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEFSTETREELFYDKAKLLENGEQWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(daa:AKL17_2228) *Defluviimonas alba*
 MALDYTRAAKYFLMDFIKGFGLGMKYFFAPKETLNYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEFSTETREELFYDKARLLDNGARWEAEIARNLEMDAPYR
 >2[4Fe-4S]ST12(yan:AYJ57_02660) *Yangia* sp. CCB-MM3
 MASIDYGRAAKYFLLADDFIKGFQGLGLKYFFAPKPTLNYPHEKGYLSPRFRGEHALRRYPN
 GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIV
 EGNPFESTETREELFYDKDKLLANGERWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(tpro:Ga0080559_TMP4774) *Salipiger profundus*
 MTQIDYGRAAKYFLLDFIKGFQGLGLRYFFAPKPTLNYPHEKGYLSPRFRGEHALRRYPN
 GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIV
 EGNPFESTETREELFYDKKLENGERWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(paby:Ga0080574_TMP4554) *Pelagibaca abyssi*
 MTQIDYGRAAKYFLLADDFIKGFALGMKYFFAPKPTLNYPHEKGPLSPRFRGEHALRRYPN
 GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIV
 EGNPFESTETREELFYDKQKLENGERWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(thw:BMG03_08295) *Thioclava nitratreducens*
 MAFDYNRAAKYFLLVDFIKGFGLGMRYFFAPKPTLNYPHEKGPLSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIDAEPRADGSRRTRYDIDMTKCIYCGFCQEACPVDIAIVE
 GPNFEFSTETREELFYDKQKLENGARWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(sil:SPO2770) *Ruegeria pomeroyi*
 MTQIDYTRAAKYFLLQDFWVGMLGLKYFFSPKATINYPHEKGPLSPRFRGEHALRRYPN
 GEERCIACKLCEAICPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIV
 EGNPFESTETREELFYDKKLLSNGDRWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(sit:TM1040_0754) *Ruegeria* sp. TM1040
 MTQIDYTRAAKYFLLQDVWQGFKLGLKYFFAPKATINYPHEKGPLSPRFRGEHALRRYPN
 GEERCIACKLCEAVCPAQAITIDAEPRDGSRRTRYDIDMTKCIYCGFCQEACPVDIAIV
 EGNPFESTETREELFYDKDKLLANGERWEAEIARNLELDAPYR
 >2[4Fe-4S]ST12(rcp:RCAP_rcc01531) *Rhodobacter capsulatus*
 MAFDYVRAAKYFVLWDFIKGFALGMKYFVAPKPTLNYPHEKGPLSPRFRGEHALRRYPSG
 EERCIACKLCEAICPAQAITIDAEPRDDGSRRTRYDIDMTKCIYCGYCQEACPVDIAIVE
 GPNFEYATETREELFYTKKLENGARWEAEIARNIEMDAPYR
 >2[4Fe-4S]ST12(rli:RLO149_c024940) *Roseobacter litoralis*

MTQIDYARHAKYFLLQDFWVGMKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCEEACPVDAIV
EGPNFEFSTETREELYDKDRLLANGERWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(pga:PGA1_c10490) *Phaeobacter inhibens* DSM 17395
MANIDYTRAAKYFLLQDFWVGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKDKLLSNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(pgl:PGA2_c10330) *Phaeobacter inhibens* 2.10
MANIDYTRAAKYFLLQDFWVGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKEKLLSNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(pgd:Gal_02444) *Phaeobacter gallaeciensis* DSM
26640
MANIDYTRAAKYFLLQDFWVGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKDKLLSNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(php:PhaeoP97_01020) *Phaeobacter porticola*
MANIDYTRAAKYFLLQDFWVGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKDKLLSNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(lmd:METH_12100) *Leisingera methylohalidivorans*
MTQIDYTRAAKYFLLQDFWVGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKDKLLANGDRWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(rsu:NHU_01353) *Rhodovulum sulfidophilum*
MAAIDWQRAGKYFLLMDFLQGFR LGMKYFFAPKATLSYPHEKGPLSPRFRGEHALRRYPS
GEERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKQKLLNGDRWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(rhc:RGUI_0424) *Rhodovulum* sp. P5
MAAIDWTRAGKYFLLMDFLEGMR LGMKYFLAPKATVNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKQKLLDNGERWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(tom:BWR18_08725) *Tateyamaria omphalii*
MTQIDYGRAAKYFLLQDFWVGMKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFSTETREELYDKEKLLNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(jan:Jann_1187) *Jannaschia* sp. CCS1
MTQIDYTRAAKYFLLADFFKGFK LGMKYFFAPKVTINYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELYDKEKLLANGERWESAIAHNLELDAPYR
>2[4Fe-4S]ST12(rde:RD1_3275) *Roseobacter denitrificans*
MTQVDYTRAAKYFLLQDFWVGMK LGMKYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCEEACPVDAIV
EGPNFEFSTETREELYDKDRLLANGERWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(dsh:Dshi_1322) *Dinoroseobacter shibae*
MAQMDYTRAAKYFLLFDFFAGFK LGKLYFFKPKATLAYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV
EGPNFEFATETREELFYDKEKLLDNGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(oar:OA238_c28590) *Octadecabacter arcticus*
MTEIDYTRAAKYFLLADFAKGFRLGFKYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIV

EGPNFEFSTETREELYDKEKLLDNGDRWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(otm:OSB_20590) *Octadecabacter temperatus*
MSQIDYTRHAKYFLMTDIIKGFALGFKYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFSTETREELYDKEKLLDNGDRWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(red:roselon_00176) *Roseibacterium elongatum*
MTQIDYTRAAKYFLLADFFKGMKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAVCPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATETREELYD KAKLLENGERWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(ptp:RCA23_c13650) *Planktomarina temperata*
MANIDYTRRVKYFLLQDFWAAFKLGMYFFRPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFSTETREELFYDKSKLLENGDRWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(malg:MALG_02350) *Marinovum algicola*
MADIDYGRAAKYFLLTDFIQGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHVLRRYPN
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATETREELFYDKAKLLENGDRWEAEIAANLAVDAPYR
>2[4Fe-4S]ST12(suam:BOO69_06655) *Sulfitobacter* sp. AM1-D1
MTQIDYSRAAKYFLLQDFAKGFALGFKQMFPRPKATVNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFSTETREELYD KAKLLANGERWEAEIARNLELDAPYR
>2[4Fe-4S]ST12(lvs:LOKVESSMR4R_01791) *Yoonia vestfoldensis*
MSKTNMDYTRAAKYFLLQDFWVGFKLGMYFFAPKATLNYPHEKGPLSPRFRGEHALRRY
PNGEERCIACKLCEAVCPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
IVEGPNFEFSTETREELYD KAKLLENGDRWESEIARNLALDAPYR
>2[4Fe-4S]ST12(kvu:EIO_2274) *Ketogulonicigenium vulgare* Y25
MSQIDYTRAAKYFLLKDVWDGFR LGMYFFRPRPTVNYPHEKVPLSPRFRGEHALRRYPS
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATESREELFYDKDKLLANGDKWEAEIARNLAADAPYR
>2[4Fe-4S]ST12(kvl:KVU_1815) *Ketogulonicigenium vulgare* WSH-001
MSQIDYTRAAKYFLLKDVWDGFR LGMYFFRPRPTVNYPHEKVPLSPRFRGEHALRRYPS
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATESREELFYDKDKLLANGDKWEAEIARNLAADAPYR
>2[4Fe-4S]ST12(kro:BVG79_01879) *Ketogulonicigenium robustum*
MSQIDYTRAAKYFLLKDVWDGFR LGMYFFRPRPTVNYPHEKVPLSPRFRGEHALRRYPS
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATESREELFYDKDRLLANGDKWEAEIARNLAADAPYR
>2[4Fe-4S]ST12(rmm:ROSMUCSMR3_00221) *Roseovarius mucosus*
MTKIDYGRAAGYFLLSDFFKGFKLGKLYFFAPKATLNYPHEKGPLSPRFRGEHALRRYPN
GEERCIACKLCEAICPAQAITIDAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
EGPNFEFATETREELFYDKARLLANGDRWEAEIARNLEMDAPYR
>2[4Fe-4S]ST12(nar:Saro_2292) *Novosphingobium aromaticivorans*
MTVGQLIKSFTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEE
RCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
NFEYATETREELLYDKAKLLSNGDKWERAIAANLEADAPYR
>2[4Fe-4S]ST12(4npp:PP1Y_AT27349) *Novosphingobium* sp. PP1Y
MTVGHLIKSFTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAAPRADGSRRTTRYDIDMTKCIYCGFCQEACPVDIV
NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
>2[4Fe-4S]ST12(npn:JI59_02950) *Novosphingobium*
pentaromativorans

MTVGHLIKSFTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITIEAAPRADGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(eli:ELI_06625) *Erythrobacter litoralis* HTCC2594
 MTTATQLLKSFTLWEFLKAHALTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEYSTETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(elq:Ga0102493_112422) *Erythrobacter litoralis*
 DSM 8509
 MTTATQLLKSFTLWEFLKAHALTLKYFFKPKVTINYPFEKSPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEYSTETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(aep:AMC99_01251) *Altererythrobacter*
epoxidivorans
 MTVGQLIKSFTLWEFVKAHALTLKYFFKPKVTINYPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITIESEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(anh:A6F65_01798) *Altererythrobacter namhicola*
 MTALQLLKSFTLWEFVKAHALTLKYFFKPKVTINYPYEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(cna:AB433_08100) *Croceicoccus naphthovorans*
 MTALQLIKSYTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(sal:Sala_1301) *Sphingopyxis alaskensis*
 MSYVGHLVKSFTLWEFVKAHALTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEYATETREELLYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sphk:SKP52_08520) *Sphingopyxis fribergensis*
 MTTIAHIVKSFTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEFATETREELLYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sphp:LH20_11430) *Sphingopyxis* sp. 113P3
 MSSIAHFVKTFTLWEFVQAHWLTLYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEFSTETREELLYDKAKLLANGDKWERTIAANLAADAPYR
 >2[4Fe-4S]ST12(smaz:LH19_09475) *Sphingopyxis macrogoltabida* 203
 MSYVAHLVKSFTLWEFVKAHALTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEFATETREELLYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(ster:AOA14_15315) *Sphingopyxis terrae*
 MSYVAHLVKSFTLWEFVKAHALTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAVPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEFATETREELLYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sgi:SGRAN_2176) *Sphingopyxis granuli*
 MSNIAHLVRTFTLWEFVQAHWLTLYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIEAEPREDGSRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
 PNFEFATETREELLYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sph1:LPB140_07145) *Sphingopyxis* sp. LPB0140
 MSNISHLIKSTLWEFAKAHWLTLKYFFKPKATINYPFEKNPISPRFRGEHALRRYPNGE

ERCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIFCGFCQEACPVDVAVEG
 PNFEYATETREELLYDKAKLLENGDKWEQAIANLAADAPYR
 >2[4Fe-4S]ST12(sphi:TS85_08835) *Sphingomonas* sp. WHSC-8
 MSVAQIIRSFTLWEFLKAHWLTLQYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPALAITIEAEPRDDGSRRTTRYDIDMTKCIYCGLCQEACPVDVAIVEGP
 NFEFSTETREELIYQKEKLLANGDRWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(cij:WG74_10875) *Citromicrobium* sp. JL477
 MSIAQTIKAFTLYEFVKAHALTLKYLFKPKVTINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIESEPRADGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYSTETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(sphg:AZE99_06140) *Sphingorhabdus* sp. M41
 MNIAQTIKAFTLWEFIGAHMLTLKYFFKAKKTINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYATETREELIYDKSKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(blas:BSY18_872) *Blastomonas* sp. RAC04
 MLQTLKAFTLYEFVKAHALTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEERC
 IACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIFCGFCQEACPVDVAIVEGP
 EYATETREELIYDKGKLENGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(aay:WYH_00626) *Altererythrobacter atlanticus*
 MSVAQLVKSFTLWEFLKAHSLTLKYFFKPKATINYPYEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYSTETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(amx:AM2010_1299) *Altererythrobacter marensis*
 MSVAHLIKSFTLWEFVKAHALTLKYFFKPKATINYPFEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(ado:A6F68_02231) *Altererythrobacter dongtanensis*
 MTIAHLIKSFTLWEFVKAHALTLKYFFKPKATVNPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(pns:A9D12_12635) *Porphyrobacter neustonensis*
 MTSVSHLIKSTLWEFLKAHALTLKYFFRKPVTINYPFEKAPLSRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIFCGFCQEACPVDVAIVEG
 PNFEYSTETREELLYDKAKLLSNGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(porl:BG023_112022) *Porphyrobacter* sp. LM 6
 MTTVSHLIKSTLWEFLKAHALTLKYFFKPKVTINYPFEKAPLSRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIESEPRDDGSRRTTRYDIDMTKCIFCGFCQEACPVDVAIVEG
 PNFEYATETREELLYDKAKLLANGDKWERAIAANLEADAPYR
 >2[4Fe-4S]ST12(swi:Swit_2993) *Sphingomonas wittichii*
 MSLGHIKSFTLWEFVKAHWLTLKYFFRAKATINYPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIFCGFCQEACPVDVAIVEGP
 NFEYSTETREELIYDKAKLLANGDRWEPATAANLAADAPYR
 >2[4Fe-4S]ST12(sphm:G432_00205) *Sphingomonas* sp. MM-1
 MSLAHYVKTFTLWEFVKAHWLTLKYFFKPKATINYPFEKNPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITIEAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEYATETREELIYDKAKLLSNGDRWESAIAANIAADAPYR
 >2[4Fe-4S]ST12(sjp:SJA_C1-13310) *Sphingobium japonicum*
 MSLGYVKSFTLWEFVKAHALTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITIEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDVAIVEGP
 NFEFSTETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sch:Sphch_1178) *Sphingobium chlorophenolicum*

MSLGYYVKSFTLWEFVKAHWLTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFSTETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(ssy:SLG_23100) *Sphingobium* sp. SYK-6
 MSVAHLIKSFTLWEFVKAHWLTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFATETREELIYDKAKLLANGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(syb:TZ53_20545) *Sphingobium* sp. YBL2
 MSLGYYVKSFTLWEFVKAHALTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFSTETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sbd:ATN00_16765) *Sphingobium baderi*
 MSLGYYIKSFTLWEFVKAHWLTLKYFFKPKATINYPHEKNPISPRFRGEHVLRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFATETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(spmi:K663_10890) *Sphingobium* sp. MI1205
 MSLGYYVKSFTLWEFVKAHWLTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFATETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sphb:EP837_02368) *Sphingobium* sp. EP60837
 MSLGYYVKSFTLWEFVKAHWLTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFATETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sphr:BSY17_159) *Sphingobium* sp. RAC03
 MSLGYYVKSFTLWEFVKAHALTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITIEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFATETREELIYDKGKLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(sinb:SIDU_07645) *Sphingobium indicum*
 MSLGYYVKSFTLWEFVKAHALTLKYFFKPKATINYPYEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAQPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGP
 NFEFSTETREELIYDKAKLLENGDKWERAIAANLAADAPYR
 >2[4Fe-4S]ST12(gdi:GDI3032) *Gluconacetobacter diazotrophicus*
 PA1 5 (Brazil)
 MGHFDRTVRSFLLAELVAGMGATFKAMFKPKVTINYPYEKGPLSPRFRGEHALRRYPNGE
 ERCIACKLCEATCPAEAITIESEPRDDGSRRTTRYDIDMTKCIYCGLCEEACPVDAIVEG
 PNYEFATETREELMYNKDKLLANGDRWESVLARRLELDAPYR
 >2[4Fe-4S]ST12(gdj:Gdia_3336) *Gluconacetobacter diazotrophicus*
 PA1 5 (JGI)
 MGHFDRTVRSFLLAELVAGMGATFKAMFKPKVTINYPYEKGPLSPRFRGEHALRRYPNGE
 ERCIACKLCEATCPAEAITIESEPRDDGSRRTTRYDIDMTKCIYCGLCEEACPVDAIVEG
 PNYEFATETREELMYNKDKLLANGDRWESVLARRLELDAPYR
 >2[4Fe-4S]ST12(aace:A0U92_11150) *Acetobacter aceti*
 MAGMDRALKAFLLTEIISGMASTFKTMFKPKVTINYPYEKGPLSPRFRGEHALRRYPNGE
 ERCIACKLCEATCPAEIVIEAEPRDDGSRRTTRYDIDMTKCIYCGLCEEACPVDAIVEG
 PNYEFATETREELMYNKEKLLSNGDRWESVLARRLELDAPYR
 >2[4Fe-4S]ST12(mgy:MGMSRv2__1319) *Magnetospirillum*
gryphiswaldense MSR-1 v2
 MAFLDRTARAFLLTELTVQGLALTFRYMFKPSVTTNYPYEKIPMSPRFRGEHALRRYANGE
 ERCIACKLCEAICPAQAITEAEPRPDGSRRRARYDLDMTKCIYCGLCQEACPVDAIVEG
 PNFEFATETRAELMYNKQKLLANGDRWEAELAMRIAADAPYR
 >2[4Fe-4S]ST12(azl:AZL_021400) *Azospirillum* sp. B510

MAFLDRAARSLFLTELVCGMALTFRYMFKPKVTINYPYEKGPISRRFRGEHVLRRYASGE
 ERCIACKLCEAVCPALAITIEAEPRDDGSRRTTRYDIDMTKCIYCGLCQEACPVDVAVMG
 PNFEFSTENREELFYNKQKLLANGDRWEAEIAQNLAEEAPYR
 >2[4Fe-4S]ST12(abs:AZOBR_100251) *Azospirillum brasilense* Sp245
 MAFLDRAARSLFLTELLGGLGLTLRYMFKPKVTLNYPFEKGPISPRFRGEHVLRRYPGGE
 ERCIACKLCEAVCPALAITIEAEPRDDGSRRTTRYDIDMTKCIYCGYCQEACPVDIVMG
 PNFEFSTENREELFYNKQKLLANGDRWEAEIAQNLAEEAPYR
 >2[4Fe-4S]ST12(abq:ABAZ39_08350) *Azospirillum brasilense* Az39
 MAFLDRAARSLFLTELLGGLGLTLRYMFKPKVTLNYPFEKGPISPRFRGEHVLRRYPGGE
 ERCIACKLCEAVCPALAITIEAEPRDDGSRRTTRYDIDMTKCIYCGYCQEACPVDIVMG
 PNFEFSTENREELFYNKQKLLANGDRWEAEIAQNLAEEAPYR
 >2[4Fe-4S]ST12(tmo:TMO_1970) *Tistrella mobilis*
 MASIGQTARAFLLTEIVKGMALTLRYFFKPKVTLNYPYEKGPISPRFRGEHVLRRYPNGE
 ERCIACKLCEAICPALAITIEAEPRADGSRRTTRYDIDMTKCIYCGFCQEACPVDIVEG
 PNFEFATETREELFYDKARLLANGDRWEREIAANLADVAPYR
 >2[4Fe-4S]ST12(magq:MGMAQ_1973) *Magnetospira* sp. QH-2
 MGFI DRTARAFLLAELVKGMALTFSYMFKPCVTLNYPMEKGPLSPRFRGEHALRRYPGGE
 ERCIACKLCEAICPALAITIEAEPRDDGSRRTSRYDIDMTKCIYCGFCQEACPVDIVEG
 PNFEYATETREELFYNDKLLANGDRWETELAARIRADAPYR
 >2[4Fe-4S]ST12(apb:SAR116_0149) *Candidatus Puniceispirillum*
marinum
 MRMLMDSIKSFLLELAKGMFLTLKYFFKPKVTINYPYEKGSLSRFRGEHALRRYPNGE
 ERCIACKLCEAVCPAQAITIEAEPRDDGSRRTTRYDIDMTKCIYCGFCQEACPVDIVEG
 PNFEFATETREELYDYDNKLLANGDRWETELIARNLAADAWE

Subtype 13

>2[4Fe-4S]ST13(gdj:Gdia_0711) *Gluconacetobacter diazotrophicus*
 PA1 5 (JGI)

MFDILRTLWLTFRHMTHRRVTVGYPETKPPLPPRYRGRIILSRDPDGQERCVACGLCAVACP
 VDCISLQKTEQDGRWYPDYFRINF SRCIFCGFCEEACPTYAIQLTPDFEMSEYVRPSL
 VYEKEDLLISGTGKYPDYSFYLVSGVTIPGKDKGEAERESPPVDVRS LMP

>2[4Fe-4S]ST13(gdi:GDI2464) *Gluconacetobacter diazotrophicus*
 PA1 5 (Brazil)

MGYPETKPPLPPRYRGRIILSRDPDGQERCVACGLCAVACP VDCISLQKTEQDGRWYPDYFR
 INF SRCIFCGFCEEACPTYAIQLTPDFEMSEYVRPSLVYEKEDLLISGTGKYPDYSFY
 LVSGVTIPGKDKGEAERESPPVDVRS LMP

Subtype 14

>2[4Fe-4S]ST14(rpb:RPB_1479) *Rhodopseudomonas palustris* HaA2

MPLASYETSVPVVVDEAKCIADKGCTVCVDVCPLDVLRLISDLTGKAFMAYDECWYCMPCEAD
CPTDAVKVNIPYLLR

>2[4Fe-4S]ST14(nwi:Nwi_0677) *Nitrobacter winogradskyi*

MPIAHTPTTVPVVVDEAKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKYDECWYCMPCE
TDCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(bja:bsr3197) *Bradyrhizobium diazoefficiens* USDA
110

MPLASYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISEMTNKAYMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(mlo:msr9193) *Mesorhizobium japonicum* MAFF 303099

MPLALSPTAVPVVVDETKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKFDECWYCMPCE
KDCPTGAVTVSIPYLLR

>2[4Fe-4S]ST14(six:BSY16_4737) *Sinorhizobium* sp. RAC02

MPLAFSPTAVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKFDECWYCMPCE
TDCPTGAVSVNIPYLLR

>2[4Fe-4S]ST14(same:SAMCFNEI73_pB0273) *Sinorhizobium Americanum*

MPLALSPTTVPVVVVDDAKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKFDECWYCMPCE
TDCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(same:SAMCFNEI73_pC1417) *Sinorhizobium Americanum*

MPLALSPTTVPVVDDAKCIADKGCTVCVDVCPLDVLRLISDLTGKAFMKFDECWYCMPCE
TDCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(xau:Xaut_2802) *Xanthobacter autotrophicus*

MPFANHPTSVPVTVDDDEKCIAEKGCRVCIDVCPLDVLAINPASGKAHMKYDECWYCMPCE
VDCPTGAVKVEIPYLLR

>2[4Fe-4S]ST14(mex:Mext_3350) *Methylobacterium extorquens* PA1

MPLAHQPSAVPVTVDDPEKCIADKGCTVCVDVCPLDVLRLISDLTGKAHMKYDECWYCMPCE
TDCPTGAVTVQIPYLLR

>2[4Fe-4S]ST14(mea:Mex_1p3569) *Methylobacterium extorquens* AM1

MPLAHQPSAVPVTVDDPEKCIADKGCTVCVDVCPLDVLRLISDLTGKAHMKYDECWYCMPCE
TDCPTGAVTVQIPYLLR

>2[4Fe-4S]ST14(mdi:METDI4145) *Methylobacterium extorquens* DM4

MPLAHQPSSTVPVTVDDPEKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKYDECWYCMPCE
TDCPTGAVTVQIPYLLR

>2[4Fe-4S]ST14(mch:Mchl_3675) *Methylobacterium extorquens* CM4

MPLAHQPSAVPVTVDDPEKCIADKGCTVCVDVCPLDVLRLISDLTGKAHMKYDECWYCMPCE
TDCPTGAVTVQIPYLLR

>2[4Fe-4S]ST14(mch:Mchl_4197) *Methylobacterium extorquens* CM4

MPIITQAKSAAVVIDDDKCIAEKGCRVCVDVCPLDILAIETRQKAYMKYDECWYCMPCE
VDCPTNAVKNIPYLLR

>2[4Fe-4S]ST14(mpo:Mpop_4190) *Methylobacterium populi*

MPLAHQPSTVPVTVDAEKCIADKGCTVCVDVCPLDVLRLISDLTGKAHMKYDECWYCMPCE
TDCPTGAVTVQIPYLLR

>2[4Fe-4S]ST14(bjp:RN69_31775) *Bradyrhizobium japonicum* E109

MPLASYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDMTGKAYMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(bbt:BBta_4883) *Bradyrhizobium* sp. BTAi1

MPIAYTPTTLPVVVDEAKCIADKGCTVCVDVCPLDVLRLISDLTGKAYMKYDECWYCMPCE
TDCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(brs:S23_48000) *Bradyrhizobium* sp. S23321

MPLASYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDMTGKAYMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(aol:S58_21790) *Bradyrhizobium oligotrophicum*

MPLATYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDMTGKAFMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(brad:BF49_1488) *Bradyrhizobium* sp. BF49

MPLASYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDMTNKAYMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(bic:LMTR13_09210) *Bradyrhizobium icense*

MPLASYQTSVPVVVDDAKCIADKGCTVCVDVCPLDVLRLISDMTGKAYMAYDECWYCMPCE
ADCPTGAVTVNIPYLLR

>2[4Fe-4S]ST14(eah:FA04_29530) *Ensifer adhaerens* Casida A

MPLALSPTTVPVVVDEAKCIADKGCTVCVEVCPLDVLRIISDLTGKAYMKFDECWYCMPCETD
CPTGAVTVNIPYLLR

Subtype 15

>2[4Fe-4S]ST15(rsp:RSP_3193) *Rhodobacter sphaeroides* 2.4.1

MIEAAVSMALGLGLGLLLGVAARRFHVESPPIVDAIEGILPGTNCGACGYPGCRGLAEAMS
EGAAPVTACAPGGRDVALALAAIVETDGGGGAVPGMAEAEPTVAFIFEDHCTGCMRCFKRCP
TDAIIGANRQIHTVVTDACIGCNACIEACPTEAIVARVKPKTLKSWYWDKPRTAFEARGTEV
AA

Subtype 16

>2[4Fe-4S]ST16(red:roselon_00015) *Roseibacterium elongatum*

MKGILDSLNVNVRKLVTKKYTRQYPEEKPDLPARYRARIVLTRDPDGQERCVCACNLCAVACP
VDCIDVVKAETEDGRWYPETFRINFARCIFCGYCEEACPTQAIQLTPDFETADYTRAGLIHD
KEDLLIAGQGKQEGYRYWSVAGKAIDGKPKGAAETEAAPINLKDLTP

Subtype 17

>2[4Fe-4S]ST17(pgv:SL003B_2077) *Polymorphum gilvum*

MGLDQAAKSLFLKEFVSAFFLAMRYFFKPKPTLNYPFEKGPVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYYSKEKLLANGDRWEREIARNIEMDAPYR

>2[4Fe-4S]ST17(meso:BSQ44_12500) *Mesorhizobium* sp. B7

MSALAQAAKSLLLKEFFGAVVLSMRQFFAPKYTINYPHEKNPQSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVE
GPNFEFSTETREELYDDKDRLLANGDRWEREIARNIALDSPYR

>2[4Fe-4S]ST17(mamo:A6B35_22200) *Mesorhizobium amorphae*

MSALSQAASLLQDFVSAFFLSMRQFFAPKETINYPHEKGPISPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVE
GPNFEFATETREELYDDKDRLLANGDRWERELARNIALDSPYR

>2[4Fe-4S]ST17(rhl:LPU83_1663) *Rhizobium favelukesii*

MAGLSNAVSSLFLKEFVSAFWLTFRYIFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVE
GPNFEFATETREELYFDKARLLENGDRWEREIARNIALDAPYR

>2[4Fe-4S]ST17(mlo:mll1359) *Mesorhizobium japonicum* MAFF 303099

MMSALSQAASLLQDFVSAFFLSMRQFFAPKETINYPHEKGPVSPRFRGEHALRRYPNG
EERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIV
EGPNFEFATETREELYDDKDKLLANGDRWERELARNISLDAPYR

>2[4Fe-4S]ST17(mln:A9174_19200) *Mesorhizobium loti* NZP2037

MSALSQAASLLQDFVSAFFLSMRQFFAPKETINYPHEKGPTS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVE
GPNFEFATETREELYDDKDKLLANGDRWERELARNISLDAPYR

>2[4Fe-4S]ST17(mci:Mesci_3293) *Mesorhizobium ciceri* (biovar Biserrulae) mci
MSALSQAAKSLLLQDFVSAFFLSMRQFFAPKETINYPHEKGPTS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFATETREELYDDKDRLLANGDRWERELARNISLDSFYR

>2[4Fe-4S]ST17(mop:Mesop_3690) *Mesorhizobium opportunistum*
MGALTQAAKSLLLQDFVSAFFLSMRQFFAPKETINYPHEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFATETREELYDDKDRLLANGDRWERELARNISLDSFYR

>2[4Fe-4S]ST17(mam:Mesau_03564) *Mesorhizobium australicum*
MSALSQAAKSLLLQDFVSAFFLSMRQFFAPKETINYPHEKG PIS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFATETREELYDDKDRLLANGDRWERELARNISLDSFYR

>2[4Fe-4S]ST17(mes:Meso_1030) *Chelativorans* sp. BNC1
MSALAQAAKSLLLKEFFGAVVLSMRQFFAPKATLNYPHEKG PLS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFATETREELYDDKDKLLANGDRWERELARNIALDAPYR

>2[4Fe-4S]ST17(hoe:IMCC20628_01659) *Hoeflea* sp. IMCC20628
MLAQAAKS LFLKEFVGAFLLSMRYFFAPKATLNYPNEKG PVS PRFRGEHALRRYPNGEER
CIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVEGP
NFEFATETREELYDDKDRLLANGDRWERELARNIAIDSPYR

>2[4Fe-4S]ST17(aak:AA2016_2936) *Aminobacter aminovorans*
MSALAQAAKSLLLQDFVGAFLLSMRQFFAPKATLNYPHEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(pla:Plav_3218) *Parvibaculum lavamentivorans*
MAWLDQSARS LFLAEFVSSFLAMRYFFKPKVTLNYPFEKG PLS PRFRGEHALRRYPNGE
ERCIACKLCEAICPALAITIEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVD AIVE
GPNFEFATETREELMYDKNRLLANGDRWEREIARNIALDAPYR

>2[4Fe-4S]ST17(sm:Sinme_1071) *Sinorhizobium meliloti* AK83
MAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFSTETREELYDDKEKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(sm:SinmeB_0901) *Sinorhizobium meliloti* BL225C
MAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFSTETREELYDDKEKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(smx:SM11_chr2300) *Sinorhizobium meliloti* SM11
MAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFSTETREELYDDKEKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(smi:BN406_01009) *Sinorhizobium meliloti* Rm41
MAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFSTETREELYDDKEKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(smeg:C770_GR4Chr1290) *Sinorhizobium meliloti* GR4
MAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
GPNFEFSTETREELYDDKEKLLANGDRWEREIARNIAMDSFYR

>2[4Fe-4S]ST17(sm:SM2011_c01922) *Sinorhizobium meliloti* 2011
MMAGLSNAVSS LFLKEFVGAFLLSMRYFFRPKATLNYPFEKG PVS PRFRGEHALRRYPNG

EERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 EGNFEEFSTETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(smer:DU99_06640) *Sinorhizobium meliloti* RMO17
 MAGLSNAVSSLFLKEFVGAFLLSMRYFFRPKATLNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFSTETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(smd:Smed_0898) *Sinorhizobium medicae*
 MAGLSNAVSSLFLKEFVGAFLLSMRYFFRPKATLNYPYEKGPISPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFSTETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(rhi:NGR_c10580) *Sinorhizobium fredii* NGR234
 MAGLSQAVSSLFLKEFVGAFLLSMRYFFRPKATLNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(sfh:SFHH103_00994) *Sinorhizobium fredii* HH103
 MAGLSQAVSSLFLKEFVGAFLLSMRYFFRPKATLNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(sfd:USDA257_c33070) *Sinorhizobium fredii* USDA
 257
 MAGLSQAVSSLFLKEFVGAFLLSMRYFFRPKATLNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(six:BSY16_1542) *Sinorhizobium* sp. RAC02
 MASLSQAVNSLFLKEFVGAFLLSMRYFFRPKATVNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDQKQKLENGDRWEREIARNIAIDSPYR
 >2[4Fe-4S]ST17(same:SAMCFNEI73_Ch1389) *Sinorhizobium Americanum*
 MAGLSQAVGSLFLKEFVGAFLLSMRYFFRPKATVNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDKEKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(ead:OV14_2323) *Ensifer adhaerens* OV14
 MMAGLSQAVSSLFLKEFVGAFLLSMRYFFKPKATLNYPFEKGPVSPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 EGNFEEFATETREELYDQKDKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(eah:FA04_05060) *Ensifer adhaerens Casida A*
 MAGLSQAVSSLFLKEFVGAFLLSMRYFFKPKATLNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYDQKDKLLANGDRWEREIARNIAMDSPYR
 >2[4Fe-4S]ST17(atu:Atu1278) *Agrobacterium fabrum*
 MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYFDKQRLLDNGDRWEREIARNLALDAPYR
 >2[4Fe-4S]ST17(ara:Arad_1857) *Agrobacterium radiobacter*
 MKMAGFSNAVSSVFLKEFVGAFLLSMRYFFKQKATINYPFEKGPVSPRFRGEHALRRYPN
 GEERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 VEGPNFEEFATETREELYFDKARLLENGDRWEREIARNIAIDSPYR
 >2[4Fe-4S]ST17(atf:Ach5_11800) *Agrobacterium tumefaciens* Ach5
 MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDIV
 GPNFEEFATETREELYFDKQRLLDNGDRWEREIARNLALDAPYR

>2[4Fe-4S]ST17(ata:AWN88_11725) *Agrobacterium tumefaciens* S33
MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQKLLDNGDRWERE IARNLALDAPYR

>2[4Fe-4S]ST17(avi:Avi_1723) *Agrobacterium vitis*
MASVSQAVRSFLFLKEFVNAAFLSMRYFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFSTESREELYFDKAKLLANGDRWERE IARNLAQDAPYR

>2[4Fe-4S]ST17(agr:AGROH133_05642-1) *Agrobacterium* sp. H13-3
MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQRLDNGDRWERE IARNLALDAPYR

>2[4Fe-4S]ST17(agr:AGROH133_05642-2) *Agrobacterium radiobacter*
MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQRLDNGDRWERE IARNLALDAPYR

>2[4Fe-4S]ST17(agr:AGROH133_05642-3) *Agrobacterium* sp. RAC06
MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQRLDNGDRWERE IARNLALDAPYR

>2[4Fe-4S]ST17(aro:B0909_07015) *Agrobacterium rhizogenes*
MASLSQAVNSLFLKEFVGAILLTMRHFFKQKATVNYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQKLLDNGDRWERE IARNLALDAPYR

>2[4Fe-4S]ST17(ret:RHE_CH01613) *Rhizobium etli* CFN 42
MASLSSSINSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rec:RHECIAT_CH0001685) *Rhizobium etli* CIAT 652
MASLSSSINSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rel:REMIM1_CH01633) *Rhizobium etli* bv. *mimosae*
Mim1
MASLSSSINSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rep:IE4803_CH01613) *Rhizobium etli* bv. *phaseoli*
IE4803
MASLSSSINSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rei:IE4771_CH01666) *Rhizobium* sp. IE4771
MASLSSSINSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rle:RL1709) *Rhizobium leguminosarum* bv. *viciae*
3841
MASLSGSISSLFLKEFVGAFLLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWERE IARNIAIDSPYR

>2[4Fe-4S]ST17(rlt:Rleg2_1269) *Rhizobium leguminosarum* bv. trifolii WSM2304
MGSLSSSISSLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rlg:Rleg_1361) *Rhizobium leguminosarum* bv. trifolii WSM2304
MASLSGSISSLFLKEFVGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rlb:RLEG3_17230) *Rhizobium leguminosarum* bv. trifolii WSM1689
MASLSGSISSLFLKEFVGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rlu:RLEG12_17425) *Rhizobium leguminosarum* bv. trifolii CB782
MGSLSSSINSFLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rtr:RTCIAT899_CH06930) *Rhizobium tropici*
MAGISNAVGSFLFLKEFVGAFFLSMRYFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIAQNIADSPYR

>2[4Fe-4S]ST17(rir:BN877_I1259) *Rhizobium* sp. IRBG74
MASLSQAVNSLFLKEFVGAIFLTMRHFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQKLLDNGDRWEREIANLALDAPYR

>2[4Fe-4S]ST17(rga:RGR602_CH01474) *Rhizobium gallicum*
MASLSNAVGSFLFLKEFVGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKQRLDNGDRWEREIANMAIDAPYR

>2[4Fe-4S]ST17(rhn:AMJ98_CH01641) *Rhizobium* sp. N1341
MASLSSSINSFLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rpha:AMC79_CH01644) *Rhizobium phaseoli*
MASLSSSINSFLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(rht:NT26_1274) *Rhizobium* sp. NT-26
MASLTQAVSSLFLKEFVGAFFLSMRYFFKPKATVNYPFEKNPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFSTETREELYDDKARLLENGDRWEREIANMAQDAPYR

>2[4Fe-4S]ST17(rhx:AMK02_CH01650) *Rhizobium* sp. N731
MASLSSSINSFLFLKEFFGAFFLSMRYFFRQKATINYPFEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYFDKARLLDNGDRWEREIANIAIDSPYR

>2[4Fe-4S]ST17(ngl:RG1141_CH11880) *Neorhizobium galegae* bv. officinalis
HAMB1 1141
MASLGQAVNSLFLKEFVGAFFLSMRYFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE

ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFSTETREELYFDKARLLENGDRWERE IARNMAIDAPYR
 >2[4Fe-4S]ST17(ngg:RG540_CH12150) *Neorhizobium galegae* bv.
 orientalis HAMBI 540
 MASLGQAVNSLFLKEFVGAFFLSMRYFFKQKATINYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYFDKARLLENGDRWERE IARNMAIDAPYR
 >2[4Fe-4S]ST17(lcc:B488_02650) *Liberibacter crescens*
 MFIQSINSLSLFLKEFVRAFFLSMRYFFKPKATINYPFEKGPVSPRFRGEHALRRYPNGEER
 CIACKLCEAICPAQAITIEAGPRQSDGTRRTIRYDIDMVKCIYCGFCQEACPVDATIVEGP
 NFEFATETREELYFDKARLLDNGDRWEKEIARNILIEAPYR
 >2[4Fe-4S]ST17(shz:shn_07060) *Shinella* sp. HZN7
 MASLSQAVNSLFLKEFVGAFFLSMRYFFRFPKATVNYPFEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFSTETREELYDDKQKLENGDRWERE IARNIAMDSPYR
 >2[4Fe-4S]ST17(bme:BMEI1150) *Brucella melitensis* bv. 1 16M
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDHWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmel:DK63_263) *Brucella melitensis* bv. 1 16M
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDHWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmi:BMEA_A0852) *Brucella melitensis* ATCC 23457
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmz:BM28_A0822) *Brucella melitensis* M28
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmg:BM590_A0820) *Brucella melitensis* M5-90
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmw:BMNI_I0802) *Brucella melitensis* NI
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmee:DK62_596) *Brucella melitensis* bv. 3 Ether
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmf:BAB1_0830) *Brucella abortus* 2308
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bmc:BAbs19_I07740A) *Brucella abortus* S19
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR

>2[4Fe-4S]ST17(baa:BAA13334_I02677) *Brucella abortus* A13334
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babo:DK55_826) *Brucella abortus* bv. 2 86/8/59
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babr:DO74_1062) *Brucella abortus* bv. 6 870
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babt:DK49_585) *Brucella abortus* 63 75
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babb:DK48_1292) *Brucella abortus* BDW
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babu:DK53_811) *Brucella abortus* bv. 9 C68
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babs:DK51_647) *Brucella abortus* BER
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(babc:DO78_732) *Brucella abortus* NCTC 10505
MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(bsui:BSP1_I0894) *Brucella suis* bv. 2 Bs143CITA
MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(bsup:BSPT1_I0906) *Brucella suis* bv. 2 PT09143
MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(bsuv:BSPT2_I0893) *Brucella suis* bv. 2 PT09172
MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWEREIARNIAMDAPYR

>2[4Fe-4S]ST17(bsuc:BSP2_I0822) *Brucella suis* bv. 2 Bs364CITA
MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE
GPNFEFATETREELYDDKDKLLANGDRWELEIARNIAMDAPYR

>2[4Fe-4S]ST17(bsz:DK67_1719) *Brucella suis* bv. 3
MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVE

GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bsw:IY71_04060) *Brucella suis* ZW043
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bsg:IY72_03790) *Brucella suis* ZW046
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bcs:BCAN_A0825) *Brucella canis* ATCC 23365
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bsk:BCA52141_I0434) *Brucella canis* HSK A52141
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bcar:DK60_874) *Brucella canis* RM6/66
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bcas:DA85_03860) *Brucella canis* SVA13
 MASITQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bpv:DK65_555) *Brucella pinnipedialis* 6/566
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bcet:V910_101165) *Brucella ceti* TE10759-12
 MASIAQAAKSLLLKEFASAFALSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(oan:Oant_2415) *Ochrobactrum anthropi* ATCC 49188
 MASFAQAAKSLLLKEFVGAFFLSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(oah:DR92_1876) *Ochrobactrum anthropi* OAB
 MASFAQAAKSLLLKEFVGAFFLSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(ops:A8A54_03620) *Ochrobactrum pseudogrignonense*
 MASFAQAAKSLLLKEFVGAFFLSMRQFFAPKATLNYPHEKGPVSPRFRGEHALRRYPNGE
 ERCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVD AIVE
 GPNFEFATETREELYDDKDKLLANGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(bja:bl14909) *Bradyrhizobium diazoefficiens* USDA
 110
 MRAVMGININATARSLLLSEFVS AFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRR
 YPNGEERC IACKLCEAVCPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACP V
 DAIVEGPNFEFATETREELFYDKAKLLANGDRWERE IAKAIELDAPYR
 >2[4Fe-4S]ST17(bju:BJ6T_47790) *Bradyrhizobium japonicum* USDA 6

MGINVNATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 EGNPFEFATETREELFYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(bjp:RN69_23295) *Bradyrhizobium japonicum* E109
 MNVNATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELFYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(bra:BRADO4176) *Bradyrhizobium* sp. ORS 278
 MNISATARSLLLQEFVSAFFLAMRYFFKPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKAKLLANGDRWEREISKAIALDAPYR
 >2[4Fe-4S]ST17(bbt:BBta_4553) *Bradyrhizobium* sp. BTAi1
 MNISATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKAKLLANGDRWEREISKAIALDAPYR
 >2[4Fe-4S]ST17(brs:S23_32720) *Bradyrhizobium* sp. S23321
 MGININATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNG
 EERCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 EGNPFEFATETREELFYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(aol:S58_34180) *Bradyrhizobium oligotrophicum*
 MNISATARSLLLQEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKAKLLANGDRWEREISKAIALDAPYR
 >2[4Fe-4S]ST17(brc:BCCGELA001_20840) *Bradyrhizobium* sp. CCGE-
 LA001
 MNINATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELFYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(brad:BF49_6647) *Bradyrhizobium* sp. BF49
 MGININATARSLLLSEFVSAFFLAMRYFFQPKPTLNYPFEKGPISPRFRGEHALRRYPNG
 EERCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 EGNPFEFATETREELFYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(bic:LMTR13_18775) *Bradyrhizobium icense*
 MSVNVNATARALLLSEFVSAFFLAMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNG
 EERCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 EGNPFEFATETREELYDYDKAKLLANGDRWEREIAKAIELDAPYR
 >2[4Fe-4S]ST17(rpb:RPB_2582) *Rhodopseudomonas palustris* HaA2
 MNINATARSLLLTEFVSAFFLAMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKARLLANGDRWEREIAKSIELDAPYR
 >2[4Fe-4S]ST17(rpc:RPC_2412) *Rhodopseudomonas palustris* BisB18
 MRVTAAARSLLLTEFVSAFFLAMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKAKLLANGDRWEREIAKSIELDAPYR
 >2[4Fe-4S]ST17(rpd:RPD_2877) *Rhodopseudomonas palustris* BisB5
 MNINATARSLLLTEFVSAFFLAMRYFFRPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDIV
 PNFEFATETREELYDYDKARLLANGDRWEREIAKSIELDAPYR
 >2[4Fe-4S]ST17(rpe:RPE_2531) *Rhodopseudomonas palustris* BisA53
 MGVTAAARSLLLTEFVSAFFLAMRYFFKPKPTLNYPFEKGPISPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTERYDIDMVKCIYCGLCQEACPVDIV

PNFEFATETREELYDYDKAKLLANGDRWEREIAKHMALDAPYR
>2[4Fe-4S]ST17(rpt:Rpal_3290) *Rhodopseudomonas palustris* TIE-1
MNVTTATARSLLLTEFVSAFFLAMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAVCPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYDYDKARLLANGDRWEREIAKAISLDAPYR
>2[4Fe-4S]ST17(rpx:Rpd_x1_2561) *Rhodopseudomonas palustris* DX-1
MNVTTAAARSLLLTEFVSAFFLAMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYDYDKARLLANGDRWEREIAKAISLDAPYR
>2[4Fe-4S]ST17(nwi:Nwi_1879) *Nitrobacter winogradskyi*
MSINATARSLLLTEFISAFFLTMRYYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAVCPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDAIVEG
PNFEFATETREELYDYDKAKLLANGDRWEREIAKAIELDAPYR
>2[4Fe-4S]ST17(nha:Nham_2212) *Nitrobacter hamburgensis*
MSINATARALLLTEFVSAFFLTMRYYFFQPKATINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTVRYDIDMVKCIYCGLCQEACPVDAIVEG
PNFEFATETREELYDYDKAKLLANGDRWEREIAKAIELDAPYR
>2[4Fe-4S]ST17(bos:BSY19_2477) *Bosea* sp. RAC05
MSLAQAAGKLLLKEFVGAFALSMRYFFKPKATINYPFEKNPQSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMTKCIYCGFCQEACPVDAIVEG
PNFEFATETREELFYDKDRLLENGARWEREIARNIAMDAPYR
>2[4Fe-4S]ST17(bvv:BHK69_20555) *Bosea vaviloviae*
MSLAQAAGKLLLKEFVGAFALSMRYFFKPKATLNYPFEKGMLSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMTKCIYCGFCQEACPVDAIVEG
PNFEFATETREELFYDKDRLLANGARWEREIARNIAMDAPYR
>2[4Fe-4S]ST17(xau:Xaut_4625) *Xanthobacter autotrophicus*
MKLDQAARGFLTELVS GF FLAMRYFFKPKATLNYPFEKGPLSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFAAETREELYDYDKEKLLANGDRWEREIARSIAMDAPYR
>2[4Fe-4S]ST17(azc:AZC_1676) *Azorhizobium caulinodans*
MKLDQAARALFTELVS GF FLAMRYFFKPKATINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYDYDKEKLLANGDRWEREIARAIAADAPYR
>2[4Fe-4S]ST17(mex:Mext_1077) *Methylobacterium extorquens* PA1
MKLDQVARSLLLKEFVS GF VFLAMKYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
PNFEFSVETREELLYDYDKQKLENGDRWEREIARNIAVDAPYR
>2[4Fe-4S]ST17(mea:Mex_1p0847) *Methylobacterium extorquens* AM1
MKLDQVARSLLLKEFVS GF VFLAMKYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
PNFEFSVETREELLYDYDKQKLENGDRWEREIARNIAVDAPYR
>2[4Fe-4S]ST17(mdi:METDI1558) *Methylobacterium extorquens* DM4
MKLDQVARSLLLKEFVS GF VFLAMKYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
PNFEFSVETREELLYDYDKQKLENGDRWEREIARNIAVDAPYR
>2[4Fe-4S]ST17(mch:Mchl_1206) *Methylobacterium extorquens* CM4
MKLDQVARSLLLKEFVS GF VFLAMKYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITIEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
PNFEFSVETREELLYDYDKQKLENGDRWEREIARNIAVDAPYR
>2[4Fe-4S]ST17(mpo:Mpop_1011) *Methylobacterium populi*
MKLDQVARSLLLKEFVS GF FLAMKYFLKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE

RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQKLLNGDRWERE IARNIAIDAPYR
 >2[4Fe-4S]ST17(mrd:Mrad2831_2051) *Methylobacterium radiotolerans*
 MKLDQVAKSLLLKEFVSGMILGMRYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQKLLNGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(met:M446_4398) *Methylobacterium* sp. 4-46
 MRLDQVARSLLLKEFVSGFALAMRYLFKPKATINYPFEMGHRSPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQRLLANGDRWERE IARNIAADAPYR
 >2[4Fe-4S]ST17(mno:Mnod_4134) *Methylobacterium nodulans*
 MRLDQVARSLLLKEFVSGFALAMRYLFKPKATINYPFEMGHRSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQKLLANGDRWERE IARNIAADAPYR
 >2[4Fe-4S]ST17(mor:MOC_2440) *Methylobacterium oryzae*
 MKLDQVAKSLLLKEFVSGMVLGMRYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQKLLNGDRWERE IARNIAMDAPYR
 >2[4Fe-4S]ST17(meta:Y590_04475) *Methylobacterium* sp. AMS5
 MKLDQVARSLLLKEFVSGFFLAMKYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKQKLLNGDRWERE IARNIAVDAPYR
 >2[4Fe-4S]ST17(maqu:Maq22A_c02875) *Methylobacterium aquaticum*
 MKLDQVARGLLLKEFVTGFALAMRYFFKPKATINYPFEMGHRGPRFRGEHALRRYPNGEE
 RCIACKLCEAVCPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGMCQEACPVDAIVEG
 PNFEFSVETREELLYDKEKLLANGDRWERE IARNIAADAPYR
 >2[4Fe-4S]ST17(bid:Bind_2390 K00338 *Beijerinckia indica*)
 MRLDSAAKALFLKEFVGAFALSMRYFFKPRPTLNYPHEKNPQSPRYRGEHALRRYPNGEE
 RCIACKLCEAICPAKAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
 PNAEFAVETREELYYDKDRLLQNGARWERE IARNIALDAPYR
 >2[4Fe-4S]ST17(msl:Msil_2926) *Methylocella silvestris*
 MKLDQAAKALFLSEFVGAFLLSMRYFFKPKPTLNYPHEKNPQSPRYRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
 PNAEFSVETREELYYDKDRLLNGARWERE IARNIALDAPYR
 >2[4Fe-4S]ST17(hdn:Hden_1934) *Hyphomicrobium denitrificans* ATCC 51888
 MSVARAAKSLFLTEIVVAFVLTTRYFFAPKKTLNYPYEKGPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVDAIVEG
 PNFEFATETREELFYDKERLLSNGDRWERE IAKNIALDAKYR
 >2[4Fe-4S]ST17(hdt:HYPDE_28883) *Hyphomicrobium denitrificans* 1NES1
 MSVARATKSLLLTEIVAAFVLTTRYFFAPKKTLNYPYEKGPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVDAIVEG
 PNFEFATETREELFYDKERLLSNGDRWERE IAKNIALDAKYR
 >2[4Fe-4S]ST17(hmc:HYPMC_2890) *Hyphomicrobium* sp. MC1
 MNVAQGVKSLFLTEFVSAFFLTMYFFSPKKTLNYPYEKGPLSPRFRGEHALRRYPNGEE
 RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVDAIVEG
 PNFEFATETREELFYDKERLLSNGDRWERE IAKNIALDAKYR
 >2[4Fe-4S]ST17(hni:W911_15990) *Hyphomicrobium nitrativorans*
 MRVAQGLKSLFLAEFVSAFFLAMRYFFAPKKTLNYPFEKGPLSPRFRGEHALRRYPNGEE

RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGLCQEACPVDATIVEG
PNFEFATETREELYDYDKERLLANGDRWEREIAARNLALDAPYR
>2[4Fe-4S]ST17(phl:KKY_1323) *Pelagibacterium halotolerans*
MKALRFLDALLLREFVSTFFLAMRYFFAPKPTINYPFEKGESVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRQNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVEG
PNFEFATETREELYFSKDRLLANGDRWERELAANIALDAPYR
>2[4Fe-4S]ST17(fil:BN1229_v1_3009) *Candidatus Filomicrobium
marinum* W
MAIAQAVRSMFLTEFVSAFFLAMRYFFMPKKTVNYPFEKGPLSPRFRGEHALRRYPNGQE
RCIACKLCEAICPALAITEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVEAIVEG
PNFEFATETREELFYDKERLLDNGDRWEREIAKNIGLDAKFR
>2[4Fe-4S]ST17(fiy:BN1229_v1_2907) *Candidatus Filomicrobium
marinum* Y
MAIAQAVRSMFLTEFVSAFFLAMRYFFMPKKTVNYPFEKGPLSPRFRGEHALRRYPNGQE
RCIACKLCEAICPALAITEAGPRRNDGTRRTTRYDIDMTKCIYCGLCQEACPVEAIVEG
PNFEFATETREELFYDKERLLDNGDRWEREIAKNIGLDAKFR
>2[4Fe-4S]ST17(deq:XM25_06955) *Devosia* sp. H5989
MRQFLNSLLLKEFVSFAFLSMRYFFSPKPTINYPFEKGHVSPRFRGEHALRRYPNGEERC
IACKLCEAICPAQAITEAGPRQNDGTRRTVRYDIDMVKCIYCGFCQEACPVDATIVEGPN
FEFATETREELYFSKEKLLANGDRWEREIAARNIALDAPYR
>2[4Fe-4S]ST17(rhz:RHPLAN_38840) *Rhodoplanes* sp. Z2-YC6860
MRLDQAARSIFLQEFVSAFFLGMRYFFKPKATLNYPFEKGPISPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGLCQEACPVDATIVEG
PNFEFATETREELYDYDKERLLANGDRWEREIAKNIALDAPYR
>2[4Fe-4S]ST17(msc:BN69_1742) *Methylocystis* sp. SC2
MKLDQAAKSLFLTEFVGAFLLSMRYFFKPKATINYPHEKNPQSPRYRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGYCQEACPVDATIVEG
PNSEFSVETREELYYNKQRLLENGDRWEREIAARNIAMDAQYR
>2[4Fe-4S]ST17(mbry:B1812_03680) *Methylocystis bryophila*
MRLDQEAASLFLLEFVAFFLGIRYIFKPKATINYPHEKNPQSPRYRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDATIVEG
PNAEFATETREELYYNKERLLENGARWEREIAARNIALDAPYR
>2[4Fe-4S]ST17(mey:TM49_13470) *Marteella endophytica*
MGSVAQAFNAIFLKEFVAFFLTMRYFFGQKSTVNYPFEKGPSVSPRFRGEHALRRYPNGE
ERCIACKLCEAICPAQAITEAGPRRNDGTRRTVRYDIDMVKCIYCGFCQEACPVEAIVE
GPNFEFATETREELYDYDKERLLANGDRWEREIAARNIAMDAPYR
>2[4Fe-4S]ST17(mcg:GL4_2076) *Methyloceanibacter caenitepidi*
MTRFAQAASLLEFVSFAFWLAMKYFVAPKATLNYPYEKGPLSPRFRGQHALRRYPNGE
ERCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVEAIVE
GPNFEFATETREELYDYDKARLLSNGDRWEREIAKNIELDSAYR
>2[4Fe-4S]ST17(psin:CAK95_22835) *Pseudorhodoplanes sinuspersici*
MRLDQAARSVFLAEFVQAFFLGMRYFFKPKPTINYPFEKNPISPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGLCQEACPVDATIVEG
PNFEFATETREELYDYDKERLLANGDRWEREIAQNIRLDAPYR
>2[4Fe-4S]ST17(psf:PSE_3429) *Pseudovibrio* sp. FO-BEG1
MGLGQAAKSLLEFVSAFFLAMRYFFKPKPTINYPFEKGPSVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMTKCIYCGFCQEACPVDATIVEG
PNFEFATETREELFYDKDKLLANGERWEREIAARNIELDAPYR
>2[4Fe-4S]ST17(pphr:APZ00_17540) *Pannonibacter phragmitetus*
MGLDQAIKSLFLKEFVSAFFLAMRYFFKPKPTVNYPFEKGPSVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDATIVEG

PNFEFATETREELYYSKEKLLANGDRWEREIARNIAMDAPYR
>2[4Fe-4S]ST17(lap:ACP90_13715) *Labrenzia* sp. CP4
MGLSQAVKSLFLQEFVSAFVLAMRYFFKPKPTVNYPFEEKGPVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYDKEKLLANGDRWEREIARNIEMDAPYR
>2[4Fe-4S]ST17(lagg:B0E33_25530) *Labrenzia aggregata*
MGLSQAVKSLFLQEFVSAFVLAMRYFFKPKPTVNYPFEEKGPVSPRFRGEHALRRYPNGEE
RCIACKLCEAICPAQAITEAGPRRNDGTRRTTRYDIDMVKCIYCGFCQEACPVDAIVEG
PNFEFATETREELYDKEKLLANGDRWEREIARNIEMDAPYR

2[4Fe-4S]Alv

Subtype 1

>2[4Fe-4S]AlvST1(mgy:MGMSRv2__1443) *Magnetospirillum*
gryphiswaldense MSR-1 v2
MSLKITEDCTSCDACVSVCPNTAISAGEVIYVIEEDRCTECVGAEDTPQCQLVCPADCIV
IGTEETPDQLQAKYEALHG
>2[4Fe-4S]AlvST1(magq:MGMAQ_1616) *Magnetospira* sp. QH-2
MALLINEDCTNCDACVPVCPNEAITEGDVIYEIDPARCTECVGAEDEPQCQLVCPADCIF
PDPANEETQEQLQAKYEALRV
>2[4Fe-4S]AlvST1(rpe:RPE_0603) *Rhodopseudomonas palustris* BisA53
MALMINEDCTGCDACRPVCPNDAIKAGDPLYRVDPARCTECVGAEDEPQCQVVCPCADCLV
ANPEWAETPEQLQEKYERLHS
>2[4Fe-4S]AlvST1(rpt:Rpal_0729) *Rhodopseudomonas palustris* TIE-1
MALMINEDCTACDACRPVCPNQAIASDTICAVDALRCTECVGAEDEPQCQLVCPADCIV
PNPDWRETPEHLQDKYQQLHS
>2[4Fe-4S]AlvST1(rpx:Rpx1_4124) *Rhodopseudomonas palustris* DX-1
MALMINEDCTACDACRPVCPNQAIASDTIYAVDALRCTECVGAEDEPQCQLVCPADCIV
PNPDWRETPEQLQDKYQQLHS
>2[4Fe-4S]AlvST1(rpa:RPA0662) *Rhodopseudomonas palustris* CGA009
MALMINEDCTACDACRPVCPNQAIASDTIYAVDALRCTECVGAEDEPQCQLVCPADCIV

PNPDWRETPEQLQDKYQQLHS

>2[4Fe-4S]AlvST1(rpc:RPC_1024)*Rhodopseudomonas palustris* BisB18
MALMINEDCTACDACRPVCPNEAIAAGDPMFVIDALRCTECVGAEDEPQCRLVCPADCIV
ANLDWSETPEELQTKYDQLHG

>2[4Fe-4S]AlvST1(rpd:RPD_1533)*Rhodopseudomonas palustris* BisB5
MALMINDDCTACDACRPVCPNEAIAAGEPLFVIDALRCTECVGAEDEPQCRLVCPAGCVV
ANPDWSETPEELQAKYDQLHS

>2[4Fe-4S]AlvST1(abs:AZOBR_70146)*Azospirillum brasilense* Sp245
MAYKIKASDCTACGACEAECPNNAISFKKGAYAINADLCTECKGQFSSPQCASVCPADCC
VPA

>2[4Fe-4S]AlvST1(abq:ABAZ39_09920)*Azospirillum brasilense* Az39
MAYKIKASDCTACGACEAECPNNAISFKKGAYAINADLCTECKGQFSSPQCASVCPADCC
VPA

Subtype 2

>2[4Fe-4S]AlvST2(bra:BRADO5432)*Bradyrhizobium* sp. ORS 278
MSNSTRDGRDWRPDYLVAIDAAKCIGCGRCYKVCGREVMTLKGINDEGEFVELDDDEDDE
VEKKIMVMHDTGACIGCGACARVCPTNCQTHSPAG

>2[4Fe-4S]AlvST2(bbt:BBta_5917)*Bradyrhizobium* sp. BTAi1
MSNSTRDGRDWKPDYLVAINPEKCIGCGRCYKVCGREVMTLKGINDEGEFVELDDDEDDE
VEKKIMVMHDTGACIGCGACARVCPTNCQTHSPAA

>2[4Fe-4S]AlvST2(aol:S58_22740)*Bradyrhizobium oligotrophicum*
MSNSTRDGRDWRPDYLVAIDAGKCIGCGRCYKVCGREVMTLKGINDEGEFVELDDDEDDE
VEKKIMVMHDTGACIGCGACARVCPTNCQTHSPAA

>2[4Fe-4S]AlvST2(brc:BCCGELA001_31120)*Bradyrhizobium* sp. CCGE-
LA001

MSSITRGGREWTPNYLDSIDAKKCIGCGRCFKVCGRNVMTLKGISEEGELVDLEDDEDDE
IEKKIMVMNDKGECIGCGACARVCPTSCQAHDPAIAAPV

>2[4Fe-4S]AlvST2(bic:LMTR13_26810)*Bradyrhizobium icense*
MSFATRDGRDWTPNYLISIDPKKCIGCGRCFKVCGRDVMTLKGINEEGDLVDLDDDEDDE

IEKKIMVMNDQGACIGCGACARVCPTNCQTHQPAATEAA

>2[4Fe-4S]AlvST2(xau:Xaut_0096) *Xanthobacter autotrophicus*
 MSNETRDGRAWQPDYLLDIDADKCIGCGRCFKVCGRDVMTLKGINEDGEVSLDDDEDDE
 VEKKVMVMNDTGACIGCGACARVCPANCQVHGHEQAAA

>2[4Fe-4S]AlvST2(azc:AZC_1034) *Azorhizobium caulinodans*
 MSQSTRDGRAWEPEYLVAIDDRKCIGCGRCYKVCGREVMTLKGITDEGEIVSLDDDEDDE
 VEKKIMVMADTGACIGCGACARVCPTNCQTHVPASQAA

>2[4Fe-4S]AlvST2(msc:BN69_2631) *Methylocystis* sp. SC2
 MSQATRDGRDWCPEYLVAIDPGKCIGCGRCFKVCGRDVMTLKGILNEDGELVALDDDEDEE
 VEKKIMVMNDIGACIGCGACARVCPTNCQTHAAEDVALV

>2[4Fe-4S]AlvST2(bja:bsr1750) *Bradyrhizobium diazoefficiens* USDA
 110
 MSFATRDGRDWMPQYLASIDAKKCIGCGRCFKVCGQDVMTLKGINEEGELVNLDNDADDE
 VEKKIMVLNDQGACIGCGACDRVCPASCQTHVPAAAA

Subtype 3

>2[4Fe-4S]AlvST3(smk:Sinme_6346) *Sinorhizobium meliloti* AK83
 MISSFVTRDGSRWMPKYLSAIDGATCIGCGRCFKVCSREVMHLHGIDDVGEILGPFDEGE
 DDFGGELNRMIMVVDFRGRCIGCGACARVCPRDCQTHVAADILAA

>2[4Fe-4S]AlvST3(smx:SM11_pC1117) *Sinorhizobium meliloti* SM11
 MISSFVTRDGSRWMPKYLSAIDGATCIGCGRCFKVCSREVMHLHGIDDVGEILGPFDEGE
 DDFGGELNRMIMVVDFRGRCIGCGACARVCPRDCQTHVAADILAA

>2[4Fe-4S]AlvST3(daa:AKL17_1557) *Defluviimonas alba*
 MPAIAHTRGGAEYVPQYLMAIDAGKCIGCGRCFKVCGRGVMTLHGLTGEGQLVRPGSDEW
 DELEDEIIKKVMALIAPENCIGCGACARVCPSPDCQSHAALS

>2[4Fe-4S]AlvST3(rcp:RCAP_rcc03275) *Rhodobacter capsulatus*
 MMPTVAYTRGGAEYTPVYLMKIDEQKCIGCGRCFKVCGRDVMSLHGLTEDGQVVAPGTDE
 WDEVEDEIVKKVMALTGAENCIGCGACARVCPSECQTHAALS

>2[4Fe-4S]AlvST3(ngl:RG1141_PB00730) *Neorhizobium galegae* bv.
 officinalis bv. officinalis HAMBI 1141
 MNRSGFTRDGCSWIPEYLNFDAGTCIGCGRCFKVCSREVMHPYGINDAGQILGVCRGAE
 EDFDGELTRVIMAVDYPGRGRCIGCGACARVCPKNCQVYVRADLLPSEPHK

Subtype 4

>2[4Fe-4S]AlvST4(rle:pRL100156) *Rhizobium leguminosarum* bv.
viciae 3841
MTSSSVTRDGSRWMPPEYLN SINPAMCIGCGRCFKVCSREVMHAHGIDEAGDMLGVCDGED
DFNGELSRVIMVIDYPGRCIGCGACARVCPKNCQTHIAVHHRSLHES

Subtype 5

>2[4Fe-4S]AlvST5(rhc:RGUI_2011) *Rhodovulum* sp. P5
MPITATTRGGTEYVPEFLVEIDMEKCIGCGRCYKVCARDVLDLKGVTDEDEIVDVDDEEY
EDDIERKIMVVSADDCIGCGACARVCPSPNCQTHAPAEAA

>2[4Fe-4S]AlvST5(rsu:NHU_01426) *Rhodovulum sulfidophilum*

MPTRSRRITGAPTDPHDRIGAPSRNRPRHDVNSKDTGQALKAAPKAAKEIRAMTITATTRG
GTEYIPEFLMAIDQGKCIGCGRCFKVCARNVLTLLKGVTDEDEIVDLDDDEEFEDDEIERRIMVI
ADGDDCIGCGACARVCPSSCQTHAPA

Subtype 6

>2[4Fe-4S]AlvST6(brs:S23_46360) *Bradyrhizobium* sp. S23321
MSSATRDGRDWRPDYLVSIDPRKCIGCGRCYKVCGREVMTLKGLEDDDEMIDLDDDDDEV
EKKVMVMNDDGACIGCGACARVCPPTNCQTHAPA

Subtype 7

>2[4Fe-4S]AlvST7(mbry:B1812_08085) *Methylocystis bryophila*
MSEFKTRDGRDYVPQYLTDIDASTCIGCGRCFKVCPQGVMAlyGVNDEGEILGAVTEDDDDD
NDFDGELNRKIMKVEEAGACIGCNACARVCPKNCQTHVSADKIAA

Subtype 8

>2[4Fe-4S]AlvST8 (msl:Msi1_3624) *Methylocella silvestris*

MSEFKTRGGAAWTPPLYLTEIDPVTCTIGCGRCFKVCPQNVMTLYGVNDEGEILGAVTQDDDDD
FDGDLNRKIMAVEHPDSCIGCNACSKVCPKNCQTHVSADALSA

Table S3. Ferredoxin protein sequences identified by datamining of published articles and Protein Data Bank (PDB). Ferredoxins were sorted as per their Fe-S cluster type and subtypes. Name of the ferredoxins includes their nomenclature name as described in the methodology followed by protein ID (either GenBank accession number or PDB ID) database and species name. Cysteine amino acids that binds to the Fe-atom of Fe-S cluster is highlighted in the sequences. In case of two Fe-S clusters, cysteine amino acids highlighted with different colors representing their binding to different Fe-S clusters.

2Fe-2S

Subtype 1

Archaea

Bacteria

>2Fe-2SST1 (3LXF) *Novosphingobium aromaticivorans*
TAILVTTRDGTRTEIQAE PGLSLMEALRDAGIDELLALCGGCCSCATCHVLVAPAFADRLPA
LSGDENDLLDSSDHRTPHSRLSCQITINDKLEGLEVEIAPED
>2Fe-2SST1 (mmi:MMAR_3155) *Mycobacterium marinum* M

MAVVTFFVSHGGEKYEAPLEEGQSLMRVATNNAVPGIDGDCGGEAACGTCHVIVDPQWSDRVG
LSGANEEEMLAMNPERQPTSRLSCQM QVSEAWDGLIVHLPEFQL

Eukaryota

>2Fe-2SST1 (AAL95709.1) *Giardia intestinalis*
MSLLSSIRRFITFRVVQQGVEHTVSGAVGQSLDLAIAKAAHIPIQDACEGHLGCGTCGVYLDK
KTYKRIPRATKEEAVLLDQVPNPKPTSRLSCAVKLSSMLEGATVRIPSFNKNVLSESDILAS
EEKKRHGQH

>2Fe-2SST1 (2WLB) *Schizosaccharomyces Pombe*
GTGIKVVFFVTPEGREIMIEGNEGDSILDLAHANNIDLEGACEGSVACSTCHVIVDPEHYELL
DPPEEDEEDMLDLAFGLEETSRLGCQVLLRKDLDGIRVRIP

>2Fe-2SST1 (2MJD) *Saccharomyces cerevisiae*
GEELKITFILKDGSQKTYEVCEGETILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDAL
PEPEDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALPQMTRNVNNDFS

>2Fe-2SST1 (2Y5C) *HOMO SAPIENS*
MASDVVNVFVDRSGQRI PVSGRVGDNVLHLAQRHGV DLEGACEASLACSTCHVYVSEDHLD
LLPPEEREDDMLDMAPLLQENSRLGCQIVLTPELEGAEFTLPK ITR

>2Fe-2SST1 (3P1M) *Homo sapiens* (9606)
MSSSEDKITVHFINRDGETLTTKGKVGDSLLDVVVENNLDIDGFGACEGTLACSTCHLIFED
HIYEKLDAITDEENDMLDLAYGLTDRSRLGCQICLT KSMDNMTVRVPETVADARQSIDVGKT
SAENLYFQ

>2Fe-2SST1 (1AYF) *Bos taurus*
EDKITVHFINRDGETLTTKGKIGDSLLDVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFE
KLEAITDEENDMLDLAYGLTDRSRLGCQICLT KAMDNM TVRVP

>2Fe-2SST1 (2739133354) *Leishmania major Friedlin V1*
MHRRFILGHVLPRLMALAPLSASRALSSAPGKVELRVKKRDGTHCHVYVPVGISLMHAL
RDVSKMDVEGTCNGAMVCATCHVKLSAASFKEIEGPSEVEEDVLARALDVEETSRLACQV
DLTPELDGLELEVELPSQETDRS
>2Fe-2SST1 (639624039) *Trypanosoma brucei brucei* 927/4 GUTat10.1
MLSATFGTLGTSCGRGFLQRQGLLTTFMGRFCHSGGGGNNQNNDSNSGNDGSSTPGAIR
VNVTTAEGEKITFSAPSGLTLMALRDVARVDIEAACDGTACSTCHVILREEDFGKLTAA
SEDEMMLDLAPQVTPTSRLACQVKLSKELDGITLQMPSETTNEMR

>2Fe-2SST1 (2739133353) *Leishmania major Friedlin V1*
MRNHSLLLATGVLLRPPMALAGALYTSRVLYSIPGKVVCARTRDGTPCDFEAPVGMSLM
HAIRDVARLEMDGACDGCAQCSTCHVYLSEACFKKLGPSEQE QDVLDKALDLQDTSRLACQ
ITLTPAMDGLEVVLPKNVTNLLM

>2Fe-2SST1 (2740751416) *Tetrapisispora blattae* CBS 6284
MLSLTNCISKKSLLWKPLTSGRLFSSLASKYALRHSTFNDPTISLRRHPKAINFYKSQ
VRSFSSTLTTFHGHNLNPPKPGELHITFVLKDGEQKTFEVSEGDSLLDIAQAHNLMEGA
CGGSCACSTCHVIVDPDYIDALPEPEDDENDMLDLAYGLTETSRLGCQVKMSKEVEGLRV
ALPAMTRNVSNNDFSNN

>2Fe-2SST1 (639507213) *Danio rerio Tuebingen*
MAAAAVRAGVNFTQRLNRISPVCRCVPLLRNRC TGAARRAVDGFSA PSRRLRTSIGV
CQSEDSSAPEEDAHAQEHIVNVYIDRSGRRI PVQARVGD NVLYLAHKHGIDLEGACEAS
LACSTCHVYVSSGHYDRLPEPEEREDDMLDMAPLLQENSRLGCQIILTPELDGMELTLPK

VTRNFYVDGHVPKPH

>2Fe-2SST1(639503139)*Danio rerio* Tuebingen

MAAAAVRAGVNFTQRLNRISPVCRCPLLRNRCCTGAARRAVDGFSAAPSRLRRTSIGV
CQSEDSSAPEEDAHAEHIVNVVYIDRSGRRIPVQARVGDNVLYLAHKHGIDLEXACEAS
LACSTCHVYVSSGHYDRLPEPEEREDDMLDMAPLLQENSRLGCQIILTPELDGMELTLPK
VTRNFYVDGHVPKPH

>2Fe-2SST1(2740681361)*Sugiyamaella lignohabitans* CBS10342

MTLRLISKLASPSALRRRCALASSKSQAFGTASLLQRSNAIRNAVSGPGGNIYTARSLHTTA
IAHHGHVHKPNPGEELHVTFITKEGEQIQLEVAEGDNLLDIAQAHNMDMEGACGGSCACS
TCHVIVDPDYDKMEEPDDDDENDMLDLAFGLTETSRLGCQIKMTKELDGVRVALPAMTRN
LQARDFQ

>2Fe-2SST1(2740744706)*Kazachstania africana* CBS 2517

MLKAVCRPNTLSRASIVLKSPNFRLLSRTMTAYQFSVRTSLNNSLVVSNSQRMHFSTAQL
LQHGHIKKPVPGEELKVTFVLKDGSSQQTYPDACEGETLLDIAQGHNLDMEGACGGSCACST
CHVIVDPDYDALPEPEDDENDMLDLAYGLTETSRLGCQLKMSKDIDGIRVALPQMTRNV
SSNDFK

>2Fe-2SST1(639333365)*Homo sapiens*

MAASMARGGV SARVLLQAARGTWWNRPGGTSGSGEGVALGTTRKFQATGSRPAGEEDAGG
PERPGDVNVVVFVDRSGQRIPVSGRVGDNVHLAQRHGV DLEGACEASLACSTCHVYVSE
DHLDLLPPPEEREDDMLDMAPLLQENSRLGCQIVLTPELEGAEFTLPKITRNFYVDGHVP
KPH

>2Fe-2SST1(2740596487)*Ustilago bromivora* UB2112

MVTPSATRTALSAATHVLRRQTLTTAPKVLTPRTIPIASSSRLFTTTPIRPHGGITRPAP
GTGVKIH FVDPKGEPLKSVEASEGDDL SVAHEYDIDLEGACEGSIACSTCHVILEPDVY
DSLEEP CDDENDMLDLAFGLTDTSRLGCQVKVTKEQDGMKVQLPAATRNMVVDGHKAGHH

>2Fe-2SST1(2740658214)*Zygosaccharomyces parabailii* ATCC 60483

MFRLQRFSSRLNQVCIALRRAPPIQTYKAMPMTAGFFPLRGRVTFTQPFSTSLKLLHGHL
TPPKPGEELHVTFILRDGTQRTFEVAEGDTLLDIAQANNLEMEGACGGSCACSTCHVIVD
PDYFDALPEPSDDENDMLDLAYGLTETSRLGCQIKMTKDIDGIRVALPAMTRNV SASDFN

>2Fe-2SST1(2740651865)*Zygosaccharomyces parabailii* ATCC 60483

MFRLQRFSSGLNQVCIALRRASPIQTCKATPMTAGLFPLRGRVTFTIQPFSTSLKLLHGHL
TPPKPGEELHVTFILRDGTQRTFEVAEGDTLLDIAQANNLEMEGACGGSCACSTCHVIVD
PDYFDALPEPSDDENDMLDLAYGLTETSRLGCQIKMTKDIDGIRVALPAMTRNV SASDFN

>2Fe-2SST1(645679239)*Zygosaccharomyces rouxii* CBS 732

MFRI PRINFMVNRAVLASRRAFHAQNHMRNLQQPVARRTILTHTKPFSTTSKLSHGHLTP
PKPGEELKVTFILKDGSRQTYEVAEGDSLDDIAQANNLEMEGACGGSCACSTCHVIVDPD
YFDALPESDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALPAMTRNVNASDFD

>2Fe-2SST1(2740641114)*Candida intermedia* CBS 141442

MLSRILARQPCLPYLGQARSVNLVGLQVRSLLQOMKLTHRLASRHFQVSASALHGHIHKP
KPGEELKITFITKDGTQHTFEVAEGDNLLDIAQAYNLDMEGACGGLCACSTCHII VDPDF
YDEIPEPDDENDMLDLAFGLTETSRLGCQVKMSKELDGIRVALPAMTRNLQSKDFS

>2Fe-2SST1(2740648393)*Candida intermedia* PYCC 4715

MLSRILTRQPCLPYLGQARSVNLVGLQVRSLLQOMKLTHHLASRHFQVSASALHGHIHKP
KPGEELKITFITKDGTQHTFEVAEGDNLLDIAQAYNLDMEGACGGLCACSTCHII VDPDF
YDEIPEPDDENDMLDLAFGLTETSRLGCQVKMSKELDGIRVALPAMTRNLQSKDFS

>2Fe-2SST1(645669254)*Candida dubliniensis* CD36
MFRLIPRLKPIIPSINRISVSIKPPPLPPPTSPSTPQQCHVLRAFHTSPISHHGHLKKPNP
GEELHITFITKDGKQLTYEVAEGDNILDIAQAHNLDMEGACGGSCACSTCHVIVDPPEYYD
KLEEPDDENDMLDLAFGLTETSRLGCQVKMTKELDGLRVALPAMTRNLQSRDFN

>2Fe-2SST1(2740733507)*Sporisorium reilianum* SRZ2
MAATLARTALTEAARQAVRRPSLAPSLALRVPTPSLRLLSTTAPRPHGGITRPAPGSGIT
IHFIDPKGEPLKTVAANEGDDLISIAHEYDIDLEGACEGSIACSTCHVILEPVDVYSLEE
PCDDENDMLDLAFGLTETSRLGCQVKVTKEQDGMKVQLPAATRNMVVDGHKAGHH

>2Fe-2SST1(2740773685)*Saccharomyces cerevisiae* YJM1078
MLKIVTRAGHTARISNIAAHLRTSPSLLTRTTTTTRFLPFSTSSFLNHGHLKKPKPGEE
LKITFILKDGSKTYEVCEGETILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALP
EPEDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALPQMTRNVNNNDFS

>2Fe-2SST1(638214378)*Saccharomyces cerevisiae* S288C
MLKIVTRAGHTARISNIAAHLRTSPSLLTRTTTTTRFLPFSTSSFLNHGHLKKPKPGEE
LKITFILKDGSKTYEVCEGETILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALP
EPEDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALPQMTRNVNNNDFS

>2Fe-2SST1(2740718184)*Saccharomyces cerevisiae* YJM1332
MLKIVTRAGHTARISNIAAHLRTSPSLLTRTTTTTRFLPFSTSSFLNHGHLKKPKPGEE
LKITFILKDGSKTYEVCEGETILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALP
EPEDDENDMLDLAYGLTETSRLGCQIKMSKDIDGIRVALPQMTRNVNNNDFS

>2Fe-2SST1(639514291)*Caenorhabditis elegans* Bristol N2
MSSVLRRLAMRAKGFSRFLAETQAFPVKNRHFMTSSVRKTGDFEYEDPKSEDEVVNITYVL
RDGTERKIRGKVGDNVMFLAHRYDIEMEGACEASLACSTCHVYVDPAFQNKLEPELEED
DMLDMAPALKDNSRLGCQIVLTKELDGITVTLPTMTRNFYVDGHVPKPH

>2Fe-2SST1(2739117763)*Candida albicans* SC5314
MFRLIPRLKPIIPSINRISLSVKPQPSTSQHCHTLRAFHTSPISLHGHLKKPNPGEELHI
TFITKDGKQLTYEVAEGDNILDIAQAHNLDMEGACGGSCACSTCHVIVDPPEYYDRLEEPD
DDENDMLDLAFGLTETSRLGCQVKMTKELDGLRVALPAMTRNLQSRDFN

>2Fe-2SST1(2740887005)*Kazachstania naganishii* CBS 8797
MFRLLLKNSMRPTILTVRSSGSSQLLNSSILTASRGFSRTRPRLHGHRLKPAKGEELKIS
FILKDGTSKTYEVAEGDTILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALQEPED
DENDMLDLAYGLTETSRLGCQVKMSKDIDGIRVALPQMTRNVNNKDFS

>2Fe-2SST1(638229415)*Candida glabrata* CBS 138
MQHILRRSIVPISRNIGLSRRFADRPLWQSSARLFSTSMMLSHGHKPKPNPGEELHVTYI
LKDGSKTYEVADGDTLLDIAQANNLDMEGACGGSCACSTCHVIVDPDYDAIPEPEDDE
NDMLDLAYGLTETSRLGCQVKMSKDIDGIRVALPAMTRNVSNNDNFQ

>2Fe-2SST1(2740687691)*Kluyveromyces marxianus* NBRC 1777
MLRTILPRQAVLLNQFRTGAMHSRMQMKPHTRLWTSNLIGKRFHGHHLHKPKPGEEELHVTF
ILKDGTSKTYEVAEGDSLDDIAQGHNLDMEGACGGSCACSTCHVIVDPPEYYDALEEPDDD
ENDMLDLAYGLTETSRLGCCIKMSKDIDGIRVALPAMTRNVSSSTDFE

>2Fe-2SST1(638233708)*Kluyveromyces lactis* NRRL Y-1140
MIRGILTRQAGHLNQLRARSITSPSISHNIWLARTNLSWKRYHGHHLHKPKPGEEELHVTFI
LKDGTSKTYEVAEGDSLDDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALEEPDDDE
NDMLDLAYGLTETSRLGCCIKMKNKDIDGIRVALPSMTRNVSSSTDFE

>2Fe-2SST1(2740668374)*Millerozyma farinosa* CBS 7064
MIRSLVRITRGPSVRANIKFVPTAQRICIPFSRGFHYSA PRNHGHKPKPGEEELKITFI
TKEGEQHTYEVAEGDNILDIAQAHNLDMEGACGGSCACSTCHIIIVDPPEYYDAIPEPDDE
NDMLDLAFGLTETSRLGCQVVMTELDGIRVALPAMTRNLQKQKDFK

>2Fe-2SST1(2740667312)*Millerozyma farinosa* CBS 7064
MIRSLVRITRGPSVRANIKFVPTAQRICIPFSRGFHYSA PRNHGHKPKPGEEELKITFI
TKEGEQHTYEVAEGDNILDIAQAHNLDMEGACGGSCACSTCHIIIVDPPEYYDAIPEPDDE

NDMLDLAFGLTETSRLGCQVVMTKELDGIRVALPAMTRNLQQKDFK
 >2Fe-2SST1(638241122)*Debaryomyces hansenii* var. *hansenii* CBS767
 MFRSILRSSRCIPKTLQNNCRSPTVVTPNLNLYKQFHQTVPKFHGHLHKPNPGEELHITFI
 TKDGEQLSFEVAEGDNVLDIAQAHNLDMEGACGGSCACSTCHVIVDPEFYDEIPEPDDDE
 NDMLDLAFGLTETSRLGCQIKMSKEIDGIRVALPAMTRNLQNKDFN
 >2Fe-2SST1(2517316129)*Eremothecium cymbalariae* DBVPG#7215
 MIGRLLVRQLRTVQSLKPLWLQGNINATARLRKPLIQQRHGHILHEPKKGEELHVTFIL
 KDGTQKTFEVCEGDTLLDIAQGHNLDEGACGGSCACSTCHVIVDPDYVDLDEPGDDEN
 DMLDLAYGLTETSRLGCCIKMSKDVDGLRVALPAMTRNVNSSDFE
 >2Fe-2SST1(2753004395)*Eremothecium sinicaudum* ATCC 58844
 MLGRLLPRSSNKIPYTALLRTQKTYPSPPLYKRSPLAKRYHYVLQKPKKGEELNVTFILK
 DGSQKTFQVCEGDSVLDIAQSNLDMEGACGGSCACSTCHVIVDPDYVDLLEEPNDDEND
 MLDLAYGLTETSRLGCCIKMNKKIDGIRLALPAMTRNVNLSDFE
 >2Fe-2SST1(645683142)*Lachancea thermotolerans* CBS 6340
 MFRIAGLSKSLRGLAVGRANIMVPKYAGFAQSALRFHGHVHKPKPGEELHVTFILKDG
 SQRQYEVSAAGDTLLDIAQANNLEMEGACGGSCACSTCHVIVDPDYDALEEPDDDENDML
 DLAYGLTETSRLGCQIKMSKDIDGIRVALPAMTRNVSNSTDFD
 >2Fe-2SST1(2740615562)*Yarrowia lipolytica* CLIB89(W29)
 MLRTFSRQVLQVSRAPVPTFRPVAPATRLFQTSAPVFHGHVHKPKPGEELIKVTFITKDGE
 QIEVDTCEGDNLLDIAQANNLDMEGACGGSCACSTCHVIVDPEYYDKLEEPDDDENDMLD
 LAFGLTETSRLGCQVCMKDLDGIRIALPAMTRNLQASDFN
 >2Fe-2SST1(638246243)*Yarrowia lipolytica* CLIB122
 MLRTFSRQVLQVSRAPVPTFRPVAPATRLFQTSAPVFHGHVHKPKPGEELIKVTFITKDGE
 QIEVDTCEGDNLLDIAQANNLDMEGACGGSCACSTCHVIVDPEYYDKLEEPDDDENDMLD
 LAFGLTETSRLGCQVCMKDLDGIRIALPAMTRNLQASDFN
 >2Fe-2SST1(645674107)*Komagataella pastoris* GS115
 MFKPVFTKRMALNYLGSIAIKYRHNPLRLPRIPVRFHGHLLKPNPGEELHITFITKDGTQ
 KTFEVAEGDSLDDIAQGNHLDMEGACGGSCACSTCHVIIDPEFYDEIPEPDDDENDMLDL
 AFGLTETSRLGCQVFMKNLDGIRVALPAMTRNLQSSDFD
 >2Fe-2SST1(2740662368)*Komagataella phaffii* CBS 7435
 MFKPVFTKRMALNYLGSIAIKYRHNPLRLPRIPVRFHGHLLKPNPGEELHITFITKDGTQ
 KTFEVAEGDSLDDIAQGNHLDMEGACGGSCACSTCHVIIDPEFYDEIPEPDDDENDMLDL
 AFGLTETSRLGCQVFMKNLDGIRVALPAMTRNLQSSDFD
 >2Fe-2SST1(2740695651)*Ashbya* sp. FD-2008
 MLGRLLPISARAVRFARAPPVVRALRAHGLSTPRKGEELQVTFILKDGSGQRTFDVAPGD
 TLLDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALEEPDDDENDMLDLAYGLTETSRL
 LGCCIRMSKDINGLRVALPAMTRNVSNNSDFN
 >2Fe-2SST1(638225492)*Eremothecium gossypii* ATCC 10895
 MLGRLLPISARAVRFARAPPFMRALRAHGLSTPRKGEELQVTFILKDGSGQRTFDVAPGD
 TLLDIAQGHNLDMEGACGGSCACSTCHVIVDPDYDALQEPDDDENDMLDLAYGLTETSRL
 LGCCIRMSKDINGLRVALPAMTRNVSNNSDFS
 >2Fe-2SST1(649342403)*Thalassiosira pseudonana* CCMP 1335
 ETVTITYVDPDGEEHPVKAIEVGKNLLDIAHENNIELEGACGGELACSTCHLVFDRDVFD
 LPPKSDEEEDMLDLAFELTDTSRLGCQICVTKEFEGIKVRIPDDGY

 >2Fe-2SST1(639494181)*Danio rerio* Tuebingen
 MAYRMCVRVLLRSSSLLACHPGSVRSHAEFHHTVPSLCSQSQSLNGSSSSKVLVHFVNQSG
 VKSSVFVTEGETLLDVVIKKNLDFSGFGACEGTLACSTCHLIFEENVFDKLEPMVDEEID
 MLDLAYGITKTSRLGCQVTVERWMDGMTVRVPQDIKDQRGKQEAUVSSK
 >2Fe-2SST1(2740677148)*Encephalitozoon romaleae* SJ-2008
 MYEASQGTGLYSLFPPLKFLSVIFALDLPAMSYAPDRASGKIKLFFKAMGQMPVKAVY

GDTVLETAHKNGVNLEGACEGNLACSTCHVILEESLYKRLGEPDKEYDLIDQAAGGTST
 SRLGCQLKVDKNFENAVLTIPRATKNMAVDGFKPEPH
 >2Fe-2SST1 (639496254) *Danio rerio* Tuebingen
 MSLPTLEQLQSSSSSKVLVHFNQSGVKSSVFVTEGETLLHVVIKSLDFIGFGACEGTL
 ACSTCHLIFEENVFDKLEPMVDEEIDMLDLAYGITKTSRLGCQVTVERWMDGMTVRVPQD
 IKDQRGKQEAUSSK
 >2Fe-2SST1 (2740826195) *Encephalitozoon hellem* ATCC 50504
 MGMSGAPDRTPGKIEVFFKAMGQVIPAETVCGDTVLEAAHKNGISLEGACEGNLACSTCH
 VILEEPLYRRLGEPDKEYDLIDQAAGGTSTSRSLGCQLKIDKSFEKAIFTIPRATKNMAV
 DGFKPKPH
 >2Fe-2SST1 (2517314586) *Encephalitozoon intestinalis* ATCC 5050
 MDMANAPDKTSGKVGLLFKTMGKMIPVNAVYGDTVLETAHKNGVLDLEGACEGNLACSTCH
 VILEEPLYRRLGEPDKEYDLIDQAAGITSTSRSLGCQLKIDKSFEKTVLTIPRATKNMAV
 DGFKPKPH
 >2Fe-2SST1 (638215829) *Encephalitozoon cuniculi* GB-M1
 MDMFSAPDRIPEQIRIFFKTMQVVPKAVCGSTVLDVAHKNGVLDLEGACEGNLACSTCH
 VILEEPLYRKLGEPSDKEYDLIDQAAGATGTSRLGCQLRVDKSFENAVFTVPRATKNMAV
 DGFKPKPH

>2Fe-2SST1 (639337880) *Homo sapiens*
 MAAAGGARLLRAASAVLGGPAGRWLHHAGSRAGSSGLLRNRGPGGSAEASRSLSVSARAR
 SSEDKITVHFIFINRDGETLTTKGKVGDSLDDVVENNLDIDGFGACEGTLACSTCHLIFE
 DHIYEKLDAITDEENDMLDLAYGLTDRSRLGCQICLTKSMNMTVRVPETVADARQSIDV
 GKTS
 >2Fe-2SST1 (639497030) *Danio rerio* Tuebingen
 MSACVLR AFLQRAAVMRQAAQQTISQTRAFFQSYTHIRGINTYANSLRAEEKVTVHFLNR
 DGKRITVKASIGESLLDVVDRDLIDGFGACEGTLACSTCHLIFEEDVYKKLGPSVDEE
 MDMLDLAYGLTDTSRSLGCQVCLRKDLGMLRVPDVISDARADSEKESSTAPPKI
 >2Fe-2SST1 (2740816765) *Babesia microti* RI
 MQYYILSQTRAYITRYFMRQNIYNNFLPLPQSNRAPYLQQCVYYSTNKLKVTFFIFQNG
 NEKVVSVESGTSILEAAHKNNDIELEGACDGCLACSTCHVILEQKVFDRLEPSEAEFDML
 DLAPCLTDTSRSLGCQVKLDEGMDGIKIKLPQITRNFYVDGHIPOAH
 >2Fe-2SST1 (2740822904) *Plasmodium knowlesi* H
 MTEDGENDYNFFSRNNTFKRALLNKIKNKCIYFNYIRAFITTQSQEEIDVTFVNQDNYEKT
 VKAKVGDSILKVAHENSINIEGACDGFCACSTCHVIIDDKYNNLLPEALDNEIDMLELAP
 CITETSRSLGCQVKLRKDLGDMKIKLPPMTRNFYVDGYVPTPH
 >2Fe-2SST1 (2740848162) *Plasmodium berghei* K173
 MNSKFSFPIRNNIFKRFLPSKSKNNYLYLNLKKKFTTQNSDEINVTFLNHDNHETTVKAQ
 VGDSILKVAHENNINIEGACEGFCACSTCHVIIDNQFYELLPEAQDNELDMLELAPCITE
 TSRLGCQVKLTKELDGMKIKLPPMTRNFYVDGYVPTPH
 >2Fe-2SST1 (2740784779) *Plasmodium yoelii* 17X
 MISRFSFPIRNNIFKRVL PSTFKNNYIYLNFKKSFTTQNSDEINVTFLNHDNHETTVKAQ
 VGDSILKVAHENNINIEGACEGFCACSTCHVIIDDEFYELLPEAQDNELDMLELAPCITE
 TSRLGCQVKLTKELDGIKIKLPPMTRNFYVDGYVPTPH
 >2Fe-2SST1 (2740576725) *Plasmodium coatneyi* Hackeri
 MITKFSFSLRNDTFKRALLNKIKNKCIYFNYIRAFITTESPEEIDVTFVNQDNYEKT VKAK
 VGDSILKVAHENSINIEGACDGFCACSTCHVIIDDKYDNLPEALDNEIDMLELAPCITE
 TSRLGCQVKLKKELDGMKIKLPPMTRNFYVDGYVPTPH
 >2Fe-2SST1 (2740790168) *Plasmodium berghei* ANKA
 MNSKFSFPIRNNIFKRFLPSKSKNNYLYLNLKKKFTTQNSDEINVTFLNHDNHETTVKAQ
 VGDSILKVAHENNINIEGACEGFCACSTCHVIIDNQFYELLPEAQDNELDMLELAPCITE

TSRLGCQVKLTKELDGMKIKLPPMTRNFYVDGYVPTPH
>2Fe-2SST1 (2740780372) *Plasmodium chabaudi* AS
MISRFSFPIRNNIFKRVLPSKSKNNYIYLNFIKNFTTQNSDEINVTFLNQDNHETSVKAK
VGDSILKVAHENNINIEGACEGFCACSTCHVIIDKEFYELLPEAQDNELDMLELAPCITE
TSRLGCQVKLTKELDGIKVQLPPMTRNFYVDGHVPTPH
>2Fe-2SST1 (2740829509) *Theileria orientalis Shintoku*
MYRLYNIINSSILLIPKPNLNTLIKAGNRNFTTNNLINISFIQYDEEINVSVPVGISILE
AAHRNNIEIEGACDGCMACSTCHVILDENVYNALPEPTEAEMDMLDLAPCLTPTSRLGCQ
VILNEKHDGIRIKLPRITRNFYVDGYTPSHH
>2Fe-2SST1 (2739112146) *Theileria annulata Ankara C9*
MKLLCNIFNNSINKFLRPNSYFFYKNFYNHSTQNIKITFVQYEDIEITVDVPVGISILEA
AHKHNIIEIEGACDGCMACSTCHVILEEDVYDALPEPSESELDMLDLAPCLTNTSRLGCQV
ILGKEHDNIRITLPRITRNFYVDGHTPTPH
>2Fe-2SST1 (638271548) *Plasmodium falciparum* 3D7
MIYLYFSFFSYFYSFYSFYFFWYSDVTFINQDNYEKTVMKAKIGDSILKVAHDNHINIEGA
CEGFCACSTCHVIIDENFHDLLPEPLDNEIDMLELAPCITETSRLGCQIKLSKELDGMKI
QLPPMTRNFYVDGHVPTPH

>2Fe-2SST1 (2739131228) *Leishmania major Friedlin V1*
MGNGRMRRLTGCTSLCLASVTVQGGSLQSRRFHGHGGDRNKPVEVEFTLPDGEKKVVMG
YEGQTLDDVCAEQGLPMEGACGGSCACSTCHVYLEEKVMDLQFQPTDDENDMIDQAFYPEPT
SRLGCQLTLKRGVHDGLKVKMPRATRNMYVDGAKVVPH

Subtype 2

Bacteria

>2Fe-2SST2 (1B9R) *Pseudomonas* sp.
PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVGE
ANPDENDLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA
>2Fe-2SST2 (1UWM) *Rhodobacter Capsulatus*
AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADC GGACACSTCHAYVDPAWVDKLPK
ALPTETDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI
>2Fe-2SST2 (1PDX) *Pseudomonas putida*
SKVVYVSHDGTRRELDVADGVSLMQAAVSNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPA
ANEREIGMLECVTAELKPNSRLCCQIIMTPELDGIVVDVPDRQW
>2Fe-2SST2 (CCH23747.1) *Corynebacterium glutamicum* K051
MSTIHFDHAGKTRTIEATVGDSVMETAVRNGVPGIVAECGGSLSATCHVFVDPAQYDALP
PMEEMEDEMLWGAAVDREDCSRLSCQIKVTEGMDLSLTPETQV

Eukaryota

>2Fe-2SST2 (ath:AT4G05450) *Arabidopsis thaliana*
MIGHRISRLGSTIVKQLAREGYLATYGTKNLHRSYGHYQLQSLPVVPRQARTSQEAWFLKSHK
FCTSSTTSSENGDEETEKITIIIFVDKDGEIIPVKVPIGMSVLEAAHENDIDLEGACEASLAC
STCHVIVMDTEYYNKL EPTDEENDMLDLAFLGTETSR LGCQVIARPELDGVRLAIP SATRN
FAVDGFV PKPH

>2Fe-2SST2 (2505189252) *Paulinella chromatophora*
MPVIRFVREGIDVECYPGENLREVALRHGIELYGIKGLGNCGGCGQCITCFVDIISPHG
SNSPSTLSARTQVENMKLRRRPDTWRLGCQVLVYGSVLVLTRPQLGLPDAEYRIAAARTA
KLSKGNMSWFSPEVNINPEQSTTSSEGDEEPALNSD TVS
>2Fe-2SST2 (2739133352) *Leishmania major Friedlin V1*
MHR LALPRVVL CARHPAASAPLTTSSGASLRWCSSPPPSLSPSTTPGKV KVHIKSETEGT
EKTVEAALGLTLMEVIRDVAKMDMEAACDGT CACSTCHVIFTAASYQKLLDAPSEDEM DMLD
LAPKVTKTSRLSCQVKIAPELDDISVTIPNEMENQMGY

>2Fe-2SST2 (640421166) *Ostreococcus lucimarinus* CCE9901
IEVTFVERDGERRAVRGLIGENLLETAHRHDVELEGACEGSLACSTCHVVFED EKV FETLPE
ACDDENDMLDLAYGLTATSRLGCQVTLERGALEGCVVILPRATRNF AVDGFV PKPH
>2Fe-2SST2 (640421163) *Ostreococcus lucimarinus* CCE9901
IEVTFVERDGERRAVRGLIGENLLETAHRHDVELEGACEGSLACSTCHVVFED EKV FETLPE
ACDDENDMLDLAYGLTATSRLGCQVTLERGALEGCVVILPRATRNF AVDGFV PKPH

>2Fe-2SST2 (639625305) *Trypanosoma brucei brucei* 927/4 GUTat10.1
MAALRYLLAPRRALVTPFLRSVTCVSSGGIFSSQRPHTFPVLWHAVRTHSND SGERSKPLTL
HVQLPCGTMRTL TAYEGQTL LDVAMEHGLPIEGACGGSCACSTCHVYLENDEAMEL FDEATD
EENDMLDMAFFPQSTSRLGCQLTLRQQKHDGLKISLPKATRNM YVDGHTITPHH

>2Fe-2SST2 (2517260843) *Thielavia terrestris* NRRL 8126
MSTPKLLAQTLPSLRLATRR TAPSIARHVVR CYTAASAAPRPAPP AWSSQPPIRRSLWSA
AFQSRPFSVSTAVSHGHIQPPKPGEELYVT FIDKEGVEHKLAVSKGDNLLDIAQAHDLEM
EGACGGSCACSTCHVIVMDQEYYDRMPEPDD DENDMLDLAFLGLQETSRLGCQVVMTPELN
GLRVKLPAMTRNLQSSDFK

>2Fe-2SST2 (2762808093) *Thielavia terrestris* NRRL 8126
MSTPKLLAQTLPSLRLATRR TAPSIARHVVR CYTAASAAPRPAPP AWSSQPPIRRSLWSA
AFQSRPFSVSTAVSHGHIQPPKPGEELYVT FIDKEGVEHKLAVSKGDNLLDIAQAHDLEM
EGACGGSCACSTCHVIVMDQEYYDRMPEPDD DENDMLDLAFLGLQETSRLGCQVVMTPELN
GLRVKLPAMTRNLQSSDFK

>2Fe-2SST2 (2762871174) *Thermothelomyces thermophila* ATCC 42464
MSAPKLFAQALPTLRRAPRLTTGAIGRRVRCYTQASAAARPTNSSRVVQAVARRSPALMR
AQRRTFSASPAVSHGHIKPPKPGEELYVT FVDKEGVEHKFAVSKGDNLLDIAQANDLEME
GACGGSCACSTCHVIVLDQEYYDKMPEPDD DENDMLDLAFLGLQETSRLGCQVVMTPELDG
LRVKLP SMTRNLQSSDFK

>2Fe-2SST2 (2517254265) *Thermothelomyces thermophila* ATCC 42464
MSAPKLFAQALPTLRRAPRLTTGAIGRRVRCYTQASAAARPTNSSRVVQAVARRSPALMR
AQRRTFSASPAVSHGHIKPPKPGEELYVT FVDKEGVEHKFAVSKGDNLLDIAQANDLEME
GACGGSCACSTCHVIVLDQEYYDKMPEPDD DENDMLDLAFLGLQETSRLGCQVVMTPELDG
LRVKLP SMTRNLQSSDFK

>2Fe-2SST2 (640296514) *Fusarium graminearum* PH-1

MSASRSFATCLAKLPATACRTTQPMRFSQNIMSQASRSQFAVIPRAVRFSPVSQRAFTTS
TQRRHGHIDPPKPGEEELYVTFTIEKDG TENKF AVSEGDNLLDIAQANDLEMEGACGGSCAC
STCHVIVADDEYFDKMPEPEDDENDMLDLAFGLTETSR LGCQVKMTKEMDGLVVKLPSMT
RNLQASDFS

>2Fe-2SST2(2740844848)*Fusarium fujikuroi* IMI 58289

MSASRSFATCLAKLPATAPRTIQPMRLGQNVVSQTSKGRSPTISRFTRFSPVSHRAFTTT
TQRRHGHIDPPKPGEEELYVTFTIEKDG TENKF AVSEGDNLLDIAQANDLEMEGACGGSCAC
STCHVIVADDA YFDKMPEPEDDENDMLDLAFGLTETSR LGCQVKMTKELDGLVVKLPSMT
RNLQASDFS

>2Fe-2SST2(639576354)*Arabidopsis thaliana Columbia*

MVFHRLSRLGSRIVKELPRERHLSMCGKRILQRSYGQYLQSSPMLQRQTRSFKEALFSNN
HKFCTSFSTTSEKGGEKTEKINVT FVDKDGE E IHIKVPVGMNILEAAHENDIELEGACEG
SLACSTCHVIVMDTKYYNKLEEPTDEENDMLDLAFGLTATSR LGCQVIAKPELDGVR LAI
PSATRNF AVDGFVPKPH

>2Fe-2SST2(639574862)*Arabidopsis thaliana Columbia*

MIGHRISRLGSTIVKQLAREGYLATYGTKNLHRSYGHY LQSLPVVPRQARTSQEAWFLKS
HKFCTSSSTTSSENGDEETEKIT IIFVDKDGE EIPVKVPIGMSVLEAAHENDIDLEGACEA
SLACSTCHVIVMDTEYYNKLEEPTDEENDMLDLAFGLTETSR LGCQVIARPELDGVR LAI
PSATRNF AVDGFVPKPH

>2Fe-2SST2(2507880113)*Zea mays mays* cv. B73

MFPRI SRLGARLLRESRAETRAGNLLNSQRIF FQD HVNRHSIPVVTPAVLSMRNALLSTA
TSGDQDESSQAKDKISVTFVNKDGSEKTICVPVGMSMLEAAHENDIELEGACEGSLACST
CHVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGMRLALPVATR N
FAVDGYVPKPH

>2Fe-2SST2(2507880112)*Zea mays mays* cv. B73

MFPRI SRLGARLLRESRAETRAGNLLNSQRIF FQD HVNRHSIPVVTPAVLSMRNALLSTA
TSGDQDESSQAKDKISVTFVNKDGSEKTICVPVGMSMLEAAHENDIELEGACEGSLACST
CHVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGMRLALPVATR N
FAVDGYVPKPH

>2Fe-2SST2(2507880116)*Zea mays mays* cv. B73

MIVEVIFLHTVNRISVTFVNKDGSEKTICVPVGMSMLEAAHENDIELEGACEGSLACSTC
HVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGMRLALPVATR NF
AVDGYVPKPH

>2Fe-2SST2(2507880115)*Zea mays mays* cv. B73

MIVEVIFLHTVNRISVTFVNKDGSEKTICVPVGMSMLEAAHENDIELEGACEGSLACSTC
HVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGMRLALPVATR NF
AVDGYVPKPH

>2Fe-2SST2(2507880114)*Zea mays mays* cv. B73

MIVEVIFLHTVNRISVTFVNKDGSEKTICVPVGMSMLEAAHENDIELEGACEGSLACSTC
HVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGMRLALPVATR NF
AVDGYVPKPH

>2Fe-2SST2(2507857107)*Zea mays mays* cv. B73

MTDVVIFLCIMHRISVTFVNKDGSEKTIRVPVGMSMLEAAHENDIELEGACEGSLACSTC
HVIVMDVNYYNKLEDPADEENDMLDLAFGLTETSR LGCQVIAKPELDGIRLALPVATR NF
AVDGYVPKPH

>2Fe-2SST2(2508320447)*Micromonas pusilla* NOUM17, RCC 299

MLEVAHKNDIELEGACEGSLACSTCHVIINDQAVYDALPEPDDDENDMLDLAFGLTETSR
LGCQVIAAKELDGMTLSLPKATRNF AVDGFVPKPH

>2Fe-2SST2(2507880117)*Zea mays mays* cv. B73

MITFPAIVATAGACEGSLACSTCHVIVMDVKYYNKLEDPADEENDMLDLAFGLTETSRLGCQ
VIAKPELDGMRLALPVATRNFVAVDGYVVKPH

Subtype 3

Archaea

>2Fe-2SST3(2545641477)*Halobiforma lacisalsi* AJ5, JCM 12983
VTGSTSTTWTVELRVPEDADLEAAGESRSIEVRENQSILSAARGAGLWLSADCQQGWCITCG
CGARLLEGEVDHANAKRYYPEDEAAGFVLTCVAQPRSDCVLEVERYDELLEHRAEHRPP
GRSKLG

>2Fe-2SST3(2509883874)*Natrinema pellirubrum* 157
MTASTTWEVELRVPDDADLEAAGESRTIAVREDEAILAAARRAGLWLSADCQQGWCITCG
ARLLEGEVDHSDAKRYYPEDEAENFVLTCVAQPRADCVIVVEQYDELLRHRADHDRPPGR
SKLG

>2Fe-2SST3(2517201353)*Natrinema* sp. J7-2
MTAPTWEVELRVPEDAAALDAAGESRTVAVREDQSILTAARAADLWLSADCQQGWCITCG
AKLRSGEVDHSRAKRYYPSEDAANFVLTCVARPRSDCVIEVERSEALLRHRADHDKPPGR
SKLE

>2Fe-2SST3(2510572427)*Natronobacterium gregoryi* SP2(2510572427)
MTAATTWTVELRVPQDADLEAAGESRTIEVPEDQSILSAARAAGIWLTAADCQQGWCITCG
ARLLEGEVDHSTAKRYYPEDERAGFVLTCVARPRSDCVLEVERDDELLRHRADHDRPPGR
SKLD

>2Fe-2SST3(648063341)*Halalkalicoccus jeotgali* B3, DSM 18796
MGETTYSVEIVVPEDADSQRAGETVETRVDEDDYVLASARSQDVWLAADCQQGWCTTCAA
ELLEGEVDQSDAKRYYESDEAAGMILPCTAKPRSDLTIRAFQYEEMLEHRAANDNPPGNS
KLD

>2Fe-2SST3(2507055677)*Halobacterium* sp. DL1
MELVVPEDCEIPQAGETVDVEVPEGEYVLWAAREAGVWLPADCQQGWCCRCAGELLSGEL
DQTDARRYFETDRDAALHLLCTAVPQSDCRIRVCQYEEMLDERAKQELPPGNSKR

>2Fe-2SST3(2540571112)*Natronomonas moolapensis* 8.8.11, DSM
18674
MSDADTDVWDVTIEIPADADLEEAGETHTIRVGSEYILAAAREQGLWVPADCQQGWCIT
CAATVLEGDVDQSDAKRYYSEDADADFALICTAKPNSDVTCLKVGAHEELLRHRADTDRPP
GSSKL

Bacteria

>2Fe-2SST3 (1CZP) *Nostoc* sp.
 ATFKVTLINEAEGTKHEIEVPDDEYILDAAEEQGYDLPFSCRAGACSTCAGKLVSGTVDQSD
 QSFLDDDDQIEAGYVLTCVAYPTSDVVIQTHKEEDLY

>2Fe-2SST3 (1RFK) *Mastigocladus laminosus*
 ATYKVTLINEAEGLNKTIEVPDDQYILDAAEEAGIDLPHYSCRAGACSTCAGKLISGTVDQSD
 QSFLDDDDQIEAGYVLTCVAYPTSDCVIETHKEEELY

>2Fe-2SST3 (ABB57529.1) *Synechococcus elongatus* PCC 7942 = FACHB-805
 MATYKVTLVNAAEGLNTTIDVADDTYILDAAEEQGIDLPHYSCRAGACSTCAGKVVSGTVDQSD
 DQSFLDDDDQIAAGFVLTCVAYPTSDVTIETHKEEDLY

>2Fe-2SST3 (4FXC) *Arthrospira platensis*
 ATYKVTLINEAEGINETIDCDDDTYILDAAEEAGLDLPYSCRAGACSTCAGTITSGTIDQSD
 QSFLDDDDQIEAGYVLTCVAYPTSDCTIKTHQEEGLY

>2Fe-2SST3 (3B2G) *Leptolyngbya boryana*
 PSFKVTLINETEGLNTTIEVPDDEYILDAAEEQGIDLPHYSCRAGACSTCAGKITAGTVDQSD
 QSFLDDDDQIQAGYVLTCVAYPTSDCTILTHQEEEDLY

>2Fe-2SST3 (1OFF) *SYNECHOCYSTIS* SP.
 MASYTVKLITPDGESSIECSDDTYILDAAEEAGLDLPYSCRAGACSTCAGKITAGSVDQSDQ
 SFLDDDDQIEAGYVLTCVAYPTSDCTIETHKEEDLY

>2Fe-2SST3 (1ROE) *Synechococcus elongatus*
 ATYKVTLVRPDGETTIDVPEDEYILDVAEEQGLDLPFSCRAGACSTCAGKLLEGEVDQSDQ
 SFLDDDDQIEKGFVLTCVAYPRSDCKILTNQEEELY

>2Fe-2SST3 (ABB58611.1) *Synechococcus elongatus* PCC 7942 = FACHB-805
 MSDTYTVRIRDRRTDEEFTVQVPPDRYILQTAEQGYELPFSCRNGACTACAVRVLGGAIEQ
 TEAMGLSAPLRQRGYALLCVSYPRSDVIVETQDEDEVYMLQFGRYFGQGKVSFGLPLDEE

>2Fe-2SST3 (ABB56370.1) *Synechococcus elongatus* PCC 7942 = FACHB-805
 MATYQVEVIYQGQSQTFTADSDQSVLDSAQAAGVDLPASCLTGVCTTCAARILSGEVDQPD
 MGVGPEPAKQGYTLLCVAYPRSDLKIETHKEDELYALQFGQPG

>2Fe-2SST3 (1IUE) *Plasmodium falciparum*
 AFYNITLRTNDGEKKIECNEDEYILDASERQNVELPHYSCRGGSCSTCAAKLVEGEVDNDDQS
 YLDEEQIKKKYILLCTCYPKSDCVIETHKEDELHDM

>2Fe-2SST3 (1FRD) *Nostoc* sp.
 ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFCHSGSCSSCVGKVVEGEVDQSD
 QIFLDDEQMGKGFALLCVTYPRSNCTIKTHQEPYLA

Eukaryota

>2Fe-2SST3 (2MH7) *Chlamydomonas reinhardtii*
 MYKVTCLKTPSGDKTIECPADTYILDAAEEAGLDLPYSCRAGACSSCAGKVAAGTVDQSDQSF
 LDDAQMGNGFVLTCVAYPTSDCTIQTHQEEALYENLYFQ

>2Fe-2SST3 (1AWD) *Chlorella fusca*
 YKVTCLKTPSGEETIECPEDTYILDAAEEAGLDLPYSCRAGACSSCAGKVESGEVDQSDQSF
 LDDAQMGKGFVLTCVAYPTSDVTILTHQEAALY

>2Fe-2SST3 (3AB5) *Cyanidioschyzon merolae*
 MYKIQLVNQKEGIDVTIQCAGDQYILDAAEEQGVDLPYSCRAGACSTCAGKLVKGSVDQSDQ
 SFLDEDQISKGFILTCVAYPTSDCVIQTTHQEEALY

>2Fe-2SST3 (1FRR) *Equisetum arvense*
 AYKTVLKTSPSGEFTLDVPEGTTILDAAEEAGYDLFPSCRAGACSSCLGKVVSGSVDESEGSF
 LDDGQMEEGFVLTCIAIPESDLVIETHKEEEELF

>2Fe-2SST3 (5H57) *Zea mays*
 AVYKVKLVGPEGEEHEFDAPDDAYILDAAETAGVELPYSCRAGACSTCAGKIESGSVDQSDG
 SFLDDGQQEEGYVLTCVSYPKSDCVIHTHKEGDLY

>2Fe-2SST3 (4ITK) *Chlamydomonas reinhardtii*
 MFKVTFKTPKGEKTIDVEADKYLLDAAEEAGMDLPYSCRSGGCSTCCGKLESGTVDQSDQNM
 LDEDQLKQGFVLTCVAYPTSDIVILTDQESKLPIGGSENLYFQ

>2Fe-2SST3 (1WRI) *Equisetum arvense*
 AYKVTCLKTPDGDITFDVEPGERLIDIGSEKADLPLSCQAGACSTCLGKIVSGTVDQSEGSFL
 DDEQIEQGYVLTCIAIPESDVVIETHKEDEL

>2Fe-2SST3 (3B2F) *Zea mays*
 ATYNVKLITPEGEVELQVPDDVYILDQAEEDGIDL PYSCRAGSCSSCAGKVVSGSVSDQSDQS
 YLDDGQIADGWVLTCHAYPTSDVVIETHKEEELTGA

>2Fe-2SST3 (4ZHO) *Arabidopsis thaliana*
 MATYKVKFITPEGELEVECDDDVYVLDAAEEAGIDL PYSCRAGSCSSCAGKVVSGSVSDQSDQ
 SFLDDEQIGEGFVLTC AAYPTSDVTIETHKEEA AIMLEHHHHHH

>2Fe-2SST3 (ath:AT1G10960) *Arabidopsis thaliana*
 MASTALSSAIVSTSFLRRQQTPI SLRSLPFANTQSLFGLKSSTARGGRVTAMATYKVKFITP
 EGEQEVECEEDVYVLDAAEEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQMSEG
 YVLTCVAYPTSDVVIETHKEEA AIM

>2Fe-2SST3 (ath:AT1G32550) *Arabidopsis thaliana*
 MALILPCTFCTSLQKKNFPINRRYITNFRRGATTATCEFRIPVEVSTPSDRGSLVVP SHKVT
 VHDRQRGVVHEFEVPEDQYILHSAESQNI SLPFACRHGCCTSCAVRVKSGELRQPQALGISA
 ELKSQGYALLCVGFPTSDLEVETQDEDEVYWLQFGRYFARGPIERDDYALELAMGDE

>2Fe-2SST3 (ath:AT2G27510) *Arabidopsis thaliana*
 MATVRISSTSMTKAVLRSQTTNKLITNKSYNLSVGSTKRVSRSFGLKCSANSGGATMSAVYK
 VKLLGPDGQEDFEVQDDQYILDAAEEAGVDLPYSCRAGACSTCAGQIVSGNVDQSDGSFLE
 DSHLEKGYVLTCVAYPQSDCVIHTHKE TELF

>2Fe-2SST3 (ath:AT5G10000) *Arabidopsis thaliana*
 MDQVLYSSYIIKIPVISRISPSQAQLTTRLNNTTYFGLSSSRGNFGKVFAKESRKVKLISPE
 GEEQEIEGNEDCCILESAENAGLELPYSCRSGTCGTCCGKLVSGKVDQSLGSFLEEEQIQKG
 YILTCIALPLEDCVVYTHKQSDLI

>2Fe-2SST3 (1PFD) *Petroselinum crispum*
 ATYNVKLITPDGEVEFKCDDDVYVLDQAEEEGIDIPYSCRAGSCSSCAGKVVSGSIDQSDQS
 FLDDDEQMDAGYVLTC HAYPTSDVVIETHKEEEIV

>2Fe-2SST3 (1A70) *Spinacia oleracea*
 AAYKVTLVPTGNVEFQCPDDVYILDAAEEEGIDL PYSCRAGSCSSCAGKLTGSLNQDDQS
 FLDDDQIDEGWVLTCAAYPVSDVTIETHKKEELTA

>2Fe-2SST3 (2508317128) *Micromonas pusilla* NOUM17, RCC 299
 MSATVTMSAVAAKTGARLSSRAISKQARALAATPRVAAKPRASLTAKAMLV TIEHEGKTY
 EVECDGHDNILD AALDAGIENLSYDCKMGVCMTCPSRVTAGKVDQQGSMLSDDVEEKGFA
 LLCCA KPLGEGVVIKTVTEEEELLDEQLCA

>2Fe-2SST3(640417898) *Ostreococcus lucimarinus* CCE9901
AVAVEIRHEGKTYNLEVADGDNILDVALDAGIDLRYDCKMGVCMMPAKVVAGAIQSGS
MLSDDVEEKGYALLCCAVPQGEDVVIQTVSEDELLEEQLCSD

>2Fe-2SST3(640417588) *Ostreococcus lucimarinus* CCE9901
SVKVTDHETGEMLELDVPEGRYILFEAEQQGWVLPNACRMGGCTKCAVKISKGSLEQPES
LGLSKELKDQGYALLCVATATEDVECVTQDEEEVYMKQFGKSFAE

>2Fe-2SST3(2505188780) *Paulinella chromatophora*
MRSSHAIIVHWSQQAYTFSHKVPEGEYILNSFEQHGALLPFNCRNGCCTTCAVQVLNGDI
DHREAFGLSSQIRNRGYGLLCVACSMNPLELETQEEDEVYNSQFGIFFGRGKVIKGLPLD
EG

>2Fe-2SST3(2505188822) *Paulinella chromatophora*
MAQIFSISIDFNGTTYSFPCSSDQTVLMGAETAGIELPSSCCSGLCTTCASKLHEGKVYQ
PDAMGIKADLSNEGYALLCVAYPLSDLKLEANQEDALYEAQFGQYQK

>2Fe-2SST3(2507842412) *Zea mays mays* cv. B73
MTCPAATATATTARIGARRGPCLWRSERRASFLVIRSTSLLPDRPARDTRARAASELQQAP
RPASATVPAHKVTVHQRGVIHEFVVPEDQYILHTAEAQDIRLPFACRHGCCTSCAVRI
KSGQIRQPEALGISAEKDKGYALLCVGFPSGDVEVETQDEDEVYWLQFGRYFARGPVER
DDYALELAMGDE

>2Fe-2SST3(639587729) *Arabidopsis thaliana* Columbia
MALILPCTFCTSLQKNFPINRRYITNFRRGATTATCEFRIPVEVSTPSDRGSLVVP SHK
VTVHQRGQGVVHEFEVPEDQYILHSAESQNISLPFACRHGCCTSCAVRVKSGELRQPQAL
GISAEKLSQGYALLCVGFPTSDLEVETQDEDEVYWLQFGRYFARGPIERDDYALELAMGD
E

>2Fe-2SST3(2740822756) *Plasmodium knowlesi* H
MTMIMLFLMLILLTEKSSTYRFSNNRTALKYMSGSRGINICAPQRRACSSFINNLVSSKK
ASCLPVGDRGVNARNTSSNLSNDGGKRRYFKSVNRNKL FYNITLRTNDGEKKIQCDEDE
YILDASERQNVLPYSCRGGSCSTCAAKLIEGEVDNEDQSYLDEEQLKKKYILLCTCYPK
SDCVIETHKEEELHDM

>2Fe-2SST3(2740578133) *Plasmodium coatneyi* Hackeri
MTAIIMFLMLLLLTEKSNTYKISNKRTTLNMYGSRGINICAPQKKACSSFISNLVNSKK
ASCLPVGDRGVNARHTSSNLSNDGGKRRYFKSANRNKL FYNITLRTNDGEKKIQCDEDE
YILDACERQNVLPYSCRGGSCSTCAAKLIEGKVDNEDQSYLDEEQLKKKYVLLCTCYPK
SDCVIETHKEEELHDM

>2Fe-2SST3(638274858) *Plasmodium falciparum* 3D7
MNIVILLILLITFSIKHSNTYKLKNTYIPINMYHNNKNILRSQKSKLFLNFLSNNQLANS
NKQTCFFKSNIKSSISNIDNYDYIRKRYINTSNKNKL FYNITLRTNDGEKKIECNEDEYI
LDASERQNVLPYSCRGGSCSTCAAKLVEGEVDNDDQSYLDEEQIKKKYILLCTCYPKSD
CVIETHKEDELHDM

>2Fe-2SST3(2740848019) *Plasmodium berghei* K173
MRVALFFLYYIFFFFKQNNYKLNPPPLNYMYGNKLIINIPRNRVCVRLINNL PNGSKH
SVFLMNSNKFNLKIGCDHNINKRRYSVSPNPGKLFYNITLRTNDGEKKIECEEDEYILDA
SERQNVLPYSCRGGSCSTCAAKLIEGEVDNEEQSYLDDEQLKKKYILLCTCYPKSDCVI
ETHKEDELHDM

>2Fe-2SST3(2740784636) *Plasmodium yoelii* 17X
MRVVLFFLYYIFFFFKQNNYKLNPPPLNYMYGNKLIINIPRNRICARLINNLANGSKH

SVFLMNSNKFNLKIGCNHNINKRRYSGSPNPGKLFYNITLRTNDGEKKIECEEDEYILDA
SERQNVLPYSCRGGSCSTCAAKLIEGEVDNEEQSYLDDEQLKQKYILLCTCYPKSDCVI
ETHKEDELHDM

>2Fe-2SST3(2740790025) *Plasmodium berghei* ANKA

MRVALFFLYYIFFFFKQNNYKLNPPPLNYMYGNKLIINIPRNRVCVRLINNLPNGSKH
SVFLMNSNKFNLKIGCDHNINKRRYSVSPNPGKLFYNITLRTNDGEKKIECEEDEYILDA
SERQNVLPYSCRGGSCSTCAAKLIEGEVDNEEQSYLDDEQLKQKYILLCTCYPKSDCVI
ETHKEDELHDM

>2Fe-2SST3(2740780229) *Plasmodium chabaudi* AS

MRVLLFFLYYIFFFFKQHNTYKLSNKSPPPLNYMYGNKLIINIPRNRICARLINNLDNGSKH
SVFLMNNNQFNLKIGCNHNINKRRYSGSPSSDKLFYNITLRTNDGEKKIECAEDEYILDA
CEKQNVLPYSCRGGSCSTCAAKLIEGEVDNEEQSYLDDEQLKQKYILLCTCYPKSDCVI
ETHKEEELHDM

>2Fe-2SST3(2740829329) *Theileria orientalis Shintoku*

MANLQGFKFLYACLGCI LAFIRGVSGISSHRWTHSAFLIAPT NFHFKSHSNLCKRQQNNQ
LDDTDLFKELNSRDRHRLRLRHAI RLILPEGEKVIESSEDEYILEAAENQGIELPYSCR
GGSCSTCAAALVIGEIDNCEQSYLSDEQIKQGYCLLCTSYAKSDCTIKTHKEEELHREEE
EQGKEKQE

>2Fe-2SST3(2739114173) *Theileria annulata* Ankara C9

MFLFFIHVCYLVFC SVVACITNRRFSTSFINS PRNFSYSLSNSNLNTFSQPFNKGIEREL
INSSKFSDRRIPLY YAVKLVLPGEGEKVIESAEDEYILESAESQGVLPYSCRGGSCSTCA
ATLVSGEIDNSEQSYLDDQVKKGYCLLCTSYAKSDCTIETHKEDKLHEEEETSTNNNII

>2Fe-2SST3(2740819274) *Babesia microti* RI

MTYVVYGGSIYLIFLVILHIINC NVVLSHRRTSYAFITSRSIQLQTNNIKSCHKVTFVTP
KGKKIVYCEEDEYVLDSAEAAGLDLPYSCRGGSCSTCNCMLTDGNMSNEDQSYLTDEELR
KGYRLICTAYPHSDCTVITHKEDELHKLRGESS

>2Fe-2SST3(639579225) *Arabidopsis thaliana Columbia*

MDQVLYSSYIIKIPVISRISPSQAQLTTRLNNTTYFGLSSSRGNFGKVFAKESRKVKLIS
PEGEEQEIEGNEDCCILESAENAGLELPYSCRSGTCGTCCGKLVSGKVDQSLGSFLEEEQ
IQKGYILTCIALPLEDCVVYTHKQSDLI

>2Fe-2SST3(2740742500) *Babesia bigemina* Bond

MRLLAEFSLLCVVVNLNIHLVVNVTGERMLHHCTLPWQQFRVGYVTHCNRFRKYRMWSTSL
VPLANDRRYFRHLRPSGLFYSVKFVTPQGDVTVDCDPDEYILEAAEKAGIDL PYSCRGG
CSTCAGKIVNGIVDNEEQSYLDNEQMSQGYCLLCTCYPRSDCTIVTHKEEELHASGSST

>2Fe-2SST3(2507852741) *Zea mays mays* cv. B73

MAATALSMSILRAPPPCFSSPLRLRVAVAKPLAAPMRRQLLRAQATYNVKLITPEGEVEL
QVPDDVYILDFAEEEGIDLPFSCRAGSCSSCAGKVVSGSVDQSDQSFLNDNQVADGWVLT
CAAYPTSDVVIETHKEDDLL

>2Fe-2SST3(640293778) *Fusarium graminearum* PH-1

MRSIDPVG NVAGV VHR TALPRISIAISDIAIGLLRLLIFHQSLNMSYKVTIKTPNEDYTF
NCGSDEYILDVAESNGIKLPYSCRAGVYSSCAGKLVSGTIQQDDQDFLDSQVEAGYVLL
CIAYPTSDCIIKANAEDEL

>2Fe-2SST3(2507831497) *Zea mays mays* cv. B73

MAAAAAALVSSNSLRAPAAFSVVVRAASRPAPVVAVVTPLPAAKAAAARGARLRAQATHN
VKLITPDGEVQLKMPGDVYILDHAEERGLDLPYSCRAGACSSCVGKIVSGSVNQFDQSFL
DDDQVAEGFVLT CIAYPTSDLVIQTHKEDALVESY

>2Fe-2SST3(2507859608) *Zea mays mays* cv. B73

MSTATAARLPAPRSGASYHYQTAAPAANTLSFAGHARQAARASGPRLSSRFVAAAAVLH
KVKLVGPDGTEHEFEAPDDTYILEAAETAGVELPFSCRAGSCSTCAGRMSAGEVDQSEGS

FLDDGQMAEGYLLTCISYPKADCVIHTHKEEDLY

>2Fe-2SST3(2507852735) *Zea mays mays* cv. B73
MATVLGSPRAPAFFFSPLRAAPAPTAVALPAKVGIMGRSASSRGRRLRAQATYNVKLI
TPEGEVELQVPDDVYILDQAEEDGIDL PYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQ
IAAGWVLTCHAYPTSDVVIETHKEEELTGA

>2Fe-2SST3(2507852738) *Zea mays mays* cv. B73
MATVLSSPRAPAFSFSRLRAAPAPTTVAMTRGGGASSRLRAQATYNVKLITPEGEVELQVP
DDVYILDYAE EEGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQIAAGWVLTCA
YPTSDVVIETHKEDDLIS

>2Fe-2SST3(2507852737) *Zea mays mays* cv. B73
MATVLSSPRAPAFSFSRLRAAPAPTTVAMTRGGGASSRLRAQATYNVKLITPEGEVELQVP
DDVYILDYAE EEGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQIAAGWVLTCA
YPTSDVVIETHKEDDLIS

>2Fe-2SST3(2507878499) *Zea mays mays* cv. B73
MATAAAAATAMCSVPGPSGSMRRRAFCTWKKADAPRVASSSVARVVRASAAVHRVKLVG
PDGSESELEVAEDTYVLDAEE EAGLELPYSCRAGSCATCAGKLASGEVDQSEGSFLDDAQ
RAEGYVLTCSYPRADCVIYTHKEEEVH

>2Fe-2SST3(2507878482) *Zea mays mays* cv. B73
MATAAAAATAMCSVPGPSGSMRRRAFCTWKKADAPRVASSSVARVVRASAAVHRVKLVG
PDGSESELEVAEDTYVLDAEE EAGLELPYSCRAGSCATCAGKLASGEVDQSEGSFLDDAQ
RAEGYVLTCSYPRADCVIYTHKEEEVH

>2Fe-2SST3(2507843362) *Zea mays mays* cv. B73
MATVLSSPRAPAFSFSRLRAAPAPTTVAMTRGGGASSRLRAQATYNVPDDVYILDFAE EEG
IDLPFSCRAGSCSSCAGKVVSGSVDQSDQSFLNDNQVADGWVLTCAAYPTSDVVIETHKE
DDL

>2Fe-2SST3(639567408) *Arabidopsis thaliana* Columbia
MATVRISSTSMTKAVLRSQTTNKLITNKSYNLSVGSTKRVSRSFGLKCSANSGGATMSAV
YKVKLLGPDGQDEFEVQDDQYILDAAEE EAGVDLPYSCRAGACSTCAGQIVSGNVDQSDG
SFLEDSHLEKGYVLTCAVY PQSDCVIHTHKE TELF

>2Fe-2SST3(2507809369) *Zea mays mays* cv. B73
MATFASPLLCNFMAIEQKNAPQLTNSRKPSRPLSFPTTRSMPTLPLPGFRARPDWRVAAV
YKVKLIGPEGQESVIQVPEDSYILDAAEE EAGIDLPYSCRAGACSTCAGKVLEGSVDQADQ
SFLDDAQVGAGYALTCVAYPTSDCVIQT HREADLY

>2Fe-2SST3(2507892092) *Zea mays mays* cv. B73
MAMATFTSSPVLCSFRTIEQKKAPLLNNSTKRPLHLGFPRSVPTSPSLRERLDLRVAAYV
KVKLLGPEGQESVLDVPEDSYILDAAEE EAGLDLPYSCRAGACSTCAGKLLLEGSVDQADQS
FLDEAQVGAGYALTCVAYPTSDCVIQT HREEDLY

>2Fe-2SST3(2507804759) *Zea mays mays* cv. B73
MSTSTFATSCTLLGNVRTTQASQTAVKSPSSLSFFSQVTKVPSLKTSKKLDVSAMAVYKV
KLVGPEGEEHEFDAPDDAYILDAAETAGVELPYSCRAGACSTCAGKIESGSVDQSDGSFL
DDGQQEEGYVLTCSYPKSDCVIHTHKEGDLY

>2Fe-2SST3(2507804758) *Zea mays mays* cv. B73
MSTSTFATSCTLLGNVRTTQASQTAVKSPSSLSFFSQVTKVPSLKTSKKLDVSAMAVYKV
KLVGPEGEEHEFDAPDDAYILDAAETAGVELPYSCRAGACSTCAGKIESGSVDQSDGSFL
DDGQQEEGYVLTCSYPKSDCVIHTHKEGDLY

>2Fe-2SST3(639589425) *Arabidopsis thaliana* Columbia
MASTALSSAIVGTSFIRRSAPISLRSLPSANTQSLFGLKSGTARGGRVTAMATYKVKFI
TPEGELEVECD DDVYVLDAEE EAGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSFLDDEQ
IGEGFVLTCAAYPTSDVTIETHKEEDIV

>2Fe-2SST3(639585313) *Arabidopsis thaliana* Columbia
MASTALSSAIVSTSFLRRQQTPISLRSLPFANTQSLFGLKSSTARGGRVTAMATYKVKFI

TPEGEQEVECEEDVYVLDAAEAEAGLDLPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQ
MSEGYVLTCVAYPTSDVVIETHKEEAIM
>2Fe-2SST3(2505189316) *Paulinella chromatophora*
MASYKVTLINE SDGLNKTIEVPDDQYILDAAEEQGIDLPYSCRAGACSTCAGKITAGTVD
QSDQSFLDDDQIEAGFVLTCVAYPTSDCTIKTHAEEELY
>2Fe-2SST3(649363878) *Thalassiosira pseudonana* CCMP 1335
MATYKVTLI SEEH DINATIDCNDDVFVLDAAEAEAGIDLPYSCRAGACSTCAGKVSDGTID
QSEQTFLLDDDQMGAGFVLTCIAYPKSDCTILVHQEDEL
>2Fe-2SST3(2508318168) *Micromonas pusilla* NOUM17, RCC 299
MSAFTLSTSTVARSAFTGRKVAVRRNAPVAKARGMKVQAFTVTLETPEGKQDISCADDY
VLDAAEAEAGIDLPYSCRAGACSSCAGKV TAGTIDQSDQSFLDDDQMGNGFVLTCVAYPTS
DCTIKTHMEEELY
>2Fe-2SST3(640421541) *Ostreococcus lucimarinus* CCE9901
MSVTAAPVASFAGARRSSAAVARRSTIARFQVTLETPEGAQAIECADDYILDAAEEAGIDL
PYSCRAGACSSCAGKV TAGSIDQSDQSFLDDDQMGNGFVLTCVAYPTSDCTVKTHMEEELY

Subtype 4

Archaea

Bacteria

>2Fe-2SST4(1I7H) *Escherichia coli*
MPKIVILPHQDLCPDGAVLEANSGETILDAALRNGIEIEHACEKSCACTTCHCIVREGFDSL
PESSEQEDDMLDKAWGLEPESRLSCQARVTDEDLVVEIPRYTINHAREH
>2Fe-2SST4(3AH7) *Pseudomonas putida*
MPLVTFLPHEKFCPEGLTVEVKPGTNI ELAHDHHIEMESACGGVKACTTCHCIVRKGFDSL
EEADELEEDMLDKAWGLEAQ SRLGCQVFVADEDLTIEIPKYSLNHAAEAPH

Eukaryota

Subtype 6

Archaea

>2Fe-2SST6(2678207143) *Halobacterium hubeiense* JI20-1
MVNTLGLLLGLGMALALVGLHLLKGTSKVPEDIASSEVLEQRASTVPETDFPEPYNRSIG
GGGAGAVAGGAAEGELEEESEDEGFDPE SIPEDVEVEYYEIEFVKEGETIEVANNESIL

DAGEEEGWDLPYACRQGQCLSCGGRVASGEDASEFIRHTNNETLSDDEMEKGMYMLTCTAH
PTTSFSVETDETP

>2Fe-2SST6(638161117)*Halobacterium salinarum* NRC-1
MVTTLGVTLGLGVTLLEFVVLHLAKGSSKPPAEDIAQDVLEHRASTVPETDFPEPYNRSIG
GGGGAGAVAGGAESELEDDGEEEDDGFDPAIADDDVEYYEIEYVKEGETIEVASNESILD
AGVDEGWDLPYACQGGQCVSCSGRVADGEDAAEYIRHSNNESLGDAEIEEGYMLTCTAHP
TASFSIETDETP

>2Fe-2SST6(641567661)*Halobacterium salinarum* R1, DSM 671
MVTTLGVTLGLGVTLLEFVVLHLAKGSSKPPAEDIAQDVLEHRASTVPETDFPEPYNRSIG
GGGGAGAVAGGAESELEDDGEEEDDGFDPAIADDDVEYYEIEYVKEGETIEVASNESILD
AGVDEGWDLPYACQGGQCVSCSGRVADGEDAAEYIRHSNNESLGDAEIEEGYMLTCTAHP
TASFSIETDETP

>2Fe-2SST6(2507054418)*Halobacterium* sp. DL1
MVDTLGLALGLGMALTLVGLHFFKGTSPVPEDIAQEVLEHRASTVPETDFPEPYNRSIG
GGGGAGAVAGAGAEGELEESEEADGFDPEIPEDDVEYYEIEFVKEGETIEVGNNENLL
DAGEEEGWDLPYACRQGQCLSCGGRVASGDDASEFIRHSNNETLGDDIEKGYMLTCTAY
PTQAFSLETDETP

>2Fe-2SST6(651266909)*Haloquadratum walsbyi* C23, DSM 16854
MVDINFLGVGIGATLTLLAVSLHYARGTGWPTADISQEVLEKRASTVPETEFPEPMNRS
IGGGAIPAGSVTGGGGELEETDTEVDESEQVPGDIPDEEAIFYFEVEFEKQGSTIEVASNQ
TVLTAGENESWDLPYACRQGQCVSCAGQITSDGNAEDYVEHDNQQLDDTELEDGYTLTC
VAYPKDDFTIETGEAP

>2Fe-2SST6(649767686)*Halogeometricum borinquense* PR3, DSM 11551
MVEINLVGLGIGMTLTLMVALHFSRGTEWTPAADISQEVLEHRASTVPETDFPEPMNRS
IGGGGVAAGAVASGEEGAEELEGEAEESSESSPADIPEDVEYFEVEYAKQGATIEVANNT
VLEAGEDEGMDLPYACRQGQCVSCAGQITSGGSSEYVVDNQQMLGDAELDDGYTLTCV
AYPKADFTIETGEAP

>2Fe-2SST6(638050380)*Haloquadratum walsbyi* HBSQ001, DSM 16790
MVDINFLGVGIGATLTLLAVSLHYARGTGWPTADISQEVLEKRASTVPETEFPEPMNRS
IGGGAIPAGSVTGGGGELEETDTEVDESEQVPGDIPDEEAIFYFEVEFEKQGSTIEVASNQ
TVLTAGEDESWDLPYACRQGQCVSCAGQITSGGNAEDYVEHDNQQLDDAELEHGYTLTC
VAYPKDDFTIETGEAP

Bacteria

>2Fe-2SST6(A9EXQ0)*Sorangium cellulosum* So ce56
MPTVVFEDGALGPAVTAEAGAGRLIDVCDDARAPIVFSRDARCATCRVEVVEGEQLLEPPA
RGERDLLERLGAPPRLRLACQAVLRAGPGLIRLRGVVGREG

Subtype 7

Bacteria

>2Fe-2SST7(5FFI)*Azotobacter vinelandii*

MATIIYFSSPLMPHNKKVQAVAGKRSTLLGVAQENGVKIPFECQDGNGSCLVKITHLDGERI
KGMLLTDKERNVLKSVGKLPKSEEERA AVRDLPP TYRLACQTI VTDEDLLEFTGEPGGA

Subtype 8

Archaea

>2Fe-2SST8 (2668364098) *uncultured marine*
MSANAVAATLELDPSSDETRPVIRFLQGPHLLGQTPFVAGKTLVEHAIEAGVEIPTNCTS
GTCGACMVTLLLGDIPDPPLPPGLDDFMAEEGARLGCIGLPNGDVDVDIRPPL

Bacteria

>2Fe-2SST8 (1JQ4) *Methylococcus capsulatus* str. Bath
MQRVHTITAVTEDGESLRFECRSEDEVITAALRQNI FL MSSCREGGCATCKALCSEG DYDLK
GCSVQALPPEEEEEGLVLLCRTPKTDLEIELPYTH

Subtype 9

Archaea

>2Fe-2SST9 (2730749706) *Haloferax gibbonsii* ARA6
VPTVHFGRGRIE CDRGDVLRDVLRAAGEPPHNGHSSWFNCRGGGSCGTCAVRVRGPVTYR
TKKERRRLRFPPHDS DSGRLACQTVVLGDLWVEKYPGFWGQRVEADESETGDAQDAEDA
QGPTG

>2Fe-2SST9 (2578421895) *Haloferax mediterranei* R-4
MPTVHFGRGRIE CDRGAVLRDVLRGAGEPPHNGHSSWLNCHGRGSCGTCAVRVQGPVTYR
TKKETRRLRLPPHDPDSGLRLACQTLVLGDIWVEKYPGFWGHHVDDDPID

>2Fe-2SST9 (2522036473) *Haloferax mediterranei* R-4
MLRGAGEPPHNGHSSWLNCHGRGSCGTCAVRVQGPVTYRTKKETRRLRLPPHDPDSGLRL
ACQTLVLGDIWVEKYPGFWGHHVDDDPID

>2Fe-2SST9 (646700503) *Haloferax volcanii* DS2, ATCC 29605
MPTVHFGRGRIE CDRGDVLRDVLRAAGESPHNGHSSWFNCRGGGSCGTCAVRVRGPATYR
TKKERRRLRFPPHDPDSGLRLACQTVVLGDLRVEKYPGFWGQRVEADESETGAVQDAEDA
QEPTD

>2Fe-2SST9 (649769286) *Halogeometricum borinquense* PR3, DSM 11551
MPTVQFRDSEIQ CERGAVLRDVLLAAGESPHNGSADMLNCRGRGTCGTCAVAVEGAVTDR
TKREETRLSFPPHHPDSGLRLSCQTRVLGDVTVEKHYPGFWGQHVEESERSEDNGTGGGDE

>2Fe-2SST9 (648063451) *Halalkalicoccus jeotgali* B3, DSM 18796
MPTISYEGERIECAVGTELREALLEAGLSPHNGASNYANCGWAVCGTCAVAVDGAVSEM
SEAERKRLSKWPHDLDSGLRLACQTHIEGDVEVRKYGGFWGQNV DQ

>2Fe-2SST9 (2545639667) *Halobiforma lacisalsi* AJ5, JCM 12983
MPTVYYRGERIECERGAILRDVLL EAGLSPHNGMADTLNCGGHATCGTCAVRVEGDVSEP
TAAERRRLSV PPLRGREGLRLACQTEVRGDLEVRKGE GFWGQREPSDDGRAESDEQSDAP

ESTG

>2Fe-2SST9(643707106) *Halorubrum lacusprofundi* ATCC 49239
MPTVSYQGEEIECEEAILRDVLEAGLSVYNGRAEQFNCRGTGSCGTCAVQVDGAVSEP
GKKEKARLWLPHPHSHDVRLACQTRVEGDVEVRKGRGLWGQHI
>2Fe-2SST9(646512551) *Haloterrigena turkmenica* VKM B-1734, DSM
5511

MPTIEFRGREIECERGRILRDVLLLEAGESPHNNGRANWLNCRGHGTCGTCAVAIEGDASEP
TAAERRRLSLPPHDPDGLRLSCQTRVDGDLEVRKYDGLWGQRPDGDAPAASDGPTAPAD
ER

>2Fe-2SST9(646647838) *Natrialba magadii* ATCC 43099
MPTITIRGRDLEECERGAVLRDVLRLADESPHNNGRADALNCRGLGTCGTCAVAVSGEVGE
GPRERLRLSTPPHDADSGRLRLACQVRVEDDLVVEKYPGFWGQHTDRTEKGNEDETEP

>2Fe-2SST9(2510573059) *Natronobacterium gregoryi* SP2
MPTVTIHDRELECETDAVLRNVLLRADESPHNNGRADTLNCRGLGSCGTCAVAVSGEVGAP
GSRERLRLSIPPHDTASGLRLACQLRVEDDLVVEKYPGYWGQHTDRTEEKADPEEP

>2Fe-2SST9(2506729650) *Natronococcus occultus* SP4, DSM 3396
MPTVTYEAEEIDCEDGAILRDVLLLEAGLSPHNGRAALLNCRGHGTCGTCAVEIDGPVSEP
TTREKRRLSVPPHDPDGLRLSCQTEVQGD LAVEKHGGFWGQHRAESSRD

>2Fe-2SST9(637723008) *Natronomonas pharaonis* Gabara, DSM 2160
MPTVTAFGREIECEEAILRDILLNAGLSPHNGRSDLLNCRGLGTCGTCAVEIDGAVSNI
GRRERSRLAVPPHDPESGRLRLACQTRVLGDVTVTKYPGFWGQHTRCESE

>2Fe-2SST9(2730750239) *Haloferax gibbonsii* ARA6
MAVISLVGVGAGLVLLVLLAVALHYSKGTGWEPTADITQEV LERRAATVAETDFPEPMNRS
IGGGGGVAAVAGGEEGAELEGEAAEEEPSPADMPEDVEYFEVEFVKQGETIELASNETV
LDQGEDAGMDLPYACRQGSCVSCAAKITNGPAEEYITHHTQETLSDEEMDNGYTLTCVAY
PKADFAIETGEAP

>2Fe-2SST9(2522037089) *Haloferax mediterranei* R-4
MAVISLVGVGAGLVLLVLLAVALHFSKGTGWEPTADITQEV LERRAATVAETDFPEPMNRS
IGGGAVAGAVAGGEEGAELEGEAAEEEPSPADMPEDVEYFEVEFVKQGETIELASNET
VLDQGEDAGMDLPYACRQGQCVSCAGKITDGPAD EYVTHFKQETLSGEEMDKGYTLTCVA
Y PKADFAIETGEAP

>2Fe-2SST9(2578423265) *Haloferax mediterranei* R-4
MAVISLVGVGAGLVLLVLLAVALHFSKGTGWEPTADITQEV LERRAATVAETDFPEPMNRS
IGGGAVAGAVAGGEEGAELEGEAAEEEPSPADMPEDVEYFEVEFVKQGETIELASNET
VLDQGEDAGMDLPYACRQGQCVSCAGKITDGPAD EYVTHFKQETLSGEEMDKGYTLTCVA
Y PKADFAIETGEAP

>2Fe-2SST9(646701083) *Haloferax volcanii* DS2, ATCC 29605
MAVISMVGVGAGLVLLVLLAVALHYSKGTGWEPTADITQEV LERRAATVAETDFPEPMNRS
IGGGGGVAAVAGGEEGAELEGEAAEEEPSPADMPEDVEYFEVEFVKQGETIELASNETV
LDQGEDAGMDLPYACRQGSCVSCAAKITDGPAD EYVTHHTQETLSDEEMDNGYTLTCVAY
PKADFAIETGEAP

>2Fe-2SST9(643707096) *Halorubrum lacusprofundi* ATCC 49239
MLNPLITTIVNPTAIVVAVIATLLVVLVSSLKGRGWEPATDISDEV LQRRAAVPETEFP
EPGNRSIGGGGGGGAIPAGGEGEEGELEDGAAGSGPGDIPEDVEYFEVEFVKQGETVE
LSNNEPILDQGEDQGWDLPYACRQGQCVSCAGRIADGPSEDFVEHDNQQMLED AEIEDGY
TLTCVAYPRGSFSIETGEAP

>2Fe-2SST9(2598064000) *Salinarchaeum* sp. Harcht-Bsk1
MELGLAFAVGVLTVLTVLVHFSRGTGWSPNEDISQAVLEQRAQTVPETDFPEPSNRTFS
AGGGAAVAAGGEEGTELEEGEEESSSPGDIPEDIEYFDVEFVKEGETIEVVNNEPLL

DQGEDHGWDLPYACREGQCVSCAGHIPDGDARDFVEHDDQEMLDDPELEDGYVLTCVAYP
RADFSLETSESP

Eukaryota

>2Fe-2SST9(2508313318)*Micromonas pusilla* NOUM17, RCC 299
MALLASSFAGAAVRALSTRSTTRVDRSKGLVCRAQDKMARTTIDLDRKIGPGTGKPIKV
TFLGANGQNVVDCPEDQYILDAGIDAGLELPFTCRGGICGACVAKCTKGSVDHRDIADL
EFTLSEEEQEEGMALLCMCYPVEASEGEGIEIETQSDWGYSLGVAEWKGATGEIGRSPT
PLMKGDLKGL
>2Fe-2SST9(640421700)*streococcus lucimarinus* CCE9901
VTFLGAGGSRVDVECGSNQYILDAGLEAGIEIPFTCRGGICGACVARCASGDVDQSDIAD
LEFTLGEDEIEAGMVLLCMARPVGDVEIETQSD

Subtype 10

Bacteria

>2Fe-2SST10(2MJ3)*Ehrlichia chaffeensis*
MPLITFISPDGSRKTYEAYDGETLLSLAHRNNVDLEGACEGSLACSTCHVIIDPSWYDIVEQ
HNEISDEENDMLDLAFGLTDTSRLGCQIILTKELDGLCVILPTETRNISFVKNS

Subtype 18

Archaea

>2Fe-2SST18(2522038754)*Haloferax mediterranei* R-4(2522038754)
MPTIEFKGETIEADVGDNLQRQTLLDAGLSPHNGKAQYTNCRGNALCGTCAVEIVEGDVSNPT
GKERRRLKLPPHSLDSGLRLSCQLTIEDDLVVEKHHPGYWGQKIEQNDS
>2Fe-2SST18(2578424680)*Haloferax mediterranei* R-4
MPTIEFKGETIEADVGDNLQRQTLLDAGLSPHNGKAQYTNCRGNALCGTCAVEIVEGDVSNPT
GKERRRLKLPPHSLDSGLRLSCQLTIEDDLVVEKHHPGYWGQKIEQNDS

Bacteria

>2Fe-2SST18(fri:FraEu1lc_3227) *Frankia* sp. Eu1lc (Frankia inefficax sp.)
MSIKVTFRLADGSARVVVAEPGTSVMRVAVENGVPGIVGECGGEMSCATCHVHVDPDLAFRS
MSADEEDMLEAVDDRLPTSRLGCQLILRDELGEIAVTVPS

Eukaryota

>2Fe-2SST18(2508319934) *Micromonas pusilla* NOUM17, RCC 299
MSLSIASPASAVRPSIACLSRRRPVGRSSRSQMRVEAASVKVTITPSDGGESITTTVDTA
SVLRTVILDTGAQLYGGMDRLMNCGGMGNCGTCLVDVVEGADLLSEQTEAELRKVKAGKL
KEGWRMSCQCLVGGDAAPEGAELSVVVRPKK

Subtype 20

Bacteria

>2Fe-2SST20(ABB56730.1) *Synechococcus elongatus* PCC 7942 = FACHB-805
MPSIRFIREDKEVFAADGANLRFKAIVENQVDLYTFGGKMMNCGGYGQCGTCIVEIVQGAENL
SPRTSFEERKLKRKPD SYRLACQATVNGPVTVLTKPNPKEAQRET LIAQDLARPIPV TAPPA
LPQTETEVAGDPPSIATAET

Eukaryota

>2Fe-2SST20(2505189500) *Paulinella chromatophora*
MPTIRFEQEGQQVGCIEGANLRKAALDAGINPYKGLNNLNCCGGVGQCGTCVVEVIEGVR
NLSPRSDVEEVYLADRPANYRLSCRTSVNGDVTVRTRPPEGVGKGSNSLLGALKALVGRN

>2Fe-2SST20(2507867603) *Zea mays mays* cv. B73
MAATAHLTGVLGVSSPPLAPSHCSCSGAKKQSCSLRQGRQRRRLRVARAVEVDAPSAGA
PEPEEAEEPSVDFAFVSPRLLPDGTPDVHYRTARGGQKLRDIMLDGYIDLYGPYDKVLLN
CSGGGVCGTCIVEVVEGKEMLSPKTDVEKELLKRKPKTWRLACQATVGNADSTGQMIIQQ
LPEWKIHEWDK

>2Fe-2SST20(2507861006) *Zea mays mays* cv. B73
MAATSSACACAAVALASFPSAASTSAPSRVSASSHRGQRHSRAATVRCSSTSPNVSQGAP
APAPPKPQIELEFVGPKPGADGSFPVDRAEAASGEKLLRDVMNENKIELYAAAYGKVMNCG
GGGSCGTCIVEIIDGKELLNERTNTENRYLKKKPD SWRLACQTIVGNKENS GKVVVQRLP
QWKR

>2Fe-2SST20(639577863) *Arabidopsis thaliana* Columbia
MASLGFNLGFTFSNAQIQQHRKVSGGGRARVISCNSSSSSSSQASSPQGISA VTPLEIEL
EFFGPKPGSDGSYPVDKAKAVSGDKLLRSIMQDNKIELYAAAYGKVMNCGGGGSCGTCIVE
ILDGRDLLNERTDTENRYLKKKPESWRLACQTIVGNKENS GKSA LDIGCRAADSTVEEVN
>2Fe-2SST20(2507829927) *Zea mays mays* cv. B73

MSGAHRTVRCSLPTVGPATCRAQIPRPTVGP KPGADGSFPLDRAEATSGEKLLCDVMNEN
KIELYVAYGKVMNCGGGGSCGTCIVEIIDGKELLNERTSTENQYLKKKPD SWRLACQTIV
GNKENS GKV VVQRLPQWKR

Subtype 23

Bacteria

>2Fe-2SST23 (ABB56928.1) *Synechococcus elongatus* PCC 7942 =
FACHB-805
MTLAETLSVRVRS LGLDQIDRHLFLCADQTKPLCCDRDRSLESWEYLKRRLRELDLDRPDTG
KPLVFRTKANCLRV CQEGPILLVYPEGIWYGRVTPEAIERILQEHLLGGQP VQELILHQHAL
PAVDPL

Subtype 24

Archaea

>2Fe-2SST24 (1E0Z) *Halobacterium Salinarium*
PTVEYLN YETLDDQGWDMDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDWPFS
CRAGACANCASIVKEGEIDMDMQQILSDEEVEEKDVRLTCIGSPA ADEVKIVYNAKHL DYLO
NRVI

>2Fe-2SST24 (1DOI) *Haloarcula marismortui*
PTVEYLN YEVDNGWDMYDDDVFG EASDMDLDD EGYGSLEVNEGEYILEAAEAQGYDWPFS
CRAGACANCAAIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHL DYLO
NRVI

>2Fe-2SST24 (2506732859) *Natronococcus occultus* SP4, DSM 3396-A
MTACDDPGHVVELRDADGAVDSLQIPPGESIVDAAESAGIDLPGCLYGACGTCTARLLE
GRCRHLEPPRALKD DDVLEDGYVLACVATPETDCTLRVGHDIQAE AIGTPWR
>2Fe-2SST24 (2540570422) *Natronomonas moolapensis* 8.8.11, DSM
18674-A

MCANAAAHSVELVRPDGR TETIRVENGETIVDAAERADVAVPYGCLYGVC GTCTAELL DG
DVRHRASPRALKTRSLDAEYVLLCIATPETDCRIRIGHGIQAEVVGTPWK

>2Fe-2SST24 (648061912) *Halalkalicoccus jeotgali* B3, DSM 18796-A
MHVVGLE RSGKRRETVRVDPDESLLAA AERSGIGLPFGCRIGVCGTCTGRVLDGEMRHVE
PPRALKDRHLEAGYVLT CIATPEVDCTVEVGT DVRLARLFENPWR

>2Fe-2SST24 (2522038515) *Haloferax mediterranei* R-4 -A
MATRHDLTLTW RDGREETVPASENETVLEAAESAGIGLPFGCRTGACATCVGRLIDGAIL
YDRPPRALKTRHIEAGYV LCCIARPRTDCRIE VGADVQTDLVSNPWK

>2Fe-2SST24 (2578421174) *Haloferax mediterranei* R-4-A
MATRHDLTLTW RDGREETVPASENETVLEAAESAGIGLPFGCRTGACATCVGRLIDGAIL
YDRPPRALKTRHIEAGYV LCCIARPRTDCRIE VGADVQTDLVSNPWK

>2Fe-2SST24 (649769257) *Halogeometricum borinquense* PR3, DSM
11551-A

MASRHTLTTLTRRSGREETTRASEDETILEAAESADISLPFGCRTGACATCVGRLIDGNIS
YDRPPRALKTRHIESGYVLCCIARPRTDCRIEIGPGVQAELVSNPWK
>2Fe-2SST24(2511547557)*Haloarcula hispanica* CGMCC 1.2049
MTEVLLDWRDSDRTETVSVDPGETILDAAEAADIGLPFGCRTGACGTCTARLLSGDVVHH
RPPRALKEQHLADGYVLLCVAEPTTDAHLAVGATVQAELVNPWK
>2Fe-2SST24(2558552774)*Haloarcula hispanica* N601
MTEVLLDWRDSDRTETVSVDPGETILDAAEAADIGLPFGCRTGACGTCTARLLSGDVVHH
RPPRALKEQHLADGYVLLCVAEPTTDAHLAVGATVQAELVNPWK
>2Fe-2SST24(2629121184)*Haloarcula* sp. CBA1115
MTEVLLDWRDSDRTETVSVDPGETILDAAEAADIGLPFGCRTGACGTCTARLLSGDVVHH
RPPRALKEQHLADGYVLLCVAEPTTDAHLAVGATVQAELVNPWK

>2Fe-2SST24(638183788)*Haloarcula marismortui* ATCC 43049
MTEVLLDWRDSDRTETIAPVDPGETILDAAAADIGLPFGCRTGACGTCTARLLSGDVVHH
RPPRALKDRHLADGYVLLCIAEPTTDTHLAVGATVQAELVNPWK
>2Fe-2SST24(648061773)*Halalkalicoccus jeotgali* B3, DSM 18796
MGHEITLWPGDRVETFSVERNITILEAAARVGIRLPYDCRSGTCAECVGQVLEGSIEHRRM
PRALEESDRREGYALLCIAVPREDCRIRTGSRLKAELGSSPWG

>2Fe-2SST24(644972966)*Halorhabdus utahensis* AX-2, DSM 12940
MPEVEYLNFDVVDENEWSIEDEDI FEKAAAADLEDEDYGVLEVEEGEFILDAAEDEGFNW
PFYCREGKCAVCGAEVLEGEIEMPDQEII TEKEKEEDNVRLTCGGTPVEDDTKIIYNAXH
LNLDWYSYV

>2Fe-2SST24(2656728473)*Halorhabdus tiamatea* SARL4B
MPTVEYLNIEVLDDHGWDMDDDDLF EKAGDAGLDEGDYGTIDVAEGEYILEAAEAQGYDW
PFSCRAGACANCASIVKEGDIDMDMQQILSDEEVEDKGVRLTCVGTPTEDVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24(644972846)*Halorhabdus utahensis* AX-2, DSM 12940
MPTVEYLNIEALDDHGWDMDDDDLF EKAESSDLGENDYGAIDVAEGEYILEAAEAQGYDW
PFSCRAGACANCAAI VKEGDIDMDMQQILSDEEVEDKGVRLTCVGTPTEDVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24(2718530466)*Halodesulfurarchaeum formicicum* HSR6
MPTVEYINIEVLDDQGWDLLEDGDLFEKAADAGLDDQDYGTLDVGEGEYILEAAEAAGYDW
PFSCRAGACANCAGVVKEGDIEMDMQQILSDEEMEEENVRLTCIGSPATDEVQLVYNAKH
LDFLQDRVI
>2Fe-2SST24(2718541652)*Halodesulfurarchaeum formicicum* HTSR1
MPTVEYINIEVLDDQGWDLLEDGDLFEKAADAGLDDQDYGTLDVGEGEYILEAAEAAGYDW
PFSCRAGACANCAGVVKEGDIEMDMQQILSDEEMEEENVRLTCIGSPATDEVQLVYNAKH
LDFLQDRVI

>2Fe-2SST24(2598065433)*Salinarchaeum* sp. Harcht-Bsk1
MPTVEYLNIDVVDDEGWDMYDDDVFAEAADMDLSDDEDYGTLDVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAI VLEGDIDMDMQQILSDEEVDEKNVRLTCIGSPAADDVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24(2511547860)*Haloarcula hispanica* CGMCC 1.2049
MDDNGWDMYDDDVFAEAASMDLDGEDYGSLEVNEGEYILEAAEAQGYDWPFSCRAGACAN
CAAI VLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHL DYLQNRVI
>2Fe-2SST24(2558553081)*Haloarcula hispanica* N601
MPTVEYLNIEVVDNNGWDMYDDDVFAEAASMDLDGEDYGSLEVNEGEYILEAAEAQGYDW

PFSCRAGACANCAAIIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2656628125) *Halanaeroarchaeum sulfurireducens* M27-
SA2

MPTVEYLNLYETLDDQGWDLDDDDIFEKAADAGFDDDEDYGTLDVADGEYILEAAEAQGYDW
PFSCRAGACANCAAILKEGEIDMDMQQILSDEEVEDEGVRLTCIGSPAEDDVKIIYNAKH
LDYLQNRVI

>2Fe-2SST24 (2629121471) *Haloarcula* sp. CBA1115

MPTVEYLNLYEVVDDNGWDMYDDDVFAEASDMDLDGEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2642205066) *Halobacteriaceae archaeon* HSR2

MPTVEYLNLYETLDDQGWDLDDDDIFEKAADAGFDDDEDYGTLDVADGEYILEAAEAQGYDW
PFSCRAGACANCAAILKEGEIDMDMQQILSDEEVEDEGVRLTCIGSPAEDDVKIIYNAKH
LDYLQNRVI

>2Fe-2SST24 (651267925) *Haloquadratum walsbyi* C23, DSM 16854

MATVEYLNLYETLDDKGWEMDDNDLFEKAADSDLDTEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVTEGEIDMDMQQILSDEEVSENRVRLTCIGSPAADNIKIVYNAKH
LDYLQNRVIG

>2Fe-2SST24 (651269612) *Haloquadratum walsbyi* C23, DSM 16854

MATVEYLNLYESLNDKGWEMDDDEDLFEKAADSDLGDEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVTEGEIDMDMQQILSDEEVSDKNVRLTCIGSPAADSVQIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (638052699) *Haloquadratum walsbyi* HBSQ001, DSM 16790

MPWRTCAILMATVEYLNLYESLNDKGWEMDDDEDLFEKAADSDLGDEDYGSLEVNEGEYILE
AAEAQGYDWPFSCRAGACANCAAIIVTEGEIDMDMQQILSDEEVSDKNVRLTCIGSPAADS
VQIVYNAKHLDYLQNRVI

>2Fe-2SST24 (638051294) *Haloquadratum walsbyi* HBSQ001, DSM 16790

MATVEYLNLYETLDDKGWEMDDNDLFEKAADSDLNEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVTEGEIDMDMQQILSDEEVSENRVRLTCIGSPAADNIKIVYNAKH
LDYLQNRVIG

>2Fe-2SST24 (648061546) *Halalkalicoccus jeotgali* B3, DSM 18796

MPTVEYLNLYETLDDQGWIDDDDLFDQAADAGLDEEDYGSLDVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAILKEGEIEMDMQQILSDEEVDDKNVRLTCIGSPAADTVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2730751553) *Haloferax gibbonsii* ARA6

MPTVTYLNLYEVLDDNGWDLDDDDLFEQAADAGLDAEDYGEMEVDNQGEYILEAAEAQGYDW
PFSCRAGACANCASILKEGEIEMDMQQILSDEEVNDKNVRLTCIGSPVEDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2522038217) *Haloferax mediterranei* R-4

MPTVTYLNLYEALDDQGWDLDDDDLFEKAADAGLDAEDYGEMEVDNQGEYILEAAEAQGYDW
PFSCRAGACANCASILKEGEIEMDMQQILSDEEVNDKNVRLTCIGSPVADEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2578423133) *Haloferax mediterranei* R-4

MPTVTYLNLYEALDDQGWDLDDDDLFEKAADAGLDAEDYGEMEVDNQGEYILEAAEAQGYDW
PFSCRAGACANCASILKEGEIEMDMQQILSDEEVNDKNVRLTCIGSPVADEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (646702237) *Haloferax volcanii* DS2, ATCC 29605

MPTVTYLNLYEVLDDNGWDLDDDGLEQAADAGLDAEDYGEMEVDNQGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIDMDMQQILSDEEVNEKNVRLTCIGSPVEDEVKIVYNAKH

LDYLQNRVI
>2Fe-2SST24 (2507080798) *halophilic archaeon* DL31
MPTVEYLNIEVLDDHGWSMDDDDLFEQAADADLSDEDYGNLDVNQGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVEGEIDMDMQQILSDEEVEERNVRLTCIGSPATDEVMIYNAKH
LDYLQNRVI
>2Fe-2SST24 (2741432121) *Halorientalis* sp. IM1011
MPTVEYLNIEVLDDHGWDMYDNETFDKAAEADLDDDEDYGS�DVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVEGEIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVRIYNAKH
LDYLQNRVI
>2Fe-2SST24 (643709246) *Halorubrum lacusprofundi* ATCC 49239
MMPTVEYLNIEVLDDHGWSMDDDDLFEAAADADLDAEDYGS�DVNQGEYILESAEAQGYD
WPFSCRAGACANCASIVMEGDIEMDMQQILSDEEVEEKNVRLTCIGSPATDEVKIVYNAK
HLDYLQNRVI
>2Fe-2SST24 (2540572293) *Natronomonas moolapensis* 8.8.11, DSM
18674
MPTVEYLNIEVLDDHGWGMDDDLFESAADADLGDEDYGEVDVAEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIDMDMQQILSDEEVEEEMVRLTCIGSPADEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (637721177) *Natronomonas pharaonis Gabara*, DSM 2160
MPTVEYLNIEVLDDHGWEMDDDDLFEAADADLDEEDYGS�DVAEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIDMDMQQILSDEEVEEKMVRLTCIGSPADEVKIVFNAKH
LDYLQNRVI
>2Fe-2SST24 (2678209622) *Halobacterium hubeiense* JI20-1
MPTVEYLNIEYTLDDQGWDMDDDDLFEKAADAGLDDEDYGTLEVAEGEYILEAAEAQGYDW
PFSCRAGACANCASIVKEGDIDMDMQQILSDEEVEEKNVRLTCIGSPADEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (638160899) *Halobacterium salinarum* NRC-1
MPTVEYLNIEYTLDDQGWDMDDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDW
PFSCRAGACANCASIVKEGEIDMDMQQILSDEEVEEKDVRLTCIGSPADEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (641567444) *Halobacterium salinarum* R1, DSM 671
MPTVEYLNIEYTLDDQGWDMDDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDW
PFSCRAGACANCASIVKEGEIDMDMQQILSDEEVEEKDVRLTCIGSPADEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (649767562) *Halogeometricum borinquense* PR3, DSM
11551
MPTVEYLNIEVLDDNGWDLDDDDLFEAADAGLDGEDYGTLEV NQGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIQMDMQQILSDEEVSEKNVRLTCIGSPETDEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (645019192) *Halomicrobium mukohataei* arg-2, DSM 12286
MPTVEYLNIEVVDKGVDMYDDGVFEDAADADLSDEDYGTLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVEGEIDMDMQQILSDEEVEEKNVRLTCIGSPDADEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (2506688985) *Halopiger xanaduensis* SH-6
MPTVEYLNIEVVDQGWDIYDDEVFEKAADAGLDDEDYGTLDVAEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVDGEIDMDMQQILSDEEVEEKNVRLTCIGSPETDEVKIVYNAKH
LDYLQNRVI
>2Fe-2SST24 (2506860215) *Halovivax ruber* XH-70, DSM 18193
MPTVEYLNIEVLDDHGWEMDDDDLFEAADAGLDDEDYGTLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAILKEGELEMDMQQILSDEEVEEKNVRLTCIGHALTDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2718328807) *Natrialbaceae archaeon* JW/NM-HA 15
MPTVEYLNIEVVDNDGWDIYDEDFETAADDEGLDEEDYGTLEVAEAGEYILEAAEAQGFWD
PFSCRAGACANCAAIIVDGEIEMDMQQILSDEEVDEKNVRLTCIGSAETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (648062459) *Halalkalicoccus jeotgali* B3, DSM
18796 (648062459)
MSSSLPNIKVGRDAEADMPEELPVHEIEYLNIEAIEPHGWDLDDDDLFKAAAADLTEK
DHGTFEIRGTRYILDGADEGQKWPFECAASCAYCTMFLYEGDVKMDMDLILTDEEVEE
RNIYLSQSIPKSEEVKVYNAMLADYLQENIVGVREV

>2Fe-2SST24 (2507057054) *Halobacterium* sp. DL1
MPTVEYLNIEYTLDDQGWDMDDDDLFKASDAGLDEEDYGTLDVAEAGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVFDGEIDMDMQILSDEEVEEKDVRLTCIGSAQTDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2545639490) *Halobiforma lacisalsi* AJ5, JCM
12983 (2545639490)
MMPTVEYLNIEVLDDQGWDMDDDDLFQAADADLDDDEDYGSLEVNEGEYILEAAEAQGYD
WPFSCRAGACANCAAIIVKEGEIDMDMQILSDEEVEEKNVRLTCIGSAETDEVKIVYNAK
HLDYLQNRVI

>2Fe-2SST24 (2510276469) *Halostagnicola larsenii* XH-48, DSM
17691 (2510276469)
MPTVEYLNIEVLDDQGWEMDDDDLFETAADAGLDEEDYGTLEVAEAGEYILEAAEAQGYDW
PFSCRAGACANCAAIITEGEIEMDMQQILSDEEVEEKNVRLTCIGSAETDEVRIYVNAKH
LDYLQNRVI

>2Fe-2SST24 (2741434959) *Haloterrigena daqingensis*
JX313 (2741434959)
MPTVEYLNIEVLDDQGWEMDDDDLFQQAADAGLDEEDYGSLDVAEAGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIQMDMQILSDEEVEDKNVRLTCIGSAETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (646510662) *Haloterrigena turkmenica* VKM B-1734, DSM
5511 (646510662)
MPTVEYLNIEVLDDQGWDMDDDDLFQAADAGLDDDEDYGTLDVAEAGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVFEGEIDMDMQILSDEEVEEKDVRLTCIGSAETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (646645505) *Natrialba magadii* ATCC 43099 (646645505)
MPTVEYLNIEVLDDQGWEMDDDDLFKAADADFGEEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVTEGEIQMDMQILSDEEVEDKNVRLTCIGSAETDEVKMYNAKH
LDYLQNRVI

>2Fe-2SST24 (2509882554) *Natrinema pellirubrum* 157 (2509882554)
MPTVEYLNIEVLDDHGWDMDDDLFDEAADAGLDDDEDYGSLDVAEAGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIDMDMQILSDEEVEEKNVRLTCIGSPETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2517200551) *Natrinema* sp. J7-2 (2517200551)
MPTVEYLNIEVLDDQGWDMDDDDLFQAADAGLDEEDYGSLEVAGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVFEGEIDMDMQILSDEEVEEKNVRLTCIGSAETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2510572065) *Natronobacterium gregoryi*
SP2 (2510572065)
MPTVEYLNIEVLDDQGWDMDDDDLFQAADADLGDEDYGSLEVNEGEYILEAAEAQGYDW
PFSCRAGACANCAAIIVKEGEIDMDMQILSDEEVEDKDVRLTCIGSAETDEVKIVYNAKH
LDYLQNRVI

>2Fe-2SST24 (2506730473) *Natronococcus occultus* SP4, DSM 3396 (2506730473)
MSPNLPHVRLGEDAAERGDSEADEGPVRTVEYLDYEVLSERGWDIEDDDLFKAAEADLD
DTDHGRIEVTGRRYILDAAEDQGFEPYECRAASCANCAGIVYEGDVEMDMDLILTEEEV
EERQITLTCQSIPKSDEVKLVYNAMYLDYLQDRVIGVREV
>2Fe-2SST24 (2506728776) *Natronococcus occultus* SP4, DSM 3396
MPTVEYLNIEVLDDQGWEMDDDDLFQAAADAGLDEEDYGTLDVAEGEYILEAAEAQGYDW
PFSCRAGACANCAAIVYEGEIDMDMQILSDEEVEDKNVRLTCIGSAETDEVQIVYNAKH
LDYLNQNRVI

>2Fe-2SST24 (2510276562) *Halostagnicola larsenii* XH-48, DSM 17691
MVETYTVEFIDEGRTIEVPANKPVLEAAEEAGLTPPYQCRMVCGVCCGMVVEDGEVDQTE
GMFLSESEKEEGYALTCIAKPRSDLRIRTDSP
>2Fe-2SST24 (646514724) *Haloterrigena turkmenica* VKM B-1734, DSM 5511
MVESYTFVDEGQAIEVPANKPILEAAEEAGLAPPYQCRMVCGVCCGLVVEDGEVDQT
EGMFLSDSEKEEGYALTCIAKPRSDLRIRTDSP
>2Fe-2SST24 (2506729454) *Natronococcus occultus* SP4, DSM 3396
MVETHTFVDEGRTLEIPENQPILEAAEEAGLTPPYQCRMVCGVCCGMIVEDGVVEQT
EGMFLSDSEKEEGYALTCVAKPRSDLRIRTDSP

>2Fe-2SST24 (2511547562) *Haloarcula hispanica* CGMCC 1.2049
MVELVGLAAGATLTLLIVVALHYAKGTGWEAPEDISQEVLEQRAATVPETDFPEPYNRSIG
GGGATAIPAGEAEGELGEGEEAEEEEDEGFDPDDIAEDEVEYYEIEFAKEGETIEVANNEP
LLDAGEEEGWDLPYACREGQCISCAGHIEDGPAEDYIRHSNNDSLMDDDMEEGYCLTCVA
YPTSDFTLETGESP
>2Fe-2SST24 (2558552779) *Haloarcula hispanica* N601
MVELVGLAAGATLTLLIVVALHYAKGTGWEAPEDISQEVLEQRAATVPETDFPEPYNRSIG
GGGATAIPAGEAEGELGEGEEAEEEEDEGFDPDDIAEDEVEYYEIEFAKEGETIEVANNEP
LLDAGEEEGWDLPYACREGQCISCAGHIEDGPAEDYIRHSNNDSLMDDDMEEGYCLTCVA
YPTSDFTLETGESP
>2Fe-2SST24 (638183793) *Haloarcula marismortui* ATCC 43049
MVELVGLAAGATLTLLIVVALHYAKGTGWEAPEDISQEVLEQRAATVPETDFAEPYNRSIG
GGGAVAIPAGEAEGELGEGEAVEEEEEDEGFDPDDIADDEVEYYEIEFAKEGETIEVANNEP
ILDAGEEEGWDLPYACREGQCISCAGHIEDGPATDHIRHSNNDSLMDDDMEEGYCLTCVA
YPTSEFTIETGESP
>2Fe-2SST24 (2629121189) *Haloarcula* sp. CBA1115
MVELVGLAAGATLTLLIVVALHYAKGTGWEAPEDISQEVLEQRAATVPETDFPEPYNRSIG
GGGATAIPAGEAEGELGEGEEAEEEEDEGFDPDDIAEDEVEYYEIEFAKEGETIEVANNEP
LLDAGEEEGWDLPYACREGQCISCAGHIEDGPAEDYIRHSNNDSLMDDDMEEGYCLTCVA
YPTSDFTLETGESP
>2Fe-2SST24 (645018736) *Halomicrobium mukohataei* arg-2, DSM 12286
MVEPVSVAAAGAVLTIVVAVHYSSGTGWEPSSEDISQNVIEKRAATVPETDFPEPYNRSIG
GGGSAAAI PAGEEGAEELEGAEEADDGFDPEIADDEVEYYEIEFAKEGETIEVANNEP
LDAGEDEGWDMPYACRQGQCVSCAGQITDGAASDYIRHSQNESLFDMMEEGYCLTCVAY
PTDEFTIETGEQP
>2Fe-2SST24 (2656727456) *Halorhabdus tiamatea* SARL4B
MVEVLGIALGVGFTLTAVLLHYAKGTGWEPAEDVSTLLERRAAAVPETDFAEPMNRSIG
GGGAAIPAGTADAEGELAGDAEEAETGFDPEAIPDEEVEHYEIEFGKEGETIEVANNEP
LEAGEDEDWDLPYSCRQGQCLSCSGHIADGPAEDFVKHSNNDTLSDEEMENGYCLTCTAH
PTTDFTIETGETP

>2Fe-2SST24(644971659)*Halorhabdus utahensis* AX-2, DSM 12940
MVEALGIALGIGFTTFTAVLLHYAKGTGWEPAEDISTLLERRAAVPETDFPEPMNRSIG
GGGAAIPAGGDAEGELADGDADEADQGFDPEAIPEDEVEHYEIEFAKEGKTIEVANNETI
LEAGEDDEDWDLPYSCRQGQCLSCSGHVEDGPAEDFVKHSNNDTLSEEEMENGYCLTCTAH
PTTDFTIETSETP

>2Fe-2SST24(2741431742)*Halorientalis* sp. IM1011
MVDAGILTGAFLTLVAVALHYSKGTGWEANEDISQEVLEKRAETVPETEFPEPMNRSIGG
GGVAAGAVAGGSEGELAEGGEEDEGFDPAIADDEVETYEIEFAKEGETIEIANNENIL
DVGEDQGWDLPYACREGSCLSCAGHIEEGPAEEYIQHSNNDTLNEEEMDNGYCLTCTAYP
TDSFTLETGEQP

>2Fe-2SST24(2507080499)*halophilic archaeon* DL31
MADYTVEFVRTGETIEIPETQTILKACLEAGIAQEYSCRVMCLACSAKIEGEVEQTVA
EHRALTPEEAEEYALTCMARPQSDLKLDRGKYPPSIEDMGAEPGDAAVSDDD

Bacteria

Eukaryota

>2Fe-2SST24(3AV8)*Aphanothece sacrum*
ASYKVTLKTPDGDNVITVPDDEYILDVAEEQGLDLPYSCRAGACSTCAGKLVSGPAPDQSDQ
SFLDDDQIQAGYILTCVAYPTGDCVIETHKEEALY

Subtype 25

Eukaryota

>2Fe-2SST25(1L5P)*Trichomonas vaginalis*
GTITAVKGGVKKQLKFEDDQTLFTVLTEAGLMSADDTTCQGNKACGKCICKHVSGKVAAAEDD
EKEFLEDQPANARLACAITLSGENDGAVFEL

Subtype 31

Archaea

>2Fe-2SST31 (2509882665) *Natrinema pellirubrum* 157
MTSHDVTLEWPDGRTRTIAVREDETVLEAAERDDSTLPFGCRTGACGTRTGRLLEDGDDALT
HRRQPRVLKDRHRAAGYVLLCLASPRADCRIAVGSSVHSELVDNPWK

Subtype 36

Bacteria

>2Fe-2SST36 (A9EY18) *Sorangium cellulosum* So ce56
MAKVRFLAHGRAWEVEAPVGSSVLQASKSVGAPEGDACGGVCACSTCHVYVTKGRELLSEAE
EDEEDILDKAFDVRSTSRLGCQARILKDGDI EAEISRESLDAFYNEHPNVKDPRKG

Subtype 37

Bacteria

>2Fe-2SST37 (A9GDT7) *Sorangium cellulosum* So ce56
MPQRKRYLFVCVNRDPDGVPKGSQAQRGAEGIHVQLKAALAERGLAKVEARACSASCLDVCW
AGPVIAVEPDGYFYGRVTPADVPEIVDALASGRRVERLVLPPEDFTEATAAPPLPAPP
RGAPPQA

Subtype 38

Archaea

>2Fe-2SST38 (2678207658) *Halobacterium hubeiense* JI20-1
MTEYTVFEFVGTEEEIQVSDKETILSACLEEGIAQEYSCRVMCLACSAKIEAGDVTQPAA
RGLTEEEAENYALTCMARPQSDLKLDGRGKYPPSIEDDAAAAAPAADDD
>2Fe-2SST38 (638159411) *Halobacterium salinarum* NRC-1
MTEYTVFEFAGAGETIEVSDTETILKACLREGIAQEYSCRVMCLACSAKIESGDVTQPAA
RGLTDAEAEYALTCMARPQTDLVLDGRGKYPPSIEEEAAVADQAAADDD
>2Fe-2SST38 (641565953) *Halobacterium salinarum* R1, DSM 671
MTEYTVFEFAGAGETIEVSDTETILKACLREGIAQEYSCRVMCLACSAKIESGDVTQPAA
RGLTDAEAEYALTCMARPQTDLVLDGRGKYPPSIEEEAAVADQAAADDD
>2Fe-2SST38 (2507055119) *Halobacterium* sp. DL1
MTEYTVFEFVGTEEEIQVSGTETVLKACLREGIAQEYSCRVMCLACSAKIEEGEVTQPAA
RGLTDEEAEYALTCMARPQSDLVLDRGKYPPSIEQDAAAADAAAADDD

>2Fe-2SST38 (2522036761) *Haloferax mediterranei* R-4
MTEYTVFEFVGTEETITVSDKQITILKACIEEGIAQEYSCRVMCLACSAEILEGDVTQPAA
RGLTEEESEKYALTCMARPQSDLKLERGIYPPSIEDDAVTAGAAADDD

>2Fe-2SST38 (649769050) *Halogeometricum borinquense* PR3, DSM 11551

MTEYTVFEFVGTGESIQVSDKQTILKACIEEGIAQEYSCRVMCLACSAEILEGDVVQPAA
RGLTEEEEREYALTCMARPQSDLKLKRGVYPPSIEEDAASAAAAADDD

>2Fe-2SST38 (2540570360) *Natronomonas moolapensis* 8.8.11, DSM 18674

MTEYTVFEFVGTDDETITVSDKQTILKRCIEEGIAQEYSCRVMCLACSAEILEGDVAQPAA
RGLTDEESESyalTCMARPQSDLKLDRGKYPPSIDDTAASEGSEPASADD

>2Fe-2SST38 (2598063374) *Salinarchaeum* sp. *Harcht*-Bsk1

MTDYTVFEFVGTGETITVADTETILSRCIEEGIAQEYSCRVMCLACSAEILEGEVTQPAA
RALTEDEAERFALTCMARPQSDLKLDRGVYPPSIEDDAETTGDATAAAD

>2Fe-2SST38 (648064315) *Halalkalicoccus jeotgali* B3, DSM 18796

MATYTVFEFVGTGETIEVTDKQTILSRCLEEGIAQEYSCRVMCLACTAEIVEGEVTQPAA
RGLSEAESEAFALTCMARPQSDLKLDRGKYPPSIAVDERANHTVNGSGSGVVADDD

>2Fe-2SST38 (2642205689) *Halobacteriaceae* *archaeon* HSR2

MTEYTVFEFVGAGETIQVSENETILTAAVREGISQEFSCRVMCLACSAEIVEGEVTQPAA
RGFTDEEAEDYALTCVARPESDLRIERGQYPPSIEEEATGANAAADD

>2Fe-2SST38 (2718531799) *Halodesulfurarchaeum formicicum* HSR6

MTTHTVFEFVGTGEEIEVAETETILDVAVREGISQEYSCRVMCLACSAEIIIEGEVTQPGA
RGLTEAEAEYALTCMARPETDLKLDRGSYPPSIEAEPTGEPADD

>2Fe-2SST38 (2718542893) *Halodesulfurarchaeum formicicum* HTSR1

MTTHTVFEFVGTGEEIEVAETETILDVAVREGISQEYSCRVMCLACSAEIIIEGEVTQPGA
RGLTEAEAEYALTCMARPETDLKLDRGSYPPSIEAEPTGEPADD

>2Fe-2SST38 (2511546217) *Haloarcula hispanica* CGMCC 1.2049

MTEYTVTFVGTGEEITVSEKETILSRCIEEGIAQEYSCRVMCLACSAKIVEGSVTQPAA
RGLTDREREDYALTCMARPQSDLKLDRGKYPPSIEADVDLEDGDPTPADD

>2Fe-2SST38 (2558551415) *Haloarcula hispanica* N601

MTEYTVTFVGTGEEITVSEKETILSRCIEEGIAQEYSCRVMCLACSAKIVEGSVTQPAA
RGLTDREREDYALTCMARPQSDLKLDRGKYPPSIEADVDLEDGDPTPADD

>2Fe-2SST38 (638182364) *Haloarcula marismortui* ATCC 43049

MTEHTVTFVGTGEEITVSEKETILSRCIEEGIAQEYSCRVMCLACSAEIVEGSVTQPAA
RGLTDRERENyalTCMARPQSDLKLDRGKYPPSIEGDVSPEDGDPTPADD

>2Fe-2SST38 (2629119461) *Haloarcula* sp. CBA1115

MTEYTVTFVGTGEEITVSEKETILSRCIEEGIAQEYSCRVMCLACSAKIVEGSVTQPAA
RGLTDREREDYALTCMARPQSDLKLDRGKYPPSIEADVDLEDGDPTPADD

>2Fe-2SST38 (2545640349) *Halobiforma lacisalsi* AJ5, JCM 12983

MTEYTVFEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIVEGEVTQPAA
RGLTEEEAEYALTCMARPQSDLKLDRGKYPPSIESEIDAEGAEGHAAADD

>2Fe-2SST38 (645021473) *Halomicrobium mukohataei* arg-2, DSM 12286

MTEYTVFEFVGTGEEITVSEKETILSRCLEEGIAQEYSCRVMCLACSAEIVDGDVVQPAA
RGLTEEEERDGYALTCMARPASDLKLDRGKYPPSIEAAGSADAAGDEQAAADD

>2Fe-2SST38 (2506691762) *Halopiger xanaduensis* SH-6

MTEYTVFEFVGTGETITCSDTETILSRCLEEGIAQEYSCRVMCLACSAEIVEGDVTQPAA

RALTEEEAENYALTCMARPQSDLKLDGRGYPPSIEDEIDAAGEGGSDDPVAVADD
 >2Fe-2SST38(651268380)*Haloquadratum walsbyi* C23, DSM 16854
 MTEYTVFEFLGTGETIEVSNKQTILKACIEAGIAQEYSCRVMCLACSAEIVEGDVVQPAA
 RGLTETERDNYALTCMARPQSDLKIRRGVYPPSIEQDATQSDMAADD
 >2Fe-2SST38(638051682)*Haloquadratum walsbyi* HBSQ001, DSM 16790
 MTEYTVFEFLGTGETIEVSNKQTILKACIEAGIAQEYSCRVMCLACSAEIVEGDVVQPAA
 RGLTETERDNYALTCMARPQSDLKIRRGVYPPSIEQDATQSDMAADD
 >2Fe-2SST38(2656727860)*Halorhabdus tiamatea* SARL4B
 MTAYTVFEFVGTGETIEVEDTETVLSRAIEEGIAQEYSCRVMCLACSAKIVEGDVTPPAA
 RGLTDEEKENYALTCMARPQSDLKLDGRGYPPSIEKEAAVEAGAGDEATADD
 >2Fe-2SST38(644971946)*Halorhabdus utahensis* AX-2, DSM 12940
 MAVYTVFEFVGTGETIEVEDTDTILSRCLDEGIAQEYSCRVMCLACSAKIIDGEVTPPAA
 RGLTDKEKENYALTCMARPQSDLKLDGRGYPPSIEAEAAVEAGAGDEAAADD
 >2Fe-2SST38(2741429520)*Halorientalis* sp. IM1011
 MTDYTVFEFAGTGEQITVSETETILRRICIEEGIAQEYSCRVMCLACSAKVVEGEVTPPAA
 HGLTDAEREEYALTCMARPQSDLVLDGRGYPPSIEADAEETAGAAADD
 >2Fe-2SST38(643708491)*Halorubrum lacusprofundi* ATCC 49239
 MTEYTVFEFVGTGETIEVADTETILQPCIEEGIAQEYSCRVMCLACSAEIVEGEVTPPAA
 RGLTDEEAEYALTCMARPQSDLKLDGRGYPPSIEDDAATDASDVGAAADDD
 >2Fe-2SST38(2510274300)*Halostagnicola larsenii* XH-48, DSM 17691
 MTEYTVFEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIVEGEVTPPAA
 RGLTEAEAEYALTCMARPNSDLKLDGRGYPPSIEAEIDSEGANGAATADD
 >2Fe-2SST38(2741435756)*Haloterrigena daqingensis* JX313
 MTEYTIEFVGTGETITCSDTETILSRCLEEGIAQEYSCRVMCLACSAEILEGEVTPPAA
 RGFTEAEAEYALTCMARPQSDLKLERGVYPPSIDGDLESEGTGDAVAVADD
 >2Fe-2SST38(646511953)*Haloterrigena turkmenica* VKM B-1734, DSM 5511
 MTEYTVFEFVGTGETITCSDTETILSRCLEEGIAQEYSCRVMCLACSAEIVEGEVTPPAA
 RGLTEEEAENYALTCMARPQSDLTLDRGYPPSIESDLEADGSNAGATADD
 >2Fe-2SST38(2506859546)*Halovivax ruber* XH-70, DSM 18193
 MTEYTVFEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACTAEIVEGEVTPPAA
 RGFTEEEAEHYALTCMARPQSDLKLERGYPPSIEGDATSAAGEAFGDD
 >2Fe-2SST38(646646543)*Natrialba magadii* ATCC 43099
 MTEYTIEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIIIEGEVTPPAA
 RGFTEEEAEAYALTCMARPQSDLKLERGYPPSIESDLEAGEAGNAGGDTAAADD
 >2Fe-2SST38(2718329544)*Natrialbaceae archaeon* JW/NM-HA 15
 MTEYTVFEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIIIEGEVTPPAA
 RGFTEQEAENYALTCMARPQSDLKLERGVYPPSIEGDLGDAAPADD
 >2Fe-2SST38(2509885737)*Natrinema pellirubrum* 157
 MTEYTIEFVGTGETITCTDKETILSRCLEEGIAQEYSCRVMCLACSAEIIAGEVTPPAA
 RGLTEEEAENYALTCMARPQSDLKLDGRGYPPSIEGDLEAVSSDGAVADD

 >2Fe-2SST38(2517204098)*Natrinema* sp. J7-2
 MTEYTIEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIIIDGEVTPPAA
 RGLTDEEAEYALTCMARPQSDLKLDGRGYPPSIEGDLEATGAIDSAAADD
 >2Fe-2SST38(2510571278)*Natronobacterium gregoryi* SP2
 MTDYTVFEFVGTGETITCSDKETILSRCLEEGIAQEYSCRVMCLACSAEIVEGEVTPPAA
 RAFTDEEAEYALTCMARPQSDLKLERGYPPSIDDDVAAEAGGDVETGSPADD
 >2Fe-2SST38(2506729413)*Natronococcus occultus* SP4, DSM 3396
 MTEYTVFEFVGTGESITCTDKETILSRCLEEGIAQEYSCRVMCLACSAEIVEGEVTPPAA

RGFTEEEAENYALTCMARPQSDLKLERGKYPPSIEGDLAGGEPARADD
 >2Fe-2SST38(637722834)*Natronomonas pharaonis* Gabara, DSM 2160
 MTDYTVFEFVGTGETITVSDKDTILSRCIEEGIAQEYFSCRVMCLACSAEIEGEVTQPAA
 RGLTDAEREDYALTCMARPQSDLKLDGRGKYPPSIEDEVDVDADGTDAAAADD
 >2Fe-2SST38(2730749936)*Haloferax gibbonsii* ARA6
 MTEYTVFEFVGTGETITVSDKQTILKACIEEGIAQEYFSCRVMCLACSAEILEGDVTQPAA
 RGLTDEEAERFALTTCMARPQSDLKLDGRGVYPPSIEGDAAGTAADDD
 >2Fe-2SST38(2578421604)*Haloferax mediterranei* R-4
 MTEYTVFEFVGTGETITVSDKQTILKACIEEGIAQEYFSCRVMCLACSAEILEGDVTQPAA
 RGLTEEESEKYALTCMARPQSDLKLERGIYPPSIEDDAVTAGAAADDD
 >2Fe-2SST38(646700738)*Haloferax volcanii* DS2, ATCC 29605
 MTEYTVFEFVGTGETITVSDKQTILKACIEEGIAQEYFSCRVMCLACSAEILEGDVTQPAA
 RGLTEEEAERFALTTCMARPQSDLKLDGRGVYPPSIEDDAAGTAADDD
 >2Fe-2SST38(2656628749)*Halanaeroarchaeum sulfurireducens* M27-
 SA2
 MTEYTVFEFVGAGETIQVSENETILTAAVREGISQEFSCRVMCLACSAEIVEGEVTQPAA
 RGFTDEEAEDYALTCVARPESDLRIERGQYPPSIEEEATGANAAADD

Eukaryota

>2Fe-2SST38(ath:AT4G14890)*Arabidopsis thaliana*
 MATLPLPTQTSTISLPPKPYLSNSFSFPLRNATLSTTTNRRNFLTGTGRIIARAYKVVEHD
 GKTTELEVEPDETILSKALDSGLDVPYDCNLGVCMTCPAKLVTGTVDQSGGMLSDDVVERGY
 TLLCASYPTSDCHIKMIPPEEELLSLQLATAND
 >2Fe-2SST38(639575667)*Arabidopsis thaliana* Columbia
 MATLPLPTQTSTISLPPKPYLSNSFSFPLRNATLSTTTNRRNFLTGTGRIIARAYKVVEHD
 GKTTELEVEPDETILSKALDSGLDVPYDCNLGVCMTCPAKLVTGTVDQSGGMLSDDVVER
 GYTLLCASYPTSDCHIKMIPPEEELLSLQLATAND
 >2Fe-2SST38(2507802064)*Zea mays mays* cv. B73
 MAAASASLLHLATPTLTRSTRVLRLPSAQLSRWPSGARIAAAQPPRAYKVVTIEHGGESR
 VVEVEEDETILSRALDEGLDVPDCKLGVCMTCPARLVSGTVDQSDGMLSDDVVARGYAL
 LCAAYPRSDCTIRVIPEDELLKVQLATADD

Subtype 39

Archaea

>2Fe-2SST39(2545639906)*Halobiforma lacisalsi* AJ5, JCM 12983
 MTEYDVTLEWPDGGTDTVAVDSRDTVLEAAQQEGIRLPADCRKGTCTTCVGRVVGVGDGAA
 GASGPVDAAEAFDYRRQPAALTDGERADGYVLLCIALPRADCRVAVGPAIRAEVGDSP
 WA
 >2Fe-2SST39(2510572047)*Natronobacterium gregoryi* SP2
 MTQYDVTLEWPDGDTDTVAVSPTETVLEVALREGIRLPYDCREGTCITCVGRVLAAGGDETP
 GAEEAVDAADAFDYRRQPKALTEDERANGYVLLCIAVPRADCRVAVGPMVRSEVGDSP
 WS

Subtype 40

Archaea

>2Fe-2SST40 (646645851) *Natrialba magadii* ATCC 43099
MTSYEVVLERPGSPDHTLEVSKRETILEAARRDGVRLPADCLKGTCTTCVGRVVGVEGEDDG
DDETTDSRPDAALAVDYRRPPQALAGHERADGYVLLCIALPRADCRIEAGPQVRAEVG
DSPWR
>2Fe-2SST40 (2545639904) *Halobiforma lacisalsi* AJ5, JCM 12983
MTSHDVTLEWPDGRTRTIVVREGETVLEGAERADVALPFGCRTGACGTCTGRLLGSEGSEPT
ATATETGRVDVGDAFSSRRRPRALKDRHREAGYVLLCIATPRTDCRFAVGSSVHTELV
DNPWK
>2Fe-2SST40 (2517200684) *Natrinema* sp. J7-2
MVTLEWPDGRTRTVAVREDETVLDGAERADISLPFGCRTGACGTCTGRLLAVDGAESEPD
SGDAEDPDIGATIAYTRPPRALKDRHRADGYVLLCLASPRADCRIAVGSSVQSELVENPW
K

Subtype 41

Archaea

>2Fe-2SST41 (2506732578) *Natronococcus occultus* SP4, DSM
3396 (2506732578)
MSSYDVTLEWSDGRSRTVAVEPRETILEAALREGVRLPYDCRKGTCITACAGRVVDLEDDAEA
NDGPPDAAAVIDYRRPPRALEESDRADGYALLCIAQPRADCRIEVGPMVRSQLGDSPW
G

>2Fe-2SST41 (2517200686) *Natrinema* sp. J7-2
MTSYDVTLEWTDGRTRTIDVGESQTVLEAAQRLGVRLPYDCRAGTCITCVGRLLALEDGDDG
TDRPLDVADALGYQRPPQALTDDERDDGYVLLCIASPRADCRIEVGPRVRAEVGDSPWA

Subtype 42

Archaea

>2Fe-2SST42 (2506689360) *Halopiger xanaduensis* SH-6
MTYDVTLEWPDGRSTETIDAPESESVLDAAQRAGVRLPYDCRKGTCITCVGRLLLEV
DGEGEREATDADSDGDGTDADSDADDSAGAPHPADAFAYRRSPAALTEGERADGYVLLCIAQPRADCRL
EVGPQIRAQVGDSPWA

Subtype 43

Archaea

>2Fe-2SST43 (646514235) *Haloterrigena turkmenica* VKM B-1734, DSM
5511

MTSHDVTLEWADGSTQTVAVAENESVLDAAQRAGARLPYDCRKGTCITCVGRLLALEGEDAE
SAEGGSEQPPDPADVFTYRRSPAALTDQEQADGYVLLCVAHPQSDCRIEVGPRVRAEVDSP
WA

>2Fe-2SST43 (2545642570) *Halobiforma lacisalsi* AJ5, JCM 12983
MPTIRFDGERIECEDGRNLLRALPRGALSSATPVSLCGNGVCGMCAVTVEGETNELTEAERN
RLSEPCEDSPCEGGDGNGDGETD DVDRSRRRLACQTEVHGDLEVTMDE

Subtype 44

Archaea

>2Fe-2SST44 (2509882667) *Natrinema pellirubrum* 157
MTTHEVTLEWTDGRTRTLDVAESQTVLEAAQRVGARLPYDCRSGTCITCVGRLLGLEDGETD
TEEGARPDVREAFAYRRQPRALTDDEQQEGYVLLCIAASPQADCRIEVGPRVRAEVDGS
PWA

>2Fe-2SST44 (2506689358) *Halopiger xanaduensis* SH-6
MASHEVVLEWPEADRERRRTIAVRADETVLEGAERADVALPFGCRTGACGTCTGRLLSVGGTD
ATGTNSEPTTVDEAFDYRRPPRALKDRHRAAGYVLLCIAAPRADCRLAVGSSVHAELV
ENPWK

Subtype 45

Archaea

>2Fe-2SST45 (646514233) *Haloterrigena turkmenica* VKM B-1734, DSM
5511

MVSQRHDVTLEWPDADRETRTIAVDEDETVLEAAERSGIALPFGCRTGACGTCTGRLLLEADG
AEPTAADDERTVDVDGAFSYRRSPRALKDRHRTAGYVLLCIASPRTDCRLAVGANVHTELVE
NPWK

Subtype 46

Archaea

>2Fe-2SST46 (651268525) *Haloquadratum walsbyi* C23, DSM 16854
MTMSENTDSIPVIVIDTDTKTKITV SIGTNLRDALRNHDFSPYGRLSETLNCGGNGLCAT
CGVRVRVYNNQQNDIADTQIHTDDNDIMYPDSGPTPNHWHDLAARFGYPRLSCQITVSE
PLVVQLLPKKLLWGGRKTKTEVTDSMRTNDADSNYR

>2Fe-2SST46 (651268525) *Haloquadratum walsbyi* HBSQ001, DSM
16790 (638051799)

MTMSENTDSIPVIVIDTDTKTKITV SIGTNLRDALRNHDFSPYGRLSETLNCGGNGLCAT
CGVRVRVYNNQQNDIADTQIHIDDNDIMYPDSGPTPDHWHDLAARFGYPRLSCQITVSE
PLVVQLLPKKLLWGGRKTKTEVTDSMRTNDVDSNYR

Subtype 47

Archaea

>2Fe-2SST47 (2540571832) *Natronomonas moolapensis* 8.8.11, DSM 18674
MNESVTTLTVREDGAETTIEAERGAILRDVLRSHGVAVYGSVSRVANCGGRGLCGTCGVRVEG
AEGGSIPAAGLHDAAAKRWGYPRLSRIRVTEPMTVEVIEKVWVGQLRPE

Subtype 48

Archaea

>2Fe-2SST48 (2730750180) *Haloferax gibbonsii* ARA6
MGDSESRPERDPPGPTVTVHVVRTDVGKVVTDLSVERGTVLRDALLEAGISPYARFTKRAN
CGGRGLCATCGVRIRSSEPTADHWHDDLAARFGYPRLSCQIRVDEPMTAELVEKTVWGGRE

>2Fe-2SST48 (2730750180) *Haloferax volcanii* DS2, ATCC 29605 (646700974)
MSDREPRVRTECDPADSTVTVRVRDVGDRVTDLEVERGTVLRDALLDAGISPYARLTKR
VNCGRGLCATCGVRVRSGEPTPDHWHDDLAARFGYPRLSCQLRVDGPLTVELVEKVWVG

Subtype 49

Archaea

>2Fe-2SST49 (2511547885) *Haloarcula hispanica* CGMCC 1.2049
MPATLTVETPGGETHELTAERGAVLRDVLLDADLSPHGRYAKRVNCGGRGICATCGVRLA
EPPDPDHWDDLADRFSYPRLSCQLRVRDGMRVELLDKRVWGSRQPDGRTD

>2Fe-2SST49 (2558553106) *Haloarcula hispanica* N601
MPATLTVETPGGETHELTAERGAVLRDVLLDADLSPHGRYAKRVNCGGRGICATCGVRLA
EPPDPDHWDDLADRFSYPRLSCQLRVRDGMRVELLDKRVWGSRQPDGRTDGRE

>2Fe-2SST49 (645019210) *Halomicrobium mukohataei* arg-2, DSM 12286
MTTATITVETPDGAVREIDCEAGRVLRDVLVEHDLSPHSRLAVANCGGRGLCATCGVRLE
TPPEADHWHDRDLADRFGYPRLSCQIEVVDMAVRIPEKRVWGRRE

>2Fe-2SST49 (638184149) *Haloarcula marismortui* ATCC 43049
MPATLTVETPAGETHELTAEPGAVLRDVLLDADLSPHGRYATRVNCGGRGICATCGVRLA
EPPDPDHWDDLADRFGYPRLSCQLQVRDGMQVKLLDKRVWGSRQAGDETD

>2Fe-2SST49(2629121497)*Haloarcula* sp. CBA1115
MPATLTVETPGGETHELTAERGAVLRDVLDDADLSPHGRYAKRVNCGGRGICATCGVRLA
EPPDPDHWDDLADRFSYPRLSQRLVRDGMRVELLDKRVWGSRQPDGRD
>2Fe-2SST49(644971717)*Halorhabdus utahensis* AX-2, DSM 12940
MSDESTAETGENDTVTVTVFDGETRTEVSVTRGRILRDGLLEQGFSPYTRLTASANCGGR
GLCATCGVRLRDGPPPKHWHDRLAARFGYPRLSCQVTVEADLTVELVADKRIWGSRNATE
NDSR

>2Fe-2SST49(2507080069)*halophilic archaeon* DL31
MSNLVSVTVVDGDEFATIEVERGATRDRDALLEREF SVYGSVSKHANCGGRGLCATCGVAV
APEPEPTHWHDIAAARFGYPRLSCQLTVEEPMTVRLLEKRIWGQLLPNRADQ

>2Fe-2SST49(637722442)*Natronomonas pharaonis* Gabara, DSM 2160
MGDDIELTVITAADSTITVERGSVLRDVLLERGFSVYGTVSSRVNCGGRGLCATCTVEV
DPPPEPAHWHDAAAVRFGYPRLSCCIEVKEPMTVRLLDKHWVGQVLPRRPDGE

>2Fe-2SST49(2545640424)*Halobiforma lacisalsi* AJ5, JCM 12983
MAEGIPVRVITGSEGGETTIRVEPGANLRESLLEHGLPVYGTVSQYANCGGRGLCSTCTV
EVDPAPEPTHWHDAAAVRFGYPRLSCCITVEGPMTVRLLDKHWVGQVLPQVAPDES

>2Fe-2SST49(2509883389)*Natrinema pellirubrum* 157
MSAAIPVTVITDESERVIEVASGTILRDALLEHGFVPYGTVSRVANCGGRGLCSTCTVEV
DPAPEPTHWHDAAAVRFGYPRLSCCLTVEEPLTVRCLDKHWVGQILPRRPSSKS

Subtype 50

Archaea

>2Fe-2SST50(651268286)*Haloquadratum walsbyi* C23, DSM 16854
MPTVTVGTTTTIECDHGAILRDVLQRYDLGIDPHNGAASVINCRGHGTCGTCAVEIRSNNHHR
KDTGTSNETITSTDTNNSVEMTADIDTSSSQNSTNNRESGDAAARINSRTAIERVRLSVPPH
TSDSELRLACQTRVLDDIRVIKHDGLWGHTDDDQDK

>2Fe-2SST50(638051606)*Haloquadratum walsbyi* HBSQ001, DSM 16790
MPTVTVGTTTTIECDHGAILRDVLQRYDLGIDPHNGAASVINCRGHGTCGTCAVEIRSNNHHR
KDTGTSNETITSTDTNNSVEMTADIDTSSSQDSTNDRESGDAAVRINSRTAIERVRLSVPPH
TSDSELRLACQTRVLDDIRVIKHDGLWGHTDDDQDK

Subtype 51

Archaea

>2Fe-2SST51(2684093833)*Methanoculleus* sp. MAB1
MPTATFLPGYRKAVVPSGTTILDAARAAGLPMNVVCGGQKGKCLVFIDGTVSFDIEDCR
RFFSNNEIASGACLACRATIVGDVRVEVPAESLIQEQLVEIPGMKEVPLKPAVWKYEVHL
TPPSLDDTTTPRPRPPAGGDRRSGRPAPPTVYTHRSRSSATSRRCSAGAGGT

Subtype 52

Archaea

>2Fe-2SST52(2506730837)*Natronococcus occultus* SP4, DSM 3396

MTDSSPLRSGRSETGSDASSCPAKTRFGLERRHVLLAAGTAGSIALSGCLDDDDTDDDDEA
AATYDITFLEDGAETEVTIEETEELLYPALEADVEIPYSCEVGSCGECTARYDGDATDVV
SHDGNEYLDEDQIADGWLLTCVAYPRDDAELEVAHPDDA

Subtype 53

Eukaryota

>2Fe-2SST53 (649342678) *Thalassiosira pseudonana* CCMP 1335
SLTFVNPDDTTTTISARVGETLLQSAHRTGIEMEGACEGVCACSTCHVILEQGLYDELDDGM
EEGALGEDEEDMLDMAFGLSQTSRLGCQVKVGVNMDGSVITLPKATRNIFYVDGCHKPKPH

Subtype 54

Eukaryota

>2Fe-2SST54 (2752781104) *Zymoseptoria tritici* ST99CH_1A5
MHDHLNGLDVRQDVATALSPASTEPGSKLTSRQTWLEKVMRSESPLYCKVGYLTQPPS
IIAFSKAMLDIEDTGTAQVLFKTSNITATWLATEDLSLLELAEKAGLKPLHGCRSAMCGT
CEVKVLKGQVYGPEGDKPQGILICQSRPATTEIELEL
>2Fe-2SST54 (2752796449) *Zymoseptoria tritici* ST99CH_3D7
MLDIEDTGTAQVLFKTSNITATWLATEDLSLLELAEKAGLKPLHGCRSAMCGTCEVKVLK
GQVYGPEGDKPQGILICQSRPATTEIELEL

Subtype 55

Archaea

>2Fe-2SST55 (648064638) *Halalkalicoccus jeotgali* B3, DSM 18796
MVETYTIEFVNEGVTLTLEVAENESILEAAENAGLDLPYQCRMGVCGVCSGMCMERGEVDQLE
GMFLSESEKEEGYALTCIAKPRSDMRIRTNESP
>2Fe-2SST55 (2718328477) *Natrialbaceae archaeon* JW/NM-HA 15
MVETYTVEFVDENRTIEVPEDKPILEAAEEAGLRPSYQCRMGVCGVCSSAMLLEGEVDQSE
GMFLSDSEQEEGYVLTTCIAKPRSDLRLRTDESP

3Fe-4S

Subtype 1

Archaea

>3Fe-4SST1 (1SJ1) *Pyrococcus furiosus*

AWKVSVDQDTCIGDAICASLCPDVFEMNDEGKAQPKVEVIEDEELYNCAKEAMEACPVS
AIT IEEA

>3Fe-4SST1 (2688749358) *Thermococcus*

piezophilus

CDGS

MVDQDTCIGDAICASLCPDVFEMNDEGKAVPVVEVIDDENLYNCAVEAAEACPVS
AIVIE EA

Bacteria

>3Fe-4SST1 (Mmar_4763) *Mycobacterium marinum*

MKVIVDENICASSGNCVMNAPEIFDQRDEDGVVLLNANPPAELAEGARRAAASCPALAIKI
EE

>3Fe-4SST1 (CAC17493.1) *Streptomyces coelicolor* A3(2)

MTLAGQAFSGRGAERDRCVGAGQCVLAAPGVFDQDEEDGLVRVLAERP
SAAESDAVRAAV RACPSGALTLR

>3Fe-4SST1 (AL006604.1) *Streptomyces venezuelae*

MDVHVDRDRCLGAGMCALTAPQVFDQDEEEGLVLLDARPPQERHAAVRVAAGVCPASVITL
TRHGSSPAS

>3Fe-4SST1 (AL013336.1) *Streptomyces venezuelae*

MSAPLLSVDRERCIGAGMCAMTAPDVFQDQDDEGLVLLLDTEPPAAHRPAARMAAGVCP
SGA ITLHEPDS

>3Fe-4SST1 (4ID8) *Rhodopseudomonas palustris*

MSEMLTIHVDQDKCQGHARCKALAPELFDLDDYGNAHEKGDGVVPADLIDKAWLAKS
NCPEN AIDITED

>3Fe-4SST1 (mmi:MMAR_4716) *Mycobacterium marinum* M

MKVWVDPQRCQGHTLCAMIAPDSFQLSDIDGSSSAISETVPADQWDLVREAAHSCPEQA
IIVI TDET

>3Fe-4SST1 (mmi:MMAR_4730) *Mycobacterium marinum* M

MRIRLDRTVCDGFGFLCAKQAPGYFTLDDWGYACLSGDGTVREEDRDAVLRALMDCPA
HAITE IGERQPDVVQHSPASAEDPAEHLKTESNEAQWGFTR

Subtype 2

Bacteria

>3Fe-4SST2 (FraEuI1c_5370) *Frankia* sp. *EuI1c* (*Frankia inefficax* sp.)

MKVFIDDDNCRGHGVCAAEC PQVFVNDDGYGEVIVDEVPAELED AVR RVVATHC PERAITVE

>3Fe-4SST2 (fri:FraEuI1c_5464) *Frankia* sp. *EuI1c* (*Frankia inefficax* sp.)

MKAEVDAAK CQGHARCWEICPEVFALDEEGFGSVVDPEVPVELEAKAREAADNC PERAIVLA

>3Fe-4SST2 (fri:FraEuI1c_2495) *Frankia* sp. *EuI1c* (*Frankia inefficax* sp.)

MKVAVDGAKCTGHARCQATAPEVFALDELGYAVPGEREIAAGAEAEARRGASAC PERAITVW
GDPLGRPAR

>3Fe-4SST2 (Rv1786) *Mycobacterium tuberculosis* H37Rv

MKVRLDPSRCVGH AQCYAVDPDLFPIDDSGNSILAEHEVRPEDMQLTRDGVAACPEMALILE
EDDAD

>3Fe-4SST2 (mmi:MMAR_2667) *Mycobacterium marinum* M

MKIRLESSKCVGH AQCYAVDPDLFPIDESGYSILEEHEVRPEDEQVARDGVASCPEMALI
LDEE

>3Fe-4SST2 (Mmar_2879) *Mycobacterium marinum* M

MRVAADREICMATGMCVMTADAFFDQDADGIVVLA AHEVPAD EERRVRNAV KLCPSGALELM
SD

>3Fe-4SST2 (mmi:MMAR_4734) *Mycobacterium marinum* M

MRIEVDWDLCE SNGICMGIVAEVFQLGDDDM LTVLQPEVTPENEELVREAVRQCPRQAISIT
R

>3Fe-4SST2 (mmi:MMAR_4736) *Mycobacterium marinum* M

MKVRVDDQRCRGHGMCLTLCPEVFSLTDDGYAVAITSDVPMELEEEAVREAIQCCPEQAISES

>3Fe-4SST2 (CAC14338.1) *Streptomyces coelicolor* A3(2)

MHIGIDKDT CIGAGQCALTAPGVFTQDDDGYSTLRPGREDGGGSALVREAA RACPVGAITVS
ERVG

>3Fe-4SST2 (Rv0763c) *Mycobacterium tuberculosis* H37Rv

MGYRVEADRDLCQGHAMCELEAPEYFRVPKRGQVEILDPEPPPEEARGVIKHAVWACPTQALS
IRETGE

>3Fe-4SST2 (Mmar_3973) *Mycobacterium marinum* M

MRVIVDETLCEANGFCESLAPDIFALGDADVQIADGPVPADRQIDVRAAVDQCPKAALRLI
E

>3Fe-4SST2 (mmi:MMAR_4933) *Mycobacterium marinum* M

MSYRIEADLDLCQGHAMCELEAPDYFRVPKRGKVEIIDPEPPEQARPEIEQAVRMCPTQALS
IKAKED

>3Fe-4SST2 (mmi:MMAR_4991) *Mycobacterium marinum* M

MLHNDHWLAQVLGKIKEGAVRVIVDRDRCEGNAVCLGIAPDIFDLDDDDYAVVKTDPIPPDQ
EALAEQAIAECPRAALLRED

Subtype 7

Bacteria

>3Fe-4SST7 (CAB59502.1) *Streptomyces coelicolor* A3 (2)

MSVQQEAAVDGEALEVWIDQDLCTGDGICAQYAPEVFELDIDGLAYVKGADDELLQAPGATT
PVPLTLLTDVVDSDAKECPGECIHVRRVSDRAEIIYGPDS

>3Fe-4SST7 (ALO07233.1) *Streptomyces venezuelae*

MTVQNEAPATGVVEALEVWIDQDLCTGDGICAQYAPEVFELDIDGLAYVKSADDELLQDSGA
TTPVPLPLLQDVVDSDAKECPGDCIHVRRVADKVEVYGPDAE

Subtype 6

Bacteria

>3Fe-4SST6 (fri:FraEuI1c_5333) *Frankia* sp. *EuI1c* (*Frankia*
inefficax sp.)

MARHITIDRDLCMGSGQCLIYAPNTFDLDDDAIATVVDPDGSDAELASAVTGCPTQAISVA
RD

>3Fe-4SST6 (fri:FraEuI1c_1414) *Frankia* sp. *EuI1c* (*Frankia*
inefficax sp.)

MTDAWRIEVDRRRCVGTGACAYAAPEVFRLDDRSLATVVVGKVDGDDAFLRDVVAECPTEALR
LSPIDDAR

>3Fe-4SST6 (FraEuI1c_4132) *Frankia* sp. *EuI1c* (*Frankia* *inefficax*
sp.)

MAGGAATIAVDRARCVGSGMCVVYAPDTFTHDEEAKVVVLDPLGDPAEVVESAVEACPTGAL
TLVTAGEAGG

>3Fe-4SST6 (ALO08019.1) *Streptomyces venezuelae*

MGDRWHVEVDRSVCIGSGMCVNHAPTAFLDRTARQSHPTDPEADAGERLLAAAEGCPVEAIL
ITLADGGEPVYPPEE

>3Fe-4SST6 (1FXD) *Desulfovibrio gigas*

PIEVNDDCMACEACVEICPDVFEMNEEGDKAVVINPDSDLDCVEEAIDSCPAEAI VRS

Subtype 3

Bacteria

>3Fe-4SST3 (mmi:MMAR_2932) *Mycobacterium marinum* M
MRLVVDLNNKCQGYAQCVPLAPEVFKLVGEEALAYDPNPDDSQRRVLRVAVASCPVQAIILEV
DPPADRDTK

>3Fe-4SST3 (CAB92987.1) *Streptomyces coelicolor* A3(2)
MRISVDPEQCYGSGDCVHRAPSVFTQVGGLGAVIPGREHDVDAPRVREAAEGCPSAAIT IAR
TEAEGVRGGGA

4Fe-4S

Subtype 7

Bacteria

>4Fe-4SST7 (ABB57779.1) *Synechococcus elongatus* PCC 7942 = FACHB-
805

MTTPDRSGLEPELGGSLRHGQARSGLEPELGGELRQKLVWVDEVTCIGCRYCSHVATNTFYI
EPDYGRSRVVRQNGDPEELVQE AIDTCPVDCIHWVNPSELRQLEAERRNQVIMPLGF PQERS
KQRRRT

>4Fe-4SST7 (1FXR) *Desulfovibrio africanus*
ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIHWE
DE

Subtype 8

Bacteria

>4Fe-4SST8 (1VJW) *Thermotoga maritima*

MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCA KDAADSCPTGAISVEE

Subtype 3

Bacteria

>4Fe-4SST3 (1IQZ) *Bacillus thermoproteolyticus*
PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAYVTLDDNQGIVEVPDILIDDMMDAFEGCP
TDSIKVADEPFDDGDPNKF

Subtype 9

Archaea

>4Fe-4SST9 (2Z8Q) *Pyrococcus furiosus* DSM 3638
AWKVSVDQDTCIGCAICASLCPDVFEMNDEGKAQPKVEVIEDEELYNCAKEAMEACPVS
AIT IEEA

Eukaryota

>4Fe-4SST9 (2508314653) *Micromonas pusilla* NOUM17, RCC 299
LGPDSETKAIFVDESTCIGCRACVTWAAGTFEMVEDQNAGRARCTRQWNDDEETMQIAVEMC
PVDCIYWVKRSQLAILE

Subtype 10

Archaea

>4Fe-4SST10 (2505972394) *Methanocella paludicola* SANA
(reannotation)
MVPKVDKELCISCGNCVDLCPDVFVWDDEGKA EVTNPGGCSTQCNCQEAAESCPTDAISL
EE

Subtype 11

Archaea

>4Fe-4SST11 (2511505707) *Thermococcus* sp. AM4
MAWKVTVDVDTTCIGDAICASLCPDVFEMGDDGKAHPVDVTDLECAQEAAEACPVGAIIL
EEA
>4Fe-4SST11 (2636844530) *Thermococcus eurythermalis*
A501
MAWKVTVDQDTCIGDAICASLCPDVFEMNDEGKAVPIVETTDLECAKEAAEACPVGAITL
EEV

>4Fe-4SST11 (2682416982) *Thermococcus guaymasensis* DSM
 11113
 MAWKVTVDQDTCIGDAICASLCPDVFEMGDDGKAHAIVETTDLECAKEAAEACPVGAILT
 EEV
 >4Fe-4SST11 (2687701486) *Thermococcus peptonophilus* OG-
 1
 MAWKVTVDQDTCIGDAICASLCPDVFEMGDDGKAHPIVETTDLECAQEAAEACPVGAILT
 EEV
 >4Fe-4SST11 (2758666062) *Thermococcus gorgonarius* W-
 12
 MAWKVTVDQDTCIGDAICASLCPDVFEMGDDGKAHPVVETTDLECAQEAAEACPVGAILT
 EEV
 >4Fe-4SST11 (638156651) *Archaeoglobus fulgidus* VC-16, DSM
 4304
 MKAVVDRDLCIGCGTCEEICPEVFRINDEGISEVIGSCDSAECCEEAMESCPASAI SLED
 >4Fe-4SST11 (644842173) *Thermococcus sibiricus* MM
 739
 MKVSVDKDTTCIGCGVCASICPDVFEMDDEGKAQALVTETDLECAKEAAESCPTGSITVE
 >4Fe-4SST11 (2685063455) *Thermococcus* sp. 2319x1
 MKVSVDKDTTCIGCGVCASICPDVFEIDDDGKAKAIVPETDLECAKEAAESCPTGAITVE
 >4Fe-4SST11 (2514742512) *Thermococcus litoralis* DSM
 5473
 MKVSVDKDACIGCGVCASICPDVFEMDDDGKAKALVAETDLECAKEAAESCPTGAITVE
 >4Fe-4SST11 (2559338294) *Thermococcus paralvinellae*
 ES1
 MKVKVDKDTTCIGCGVCASICPDVFEMDDDGKAKTLVEETDLECAKEAAESCPTGAIIEE
 >4Fe-4SST11 (650727821) *Thermococcus barophilus* MP, DSM
 11836
 MKVKLDKDTTCIGCGVCASICPDVFEMDDDGKAKVIMEETDLECAKEAAESCPTGSITIEE
 >4Fe-4SST11 (2684671857) *Thermococcus barophilus* CH5
 MKVKLDKDTTCIGCGVCASICPDVFEMDDDGKAKVIMEETDLECAKEAAESCPTGSITIEE

Subtype 12

Archaea

>4Fe-4SST12 (2635974192) *Geoglobus acetivorans* SBH6
 MMKVVIDESTCTGCGTCEISICPEVFQLGDDGLAHVVGECEGLEECCQEAAADNCPVEAITI
 E
 >4Fe-4SST12 (646611275) *Ferroglobus placidus* AEDII12DO, DSM 10642
 MPAKVVDENLCTGCGLCEEICPEVFKLDENGISRVDGCEANIDCCQEAAESCPAGAITIE

7Fe-8S

Subtype 1

Bacteria

>7Fe-8SST1 (2V2K) MYCOBACTERIUM SMEGMATIS
TYVIAEPCVDVKDKACIEECPVDCIYEGARMLYIHPDECVDGACEPVCPVEAIYYEDDVPD
QWSSYAQANADFFAELGSPGGASKVGQTDNDPQAIKDLPPQGE

>7Fe-8SST1 (Rv1177) Mycobacterium tuberculosis strain ATCC 25618
/ H37Rv
MTYTIAEPCVDIKDKACIEECPVDCIYEGARMLYIHPDECVDGACEPVCPVEAIFYEDDVP
EQWSHYTQINADFFAELGSPGGAAKVGMTENDPQAVKDLAPQSEDA

>7Fe-8SST1 (1BD6) Bacillus schlegelii
AYVITEPCIGTKDASCVEVCPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPE
EWKSYIQKNRDFFKK

>7Fe-8SST1 (CCH24277.1) Corynebacterium glutamicum K051
MTYTIAQPCVDVLDRAECVVECPVDCIYEGKRMPLYIHPDECVDGACEPACPVVEAIFYEDDVP
DEWLDYNDANAAFFDDLGLSPGGAAKLGPDQFDHPMIAALPPQA

>7Fe-8SST1 (CCH26076.1) Corynebacterium glutamicum K051
MTYTIAQPCVDVLDRAECVVECPVDCIYEGKRMPLYIHPDECVDGACEPVCPVEAIFYEDDVP
HEWWDYTGANAAFFDDLGLSPGGAAKLGPDQFDQALVAVLPPQNQN

>7Fe-8SST1 (CAC04216.1) Streptomyces coelicolor A3(2)
MTYVIAQPCVDIKDRACVTECPVDCIYEGARTLYINPAECVDCHACEPVCPVEAIFHEDDLP
RHWAHYLAVNAEYFDEAASPSRARRDAVGDPHFAVEALPPQSGPHKKEISFFTVRKEEAADAD
LWFPS

>7Fe-8SST1 (CAC05765.1) Streptomyces coelicolor A3(2)
MTYVIAQPCVDVKDKACIEECPVDCIYEGQRSLYIHPDECVDGACEPVCPVEAIFYEDDTP
EEWKDYYKANVEFFDELGLSPGGASKLGLIERDHPFVAALPPQNQ

>7Fe-8SST1 (ALO10852.1) Streptomyces venezuelae
MTYVIAQPCVDVKDKACIEECPVDCIYEGKRSLYIHPDECVDGACEPVCPVEAIFYEDDTP
EEWKDYYKANVEFFDELGLSPGGASKLGEIERDHPFIAALPPQNG

>7Fe-8SST1 (azo:azo1031) Azoarcus olearius BH72
MAYVVTECIRCKYTDCVDVCPVDCFREGENFLVIDPEECIDCTLCAECPVEAIYAEDDVP
ADQQQFIALNAELARTWKPIVERKEPLPDAEQWAKVKGKTGELKR

>7Fe-8SST1 (WP_063541473.1) Pseudomonas stutzeri
MTFVVTDNCKYKTYTDCVEVCPVDCFYEGPNFLVIHPDECIDCALCEPECQAQAI FSEDEV
EDQQEFIE
LNTDLAEVWPNITEKKDALADAEEDWGVKDKLQYLER

>7Fe-8SST1 (P0CY91) *Rhodobacter capsulatus* OX=1061

MTYVVTDNCIACKYTDCEVCPVDCFYEGENTLVIHPDECIDCGVCEPECPADAIRPDTEPG
MEDWVEFNRTYASQWPVITIKKDPMPDHKKYDGETGKREKYFSPNPGTGD

>7Fe-8SST1 (7FDR) *Azotobacter vinelandii*

AFVVTDNCIKCKYTDCVEVCPVDCFYEGPNFLVIHPDECIDCALCEPECQAQAIFFSEDEVPE
DMQEFIQLNAEAEVWPNI TEKKDPLPDAEDWDGVKGKLGHLER

>7Fe-8SST1 (Rv2007c) *Mycobacterium tuberculosis* H37Rv

MTYVIGSECVDMVKSCVQECPVDCIYEGARMLYINPDECVDGACKPACRVEAIYWEGDLP
DDQHQLGDNAAFFHQVLPGRVAPLGSPGGAAVGPIGVDTPLVAAIPVECP

Subtype 5

Archaea

>7Fe-8SST5 (2VKR) *Acidianus Ambivalens*

GIDPNYRTSRQVVGEGHQGHKVYGPVDPKVLGIHGTIVGVDFDLICIADGSCITACPVNVFQW
YDTPGHPASEKKADPINEQACIFCMACVNVCPVAAIDVKPP

Subtype 6

Bacteria

>7Fe-8SST6 (ABB56846.1) *Synechococcus elongatus* PCC 7942 = FACHB-805

MAHTIVTNTCEGVADCVDACPVACIQEGPGRNQKGTWYWIDFSTCIDCGICLQVCPVEGAI
LPEERPEL
QQTP

Eukaryota

>7Fe-8SST6 (2505188782) *Paulinella chromatophora*

MAHTIVTDICEGIADCVNACPVACIHMGNKNGINKKGTNIFYWIDFNTCIDCGICLQVCPLN
AILAEERSELQQIN

Subtype 7

Bacteria

>7Fe-8SST7(1H98) *Thermus Aquaticus*
PHVICEPCIGVKDQSCVEVCPVECIYDGGDQFYIHPEECIDCGACVPACPVNAIYPEEDVPE
QWKSYIEKNRKLABLE

Subtype 8

Archaea

>7Fe-8SST8(2509663901) *Methanomethylovorans hollandica* DSM 15978
MPAKVDPNICEGIGACKESCPEDVFEMKDDGQGLKSVVVHPDNCIEGLCVDACPMGAIT
IE

>7Fe-8SST8(2633313307) *Methanosarcina lacustris* Z-
7289
MYPKIDYDKCVGSLECYDVCPADVDEEETKDGKRAVVARPDECTECEQCIDACPTDAIE
LVE

>7Fe-8SST8(2629258817) *Methanosarcina* sp. WWM596
MHPKIDYDKCVGSLECYDVCPADVDEEETKDGKRAVVARPDECTECEQCIDACPTDAIE
MVD

>7Fe-8SST8(2628411983) *Methanosarcina* sp. WH1
MHPKIDYDKCVGSLECYDVCPADVDEEETKDGKRAVVARPDECTECEQCIDACPTDAIE
MVD

>7Fe-8SST8(2653181245) *Methanosarcina* sp. MTP4
MYPKIDYDKCVGSLECYDVCPDVTVDKETEDGKRAVVARPDDCTECEQCIDVCPDPTDAIE
LVD

>7Fe-8SST8(2633313308) *Methanosarcina lacustris* Z-
7289
MHPVIDYHKCTGALACYEVC PGDVFDIKEMEAGKKAVVARPDDCIECDQCVDACPEDAIE
LVD

>7Fe-8SST8(2629258818) *Methanosarcina* sp. WWM596
MHPVIDYHKCTGALACYEVC PGDVFDVKEMEAGKKAVVARPDDCIECDQCVDACPEDAIE
LVD

>7Fe-8SST8(2628411984) *Methanosarcina* sp. WH1
MHPVIDYHKCTGALACYEVC PGDVFDVKEMEAGKKAVVARPDDCIECDQCVDACPEDAIE
LVD

>7Fe-8SST8(2509663901) *Methanomethylovorans hollandica* DSM 15978
MPAKVDPNICEGIGACKESCPEDVFEMKDDGQGLKSVVVHPDNCIEGLCVDACPMGAIT
IE

Subtype 9

Archaea

>7Fe-8SST9(2502871345)*Methanosalsum zhilinae* WeN5, DSM 4017
MVAIIDPDKCNGYTLCADACPVDAITIREDDIAIVDPDICTDCGECVDACPVGAIK

Subtype 10

Archaea

>7Fe-8SST10(638164976)*Methanosarcina mazei* Go1
MHCSLECYDTCVPDVFDAEETEEGKRAVVARPEDCIECEQCVEVCPTDAIELVED
>7Fe-8SST10(2629268101)*Methanosarcina mazei* S-6
MHCSLECYDTCVPDVFDAEETEEGKRAVVARPEDCIECEQCVEVCPTDAIELVED

2[4Fe-4S]

Subtype 2

Bacteria

>2[4Fe-4S]ST2(3EUN)*Allochromatium vinosum*
ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDIAIKDP
SHEETEDELRAKYERITG
EG

>2[4Fe-4S]ST2(2ZVS)*Escherichia coli* K-12
ALLITKKCINCDMCEPECPNEAISMGDHIYEINSDKCTECVGHYETPTCQKVCPIPNITIVKD
PAHVETEEQLWDKFVLMH
HADKI

>2[4Fe-4S]ST2(P0CY90)*Rhodobacter capsulatus*
MAMKIDPELCTSCGDCEPVCPTNAIAPKKG VYVINADTCTECEGEHDL PQCVNACMTDNCIN
PAA

>2[4Fe-4S]ST2(A9FH21)*Sorangium cellulosum* So ce56
MATYITEDCINCGACEPECPNEAISEGDEIYVIDPELCTECVG FYDHEACQAVCPVECCLPN
PQIVETEEVLIARAVRLHPDDGELKKRAAANDYPSRFRK

Subtype 3

Bacteria

>2[4Fe-4S]ST3(A9GFT9)*Sorangium cellulosum* So ce56
MIELVSDARCIGCDLCVEVCPTDVFDRVPGGAPVIARQGDQCFCMCEAYCPVDALYVAP
EAERPVAVDAERLEASGLLSYRAAVGWGTRRKPGAAADETFRVLTVARQT

Archaea

>2[4Fe-4S]ST3(638175208)*Methanosarcina acetivorans* C2A
MPAKVNKEECTACGTCVVEECPVEAIVIDEDEGCAVVDDEDECVDGACEEACPVGAIKTE
>2[4Fe-4S]ST3(638166185)*Methanosarcina mazei* Go1
MVAKNKEECTGCGTCVDECPVEAIIIDEDEGCAVVDDEDECVDGACEDVCPIGAIVKE
>2[4Fe-4S]ST3(2637280920)*Methanosarcina thermophila* TM-1
MPAKVNKEECTGCGTCVVEECPVEAIVIDEDEGCAAVDEEECVCEGACEEVCPIEAIEVE
>2[4Fe-4S]ST3(649737917)*Methanothermus fervidus* V24S, DSM
2088
MKIIVNDKCNCGVCRLVCPKGGKIWKINKKAKATNLEYCHLCMICATRCPTQAIKIIR
>2[4Fe-4S]ST3(2649849577)*Methanosarcina barkeri* 3
MPATVNADECSGCGTCVDECPNDAIALDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE

>2[4Fe-4S]ST3(2632753581)*Methanosarcina barkeri*
Wiesmoor
MPAIVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(637699650)*Methanosarcina barkeri* Fusaro, DSM
804
MPAIVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2632830895)*Methanosarcina barkeri*
227
MPATVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2635680194)*Methanosarcina barkeri*
CM1
MPATVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2648886128)*Methanosarcina vacuolata* Z-
761
MPATVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2633008971)*Methanosarcina barkeri* MS
MPATVNADECSGCGTCVDECPNDAITLDEEEKGIAVVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2628281869)*Methanosarcina* sp.
Kolksee
MPATVNADECSGCGTCVDECPNDAITLDEEEKGIAIVDNDECVECGACEEACPNQAIKVEE
>2[4Fe-4S]ST3(2653181867)*Methanosarcina* sp. MTP4
MPAIVNEEECSGCGTCVDECPSEAITLDDDKGIAVVDQDECVECGACEEACPNDAIKVEE
>2[4Fe-4S]ST3(2633310938)*Methanosarcina lacustris* Z-
7289
MPAIVNADECSGCGTCVDECPSEAITLDEEEKGVAVVDQDECVECGACEEACPNQAIKVQE
>2[4Fe-4S]ST3(2630864270)*Methanosarcina horonobensis* HB-
1
MPALVNADECSGCGTCVDECPSEAITLDEEEKGCAVVDQDECVECGACEEACPNQAIKVQE

>2 [4Fe-4S] ST3 (2630385317) *Methanosarcina thermophila* CHTI-55
 MPALVNADECSGCGSCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2637280903) *Methanosarcina thermophila* TM-1
 MPALVNADECSGCGSCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2683957013) *Methanosarcina* sp. 795 OTU795
 MPALVNADECSGCGSCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2641569127) *Methanosarcina mazei* WWM610
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (638166151) *Methanosarcina mazei* Go1
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2629270533) *Methanosarcina mazei* S-6
 MPALVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2633686767) *Methanosarcina mazei* LYC
 MPALVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2540563552) *Methanosarcina mazei* Tuc01
 MPALVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2651207974) *Methanosarcina mazei* SarPi
 MPALVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2638501146) *Methanosarcina mazei* C16
 MPALVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVTE

>2 [4Fe-4S] ST3 (2645882981) *Methanosarcina siciliae* HI350
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2653161569) *Methanosarcina siciliae* T4/M
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2628823615) *Methanosarcina siciliae* C2J
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (638175176) *Methanosarcina acetivorans* C2A
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGLAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2628409721) *Methanosarcina* sp. WH1
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2629256159) *Methanosarcina* sp. WWM596
 MPAIVNADECSGCGTCVDECPSEAITLDEEEKGIAVVDQDECVECGACEEACPNQAIKVEE

>2 [4Fe-4S] ST3 (2653181688) *Methanosarcina* sp. MTP4
 MPAKVNKEECTGCRCTVEECPVEAITLDEEEGVAVVDEEECVCEGACEETCTSEAIKVE

>2 [4Fe-4S] ST3 (2628409753) *Methanosarcina* sp. WH1
 MPAKVNKEKCTGCGTCVDECPSEAITLDEKEGIAVVNEDECVDGACEDVCPAEAIKVE

>2 [4Fe-4S] ST3 (2629256189) *Methanosarcina* sp. WWM596
 MPAKVNKEKCTGCGTCVDECPSEAITLDEKEGIAVVNEDECVDGACEDVCPAEAIKVE

>2 [4Fe-4S] ST3 (2630385334) *Methanosarcina thermophila* CHTI-55
 MPAKVNKEECTGCGTCVVEECPVEAIVIDEDEGCAAVDEEECVCEGACEEVCPIEAIEVE
 >2 [4Fe-4S] ST3 (2637280920) *Methanosarcina thermophila* TM-1
 MPAKVNKEECTGCGTCVVEECPVEAIVIDEDEGCAAVDEEECVCEGACEEVCPIEAIEVE
 >2 [4Fe-4S] ST3 (2649849596) *Methanosarcina barkeri* 3
 MPAKVKKEECTGCGTCVVEECPVEAIIIDEDEGCAVVDEEECVDCGACEEVCPIQAIKVE
 >2 [4Fe-4S] ST3 (2683957030) *Methanosarcina* sp. 795
 OTU795
 MPAKVNKEECTGCGTCVVEECPVEAIVIDEDEGCAAVDEEECVCEGACEEVCPIEAIEVE
 >2 [4Fe-4S] ST3 (2628281904) *Methanosarcina* sp.
Kolksee
 MPAKVNKEECTGCGTCVDECPVEAIVIDEDEGCAVVDEDECVECGACEEACPNIAITIEQ
 PE
 >2 [4Fe-4S] ST3 (2648886164) *Methanosarcina vacuolata* Z-761
 MPAKVNKEECTGCGTCVDECPVEAIVIDEDEGCAVVDEDECVECGACEEACPNIAITIEQ
 PE
 >2 [4Fe-4S] ST3 (2632753604) *Methanosarcina barkeri*
Wiesmoor
 MPAKVKKEECTGCGTCVDECPVEAIVIDEDEEGCAVVDEDECVECGACEEACPNIAITIE
 >2 [4Fe-4S] ST3 (637699628) *Methanosarcina barkeri Fusaro*, DSM
 804
 MPAKVKKEECTGCGTCVDECPVEAIVIDEDEEGCAVVDEDECVECGACEEACPNIAITIE
 >2 [4Fe-4S] ST3 (2632830873) *Methanosarcina barkeri*
 227
 MPAKVNKEECTGCGTCVDECPVEAIVIDEDEEGCAVVDEDECVECGACEEACPNIAITSE
 >2 [4Fe-4S] ST3 (2635680168) *Methanosarcina barkeri*
 CM1
 MPAKVNKEECTGCGTCVDECPVEAIVIDEDEEGCAVVDEDECVECGACEEACPNIAITSE
 >2 [4Fe-4S] ST3 (2633008995) *Methanosarcina barkeri* MS
 MPAKVNKEECTGCGTCVDECPVEAIVIDEDEEGCAVVDEDECVECGACEEACPNIAITSE
 >2 [4Fe-4S] ST3 (638166185) *Methanosarcina mazei* Go1
 MPAKVNKEECTGCGTCVDECPVEAIIIDEDEGCAVVDEDECVDCGACEDVCPIGAIIKVE
 >2 [4Fe-4S] ST3 (2651207934) *Methanosarcina mazei*
 SarPi
 MPAKVNKEECTGCGTCVDECPVEAIIIDEDEGCAVVDEDECVDCGACEDVCPIGAIIKVE
 >2 [4Fe-4S] ST3 (638175208) *Methanosarcina acetivorans*
 C2A
 MPAKVNKEECTACGTCVVEECPVEAIVIDEDEGCAVVDEDECVDCGACEEACPVGAIIKTE
 >2 [4Fe-4S] ST3 (2645883005) *Methanosarcina siciliae*
 HI350
 MPAKVNKEECTACGTCVVEECPVEAIIIDEDEGCAVVDEDECVDCGACEEACPVGAIIKVE
 >2 [4Fe-4S] ST3 (2653161596) *Methanosarcina siciliae*
 T4/M
 MPAKVNKEECTACGTCVVEECPVEAIIIDEDEGCAVVDEDECVDCGACEEACPVGAIIKVE
 >2 [4Fe-4S] ST3 (2628823643) *Methanosarcina siciliae*
 C2J
 MPAKVNKEECTACGTCVVEECPVEAIIIDEDEGCAVVDEDECVDCGACEEACPVGAIIKVE

>2[4Fe-4S]ST3(2630864246)*Methanosarcina horonobensis* HB-1
 MAAKVNKEECTGCGTCVVEECPVEAIIIDEDEGCAVVDEDECVDCGACEEACPIGAIKTE

Subtype 8

Archaea

>2[4Fe-4S]ST8(650943090)*Pyrococcus yayanosii* CH1
 MTEVKVAPEEKVRKKPSFVKPWLGLKYLFKRPVTIKIPDEKIDPAPKYRGFHTLDWKKCV
 GCNFCGQICPARAIEMTWIEGEKRPHPKIDYGRCTFCQFCVDVCPTGALSFIESYILTTT
 WREEELELYDWVPIPPDKFREMQEKF GDYRFPLEKMEFNRETKEVTTYLLRDGEVMKFKIL
 GYGIKPPKSPA EKAYEK

>2[4Fe-4S]ST8(639772936)*Thermofilum pendens* Hrk 5
 MGIRQILKIALREGVATLEYPPFKPEEAPEDFRGKPEIDPSICMGCACANVCPPDAITCV
 DDLERGLRTWKIFYGRCIFCGRCEEACPLSAIRQSKEYELASKTREDLEV VVETPLARCS
 TCGKYFPVTEREVAQAAQILAEAKTLPRSVLELLENGVECPECKRRRTVLSIVKSARPGV
 KPLSVTGEEGGRHE

Subtype 9

Archaea

>2[4Fe-4S]ST9(2632831998)*Methanosarcina barkeri* 227
 MDQFFSSLLKKSIIIPLENPPKWAKLFPYAFMLFLILISAVFLIPIFCAYICPLRIIYDPP
 AVTTTTFQWITALIFVTGGLIFLVIGPLLTKKRLFC SFICPLMPANTLIGVINPFKVKINI
 DLCKKCGLCVKSCELFAITKESLAKGKTIIECAECGKCMDKCPAGAI DYKLMFTDQNI RF
 FYSAGNYL

>2[4Fe-4S]ST9(2638498581)*Methanosarcina mazei* C16
 MSEMNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSIIYM
 E

>2[4Fe-4S]ST9(638165095)*Methanosarcina mazei* Go1
 VVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSIIYME

>2[4Fe-4S]ST9(2641566654)*Methanosarcina mazei*
 WWM610

MSEMNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSIIYM
 E

>2[4Fe-4S]ST9(2630861022)*Methanosarcina horonobensis* HB-1

MSDTNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDPEKCNLCMKCIDECTNRSIIYM
 D

>2[4Fe-4S]ST9(2683956731)*Methanosarcina* sp. 795
 OTU795

MSEKTGYVVVFGCKRCGKCKNICPVDAIYEENELSKIDTEKCTLCMKCIDECTNRAI IYM
E

>2 [4Fe-4S] ST9 (2637280624) *Methanosarcina thermophila* TM-
1

MSEKTGYVVVFGCKRCGKCKNICPVDAIYEENELSKIDTEKCTLCMKCIDECTNRAI IYM
E

>2 [4Fe-4S] ST9 (2630385038) *Methanosarcina thermophila* CHTI-
55

MSEKTGYVVVFGCKRCGKCKNICPVDAIYEENELSKIDTEKCTLCMKCIDECTNRAI IYM
E

>2 [4Fe-4S] ST9 (637699166) *Methanosarcina barkeri Fusaro*, DSM
804

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENELSKIDQDKCTRCMKCIDVCTNKAI IYM

>2 [4Fe-4S] ST9 (2628282245) *Methanosarcina* sp.
Kolksee

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENEISKIDQDKCTRCMKCIDVCTNKAI IYM
E

>2 [4Fe-4S] ST9 (2648886514) *Methanosarcina vacuolata* Z-
761

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENEISKIDQDKCTRCMKCIDVCTNKAI IYM
E

>2 [4Fe-4S] ST9 (2632831489) *Methanosarcina barkeri*
227

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENELSKIDQDKCTRCMKCIDVCPNKAI IYM
E

>2 [4Fe-4S] ST9 (2635679565) *Methanosarcina barkeri*
CM1

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENELSKIDQDKCTRCMKCIDVCPNKAI IYM
E

>2 [4Fe-4S] ST9 (2633011636) *Methanosarcina barkeri* MS

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENELSKIDQDKCTRCMKCIDVCPNKAI IYM
E

>2 [4Fe-4S] ST9 (2632754104) *Methanosarcina barkeri*
Wiesmoor

MSEQNGYVVVFGCKRCGKCKDVCPVDAIYEENELSKIDQDKCTRCMKCIDVCTNKAI IYM
E

>2 [4Fe-4S] ST9 (2649850361) *Methanosarcina barkeri* 3

MSEQNGYVVVFGCKRCGKCKDVCPVGAIYEENELAKIDPKKCTLCMKCIDECTNRSI IYM
E

>2 [4Fe-4S] ST9 (2628412039) *Methanosarcina* sp. WH1

MSEKEGYVVVFGCKRCGKCKDVCPVGAIYEENELAKIDPEKCNLCMKCIDECTNRSI IYM
E

>2 [4Fe-4S] ST9 (2629258757) *Methanosarcina* sp. WWM596

MSEKEGYVVVFGCKRCGKCKDVCPVGAIYEENELAKIDPEKCNLCMKCIDECTNRSI IYM
E

>2 [4Fe-4S] ST9 (2629267979) *Methanosarcina mazei* S-6

MSEMNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSI IYM

E
>2 [4Fe-4S] ST9 (2633684230) *Methanosarcina mazei* LYC
MSEMNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSIIYM
E
>2 [4Fe-4S] ST9 (2651205513) *Methanosarcina mazei*
SarPi
MSEMNGYVVVFGCKRCGKCRDVCPVGAIYEENELAKIDTEKCNLCMKCIDECTNRSIIYM
E
>2 [4Fe-4S] ST9 (2685268711) *Methanobacterium formicicum*
Mb91
MIVREWCMYCGECAGVCPLNIIQVRELTLEFDEEKCNNCKICVKACPVNALEEEVV
>2 [4Fe-4S] ST9 (2647505556) *Methanobacterium formicicum* DSM
1535
MIVREWCMYCGECAGVCPLNIIQVRELTLEFDEEKCNNCKICVKACPVNALEEEVV

>2 [4Fe-4S] ST9 (2637993349) *Methanobacterium* sp. MB1
MIVREWCMYCGECAGVCPLNIIQIRELTLEFDEKKCNNCKICVKACPVNALEEEVV

>2 [4Fe-4S] ST9 (2637992165) *Methanobacterium* sp. MB1
MIVNEWCMYCGECAGVCPRNLIEVREISLKINQEGCKDCGICIQVCPVQALQGDD

>2 [4Fe-4S] ST9 (2647504296) *Methanobacterium formicicum* DSM
1535
MIVNEWCMYCGECAGVCPRNLIEVREISLKINHDECKDCGICIKVCPVQALQGDD
>2 [4Fe-4S] ST9 (2631418098) *Methanobacterium formicicum*
BRM9
MIVNEWCMYCGECAGVCPRNLIEVREISLKINHDECKDCGICIKVCPVQALQGDD

>2 [4Fe-4S] ST9 (2685267232) *Methanobacterium formicicum*
Mb91
MIVNEWCMYCGECAGVCPRNLIEVRELSLKINHDECKDCGICIKVCPVQALQGDD
>2 [4Fe-4S] ST9 (650870970) *Methanobacterium paludis* SWAN-
1
MIVKEWCMYCGECAGVCPRTLIEVQETNLI FNKEGCKDCQICIQVCPVQALVKEE
>2 [4Fe-4S] ST9 (650752141) *Methanobacterium lacus* AL-
21
MIVKEWCMYCGECAGVCPRALIEVRETS LIFNEEGCKDCRICVSVCPINALDKED
>2 [4Fe-4S] ST9 (638154785) *Methanothermobacter thermautotrophicus*
Delta H
LITMKVKEWCMFCGECAGVCPRNLIEVRETS LKFREDECRECNICIQVCPVRALER
>2 [4Fe-4S] ST9 (2540853929) *Methanobrevibacter* sp.
AbM4
MIVKDWCVYCGECAGVCPRNLITVRETNLEFKTDECKECSTCVDACPINALEQE
>2 [4Fe-4S] ST9 (2655683698) *Methanobrevibacter millerae*
SM9
MIVKEWCSFCGECAGVCPRNLIQVREYSLVFKEDECRDCDTCIKACPINALEKED
>2 [4Fe-4S] ST9 (640593524) *Methanobrevibacter smithii* PS, ATCC
35061
MIVKDWCSFCGECAGVCPRNLIQVKEYSLVFDESECRECSTCVDACPINALEKED
>2 [4Fe-4S] ST9 (2522261378) *Archaeoglobus sulfaticallidus* PM70-1,
DSM 19444 (Asulf_version1)

MLVIDRYKCAYCGACISVCKFNANELVETFVRVDEEKCTLCKMCVRVCPMG AISVEE
 >2 [4Fe-4S] ST9 (638156977) *Archaeoglobus fulgidus* VC-16, DSM
 4304
 MARKAIVDRRKAYCGACVAVCPADANELVETFLEIYDDRCTGCGICVKMCPMGALAMVE
 VD
 >2 [4Fe-4S] ST9 (2635973664) *Geoglobus acetivorans*
 SBH6
 MKKLIVNRYRCGYCGACVAVCKFNANELVETYLEIYEDKCTLQACVRTCPMNALEVVE
 >2 [4Fe-4S] ST9 (646611498) *Ferroglobus placidus* AEDII12DO, DSM
 10642
 MKRIVVNRYKCAYCGACVSVCKFDANELVETYLEIYPDKCTLCMVCVKTCPMGALEVVE
 >2 [4Fe-4S] ST9 (646366977) *Methanocaldococcus vulcanius* M7, DSM
 12094
 MVKVNYKRCGYCGACVGVCECNLAINLIEHIVVIDEKKCSNCLCIIVCPLNALEGE
 >2 [4Fe-4S] ST9 (646622816) *Methanocaldococcus* sp. FS406-
 22
 MVKINYKKCGYCGACVGVCEKLAINLIEHIIVIDEEKCSNCKLCTIVCPLNALEGE
 >2 [4Fe-4S] ST9 (638201852) *Methanocaldococcus jannaschii* DSM
 2661
 MVKIDYKKCGYCGACVGVCEKLAINLIEHIIVIDEKKCNNCKLCTIVCPLNALEGE
 >2 [4Fe-4S] ST9 (644969457) *Methanocaldococcus fervens*
 AG86
 MVKINYKKCGYCGACVGVCECNLAINLIEHIIVIDEKKCNNCKLCTIVCPLNALEGE
 >2 [4Fe-4S] ST9 (646860138) *Methanococcus voltae* A3
 MKVNTLKCgyCGACVGVICPRNAIELIENKIEIDTEKCKGCKLCKEICPVNALEE
 >2 [4Fe-4S] ST9 (640788721) *Methanococcus aeolicus* Nankai-
 3
 MEVNIEKCGYCGACVGVCNRLAIELIENTVIIIDNEKCNGLCAIVCPLNALNTLEE
 >2 [4Fe-4S] ST9 (650855714) *Methanotorris igneus* Kol5, DSM
 5666
 MKVNYERCGYCGACVGVCDKMAIELVENLIIINNEKCTNCKLCMIVCPLNALVDG
 >2 [4Fe-4S] ST9 (650917389) *Methanothermococcus okinawensis*
 IH1
 MKVNHEKCGYCGACVGVCKELAIELVENMIVIDNKKCNNCKLCMIVCPLNALEE
 >2 [4Fe-4S] ST9 (640793945) *Methanococcus maripaludis*
 C7
 MKVNYSKCGYCGACVGVCKSMAIELIENKLYIDDKCNKCTLCMIVCPLNALEE
 >2 [4Fe-4S] ST9 (640787073) *Methanococcus vanniellii* SB
 MNVDYNKCGYCGACVGVCKSMAIELIENKIIYDEKCNNCKLCAVVCPLNALEE
 >2 [4Fe-4S] ST9 (2563556328) *Methanococcus maripaludis*
 S2
 MKVNYSKCGYCGACVGVCKSMAIELIENKLYIEEEKCNNCKLCTVVC PVNALEE
 >2 [4Fe-4S] ST9 (2511671152) *Methanococcus maripaludis*
 X1
 MKVNYSKCGYCGACVGVCKSMAIELIENKLYIEEEKCNNCKLCTVVC PVNALEE
 >2 [4Fe-4S] ST9 (641282982) *Methanococcus maripaludis*
 C6
 MKVNYNKCGYCGACVGVCKSMAIELIENKLYIEEEKCNNCKLCAVVC PVNALEE
 >2 [4Fe-4S] ST9 (640166740) *Methanococcus maripaludis*
 C5
 MKVNYNKCGYCGACVGVCSMAIELIENKLYIEEEKCNNCKLCAVVC PVNALEE

>2 [4Fe-4S] ST9 (646648629) *Aciduliprofundum boonei*
 T469
 MNMMNVDP AICNYCGACV GSCP VNCMFLDETIVRIDEDKCIKCGFCIRACPVGAISADWW
 SE
 >2 [4Fe-4S] ST9 (2509054261) *Aciduliprofundum* sp. MAR08-
 339
 MMKVDP SVCNYCGACV GSCP VNCMFLDETIVRIDEDKCIKCGFCIRACPVGAIDA EWWSE
 >2 [4Fe-4S] ST9 (2632754767) *Methanosarcina barkeri*
Wiesmoor
 VSLKINRYKCGYCGACVGVCPKGALELVETWVEVDESTCITCGICGRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (637702249) *Methanosarcina barkeri Fusaro*, DSM
 804
 MSLKINRYKCGYCGACVGVCPKGALELVETWVEVDESTCITCGICGRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (2630863250) *Methanosarcina horonobensis* HB-
 1
 VSININRYKCGYCGACVGVCPKGALELVETWIEVDESVCIVCGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (638176262) *Methanosarcina acetivorans*
 C2A
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESTCICGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (2641568266) *Methanosarcina mazei*
 WWM610
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK

 >2 [4Fe-4S] ST9 (2629269631) *Methanosarcina mazei* S-6
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (2633686608) *Methanosarcina mazei* LYC
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (638167059) *Methanosarcina mazei* Go1
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (2651207081) *Methanosarcina mazei*
 SarPi
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK
 >2 [4Fe-4S] ST9 (2638500251) *Methanosarcina mazei* C16
 VSVNINRYKCGYCGACVGVCPKGALELVETWIEVDESICIVCGICDRICPVGAIEVMK

 >2 [4Fe-4S] ST9 (648194279) *Methanolacinia petrolearia* DSM
 11571
 MVA VVDADKCTGCETCVDVCPSEAINMEDGIAVVDADACVDCE SCVDECPAEAIHME

 >2 [4Fe-4S] ST9 (640116147) *Methanoculleus marisnigri* JR1, DSM 1498

 MAAVVDIEKCTGCETCVDVCPASAITMEDGKAKVDVDLCVDCETCVDECPSE AISME

 >2 [4Fe-4S] ST9 (2540642432) *Methanoculleus bourgensis*
 MS2
 MTAVVDPELCTGCETCVDVCPAAAIRMEEGKAEVDPGLCVDCGTCVDECPSGAIHLE

 >2 [4Fe-4S] ST9 (640868631) *Methanoregula boonei* 6A8
 MVAVIDMTKCTGCETCVSECPASAISMENEKAKVDKDMCVDCQTCVDACPSEAIQME

>2[4Fe-4S]ST9(2509038734)*Methanoregula formicica* SMSP, DSM 22288
MVAIVDNDKCTGCETCVSECPASAIAMENDKAKVDKDMCVDQCQTCVDVCPSEAIHME
>2[4Fe-4S]ST9(2730776139)*Methanomicrobiales* archaeon
Methan_06
MTAIIIDKDKCTGCETCVDECPATAITMENEKAVVNNELCVDCGSCVDVCPAEAITME
>2[4Fe-4S]ST9(637897125)*Methanospirillum hungatei* JF-1
MTAIIIDKDKCTGCETCVDECPATAITMENEKAVVNNELCVDCGSCVDVCPAEAITME
>2[4Fe-4S]ST9(640116728)*Methanoculleus marisnigri* JR1, DSM 1498
MAAIIIDPELCTGCETCVGACPAGAIRMEDVKPKIDTGLCIDCGTCVDECPTGAVRLE
>2[4Fe-4S]ST9(643569118)*Methanosphaerula palustris* E1-9c, DSM 19958
MVAKVDSDLVGCETCVDECPAEAIAMANGIAVIDKDKCVDCGSCVEVCPSSAITMD
>2[4Fe-4S]ST9(2507146443)*Methanofollis liminatans* GKZPZ, DSM 4140
MVAVVDPDLCVGCETCVDECPSEAITMEDGIAVIDKDNCVDCGTCVDVCPSSAAIHME
>2[4Fe-4S]ST9(640099186)*Methanocorpusculum labreanum* Z
MPAVVNKEKCTGCATCVDICPSAAIELVDDKAVISVDDCVDCECTCVDECPESAIHME
>2[4Fe-4S]ST9(2730778952)*Methanomicrobiales* archaeon
Methan_05
MPAVVNKEKCTGCATCVDICPSAAIELVDDKAVVNADECVDCESCVDECPESAIHME
>2[4Fe-4S]ST9(2507147516)*Methanofollis liminatans* GKZPZ, DSM 4140
MLTIHREICGYCGACVSVCPGEGALELVDAYLTVDTGACIGCGLCTKACPLGALEVTDEE
>2[4Fe-4S]ST9(2730778409)*Methanomicrobiales* archaeon
Methan_05
MAYVINTDECIACGACEAECPEGAISEVNGAYMIDPAKCSECGTCADVCPSPGSPQKA

Bacteria

>2[4Fe-4S]ST9(2FDN)*Clostridium acidurici*
AYVINEACISCGACEPECPVNAISSGDDRYVIDADTCIDCGACAGVCPVDAPVQA
>2[4Fe-4S]ST9(1CLF)*Clostridium pasteurianum*
AYKIADSCVSCGACASECPVNAISQGDSIFVIDADTCIDCGNCANVCPVGAPVQE
>2[4Fe-4S]ST9(1FCA)*Gottschalkia acidurici*
AYVINEACISCGACEPECPVDAISQGGSRVVIDADTCIDCGACAGVCPVDAPVQA

Eukaryota

>2[4Fe-4S]ST9(AAA29098.1)*Entamoeba histolytica*
MGKITIVNIDDCVACGACSGTCPQSVLEVNDHVEIKNPDDCIGCGACVDACPQGVLKVE

Subtype 10

Archaea

>2[4Fe-4S]ST10(637896763)*Methanospirillum hungatei* JF-1
MIEVHREICAYCGCCVSVCPGEGALELVDAYLDIDTNTCKNCGICVRVCPLGALEAKK
>2[4Fe-4S]ST10(2730776450)*Methanomicrobiales archaeon Methan_06*
MIEVHREICAYCGCCVSVCPGEGALELVDAYLDIDTNTCKNCGICVRVCPLGALEAKK

Subtype 12

Eukaryota

>2[4Fe-4S]ST12(640421311)*Ostreococcus lucimarinus* CCE9901
MPTDLAGVLDASAKTLVLTELLRGMSLTLKYFFDKKVTINYPFEKGPLSPRFRGEHALRR
YPTGEERCIACKLCEAICPAQAITIEAEEREDGSRRTTRYDIDMTKCIFCGFCQEACPVD
AIVEGPNFEYATFSHEELLYDKEKLLSNGDRWEKEIARNLQSEAMYR
>2[4Fe-4S]ST12(649349337)*Thalassiosira pseudonana* CCMP 1335
MTEIWRAFWLSGEVALPKPKVTINYPYEKGYLSRFRGEHALRRYPSGDERCIACKLCEAA
CPAQAITIDAEEREDGARRTTRYDIDMTKCIYCGFCQEACPVD AIVEGPNFEFATETHEE
LLYDKEKLLSNGDKWEKQIAKNLLSEHLYR

Archaea

>2[4Fe-4S]ST12(640897719)*Ignicoccus hospitalis* KIN4/I, DSM 18386
MEERRFVEVRERWGRKTNALGVLKSLKAVA EYLVQSRPTTLYPFEKNDLPENFRGVLVYD
IEKCI GCGACVLACPNNCLYRRPGPKTEKNKPGIYIAFEPTHCLFCGLCVDACPPVASSL
RHSNVVSIVSTKKKI IWE PWEWAAFTKLIEEKGWENDAIDYDRVEHLVKERAEQIKKALE
EEAEKGAKK

Subtype 15

Archaea

>2[4Fe-4S]ST15(2540562111)*Methanosarcina mazei* Tuc01
 MKIKICIPTEIRHNPIISESIIETGILLNIMVANIDSTYGELIADVKSDFDKIKNALES
 RGAIVAILDRPIHRDEEECEGACISVCPMNVYAFDEDDWSLCVDEKKCIQCGMCIKMCP
 HGALKLGVFSFLSFSFFISRLCPFFFFSLSFLLFPSLCLFFPFSFFSAFYPVHKIQIRVY
 ECIPISISKLPFLFID
 >2[4Fe-4S]ST15(2509663232)*Methanomethylovorans hollandica* DSM
 15978
 MFIAVYKNKCTGCGLCVITCQNQVLTIEDGSCRAVRTEDCRYCMDCVASCDFDAIKVYV
 >2[4Fe-4S]ST15(2574367197)*Uncultured* *Crenarchaeota*
 C2
 MVKIVVDPKCTGCETCVNTCPVGVYEIKDGKSTPTKVSECLVCRACEAQCPGAIQVIE
 >2[4Fe-4S]ST15(650798190)*Methanothrix soehngenii* GP-
 6
 MPAVVNRDECVSCGTCVEECPEEAISLDDEEIAVVNKEKCTECKTCVEACPSEAISME
 >2[4Fe-4S]ST15(2730780243)*Methanosarcinales* *archaeon*
Methan_04
 MPAVVNRDECVSCGTCVEECPEEAISLDDEEIAVVNKEKCTECKTCVEACPSEAISME
 >2[4Fe-4S]ST15(639700283)*Methanothrix thermoacetophila*
 PT
 MPAVVNREECVSCGTCVEECPEEAIKLDDEEIAVVDPEKCTECGTCVEACPSEAIHIE
 >2[4Fe-4S]ST15(2730785794)*Methanosarcinales* *archaeon*
Methan_02
 MPAVVNREECVSCGTCVEECPENAITMDDEEIAVVNVDKCTECGSCVEACPSEAISIE
 >2[4Fe-4S]ST15(2512008612)*Methanosaeta harundinacea*
 6Ac
 MPAVVNREECVSCGTCVEECPENAITMDDEEIAVVNVDKCTECGSCVEACPSEAISIE
 >2[4Fe-4S]ST15(2730786947)*Methanosarcinales* *archaeon*
Methan_01
 MPAVVNREECVSCGTCVEECPENAIALDDEEIAVVNADKCTECGTCVEACPSEAISIE
 >2[4Fe-4S]ST15(648056844)*Methanohalobium evestigatum* Z-7303,
 DSM 3721
 MVAVIISENCVGCATCVDECPVEAISLDGENIAVVDEGECSDCGECVDVCPTEAIEIE
 >2[4Fe-4S]ST15(646706178)*Methanohalophilus mahii* SLP, DSM
 5219
 MVAVINVDECVGCGACVDECPSEAISMNDENIAVVDAAEECVDCGVCVDVCPTEAITME
 >2[4Fe-4S]ST15(2641586738)*Methanococcoides methylutens*
 MM1
 MVAVINRDECVGCGVCVDDCPAEAISMDGDNIAVVDADACTECGICVDSCPSEAISME
 >2[4Fe-4S]ST15(2519473217)*Methanolobus psychrophilus*
 R15
 MVAIIIVDECVGCGTCVDECPSEAISMNGDNIAVVVADECLDCGACVDVCPPTDAIKME
 >2[4Fe-4S]ST15(637959326)*Methanococcoides burtonii* DSM
 6242
 MVAVINRDECVGCGTCVDDCPSEAISMNDGENIAVVNADECIDCGACVDSCPTDAISME
 >2[4Fe-4S]ST15(2641587503)*Methanococcoides methylutens*
 MM1
 MVAIINRDECVGCGTCVDDCPSEAISMNDGENIAVVNDDECLDCGACVDSCPTDAITME
 >2[4Fe-4S]ST15(2502871991)*Methanosalsum zhilinae* WeN5, DSM 4017
 MVAIVDPDECLGCGPCVDACPVDAITINDDDLAIIDPDLCTDCGECVDACPTEAISME

>2[4Fe-4S]ST15(2502871345)*Methanosalsum zhilinae* WeN5, DSM 4017

MVAIIDPDKCNGYTLCADACPVDAITIREDDIAIVDPDICTDCGECVDACPVGAITIK

>2[4Fe-4S]ST15(648055440)*Methanohalobium evestigatum* Z-7303, DSM 3721

MPAVVDSEICTGCEACVDECPVDAISMNDDGIAVVDEEECTDCEACVDICPVEAISMK

>2[4Fe-4S]ST15(2519472560)*Methanolobus psychrophilus* R15

MPAIVDKDLCTGCGACVDSCPVEAISMNDKDLAVVDPDTCVDCGDCVDTCPVDAISMS

>2[4Fe-4S]ST15((2641566495)*Methanosarcina mazei* WWM610

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2629267826)*Methanosarcina mazei* S-6

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2633684037)*Methanosarcina mazei* LYC

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((638165255)*Methanosarcina mazei* Go1

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2540562642)*Methanosarcina mazei* Tuc01

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2651205358)*Methanosarcina mazei* SarPi

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2638498430)*Methanosarcina mazei* C16

MVAKIDADACTGCGTCVDECPAAAISLNDDDIADVDEDECLDCGACVDACPNGAITLE

>2[4Fe-4S]ST15((2633313730)*Methanosarcina lacustris* Z-7289

MVAKIDADACTGCGSCIDECPAAAISLSDDDFAVVDEAECLDCGACEDVCPNGAITLE

>2[4Fe-4S]ST15((2628412522)*Methanosarcina* sp. WH1

MVAKIDADACTGCGSCIDECPAAAISLSDDDIADVDEDECLDCGACEDTCPNGAITIE

>2[4Fe-4S]ST15((2629258225)*Methanosarcina* sp. WWM596

MVAKIDADACTGCGSCIDECPAAAISLSDDDIADVDEDECLDCGACEDTCPNGAITIE

>2[4Fe-4S]ST15((2630860837)*Methanosarcina horonobensis* HB-1

MVAKIDADACTGCGSCIDECPAAAITLSDDDIADVDEDECLDCGACEDACPNGAITLE

>2[4Fe-4S]ST15((638179083)*Methanosarcina acetivorans* C2A

MVAKIDADACTGCGSCIDECPAAAISLSDDDIADVDEDECLDCGACEDACPNGAITLE

>2[4Fe-4S]ST15((2645886312)*Methanosarcina siciliae* HI350

MVAKIDADACTGCGSCIDECPAAAISLSDDDEIAVVDEDECLDCGACEDACPNGAITLE

>2[4Fe-4S]ST15((2653164945)*Methanosarcina siciliae* T4/M

MVAKIDADACTGCGSCIDECPAAAISLSDDDEIAVVDEDECLDCGACEDACPNGAITLE

>2[4Fe-4S]ST15((2628827425)*Methanosarcina* *siciliae*
 C2J
 MVAKIDADACTGCGSCIDECPAAAISSLSDDEIAVVDESECLDCGACEDACPNGAITIE
 >2[4Fe-4S]ST15((2630385164)*Methanosarcina thermophila* CHTI-
 55
 MVAKVNVDLCTGCGSCVDECPAAAISSLNDDGIATVDESECLDCGSCEDACPNNAITIE

 >2[4Fe-4S]ST15((2637280752)*Methanosarcina thermophila* TM-
 1
 MVAKVNVDLCTGCGSCVDECPAAAISSLNDDGIATVDESECLDCGSCEDACPNNAITIE

 >2[4Fe-4S]ST15((2683956857)*Methanosarcina* sp. 795
 OTU795
 MVAKVNVDLCTGCGSCVDECPAAAISSLNDDGIATVDESECLDCGSCEDACPNNAITIE
 >2[4Fe-4S]ST15((2649850193)*Methanosarcina barkeri*
 3
 MVAKVNAEVCTGCGSCVDECPAAAISSLSDDDIAVVDESECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2632831652)*Methanosarcina barkeri*
 227
 MVAKVNADICTGCGTCVDECPAGAISSLNDDDIADVDESECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2635680791)*Methanosarcina barkeri*
 CM1
 MVAKVNADICTGCGTCVDECPAGAISSLNDDDIADVDESECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2633011800)*Methanosarcina barkeri*
 MS
 MVAKVNADICTGCGTCVDECPAGAISSLNDDDIADVDESECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2628282522)*Methanosarcina* sp.
 Kolksee
 MVAKVNADSCTGCGTCVDECPAAAISSLSDDDIAVVDENECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2648886797)*Methanosarcina vacuolata* Z-
 761
 MVAKVNADSCTGCGTCVDECPAAAISSLSDDDIAVVDENECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2632754257)*Methanosarcina barkeri*
 Wiesmoor
 MVAKVNADSCTGCGTCVDECPAAAISSLNDNDIAVVDENECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((637699021)*Methanosarcina barkeri Fusaro*, DSM
 804
 MVAKVNADSCTGCGTCVDECPAAAISSLNDNDIAVVDENECLDCGACEDACPNNAITIE
 >2[4Fe-4S]ST15((2522260427)*Archaeoglobus sulfaticallidus* PM70-
 1, DSM 19444 (Asulf_version1)
 MIAVLNCQGCCTCDRVCKTGAIIRNGAKVARIDHDKCLECYDCVEACPYGALIVMD

 >2[4Fe-4S]ST15((638158725)*Archaeoglobus fulgidus* VC-16, DSM
 4304
 MIAVLGCQGCCTCSRVCPTDAIIREGGKVVRIDQSKCKEYECVKACPYGALIVMD

 >2[4Fe-4S]ST15((2635974282)*Geoglobus* *acetivorans*
 SBH6
 MPPAVLGCQGCGRCSQVCPTDALIRQGGKVVRIDADRCMECYKCVVEVCPYGALIKMD

>2[4Fe-4S]ST15((646611290)*Ferroglobus placidus* AEDII12DO, DSM 10642
 MSI AVLSCQGCGKCSQVCPTDAIVREGGKVVRIDESKCLKCYKCV E VCPY GALIKMD
 >2[4Fe-4S]ST15(2635678339)*Methanosarcina barkeri*
 CM1
 MVAKINADACTSCGSCIG ECPACAISLNDNDVSFVVEDKCND CGVCLYVCVHG AITIV

>2[4Fe-4S]ST15(2632829309)*Methanosarcina barkeri*
 227
 MVAKINADACTSCGSCIG ECPACAISLNDNDVSFVVEDKCND CGVCLYVCVHG AITIV
 >2[4Fe-4S]ST15(2649848043)*Methanosarcina barkeri* 3
 MVAKIDANSC ESCGNCIG ECPACAISINDDV SFVIEDKCND CGICLNACVHG AITIV

>2[4Fe-4S]ST15(2633010610)*Methanosarcina barkeri*
 MS
 MVAKINADACTSCGSCIG ECPACAISLNDNDVSFVVEDKCND CGVCLYVCVHG AITIV
 >2[4Fe-4S]ST15(2628282755)*Methanosarcina* sp.
Kolksee
 MVAKINPESC ASCGSCIG ECPACAISLND DDV SFVIEDKCND CGVCLDVCVHG AITII
 >2[4Fe-4S]ST15(2648887041)*Methanosarcina vacuolata* Z-
 761
 MVAKINPESC ASCGSCIG ECPACAISLND DDV SFVIEDKCND CGVCLDVCVHG AITII
 >2[4Fe-4S]ST15(2632755851)*Methanosarcina barkeri*
Wiesmoor
 MVAKINPESC ASCGSCIG ECPVCAISINDNDV SFVLEDKCND CGVCLYVCVHG AITIV
 >2[4Fe-4S]ST15(637701322)*Methanosarcina barkeri Fusaro*, DSM 804
 MVAKINPESC ASCGSCIG ECPVCAISINDNDV SFVLEDKCND CGVCLYVCVHG AITIV

>2[4Fe-4S]ST15(638157550)*Archaeoglobus fulgidus* VC-16, DSM 4304
 MAIIVLETCNGCKVCEEVCPFHVFEVIDGFAVAVNSDECIECCACVEACPESAIIVSGCG

Subtype 17

Eukaryota

>2[4Fe-4S]ST17(639591493)*Arabidopsis thaliana Columbia*
 MLPMITGFMNYGQQT LRAARYIGQGMITLSHTNRLPVTIQYPYEKLITSERFRGRIHFE
 FDKCIACEVCVRVCPIDLPVVDWKLETNIRKKRLNYSIDFGICIFCGNCVEYCPTNCLS
 MTEEYEFSTYDRHELNYNQIALGRLPMSVIDDYTIRTIWNSPQTKNGVNPLI
 >2[4Fe-4S]ST17(2507872390)*Zea mays mays* cv. B73
 MFPMLTG FITYGQQTIRAARYIGQSFIITLSHTNRLPITIHYPEKSITLERFLGRIHFE
 FDKCIACEVCVRVCPIDLPFVDWRF EKDIKRKQLLNYSIDFGVCIFCGNCVEYCPTSCLS
 TTEEYELSTYDRHELNYNQIALSRLP

Subtype 18

Bacteria

>2[4Fe-4S]ST18(1BWE)*Bacillus schlegelii*(mutantD13C)
AYVITEPCIGTKASCVEVCPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPE
EWKSYIQKNRDFFKK

Archaea

>2[4Fe-4S]ST18(2574367207)*Uncultured Crenarchaeota* C2
MPEKNASAVDIFGLLSEDSPEQAKKKRRQELLEPTGVKELFKGGNISVNKYTCDGVQCKL
CVKACPTNALYWKAGEVGIIEDLCVYCGACVLNCMVDDCIKIERKREDGKVERFSKPQDV
IMLEEKVNGKKRFDRVKAIFFPTADAYCEKYTVKPEDINLFLGKTAGNRNTDKQKHFTKP
RKRRRQPKHE

Subtype 19

Bacteria

>2[4Fe-4S]ST19(ALO12934.1)*Streptomyces venezuelae*
MPLVPQRADVPTIDESKCIDGCTLCVEMCPLDSLAIREDNGKAYMHVDECWYCGPCAARCP
TGAVTVNM
PYLLR
>2[4Fe-4S]ST19(A9GAV0)*Sorangium cellulosum* So ce56
MGHLLNRESVKAQSARSVGHAEAAVRLDLPVVIDEASCIKGCRCIDSCPVDCLAIDPETKK
ARMAYDECWYCLACEIDCPKEAITVKIPFLIR

Subtype 20

Bacteria

>2[4Fe-4S]ST20(1DUR)*Peptoniphilus asaccharolyticus*
AYVINDSCIACGACKPECPVNCIQEGSIYAIDADSCIDCGSCASVCPVGAPNPED

Archaea

>2[4Fe-4S]ST20(637846037)*Methanosphaera stadtmanae* DSM 3091
MAGNPYKINDNCVACGLCVNACPIDAIAEGNPYVIDEEKCVGCGVCAEACPTQAIEEVA
>2[4Fe-4S]ST20(2645883269)*Methanosarcina siciliae* HI350
MEDPLEFLRNISVAVATVDDGKPAVRMNDVMLVENEKLYFLTARGKPYRQLKENPEIA
LVGMDKNYVMVRVRGRIEFVENIFLEKIFEANPILDEIYPGDTKHILEVFCLSSGVGEMY
DLSGIPPKRERFAFGGAKVAESGYKITEKCTACGICKDLCPSGAISKGKIYKIDGSICLE

CGRCAENCPYDAIEPPSGI
 >2[4Fe-4S]ST20(2653161894)*Methanosarcina siciliae* T4/M
 MEDPLEFLRNIKSVAVATVDDGKPAVRMNDVMLVENEKLYFLTARGKPYYRQLKENPEIA
 LVGMDKNYVMVRVRGRIEFVENIFLEKIFEANPILDEIYPGDTKHILEVFCLSSSGVGEMY
 DLSGIPPKRERFAFGGAKVAESGYKITEKCTACGICKDLCPSGAISKGKIYKIDGSICLE
 CGRCAENCPYDAIEPPSGI
 >2[4Fe-4S]ST20(2641586371)*Methanococcoides methylutens* MM1
 MEDPLEFLRNIKSVSVATVNNGTPAVRIADVMLHEDDKLYFLTARGKPYYKQLKENPEIA
 IVAMDENYVTVRVKGKIEFVDRALLERIFEANPVMNHIYPGDTREILDVFCLPKGIGEVF
 DLSIVPPKRERFAFGGAEVVESGYRINENCIACGICKGSCPTGAISEGNIYSIDSSICLE
 CGNCYEKCPNDAIDLPAEF
 >2[4Fe-4S]ST20(2628412320)*Methanosarcina* sp. WH1
 MEDPLEFLRNIKSVAVATVDEGKPAVRMSDVMLVENEKLYFLTARGKPYYKQLKKNPEIA
 LVGMDNNYVMVRVRGKIEFVENSFLEKIFEINPVLDEIYPEDTKDILEVFCLFSGVGEMF
 DLSGTPPRRERFSFGGANVAEPGYKITEKCTACGICEELCPSGAISKGEIYKIDGSICLE
 CGRCAEYCPYDAIEPPSSI
 >2[4Fe-4S]ST20(2628823930)*Methanosarcina siciliae* C2J
 MEDPLEFLRNIKSVAVATVDDGKPAVRMNDVMLVENEKLYFLTARGKPYYRQLKENPEIA
 LVGMDKNYVMVRVRGRIEFVENIFLEKIFEANPILDEIYPGDTKHILEVFCLSSSGVGEMY
 DLSGIPPKRERFAFGGAKVAEPGYKITEKCTACGICKDLCPSGAISKGKIYKIDGSICLE
 CGRCAENCPYDAIEPPSGI
 >2[4Fe-4S]ST20(2629258468)*Methanosarcina* sp. WWM596
 MEDPLEFLRNIKSVAVATVDEGKPAVRMSDVMLVENEKLYFLTARGKPYYKQLKKNPEIA
 LVGMDNNYVMVRVRGKIEFVENSFLEKIFEINPVLDEIYPEDTKDILEVFCLFSGVGEMF
 DLSGTPPRRERFSFGGANVAEPGYKITEKCTACGICEELCPSGAISKGEIYKIDGSICLE
 CGRCAEYCPYDAIEPPSSI
 >2[4Fe-4S]ST20(2633311162)*Methanosarcina lacustris* Z-7289
 MEDPLELLRNIKSVAFATIEGGKPAVRMSDVMLYENGKLYFLTARGKPYYKQLKKNPEIA
 IVGMNKNYVMVRVRGKIEFVDNSFLEKIFEINPVLDDIYPKDTKDILEVFCISAGVGEIF
 DLSVAPPKRERFAFGGATVEEPGYKITEKCTACGICEDLCPTRAISKGKIYKIDGSICLE
 CGRCYENCPYDAIEPASGL
 >2[4Fe-4S]ST20(2682306712)*Methanobrevibacter olleyae* YLM1
 MPVFAGRIPETARERLSKLKGNNTKAIYVNYGNAQVADALVELVDILQENNFDVIAAAS
 TISHHSIFDGVAIGRPDDEDIAKINEFAQNAIEKIENGGSLESSIPGNRPYIDYKQLPFI
 VSCDVNKCVCLECVSVCPEKAIPDDDPADVLDLCSRCTSCINICPENARAFTGEAFKA
 KKPAFESANAERKEPEFYF
 >2[4Fe-4S]ST20(2758463438)*Methanopyrus* sp. SNP6
 MWLAITGGKGGVGKTTVAHVHRI LGWDALDLVTTPNLHLYLDCEEIDRSDVYIPCPKL
 EDEDECDLCGT CARACAPGALVVGSRWDLDPHLCHGCGLCVESCPNGALAYDCVRIGEVR
 RYQVSVTGAILTSGTLDVGDRRSRHLVRTLLEGADDGKDLILDTPAGAGKDVYDALKAAD
 AAIAVTQPTPAAAT
 >2[4Fe-4S]ST20(638169710)*Methanopyrus* *kandleri*
 AV19
 LKVMVERCLGCAACAAVCPKDALTISGGKPEFGPECDDCGICAKVCPTGAIENEGE

 >2[4Fe-4S]ST20(640786286)*Methanococcus* *vannielii*
 SB
 MYNIVVTMKILECCVGCCTCVPFPCNGAITSIGNAEIECEKCTKCGLCVSYCPLNAIKN
 >2[4Fe-4S]ST20(650856884)*Methanotorris igneus* Kol5, DSM
 5666
 MRILDRCVGCGECVPFPCPF EAIKTYGKAIIDKEKCTNCGICIKYCPISAIEEDN

>2 [4Fe-4S] ST20 (638201948) *Methanocaldococcus jannaschii* DSM 2661

MGIKILEKCVGCGNCVVFPCPRRAIKTYGVAIVDENKCSNCGICARYCPINAIKVDTSL

>2 [4Fe-4S] ST20 (646623544) *Methanocaldococcus* sp. FS406-22

MGIKILEKCVGCGNCVVFPCPKKAIKTYGIAIVDKNRCSNCGICVRYCPINAIKIEV

>2 [4Fe-4S] ST20 (2504145967) *Archaeoglobus veneficus* SNP6, DSM 11195

MIVTTSSCVGCAFCCKLVCPEEAIEVFGRAEIDSQKCVECKKCVIYCPIEAIAIKVVEE

>2 [4Fe-4S] ST20 (637846037) *Methanosphaera stadtmanae* DSM 3091

MAGNPYKINDNCVACGLCVNACPIDAIAEGNPYVIDEEKCVGCGVCAEACPTQAIEEVA

>2 [4Fe-4S] ST20 (2566176904) *Thermoplasmatales* archaeon
BRNA1

MPKVIEDKCVGCGNCADVCPNDAIEIKDVAVIDEAKCVECDACVDECPSGAIEPSD

>2 [4Fe-4S] ST20 (2637997696) *Candidatus Methanoplasma termitum*
Mpt1

MPPKVNAAEVCVACGSCADVCPQDAITIDDIIVIDASKCVDCGACVDECPPGAITE

>2 [4Fe-4S] ST20 (2661857974) *Methanogenic* archaeon ISO4-H5

MPKIIAENCVACGACADACPQEAITIDDIIVIDESKCVDCGACIDECNSDAIEE

>2 [4Fe-4S] ST20 (2566176906) *Thermoplasmatales* archaeon
BRNA1

MPKIIAENCVACGACADACPEGAITMEDVAVIDDSKCIDCGACVDECSSDAIEN

>2 [4Fe-4S] ST20 (2566176905) *Thermoplasmatales* archaeon
BRNA1

MPKIIAENCVACGACADVCPPEGAITIDDVVIDDSKCVDCGACVDECNSDAIEN

>2 [4Fe-4S] ST20 (2540667538) *Candidatus Methanomethylophilus alvus*
Mx1201

MPKVIADNCVACGACVDACPNGAITVDDIIVIDASKCTDCGACIDACPSEAIEN

>2 [4Fe-4S] ST20 (2661857975) *Methanogenic* archaeon ISO4-H5

MPKVIADNCVACGACADACPESAITVDDVAVIDESKCVDCGACVDECPSSEAIEN

Subtype 21

Bacteria

>2[4Fe-4S]ST21(A9G317)*Sorangium cellulosum* So ce56
MAYVIAEPCVATCDTACVPVCPVDCIHGPLAADEISRIPEGERKTRLAGLQLYIDPESCICC
GACENECPVGAIFDEDELPAEWQRYREINARFFDDRAKERAPEET

Subtype 22

Eukaryota

>2[4Fe-4S]ST22(639591453)*Arabidopsis thaliana* Columbia
MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVGCKRCESACPT
DFLSVRVYLWHETTTRSMGLAY
>2[4Fe-4S]ST22(2505189083)*Paulinella chromatophora*
MSHSVKIYDTCIGCTQCVRACPLDVLEMVPWDGCKASQIASSPRTEDCVGCKRCETACPT
DFLSIRVYLGDETTRSMGLAY
>2[4Fe-4S]ST22(649363882)*Thalassiosira pseudonana* CCMP 1335
MSHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKSGQIASSPRVEDCVGCKRCETACPT
DFLSVRVYLGAEETTRSLGLAY
>2[4Fe-4S]ST22(2507813137)*Zea mays mays* cv. B73
MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVGCKRCESACPT
DFLSVRIYLGPEETTRSMALSY
>2[4Fe-4S]ST22(2507833286)*Zea mays mays* cv. B73
MSHSVKIYDTCIGCTQCVRACPTDVLEMIHWDGCKAKQIASAPRTEDCVGCKRCESACPT
EFLSVSVYLGPEETTRSMALS
>2[4Fe-4S]ST22(2507863669)*Zea mays mays* cv. B73
MSHSVKIYDTCIGCTQCVRACPTDVLEMIPWDGCKAKQIASAPRTEDCVGCKRCESACPT
DF

Subtype 23

Eukaryota

>2[4Fe-4S]ST23(2505188940)*Paulinella chromatophora*
MLGFLRQVG DYTRD TVDAARNIVQGLSVTFDHLKRRPITVQYPYEKLIPSPRYRGRIHFE
LDKCIACEVCVKVCPINLPVVDFVPGPTSKVGKELRNYSIDFGVCIFCANCVEYCPTQCL
SMTEEYELTSFDRHNLNYDNVALGRPLSIRADSSVIPLRELAELPKGDLDPHTSG

Subtype 24

Archaea

>2[4Fe-4S]ST24(2730778604)*Methanomicrobiales archaeon* Methan_05
MTSAKAYKDAALAARLSDRYYRPKQDSDPSFTAEEKIGGTEAHICFQCGTCTGSCPSAA

RSSYRIRNFMRRVNLGMRDVCLNDPDLWLCTTCYTCADRCPRDLIPTDVIMAMRNIAAKQ
 GIVPKNFLATVNFIIYNTGHGVPNNDANRAARVKLGLEAEPETTSKYPEYIPAIRKILEIY
 GTKQLADRVLAEQ
 >2[4Fe-4S]ST24(648195480)*Methanolacinia petrolearia* DSM 11571
 MAVEKNYGNPDLEKKLADRNYTSDSHKDFSKRVEKISGTMSHMCFCQCGTCTGSCPSAPR
 SSYRIRLFMRRAVLGLEDEALDTPDLWLCTTCYSCSDRCPRDLFPTDVIMAMRNLA FERD
 IVPRNFLQTVNLIYTS GHGVPNNDVNRAAREKLGLPRDPPTTHSYPEYLEGIRKIIDHYK
 LKENADRILSEGGN
 >2[4Fe-4S]ST24(648195474)*Methanolacinia petrolearia* DSM 11571
 MAVEKNYGNPDLEKKLADRNYTSDSHKDFSKRVEKISGTMSHMCFCQCGTCTGSCPSAPR
 SSYRIRLFMRRAVLGLEDEALDTPDLWLCTTCYSCSDRCPRDLFPTDVIMAMRNLA FERD
 IVPRNFLQTVNLIYTS GHGVPNNDVNRAAREKLGLPRDPPTTHSYPEYLEGIRKIIDHYK
 LKENADRILSEGGN
 >2[4Fe-4S]ST24(640098885)*Methanocorpusculum labreanum* Z
 MTSKAYKDAALARS DRYRKPQSDPSFTA EVEKIGGTEAHICYQCGTCTGSCPSGA
 RSTYRIRNFMRRVNLGMRDVCLNDPDLWLCTTCYTCSDRCPRNLIPTDVIMAMRNIAARQ
 GIVPKNFLATVNFIIYNTGHGVPNSDANRAARVKLGLEAEPETTCKYPEYIPAIRKILEAY
 GTKQLADKVLAEQ
 >2[4Fe-4S]ST24(643570853)*Methanosphaerula palustris* E1-9c, DSM
 19958
 MAQSKGYPDAKLNEKLDRYMRGSDTNPQFTQDIRDISKTTAHMCFQCGTCTGSCPSAPR
 STYRIREFMRKGVGLDDEALDTPDLWLCTTCYSCDRCPRDIAPTDVIMAMRNLA FKRD
 IIPINFLKTVLAIYKTGHGVPNNDVNRAAREKLGLTRDPPTTHMYPEYIKGIQKILDHYE
 LKENADRILAEQ
 >2[4Fe-4S]ST24(640115307)*Methanoculleus marisnigri* JR1, DSM
 1498
 MAVKKDYKDQKLAEKLRDRKYYIPDSNPEFIKEVEKIGQTAAHMCYQCGTCTGSCPSAPR
 SSYRIRLFMRKAILGLEEEILTDPDLWLCTTCYSCDRCPRDLAPTDAIMAMRNLAARRD
 IVPRNFLQTVQLIYKSGHGVNNDANRAARKKLGLEEEPE TTHKYPEYLP GIRKIIDHYG
 LKDRADKILSEGE
 >2[4Fe-4S]ST24(2509039562)*Methanoregula formicica* SMSP, DSM
 22288
 MARTKGYPEALEKKLRDQRYVREDSNPEFLKNVKSISRTIAHMCYQCGTCTGSCPSAPRS
 SYRIRHFMRRRAVLGLENEALDTPDLWLCTTCYSCSDRCPRDI IPTDVIMAMRNLA FKRD
 VPVNFLKTVQAIYSSGHGVNNDVNRAAREKLGLTRDPPTTHMYPEYMPGIRKILDHYKL
 KANADRIVKEREQ
 >2[4Fe-4S]ST24(2730773254)*Methanomicrobiales archaeon* Methan_07
 MAVKKDYKDQKLAERLRDRKYYIPDSNPEFIKDVEKIGRTAAHMCYQCGTCTGSCPSAPR
 SSYRIRLFMRKAILGLEEEALDTPDLWLCTTCYSCDRCPRDLAPTDAIMAMRNLA FKRD
 IVPRNFLKTAQLIYQSGHGVNNAANRVAREKLGLEAEPETTTHKYPEYLP GIRKIMDHYR
 LKENADRILAEQ
 >2[4Fe-4S]ST24(2540643946)*Methanoculleus bourgensis* MS2
 MAVKKDYKDQKLAEKLRDRSYVSDSNPEFIKEVERLGRTAAHMCYQCGTCTGSCPSAPR
 SSYRIRLFMRKAILGLDEEVLTPDLWLCTTCYSCDRCPRDLAPTDAIMAMRNLA FKRD
 IVPRNFLKTVQAIYKTGHGVPNNDTNRAAREKLGLEADPETTHKYPEYLP GIRKIMDHYA
 MKENADRILAEQ
 >2[4Fe-4S]ST24(2684091568)*Methanoculleus* sp. MAB1
 MAVKKDYKDQKLAEKLRDRNYASDSNPEFIKEVERLGRTAAHMCYQCGTCTGSCPSAPR
 SSYRIRLFMRKAILGLDEEVLTPDLWLCTTCYSCDRCPRDLAPTDAIMAMRNLA FKRD
 IVPRNFLKTVQAIYKTGHGVPNNDTNRAAREKLGLEADPETTHKYPEYLP GIRKIMDHYA
 MKENADRILAEQ

>2[4Fe-4S]ST24(640867809)*Methanoregula boonei* 6A8
 MVRTKGYPEALEKKLHDQRYREDSTADFMKRVEASSRTIAHMCYQCGTCTGSCPSAPRS
 TYRIRKFMRRAVLGFETEALDTPDLWLCTTCYSCTDRCPRDIAPTDVIMSMRNMAFTHDI
 IPVNFLKTVTAIYASGHGVPNNNDVNRAAREKLGLTRDPPTTHMYPEYMPAIRKILDHYHL
 KENADRRIKEREK

>2[4Fe-4S]ST24(2688749754)*Methanoculleus bourgensis* MBBA
 MAVKKDYKDQKLAEKQLDRNYYASDSNPEFIKEVERLGRTAAHMCYQCGTCTGSCPSAPR
 SSYRIRLFMRKAILGLDEEVLTDPDLWLCTTCYSCTDRCPRDLAPTDAIMAMRNLAFKRD
 IVPRNFLKTVQAIYKTGHGVPNNNDTNRAAREKLGLEADPETTHKYPEYLPGIRKIMDHYA
 MKENADRILAEKE

>2[4Fe-4S]ST24(637897455)*Methanospirillum hungatei* JF-1
 MAAKSYNIPELDKKLADRRYHLSDTNPEFTQKILKTSRTIANMCYQCGTCTGSCPSAPRS
 SYRIRLFMRRCVLGLENEALDTPDLWLCTTCYSCTDRCPRDIAPTDVIMAMRNLAFKRDI
 VPKNFLQTVQLIYNSGHGVPNNNDVNRAARTKLGLPADPPTTHSYPEFVKGIQKIIDHYEL
 KENADRILKGD

>2[4Fe-4S]ST24(2507146036)*Methanofollis liminatans* GKZPZ, DSM
 4140
 MAKGYNDPAMEKKFQDRYYHAADNPEFTKEVERIGRTMAHMCYQCGTCTGSCPSAPRSSY
 RIRKFVRRVAVMGLEREALDTPDLWLCTTCYSCTDRCPRGIAPTDIIMAMRNLAFKWDIVP
 RNFLKTIQLIYTTGHGVPNNNDVNRAARVKLGLDAEPETTHKYPEFLPGIQKIMDHYKMKE
 NADRILSEGEH

>2[4Fe-4S]ST24(2730775518)*Methanomicrobiales archaeon Methan_06*
 MAAKSYNIPELDQKLADRRYHLSDTNPEFTQKIIKTSRTIANMCYQCGTCTGSCPSAPRS
 SYRIRLFMRRCVLGLEDEALDTPDLWLCTTCYSCTDRCPRDIAPTDVIMAMRNLAFKRDI
 VPKNFLQTCQLIYNSGHGVPNNNDVNRAARTKLGLPADPPTTHSYPEFIKGIQKIMDHYEL
 KENADRILKGD

>2[4Fe-4S]ST24(2730775515)*Methanomicrobiales archaeon Methan_06*
 MAAKSYNIPELDKKLADRRYHLSDTNPEFTQNILKTSRTIANMCYQCGTCTGSCPSAPRS
 SYRIRLFMRRCVLGLENEALDTPDLWLCTTCYSCTDRCPRDIAPTDVIMAMRNLAFKRDI
 VPKNFLQTCQLIYNSGHGVPNNNDVNRAARTKLGLPADPPTTHSYPEFIKGIQKIMDHYEL
 KENADRILKGD

>2[4Fe-4S]ST24(650856113)*Methanotorris igneus* Kol5, DSM 5666
 MLLKSEKDFDNNFVNEIIETGRTILGEGHVASFACQYQCGTCTGSCPSGRITAFKTRKLI
 KYAQFGMRKFAVESEDLWMCTTCYECYERCPREVKITDIIKVIRNIAAREGRMAKAHRMT
 ALYVFKTGHAVPINEETRKARKSIGLSEVPPTTHKYPEVLEVIRGIMKDMKFCDIVGICT
 ESMELKPVEWKDMSE

>2[4Fe-4S]ST24(638202080)*Methanocaldococcus jannaschii* DSM 2661
 MVIYAQKDISNDFIKEIIKTGEILGEGHVSSFKACYQCGTCTGSCPSGRITAFRTRKLIR
 YAQFGMKSIIIDSEDLWMCTTCYECYERCPRTVKITDIIKVLNRNIAAREGKMAEAHKKTA
 LYVFKTGHAVPINDQIKKARKEIGLTEIPPTTHKYPDALEVVRGIMKDLRFCDMVGICTE
 TMQLKPVEWKDMSE

>2[4Fe-4S]ST24(646366951)*Methanocaldococcus vulcanius* M7, DSM
 12094
 MVIYAQKDISNDFIEEIIKAGEILGEGHVSSFKACYQCGTCTGSCPSGRITAFRTRKLIR
 YAQFGMKSIIIDSEDLWMCTTCYECYERCPRTVKITDIIKVLNRNIAAREGKMAEAHKKTA
 LYVFKTGHAVPINDQIKKARKEIGLTEIPPTTHKYPDALEVVRGIMKDLKFCDMVGICTE
 TMQLKPMVEWKDMSE

>2[4Fe-4S]ST24(638168586)*Methanopyrus kandleri* AV19
 MVEPRDTVIREEDLNPDFLEELSELVEPVFEEEEEVLSVQACYQCGTCTGSCPSGRRTSYR
 TRLIMRKLQLGLVDEVIKSDELWMCTTCYTCYERCPRGVKIVDAVKAARNLAAKGYMAK
 AHRMVAMFVIKTGHAVPINDEIREVRKNIGLDEVPTTHRYEEALEEVQKLVKINEFDKL

IGYDWEEGDLVD

>2[4Fe-4S]ST24(2758462870)*Methanopyrus* sp. SNP6

LVEPRDTVIREEDLNPDFLEELSELVEPVFEEEEVLSVQACYQCGTCTGSCPSGRRTSYR
TRLIMRKLQLGLVDEVIKSDELWMCTTCYTCYERCPRGVKIVDAVKAARNLAAKEGHMAK
AHRMVAMFVIKTGHAVPINDEIREVRKNIGLDEVPPPTTHRYEEALEEVQKLVKINEFDKL
IGYDWEEGDLVD

>2[4Fe-4S]ST24(2758473009)*Methanopyrus* sp. KOL6

LVEPRDTVIREEDLNPDFLEELSELVEPVFEEEEVLSVQACYQCGTCTGSCPSGRRTSYR
TRLIMRKLQLGLVDEVIKSDELWMCTTCYTCYERCPRGVKIVDAVKAARNLAAKEGHMAK
AHRMVAMFVIKTGHAVPINDEIREVRKNIGLDEVPPPTTHRYEEALEEVQKLVKINEFDKL
IGYDWEEGDLVD

Subtype 25

Archaea

>2[4Fe-4S]ST25(650916849)*Methanothermococcus okinawensis* IH1
MVLSSKDFNPKFPEKVIEAGKAIGEDEATKSFRRCYQCGTCTGSCPSGRITAFRTRKLI
SAMLGLGDYIKSEDLWKCTTCYTCYERCPRNVKITDIKAMRNVASQMGYMALAHRKTTL
YVYLTGHAVPVNDQIKEVRKNIGLTEIPPTTHKYPEALEDVIRGIMNDMGLCDKVGICPTT
KKLEELKPIEWEDLSE

>2[4Fe-4S]ST25(646777310)*Methanocaldococcus infernus* ME
MVLTKNDFDPKFSEEIIVKVAEEIGEEEVVKSFRRCYQCGTCTGGCPSGRHTAYRVRVLIR
SALMGFYKYIESEDLWMCTTCYTCYERCPRDVKITEIIVKAMRNLAARLGLMAEAHRKTCL
YVYLTGHAVPINDKIKEVRKKLGLSEVPPTTYKYPEVLEHIRGIMQDMKLCEKVGICPTS
KTLKELTPVKWEEMSE

>2[4Fe-4S]ST25(640787700)*Methanococcus aeolicus* Nankai-3
MTIKSTDLPNPKFTEKIIIEAGEAIGEGDIISFRCYQCGTCTGGCPSGRITAYRVRQLIR
SAMFGLGDYVKTEDLWKCTTCYTCYERCPRDVKITEIIVKAMRNVAQMGYLATAHRKTCL
YVFLTGHAVPVNDEIIVKVRKKLGLTEIPPTTHKYPEVVEEMRGIMEDLKLCEKVGICPTT
KKLQELTPMDWSDMSE

>2[4Fe-4S]ST25(640786137)*Methanococcus vanniellii* SB
MVFKSSEFNPNFPKKIVDAGKEVFGANNASSFQKCYQCGTCTGACPSGRITALRTRKLI
SALSGMDNLLKSDDLWMCTTCYECYEKCPREVKITDIKTIRNIAAEEGYIAEPHRKTSL
LVFKTGHAVPVNDEIIVKARLAIGLTEIPPTTHKYPEALEMVRDIMDDLKFCKKVGICRET
MDLEPLKVKKSKY

>2[4Fe-4S]ST25(646859226)*Methanococcus voltae* A3
MVLNSKDYKKEFSEAIVNAGIDFLGEDKSNSFRRCYQCGTCTGACPSGRITGFRTRKVIR
QALLGSEELLSSDDLWMCTTCYECYEKCPRDVKITDLIKVIRNLASEKGYIADHRKTSL
YVFKTGHAVPVNADIIVKARLELGLTEIPPTTHKYPEALQMIKDIMSELEFCKKVGICEET
GELTELDLKYASE

>2[4Fe-4S]ST25(2563557097)*Methanococcus maripaludis* S2
MVLKSSEFNPDFPKQIIIESGEWIFGDHASSFQKCYQCGTCTGACPSGRITALRTRKLIRS
ALAGIDSILSGDDLWMCTTCYECYEKCPREVKITDIIVKIRNIAAEKGYIAEPHRKTSL
VFKTGHAVPVNDEIIVKARLAIGLTEIPPTTHKYPEALEIVRDIMEDLNFCCKKVGICRET
DLEPLNVQKSEE

>2[4Fe-4S]ST25(641284018)*Methanococcus maripaludis* C6

MVLKSSEFNPDFPKQII EAGEWIFGNNASSFQKCYQCGTCTGACPSGRITPLRTRKLIRS
ALGGIDSILSSDDLWMCTTCYECYEKCPREVKITDIIKIVRNIAAERGYYAEPHRKTSLL
VFKTGHAVPVNDEIKKARLAIGLTEIPPTTHKYPEALEMVRDIMDELNFCKKVGICRETM
DLEPLNVQRSGE

>2 [4Fe-4S] ST25 (640792923) *Methanococcus maripaludis* C7

MVLKSTEFNADFPKQII EAGEWIFGKNASSFQKCYQCGTCTGACPSGRITPLRTRKLIRS
ALAGIDSILSGDDLWMCTTCYECYEKCPREVKITDIIKII RNIAAEKGYIAEPHRKTSLL
VFKTGHAVPVNDEIKKARLAIGLTEIPPTTHKYPEALEIVRDIMDDLNFCKKVGICRETM
DLEPLNVQKSGE

>2 [4Fe-4S] ST25 (640165937) *Methanococcus maripaludis* C5

MVLKSSEFNPDFPKQII EAGEWIFGKNASSFQKCYQCGTCTGACPSGRITPLRTRKLIRS
ALAGIDSILSSDDLWMCTTCYECYEKCPREVKITDIIKIVRNVA AEKGYIAEPHRKTSLL
VFKTGHAVPVNDEIKKARLAIGLTEIPPTTHKYPEALEMVRDIMDELNFCKKVGICRETM
DLEPLNVQKTGE

>2 [4Fe-4S] ST25 (2511672054) *Methanococcus maripaludis* X1

MVLKSSEFNPDFPKQII ESGEWIFGDHASSFQKCYQCGTCTGACPSGRIT ALRTRKLIRS
ALAGIDSILSGDDLWMCTTCYECYEKCPREVKITDIIKII RNIAAEKGYIAEPHRKTSLL
VFKTGHAVPVNDEIKKARLAIGLTEIPPTTHKYPEALEIVRDIMEDLNFCKKVGICRETM
DLEPLNVQKSEE

>2 [4Fe-4S] ST25 (2655683303) *Methanobrevibacter millerae* SM9

MTSKQNIDDSPVDFAEKII MDVKN SKDEGV LKCVQCGMCTSTCPAARHSDYNPRDIIERV
LAGDESILQDDLIWNC FYCYTCHSVCPVGNSVCEVNQILKQIAISRQIGYDKLYEYMGFA
DSYFTAAIGA IPEIFFDDIKNDVPGWWEFRTNLGEIREELELDPPLMPPKETIDEVSKIL
TITGFKEKIEKIRASQEA EK

>2 [4Fe-4S] ST25 (2682306669) *Methanobrevibacter olleyae* YLM1

MNKELINNNPIEFAVDI ISHDKNTKENGVLKCVQCGMCTSTCPAARHSSYNPRDIIERVL
NGDEAILEEEDIWNC FYCYTCHSVCPVGNSVCEVNQILKQNAISKGIAYEKLYDYLGFAD
SYFNAAIGA IPEAFFEDIKDDVDGWWEFRQDLVNIRNKLNLGPLFPSEDVIDEVSIIITN
TGFKSRMDEIRKSQEDKI

>2 [4Fe-4S] ST25 (650751329) *Methanobacterium lacus* AL-21

MRTIKLNKNSHKLVDVLKDLKASPD LGIYKCVQCGMCTSI CP GASQSDYDPRDMVRRVL
EDDVSIVDDENIWNCFSCYTCNSVCPSGNNASEVNQILRQMSIDKGE GILKIQSFAAYGD
SFIELGVGSVPSKFFDDMVKDVGP EYMN LKLNIEDIRSDLGLGSYILPEKSIDEEVEEILD
KSGFKARLKRIKGCKK

>2 [4Fe-4S] ST25 (2647504051) *Methanobacterium formicicum* DSM 1535

MRTLKLNEDSSKLAKEVIGDLKASPSLELFKCIQCGMCTSLCPGARYSDYNPREMV KRVL
DGDESVIYDDDIWNC FYCYTCNSVCPANNSASVVNQILRQKAIN EGKQTDRLSAFLTYGD
SFLEIGIGSIPAAFFDVLVKDFGPEWLDLKMNLDDVRKELGLGSVTLPEDSVEEINEILK
ITGFTRKMEKIRGSP

>2 [4Fe-4S] ST25 (2685267469) *Methanobacterium formicicum* Mb91

MRTLKLNEDSSKLAKEVIGDLKASPSLELFKCIQCGMCTSLCPGARYSDYNPREMV KRVL
DGDESVIYDDDIWNC FYCYTCNSVCPANNSASVVNQILRQKAIN EGKQTDRLSAFLTYGD
SFLEIGIGSIPAAFFDVLVKDFGPEWLDLKMNLDDVRKELGLGPVTLPEDSVEEINEILK
ITGFTRKMEKIRGSP

>2 [4Fe-4S] ST25 (650751372) *Methanobacterium lacus* AL-21

MRTIKLKKDPLKLLNDVLKHLKASPELGIFKCVQCGMCSSVCPAAKRTDYDPK EMLGRVL
QDDET VVDDDTIWYCFSCYTCNSVCPSGNNACEVNQILRQMAIDKGDVQRIESFTPYGDS
FMKKGIGTIPEKY EDMVSDSGPECMNIKMDIQNIRSSLGLGNYILPDDAVNEIDLILKN
SGFMERIEMIKGCKK

>2[4Fe-4S]ST25(2631417857)*Methanobacterium formicicum* BRM9
MRTLKLNEDSSKLAKEVIGDLKASPSLELFKCIQCGMCTSLCPGARYSDYNPREMVKRVL
DGDESVIYDDDIWNCFCYCYTCNSVCPANNSASVVNQILRQKAINEGKQTDRLSAFLTYGD
SFLEIGIGSIPAAFFDVLVKDFGPEWLDLKMNLDDVRKELGLGPVTLPEDSVEEINEILK
ITGFTRKMEKIRGSP

>2[4Fe-4S]ST25(2637992676)*Methanobacterium* sp. MB1
MRTLKLNEDSSKLAKEVVGDLKASPSLKLFKCIQCGMCTSLCPGARYSDYNPREMVKRVL
DGDESVIYDDDIWNCFCYCYTCNSVCPANNSASVVNQILRQKAINEGKQTERLSAFLTYGD
SFLEIGIGSIPAAFFDVLVNDFGPKWLDLKMNLDDVRKELGLEPTTLPEDSIEEINKILK
ITGFTRKMEKIRGSP

>2[4Fe-4S]ST25(637846015)*Methanosphaera stadtmanae* DSM
3091
MGQSKKDDLAYKVLKDIKASPDGLLLRCVQCGMCASSCPAARHSEYDPRVVIKRVLDDDK
TLLEDKYIWNCFYCYNCHSVCPVGNVCEVNQILRQMAIDKDTGKKEIESFMSFADSFLD
TGLGVIPKEYHKQLFKDYGPHWDRLLQQQLEDVRKTLNLESMFLLPEAEKEVDKTLAIGF
KNRVKKIKDVRDKK

>2[4Fe-4S]ST25(648117290)*Acidilobus saccharovorans* 345-15
MPARPSLKRVPRAFLGAIAGNLGALIVGVKYFIDPNRITLLYPHEYIKLRQGYRGYIV
LIFDKCISCASCARICPARAMKMTMEVKDKLNRAMKKKYPVINYNRCIFCGYCVDVCP
TEALYHVPYHDLVYLNMQDMILNVEEFQKEPEFVTAKEGVPVTVVFDEKRGLVKVSVEES
SNQGSSSQPAGGGGSS

>2[4Fe-4S]ST25(2512784226)*Methanocella conradii* HZ254
MSIVFFGSMRVALRNVAEPGDFRLEETCGYEKCMQCGRCTASCPAAFIYEDYRPRDVMR
MLQIGDREALMRVIWRCGQCYSCAARCPRNNSVGAGILALRESAMAAGLAPEGIMATAAM
IRKNLYGHGETFLPATFDFLEEFGPKTTQRCRDNASRRVRLGFDRDDARARPIPANSMKE
IRALIDMTWPGGEADA

>2[4Fe-4S]ST25(2505970216)*Methanocella arvoryzae* MRE50
(reannotation)
MATRIPLGISRSSNGCSTDPRLSGSGYEKCMQCGRCTASCPAAYTFDDYIPRSVMSRLAL
GMGDSLAEAVWRGQCYSRCRARCPRNNSVGEAVLALRERFGAEGRVPTTIKSVRSLLLNN
LHSRGETFLPQMLTDKLLREFGPATYSRCAGNIEKRARLGYEKEDARACRIPDDAMEEIR
HILTATGCSDDTDQK

>2[4Fe-4S]ST25(648117290)*Acidilobus saccharovorans* 345-15
MPARPSLKRVPRAFLGAIAGNLGALIVGVKYFIDPNRITLLYPHEYIKLRQGYRGYIV
LIFDKCISCASCARICPARAMKMTMEVKDKLNRAMKKKYPVINYNRCIFCGYCVDVCP
TEALYHVPYHDLVYLNMQDMILNVEEFQKEPEFVTAKEGVPVTVVFDEKRGLVKVSVEES
SNQGSSSQPAGGGGSS

Subtype 26

Archaea

>2[4Fe-4S]ST26(650508321)*Vulcanisaeta moutnovskia* 768-28
MVIKIKEPRGTLAEDIVYHAKALITGFKEAIEPNRLTIQYPREVRWVPERFRGWIMLDIK
KCISCFQCAWACPVNAIQMYRAPNGKFYPGIRYTECILCHFCVDACPVGALIPTPIHDIA
YVDFDEVKFKPEDMSRSPEYIYDESERVIKYEIKNGRLLKIALPKDEIKRRLEELDKVIE

QSGGATAAAESSSA

>2[4Fe-4S]ST26(648201390)*Vulcanisaeta distributa* DSM 14429
MVIKIKPPKGTLAEDIIYHAKALITGFKEAVEPNRLTIQYPREVRWIPERFRGWIMLDIK
KCISCFQCAWACPVNAIQMYRAPNGKFYPGIRYTECILCHFCVDACPVGALIPTPIHDIA
YVDFDEVKFKPEDMSRPPEYVFDESERVIKYEIKDGRLLKIALPKDEIKKRIEELDKVIE
QSGGAPAAAESSSA

Subtype 27

Archaea

>2[4Fe-4S]ST27(646510256)*Archaeoglobus profundus* Av18, DSM 5631
MEMMEEGVDPVINLSYLAEREETELEKRVAEI IKELGAERLMYCMQCGACASICPLARVG
FEWYNKKLIKALILGLRDELDDPTPWACVACNRCTEICPRRVSPFEVMFAMRRMLAEEY
AIGSLAIEGLRSLYEYGHAVYMAGREARKKVGLPEKPPSTESDPKALEDLRKILKQTKLA
ELGLVPME

Subtype 28

Archaea

>2[4Fe-4S]ST28(2730780308)*Methanosarcinales* *archaeon*
Methan_04

MIVLIVSIGGIFYPKLGYIILLVLFATLLIIAPFRGRWFECGNLCPRGSFVDFWLAPLSRRL
AIPFLRSMWIRIPIFIALMGFMIYRLLGTQGVVDRIGMVFTLTCIITTSIAILFGVIIA
PRTWCTFCPMGTLQRIMGGSKYQLKLDGDLCDCKRCQKVCMPQLRVFELQDLPDCIKCG
RCIDACPKDALIFH

>2[4Fe-4S]ST28(650798726)*Methanothrix soehngenii* GP-6
MIVLIVSIGGIFYPKLGYIILLVLFATLLIIAPFRGRWFECGNLCPRGSFVDFWLAPLSRRL
AIPFLRSMWIRIPIFIALMGFMIYRLLGTQGVVDRIGMVFTLTCIITTSIAILFGVIIA
PRTWCTFCPMGTLQRIMGGSKYQLKLDGDLCDCKRCQKVCMPQLRVFELQDLPDCIKCG
RCVDACPKDALIFH

Subtype 29

Archaea

>2[4Fe-4S]ST29(2512783241)*Methanocella conradii* HZ254
MLEKLKASGELIANFFKRPVTVKESFGFVAEAFRWLPRRNDDLCTGCGACVERCSSGATS
ITDRGDTRVVSIDGLRCIFCGRCAEVCPEKALELTLEDAPPAQGSPTARVSLSRGAEEP
RPTVDTVLKLQRCSVCGEVMPVTEKYLDIAKERTLRNLKPETA AIVEKDMERYLKTCINC
RRVHSLEWDTHPRKFI

>2[4Fe-4S]ST29(2505974063)*Methanocella paludicola* SANAE
(reannotation)

MSIVGKLKAFGDLALNFFRKPVTVDSEYGF TAENFRWLPRRNADLCTGCGACNERCSSGA
TSLTDADGERTVVSIDGLRCIFCGRCADVCPERALELTLEPKKEGETDTGRVSLSHGSEEP
RPTVDTKLKLQKCRICGEYMPVTEKYVAVVRDRTLKNLKPETA AIVEKDMKEYLTVCVNC
RRKYSIEWDTHPRKFI

Subtype 30

Archaea

>2[4Fe-4S]ST30(2629270190)*Methanosarcina mazei* S-6

MDENFQAGKDGLMYAASKGLGIVIMEPMRGGYLVSGMPPEIQEIWDSADIQRSPVEWSLR
YLWDYPEIAVVLSGMSEIKHVEDNVKFASGGLPDSLTERERELISRVKKIYMSKTRVNCT
GCRYCMPCPSGVNI PENFKYLNNAEMFDNAEGEKALYSGLEGQASNCTECGQCEEKCPQK
IPVSQMLKEVVKLF GK

Subtype 31

Archaea

>2 [4Fe-4S] ST31 (641283839) *Methanococcus* *maripaludis*
C6

MSVVIDYDKCKGPECAECVNTCPVEVF EIQGDKVVVARESDCTFCLVCVDVCPTG AITVK
ED

>2 [4Fe-4S] ST31 (640165763) *Methanococcus* *maripaludis*
C5

MSVVIDYDKCKGPECAECVNTCPVEVF EIQGDKVVVARESDCTFCLVCVDVCPTG AITVK
ED

>2 [4Fe-4S] ST31 (640793100) *Methanococcus* *maripaludis*
C7

MSVVIDYDKCKGPECAECVNTCPVEVF EIQGNKVVVARESDCTLCMVCVDVCPTN AITVK
ED

>2 [4Fe-4S] ST31 (2511672226) *Methanococcus* *maripaludis*
X1

MSVVIDYDKCKGPECAECVNTCPVEVF EIQDDKVVIAKESDCTLCMVCVDVCPTD AITVK
ED

>2 [4Fe-4S] ST31 (650917829) *Methanothermococcus* *okinawensis*
IH1

MSVTIDYDKCKGPECAECVNACPM EVF EIQGDKVVVVREEDCTFCLVCEDVCPTG AVKVK
ED

>2 [4Fe-4S] ST31 (2563557278) *Methanococcus* *maripaludis*
S2

MSVVIDYDKCKGPECAECVNTCPVEVF EIQDDKVVVAKESDCTLCMVCVDVCPTD AITVK
ED

>2 [4Fe-4S] ST31 (640786308) *Methanococcus* *vannielii*
SB

MSVIIDYDKCKGPECAECVNTCPTEVF EIKENKVIVMRES DCTFCLVCIDVCPTD AIIVK
ED

>2 [4Fe-4S] ST31 (640788487) *Methanococcus* *aeolicus* *Nankai-*
3

MSVIINYNKCDGVDCAECMNACPM EVFTIEDNKVVVSKED ECTFCMICEDVCPNG AVKVK
D

>2 [4Fe-4S] ST31 (640788851) *Methanococcus* *aeolicus* *Nankai-*
3

MVVEIDYNNCDGIDCSGCKDACPTD VFGVEGSKIIVVSNAD ECTFCMMCEDLCPAD AVKVK

N

>2[4Fe-4S]ST31(646368154)*Methanocaldococcus vulcanius* M7, DSM
12094

MAVTIDYNLCKGAECAECANNCPEVFEIDGDKVVVARPDDCTYCGVCEDVCPTGAVKVE
PE

>2[4Fe-4S]ST31(646622590)*Methanocaldococcus* sp. FS406-
22

MAVTIDYNLCKGAECAECVNNCPMEVFEIEGDRVVVAREEDCTYCGVCEDVCPTGAVKVE
PE

>2[4Fe-4S]ST31(646777180)*Methanocaldococcus infernus*
ME

MAVTIDYSKCKGPDCAECVNNCPMEVFEIEGDKVVVANPDECTYCGVCEDVCPTSAVKVE
PE

>2[4Fe-4S]ST31(650856556)*Methanotorris igneus* Kol5, DSM
5666

MAVTIDYSKCKGPECAECVNTPMEVFEIQGDKVVVAKEDECTFCGVCEDVCPTKAIKVT
QE

>2[4Fe-4S]ST31(650855791)*Methanotorris igneus* Kol5, DSM
5666

MKVTINYDLCKGPECAECVNACPMEVFEIQGDKVVVAREEDCSGCGVCMDVCPTNAVKVE
D

>2[4Fe-4S]ST31(646622552)*Methanocaldococcus* sp. FS406-
22

MAVKINYDLCKGAECAECVDACPMEVFEVDGDKIIVAKEEDCTYCGVCVDSCPNNAILLE
E

>2[4Fe-4S]ST31(637846751)*Methanosphaera stadtmanae* DSM
3091

MIININYEDCRGIDCLDCLDICPMNVFDTVDDVLIKKLDNCCGCQVCVDVCPNNAISIE
Y

>2[4Fe-4S]ST31(2647503509)*Methanobacterium formicicum* DSM
1535

MPNVIIDYEKCEGTECGECAEVCSMEVLAIIDGDKITVKNQDGC SLCEICTDVCPNEAIKL
VD

>2[4Fe-4S]ST31(2685266675)*Methanobacterium formicicum*
Mb91

MPNVIIDYEKCEGTECGECAEVCSMEVLAIIDGDKITVKNQDGC SLCEICTDVCPNEAIKL
VD

>2[4Fe-4S]ST31(2631416651)*Methanobacterium formicicum*
BRM9

MPNVIIDYEKCEGTECGECAEVCSMEVLAIIDGDKITVKNQDGC SLCEICTDVCPNEAIKL

VD
>2 [4Fe-4S] ST31 (2637991649) *Methanobacterium* sp. MB1
MPNVIIDYEKCEGTECGECAEVCSMEVLAIIDGDKITVKNHDCSLCEICTDVCPNEAIKL
VD
>2 [4Fe-4S] ST31 (2631416840) *Methanobacterium* *formicicum*
BRM9
MVKITVDQEKCEGADCAECVDVCPMEVLILIDGKVVVRNTEDCSLCEVCMDVCPNEAVKV
EDE
>2 [4Fe-4S] ST31 (2637992333) *Methanobacterium* sp. MB1
MVKITIDQEKCEGADCAECVDVCPMEVILIDGKVKVRNTEDCSLCEVCMDVCPNEAINV
EDE
>2 [4Fe-4S] ST31 (650871787) *Methanobacterium* *paludis* SWAN-
1
MVKITIDYDKCEGADCAECTDVCPMEILVLEGDKIVIKNKEDCSLCEVCMDVCPNEAVNV
EE
>2 [4Fe-4S] ST31 (2730764719) *Methanobacterium* *congolense* Buetzberg
MVKITIDYDKCDGADCAECVDVCPMEVLIIIDGKIVIQNKEECSLCEVCMDVCPNEAVNV
EE

Subtype 32

Archaea

>2 [4Fe-4S] ST32 (2758472322) *Methanopyrus* sp. KOL6
VPKVVIDYDACVGVSECGECIEACPMDVLDEEDDKPVVVNEDDCTGCGLCEQACPHGAIV
VEV
>2 [4Fe-4S] ST32 (2758462178) *Methanopyrus* sp. SNP6
VPKVVIDYDACVGVSECGECIEACPMDVLDEEDDKPVVVNEDDCTGCGLCEQACPHGAIV
VEV
>2 [4Fe-4S] ST32 (640788362) *Methanococcus* *aeolicus* Nankai-
3
MVSVTINYDTCKGAKECGECEKNCPMEVFEVDGKVVVAHEDECTGCGVCEDVCPTGAVK
VKF

Subtype 33

Archaea

>2[4Fe-4S] ST33 (2512783147) *Methanocella* *conradii*
 HZ254
 MRISQACVGCGHCKAICPVDAIETCGVSRITGNCIECGKCKGYCAIGAIEEDA
 >2[4Fe-4S] ST33 (2505974308) *Methanocella* *paludicola* SANAE
 (reannotation)
 MRITQACVGCGHCKVFCPAGAIETCGVSRINDKCIECGKCKGYCALGAITEEP

 >2[4Fe-4S] ST33 (2509662603) *Methanomethylovorans* *hollandica* DSM
 15978
 MKIDERCVGCGQCTAFCKPKNAIIVKGNWITADCIQCKICIAAYCPMKAIEESV
 >2[4Fe-4S] ST33 (2630384638) *Methanosarcina* *thermophila* CHTI-
 55
 MKINDNCVGCGQCASFCKMKEAIEVKGKARTTNACIDCGICAVYCPVKAIEVPA
 >2[4Fe-4S] ST33 (638176270) *Methanosarcina* *acetivorans*
 C2A
 VDRMKINDNCVGCGQCASFCKKGAIEVRGRARATDACVECGLCVPYCPVKAIEVLV
 >2[4Fe-4S] ST33 (2641568259) *Methanosarcina* *mazei*
 WWM610
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGMCIPYCPVKAIEVPA
 >2[4Fe-4S] ST33 (2629269638) *Methanosarcina* *mazei* S-6
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGMCIPYCPVKAIEVPA
 >2[4Fe-4S] ST33 (2633686601) *Methanosarcina* *mazei* LYC
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGMCIPYCPVKAIEVPA

 >2[4Fe-4S] ST33 (638167052) *Methanosarcina* *mazei* Go1
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGMCIPYCPVKAIEVPA
 >2[4Fe-4S] ST33 (2645884218) *Methanosarcina* *siciliae*
 HI350
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGLCVPYCPVKAIEVPA

 >2[4Fe-4S] ST33 (2653162866) *Methanosarcina* *siciliae*
 T4/M
 MKINDNCVGCGQCASFCKKGAIEVRGRARATDACVDCGLCVPYCPVKAIEVPA
 >2[4Fe-4S] ST33 (2632829510) *Methanosarcina* *barkeri*
 227
 MKINDNCVGCGQCASFCKKGAIEVRGKARATDACIDCGICVLYCPVKAIEVVA
 >2[4Fe-4S] ST33 (2628283144) *Methanosarcina* sp.
 Kolksee
 MKINDNCVGCGQCASFCKKGAIEVKGKAQATDACIDCGICALYCPVKAIEVLA
 >2[4Fe-4S] ST33 (646707657) *Methanohalophilus* *mahii* SLP, DSM
 5219
 MRVNEKCVGCGQCTAFCKQDAIVVKGNAYITEKCTNCGVCAFYCPLKAIEAEK
 >2[4Fe-4S] ST33 (637959063) *Methanococcoides* *burtonii* DSM
 6242
 MKINDNCVGCGQCTAFCKIDAIIVKSKAHITDACVNCGICATYCPMKAIEADE
 >2[4Fe-4S] ST33 (2641587135) *Methanococcoides* *methylutens*
 MM1
 MKVNENCVGCGQCTAFCKKDAIIVKSKARITDKCVECIGICAAAYCPMKAIEVGE

Subtype 11

Archaea

>2[4Fe-4S]ST11(2730777729)*Methanomicrobiales archaeon* Methan_05

MIHIRRDVCGYCGACVSVCPRGALELIDAYLTVDETLCKNKCKICSTVCPLGAIELEEQ

>2[4Fe-4S]ST11(640099088)*Methanocorpusculum labreanum*
Z

MIHIRRDVCGYCGACVSVCPRGALELIDAYLTVDETLCKNKCKICQTVCPPLGAIEQEEQ

2[4Fe-4S]Alv

Subtype 1

Bacteria

>2[4Fe-4S]AlvST1(2FGO)*Pseudomonas aeruginosa*

SLKITDDCINCDVCEPECPNGAISQGEEIYVIDPNLCTECVGHYDEPQCQQVCPVDCIPLDD
ANVESKDQLMEKYRKITGKA

>2[4Fe-4S]AlvST1(1BLU)*Allochromatium vinosum*

ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDCIIKDP
SHEETEDELRAKYERITGEG

>2[4Fe-4S]AlvST1(3EXY)*Allochromatium vinosum*

ALMITDECINCDGCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDCIIKDP
SHEETEDELRAKYERITG

EG

>2[4Fe-4S]AlvST1(1RGV)*Thauera aromatica* K172

ALYINDDCTACDACVEECPNEAITPGDPIYVIDPTKSECVGAFDEPQCRLVCPADCIPDNP
DYRETREELQEKYDRLHG

>2[4Fe-4S]AlvST1(Q9I6D2_PSEAE)*Pseudomonas aeruginosa* (strain
ATCC 15692)

MSLKITDDCINCDVCEPECPNGAISQGEEIYVIDPNLCTECVGHYDEPQCQQVCPVDCIPLD
DANVESKDQLMEKYRKITGKA

Subtype 3

Bacteria

>2[4Fe-4S]AlvST3(P20624)*Rhodobacter capsulatus*

MPTVAYTRGGAEYTPVYLMKIDEQKCIGCGRCFKVCGRDVMSLHGLTEDGQVVAPGTDEWDE
VEDEIVKKVMALTGAENCIGCGACARVCPSECQTHAALS

Subtype 9

Archaea

>2[4Fe-4S]AlvST9(650798943)*Methanotherix soehngeni* GP-6
MLKRKMIKNFTWPLKTASREIEVTRLYPEFMMELPDAERGIHELDTICIGCGSCARVCP
NSCIEMVHFKEFGNPLKNKKMQFPQIDYGRCMFCGLCVDECPVECLKMGKKVIMAGWERKD
IVKGPDFLATKRFSAKEVADLEAEAKRIAAEKAAAKKAAAKDAAAAGDKKPAKEGANAEK
KKAVAKPAEGGAS
>2[4Fe-4S]AlvST9(2730779891)*Methanosarcinales* *archaeon*
Methan_04
MLKRKMIKNFTWPLKTASREIEVTRLYPEFMMELPDAERGIHELDTICIGCGSCARVCP
NSCIEMVHFKEFGNPLKNKKMQFPQIDYGRCMFCGLCVDECPVECLKMGKKVIMAGWERKD
IVKGPDFLATKRFSAKEVADLEAEAKRIAAEKAAAKKAAAKDAAAAGDKKPAKEGANAEK
KKAVAKPAEGGAS

Subtype 10

Archaea

>2[4Fe-4S]AlvST10(646859885)*Methanococcus* *voltae*
A3
MUYAVNAEECIACGACVPVCAVEAISEMDDGKAVIDANKCNDGDCADVCPVECIKQQ
>2[4Fe-4S]AlvST10(640786788)*Methanococcus* *vannielii*
SB
MVFKVIEDECIACGACVPSPVDAISEKDDGKAVIDASKCNSCGDCVDICPVDCIKEEKG
CC
>2[4Fe-4S]AlvST10(640793644)*Methanococcus* *maripaludis*
C7
MAYKVNEDECIACGACVPSPPENAISEKADGKAVIDPAKCTGCGDCADICPVACIKEE
>2[4Fe-4S]AlvST10(641283324)*Methanococcus* *maripaludis*
C6
MAYKVNEDDCIACGACVPSPPENAISEKADGKAVIDPAKCTSCGDCADICPVACIKEE
>2[4Fe-4S]AlvST10(640167082)*Methanococcus* *maripaludis*
C5
MAYVVKEDDECIACGACVPSPPENAISEKDDGKAVIDPAKCTGCGDCADICPVACIKEE
>2[4Fe-4S]AlvST10(2730767665)*Methanothermobacter* *wolfeii*
SIV6
MAKIIIDYDECDACGECVDVCPMEVLIIVDGKLVQHPEECNECEVCMDVCPNECIEVQE
D
>2[4Fe-4S]AlvST10(648151922)*Methanothermobacter* *marburgensis*
Marburg DSM 2133

MAKIIIDYDECDACGECVDVCPMEVLIIVDGKLVQHPEECNECEVCMDVCPNECIEVEE
D

>2[4Fe-4S]AlvST10(640591992)*Methanobrevibacter smithii* PS, ATCC
35061

MADIIIDNNECDNCGDCADVCPMEVLILEDEKLTVNEPDECSYCESCVDICPNECITIE