Phyre2

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Description	P40120
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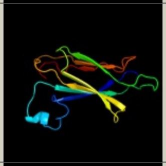
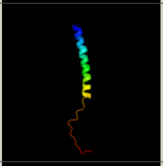
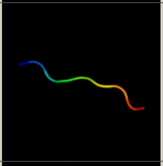
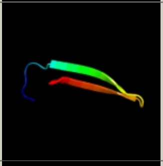
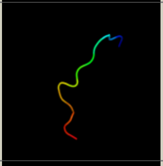
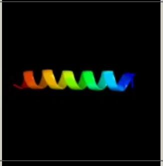
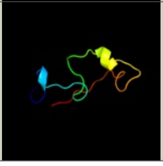
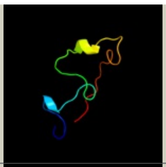
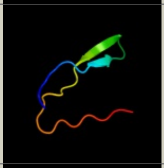
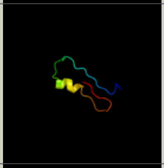
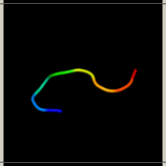
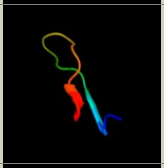
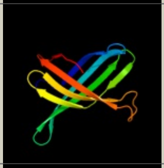
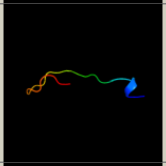
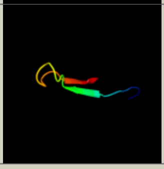
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1txkA_	Alignment		100.0	36	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
2	d1txka2	Alignment		100.0	41	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
3	d1txka1	Alignment		100.0	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
4	c2e76D_	Alignment		53.0	11	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
5	c2r5oA_	Alignment		44.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative atp binding component of abc- **PDBTitle:** crystal structure of the c-terminal domain of wzt
6	d1nkra1	Alignment		21.4	44	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
7	d2d7na1	Alignment		20.6	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
8	d2jnaa1	Alignment		20.4	17	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
9	d2noca1	Alignment		19.6	14	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
10	c1p84E_	Alignment		18.5	9	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
11	c1se9A_	Alignment		17.8	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**ubiquitin family; **PDBTitle:** structure of at3g01050, a ubiquitin-fold protein from2 arabidopsis thaliana

12	d1se9a_	Alignment		17.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
13	c3on7C_	Alignment		17.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family; **PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
14	c3rhfB_	Alignment		17.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
15	c2l6mA_	Alignment		16.5	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein dicer; **PDBTitle:** structure of c-terminal dsrbd of the fission yeast dicer (dcr1)
16	d1oisa_	Alignment		15.6	24	**Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
17	d1jmxa5	Alignment		15.3	13	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
18	c2r3aA_	Alignment		15.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
19	d2dl2a1	Alignment		15.0	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
20	d1xbwa_	Alignment		13.7	32	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
21	c3r0eC_	Alignment	not modelled	12.8	16	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
22	c3ooxA_	Alignment	not modelled	12.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
23	d1dmla1	Alignment	not modelled	11.9	26	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
24	c3exmA_	Alignment	not modelled	11.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase sc4828; **PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
25	c2l3bA_	Alignment	not modelled	11.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
26	d1k4ta3	Alignment	not modelled	11.4	24	**Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
27	c2i1jA_	Alignment	not modelled	11.4	35	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms

						resolution
28	c2fynO_	Alignment	not modelled	11.3	17	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
29	c2l7qA_	Alignment	not modelled	11.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
30	d1ee8a2	Alignment	not modelled	11.3	22	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
31	d1csya_	Alignment	not modelled	11.0	18	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
32	c2fyuE_	Alignment	not modelled	10.8	22	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
33	d1qcsa1	Alignment	not modelled	10.2	43	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
34	c3phuA_	Alignment	not modelled	10.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase l; **PDBTitle:** otu domain of crimean congo hemorrhagic fever virus
35	d1ix2a_	Alignment	not modelled	9.8	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
36	d1ml9a_	Alignment	not modelled	9.4	13	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
37	c2p8zS_	Alignment	not modelled	9.3	56	**PDB header:**translation **Chain:** S: **PDB Molecule:**elongation factor tu-b; **PDBTitle:** fitted structure of adpr-eef2 in the 80s:adpr-2 eef2:gdpnp:sordarin cryo-em reconstruction
38	d1erna1	Alignment	not modelled	9.2	34	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
39	d1h95a_	Alignment	not modelled	9.2	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
40	d1e09a_	Alignment	not modelled	9.1	23	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
41	d1p1la_	Alignment	not modelled	9.0	40	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
42	d1ja1a3	Alignment	not modelled	9.0	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
43	c3d3zA_	Alignment	not modelled	8.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**actibind; **PDBTitle:** crystal structure of actibind a t2 rnase
44	c3o0lB_	Alignment	not modelled	8.7	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
45	c3camB_	Alignment	not modelled	8.7	56	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cold-shock domain family protein; **PDBTitle:** crystal structure of the cold shock domain protein from neisseria2 meningitidis
46	d1a8pa2	Alignment	not modelled	8.6	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
47	d1fdra2	Alignment	not modelled	8.5	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
48	c1a31A_	Alignment	not modelled	8.4	24	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
49	c1dmlG_	Alignment	not modelled	8.4	26	**PDB header:**dna binding protein/transferase **Chain:** G: **PDB Molecule:**dna polymerase processivity factor; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-2 terminus of hsv pol
50	d1dq3a3	Alignment	not modelled	8.2	40	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
51	c3adyA_	Alignment	not modelled	8.2	29	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**dotd; **PDBTitle:** crystal structure of dotd from legionella
52	d1ef1a2	Alignment	not modelled	8.2	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
53	c3nezA_	Alignment	not modelled	8.1	22	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**mrojoa;

						PDBTitle: mrojoa
54	d1kr4a_	Alignment	not modelled	7.9	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
55	d1b2pa_	Alignment	not modelled	7.9	19	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
56	c1ckwA_	Alignment	not modelled	7.8	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
57	c1nh3A_	Alignment	not modelled	7.8	24	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
58	c2rocB_	Alignment	not modelled	7.8	33	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-binding component 3; **PDBTitle:** solution structure of mcl-1 complexed with puma
59	d1f20a2	Alignment	not modelled	7.8	56	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
60	d2ozga1	Alignment	not modelled	7.7	26	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
61	d1oq1a_	Alignment	not modelled	7.7	16	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Hypothetical protein YesU
62	d1ukua_	Alignment	not modelled	7.6	0	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
63	d1pjca1	Alignment	not modelled	7.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
64	d2oq1a2	Alignment	not modelled	7.5	9	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
65	c2k7pA_	Alignment	not modelled	7.5	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
66	d2a5yb1	Alignment	not modelled	7.5	47	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CED-4 C-terminal domain-like
67	c2qsdB_	Alignment	not modelled	7.5	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of a protein il1583 from idiomarina loihiensis
68	d1kbia1	Alignment	not modelled	7.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
69	c3czpA_	Alignment	not modelled	7.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
70	c2ns2A_	Alignment	not modelled	7.3	29	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spindlin-1; **PDBTitle:** crystal structure of spindlin1
71	d1ddga2	Alignment	not modelled	7.3	44	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
72	c2wclA_	Alignment	not modelled	7.3	36	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general odorant-binding protein 1; **PDBTitle:** structure of bmori gobp2 (general odorant binding protein 2)2 with (8e,10z)-hexadecadien-1-ol
73	d1p7hl1	Alignment	not modelled	7.3	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
74	c2kl5A_	Alignment	not modelled	7.3	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yutd; **PDBTitle:** solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
75	c3a0jB_	Alignment	not modelled	7.2	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cold shock protein; **PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
76	c2b9sA_	Alignment	not modelled	7.2	29	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
77	d1d6za3	Alignment	not modelled	7.2	17	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
78	d1imhc1	Alignment	not modelled	7.1	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
79	d1dlpa2	Alignment	not modelled	7.1	24	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
						Fold: Immunoglobulin-like beta-sandwich

80	d1nkra2	Alignment	not modelled	7.0	50	**Superfamily:**Immunoglobulin **Family:**I set domains
81	c1wrgA_	Alignment	not modelled	6.8	80	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
82	c1ibtC_	Alignment	not modelled	6.8	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase beta chain; **PDBTitle:** structure of the d53,54n mutant of histidine decarboxylase at-170 c
83	c3r2nC_	Alignment	not modelled	6.7	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae
84	c2jp2A_	Alignment	not modelled	6.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sprouty-related, evh1 domain-containing protein **PDBTitle:** solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spred2 protein3 (sprouty-related protein with evh1 domain isoform 2)
85	d2bk0a1	Alignment	not modelled	6.7	27	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
86	d1kfia4	Alignment	not modelled	6.6	21	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
87	d1my7a_	Alignment	not modelled	6.6	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
88	c1meqA_	Alignment	not modelled	6.6	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**exterior membrane glycoprotein (gp120); **PDBTitle:** hiv gp120 c5
89	d2k54a1	Alignment	not modelled	6.6	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
90	c2eiuE_	Alignment	not modelled	6.6	31	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein aq_1627; **PDBTitle:** crystal structure of a putative protein (aq1627) from aquifex aeolicus
91	c1ckxA_	Alignment	not modelled	6.6	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
92	d1h4ra2	Alignment	not modelled	6.6	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
93	c2kvhA_	Alignment	not modelled	6.5	63	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
94	c2a48A_	Alignment	not modelled	6.5	20	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**gfp-like fluorescent chromoprotein amfp486; **PDBTitle:** crystal structure of amfp486 e150q
95	d1m4ka2	Alignment	not modelled	6.5	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
96	c3pt2A_	Alignment	not modelled	6.5	11	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**rna polymerase; **PDBTitle:** structure of a viral otu domain protease bound to ubiquitin
97	d1x9na2	Alignment	not modelled	6.4	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
98	d1gawa2	Alignment	not modelled	6.4	56	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
99	d1jb9a2	Alignment	not modelled	6.4	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases