Phyre2

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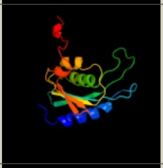
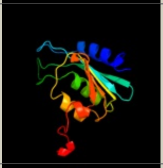
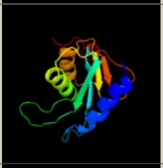
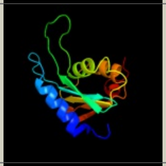
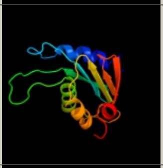
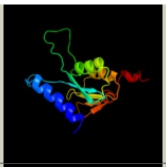
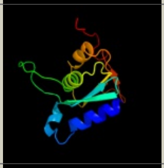
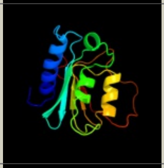
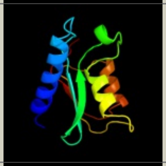
Description	P0ABF6
Date	Thu Jan 5 11:15:23 GMT 2012
Unique Job ID	bca4e904538aff92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1alnA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase complexed with 3-deazacytidine
2	d1alna1	Alignment		100.0	100	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
3	d1alna2	Alignment		100.0	100	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
4	d1r5ta_	Alignment		100.0	29	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
5	d1uwza_	Alignment		100.0	28	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
6	d1mq0a_	Alignment		100.0	31	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
7	d2fr5a1	Alignment		100.0	31	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
8	c3ijfX_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
9	c3dmoD_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytidine deaminase; **PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei
10	d2d30a1	Alignment		100.0	29	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
11	c3r2nC_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae

12	c3b8fB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative blasticidin s deaminase; **PDBTitle:** crystal structure of the cytidine deaminase from bacillus anthracis
13	c3oj6C_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**blasticidin-s deaminase; **PDBTitle:** crystal structure of blasticidin s deaminase from coccidioides immitis
14	d2z3ga1	Alignment		100.0	21	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
15	c2hvwC_	Alignment		98.4	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans
16	c2w4lC_	Alignment		98.1	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** human dcmp deaminase
17	d1z3aa1	Alignment		97.8	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
18	d1p6oa_	Alignment		97.7	16	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
19	c3ocqA_	Alignment		97.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytosine/adenosine deaminase; **PDBTitle:** crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
20	d1wkqa_	Alignment		97.6	11	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
21	d1wwra1	Alignment	not modelled	97.5	20	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
22	d2g84a1	Alignment	not modelled	97.5	20	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
23	d2b3ja1	Alignment	not modelled	97.5	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
24	d1vq2a_	Alignment	not modelled	97.4	21	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
25	d2a8na1	Alignment	not modelled	97.2	19	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
26	c2hxvA_	Alignment	not modelled	97.1	28	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- **PDBTitle:** crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
27	c2nx8A_	Alignment	not modelled	96.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase; **PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
						PDB header:hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd;

28	c2o7pA_	Alignment	not modelled	96.5	23	**PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
29	c2d5nB_	Alignment	not modelled	95.8	30	**PDB header:**hydrolase, oxidoreductase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
30	d2hxva2	Alignment	not modelled	95.7	15	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
31	c3dh1D_	Alignment	not modelled	95.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**trna-specific adenosine deaminase 2; **PDBTitle:** crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
32	d2b3za2	Alignment	not modelled	95.1	29	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
33	d3d37a2	Alignment	not modelled	57.7	16	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
34	c2d9sA_	Alignment	not modelled	45.2	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
35	c3gv1A_	Alignment	not modelled	44.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
36	c2do6A_	Alignment	not modelled	43.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
37	c2eqjA_	Alignment	not modelled	40.7	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
38	c2jnhA_	Alignment	not modelled	37.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
39	d2fug21	Alignment	not modelled	28.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
40	c3dmlA_	Alignment	not modelled	28.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
41	c3g9bA_	Alignment	not modelled	27.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
42	c2hlsB_	Alignment	not modelled	26.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
43	c2r2jA_	Alignment	not modelled	26.3	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
44	c1jn9B_	Alignment	not modelled	25.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
45	c1t3mD_	Alignment	not modelled	25.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
46	c1t3mB_	Alignment	not modelled	25.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
47	c3p8dB_	Alignment	not modelled	25.4	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72; **PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form)
48	d1fo5a_	Alignment	not modelled	24.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
49	c2ju5A_	Alignment	not modelled	24.0	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
50	c2zalB_	Alignment	not modelled	23.5	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
51	c1a8yA_	Alignment	not modelled	22.2	11	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**calsequestrin; **PDBTitle:** crystal structure of calsequestrin from rabbit skeletal muscle2 sarcoplasmic reticulum at 2.4 a resolution
52	d1z67a1	Alignment	not modelled	21.9	28	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
53	c3kp8A_	Alignment	not modelled	21.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
						Fold: Thioredoxin fold

54	d1zmaa1	Alignment	not modelled	21.0	29	**Superfamily:**Thioredoxin-like **Family:**Thioltransferase
55	c1x5eA_	Alignment	not modelled	20.7	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain containing protein 1; **PDBTitle:** the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
56	c3gwlB_	Alignment	not modelled	20.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fad-linked sulfhydryl oxidase; **PDBTitle:** crystal structure of asfv pb119l, a viral sulfhydryl oxidase
57	c3dxbE_	Alignment	not modelled	19.7	17	**PDB header:**splicing, transcription **Chain:** E: **PDB Molecule:**thioredoxin n-terminally fused to puf60(uhm); **PDBTitle:** structure of the uhm domain of puf60 fused to thioredoxin
58	c2e5qA_	Alignment	not modelled	19.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
59	d1jr8a_	Alignment	not modelled	19.3	42	**Fold:**Four-helical up-and-down bundle **Superfamily:**FAD-dependent thiol oxidase **Family:**FAD-dependent thiol oxidase
60	c2zalD_	Alignment	not modelled	19.2	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
61	c3f8uA_	Alignment	not modelled	18.1	23	**PDB header:**immune system/isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3erp57; **PDBTitle:** tapasin/erp57 heterodimer
62	c3gwnA_	Alignment	not modelled	18.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-linked sulfhydryl oxidase r596; **PDBTitle:** crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
63	d1sena_	Alignment	not modelled	17.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
64	c1senA_	Alignment	not modelled	17.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881
65	c2ppvA_	Alignment	not modelled	17.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
66	c1t3bA_	Alignment	not modelled	17.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
67	c2nytB_	Alignment	not modelled	17.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
68	d1y0ua_	Alignment	not modelled	16.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
69	d1hyua4	Alignment	not modelled	16.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
70	c3l9vE_	Alignment	not modelled	15.5	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
71	c2zakB_	Alignment	not modelled	15.5	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
72	d1v58a1	Alignment	not modelled	15.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
73	d1j9ba_	Alignment	not modelled	14.8	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
74	c2r41A_	Alignment	not modelled	14.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein of unknown function from enterococcus2 faecalis
75	c1zy7A_	Alignment	not modelled	14.2	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-specific adenosine deaminase b1, isoform **PDBTitle:** crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
76	c1jzdA_	Alignment	not modelled	13.9	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
77	c3f46A_	Alignment	not modelled	13.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
78	c1k2xB_	Alignment	not modelled	13.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene

79	c1jn9D_	Alignment	not modelled	13.7	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
80	c1k2xD_	Alignment	not modelled	13.7	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
81	c3feuA_	Alignment	not modelled	13.6	71	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
82	c2albA_	Alignment	not modelled	13.2	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57
83	c2hj3A_	Alignment	not modelled	13.1	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase erv1p; **PDBTitle:** structure of the arabidopsis thaliana erv1 thiol oxidase
84	d1qjta_	Alignment	not modelled	12.8	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
85	c3idvA_	Alignment	not modelled	12.7	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** crystal structure of the a0a fragment of erp72
86	d1rioa_	Alignment	not modelled	12.6	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
87	c1sjiA_	Alignment	not modelled	12.5	0	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsequestrin, cardiac muscle isoform; **PDBTitle:** comparing skeletal and cardiac calsequestrin structures and2 their calcium binding: a proposed mechanism for coupled3 calcium binding and protein polymerization
88	c1p4vA_	Alignment	not modelled	11.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(4)-(beta-n-acetylglucosaminyl)-l-asparaginase **PDBTitle:** crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
89	c3cawB_	Alignment	not modelled	11.7	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**o-succinylbenzoate synthase; **PDBTitle:** crystal structure of o-succinylbenzoate synthase from2 bdellovibrio bacteriovorus liganded with mg
90	c2gezF_	Alignment	not modelled	11.6	24	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-asparaginase beta subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
91	c2b5eA_	Alignment	not modelled	11.4	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of yeast protein disulfide isomerase
92	c2kboA_	Alignment	not modelled	11.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
93	c2wz9A_	Alignment	not modelled	11.2	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
94	c1zypB_	Alignment	not modelled	11.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
95	d2hzba1	Alignment	not modelled	10.9	20	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
96	d1f9ma_	Alignment	not modelled	10.7	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
97	d1oqca_	Alignment	not modelled	10.5	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**FAD-dependent thiol oxidase **Family:**FAD-dependent thiol oxidase
98	c1j08A_	Alignment	not modelled	10.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
99	d1j08a1	Alignment	not modelled	10.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like