Phyre2

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Description	P0AA25
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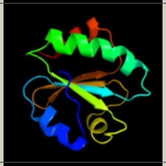
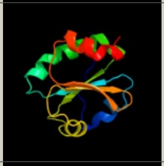
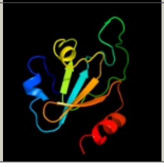
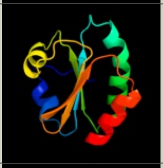
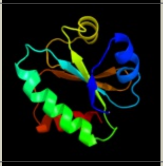
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2trxa_	Alignment		100.0	100	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
2	c3dxbE_	Alignment		100.0	100	**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
3	c2i4aA_	Alignment		99.9	58	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
4	d1thxa_	Alignment		99.9	43	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
5	c1t00A_	Alignment		99.9	55	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
6	c3p2aB_	Alignment		99.9	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
7	c2pptA_	Alignment		99.9	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
8	c3p2aA_	Alignment		99.9	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
9	c3hz4A_	Alignment		99.9	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
10	d1dbya_	Alignment		99.9	45	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
11	d1oaza_	Alignment		99.9	83	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

12	c2vocA_	Alignment		99.9	48	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
13	c2i1uA_	Alignment		99.9	52	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
14	c3gnjD_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
15	d1fb6a_	Alignment		99.9	48	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c1w89E_	Alignment		99.9	33	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
17	c3qdnA_	Alignment		99.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
18	c2o7kA_	Alignment		99.9	52	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
19	c3tcoA_	Alignment		99.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
20	c3f8uA_	Alignment		99.9	33	**PDB header:**immune system/isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3erp57; **PDBTitle:** tapasin/erp57 heterodimer
21	d1f9ma_	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
22	c3ed3A_	Alignment	not modelled	99.9	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase mpd1; **PDBTitle:** crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p
23	c2albA_	Alignment	not modelled	99.9	34	**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
24	c2e0qA_	Alignment	not modelled	99.9	39	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
25	c1x5dA_	Alignment	not modelled	99.9	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
26	c2yzuA_	Alignment	not modelled	99.9	51	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
27	c2r2jA_	Alignment	not modelled	99.9	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
28	c3hypB_	Alignment	not modelled	99.9	44	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
						PDB header:oxidoreductase

29	c3apoA_	Alignment	not modelled	99.9	26	**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
30	c2l5lA_	Alignment	not modelled	99.9	42	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
31	c2b5eA_	Alignment	not modelled	99.9	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of yeast protein disulfide isomerase
32	c2dmlA_	Alignment	not modelled	99.9	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
33	c3apsA_	Alignment	not modelled	99.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of trx4 domain of erdj5
34	d1ep7a_	Alignment	not modelled	99.9	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
35	c2vafA_	Alignment	not modelled	99.9	17	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**calsequestrin-2; **PDBTitle:** crystal structure of human cardiac calsequestrin
36	c1a8yA_	Alignment	not modelled	99.9	18	**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
37	c1sjiA_	Alignment	not modelled	99.9	18	**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
38	d1xfla_	Alignment	not modelled	99.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
39	d1xwaa_	Alignment	not modelled	99.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
40	c2l6dA_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
41	d1nw2a_	Alignment	not modelled	99.9	49	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
42	c2dizA_	Alignment	not modelled	99.9	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 5; **PDBTitle:** the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5
43	c2j23A_	Alignment	not modelled	99.9	34	**PDB header:**immune protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
44	c2wz9A_	Alignment	not modelled	99.9	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
45	d1gh2a_	Alignment	not modelled	99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
46	c2vlvA_	Alignment	not modelled	99.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
47	c1x5cA_	Alignment	not modelled	99.9	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase
48	d1m7ta_	Alignment	not modelled	99.9	57	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
49	c3ul3A_	Alignment	not modelled	99.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
50	c2dj1A_	Alignment	not modelled	99.9	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4
51	c2xbqB_	Alignment	not modelled	99.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
52	d1a8ya1	Alignment	not modelled	99.9	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
53	d1j08a2	Alignment	not modelled	99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
54	d1ti3a_	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
55	d2b5ea4	Alignment	not modelled	99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family:PDI-like
56	c1x5eA_	Alignment	not modelled	99.9	23	**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
57	c2vimA_	Alignment	not modelled	99.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
58	d1a8la2	Alignment	not modelled	99.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
59	c3h79A_	Alignment	not modelled	99.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein; **PDBTitle:** crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
60	c1v98A_	Alignment	not modelled	99.9	47	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
61	c2dj0A_	Alignment	not modelled	99.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-related transmembrane protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
62	d1syra_	Alignment	not modelled	99.9	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
63	d1r26a_	Alignment	not modelled	99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
64	c2f51B_	Alignment	not modelled	99.9	35	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
65	c2diyA_	Alignment	not modelled	99.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
66	c2dj3A_	Alignment	not modelled	99.9	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the third thioredoxin domain of2 mouse protein disulfide-isomerase a4
67	d1qgva_	Alignment	not modelled	99.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
68	d2b5ea1	Alignment	not modelled	99.9	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
69	c1xbsA_	Alignment	not modelled	99.9	19	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
70	c2qc7A_	Alignment	not modelled	99.9	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmic reticulum protein erp29; **PDBTitle:** crystal structure of the protein-disulfide isomerase related chaperone2 erp29
71	c2dj2A_	Alignment	not modelled	99.9	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the second thioredoxin domain of2 mouse protein disulfide-isomerase a4
72	d1meka_	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
73	d2ifqa1	Alignment	not modelled	99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
74	c2oe0B_	Alignment	not modelled	99.9	28	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
75	c2vm2C_	Alignment	not modelled	99.8	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
76	c3d22A_	Alignment	not modelled	99.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
77	c3cxgA_	Alignment	not modelled	99.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
78	c2qsiB_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
79	c3emxB_	Alignment	not modelled	99.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
80	c2i9hA_	Alignment	not modelled	99.8	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
						PDB header:isomerase

81	c3idvA_	Alignment	not modelled	99.8	27	**Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** crystal structure of the a0a fragment of erp72
82	c2dmmA_	Alignment	not modelled	99.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** the solution structure of the second thioredoxin domain of2 human protein disulfide-isomerase a3
83	c3apqB_	Alignment	not modelled	99.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
84	c1ovnA_	Alignment	not modelled	99.8	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**windbeutel; **PDBTitle:** crystal structure and functional analysis of drosophila2 wind-- a pdi-related protein
85	c3uemA_	Alignment	not modelled	99.8	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of human pdi bb'a' domains
86	d1g7ea_	Alignment	not modelled	99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
87	d1zmaa1	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
88	d2djja1	Alignment	not modelled	99.8	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
89	d2c0ga2	Alignment	not modelled	99.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
90	c1j08A_	Alignment	not modelled	99.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
91	c2dbcA_	Alignment	not modelled	99.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
92	c3d6iB_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
93	c2l57A_	Alignment	not modelled	99.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
94	d1fo5a_	Alignment	not modelled	99.8	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
95	d2hfda1	Alignment	not modelled	99.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
96	c1b9xC_	Alignment	not modelled	99.8	24	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**protein (phosducin); **PDBTitle:** structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
97	c3dmlA_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
98	c3g9bA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
99	d1a8la1	Alignment	not modelled	99.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
100	d2trcp_	Alignment	not modelled	99.7	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
101	d2fwha1	Alignment	not modelled	99.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
102	c2hlsB_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
103	d1v9wa_	Alignment	not modelled	99.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
104	d1nhoa_	Alignment	not modelled	99.7	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
105	c1zypB_	Alignment	not modelled	99.7	10	**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
106	d1j08a1	Alignment	not modelled	99.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
107	c2kucA_	Alignment	not modelled	99.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
						PDB header:oxidoreductase

108	c3kp8A_	Alignment	not modelled	99.7	17	**Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
109	d1a0rp_	Alignment	not modelled	99.7	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
110	d1woua_	Alignment	not modelled	99.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
111	c2aytB_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
112	c2fgxA_	Alignment	not modelled	99.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
113	d1z5ye1	Alignment	not modelled	99.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
114	d1hyua4	Alignment	not modelled	99.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
115	c3f9uA_	Alignment	not modelled	99.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
116	c2ju5A_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
117	c3fk8A_	Alignment	not modelled	99.5	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
118	c2hyxA_	Alignment	not modelled	99.5	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
119	d1knga_	Alignment	not modelled	99.5	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
120	c1senA_	Alignment	not modelled	99.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881