Phyre^2

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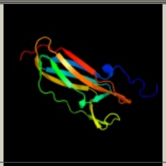
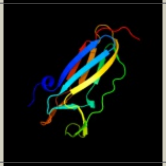
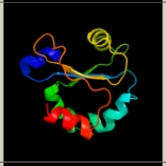
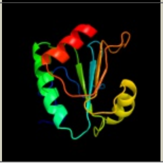
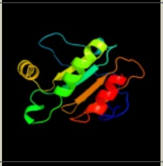
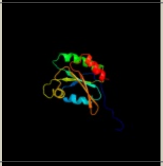
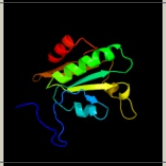
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l6pa_	Alignment		100.0	100	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha) **Family:**Thiol:disulfide interchange protein DsbD, N-terminal domain (DsbD-alpha)
2	c1jpeA_	Alignment		100.0	100	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dsbd-alpha; **PDBTitle:** crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd
3	c2k0rA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbd; **PDBTitle:** solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
4	d2fwha1	Alignment		99.9	100	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
5	c3f9uA_	Alignment		99.8	21	**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
6	c2ju5A_	Alignment		99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
7	d2dlxa1	Alignment		99.8	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
8	c2kucA_	Alignment		99.8	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
9	c3iraA_	Alignment		99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
10	c3fk8A_	Alignment		99.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
11	c2l57A_	Alignment		99.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens

12	d1sena_	Alignment		99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
13	c1senA_	Alignment		99.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881
14	c2hyxA_	Alignment		99.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
15	c2pptA_	Alignment		99.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
16	c3p2aB_	Alignment		99.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
17	c2diyA_	Alignment		99.6	14	**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
18	c3p2aA_	Alignment		99.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
19	d1z5ye1	Alignment		99.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	c3ul3A_	Alignment		99.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
21	c2vlvA_	Alignment	not modelled	99.6	23	**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
22	d1knga_	Alignment	not modelled	99.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	d1qgva_	Alignment	not modelled	99.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
24	c2f51B_	Alignment	not modelled	99.5	18	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
25	d1gh2a_	Alignment	not modelled	99.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
26	d1xwaa_	Alignment	not modelled	99.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	d1m7ta_	Alignment	not modelled	99.5	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	c2l6dA_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
29	d2ifqa1	Alignment	not modelled	99.5	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family: Thioltransferase
30	c3hypB_	Alignment	not modelled	99.5	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
31	c2vimA_	Alignment	not modelled	99.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
32	d1ti3a_	Alignment	not modelled	99.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	d1xfla_	Alignment	not modelled	99.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
34	c2l5lA_	Alignment	not modelled	99.5	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
35	c3d22A_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
36	c3dmlA_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
37	c2vm2C_	Alignment	not modelled	99.5	22	**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
38	c2xbqB_	Alignment	not modelled	99.5	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
39	c3qdnA_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
40	c2e0qA_	Alignment	not modelled	99.5	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
41	c3razA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
42	c2wz9A_	Alignment	not modelled	99.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
43	d2fy6a1	Alignment	not modelled	99.5	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d1ep7a_	Alignment	not modelled	99.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
45	c3gnjD_	Alignment	not modelled	99.5	15	**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
46	c1xbsA_	Alignment	not modelled	99.5	19	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
47	d1nw2a_	Alignment	not modelled	99.5	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
48	d1lu4a_	Alignment	not modelled	99.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
49	c2oe0B_	Alignment	not modelled	99.5	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
50	c3lwaA_	Alignment	not modelled	99.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**secreted thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
51	d1a8la2	Alignment	not modelled	99.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
52	c3hz4A_	Alignment	not modelled	99.4	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
53	d1f9ma_	Alignment	not modelled	99.4	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
54	c2b1kA_	Alignment	not modelled	99.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
55	d1r26a_	Alignment	not modelled	99.4	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
						PDB header:electron transport

56	c2i1uA_	Alignment	not modelled	99.4	25	**Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
57	d1dbya_	Alignment	not modelled	99.4	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
58	d1st9a_	Alignment	not modelled	99.4	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
59	c1v98A_	Alignment	not modelled	99.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
60	d1zzoa1	Alignment	not modelled	99.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
61	d1j08a2	Alignment	not modelled	99.4	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
62	c3or5A_	Alignment	not modelled	99.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein, thioredoxin family **PDBTitle:** crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum tls
63	d1syra_	Alignment	not modelled	99.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
64	c1w89E_	Alignment	not modelled	99.4	23	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
65	c2vocA_	Alignment	not modelled	99.4	18	**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
66	d1thxa_	Alignment	not modelled	99.4	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
67	c2i4aA_	Alignment	not modelled	99.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
68	c3erwG_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
69	d2b5xa1	Alignment	not modelled	99.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
70	c2yzuA_	Alignment	not modelled	99.4	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
71	c3tcoA_	Alignment	not modelled	99.4	28	**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
72	c1t00A_	Alignment	not modelled	99.4	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
73	c3emxB_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
74	c3kh7A_	Alignment	not modelled	99.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
75	d1fb6a_	Alignment	not modelled	99.4	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
76	d2trxa_	Alignment	not modelled	99.4	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
77	c3cmiA_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
78	d1zmaa1	Alignment	not modelled	99.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
79	c3hczA_	Alignment	not modelled	99.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
80	c3cxgA_	Alignment	not modelled	99.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
81	c3hdcA_	Alignment	not modelled	99.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
82	c2o7kA_	Alignment	not modelled	99.3	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin;

						PDBTitle: s. aureus thioredoxin
83	c2albA_	Alignment	not modelled	99.3	23	**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
84	c3lorB_	Alignment	not modelled	99.3	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**thiol-disulfide isomerase and thioredoxins; **PDBTitle:** the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
85	d1v9wa_	Alignment	not modelled	99.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
86	c3gl3D_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative thiol:disulfide interchange protein **PDBTitle:** crystal structure of a putative thiol:disulfide interchange2 protein dsbe from chlorobium tepidum
87	d1o8xa_	Alignment	not modelled	99.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
88	c3dxbE_	Alignment	not modelled	99.3	20	**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
89	c2j23A_	Alignment	not modelled	99.3	25	**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
90	d1o73a_	Alignment	not modelled	99.3	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
91	c2l5oA_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution structure of a putative thioredoxin from neisseria2 meningitidis
92	d1i5ga_	Alignment	not modelled	99.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
93	c1x5dA_	Alignment	not modelled	99.3	20	**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
94	c3ewlA_	Alignment	not modelled	99.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein bf1870; **PDBTitle:** crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
95	d1woua_	Alignment	not modelled	99.3	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
96	d1jfua_	Alignment		99.3	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
97	c3d6iB_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
98	c2dbcA_	Alignment	not modelled	99.3	18	**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)
99	c3eytA_	Alignment	not modelled	99.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
100	c2dmlA_	Alignment	not modelled	99.3	18	**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
101	c2qsiB_	Alignment	not modelled	99.2	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
102	c3eurA_	Alignment	not modelled	99.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
103	c2i9hA_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
104	c3ia1A_	Alignment	not modelled	99.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
105	d1oaza_	Alignment	not modelled	99.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
						PDB header:electron transport

106	c2dizA_	Alignment	not modelled	99.2	18	**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
107	d1gp1a_	Alignment	not modelled	99.2	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
108	d1meka_	Alignment	not modelled	99.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
109	c3kcmC_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
110	c3fw2A_	Alignment	not modelled	99.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
111	d2c0ga2	Alignment	not modelled	99.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
112	c2dj0A_	Alignment	not modelled	99.2	16	**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
113	c2obiA_	Alignment	not modelled	99.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phospholipid hydroperoxide glutathione **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpx4)
114	d2b5ea4	Alignment	not modelled	99.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
115	c2dj1A_	Alignment	not modelled	99.1	21	**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
116	d1j08a1	Alignment	not modelled	99.1	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
117	d1a8la1	Alignment	not modelled	99.1	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
118	c3ha9A_	Alignment	not modelled	99.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized thioredoxin-like protein; **PDBTitle:** the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
119	c3fkfC_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
120	c2r37A_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)