Phyre^2

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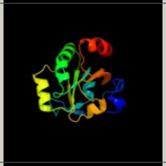
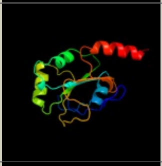
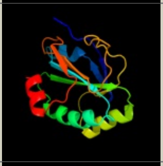
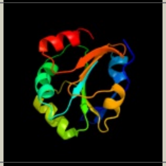
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b1kA_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
2	c3kh7A_	Alignment		100.0	53	**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
3	c2hyxA_	Alignment		100.0	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
4	d1z5ye1	Alignment		100.0	99	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
5	d1knga_	Alignment		99.9	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
6	c3lwaA_	Alignment		99.9	19	**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
7	d2b5xa1	Alignment		99.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
8	c3hczA_	Alignment		99.9	19	**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.
9	c3gl3D_	Alignment		99.9	31	**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
10	c3fw2A_	Alignment		99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
11	d1jfua_	Alignment		99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

12	c2l5oA_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution structure of a putative thioredoxin from neisseria2 meningitidis
13	c3or5A_	Alignment		99.9	24	**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
14	c3fkfC_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
15	d1zzoa1	Alignment		99.9	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
16	c3lorB_	Alignment		99.9	19	**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
17	d1lu4a_	Alignment		99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
18	c3ewlA_	Alignment		99.9	12	**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
19	d1st9a_	Alignment		99.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	c2ywiA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
21	c3hdcA_	Alignment	not modelled	99.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
22	c3ia1A_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
23	c3eurA_	Alignment	not modelled	99.9	11	**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
24	d2cvba1	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
25	c3kcmC_	Alignment	not modelled	99.9	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
26	c3eytA_	Alignment	not modelled	99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
27	d2fy6a1	Alignment	not modelled	99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
28	c3erwG_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
						PDB header:structural genomics, unknown function

29	c3ha9A_	Alignment	not modelled	99.9	20	**Chain:** A: **PDB Molecule:**uncharacterized thioredoxin-like protein; **PDBTitle:** the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
30	c3cynC_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
31	c3razA_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
32	d2bmxa1	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
33	d1qmva_	Alignment	not modelled	99.9	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
34	c2bmxB_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
35	c3cmiA_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
36	d2b7ka1	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
37	d1uula_	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
38	c2p5qA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
39	c2yzhD_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** crystal structure of peroxiredoxin-like protein from aquifex aeolicus
40	d1o8xa_	Alignment	not modelled	99.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
41	d1n8ja_	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
42	c3drnB_	Alignment	not modelled	99.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
43	d2zcta1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d1o73a_	Alignment	not modelled	99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
45	d2a4va1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
46	d1qq2a_	Alignment	not modelled	99.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
47	c1zyeL_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
48	c3kebB_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
49	c1zofB_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
50	c3me8B_	Alignment	not modelled	99.8	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative electron transfer protein aq_2194 from2 aquifex aeolicus vf5
51	c2c0dA_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
52	c2obiA_	Alignment	not modelled	99.8	17	**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)
53	c2he3A_	Alignment	not modelled	99.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
54	c3gknA_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
						PDB header:oxidoreductase

55	c2v1mA_	Alignment	not modelled	99.8	17	**Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
56	d2h01a1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
57	d1xvwa1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	d1zyea1	Alignment	not modelled	99.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
59	c2h66G_	Alignment	not modelled	99.8	19	**PDB header:**structural genomics/oxidoreductase **Chain:** G: **PDB Molecule:**pv-pf14_0368; **PDBTitle:** the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
60	d1yexa1	Alignment	not modelled	99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
61	d2f8aa1	Alignment	not modelled	99.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
62	d1gp1a_	Alignment	not modelled	99.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
63	c3dwvB_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
64	d1i5ga_	Alignment	not modelled	99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
65	d1we0a1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
66	d1zofa1	Alignment	not modelled	99.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
67	c2rliA_	Alignment	not modelled	99.8	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
68	c2r37A_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
69	c2p31B_	Alignment	not modelled	99.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
70	c2b7kD_	Alignment	not modelled	99.8	16	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
71	d1xcca_	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	c2jszA_	Alignment	not modelled	99.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** solution structure of tpx in the reduced state
73	d1e2ya_	Alignment	not modelled	99.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
74	d1wp0a1	Alignment	not modelled	99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
75	d1psqa_	Alignment	not modelled	99.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
76	c2v2gC_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
77	d2cx4a1	Alignment	not modelled	99.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
78	c2xpdC_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
79	c3f9uA_	Alignment	not modelled	99.8	16	**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
80	c3ixrA_	Alignment	not modelled	99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
81	d1q98a_	Alignment	not modelled	99.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

82	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
83	d1xvqa_	Alignment	not modelled	99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
84	c2xhfA_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana
85	d1qxha_	Alignment	not modelled	99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
86	d1xzoa1	Alignment	not modelled	99.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
87	d1prxa_	Alignment	not modelled	99.7	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
88	c2ywnA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin-like protein; **PDBTitle:** crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
89	c2k6vA_	Alignment	not modelled	99.7	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**putative cytochrome c oxidase assembly protein; **PDBTitle:** solution structures of apo sco1 protein from thermus2 thermophilus
90	c2wfcD_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from arenicola marina
91	d2cv4a1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
92	c2pptA_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
93	c2kucA_	Alignment	not modelled	99.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
94	c3p2aB_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
95	d1hd2a_	Alignment	not modelled	99.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
96	c1v98A_	Alignment	not modelled	99.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
97	c2ju5A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
98	c3p2aA_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
99	d2fwha1	Alignment	not modelled	99.6	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
100	c3emxB_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
101	c3hypB_	Alignment	not modelled	99.6	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
102	c2l6dA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
103	d1gh2a_	Alignment	not modelled	99.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
104	c3ul3A_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
105	c3hz4A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
106	c3gnjD_	Alignment	not modelled	99.6	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
107	d1j08a2	Alignment	not modelled	99.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
108	c2divA	Alignment	not modelled	99.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2;

108	c2diyA_	Alignment	not modelled	99.6	15	**PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
109	c2l5lA_	Alignment	not modelled	99.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
110	d1nm3a2	Alignment	not modelled	99.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
111	c2e0qA_	Alignment	not modelled	99.5	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
112	d1tp9a1	Alignment	not modelled	99.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
113	c3d22A_	Alignment	not modelled	99.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
114	c3dmlA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
115	c3umaC_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**hypothetical peroxiredoxin protein; **PDBTitle:** crystal structure of a hypothetical peroxiredoxin protein frm2 sinorhizobium meliloti
116	d1nw2a_	Alignment	not modelled	99.5	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
117	d1z6na1	Alignment	not modelled	99.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
118	d1a8la2	Alignment	not modelled	99.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
119	d1xwaa_	Alignment	not modelled	99.5	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
120	c2vocA_	Alignment	not modelled	99.5	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