Phyre^2

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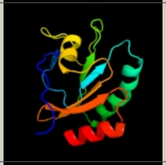
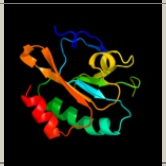
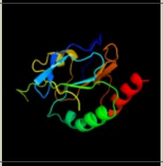
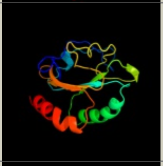
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hyxA_	Alignment		99.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
2	c3lwaA_	Alignment		99.8	12	**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
3	d2fy6a1	Alignment		99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
4	d1knga_	Alignment		99.8	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
5	d1jfua_	Alignment		99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
6	c3erwG_	Alignment		99.8	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
7	d2b5xa1	Alignment		99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
8	d1z5ye1	Alignment		99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
9	c3ia1A_	Alignment		99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
10	d1zzoa1	Alignment		99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
11	c3or5A_	Alignment		99.8	22	**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

12	c3razA_	Alignment		99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
13	d1lu4a_	Alignment		99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
14	c3lorB_	Alignment		99.8	20	**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
15	c3kh7A_	Alignment		99.8	13	**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
16	c2ywiA_	Alignment		99.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
17	c3hczA_	Alignment		99.7	16	**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.
18	c2b1kA_	Alignment		99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
19	c3cynC_	Alignment		99.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
20	d2cvba1	Alignment		99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
21	d1o8xa_	Alignment	not modelled	99.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
22	d1st9a_	Alignment	not modelled	99.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	c3cmiA_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
24	c3fw2A_	Alignment	not modelled	99.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
25	c3gl3D_	Alignment	not modelled	99.7	24	**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
26	d1o73a_	Alignment	not modelled	99.7	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
27	c3fkfC_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
28	d1i5ga_	Alignment	not modelled	99.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

29	c3eytA_	Alignment	not modelled	99.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
30	c2l57A_	Alignment	not modelled	99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
31	c2l5oA_	Alignment	not modelled	99.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution structure of a putative thioredoxin from neisseria2 meningitidis
32	c3ha9A_	Alignment	not modelled	99.7	16	**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
33	c2pptA_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
34	c3f9uA_	Alignment	not modelled	99.7	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
35	d2f8aa1	Alignment	not modelled	99.7	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
36	c3ewlA_	Alignment	not modelled	99.7	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
37	c2p5qA_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
38	c3kcmC_	Alignment	not modelled	99.7	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
39	d1gp1a_	Alignment	not modelled	99.7	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
40	c3hdcA_	Alignment	not modelled	99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
41	c3dwvB_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
42	d2b7ka1	Alignment	not modelled	99.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
43	c3p2aB_	Alignment	not modelled	99.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
44	c2he3A_	Alignment	not modelled	99.7	10	**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)
45	c2r37A_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
46	c3p2aA_	Alignment	not modelled	99.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
47	c2p31B_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
48	c3emxB_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
49	c2b7kD_	Alignment	not modelled	99.6	17	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
50	c1v98A_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
51	d1wp0a1	Alignment	not modelled	99.6	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
52	c2rliA_	Alignment	not modelled	99.6	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
53	c3eurA_	Alignment	not modelled	99.6	15	**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
54	c2l5lA_	Alignment	not modelled	99.6	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides

						vulgatus
55	c2v1mA_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
56	c3hypB_	Alignment	not modelled	99.6	24	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
57	c2obiA_	Alignment	not modelled	99.6	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)
58	d1uula_	Alignment	not modelled	99.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
59	d2bmxa1	Alignment	not modelled	99.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
60	d1a8la2	Alignment	not modelled	99.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
61	c3hz4A_	Alignment	not modelled	99.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
62	d1j08a2	Alignment	not modelled	99.6	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
63	c2bmxB_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
64	c3dmlA_	Alignment	not modelled	99.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
65	c2l6dA_	Alignment	not modelled	99.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
66	d1qmva_	Alignment	not modelled	99.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
67	c3ul3A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
68	c3gnjD_	Alignment	not modelled	99.6	22	**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
69	c2c0dA_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
70	c2yzhD_	Alignment	not modelled	99.5	9	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** crystal structure of peroxiredoxin-like protein from aquifex aeolicus
71	d2zcta1	Alignment	not modelled	99.5	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	d2h01a1	Alignment	not modelled	99.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
73	d1zmaa1	Alignment	not modelled	99.5	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
74	d1thxa_	Alignment	not modelled	99.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
75	c3dxbE_	Alignment	not modelled	99.5	22	**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
76	c2ju5A_	Alignment	not modelled	99.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
77	c3qdnA_	Alignment	not modelled	99.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
78	c3kebB_	Alignment	not modelled	99.5	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
79	d1dbya_	Alignment	not modelled	99.5	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
80	c1zofB_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori

81	c2kucA_	Alignment	not modelled	99.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
82	c2vocA_	Alignment	not modelled	99.5	15	**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
83	c2v2gC_	Alignment	not modelled	99.5	18	**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
84	d2a4va1	Alignment	not modelled	99.5	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	d1zofa1	Alignment	not modelled	99.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
86	c2i1uA_	Alignment	not modelled	99.5	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
87	d2fwha1	Alignment	not modelled	99.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
88	c2i4aA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
89	c1w89E_	Alignment	not modelled	99.5	19	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
90	d1nw2a_	Alignment	not modelled	99.5	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
91	c1xbsA_	Alignment	not modelled	99.5	20	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
92	c2e0qA_	Alignment	not modelled	99.5	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
93	c3me8B_	Alignment	not modelled	99.5	11	**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
94	d1n8ja_	Alignment	not modelled	99.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	d1a8la1	Alignment	not modelled	99.5	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
96	d1zyea1	Alignment	not modelled	99.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
97	d1qq2a_	Alignment	not modelled	99.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
98	d1ep7a_	Alignment	not modelled	99.5	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
99	c1t00A_	Alignment	not modelled	99.5	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
100	d1qgva_	Alignment	not modelled	99.5	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
101	c3drnB_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
102	d1xwaa_	Alignment	not modelled	99.5	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
103	c2f51B_	Alignment	not modelled	99.5	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
104	d1gh2a_	Alignment	not modelled	99.5	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
105	d1fb6a_	Alignment	not modelled	99.4	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
106	c3gknA_	Alignment	not modelled	99.4	17	**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
107	d2trxa_	Alignment	not modelled	99.4	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

108	c3d22A_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
109	c1x5dA_	Alignment	not modelled	99.4	18	**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
110	d1j08a1	Alignment	not modelled	99.4	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
111	c2diyA_	Alignment	not modelled	99.4	30	**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
112	c2o7kA_	Alignment	not modelled	99.4	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
113	c2yzuA_	Alignment	not modelled	99.4	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
114	c3ixrA_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
115	c2h66G_	Alignment	not modelled	99.4	13	**PDB header:**structural genomics/oxidoreductase **Chain:** G: **PDB Molecule:**pv-pf14_0368; **PDBTitle:** the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
116	c2xbqB_	Alignment	not modelled	99.4	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
117	d1yexa1	Alignment	not modelled	99.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
118	c3tcoA_	Alignment	not modelled	99.4	23	**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
119	c2dmlA_	Alignment	not modelled	99.4	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
120	d1e2ya_	Alignment	not modelled	99.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like