Phyre2

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Description	P0AE08
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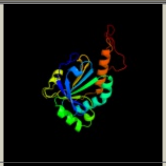
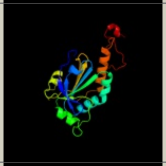
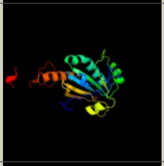
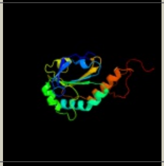
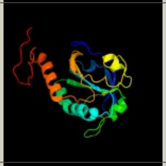
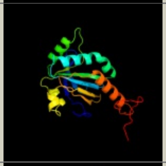
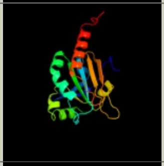
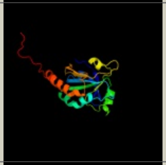
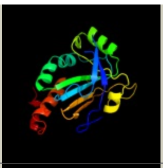
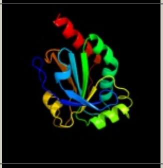
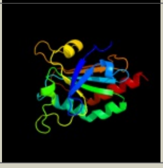
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n8ja_	Alignment		100.0	98	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
2	d1qmva_	Alignment		100.0	36	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
3	d1uula_	Alignment		100.0	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
4	d1xcca_	Alignment		100.0	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
5	c2v2gC_	Alignment		100.0	29	**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
6	d1prxa_	Alignment		100.0	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
7	d2zcta1	Alignment		100.0	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
8	d1yexa1	Alignment		100.0	98	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
9	d2h01a1	Alignment		100.0	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
10	c1zofB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
11	d1we0a1	Alignment		100.0	62	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

12	c2bmxB_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
13	c2c0dA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
14	c2h66G_	Alignment		100.0	30	**PDB header:**structural genomics/oxidoreductase **Chain:** G: **PDB Molecule:**pv-pf14_0368; **PDBTitle:** the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
15	d1qq2a_	Alignment		100.0	36	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
16	d1e2ya_	Alignment		100.0	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
17	c1zyeL_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
18	d2bmxa1	Alignment		100.0	32	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
19	d1zofa1	Alignment		100.0	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	d1zyea1	Alignment		100.0	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
21	c2ywiA_	Alignment	not modelled	100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
22	d2cv4a1	Alignment	not modelled	100.0	34	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	d2cvba1	Alignment	not modelled	100.0	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
24	c3kebB_	Alignment	not modelled	100.0	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
25	d1xvwa1	Alignment	not modelled	100.0	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
26	c3umaC_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**hypothetical peroxiredoxin protein; **PDBTitle:** crystal structure of a hypothetical peroxiredoxin protein frm2 sinorhizobium meliloti
27	d1nm3a2	Alignment	not modelled	100.0	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
28	c2wfcD_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from arenicola marina
						Fold: Thioredoxin fold

29	d1hd2a_	Alignment	not modelled	100.0	26	**Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
30	c3gknA_	Alignment	not modelled	100.0	24	**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
31	d1tp9a1	Alignment	not modelled	100.0	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
32	c2jszA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** solution structure of tpx in the reduced state
33	c2xhfA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana
34	d1psqa_	Alignment	not modelled	99.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
35	c2yzhD_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** crystal structure of peroxiredoxin-like protein from aquifex aeolicus
36	c3ixrA_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
37	d2cx4a1	Alignment	not modelled	99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
38	d1xiya1	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
39	c2xpdC_	Alignment	not modelled	99.9	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
40	d1xvqa_	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
41	c2hyxA_	Alignment	not modelled	99.9	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
42	d1qxha_	Alignment	not modelled	99.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
43	d1q98a_	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	c2pwjB_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**mitochondrial peroxiredoxin; **PDBTitle:** structure of a mitochondrial type ii peroxiredoxin from2 pisum sativum
45	c3drnB_	Alignment	not modelled	99.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
46	c3hdcA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
47	d2a4va1	Alignment	not modelled	99.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
48	c2ywnA_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin-like protein; **PDBTitle:** crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
49	d1jfua_	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
50	d2b7ka1	Alignment	not modelled	99.9	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
51	c3gl3D_	Alignment	not modelled	99.9	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
52	c3kcmC_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
53	c3kh7A_	Alignment	not modelled	99.9	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
54	c3ha9A_	Alignment	not modelled	99.9	12	**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
55	c2l5oA	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin;

						PDBTitle: solution structure of a putative thioredoxin from neisseria2 meningitidis
56	c2b1kA_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
57	d1lu4a_	Alignment	not modelled	99.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	c3hczA_	Alignment	not modelled	99.9	15	**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.
59	d2b5xa1	Alignment	not modelled	99.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
60	d1st9a_	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
61	c3me8B_	Alignment	not modelled	99.9	14	**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
62	c1nm3B_	Alignment	not modelled	99.9	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
63	d1xzoa1	Alignment	not modelled	99.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
64	c2b7kD_	Alignment	not modelled	99.9	15	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
65	c3lorB_	Alignment	not modelled	99.9	13	**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
66	c3or5A_	Alignment	not modelled	99.9	17	**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
67	c3lwaA_	Alignment	not modelled	99.9	17	**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
68	c3eytA_	Alignment	not modelled	99.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
69	c3erwG_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
70	c2rliA_	Alignment	not modelled	99.8	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
71	c2k6vA_	Alignment	not modelled	99.8	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
72	c3eurA_	Alignment	not modelled	99.8	10	**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
73	c3fkfC_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
74	c3ia1A_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
75	c3ewlA_	Alignment	not modelled	99.8	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
76	d1zzoa1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
77	d2fy6a1	Alignment	not modelled	99.8	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
78	c3fw2A_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
79	d1wp0a1	Alignment	not modelled	99.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
80	c3cynC_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8

81	d1knga_	Alignment	not modelled	99.8	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
82	c2p5qA_	Alignment	not modelled	99.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
83	c2v1mA_	Alignment	not modelled	99.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
84	c3dwvB_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
85	c2he3A_	Alignment	not modelled	99.8	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)
86	d2f8aa1	Alignment	not modelled	99.8	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
87	c2p31B_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
88	d1o8xa_	Alignment	not modelled	99.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
89	c3cmiA_	Alignment	not modelled	99.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
90	d1gp1a_	Alignment	not modelled	99.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
91	c2obiA_	Alignment	not modelled	99.7	9	**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)
92	d1o73a_	Alignment	not modelled	99.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
93	c3razA_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
94	d1z5ye1	Alignment	not modelled	99.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	d1i5ga_	Alignment	not modelled	99.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
96	c2r37A_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
97	c3f9uA_	Alignment	not modelled	99.3	8	**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
98	c2l57A_	Alignment	not modelled	99.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
99	c2ju5A_	Alignment	not modelled	98.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
100	c2kucA_	Alignment	not modelled	98.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
101	d1z6na1	Alignment	not modelled	98.7	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
102	d2fwha1	Alignment	not modelled	98.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
103	c2pptA_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
104	d1j08a2	Alignment	not modelled	98.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
105	c3p2aB_	Alignment	not modelled	98.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
106	c3ul3A_	Alignment	not modelled	98.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
						PDB header:isomerase

107	c3fk8A_	Alignment	not modelled	98.3	11	**Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
108	d1sena_	Alignment	not modelled	98.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
109	c1senA_	Alignment	not modelled	98.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881
110	c3p2aA_	Alignment	not modelled	98.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
111	c1v98A_	Alignment	not modelled	98.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
112	c3emxB_	Alignment	not modelled	98.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
113	d1m7ta_	Alignment	not modelled	98.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
114	d1f9ma_	Alignment	not modelled	98.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
115	c2xbqB_	Alignment	not modelled	98.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
116	c2vlvA_	Alignment	not modelled	98.2	17	**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
117	d1gh2a_	Alignment	not modelled	98.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
118	c2i1uA_	Alignment	not modelled	98.2	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
119	c2diyA_	Alignment	not modelled	98.2	16	**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
120	d1xwaa_	Alignment	not modelled	98.2	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase