Phyre^2

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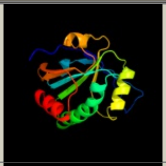
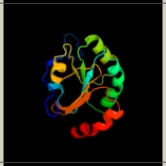
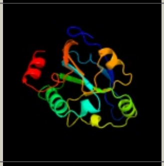
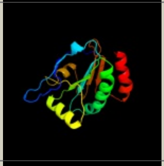
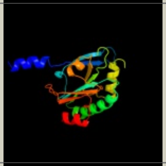
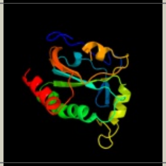
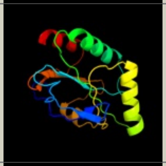
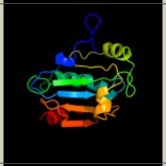
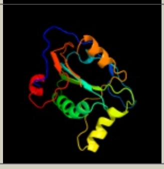
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1st9a_	Alignment		98.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
2	c3kh7A_	Alignment		98.4	15	**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		98.3	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
4	c3hdcA_	Alignment		98.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
5	c3lorB_	Alignment		98.3	11	**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
6	d2cvba1	Alignment		98.2	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
7	d1knga_	Alignment		98.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
8	c3gl3D_	Alignment		98.2	15	**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
9	c3kcmC_	Alignment		98.2	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
10	c3drnB_	Alignment		98.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxiredoxin, bacterioferritin comigratory protein **PDBTitle:** the crystal structure of bcp1 from sulfolobus sulfataricus
11	c3hczA_	Alignment		98.1	12	**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.

12	d2b5xa1	Alignment		98.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
13	c3ha9A_	Alignment		98.0	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
14	c2l5oA_	Alignment		98.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution structure of a putative thioredoxin from neisseria2 meningitidis
15	c3lwaA_	Alignment		98.0	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
16	d1e2ya_	Alignment		98.0	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
17	c2b1kA_	Alignment		98.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
18	c3fkfC_	Alignment		98.0	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
19	d2fy6a1	Alignment		97.9	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	d1jfua_	Alignment		97.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
21	d2bmxa1	Alignment	not modelled	97.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
22	d1zofa1	Alignment	not modelled	97.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
23	c3or5A_	Alignment	not modelled	97.9	13	**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
24	d1qq2a_	Alignment	not modelled	97.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
25	c3kebB_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** thiol peroxidase from chromobacterium violaceum
26	c1zofB_	Alignment	not modelled	97.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide-reductase; **PDBTitle:** crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
27	c2yzhD_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** crystal structure of peroxiredoxin-like protein from aquifex aeolicus
28	c2jszA_	Alignment	not modelled	97.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable thiol peroxidase; **PDBTitle:** solution structure of tpx in the reduced state

29	d2cx4a1	Alignment	not modelled	97.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
30	c2c0dA_	Alignment	not modelled	97.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin peroxidase 2; **PDBTitle:** structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
31	d1xvwa1	Alignment	not modelled	97.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
32	c3razA_	Alignment	not modelled	97.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
33	c2h66G_	Alignment	not modelled	97.7	15	**PDB header:**structural genomics/oxidoreductase **Chain:** G: **PDB Molecule:**pv-pf14_0368; **PDBTitle:** the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
34	c2ywiA_	Alignment	not modelled	97.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
35	c3erwG_	Alignment	not modelled	97.7	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
36	c3gknA_	Alignment	not modelled	97.7	12	**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
37	c3eytA_	Alignment	not modelled	97.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
38	c2bmxB_	Alignment	not modelled	97.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxidase c; **PDBTitle:** mycobacterium tuberculosis ahpc
39	d1qmva_	Alignment	not modelled	97.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
40	d1lu4a_	Alignment	not modelled	97.7	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
41	c3ia1A_	Alignment	not modelled	97.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
42	c3cmiA_	Alignment	not modelled	97.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
43	d1zzoa1	Alignment	not modelled	97.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d1psqa_	Alignment	not modelled	97.6	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
45	c3ixrA_	Alignment	not modelled	97.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
46	d1z5ye1	Alignment	not modelled	97.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
47	c2p31B_	Alignment	not modelled	97.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
48	c3me8B_	Alignment	not modelled	97.4	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
49	c3ewlA_	Alignment	not modelled	97.4	10	**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
50	c1zyeL_	Alignment	not modelled	97.3	14	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**thioredoxin-dependent peroxide reductase; **PDBTitle:** crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
51	c2p5qA_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
52	c3fw2A_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
53	c3cynC_	Alignment	not modelled	97.2	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
54	d1uula_	Alignment	not modelled	97.2	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like

55	d2zcta1	Alignment	not modelled	97.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
56	d1we0a1	Alignment	not modelled	97.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
57	c2ywnA_	Alignment	not modelled	97.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin-like protein; **PDBTitle:** crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
58	d1zyea1	Alignment	not modelled	97.0	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
59	d1qxha_	Alignment	not modelled	97.0	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
60	c3eurA_	Alignment	not modelled	97.0	14	**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
61	d2b7ka1	Alignment	not modelled	96.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
62	d1xzoa1	Alignment	not modelled	96.9	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
63	d1n8ja_	Alignment	not modelled	96.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
64	c2v1mA_	Alignment	not modelled	96.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase
65	c2xpdC_	Alignment	not modelled	96.8	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
66	d1gp1a_	Alignment	not modelled	96.7	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
67	c2he3A_	Alignment	not modelled	96.7	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)
68	d1yexa1	Alignment	not modelled	96.6	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
69	d2h01a1	Alignment	not modelled	96.5	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
70	d1prxa_	Alignment	not modelled	96.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
71	c3dwvB_	Alignment	not modelled	96.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
72	c2obiA_	Alignment	not modelled	96.3	11	**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)
73	c2xhfA_	Alignment	not modelled	96.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana
74	d1q98a_	Alignment	not modelled	96.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
75	d2f8aa1	Alignment	not modelled	96.1	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
76	d1wp0a1	Alignment	not modelled	96.0	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
77	d1hd2a_	Alignment	not modelled	95.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
78	d2a4va1	Alignment	not modelled	95.7	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
79	d1xcca_	Alignment	not modelled	95.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
80	c2r37A_	Alignment	not modelled	95.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 3; **PDBTitle:** crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
81	c2v2gC_	Alignment	not modelled	94.9	12	**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
82	c2rliA_	Alignment	not modelled	94.8	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
83	d2cv4a1	Alignment	not modelled	94.8	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
84	d1o8xa_	Alignment	not modelled	94.5	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	d1xvqa_	Alignment	not modelled	94.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
86	d1z6na1	Alignment	not modelled	94.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	c2wfcD_	Alignment	not modelled	93.4	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from arenicola marina
88	c2b7kD_	Alignment	not modelled	92.8	10	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
89	d1o73a_	Alignment	not modelled	91.7	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
90	c2k6vA_	Alignment	not modelled	91.4	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**putative cytochrome c oxidase assembly protein; **PDBTitle:** solution structures of apo sco1 protein from thermus2 thermophilus
91	c2l57A_	Alignment	not modelled	90.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
92	c3umaC_	Alignment	not modelled	88.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**hypothetical peroxiredoxin protein; **PDBTitle:** crystal structure of a hypothetical peroxiredoxin protein frm2 sinorhizobium meliloti
93	c2pwjB_	Alignment	not modelled	86.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**mitochondrial peroxiredoxin; **PDBTitle:** structure of a mitochondrial type ii peroxiredoxin from2 pisum sativum
94	d1tp9a1	Alignment	not modelled	86.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	c2kucA_	Alignment	not modelled	76.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
96	d1i5ga_	Alignment	not modelled	76.0	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
97	d1y6ja2	Alignment	not modelled	72.9	17	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
98	c2v6bB_	Alignment	not modelled	72.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
99	d1xiya1	Alignment	not modelled	68.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
100	d1t2da2	Alignment	not modelled	67.3	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
101	d1oc4a2	Alignment	not modelled	64.0	9	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
102	c3gnjD_	Alignment	not modelled	57.6	14	**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
103	c2ju5A_	Alignment	not modelled	57.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
104	c3hz4A_	Alignment	not modelled	53.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
105	c3f9uA_	Alignment	not modelled	50.2	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
106	d1zmaa1	Alignment	not modelled	48.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
107	d1pzga2	Alignment	not modelled	46.6	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain

108	c2wshC_	Alignment	not modelled	46.1	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
109	c3gr0D_	Alignment	not modelled	46.0	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
110	c3fk8A_	Alignment	not modelled	44.7	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
111	d2d30a1	Alignment	not modelled	41.9	27	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
112	c2l6dA_	Alignment	not modelled	40.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
113	d2fwha1	Alignment	not modelled	40.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
114	d1nw2a_	Alignment	not modelled	39.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
115	c2e0qA_	Alignment	not modelled	39.2	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
116	c2pptA_	Alignment	not modelled	37.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
117	d2ooka1	Alignment	not modelled	35.7	19	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Sfri0576-like
118	d5mdha2	Alignment	not modelled	35.0	9	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
119	c3ul3A_	Alignment	not modelled	34.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
120	d1nm3a2	Alignment	not modelled	33.9	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like