

# Phyre<sup>2</sup>

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gp1a_	Alignment		100.0	36	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
2	c2v1mA_	Alignment		100.0	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase; <b>PDBTitle:</b> crystal structure of schistosoma mansoni glutathione2 peroxidase
3	d2f8aa1	Alignment		100.0	37	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
4	c2r37A_	Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 3; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
5	c2he3A_	Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 2; <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
6	c3cynC_	Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable glutathione peroxidase 8; <b>PDBTitle:</b> the structure of human gpx8
7	c2p5qA_	Alignment		100.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 5; <b>PDBTitle:</b> crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
8	c3dwvB_	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
9	c2obiA_	Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipid hydroperoxide glutathione <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpx4)
10	c2p31B_	Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase 7; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 7
11	c2hyxA_	Alignment		99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein dipz; <b>PDBTitle:</b> structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis

12	<a href="#">c3cmiA</a>		99.9	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin hyr1; <b>PDBTitle:</b> crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast <i>saccharomyces cerevisiae</i>	
13	<a href="#">c3me8B</a>		99.9	9	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative electron transfer protein aq_2194 from2 <i>aquifex aeolicus</i> vf5	
14	<a href="#">c3lorB</a>		99.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol-disulfide isomerase and thioredoxins; <b>PDBTitle:</b> the crystal structure of a thiol-disulfide isomerase from2 <i>corynebacterium glutamicum</i> to 2.2a	
15	<a href="#">c2rlia</a>		99.9	10	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> sco2 protein homolog, mitochondrial; <b>PDBTitle:</b> solution structure of cu(i) human sco2	
16	<a href="#">d1jfua</a>		99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like	
17	<a href="#">d1xzao1</a>		99.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like	
18	<a href="#">d1wp0a1</a>		99.9	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like	
19	<a href="#">c3lwaA</a>		99.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a secreted thiol-disulfide2 isomerase from <i>corynebacterium glutamicum</i> to 1.75a	
20	<a href="#">c3eytA</a>		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein spoa0173; <b>PDBTitle:</b> crystal structure of thioredoxin-like superfamily protein spoa0173	
21	<a href="#">c2l5oA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution structure of a putative thioredoxin from <i>neisseria2 meningitidis</i>
22	<a href="#">c3kcmC</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from <i>geobacter2 metallireducens</i>
23	<a href="#">c3or5A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein, thioredoxin family <b>PDBTitle:</b> crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from <i>chlorobium tepidum</i> tis
24	<a href="#">c2b7kd</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> sco1 protein; <b>PDBTitle:</b> crystal structure of yeast sco1
25	<a href="#">c2yw1A</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 <i>geobacillus kaustophilus</i>
26	<a href="#">d2b7ka1</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
27	<a href="#">c3gl3D</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative thiol:disulfide interchange protein <b>PDBTitle:</b> crystal structure of a putative thiol:disulfide interchange2 protein dsbe from <i>chlorobium tepidum</i>
28	<a href="#">c2k6vA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome c oxidase assembly protein;

					<b>PDBTitle:</b> solution structures of apo sco1 protein from thermus2 thermophilus
29	<a href="#">d2cvba1</a>	Alignment	not modelled	99.9	21 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
30	<a href="#">d1lu4a_</a>	Alignment	not modelled	99.9	13 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
31	<a href="#">c3hcza_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiol-disulfide isomerase; <b>PDBTitle:</b> the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
32	<a href="#">c3gkna_</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
33	<a href="#">c3ha9A_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized thioredoxin-like protein; <b>PDBTitle:</b> the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
34	<a href="#">c3razA_</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
35	<a href="#">d1st9a_</a>	Alignment	not modelled	99.9	22 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
36	<a href="#">d2fy6a1</a>	Alignment	not modelled	99.9	15 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
37	<a href="#">d2b5xa1</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
38	<a href="#">c3fkfC_</a>	Alignment	not modelled	99.9	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
39	<a href="#">d1xvwa1</a>	Alignment	not modelled	99.9	18 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
40	<a href="#">c3ixrA_</a>	Alignment	not modelled	99.9	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein; <b>PDBTitle:</b> crystal structure of xylella fastidiosa prxq c47s mutant
41	<a href="#">c3fw2A_</a>	Alignment	not modelled	99.9	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase; <b>PDBTitle:</b> c-terminal domain of putative thiol-disulfide oxidoreductase from2 bacteroides thetaiotaomicron.
42	<a href="#">c3hdcA_</a>	Alignment	not modelled	99.9	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> the crystal structure of thioredoxin protein from geobacter2 metallireducens
43	<a href="#">c3kebB_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> thiol peroxidase from chromobacterium violaceum
44	<a href="#">c3eura_</a>	Alignment	not modelled	99.9	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343
45	<a href="#">d2cx4a1</a>	Alignment	not modelled	99.9	14 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
46	<a href="#">d2bmxa1</a>	Alignment	not modelled	99.8	11 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
47	<a href="#">c3ewlA_</a>	Alignment	not modelled	99.8	10 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein bf1870; <b>PDBTitle:</b> crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
48	<a href="#">c3erwG_</a>	Alignment	not modelled	99.8	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation thiol-disulfide oxidoreductase a; <b>PDBTitle:</b> crystal structure of sto4 from bacillus subtilis
49	<a href="#">c3drnB_</a>	Alignment	not modelled	99.8	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxiredoxin, bacterioferritin comigratory protein <b>PDBTitle:</b> the crystal structure of bcp1 from sulfolobus sulfataricus
50	<a href="#">c2yzhD_</a>	Alignment	not modelled	99.8	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> crystal structure of peroxiredoxin-like protein from aquifex aeolicus
51	<a href="#">c3kh7A_</a>	Alignment	not modelled	99.8	10 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
52	<a href="#">d1qq2a_</a>	Alignment	not modelled	99.8	10 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
53	<a href="#">d1knga_</a>	Alignment	not modelled	99.8	17 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
54	<a href="#">d1zzoa1</a>	Alignment	not modelled	99.8	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like

					<b>Family:</b> Glutathione peroxidase-like
55	<u>c2bmxB_</u>	Alignment	not modelled	99.8	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxidase c; <b>PDBTitle:</b> mycobacterium tuberculosis ahpc
56	<u>d1e2ya_</u>	Alignment	not modelled	99.8	13 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
57	<u>d1we0a1</u>	Alignment	not modelled	99.8	12 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
58	<u>d1qmva_</u>	Alignment	not modelled	99.8	11 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
59	<u>d1n8ja_</u>	Alignment	not modelled	99.8	12 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
60	<u>c2jszA_</u>	Alignment	not modelled	99.8	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> solution structure of tpx in the reduced state
61	<u>d1yexa1</u>	Alignment	not modelled	99.8	12 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
62	<u>d1psqa_</u>	Alignment	not modelled	99.8	14 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
63	<u>d1uula_</u>	Alignment	not modelled	99.8	14 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
64	<u>d1zofa1</u>	Alignment	not modelled	99.8	19 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
65	<u>c2ywnA_</u>	Alignment	not modelled	99.8	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin-like protein; <b>PDBTitle:</b> crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
66	<u>d1zyea1</u>	Alignment	not modelled	99.8	10 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
67	<u>c2xpdC_</u>	Alignment	not modelled	99.8	11 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol peroxidase; <b>PDBTitle:</b> reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
68	<u>d1q98a_</u>	Alignment	not modelled	99.8	8 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
69	<u>c3ia1A_</u>	Alignment	not modelled	99.8	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thio-disulfide isomerase/thioredoxin; <b>PDBTitle:</b> crystal structure of thio-disulfide isomerase from thermus2 thermophilus
70	<u>d1prxa_</u>	Alignment	not modelled	99.8	12 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
71	<u>c1zofB_</u>	Alignment	not modelled	99.8	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide-reductase; <b>PDBTitle:</b> crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
72	<u>d2zcta1</u>	Alignment	not modelled	99.8	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
73	<u>c1zyel_</u>	Alignment	not modelled	99.8	10 <b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase; <b>PDBTitle:</b> crystal strucutre analysis of bovine mitochondrial peroxiredoxin iii
74	<u>c2c0dA_</u>	Alignment	not modelled	99.8	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin peroxidase 2; <b>PDBTitle:</b> structure of the mitochondrial 2-cys peroxiredoxin from2 plasmodium falciparum
75	<u>c2b1kA_</u>	Alignment	not modelled	99.8	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of e. coli ccmg protein
76	<u>d2h01a1</u>	Alignment	not modelled	99.8	15 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
77	<u>c2v2gC_</u>	Alignment	not modelled	99.8	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> peroxiredoxin 6; <b>PDBTitle:</b> crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
78	<u>d2a4va1</u>	Alignment	not modelled	99.8	16 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
79	<u>d1xcc1</u>	Alignment	not modelled	99.7	11 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
80	<u>d1qxha_</u>	Alignment	not modelled	99.7	11 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
81	<u>c2h66G</u>	Alignment	not modelled	99.7	16 <b>PDB header:</b> structural genomics/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pv-pf14_0368;

81	<a href="#">c21000</a>	Alignment	not modelled	99.7	10	<b>PDBTitle:</b> the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
82	<a href="#">d1o8xa</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
83	<a href="#">d1z5ye1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
84	<a href="#">d1xvqa</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
85	<a href="#">c2xhfA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> peroxiredoxin 5; <b>PDBTitle:</b> crystal structure of peroxiredoxin 5 from alvinella pompejana
86	<a href="#">d1o73a</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
87	<a href="#">d1i5ga</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
88	<a href="#">d2cv4a1</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
89	<a href="#">d1hd2a</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
90	<a href="#">c2wfcD</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> peroxiredoxin 5; <b>PDBTitle:</b> crystal structure of peroxiredoxin 5 from arenicola marina
91	<a href="#">d1xiya1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
92	<a href="#">c2pwjB</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> mitochondrial peroxiredoxin; <b>PDBTitle:</b> structure of a mitochondrial type ii peroxiredoxin from2 pismum sativum
93	<a href="#">d1tp9a1</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
94	<a href="#">d1nm3a2</a>	Alignment	not modelled	99.5	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
95	<a href="#">c3umaC</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical peroxiredoxin protein; <b>PDBTitle:</b> crystal structure of a hypothetical peroxiredoxin protein frm2 sinorhizobium meliloti
96	<a href="#">c3f9uA</a>	Alignment	not modelled	99.3	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative exported cytochrome c biogenesis-related protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
97	<a href="#">c2l57A</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
98	<a href="#">c2ju5A</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase
99	<a href="#">c2kucA</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> putative disulphide-isomerase; <b>PDBTitle:</b> solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
100	<a href="#">c3p2aB</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> putative thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from yersinia pestis
101	<a href="#">c2pptA</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
102	<a href="#">c3p2aA</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from yersinia pestis
103	<a href="#">d2fwha1</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
104	<a href="#">c1v98A</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure analysis of thioredoxin from thermus thermophilus
105	<a href="#">d1sena</a>	Alignment	not modelled	98.8	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
106	<a href="#">c1senA</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin-like protein p19; <b>PDBTitle:</b> endoplasmic reticulum protein rp19 o95881
107	<a href="#">c3hypB</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of bacteroides fragilis trxp_s105g mutant

108	<a href="#">c3fk8A_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> disulphide isomerase; <b>PDBTitle:</b> the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
109	<a href="#">d1z6na1</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
110	<a href="#">c2vocA_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
111	<a href="#">c3gnjD_</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin domain protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
112	<a href="#">d1j08a2</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
113	<a href="#">c1nm3B_</a>	Alignment	not modelled	98.7	10	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein hi0572; <b>PDBTitle:</b> crystal structure of haemophilus influenza hybrid-prx5
114	<a href="#">d1xwaa</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
115	<a href="#">d1gh2a_</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
116	<a href="#">c2l5IA_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of thioredoxin from bacteroides vulgaris
117	<a href="#">c3ul3A_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
118	<a href="#">c2e0qA_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
119	<a href="#">d1thxa_</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
120	<a href="#">c3emxB_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from aeropyrum pernix