



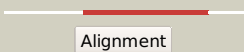




# Phyre2

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Description	RVBD3673c_(-)_4114652_4115335
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	ae4858dc7578fbf1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hyxA_</a>	 Alignment		100.0	19	<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
2	<a href="#">c6gc1A_</a>	 Alignment		100.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> nhl repeat-containing protein 2; <b>PDBTitle:</b> crystal structure of trx-like and nhl repeat containing domains of 2 human nhlrc2
3	<a href="#">c4tr3A_</a>	 Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> type iii iodothyronine deiodinase; <b>PDBTitle:</b> mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
4	<a href="#">d2b5xa1</a>	 Alignment		99.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
5	<a href="#">c4eo3A_</a>	 Alignment		99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> bacterioferritin comigratory protein/nadh dehydrogenase; <b>PDBTitle:</b> peroxiredoxin nitroreductase fusion enzyme
6	<a href="#">d1knga_</a>	 Alignment		99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
7	<a href="#">c4ka0C_</a>	 Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> putative thiol-disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative thiol-disulfide oxidoreductase from 2 bacteroides vulgatus (target nysgrc-011676), space group p21221
8	<a href="#">c3lwaA_</a>	 Alignment		99.9	22	<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-disulfide isomerase from 2 corynebacterium glutamicum to 1.75a
9	<a href="#">c2ywiA_</a>	 Alignment		99.9	18	<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 from 2 geobacillus kaustophilus
10	<a href="#">d1jfua_</a>	 Alignment		99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
11	<a href="#">c4pq1B_</a>	 Alignment		99.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> putative electron transport related protein; <b>PDBTitle:</b> crystal structure and functional implications of a dsbf homologue from 2 corynebacterium diphtheriae

12	<a href="#">c3or5A_</a>	Alignment		99.9	19	<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 chlorobium tepidum t1s
13	<a href="#">d1lu4a_</a>	Alignment		99.9	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
14	<a href="#">d1z5ye1</a>	Alignment		99.9	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
15	<a href="#">c3lorB_</a>	Alignment		99.9	19	<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 corynebacterium glutamicum to 2.2a
16	<a href="#">c3erwG_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation thiol-disulfide oxidoreductase a; <b>PDBTitle:</b> crystal structure of stoa from bacillus subtilis
17	<a href="#">c3raza_</a>	Alignment		99.9	20	<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
18	<a href="#">d2fy6a1</a>	Alignment		99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
19	<a href="#">c3gl3D_</a>	Alignment		99.9	17	<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 chlorobium tepidum
20	<a href="#">d2cvba1</a>	Alignment		99.9	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
21	<a href="#">c2b1kA_</a>	Alignment	not modelled	99.9	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
22	<a href="#">d1zzoa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
23	<a href="#">c3eytA_</a>	Alignment	not modelled	99.9	16	<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
24	<a href="#">c4yodA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of a thioredoxin-like protein (baccac_02376) from2 bacteroides caccae atcc 43185 at 1.90 a resolution
25	<a href="#">c5um7B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin signature protein; <b>PDBTitle:</b> crystal structure of the reduced state of the thiol-disulfide2 reductase sdba from streptococcus gordonii
26	<a href="#">c3ha9A_</a>	Alignment	not modelled	99.9	13	<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
27	<a href="#">d1st9a_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
28	<a href="#">c3fkfC_</a>	Alignment	not modelled	99.9	11	<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
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3kh7A_</a>	Alignment	not modelled	99.9	17	<b>Chain:</b> A: <b>PDB Molecule:</b> thio-disulfide interchange protein dsbe; <b>PDBTitle:</b> crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
30	<a href="#">c3fw2A_</a>	Alignment	not modelled	99.9	14	<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.
31	<a href="#">c3kcmC_</a>	Alignment	not modelled	99.9	23	<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 geobacter2 metallireducens
32	<a href="#">c2l5oA_</a>	Alignment	not modelled	99.9	19	<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 neisseria2 meningitidis
33	<a href="#">c3u5rG_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein smc02350 from2 sinorhizobium meliloti 1021
34	<a href="#">c3ewlA_</a>	Alignment	not modelled	99.9	13	<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
35	<a href="#">c3hczA_</a>	Alignment	not modelled	99.9	9	<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.
36	<a href="#">c3eurA_</a>	Alignment	not modelled	99.9	7	<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
37	<a href="#">c4evmA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of soluble domain of membrane-anchored2 thioredoxin family protein from streptococcus pneumoniae strain3 canada mdr_19a
38	<a href="#">d1uuuA_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
39	<a href="#">c2m72A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized thioredoxin-like protein; <b>PDBTitle:</b> solution structure of uncharacterized thioredoxin-like protein pg_21752 from porphyromonas gingivalis
40	<a href="#">d1qmva_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
41	<a href="#">c2lrtA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the uncharacterized thioredoxin-like protein2 bv_1432 from bacteroides vulgatus
42	<a href="#">c4fyuB_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from wuchereria bancrofti at 2.02 angstrom
43	<a href="#">c2ls5A_</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> solution structure of a putative protein disulfide isomerase from2 bacteroides thetaiotaomicron
44	<a href="#">c4nmuB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol-disulfide oxidoreductase resa; <b>PDBTitle:</b> crystal structure of thiol-disulfide oxidoreductase from bacillus str.2 'ames ancestor'
45	<a href="#">d1i5ga_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
46	<a href="#">c3ia1A_</a>	Alignment	not modelled	99.9	21	<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
47	<a href="#">c6feuj_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus
48	<a href="#">c4fo5A_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein; <b>PDBTitle:</b> crystal structure of a thioredoxin-like protein (bdi_1100) from2 parabacteroides distasonis atcc 8503 at 2.02 a resolution
49	<a href="#">d1wp0a1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
50	<a href="#">d1n8ja_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
51	<a href="#">c2yp6A_</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> crystal structure of the pneumococcal exposed lipoprotein2 thioredoxin sp_1000 (etrx2) from streptococcus pneumoniae3 strain tigr4 in complex with cyclofos 3 tm
52	<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
53	<a href="#">d1xcca_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
54	<a href="#">d1o73a_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

55	<a href="#">c2bmxB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxidase c; <b>PDBTitle:</b> mycobacterium tuberculosis ahpc
56	<a href="#">d1o8xa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
57	<a href="#">c2lusA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> nmr structure of carinoscorpis rotundicauda thioredoxin related2 protein 16 and its role in regulating transcription factor nf-kb3 activity
58	<a href="#">c3me8B</a>	Alignment	not modelled	99.9	16	<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 aquifex aeolicus vf5
59	<a href="#">c3cynC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable glutathione peroxidase 8; <b>PDBTitle:</b> the structure of human gp8
60	<a href="#">c3tkpB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxiredoxin-4; <b>PDBTitle:</b> crystal structure of full-length human peroxiredoxin 4 in the reduced2 form
61	<a href="#">c3sbcG</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> peroxiredoxin tsa1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae tsa1c47s mutant protein
62	<a href="#">c3s9fA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> tryparedoxin; <b>PDBTitle:</b> the structure of tryparedoxin i from leishmania major
63	<a href="#">d2f8aa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
64	<a href="#">d2bmx1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
65	<a href="#">c3ztIB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin peroxidase; <b>PDBTitle:</b> crystal structure of decameric form of peroxiredoxin i from2 schistosoma mansoni
66	<a href="#">d1gp1a</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
67	<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
68	<a href="#">c2obiA</a>	Alignment	not modelled	99.9	12	<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 (gp4)
69	<a href="#">d2b7ka1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
70	<a href="#">c3w6gP</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> probable peroxiredoxin; <b>PDBTitle:</b> structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii
71	<a href="#">c2v1mA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase; <b>PDBTitle:</b> crystal structure of schistosoma mansoni glutathione peroxidase
72	<a href="#">c5jcgC</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase, mitochondrial; <b>PDBTitle:</b> structure of human peroxiredoxin 3 as three stacked rings
73	<a href="#">c5enuB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase/ thiol specific antioxidant/ <b>PDBTitle:</b> crystal structure of an alkyl hydroperoxide reductase from burkholderia2 ambifaria
74	<a href="#">c2p5qA</a>	Alignment	not modelled	99.9	14	<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 in the2 reduced form
75	<a href="#">c2lrnA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> solution structure of a thiol:disulfide interchange protein from2 bacteroides sp.
76	<a href="#">c2rliA</a>	Alignment	not modelled	99.8	25	<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
77	<a href="#">c3gknA</a>	Alignment	not modelled	99.8	21	<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
78	<a href="#">c2b7kD</a>	Alignment	not modelled	99.8	16	<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
79	<a href="#">d2zcta1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
						<b>PDB header:</b> oxidoreductase

80	<a href="#">c5zteA</a>	Alignment	not modelled	99.8	11	<b>Chain:</b> A: <b>PDB Molecule:</b> 2-cys peroxidoredoxin bas1, chloroplastic; <b>PDBTitle:</b> crystal structure of prxa c119s mutant from arabidopsis thaliana
81	<a href="#">c5y63E</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> alkyl hydroperoxide reductase, c subunit; <b>PDBTitle:</b> crystal structure of enterococcus faecalis ahpc
82	<a href="#">d2h01a1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
83	<a href="#">c2i81B</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-cys peroxidoredoxin; <b>PDBTitle:</b> crystal structure of plasmodium vivax 2-cys peroxidoredoxin,2 reduced
84	<a href="#">d2cv4a1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
85	<a href="#">c2c0dA</a>	Alignment	not modelled	99.8	11	<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 peroxidoredoxin from2 plasmodium falciparum
86	<a href="#">d1zyea1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
87	<a href="#">c2he3A</a>	Alignment	not modelled	99.8	19	<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 glutathione peroxidase 2 (gpx2)
88	<a href="#">c3dvwB</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type trypanredoxin peroxidase, oxidized form
89	<a href="#">c5ykjA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxidoredoxin prx1, mitochondrial; <b>PDBTitle:</b> structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxidoredoxin via glutathione/thioredoxin systems
90	<a href="#">c2p31B</a>	Alignment	not modelled	99.8	16	<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
91	<a href="#">c3ixrA</a>	Alignment	not modelled	99.8	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 prqx c47s mutant
92	<a href="#">c6n5uC</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein sco1 homolog 1, mitochondrial; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana sco1 with copper bound
93	<a href="#">c2v2gC</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> peroxidoredoxin 6; <b>PDBTitle:</b> crystal structure of the c45s mutant of the peroxidoredoxin 62 of arenicola marina. monoclinic form
94	<a href="#">c3cmiA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxidoredoxin hyr1; <b>PDBTitle:</b> crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
95	<a href="#">d1yexa1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
96	<a href="#">c3tueB</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trypanredoxin peroxidase; <b>PDBTitle:</b> the structure of trypanredoxin peroxidase i from leishmania major
97	<a href="#">c1zofB</a>	Alignment	not modelled	99.8	15	<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
98	<a href="#">c5ovqL</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> peroxidoredoxin; <b>PDBTitle:</b> crystal structure of the peroxidoredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
99	<a href="#">d1xvwa1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
100	<a href="#">d1qq2a</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
101	<a href="#">c1zyeL</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase; <b>PDBTitle:</b> crystal structure analysis of bovine mitochondrial peroxidoredoxin iii
102	<a href="#">c2r37A</a>	Alignment	not modelled	99.8	11	<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)
103	<a href="#">c2yzhD</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> crystal structure of peroxidoredoxin-like protein from aquifex aeolicus
104	<a href="#">c2k6vA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> electron transport protein; <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome c oxidase assembly protein; <b>PDBTitle:</b> solution structures of apo sco1 protein from thermophilus
105	<a href="#">c2xhfA</a>	Alignment	not modelled	99.8	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxidoredoxin 5; <b>PDBTitle:</b> crystal structure of peroxidoredoxin 5 from alvinella pompejana

106	<a href="#">d1e2ya_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
107	<a href="#">c4txoB_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase/copper binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> blr1131 protein; <b>PDBTitle:</b> crystal structure of the mixed disulfide complex of thioredoxin-like2 tlpas(c110s) and copper chaperone scois(c74s)
108	<a href="#">c4bpyA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sco protein; <b>PDBTitle:</b> crystal structure of the c90a mutant of the sco copper chaperone2 protein from streptomyces lividans
109	<a href="#">d2cx4a1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
110	<a href="#">c3drnB_</a>	Alignment	not modelled	99.8	8	<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
111	<a href="#">d2a4va1</a>	Alignment	not modelled	99.8	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
112	<a href="#">c3f9uA_</a>	Alignment	not modelled	99.8	10	<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
113	<a href="#">c4hdeA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sco1/senc family lipoprotein; <b>PDBTitle:</b> the crystal structure of a sco1/senc family lipoprotein from bacillus2 anthracis str. ames
114	<a href="#">c2xpdC_</a>	Alignment	not modelled	99.8	18	<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
115	<a href="#">c2h66G_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pv-pf14_0368; <b>PDBTitle:</b> the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
116	<a href="#">d1psqa_</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
117	<a href="#">d1we0a1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
118	<a href="#">c4fybA_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein (dsbc); <b>PDBTitle:</b> structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
119	<a href="#">c2jszA_</a>	Alignment	not modelled	99.8	14	<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
120	<a href="#">c5e37A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing thioredoxin; <b>PDBTitle:</b> redox protein from chlamydomonas reinhardtii