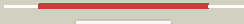



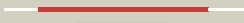



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2238c_ahpE_2510723_2511184
Date	Mon Aug 5 13:25:37 BST 2019
Unique Job ID	503d2156dfeca173

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1xvwa1</a>	 Alignment		100.0	95	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
2	<a href="#">c5ykjA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin prx1, mitochondrial; <b>PDBTitle:</b> structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
3	<a href="#">c2v2gC_</a>	 Alignment		100.0	16	<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
4	<a href="#">d1prxa_</a>	 Alignment		100.0	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
5	<a href="#">c6feuj_</a>	 Alignment		100.0	22	<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 sulfolobus islandicus
6	<a href="#">c3sbcG_</a>	 Alignment		100.0	30	<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
7	<a href="#">c3tkpB_</a>	 Alignment		100.0	31	<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
8	<a href="#">c5zteA_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-cys peroxiredoxin bas1, chloroplastic; <b>PDBTitle:</b> crystal structure of prxa c119s mutant from arabidopsis thaliana
9	<a href="#">c5ovqL_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
10	<a href="#">d1luula_</a>	 Alignment		100.0	28	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
11	<a href="#">d1xcca_</a>	 Alignment		100.0	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

12	<a href="#">d1qmva_</a>	Alignment		100.0	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
13	<a href="#">d2bmx1</a>	Alignment		100.0	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
14	<a href="#">c3ztlB_</a>	Alignment		100.0	31	<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
15	<a href="#">c2i81B_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-cys peroxiredoxin; <b>PDBTitle:</b> crystal structure of plasmodium vivax 2-cys peroxiredoxin,2 reduced
16	<a href="#">c3drnB_</a>	Alignment		100.0	27	<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
17	<a href="#">c2h66G_</a>	Alignment		100.0	25	<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
18	<a href="#">c5y63E_</a>	Alignment		100.0	25	<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
19	<a href="#">c3w6gP_</a>	Alignment		100.0	24	<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
20	<a href="#">d1qq2a_</a>	Alignment		100.0	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
21	<a href="#">d1e2ya_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
22	<a href="#">c3tueB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tryparedoxin peroxidase; <b>PDBTitle:</b> the structure of tryparedoxin peroxidase i from leishmania major
23	<a href="#">c5jcgC_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase, mitochondria; <b>PDBTitle:</b> structure of human peroxiredoxin 3 as three stacked rings
24	<a href="#">d2cx4a1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
25	<a href="#">c2bmxB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxidase c; <b>PDBTitle:</b> mycobacterium tuberculosis ahpc
26	<a href="#">c1zofB_</a>	Alignment	not modelled	100.0	25	<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
27	<a href="#">c5epfA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin; <b>PDBTitle:</b> crystal structure of peroxidoxin bcpb from mycobacterium tuberculosis
28	<a href="#">d1n8ja_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

29	<a href="#">c2c0dA</a>	Alignment	not modelled	100.0	27	<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
30	<a href="#">d1zofa1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
31	<a href="#">c2jszA</a>	Alignment	not modelled	99.9	21	<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
32	<a href="#">d1psqa</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
33	<a href="#">c1zyeL</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> thioredoxin-dependent peroxide reductase; <b>PDBTitle:</b> crystal structre analysis of bovine mitochondrial peroxiredoxin iii
34	<a href="#">c3gknA</a>	Alignment	not modelled	99.9	26	<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
35	<a href="#">c3kebB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> thiol peroxidase from chromobacterium violaceum
36	<a href="#">c4kb3B</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxidoxin; <b>PDBTitle:</b> crystal structure of the mitochondrial peroxiredoxin from leishmania2 braziliensis in the decameric form
37	<a href="#">d1yexa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
38	<a href="#">d2h01a1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
39	<a href="#">d2zcta1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
40	<a href="#">d1we0a1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
41	<a href="#">d1q98a</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
42	<a href="#">c2xpdC</a>	Alignment	not modelled	99.9	27	<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
43	<a href="#">c4je1A</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiol peroxidase; <b>PDBTitle:</b> crystal structure of thiol peroxidase from burkholderia cenocepacia2 j2315
44	<a href="#">c2yzhD</a>	Alignment	not modelled	99.9	19	<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
45	<a href="#">d1hd2a</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
46	<a href="#">c4f82A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> x-ray crystal structure of a putative thioredoxin reductase from2 burkholderia cenocepacia
47	<a href="#">d1zyea1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
48	<a href="#">c3u5rG</a>	Alignment	not modelled	99.9	24	<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
49	<a href="#">c5enuB</a>	Alignment	not modelled	99.9	24	<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 hyroperoxide reductase from burkholderia2 ambifaria
50	<a href="#">c2wfcD</a>	Alignment	not modelled	99.9	17	<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
51	<a href="#">d2a4va1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
52	<a href="#">d1qxha</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
53	<a href="#">c4eo3A</a>	Alignment	not modelled	99.9	27	<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
54	<a href="#">c2ywiA</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 geobacillus kaustophilus

55	<a href="#">c5k2jG</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 1-cys peroxiredoxin; <b>PDBTitle:</b> crystal structure of reduced prx3 in complex with h2o2 from vibrio2 vulnificus
56	<a href="#">c2xhfA</a>	Alignment	not modelled	99.9	15	<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
57	<a href="#">d1xvqa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
58	<a href="#">c3ixrA</a>	Alignment	not modelled	99.9	25	<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
59	<a href="#">c5j9bB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxiredoxin asp f3; <b>PDBTitle:</b> crystal structure of peroxiredoxin asp f3
60	<a href="#">c2ywnA</a>	Alignment	not modelled	99.9	29	<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 from sulfobolus2 tokodaii
61	<a href="#">c3umaC</a>	Alignment	not modelled	99.9	19	<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 melloti
62	<a href="#">d1tp9a1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
63	<a href="#">c2hyxA</a>	Alignment	not modelled	99.9	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
64	<a href="#">d2cvba1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
65	<a href="#">c2ls5A</a>	Alignment	not modelled	99.9	19	<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 thetaiotaomicon
66	<a href="#">c3hdcA</a>	Alignment	not modelled	99.9	28	<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
67	<a href="#">d1xiya1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
68	<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
69	<a href="#">c4tr3A</a>	Alignment	not modelled	99.9	20	<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
70	<a href="#">d1jfua</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
71	<a href="#">c4ka0C</a>	Alignment	not modelled	99.9	14	<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 from2 bacteroides vulgatus (target nysgrc-011676), space group p21221
72	<a href="#">c6gc1A</a>	Alignment	not modelled	99.9	15	<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 of2 human nhlrc2
73	<a href="#">c3me8B</a>	Alignment	not modelled	99.9	14	<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
74	<a href="#">c3kcmC</a>	Alignment	not modelled	99.9	20	<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
75	<a href="#">c2pwjB</a>	Alignment	not modelled	99.9	11	<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 pisum sativum
76	<a href="#">c3or5A</a>	Alignment	not modelled	99.9	16	<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
77	<a href="#">d1nm3a2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
78	<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 neisseria2 meningitidis
79	<a href="#">c4nmuB</a>	Alignment	not modelled	99.9	20	<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'
80	<a href="#">c3hczA</a>	Alignment	not modelled	99.9	16	<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. <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
81	<a href="#">c3ewlA_</a>	Alignment	not modelled	99.9	16	
82	<a href="#">d1lu4a_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
83	<a href="#">c3eurA_</a>	Alignment	not modelled	99.9	13	<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
84	<a href="#">d1st9a_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
85	<a href="#">c2yp6A_</a>	Alignment	not modelled	99.9	21	<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
86	<a href="#">c4yodA_</a>	Alignment	not modelled	99.9	11	<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
87	<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 chlorobium tepidum
88	<a href="#">d1xzoa1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
89	<a href="#">c5um7B_</a>	Alignment	not modelled	99.9	13	<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
90	<a href="#">c3ha9A_</a>	Alignment	not modelled	99.9	18	<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
91	<a href="#">d2b7ka1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
92	<a href="#">c2lrnA_</a>	Alignment	not modelled	99.9	13	<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.
93	<a href="#">c4hdeA_</a>	Alignment	not modelled	99.8	10	<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
94	<a href="#">c3lorB_</a>	Alignment	not modelled	99.8	17	<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
95	<a href="#">c4pq1B_</a>	Alignment	not modelled	99.8	14	<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 from2 corynebacterium diphtheriae
96	<a href="#">c3cynC_</a>	Alignment	not modelled	99.8	14	<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
97	<a href="#">c2v1mA_</a>	Alignment	not modelled	99.8	17	<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
98	<a href="#">d2b5xa1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
99	<a href="#">c2p5qA_</a>	Alignment	not modelled	99.8	16	<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
100	<a href="#">c3kh7A_</a>	Alignment	not modelled	99.8	18	<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
101	<a href="#">c4evmA_</a>	Alignment	not modelled	99.8	23	<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
102	<a href="#">c2rliA_</a>	Alignment	not modelled	99.8	16	<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
103	<a href="#">c3eytA_</a>	Alignment	not modelled	99.8	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
104	<a href="#">c3lwaA_</a>	Alignment	not modelled	99.8	11	<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 from2 corynebacterium glutamicum to 1.75a
105	<a href="#">d1zzoa1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like

106	<a href="#">c3fw2A_</a>	Alignment	not modelled	99.8	10	<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.
107	<a href="#">c2m72A_</a>	Alignment	not modelled	99.8	15	<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
108	<a href="#">c2b7kD_</a>	Alignment	not modelled	99.8	15	<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
109	<a href="#">c2he3A_</a>	Alignment	not modelled	99.8	12	<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)
110	<a href="#">c3cmiA_</a>	Alignment	not modelled	99.8	10	<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 saccharomyces cerevisiae
111	<a href="#">d2f8aa1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
112	<a href="#">d2cv4a1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
113	<a href="#">c2lrtA_</a>	Alignment	not modelled	99.8	12	<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
114	<a href="#">c2b1kA_</a>	Alignment	not modelled	99.8	15	<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
115	<a href="#">d1gp1a_</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
116	<a href="#">c3fkfC_</a>	Alignment	not modelled	99.8	15	<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
117	<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 tryparedoxin peroxidase, oxidized form
118	<a href="#">c4fo5A_</a>	Alignment	not modelled	99.8	19	<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
119	<a href="#">c2obiA_</a>	Alignment	not modelled	99.8	18	<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)
120	<a href="#">c4fyuB_</a>	Alignment	not modelled	99.8	13	<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