



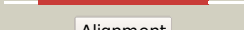

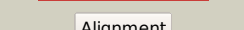

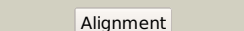





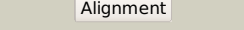

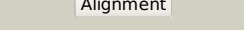

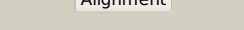

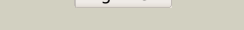



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2521\_(bcp)\_2837694\_2838167  
 Date Wed Aug 7 12:50:15 BST 2019  
 Unique Job ID 4ec15cb943244626

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gknA_</a>	 Alignment		100.0	34	<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
2	<a href="#">c5enuB_</a>	 Alignment		100.0	36	<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 hydropoxide reductase from burkholderia2 ambifaria
3	<a href="#">c3ixrA_</a>	 Alignment		99.9	33	<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
4	<a href="#">c3kebB_</a>	 Alignment		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
5	<a href="#">d1prxa_</a>	 Alignment		99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
6	<a href="#">c6feuj_</a>	 Alignment		99.9	21	<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
7	<a href="#">d1e2ya_</a>	 Alignment		99.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
8	<a href="#">c3tueB_</a>	 Alignment		99.9	23	<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
9	<a href="#">c3tkpB_</a>	 Alignment		99.9	25	<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
10	<a href="#">d1qmva_</a>	 Alignment		99.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
11	<a href="#">c5ykjA_</a>	 Alignment		99.9	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

12	<a href="#">c2hyxA_</a>	Alignment		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
13	<a href="#">c5ovqL_</a>	Alignment		99.9	25	<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
14	<a href="#">c3sbcG_</a>	Alignment		99.9	25	<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
15	<a href="#">c4eo3A_</a>	Alignment		99.9	31	<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
16	<a href="#">c4ka0C_</a>	Alignment		99.9	17	<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
17	<a href="#">c5y63E_</a>	Alignment		99.9	24	<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
18	<a href="#">d1uuuA_</a>	Alignment		99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
19	<a href="#">c4je1A_</a>	Alignment		99.9	22	<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
20	<a href="#">c3zt1B_</a>	Alignment		99.9	29	<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
21	<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'
22	<a href="#">d2bmx1_1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
23	<a href="#">c6gc1A_</a>	Alignment	not modelled	99.9	12	<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 nhlr2
24	<a href="#">c4kb3B_</a>	Alignment	not modelled	99.9	24	<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
25	<a href="#">d1xvwa1</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
26	<a href="#">d1xcca_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
27	<a href="#">d2zcta1</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="#">c5jcgC_</a>	Alignment	not modelled	99.9	24	<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

29	<a href="#">d1qq2a_</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
30	<a href="#">c2v2gC_</a>	Alignment	not modelled	99.9	21	<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
31	<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 structure analysis of bovine mitochondrial peroxiredoxin iii
32	<a href="#">c4pq1B_</a>	Alignment	not modelled	99.9	17	<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
33	<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
34	<a href="#">d1we0a1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
35	<a href="#">d1n8ja_</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="#">c3lorB_</a>	Alignment	not modelled	99.9	20	<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
37	<a href="#">d2cx4a1</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
38	<a href="#">c3drnB_</a>	Alignment	not modelled	99.9	35	<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
39	<a href="#">d1yexa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
40	<a href="#">c5epfA_</a>	Alignment	not modelled	99.9	35	<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
41	<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
42	<a href="#">c2ls5A_</a>	Alignment	not modelled	99.9	21	<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
43	<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
44	<a href="#">d1q98a_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
45	<a href="#">c2l5oA_</a>	Alignment	not modelled	99.9	22	<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
46	<a href="#">d1jfua_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
47	<a href="#">c3w6gP_</a>	Alignment	not modelled	99.9	22	<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
48	<a href="#">c2i81B_</a>	Alignment	not modelled	99.9	24	<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
49	<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 sulfolobus2 tokodaii
50	<a href="#">c2bmxB_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxidase c; <b>PDBTitle:</b> mycobacterium tuberculosis ahpc
51	<a href="#">c2xpdC_</a>	Alignment	not modelled	99.9	17	<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
52	<a href="#">c5zteA_</a>	Alignment	not modelled	99.9	27	<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
53	<a href="#">c3u5rG_</a>	Alignment	not modelled	99.9	28	<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
54	<a href="#">d1zyea1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like

						<b>Family:</b> Glutathione peroxidase-like
55	<a href="#">c2yzhD_</a>	Alignment	not modelled	99.9	16	<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
56	<a href="#">c4tr3A_</a>	Alignment	not modelled	99.9	16	<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
57	<a href="#">c2jszA_</a>	Alignment	not modelled	99.9	26	<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
58	<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
59	<a href="#">c3me8B_</a>	Alignment	not modelled	99.9	15	<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
60	<a href="#">c3lwaA_</a>	Alignment	not modelled	99.9	16	<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
61	<a href="#">c2c0dA_</a>	Alignment	not modelled	99.9	23	<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
62	<a href="#">d2b7ka1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
63	<a href="#">c2lrnA_</a>	Alignment	not modelled	99.9	20	<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.
64	<a href="#">c3kcmC_</a>	Alignment	not modelled	99.9	28	<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
65	<a href="#">d1psqa_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
66	<a href="#">c3gl3D_</a>	Alignment	not modelled	99.9	23	<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
67	<a href="#">d1lu4a_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
68	<a href="#">c3ha9A_</a>	Alignment	not modelled	99.9	17	<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
69	<a href="#">d2a4va1</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
70	<a href="#">d2cvba1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
71	<a href="#">c1zofB_</a>	Alignment	not modelled	99.9	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
72	<a href="#">c2h66G_</a>	Alignment	not modelled	99.9	23	<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
73	<a href="#">d1hd2a_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
74	<a href="#">c2p5qA_</a>	Alignment	not modelled	99.9	15	<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="#">d2b5xa1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
76	<a href="#">d1zofa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
77	<a href="#">c3hczA_</a>	Alignment	not modelled	99.9	14	<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.
78	<a href="#">d1qxha_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
79	<a href="#">c3hdcA_</a>	Alignment	not modelled	99.9	26	<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
80	<a href="#">c2ywiA_</a>	Alignment	not modelled	99.9	25	<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
						<b>PDB header:</b> structural genomics, unknown function

81	<a href="#">c3eurA</a>	Alignment	not modelled	99.9	13	<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
82	<a href="#">c3eytA</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 spoa0173; <b>PDBTitle:</b> crystal structure of thioredoxin-like superfamily protein spoa0173
83	<a href="#">c3cynC</a>	Alignment	not modelled	99.9	17	<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
84	<a href="#">d1wp0a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
85	<a href="#">c3ia1A</a>	Alignment	not modelled	99.9	24	<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
86	<a href="#">d1xzoa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
87	<a href="#">c4hdeA</a>	Alignment	not modelled	99.9	16	<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
88	<a href="#">c5k2jG</a>	Alignment	not modelled	99.9	14	<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
89	<a href="#">c2b7kD</a>	Alignment	not modelled	99.9	18	<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
90	<a href="#">c2obiA</a>	Alignment	not modelled	99.9	14	<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)
91	<a href="#">c3kh7A</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 the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
92	<a href="#">d1xvqa</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
93	<a href="#">c4evmA</a>	Alignment	not modelled	99.9	19	<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
94	<a href="#">c2v1mA</a>	Alignment	not modelled	99.9	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
95	<a href="#">c2rliA</a>	Alignment	not modelled	99.9	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
96	<a href="#">c3fw2A</a>	Alignment	not modelled	99.9	15	<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.
97	<a href="#">c4yodA</a>	Alignment	not modelled	99.9	13	<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
98	<a href="#">d2h01a1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
99	<a href="#">c3ewlA</a>	Alignment	not modelled	99.9	15	<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
100	<a href="#">c2p31B</a>	Alignment	not modelled	99.9	17	<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
101	<a href="#">d2f8aa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
102	<a href="#">d1zzoa1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
103	<a href="#">d1gp1a</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
104	<a href="#">c3fkfC</a>	Alignment	not modelled	99.9	23	<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
105	<a href="#">c3erwG</a>	Alignment	not modelled	99.9	20	<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
106	<a href="#">c3dwvB</a>	Alignment	not modelled	99.8	14	<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
107	<a href="#">c4txoB_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidodreductase/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="#">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)
109	<a href="#">c6n5uC_</a>	Alignment	not modelled	99.8	14	<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 scoi with copper bound
110	<a href="#">c2wfcD_</a>	Alignment	not modelled	99.8	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
111	<a href="#">c2xhfA_</a>	Alignment	not modelled	99.8	21	<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
112	<a href="#">c4f82A_</a>	Alignment	not modelled	99.8	16	<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
113	<a href="#">c2m72A_</a>	Alignment	not modelled	99.8	20	<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
114	<a href="#">c2lrtA_</a>	Alignment	not modelled	99.8	18	<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 bvu_1432 from bacteroides vulgatus
115	<a href="#">d2fy6a1</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="#">c2b1kA_</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 e. coli ccmg protein
117	<a href="#">c2k6vA_</a>	Alignment	not modelled	99.8	23	<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
118	<a href="#">c4fo5A_</a>	Alignment	not modelled	99.8	14	<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="#">c3umaC_</a>	Alignment	not modelled	99.8	16	<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
120	<a href="#">d1tp9a1</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like