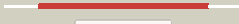



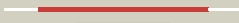
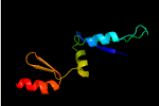









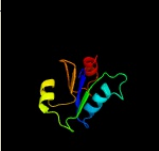












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0508 (-) _600101_600394
Date	Fri Jul 26 01:50:05 BST 2019
Unique Job ID	eb2eb12cdedc72f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1ttza_</a>	 Alignment		99.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
2	<a href="#">d1wjka_</a>	 Alignment		99.7	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
3	<a href="#">d1r7ha_</a>	 Alignment		99.7	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
4	<a href="#">d1h75a_</a>	 Alignment		99.7	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
5	<a href="#">c2fgxA_</a>	 Alignment		99.7	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
6	<a href="#">c3zija_</a>	 Alignment		99.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of the thioredoxin-like protein bc3987
7	<a href="#">c3znzA_</a>	 Alignment		99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
8	<a href="#">c3ic4A_</a>	 Alignment		99.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutaredoxin (grx-1); <b>PDBTitle:</b> the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
9	<a href="#">c2lqoA_</a>	 Alignment		99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative glutaredoxin rv3198.1/mt3292; <b>PDBTitle:</b> mrx1 reduced
10	<a href="#">c1nm3B_</a>	 Alignment		99.6	19	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> protein hi0572; <b>PDBTitle:</b> crystal structure of heamophilus influenza hybrid-prx5
11	<a href="#">c4tr1A_</a>	 Alignment		99.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glutaredoxin 3; <b>PDBTitle:</b> crystal structure of gsh-bound cgrx2/c15s

12	<a href="#">c3lgcA_</a>	Alignment		99.5	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 1; <b>PDBTitle:</b> crystal structure of glutaredoxin 1 from francisella tularensis
13	<a href="#">d1fova_</a>	Alignment		99.5	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
14	<a href="#">c2klxA_</a>	Alignment		99.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> solution structure of glutaredoxin from bartonella henselae str.2 houston
15	<a href="#">c2khpA_</a>	Alignment		99.5	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> solution structure of glutaredoxin from brucella melitensis
16	<a href="#">d1legoa_</a>	Alignment		99.5	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
17	<a href="#">c3qmxA_</a>	Alignment		99.5	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin a; <b>PDBTitle:</b> x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
18	<a href="#">d1nm3a1</a>	Alignment		99.4	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
19	<a href="#">c2mygA_</a>	Alignment		99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dithiol glutaredoxin 1; <b>PDBTitle:</b> solution structure of the dithiolic glutaredoxin 2-c-grx1 from the2 pathogen trypanosoma brucei brucei
20	<a href="#">c3h8qB_</a>	Alignment		99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 3; <b>PDBTitle:</b> crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
21	<a href="#">c2cq9A_</a>	Alignment	not modelled	99.3	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glrx2 protein; <b>PDBTitle:</b> solution structure of rsgi ruh-044, an n-terminal domain of2 glutaredoxin 2 from human cdna
22	<a href="#">c2e7pC_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
23	<a href="#">c4kjeA_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> atomic resolution structure of pfgrx1
24	<a href="#">c2ht9A_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-2; <b>PDBTitle:</b> the structure of dimeric human glutaredoxin 2
25	<a href="#">c3uiwB_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin 2; <b>PDBTitle:</b> zebrafish grx2 (apo)
26	<a href="#">c3fzaA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
27	<a href="#">c2mxnA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mono-cysteine glutaredoxin; <b>PDBTitle:</b> nmr structure of the mature form of trypanosoma brucei 1cgrx1
28	<a href="#">c5zvlB_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of wheat glutaredoxin
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c2m80A_</a>	Alignment	not modelled	99.3	15	<b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-8; <b>PDBTitle:</b> solution structure of yeast dithiol glutaredoxin grx8
30	<a href="#">c5y4uA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-3; <b>PDBTitle:</b> crystal structure of grx domain of grx3 from saccharomyces cerevisiae
31	<a href="#">c1ykaA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin ydhd; <b>PDBTitle:</b> solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
32	<a href="#">c2hzfA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
33	<a href="#">c5gtxA_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> buckwheat glutaredoxin; <b>PDBTitle:</b> crystal structure of mutated buckwheat glutaredoxin
34	<a href="#">d1jhba_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
35	<a href="#">c2ltkA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mono-cysteine glutaredoxin; <b>PDBTitle:</b> solution structure of a monomeric truncated mutant of trypanosoma2 brucei 1-c-grx1
36	<a href="#">c3d5jB_</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-2, mitochondrial; <b>PDBTitle:</b> structure of yeast grx2-c30s mutant with glutathionyl mixed disulfide
37	<a href="#">c4i2uA_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of the reduced glutaredoxin from chlorella2 sorokiniana t-89 in complex with glutathione
38	<a href="#">d1wika_</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
39	<a href="#">c2jadA_</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> yellow fluorescent protein glutaredoxin fusion protein; <b>PDBTitle:</b> yellow fluorescent protein - glutaredoxin fusion protein
40	<a href="#">c3c1sA_</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> crystal structure of grx1 in glutathionylated form
41	<a href="#">c3l4nA_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-6; <b>PDBTitle:</b> crystal structure of yeast monothiol glutaredoxin grx6
42	<a href="#">d1ktea_</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
43	<a href="#">c3ipzA_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-s14, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis monothiol glutaredoxin atrgxcp
44	<a href="#">c2jacA_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-1; <b>PDBTitle:</b> glutaredoxin grx1p c30s mutant from yeast
45	<a href="#">d1iloa_</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
46	<a href="#">c1zypB_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
47	<a href="#">c3gx8A_</a>	Alignment	not modelled	99.1	8	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-5, mitochondrial; <b>PDBTitle:</b> structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
48	<a href="#">d1hyua4</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
49	<a href="#">c3zywB_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-3; <b>PDBTitle:</b> crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)
50	<a href="#">d1nhoa_</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
51	<a href="#">c2wulB_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin related protein 5; <b>PDBTitle:</b> crystal structure of the human glutaredoxin 5 with bound glutathione2 in an fes cluster
52	<a href="#">d1abaa_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
53	<a href="#">d1t1va_</a>	Alignment	not modelled	99.0	9	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> SH3BGR (SH3-binding, glutamic acid-rich protein-like)
54	<a href="#">d1fo5a_</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
55	<a href="#">c1hyuA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf

56	<a href="#">c4mnnA</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin related protein; <b>PDBTitle:</b> the crystal structure of sso1120 from sulfolobus solfataricus
57	<a href="#">c5h29A</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase/glutathione-related protein; <b>PDBTitle:</b> crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583)
58	<a href="#">c2hlsB</a>	Alignment	not modelled	98.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein disulfide oxidoreductase; <b>PDBTitle:</b> the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
59	<a href="#">c2l6dA</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of desulfthioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
60	<a href="#">c2m46A</a>	Alignment	not modelled	98.6	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase, putative; <b>PDBTitle:</b> solution nmr structure of saci0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
61	<a href="#">d2axoa1</a>	Alignment	not modelled	98.6	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Atu2684-like
62	<a href="#">c2axoA</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu2684; <b>PDBTitle:</b> x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
63	<a href="#">c2kokA</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
64	<a href="#">d1j08a2</a>	Alignment	not modelled	98.6	7	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
65	<a href="#">d1a8la2</a>	Alignment	not modelled	98.5	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
66	<a href="#">d1zmaa1</a>	Alignment	not modelled	98.5	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
67	<a href="#">d1j08a1</a>	Alignment	not modelled	98.5	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
68	<a href="#">d1z9ha2</a>	Alignment	not modelled	98.5	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
69	<a href="#">c3d22A</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h-type; <b>PDBTitle:</b> crystal structure of a poplar thioredoxin h mutant, ptxrh4c61s
70	<a href="#">c2mu0A</a>	Alignment	not modelled	98.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> solution structure of a putative arsenate reductase from brucella2 melitensis. seattle structural genomics center for infectious disease3 target braba.00073.a
71	<a href="#">c2v1vA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h isoform 2.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state
72	<a href="#">c2ct6A</a>	Alignment	not modelled	98.4	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like <b>PDBTitle:</b> solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
73	<a href="#">c4i8bA</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from schistosoma japonicum
74	<a href="#">c2l57A</a>	Alignment	not modelled	98.4	12	<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 thioredoxin-like protein from2 clostridium perfringens
75	<a href="#">d1z3ea1</a>	Alignment	not modelled	98.4	25	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> ArsC-like
76	<a href="#">c2aytB</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-like protein; <b>PDBTitle:</b> the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
77	<a href="#">c3kp8A</a>	Alignment	not modelled	98.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vkorc1/thioredoxin domain protein; <b>PDBTitle:</b> the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
78	<a href="#">c2xbqB</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
79	<a href="#">d2ifqa1</a>	Alignment	not modelled	98.4	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
80	<a href="#">c2wz9A</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-3; <b>PDBTitle:</b> crystal structure of the thioredoxin domain of human txn12

81	<a href="#">d1oyja2</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
82	<a href="#">c6i1cB_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin f2; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii thioredoxin f2
83	<a href="#">c2vimA_</a>	Alignment	not modelled	98.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> x-ray structure of fasciola hepatica thioredoxin
84	<a href="#">c6g61A_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin o1, mitochondrial; <b>PDBTitle:</b> crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
85	<a href="#">c5e37A_</a>	Alignment	not modelled	98.3	13	<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
86	<a href="#">c4euyA_</a>	Alignment	not modelled	98.3	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 thioredoxin-like protein bce_0499 from bacillus2 cereus atcc 10987
87	<a href="#">d1k0ma2</a>	Alignment	not modelled	98.3	29	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
88	<a href="#">d1ep7a_</a>	Alignment	not modelled	98.3	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
89	<a href="#">c2voiA_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> leca thioredoxin; <b>PDBTitle:</b> crystal structure of ancestral thioredoxin relative to last eukaryotes2 common ancestor (leca) from the precambrian period
90	<a href="#">c1z9hB_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> membrane-associated prostaglandin e synthase-2; <b>PDBTitle:</b> microsomal prostaglandin e synthase type-2
91	<a href="#">d1xwaa_</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
92	<a href="#">d1gwca2</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
93	<a href="#">c3f0IA_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> arsenate reductase from vibrio cholerae.
94	<a href="#">d1syra_</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
95	<a href="#">d1a8la1</a>	Alignment	not modelled	98.3	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
96	<a href="#">c2diyA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein 2; <b>PDBTitle:</b> the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
97	<a href="#">c6ckpA_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a thioredoxin domain 2 from brucella melitensis2 at 1.15 angstrom resolution
98	<a href="#">c3p2aA_</a>	Alignment	not modelled	98.3	17	<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
99	<a href="#">c3p2aB_</a>	Alignment	not modelled	98.3	17	<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
100	<a href="#">c3hz4A_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
101	<a href="#">d1r26a_</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
102	<a href="#">d1ti3a_</a>	Alignment	not modelled	98.3	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
103	<a href="#">d1gh2a_</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
104	<a href="#">d1dbya_</a>	Alignment	not modelled	98.2	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
105	<a href="#">c2l5IA_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of thioredoxin from bacteroides vulgatus
106	<a href="#">c2oe0B_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin-3; <b>PDBTitle:</b> crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
107	<a href="#">d1xfla_</a>	Alignment	not modelled	98.2	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase

108	<a href="#">c5w1jA_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)
109	<a href="#">c2j23A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> immune protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
110	<a href="#">c3l78A_</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein spx; <b>PDBTitle:</b> the crystal structure of smu.1142c from streptococcus mutans ua159
111	<a href="#">c1u6tA_</a>	Alignment	not modelled	98.2	4	<b>PDB header:</b> protein binding, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sh3 domain-binding glutamic acid-rich-like <b>PDBTitle:</b> crystal structure of the human sh3 binding glutamic-rich2 protein like
112	<a href="#">c2pptA_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
113	<a href="#">d1g7oa2</a>	Alignment	not modelled	98.2	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
114	<a href="#">c2lrcA_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable thioredoxin; <b>PDBTitle:</b> structure of thioredoxin 2 from pseudomonas aeruginosa pao1 in its2 reduced form
115	<a href="#">c3hypB_</a>	Alignment	not modelled	98.2	18	<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
116	<a href="#">c5dbqA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of insect thioredoxin at 1.95 angstroms
117	<a href="#">c2aheA_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloride intracellular channel protein 4; <b>PDBTitle:</b> crystal structure of a soluble form of clic4. intercellular2 chloride ion channel
118	<a href="#">c4cw9A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> entamoeba histolytica thioredoxin c34s mutant
119	<a href="#">d1eema2</a>	Alignment	not modelled	98.2	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
120	<a href="#">c4kndA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin from anaeromyxobacter dehalogenans.