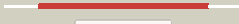



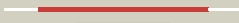







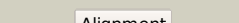











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3198A (- )_3571332_3571586
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	620104173d0b561f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lqoA_</a>	 Alignment		99.9	99	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutaredoxin rv3198.1/mt3292; <b>PDBTitle:</b> mrx1 reduced
2	<a href="#">c3znzA_</a>	 Alignment		99.7	24	<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
3	<a href="#">c3zizA_</a>	 Alignment		99.7	27	<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
4	<a href="#">c4tr1A_</a>	 Alignment		99.7	30	<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
5	<a href="#">d1r7ha_</a>	 Alignment		99.7	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
6	<a href="#">c3ic4A_</a>	 Alignment		99.7	21	<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
7	<a href="#">c3lqcA_</a>	 Alignment		99.7	31	<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
8	<a href="#">c3qmxA_</a>	 Alignment		99.7	25	<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
9	<a href="#">d1h75a_</a>	 Alignment		99.6	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
10	<a href="#">c2khpA_</a>	 Alignment		99.6	19	<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
11	<a href="#">d1fova_</a>	 Alignment		99.6	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase

12	<a href="#">c1nm3B_</a>	Alignment		99.6	20	<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
13	<a href="#">d1nm3a1</a>	Alignment		99.6	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
14	<a href="#">c2kixA_</a>	Alignment		99.5	18	<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="#">c2mygA_</a>	Alignment		99.5	16	<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
16	<a href="#">c2e7pC_</a>	Alignment		99.5	24	<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
17	<a href="#">c3fzaA_</a>	Alignment		99.5	18	<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
18	<a href="#">c2mxnA_</a>	Alignment		99.5	17	<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
19	<a href="#">c2ltkA_</a>	Alignment		99.5	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
20	<a href="#">c3uiwB_</a>	Alignment		99.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin 2; <b>PDBTitle:</b> zebrafish grx2 (apo)
21	<a href="#">c5y4uA_</a>	Alignment	not modelled	99.5	17	<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
22	<a href="#">d1wika_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
23	<a href="#">c3h8qB_</a>	Alignment	not modelled	99.5	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
24	<a href="#">c2ht9A_</a>	Alignment	not modelled	99.5	16	<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="#">c5zv1B_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> crystal structure of wheat glutarredoxin
26	<a href="#">c2cq9A_</a>	Alignment	not modelled	99.5	17	<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
27	<a href="#">c1ykaA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin ydhg; <b>PDBTitle:</b> solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
28	<a href="#">c5gtxA_</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> buckwheat glutaredoxin; <b>PDBTitle:</b> crystal structure of mutated buckwheat glutaredoxin
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c2m80A_</a>	Alignment	not modelled	99.4	17	<b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-8; <b>PDBTitle:</b> solution structure of yeast dithiol glutaredoxin grx8
30	<a href="#">c4kjeA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> atomic resolution structure of pfgrx1
31	<a href="#">c4i2uA_</a>	Alignment	not modelled	99.4	24	<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
32	<a href="#">c2hzfA_</a>	Alignment	not modelled	99.4	23	<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 and 2 reduced states show redox-correlated structural changes
33	<a href="#">d1legoa_</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
34	<a href="#">c2jadA_</a>	Alignment	not modelled	99.4	19	<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
35	<a href="#">d1abaa_</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
36	<a href="#">d1jhba_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
37	<a href="#">c2wulB_</a>	Alignment	not modelled	99.4	13	<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
38	<a href="#">c3ipzA_</a>	Alignment	not modelled	99.4	13	<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 atgrxcp
39	<a href="#">c3l4nA_</a>	Alignment	not modelled	99.3	19	<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
40	<a href="#">c3zywB_</a>	Alignment	not modelled	99.3	17	<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)
41	<a href="#">d1ktea_</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
42	<a href="#">c3d5jB_</a>	Alignment	not modelled	99.3	16	<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
43	<a href="#">c3gx8A_</a>	Alignment	not modelled	99.3	16	<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
44	<a href="#">c3c1sA_</a>	Alignment	not modelled	99.3	18	<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
45	<a href="#">c2jacA_</a>	Alignment	not modelled	99.3	18	<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
46	<a href="#">d1t1va_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> SH3BGR (SH3-binding, glutamic acid-rich protein-like)
47	<a href="#">c2fgxA_</a>	Alignment	not modelled	99.3	20	<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.
48	<a href="#">d1wjka_</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
49	<a href="#">d1g7oa2</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
50	<a href="#">c5e37A_</a>	Alignment	not modelled	99.2	17	<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
51	<a href="#">c2pptA_</a>	Alignment	not modelled	99.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
52	<a href="#">d1hyua4</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
53	<a href="#">d1nhoa_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
54	<a href="#">c2l6dA_</a>	Alignment	not modelled	99.1	25	<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
55	<a href="#">c4agsA_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol-dependent reductase 1; <b>PDBTitle:</b> leishmania tdr1 - a unique trimeric glutathione

						transferase
56	<a href="#">c1zypB</a>	Alignment	not modelled	99.0	21	<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
57	<a href="#">c2vlvA</a>	Alignment	not modelled	99.0	24	<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
58	<a href="#">d1ep7a</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
59	<a href="#">d1ttza</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
60	<a href="#">c4g10A</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase homolog; <b>PDBTitle:</b> ligg from sphingobium sp. syk-6 is related to the glutathione2 transferase omega class
61	<a href="#">d1fo5a</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
62	<a href="#">d1a8la2</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
63	<a href="#">d1j08a2</a>	Alignment	not modelled	99.0	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
64	<a href="#">c2wz9A</a>	Alignment	not modelled	98.9	18	<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
65	<a href="#">c2vm2C</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin h isoform 1.; <b>PDBTitle:</b> crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
66	<a href="#">d1syra</a>	Alignment	not modelled	98.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
67	<a href="#">c4kndA</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin from anaeromyxobacter dehalogenans.
68	<a href="#">d1xfla</a>	Alignment	not modelled	98.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
69	<a href="#">d1eema2</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
70	<a href="#">c4mnnA</a>	Alignment	not modelled	98.9	16	<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
71	<a href="#">c2lrcA</a>	Alignment	not modelled	98.9	22	<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
72	<a href="#">c3d22A</a>	Alignment	not modelled	98.9	16	<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
73	<a href="#">c5dbqA</a>	Alignment	not modelled	98.9	21	<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
74	<a href="#">c1w89E</a>	Alignment	not modelled	98.9	28	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of the reduced form of human thioredoxin 2
75	<a href="#">c2vimA</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> x-ray structure of fasciola hepatica thioredoxin
76	<a href="#">c2xbqB</a>	Alignment	not modelled	98.9	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
77	<a href="#">c2yoiA</a>	Alignment	not modelled	98.9	22	<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
78	<a href="#">c6bkvB</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from helicobacter pylori (strain g27)
79	<a href="#">d1gh2a</a>	Alignment	not modelled	98.9	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
80	<a href="#">c6i1cB</a>	Alignment	not modelled	98.9	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
81	<a href="#">d1ti3a</a>	Alignment	not modelled	98.9	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
82	<a href="#">d1xwaa</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like

						<b>Family:</b> Thioltransferase
83	<a href="#">c2diyA</a>	Alignment	not modelled	98.9	18	<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
84	<a href="#">c2oe0B</a>	Alignment	not modelled	98.9	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
85	<a href="#">c3hypB</a>	Alignment	not modelled	98.9	21	<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
86	<a href="#">c3p2aA</a>	Alignment	not modelled	98.9	22	<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
87	<a href="#">d1r26a</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
88	<a href="#">c6g61A</a>	Alignment	not modelled	98.9	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
89	<a href="#">c3p2aB</a>	Alignment	not modelled	98.9	22	<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
90	<a href="#">c3zzxB</a>	Alignment	not modelled	98.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystallographic structure of thioredoxin from litopenaeus vannamei
91	<a href="#">c4i8bA</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from schistosoma japonicum
92	<a href="#">d1dbya</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
93	<a href="#">c3ul3A</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
94	<a href="#">c3gnjD</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin domain protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
95	<a href="#">c3kp8A</a>	Alignment	not modelled	98.8	17	<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.
96	<a href="#">c6ibbB</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin 1,beta-1 adrenergic receptor; <b>PDBTitle:</b> activated turkey beta1 adrenoceptor with bound agonist formoterol and2 nanobody nb80
97	<a href="#">c2e0qA</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
98	<a href="#">c2nbsA</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> e_1r26; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for designed2 protein e_1r26
99	<a href="#">d2ifqa1</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
100	<a href="#">c2j23A</a>	Alignment	not modelled	98.8	25	<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
101	<a href="#">c2l5lA</a>	Alignment	not modelled	98.8	21	<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
102	<a href="#">c3qdnA</a>	Alignment	not modelled	98.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin protein; <b>PDBTitle:</b> putative thioredoxin protein from salmonella typhimurium
103	<a href="#">d1oyja2</a>	Alignment	not modelled	98.8	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
104	<a href="#">c6ckpA</a>	Alignment	not modelled	98.8	30	<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
105	<a href="#">c2l57A</a>	Alignment	not modelled	98.8	16	<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
106	<a href="#">c5jy5A</a>	Alignment	not modelled	98.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
107	<a href="#">c6j3gA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase; <b>PDBTitle:</b> crystal structure of an apo form of the glutathione s-transferase,2 csgst83044, of ceriporiopsis subvermispora
108	<a href="#">c1g7oA</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 2; <b>PDBTitle:</b> nmr solution structure of reduced e. coli glutaredoxin 2

109	<a href="#">c3cxgA_</a>	Alignment	not modelled	98.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin; <b>PDBTitle:</b> crystal structure of plasmodium falciparum thioredoxin, pfi0790w
110	<a href="#">d1fb6a_</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
111	<a href="#">c3hz4A_</a>	Alignment	not modelled	98.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
112	<a href="#">c2f51B_</a>	Alignment	not modelled	98.8	29	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of trichomonas vaginalis thioredoxin
113	<a href="#">d1gwca2</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
114	<a href="#">c4kf9A_</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione s-transferase protein; <b>PDBTitle:</b> crystal structure of a glutathione transferase family member from2 ralstonia solanacearum, target efi-501780, with bound gsh coordinated3 to a zinc ion, ordered active site
115	<a href="#">d1thxa_</a>	Alignment	not modelled	98.7	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
116	<a href="#">c2hlsB_</a>	Alignment	not modelled	98.7	19	<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
117	<a href="#">d1qgva_</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
118	<a href="#">c6esxC_</a>	Alignment	not modelled	98.7	26	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin 1; <b>PDBTitle:</b> caulobacter crescentus trx1
119	<a href="#">c4cw9A_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> entamoeba histolytica thioredoxin c34s mutant
120	<a href="#">c1u6tA_</a>	Alignment	not modelled	98.7	21	<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