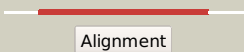

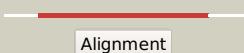

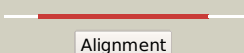

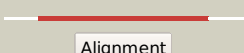





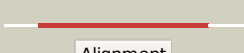

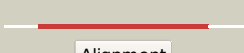


















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2466c (- )_2768271_2768894
Date	Wed Aug 7 12:50:09 BST 2019
Unique Job ID	68905e035da83252

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4nxiB_</a>			100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
2	<a href="#">c2imeA_</a>			100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
3	<a href="#">d1r4wa_</a>			100.0	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
4	<a href="#">c1yvxB_</a>			100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glutathione s-transferase kappa 1; <b>PDBTitle:</b> crystal structure of human kappa class glutathione transferase
5	<a href="#">c3fz5C_</a>			100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> possible 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
6	<a href="#">c5cohA_</a>			100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> frne protein; <b>PDBTitle:</b> crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
7	<a href="#">c3gl5A_</a>			100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative dsba oxidoreductase sco1869; <b>PDBTitle:</b> crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
8	<a href="#">c2in3A_</a>			100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
9	<a href="#">c5hfiA_</a>			99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein, cytosolic disulfide reductase <b>PDBTitle:</b> cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
10	<a href="#">c3kzqE_</a>			99.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E; <b>PDB Molecule:</b> putative uncharacterized protein vp2116; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
11	<a href="#">c6ghbB_</a>			99.9	17	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> upf0413 protein gk0824; <b>PDBTitle:</b> crystal structure of spx in complex with yjbh (oxidized)

12	<a href="#">c4pwoA</a>	Alignment		99.9	19	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> dsba; <b>PDBTitle:</b> crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae
13	<a href="#">c4jr6A</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible conserved membrane or secreted protein; <b>PDBTitle:</b> crystal structure of dsba from mycobacterium tuberculosis (reduced)
14	<a href="#">d1beda</a>	Alignment		99.9	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
15	<a href="#">c6bo0A</a>	Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mdba protein; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchotii
16	<a href="#">c4z7xA</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mdba; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from actinomyces oris.
17	<a href="#">c4p3yB</a>	Alignment		99.9	16	<b>PDB header:</b> translation/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
18	<a href="#">c5c00B</a>	Alignment		99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> mdba protein; <b>PDBTitle:</b> mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 diphtheriae
19	<a href="#">c3hd5A</a>	Alignment		99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
20	<a href="#">c4jrrC</a>	Alignment		99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of disulfide bond oxidoreductase dsba1 from2 legionella pneumophila
21	<a href="#">c3gn3B</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative protein-disulfide isomerase; <b>PDBTitle:</b> crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
22	<a href="#">c3h93A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba
23	<a href="#">c3bciA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond protein a; <b>PDBTitle:</b> crystal structure of staphylococcus aureus dsba
24	<a href="#">c3dvwA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of reduced dsba1 from neisseria2 meningitidis
25	<a href="#">c4k2dA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> crystal structure of burkholderia pseudomallei dsba
26	<a href="#">c3gykC</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 27kda outer membrane protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
27	<a href="#">c6dxC</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of dsba disulfide2 interchange protein from klebsiella pneumoniae.
28	<a href="#">c2remB</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase dsba from xylella fastidiosa
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3l9vE</a>	Alignment	not modelled	99.8	15	<b>Chain:</b> E: <b>PDB Molecule:</b> putative thiol-disulfide isomerase or thioredoxin; <b>PDBTitle:</b> crystal structure of salmonella enterica serovar typhimurium srga
30	<a href="#">c3ghaA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond formation protein d; <b>PDBTitle:</b> crystal structure of etda-treated bdbd (reduced)
31	<a href="#">c4od7A</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein; <b>PDBTitle:</b> complex structure of proteus mirabilis dsba (c30s) with a non-2 covalently bound peptide pwatcds
32	<a href="#">c3gmfA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-disulfide isomerase; <b>PDBTitle:</b> crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
33	<a href="#">c6eezC</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> dsba-like disulfide oxidoreductase; <b>PDBTitle:</b> crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipientis
34	<a href="#">c3c7mB</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba-like; <b>PDBTitle:</b> crystal structure of reduced dsbl
35	<a href="#">d1fvka</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
36	<a href="#">c2znmA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> oxidoreductase nmdbas3 from neisseria meningitidis
37	<a href="#">c3f4tA</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
38	<a href="#">c4xvwK</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> K: <b>PDB Molecule:</b> dsba-like protein; <b>PDBTitle:</b> crystal structure of proteus mirabilis scsc in a compact conformation
39	<a href="#">c4gxzB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> suppression of copper sensitivity protein; <b>PDBTitle:</b> crystal structure of a periplasmic thioredoxin-like protein from2 salmonella enterica serovar typhimurium
40	<a href="#">c5kbcA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dsba; <b>PDBTitle:</b> crystal structure of chlamydia trachomatis dsba
41	<a href="#">c4n30A</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide isomerase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba2
42	<a href="#">c3feuA</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
43	<a href="#">d1z6ma1</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
44	<a href="#">d1v58a1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
45	<a href="#">d1eeja1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
46	<a href="#">c1v57A</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbg; <b>PDBTitle:</b> crystal structure of the disulfide bond isomerase dsbg
47	<a href="#">c1jzdA</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> dsbc-dsbdalpha complex
48	<a href="#">d1t3ba1</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbC/DsbG C-terminal domain-like
49	<a href="#">c4npbA</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> protein disulfide isomerase ii; <b>PDBTitle:</b> the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
50	<a href="#">c1t3bA</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbc; <b>PDBTitle:</b> x-ray structure of dsbc from haemophilus influenzae
51	<a href="#">c3gv1A</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide interchange protein; <b>PDBTitle:</b> crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
52	<a href="#">c4ml1D</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> dsbp; <b>PDBTitle:</b> disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
53	<a href="#">d1un2a</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
54	<a href="#">c5h29A</a>	Alignment	not modelled	97.7	12	<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) <b>PDB header:</b> oxidoreductase

55	<a href="#">c1zypB</a>	Alignment	not modelled	95.1	19	<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
56	<a href="#">d1j08a1</a>	Alignment	not modelled	94.6	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
57	<a href="#">c2ht9A</a>	Alignment	not modelled	94.0	31	<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
58	<a href="#">c5e37A</a>	Alignment	not modelled	93.8	20	<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
59	<a href="#">c4kjeA</a>	Alignment	not modelled	92.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> atomic resolution structure of pfgrx1
60	<a href="#">d1hyua4</a>	Alignment	not modelled	91.4	7	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
61	<a href="#">c4mnnA</a>	Alignment	not modelled	90.2	18	<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
62	<a href="#">d1wjka</a>	Alignment	not modelled	87.8	10	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
63	<a href="#">d2trcp</a>	Alignment	not modelled	87.2	9	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Phosducin
64	<a href="#">c3nznA</a>	Alignment	not modelled	87.1	14	<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
65	<a href="#">c3zija</a>	Alignment	not modelled	86.5	18	<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
66	<a href="#">d1zmaa1</a>	Alignment	not modelled	86.0	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
67	<a href="#">d1nhoa</a>	Alignment	not modelled	86.0	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
68	<a href="#">d1a8la1</a>	Alignment	not modelled	85.4	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
69	<a href="#">c2l5IA</a>	Alignment	not modelled	84.9	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
70	<a href="#">c2fgxA</a>	Alignment	not modelled	84.8	10	<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.
71	<a href="#">d1v9wa</a>	Alignment	not modelled	84.5	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Txn15-like
72	<a href="#">d1j08a2</a>	Alignment	not modelled	84.4	20	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
73	<a href="#">c4kndA</a>	Alignment	not modelled	84.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> thioredoxin from anaeromyxobacter dehalogenans.
74	<a href="#">c2dbcA</a>	Alignment	not modelled	83.5	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> unnamed protein product; <b>PDBTitle:</b> solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
75	<a href="#">c3p2aB</a>	Alignment	not modelled	83.0	29	<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
76	<a href="#">c3kp8A</a>	Alignment	not modelled	82.7	23	<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.
77	<a href="#">c2pptA</a>	Alignment	not modelled	82.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
78	<a href="#">c2qsiB</a>	Alignment	not modelled	82.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
79	<a href="#">d1a8la2</a>	Alignment	not modelled	81.4	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
80	<a href="#">d1a0rp</a>	Alignment	not modelled	81.1	9	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Phosducin
81	<a href="#">d2axoa1</a>	Alignment	not modelled	81.0	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like

						Family:Atu2684-like
82	<a href="#">c4tr3A_</a>	Alignment	not modelled	80.8	13	<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
83	<a href="#">d1woua_</a>	Alignment	not modelled	80.1	19	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> TxnI5-like
84	<a href="#">c3emxB_</a>	Alignment	not modelled	80.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from aeropyrum pernix
85	<a href="#">c4agsA_</a>	Alignment	not modelled	79.9	15	<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
86	<a href="#">d1iloa_</a>	Alignment	not modelled	79.9	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
87	<a href="#">c1nm3B_</a>	Alignment	not modelled	79.8	30	<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
88	<a href="#">d1fova_</a>	Alignment	not modelled	79.7	8	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
89	<a href="#">c3ul3A_</a>	Alignment	not modelled	79.6	13	<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
90	<a href="#">c5nymA_</a>	Alignment	not modelled	79.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein 2.1; <b>PDBTitle:</b> crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state
91	<a href="#">c1b9xC_</a>	Alignment	not modelled	79.1	9	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein (phosducin); <b>PDBTitle:</b> structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
92	<a href="#">d1abaa_</a>	Alignment	not modelled	78.8	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
93	<a href="#">c2i4aA_</a>	Alignment	not modelled	78.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from the acidophile acetobacter aceti
94	<a href="#">c3qmxA_</a>	Alignment	not modelled	78.3	9	<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
95	<a href="#">c2lrcA_</a>	Alignment	not modelled	78.2	13	<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
96	<a href="#">c6ib1B_</a>	Alignment	not modelled	77.8	14	<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="#">c3lgcA_</a>	Alignment	not modelled	77.5	10	<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
98	<a href="#">c3p2aA_</a>	Alignment	not modelled	77.2	29	<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="#">d1knga_</a>	Alignment	not modelled	76.9	16	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
100	<a href="#">c4euyA_</a>	Alignment	not modelled	76.3	17	<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
101	<a href="#">c2l6dA_</a>	Alignment	not modelled	75.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
102	<a href="#">d1legoa_</a>	Alignment	not modelled	75.6	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
103	<a href="#">c3hz4A_</a>	Alignment	not modelled	75.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
104	<a href="#">c2axoA_</a>	Alignment	not modelled	75.3	15	<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.
105	<a href="#">d1z3ea1</a>	Alignment	not modelled	75.3	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> ArsC-like
106	<a href="#">d1h75a_</a>	Alignment	not modelled	75.0	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
107	<a href="#">d1eema2</a>	Alignment	not modelled	74.4	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain

108	<a href="#">c3vfiA_</a>	Alignment	not modelled	74.1	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a metagenomic thioredoxin
109	<a href="#">d1fo5a_</a>	Alignment	not modelled	73.7	24	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
110	<a href="#">c1yy7A_</a>	Alignment	not modelled	72.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stringent starvation protein a; <b>PDBTitle:</b> crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor
111	<a href="#">c2ywiA_</a>	Alignment	not modelled	72.6	13	<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
112	<a href="#">c3qdnA_</a>	Alignment	not modelled	72.6	10	<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
113	<a href="#">c5y1aA_</a>	Alignment	not modelled	72.2	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> 35 kda hemin binding protein; <b>PDBTitle:</b> hbp35 of porphyromonas gingivalis
114	<a href="#">c4ri7A_</a>	Alignment	not modelled	72.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phi class glutathione transferase gstf1; <b>PDBTitle:</b> crystal structure of poplar glutathione transferase f1 mutant ser 132 cys
115	<a href="#">c6bkvB_</a>	Alignment	not modelled	71.8	18	<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)
116	<a href="#">d1r7ha_</a>	Alignment	not modelled	71.7	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
117	<a href="#">d1nm3a1</a>	Alignment	not modelled	71.1	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
118	<a href="#">d1r5aa2</a>	Alignment	not modelled	70.8	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
119	<a href="#">c2mygA_</a>	Alignment	not modelled	70.6	9	<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
120	<a href="#">c3ic4A_</a>	Alignment	not modelled	70.6	16	<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