



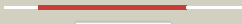



















Phyre2

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Description	RVBD2286c (-) _2558887_2559579
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	df6dca427c99d6cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nxiB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
2	c1yzxB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase kappa 1; PDBTitle: crystal structure of human kappa class glutathione transferase
3	d1r4wa_	 Alignment		100.0	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
4	c2imeA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
5	c3fz5C_	 Alignment		100.0	19	PDB header: isomerase Chain: C: PDB Molecule: possible 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: crystal structure of possible 2-hydroxychromene-2-carboxylate2 isomerase from rhodobacter sphaeroides
6	c5cohA_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: frne protein; PDBTitle: crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
7	c2in3A_	 Alignment		99.9	14	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
8	c3kzqE_	 Alignment		99.9	16	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: putative uncharacterized protein vp2116; PDBTitle: the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
9	c3gl5A_	 Alignment		99.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dsba oxidoreductase sco1869; PDBTitle: crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
10	c6ghbB_	 Alignment		99.9	15	PDB header: protein binding Chain: B: PDB Molecule: upf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
11	c5hfiA_	 Alignment		99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein, cytosolic disulfide reductase PDBTitle: cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh

12	d1beda_	Alignment		99.9	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
13	c4pwoA_	Alignment		99.9	15	PDB header: structural genomics Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae
14	c4p3yB_	Alignment		99.8	13	PDB header: translation/oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
15	c4z7xA_	Alignment		99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: mdba; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from actinomyces oris.
16	c3hd5A_	Alignment		99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
17	c4jr6A_	Alignment		99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: possible conserved membrane or secreted protein; PDBTitle: crystal structure of dsba from mycobacterium tuberculosis (reduced)
18	c3dvwA_	Alignment		99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis
19	c4k2dA_	Alignment		99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of burkholderia pseudomallei dsba
20	c3bciA_	Alignment		99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond protein a; PDBTitle: crystal structure of staphylococcus aureus dsba
21	c3h93A_	Alignment	not modelled	99.8	17	PDB header: transcription regulator Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of pseudomonas aeruginosa dsba
22	c4jrrC_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of disulfide bond oxidoreductase dsba1 from2 legionella pneumophila
23	c2remB_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: disulfide oxidoreductase; PDBTitle: crystal structure of oxidoreductase dsba from xylella fastidiosa
24	c3ghaA_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein d; PDBTitle: crystal structure of etda-treated bdbd (reduced)
25	c3l9vE_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
26	c3gmfA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-disulfide isomerase; PDBTitle: crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
27	c3gykC_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C: PDB Molecule: 27kda outer membrane protein; PDBTitle: the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
28	c3gn3B_	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative protein-disulfide isomerase; PDBTitle: crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.

29	c6dxnC	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: 1.95 angstrom resolution crystal structure of dsba disulfide2 interchange protein from klebsiella pneumoniae.
30	c4od7A	Alignment	not modelled	99.8	17	PDB header: oxidoreductase/peptide Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: complex structure of proteus mirabilis dsba (c30s) with a non-2 covalently bound peptide pwatcds
31	c6eezC	Alignment	not modelled	99.8	10	PDB header: isomerase Chain: C: PDB Molecule: dsba-like thiol-disulfide oxidoreductase; PDBTitle: crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipientis
32	c2znmA	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: oxidoreductase nmdsba3 from neisseria meningitidis
33	c3c7mB	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
34	c5c00B	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 diphtheriae
35	c6bo0A	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchotii
36	c3f4tA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
37	c4gxzB	Alignment	not modelled	99.7	15	PDB header: isomerase Chain: B: PDB Molecule: suppression of copper sensitivity protein; PDBTitle: crystal structure of a periplasmic thioredoxin-like protein from2 salmonella enterica serovar typhimurium
38	c5kbcA	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of chlamydia trachomatis dsba
39	c4xvwK	Alignment	not modelled	99.7	11	PDB header: isomerase Chain: K: PDB Molecule: dsba-like protein; PDBTitle: crystal structure of proteus mirabilis scsc in a compact conformation
40	d1fvka	Alignment	not modelled	99.7	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsBA-like
41	c3feuA	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
42	c4n30A	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein disulfide isomerase; PDBTitle: crystal structure of pseudomonas aeruginosa dsba2
43	d1z6ma1	Alignment	not modelled	99.6	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsBA-like
44	d1v58a1	Alignment	not modelled	99.3	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
45	c1v57A	Alignment	not modelled	99.3	16	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
46	d1eeja1	Alignment	not modelled	99.3	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
47	c4npbA	Alignment	not modelled	99.2	18	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
48	d1t3ba1	Alignment	not modelled	99.2	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
49	c1jzdA	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
50	c1t3bA	Alignment	not modelled	99.2	21	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
51	c3gv1A	Alignment	not modelled	99.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
52	d1un2a	Alignment	not modelled	99.0	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsBA-like
53	c4ml1D	Alignment	not modelled	98.9	16	PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
54	c5h29A	Alignment	not modelled	97.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase/glutathione-related protein; PDBTitle: crystal structure of the ntd_n/c domain of alkylhydroperoxide2 reductase ahpf from enterococcus faecalis (v583)

55	d1nhoa_	Alignment	not modelled	96.4	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
56	d1iloa_	Alignment	not modelled	96.3	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
57	d1j08a1	Alignment	not modelled	95.8	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
58	d1a8la1	Alignment	not modelled	95.1	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
59	c1zypB_	Alignment	not modelled	94.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
60	c3emxB_	Alignment	not modelled	93.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
61	c3zija_	Alignment	not modelled	90.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of the thioredoxin-like protein bc3987
62	c4mnnA_	Alignment	not modelled	90.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin related protein; PDBTitle: the crystal structure of sso1120 from sulfolobus solfataricus
63	c4tr1A_	Alignment	not modelled	88.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
64	d1k0da2	Alignment	not modelled	88.4	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
65	d1zmaa1	Alignment	not modelled	88.3	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
66	d1hyua4	Alignment	not modelled	88.1	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
67	d1h75a_	Alignment	not modelled	87.1	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
68	c2khpA_	Alignment	not modelled	85.0	21	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from brucella melitensis
69	c2kxA_	Alignment	not modelled	84.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from bartonella henselae str.2 houston
70	c2I57A_	Alignment	not modelled	84.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an uncharacterized thioredoxin-like protein from2 clostridium perfringens
71	c3nznA_	Alignment	not modelled	83.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin; PDBTitle: the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
72	d1legoa_	Alignment	not modelled	83.2	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
73	d1nm3a1	Alignment	not modelled	82.4	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
74	c4ivfH_	Alignment	not modelled	81.8	23	PDB header: transferase Chain: H: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of glutathione transferase homolog from lodderomyces2 elongisporus, target efi-501753, with two gsh per subunit
75	c2fgxA_	Alignment	not modelled	81.1	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
76	d1k0dd2	Alignment	not modelled	80.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
77	c1ljrB_	Alignment	not modelled	80.5	17	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: glutathione transferase (hgst t2-2) from human
78	d1j08a2	Alignment	not modelled	79.2	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
79	d1fo5a_	Alignment	not modelled	78.4	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
80	c4agsA_	Alignment	not modelled	77.8	17	PDB header: transferase Chain: A: PDB Molecule: thiol-dependent reductase 1; PDBTitle: leishmania tdr1 - a unique trimeric glutathione transferase
81	d1r7ha_	Alignment	not modelled	77.5	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like

						Family:Thioltransferase
82	c1k0dB_	Alignment	not modelled	77.3	14	PDB header: gene regulation Chain: B: PDB Molecule: ure2 protein; PDBTitle: ure2p in complex with glutathione
83	c3lqcA_	Alignment	not modelled	77.1	18	PDB header: unknown function Chain: A: PDB Molecule: glutaredoxin 1; PDBTitle: crystal structure of glutaredoxin 1 from francisella tularensis
84	d1v9wa_	Alignment	not modelled	77.0	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Txn15-like
85	c3vk9C_	Alignment	not modelled	76.9	22	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase delta; PDBTitle: crystal structure of delta-class glutathione transferase from silkworm
86	c2lqoA_	Alignment	not modelled	76.4	4	PDB header: oxidoreductase Chain: A: PDB Molecule: putative glutaredoxin rv3198.1/mt3292; PDBTitle: mrx1 reduced
87	d1r5aa2	Alignment	not modelled	76.2	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
88	c3kp8A_	Alignment	not modelled	75.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: svkorc1/thioredoxin domain protein; PDBTitle: the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
89	d1gwca2	Alignment	not modelled	73.9	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
90	c3qmxA_	Alignment	not modelled	73.9	12	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
91	c2yv7A_	Alignment	not modelled	73.8	8	PDB header: metal transport Chain: A: PDB Molecule: cg10997-pa; PDBTitle: crystal structure of the clic homolog from drosophila2 melanogaster
92	c1nm3B_	Alignment	not modelled	73.7	22	PDB header: electron transport Chain: B: PDB Molecule: protein hi0572; PDBTitle: crystal structure of heamophilus influenza hybrid-prx5
93	c6cckA_	Alignment	not modelled	73.5	8	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of a thioredoxin domain 2 from brucella melitensis2 at 1.15 angstrom resolution
94	c6bkbB_	Alignment	not modelled	73.3	11	PDB header: electron transport Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from helicobacter pylori (strain g27)
95	c5zfgB_	Alignment	not modelled	73.1	11	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a diazinon-metabolizing glutathione s-transferase2 in the silkworm, bombyx mori
96	d1z9ha2	Alignment	not modelled	72.8	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
97	c5e37A_	Alignment	not modelled	72.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ref-hand domain-containing thioredoxin; PDBTitle: redox protein from chlamydomonas reinhardtii
98	d1ljra2	Alignment	not modelled	72.6	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
99	c2i4aA_	Alignment	not modelled	72.6	3	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from the acidophile acetobacter aceti
100	d2trcp_	Alignment	not modelled	72.4	6	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin
101	c1oyjC_	Alignment	not modelled	72.0	17	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
102	c1eemA_	Alignment	not modelled	71.8	26	PDB header: transferase Chain: A: PDB Molecule: glutathione-s-transferase; PDBTitle: glutathione transferase from homo sapiens
103	c3h8qB_	Alignment	not modelled	71.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 3; PDBTitle: crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
104	d1a8la2	Alignment	not modelled	70.9	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
105	c3ic4A_	Alignment	not modelled	70.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin (grx-1); PDBTitle: the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
106	d1woua_	Alignment	not modelled	70.3	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Txn15-like
107	c1x5cA_	Alignment	not modelled	70.3	11	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase
						Fold: Thioredoxin fold

108	d1hyua3	Alignment	not modelled	69.8	24	Superfamily: Thioredoxin-like Family: PDI-like
109	c2mygA_	Alignment	not modelled	69.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dithiol glutaredoxin 1; PDBTitle: solution structure of the dithiolic glutaredoxin 2-c-grx1 from the2 pathogen trypanosoma brucei brucei
110	c1v2aD_	Alignment	not modelled	69.3	21	PDB header: transferase Chain: D: PDB Molecule: glutathione transferase gst1-6; PDBTitle: glutathione s-transferase 1-6 from anopheles dirus species b
111	d1eema2	Alignment	not modelled	68.8	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
112	d1fova_	Alignment	not modelled	68.6	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
113	d1a0rp_	Alignment	not modelled	68.3	7	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin
114	c2m46A_	Alignment	not modelled	68.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of saci0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
115	d1oyja2	Alignment	not modelled	67.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
116	c1b9xC_	Alignment	not modelled	67.7	7	PDB header: signaling protein Chain: C: PDB Molecule: protein (phosducin); PDBTitle: structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
117	d1gnwa2	Alignment	not modelled	67.6	6	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
118	c4ri7A_	Alignment	not modelled	67.2	17	PDB header: transferase Chain: A: PDB Molecule: phi class glutathione transferase gstf1; PDBTitle: crystal structure of poplar glutathione transferase f1 mutant ser 132 cys
119	d1z3ea1	Alignment	not modelled	67.2	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
120	c6ghfA_	Alignment	not modelled	67.1	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: pvgmgstug; PDBTitle: crystal structure of a gst variant