Phyre2

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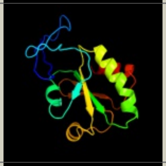
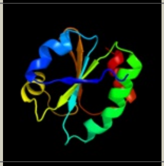
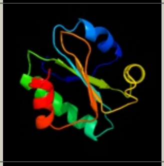
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p2aB_	Alignment		100.0	76	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
2	c2pptA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
3	c3p2aA_	Alignment		100.0	76	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
4	c3dxbE_	Alignment		99.9	38	**PDB header:**splicing, transcription **Chain:** E: **PDB Molecule:**thioredoxin n-terminally fused to puf60(uhm); **PDBTitle:** structure of the uhm domain of puf60 fused to thioredoxin
5	c3hz4A_	Alignment		99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
6	d1dbya_	Alignment		99.9	43	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
7	c3tcoA_	Alignment		99.9	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
8	c3qdnA_	Alignment		99.9	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
9	c2yzuA_	Alignment		99.9	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
10	c2vocA_	Alignment		99.9	34	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate
11	d2trxa_	Alignment		99.9	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

12	c2o7kA_	Alignment		99.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
13	c2i4aA_	Alignment		99.9	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
14	d1thxa_	Alignment		99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
15	d1nw2a_	Alignment		99.9	39	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c2l5lA_	Alignment		99.9	42	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
17	d1fb6a_	Alignment		99.9	39	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
18	c3gnjD_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
19	c2r2jA_	Alignment		99.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 4; **PDBTitle:** crystal structure of human erp44
20	c1t00A_	Alignment		99.9	37	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
21	c2e0qA_	Alignment	not modelled	99.9	36	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
22	c2i1uA_	Alignment	not modelled	99.9	36	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
23	d1ep7a_	Alignment	not modelled	99.9	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
24	c1w89E_	Alignment	not modelled	99.9	29	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
25	c3apoA_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
26	c1x5dA_	Alignment	not modelled	99.9	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
27	d1xwaa_	Alignment	not modelled	99.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	c2l6dA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
						Fold: Thioredoxin fold

29	d1f9ma_	Alignment	not modelled	99.9	30	**Superfamily:**Thioredoxin-like **Family:**Thioltransferase
30	c3hypB_	Alignment	not modelled	99.9	36	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
31	d1xfla_	Alignment	not modelled	99.9	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
32	c3f8uA_	Alignment	not modelled	99.9	26	**PDB header:**immune system/isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3erp57; **PDBTitle:** tapasin/erp57 heterodimer
33	c2albA_	Alignment	not modelled	99.9	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57
34	d1m7ta_	Alignment	not modelled	99.9	34	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
35	c2b5eA_	Alignment	not modelled	99.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of yeast protein disulfide isomerase
36	c1a8yA_	Alignment	not modelled	99.9	18	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**calsequestrin; **PDBTitle:** crystal structure of calsequestrin from rabbit skeletal muscle2 sarcoplasmic reticulum at 2.4 a resolution
37	c2vafA_	Alignment	not modelled	99.9	13	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**calsequestrin-2; **PDBTitle:** crystal structure of human cardiac calsequestrin
38	d1r26a_	Alignment	not modelled	99.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
39	d1oaza_	Alignment	not modelled	99.9	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
40	d1syra_	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
41	c2wz9A_	Alignment	not modelled	99.9	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
42	c3ed3A_	Alignment	not modelled	99.9	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase mpd1; **PDBTitle:** crystal structure of the yeast dithiol/disulfide2 oxidoreductase mpd1p
43	c2j23A_	Alignment	not modelled	99.9	35	**PDB header:**immune protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
44	d1a8la2	Alignment	not modelled	99.9	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
45	c2vlvA_	Alignment	not modelled	99.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
46	c3d22A_	Alignment	not modelled	99.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
47	d1ti3a_	Alignment	not modelled	99.9	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
48	c1sjiA_	Alignment	not modelled	99.9	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsequestrin, cardiac muscle isoform; **PDBTitle:** comparing skeletal and cardiac calsequestrin structures and2 their calcium binding: a proposed mechanism for coupled3 calcium binding and protein polymerization
49	d1j08a2	Alignment	not modelled	99.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
50	d1gh2a_	Alignment	not modelled	99.9	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
51	c3ul3A_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
52	c2diyA_	Alignment	not modelled	99.9	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-like protein 2
53	c1v98A_	Alignment	not modelled	99.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
54	d1qgva_	Alignment	not modelled	99.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
55	c2dizA_	Alignment	not modelled	99.9	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 5; **PDBTitle:** the solution structure of the third thioredoxin domain of2

						human thioredoxin domain-containing protein 5
56	c3emxB_	Alignment	not modelled	99.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
57	c3apsA_	Alignment	not modelled	99.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of trx4 domain of erdj5
58	c2xbqB_	Alignment	not modelled	99.9	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
59	c2dj1A_	Alignment	not modelled	99.9	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4
60	c2dmlA_	Alignment	not modelled	99.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
61	c2oe0B_	Alignment	not modelled	99.9	26	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
62	c2vimA_	Alignment	not modelled	99.9	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
63	d2b5ea4	Alignment	not modelled	99.9	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
64	c2vm2C_	Alignment	not modelled	99.9	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
65	d2ifqa1	Alignment	not modelled	99.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
66	d1a8ya1	Alignment	not modelled	99.9	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
67	c2dj0A_	Alignment	not modelled	99.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-related transmembrane protein 2; **PDBTitle:** the solution structure of the thioredoxin domain of human2 thioredoxin-related transmembrane protein 2
68	c1xbsA_	Alignment	not modelled	99.9	20	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
69	c2dj2A_	Alignment	not modelled	99.9	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the second thioredoxin domain of2 mouse protein disulfide-isomerase a4
70	d1meka_	Alignment	not modelled	99.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
71	c2qc7A_	Alignment	not modelled	99.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmic reticulum protein erp29; **PDBTitle:** crystal structure of the protein-disulfide isomerase related chaperone2 erp29
72	c1x5eA_	Alignment	not modelled	99.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain containing protein 1; **PDBTitle:** the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
73	d1zmaa1	Alignment	not modelled	99.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
74	c1x5cA_	Alignment	not modelled	99.8	23	**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
75	c2qsiB_	Alignment	not modelled	99.8	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
76	c2i9hA_	Alignment	not modelled	99.8	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
77	c2f51B_	Alignment	not modelled	99.8	24	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
78	d1g7ea_	Alignment	not modelled	99.8	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
79	c3h79A_	Alignment	not modelled	99.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein; **PDBTitle:** crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
80	c2l57A_	Alignment	not modelled	99.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
81	c2dj3A_	Alignment	not modelled	99.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4;

81	c2dj3A_	Alignment	not modelled	99.8	23	**PDBTitle:** the solution structure of the third thioredoxin domain of2 mouse protein disulfide-isomerase a4
82	c3idvA_	Alignment	not modelled	99.8	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** crystal structure of the a0a fragment of erp72
83	c2dbcA_	Alignment	not modelled	99.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
84	d2b5ea1	Alignment	not modelled	99.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
85	c1ovnA_	Alignment	not modelled	99.8	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**windbeutel; **PDBTitle:** crystal structure and functional analysis of drosophila2 wind-- a pdi-related protein
86	d2c0ga2	Alignment	not modelled	99.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
87	c3apqB_	Alignment	not modelled	99.8	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
88	c3dmlA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
89	d1fo5a_	Alignment	not modelled	99.8	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	d2hfda1	Alignment	not modelled	99.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
91	c2kucA_	Alignment	not modelled	99.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
92	d2djja1	Alignment	not modelled	99.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
93	c3cxgA_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
94	c3d6iB_	Alignment	not modelled	99.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
95	d1a8la1	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
96	c2dmmA_	Alignment	not modelled	99.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** the solution structure of the second thioredoxin domain of2 human protein disulfide-isomerase a3
97	c1b9xC_	Alignment	not modelled	99.8	25	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**protein (phosducin); **PDBTitle:** structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
98	c3uemA_	Alignment	not modelled	99.8	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** crystal structure of human pdi bb'a' domains
99	c1j08A_	Alignment	not modelled	99.8	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
100	d1j08a1	Alignment	not modelled	99.8	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
101	c3kp8A_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.
102	d2fwha1	Alignment	not modelled	99.7	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
103	d1nhoa_	Alignment	not modelled	99.7	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
104	d2trcp_	Alignment	not modelled	99.7	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
105	d1a0rp_	Alignment	not modelled	99.7	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
106	d1v9wa_	Alignment	not modelled	99.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
107	d1woua_	Alignment	not modelled	99.7	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c

108	c3f9uA_	Alignment	not modelled	99.7	17	biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
109	c2hlsB_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
110	c2aytB_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
111	d1z5ye1	Alignment	not modelled	99.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
112	c2hyxA_	Alignment	not modelled	99.7	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
113	c2fgxA_	Alignment	not modelled	99.7	9	**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.
114	c3g9bA_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
115	c1zypB_	Alignment	not modelled	99.6	10	**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
116	c3fk8A_	Alignment	not modelled	99.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
117	c2ju5A_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
118	d1hyua4	Alignment	not modelled	99.6	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
119	d2b5xa1	Alignment	not modelled	99.6	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
120	c1senA_	Alignment	not modelled	99.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881