



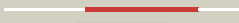







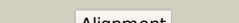











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1084 (-) _1207641_1209662
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	c2886363cba4683c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3iraA_</a>	 Alignment		100.0	47	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> the crystal structure of one domain of the conserved protein from <i>Methanosarcina mazei</i> go1
2	<a href="#">c5zigD_</a>	 Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> D; <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> the structure of cellobiose 2-epimerase from <i>Spirochaeta thermophila</i> DSM 6192
3	<a href="#">c5x32B_</a>	 Alignment		100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of d-mannose isomerase
4	<a href="#">c2gz6B_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetyl-d-glucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of <i>Anabaena</i> sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 Å
5	<a href="#">c3wkgA_</a>	 Alignment		100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of cellobiose 2-epimerase in complex with 2 glucosylmannose
6	<a href="#">c3gt5A_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of an n-acetylglucosamine 2-epimerase family protein 2 from <i>Xylella fastidiosa</i>
7	<a href="#">c3vw5B_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of sugar epimerase from ruminal bacterium
8	<a href="#">c4z4IA_</a>	 Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of cellobiose 2-epimerase from <i>Caldicellulosiruptor 2 saccharolyticus</i> DSM 8903
9	<a href="#">c4mu9B_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycoside hydrolase family 73; <b>PDBTitle:</b> crystal structure of a putative glycosylhydrolase (bt_3782) from <i>Methanobacterium thermoautotrophicum</i> strain delta H at 1.89 Å resolution
10	<a href="#">d1fp3a_</a>	 Alignment		100.0	14	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> N-acetylglucosamine (NAG) epimerase
11	<a href="#">c5zhhB_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> structure of cellobiose 2-epimerase from <i>Bacillus thermoamylovorans</i> DSM 24167

12	<a href="#">c4v1sA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,6-mannanase; <b>PDBTitle:</b> structure of the gh76 alpha-mannanase bt2949 from2 bacteroides thetaiotaomicron
13	<a href="#">c2zzrA_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> unsaturated glucuronyl hydrolase; <b>PDBTitle:</b> crystal structure of unsaturated glucuronyl hydrolase from2 streptococcus agalactiae
14	<a href="#">c4bojC_</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-1,6-mannanase; <b>PDBTitle:</b> crystal structure of bacillus circulans tn-31 aman6 in2 complex with mannobiose
15	<a href="#">c3k7xA_</a>	Alignment		99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0763 protein; <b>PDBTitle:</b> crystal structure of the lin0763 protein from listeria innocua.2 northeast structural genomics consortium target lkr23.
16	<a href="#">d2afaa1</a>	Alignment		99.8	19	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> N-acylglucosamine (NAG) epimerase
17	<a href="#">c2k8vA_</a>	Alignment		99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 12; <b>PDBTitle:</b> solution structure of oxidised erp18
18	<a href="#">c3wiwA_</a>	Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 88; <b>PDBTitle:</b> crystal structure of unsaturated glucuronyl hydrolase specific for2 heparin
19	<a href="#">d2d5ja1</a>	Alignment		99.8	17	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Glycosyl Hydrolase Family 88
20	<a href="#">c2ju5A_</a>	Alignment		99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase
21	<a href="#">c4c1sA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 76 mannosidase; <b>PDBTitle:</b> glycoside hydrolase family 76 (mannosidase) bt3792 from2 bacteroides thetaiotaomicron vpi-5482
22	<a href="#">c3f9uA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative exported cytochrome c biogenesis-related protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
23	<a href="#">d2dlxa1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> UAS domain
24	<a href="#">c3fk8A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> disulphide isomerase; <b>PDBTitle:</b> the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
25	<a href="#">c2lstA_</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> solution structure of a thioredoxin from thermus thermophilus
26	<a href="#">c1senA_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-like protein p19; <b>PDBTitle:</b> endoplasmic reticulum protein rp19 o95881
27	<a href="#">d1sena_</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
28	<a href="#">c4yiwB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 105 protein;

28	<a href="#">c4xuvb_</a>	Alignment	not modelled	99.0	14	<b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 105 (gh105) enzyme2 from thielavia terrestris
29	<a href="#">d1nc5a_</a>	Alignment	not modelled	99.5	11	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Hypothetical protein YteR
30	<a href="#">c2kucA_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative disulphide-isomerase; <b>PDBTitle:</b> solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
31	<a href="#">c4wu0B_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> similar to yter (bacilus subtilis); <b>PDBTitle:</b> structural analysis of c. acetobutylicum atcc 824 glycoside hydrolase2 from family 105
32	<a href="#">c4ce7B_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> unsaturated 3s-rhamnoglycuronyl hydrolase; <b>PDBTitle:</b> crystal structure of a novel unsaturated beta-glucuronyl2 hydrolase enzyme, belonging to family gh105, involved in3 ulvan degradation
33	<a href="#">c6dnuB_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsbd; <b>PDBTitle:</b> crystal structure of neisseria meningitidis dsbd c-terminal domain in2 the oxidised form
34	<a href="#">c6ex6A_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> six-hairpin glycosidase; <b>PDBTitle:</b> the gh127, beta-arabinofuranosidase, bt3674
35	<a href="#">c5mqoA_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> glycoside hydrolase bt_1003
36	<a href="#">c3wkaA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form
37	<a href="#">d2fwha1</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
38	<a href="#">c5noaA_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> family 88 glycosyl hydrolase; <b>PDBTitle:</b> polysaccharide lyase baccell_00875
39	<a href="#">c4qk0C_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gh127 beta-l-arabinofuranosidase; <b>PDBTitle:</b> crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
40	<a href="#">c3pmmA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
41	<a href="#">c5opiA_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rhamnogalacturonan lyase; <b>PDBTitle:</b> rhamnogalacturonan lyase
42	<a href="#">c4fybA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein (dsbc); <b>PDBTitle:</b> structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
43	<a href="#">c5zf2A_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (h-type,trx-h); <b>PDBTitle:</b> crystal structure of trxp from edwardsiella tarda eib202
44	<a href="#">c2ec4A_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> fas-associated factor 1; <b>PDBTitle:</b> solution structure of the uas domain from human fas-2 associated factor 1
45	<a href="#">c4q88B_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> glycosyl hydrolase family 88 from bacteroides vulgatus
46	<a href="#">c3k11A_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
47	<a href="#">c2i57A_</a>	Alignment	not modelled	98.8	20	<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 thioredoin-like protein from2 clostridium perfringens
48	<a href="#">c3e6uA_</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> lanc-like protein 1; <b>PDBTitle:</b> crystal structure of human lanc1
49	<a href="#">d1a8la2</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
50	<a href="#">c3ul3A_</a>	Alignment	not modelled	98.6	15	<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
51	<a href="#">c5gxyA_</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucanase; <b>PDBTitle:</b> crystal structure of endoglucanase celq from clostridium thermocellum2 complexed with cellobiose and tris
52	<a href="#">c2pptA_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-2; <b>PDBTitle:</b> crystal structure of thioredoxin-2
53	<a href="#">c2f51B_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structure of trichomonas vaginalis thioredoxin

54	<a href="#">c2xfgA</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> hydrolase/sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase 1; <b>PDBTitle:</b> reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
55	<a href="#">d1g87a1</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
56	<a href="#">d1ep7a</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
57	<a href="#">c5nymA</a>	Alignment	not modelled	98.3	11	<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
58	<a href="#">c2vfvA</a>	Alignment	not modelled	98.2	21	<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
59	<a href="#">c1ga2A</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase 9g; <b>PDBTitle:</b> the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
60	<a href="#">c3qdnA</a>	Alignment	not modelled	98.2	15	<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
61	<a href="#">d1j08a2</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> PDI-like
62	<a href="#">c4xhmB</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin (trx-3); <b>PDBTitle:</b> archaeoglobus fulgidus thioredoxin 3 m60h
63	<a href="#">d1ia6a</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
64	<a href="#">c3gnjD</a>	Alignment	not modelled	98.1	15	<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
65	<a href="#">d1m7ta</a>	Alignment	not modelled	98.1	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
66	<a href="#">c1js4B</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo/exocellulase e4; <b>PDBTitle:</b> endo/exocellulase:cellobiose from thermomonospora
67	<a href="#">c2i4aA</a>	Alignment	not modelled	98.1	15	<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
68	<a href="#">c2yzuA</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
69	<a href="#">c6bkbB</a>	Alignment	not modelled	98.1	20	<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)
70	<a href="#">c6gn9A</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a thioredoxin from clostridium acetobutylicum at2 1.75 a resolution
71	<a href="#">c3d22A</a>	Alignment	not modelled	98.0	20	<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
72	<a href="#">c3x17B</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of metagenome-derived glycoside hydrolase family 92 endoglucanase
73	<a href="#">d1nw2a</a>	Alignment	not modelled	98.0	26	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
74	<a href="#">d1ks8a</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
75	<a href="#">d1ti3a</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
76	<a href="#">c1w89E</a>	Alignment	not modelled	98.0	18	<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
77	<a href="#">d1dbya</a>	Alignment	not modelled	98.0	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
78	<a href="#">c2e0qA</a>	Alignment	not modelled	98.0	20	<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
79	<a href="#">c4ruvA</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
						<b>Fold:</b> Thioredoxin fold

80	<a href="#">d1xfla_</a>	Alignment	not modelled	98.0	15	<b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
81	<a href="#">d1nxca_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1;2-mannosidase, catalytic domain
82	<a href="#">c3p2aB_</a>	Alignment	not modelled	97.9	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
83	<a href="#">c3tcoA_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin (trxa-1); <b>PDBTitle:</b> crystallographic and spectroscopic characterization of sulfobolus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
84	<a href="#">c3hypB_</a>	Alignment	not modelled	97.9	17	<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
85	<a href="#">d1r26a_</a>	Alignment	not modelled	97.9	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
86	<a href="#">c2v8kA_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pectate lyase; <b>PDBTitle:</b> structure of a family 2 pectate lyase in complex with trigalacturonic2 acid
87	<a href="#">c5a29A_</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolygalacturonate lyase; <b>PDBTitle:</b> family 2 pectate lyase from vibrio vulnificus
88	<a href="#">c3t33A_</a>	Alignment	not modelled	97.9	8	<b>PDB header:</b> signaling protein receptor <b>Chain:</b> A: <b>PDB Molecule:</b> g protein coupled receptor; <b>PDBTitle:</b> crystal structure of arabidopsis gcr2
89	<a href="#">c1ut9A_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> structural basis for the exocellulase activity of the2 cellobiohydrolase cbha from c. thermocellum
90	<a href="#">c3hz4A_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from methanosarcina mazei
91	<a href="#">d1tf4a1</a>	Alignment	not modelled	97.9	20	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
92	<a href="#">c3wc3A_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1, 4-beta-glucanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-glucanase from eisenia fetida
93	<a href="#">d2g0da1</a>	Alignment	not modelled	97.8	11	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> LanC-like <b>Family:</b> LanC-like
94	<a href="#">c5jv5A_</a>	Alignment	not modelled	97.8	17	<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
95	<a href="#">c5u2oA_</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sj30 cch; <b>PDBTitle:</b> crystal structure of zn-binding triple mutant of gh family 92 endoglucanase j30
96	<a href="#">c6ib1B_</a>	Alignment	not modelled	97.8	21	<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="#">c6g61A_</a>	Alignment	not modelled	97.8	12	<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
98	<a href="#">c6fhnA_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein; <b>PDBTitle:</b> structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
99	<a href="#">c2vm2C_</a>	Alignment	not modelled	97.8	22	<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
100	<a href="#">c5e37A_</a>	Alignment	not modelled	97.8	14	<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
101	<a href="#">c1g6iA_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> class i alpha-1,2-mannosidase; <b>PDBTitle:</b> crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution
102	<a href="#">d1qgva_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> spliceosomal protein U5-15Kd
103	<a href="#">c3p2aA_</a>	Alignment	not modelled	97.8	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
104	<a href="#">d1dl2a_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1;2-mannosidase, catalytic domain
105	<a href="#">c3vfiA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of a metagenomic thioredoxin
106	<a href="#">c6fhjA_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein,protein; <b>PDBTitle:</b> structural dynamics and catalytic properties of a multi-



						modular2 xanthanase, native. <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure of thioredoxin from schistosoma japonicum
107	<a href="#">c4i8bA_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> oxidoreductase <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
108	<a href="#">c2nbsA_</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystallographic structure of thioredoxin from litopenaeus vannamei
109	<a href="#">c3zzxB_</a>	Alignment	not modelled	97.7	20	<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
110	<a href="#">c2l5IA_</a>	Alignment	not modelled	97.7	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> spliceosomal protein dib1; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrp at2 3.7 angstrom
111	<a href="#">c5ganD_</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> the structure of thioredoxin from s. coelicolor
112	<a href="#">c1t00A_</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the periplasmic thioredoxin soxs from paracoccus2 pantotrophus (reduced form)
113	<a href="#">c3dmIA_</a>	Alignment	not modelled	97.7	15	<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
114	<a href="#">c2yoiA_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glucuronyl c5 epimerase b; <b>PDBTitle:</b> crystal structure of d-glucuronyl c5 epimerase
115	<a href="#">c4pw2A_</a>	Alignment	not modelled	97.6	13	<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
116	<a href="#">c2oe0B_</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structure of a. acidocaldarius cellulase cela
117	<a href="#">c3gzkA_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transcription, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dim1-like protein; <b>PDBTitle:</b> crystal structure of human dim2: a dim1-like protein
118	<a href="#">c1xbsA_</a>	Alignment	not modelled	97.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha- <b>PDBTitle:</b> crystal structure of human class i alpha-1,2-mannosidase in complex2 with thio-disaccharide substrate analogue
119	<a href="#">c1x9dA_</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1;2-mannosidase, catalytic domain
120	<a href="#">d1x9da1</a>	Alignment	not modelled	97.6	11	