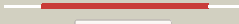



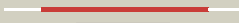



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3459c_(rpsK)_3879452_3879871
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	9d4df9a48438c681

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2qalk1</a>	 Alignment		100.0	61	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
2	<a href="#">c5o5jK_</a>	 Alignment		100.0	96	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> 30s ribosomal protein s11; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
3	<a href="#">d2uubk1</a>	 Alignment		100.0	60	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
4	<a href="#">c3j6vK_</a>	 Alignment		100.0	43	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> 28s ribosomal protein s11, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
5	<a href="#">c3bbnK_</a>	 Alignment		100.0	49	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> ribosomal protein s11; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
6	<a href="#">c3jyvK_</a>	 Alignment		100.0	37	<b>PDB header:</b> ribosome <b>Chain:</b> K; <b>PDB Molecule:</b> 40s ribosomal protein s14(a); <b>PDBTitle:</b> structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
7	<a href="#">c2zkqk_</a>	 Alignment		100.0	36	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> K; <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
8	<a href="#">c3j20M_</a>	 Alignment		100.0	47	<b>PDB header:</b> ribosome <b>Chain:</b> M; <b>PDB Molecule:</b> 30s ribosomal protein s11p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
9	<a href="#">c5o60P_</a>	 Alignment		97.9	18	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
10	<a href="#">c4v19S_</a>	 Alignment		97.6	12	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> mitoribosomal protein ul18m, mrpl18; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
11	<a href="#">d1vqon1</a>	 Alignment		97.5	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11

12	<a href="#">c4ce4S_</a>	Alignment		97.4	11	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> mrp18; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
13	<a href="#">d1ovya_</a>	Alignment		97.1	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
14	<a href="#">d2gycm1</a>	Alignment		97.1	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
15	<a href="#">c3bboQ_</a>	Alignment		97.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> ribosomal protein l18; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
16	<a href="#">c3j3vO_</a>	Alignment		96.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> O; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
17	<a href="#">c3j21O_</a>	Alignment		96.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> O; <b>PDB Molecule:</b> 50s ribosomal protein l18p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
18	<a href="#">c2j18S_</a>	Alignment		96.6	23	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> 50s ribosomal protein l18; <b>PDBTitle:</b> insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
19	<a href="#">d2j01s1</a>	Alignment		96.4	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
20	<a href="#">d2zjr1</a>	Alignment		95.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
21	<a href="#">c3j3bD_</a>	Alignment	not modelled	91.2	23	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
22	<a href="#">c4a1aM_</a>	Alignment	not modelled	87.6	25	<b>PDB header:</b> ribosome <b>Chain:</b> M; <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
23	<a href="#">c3izcQ_</a>	Alignment	not modelled	87.1	30	<b>PDB header:</b> ribosome <b>Chain:</b> Q; <b>PDB Molecule:</b> 60s ribosomal protein rpl5 (l18p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
24	<a href="#">c2zkrn_</a>	Alignment	not modelled	82.0	20	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> N; <b>PDB Molecule:</b> rrna expansion segment es27; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
25	<a href="#">c3zf7u_</a>	Alignment	not modelled	80.1	27	<b>PDB header:</b> ribosome <b>Chain:</b> U; <b>PDB Molecule:</b> 60s ribosomal protein l21e, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 Brucei ribosome
26	<a href="#">c3j39D_</a>	Alignment	not modelled	78.7	23	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> 60s ribosomal protein l5; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
27	<a href="#">d1bgva1</a>	Alignment	not modelled	75.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
28	<a href="#">d1v9la1</a>	Alignment	not modelled	61.1	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

						<b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
29	<a href="#">d1euza1</a>	Alignment	not modelled	58.7	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
30	<a href="#">c1v9lA</a>	Alignment	not modelled	58.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
31	<a href="#">c5ijzH</a>	Alignment	not modelled	56.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum
32	<a href="#">c2bmaA</a>	Alignment	not modelled	54.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase (nadp+); <b>PDBTitle:</b> the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
33	<a href="#">c2yfqA</a>	Alignment	not modelled	54.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
34	<a href="#">c3sboA</a>	Alignment	not modelled	52.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> structure of e.coli gdh from native source
35	<a href="#">d1gtma1</a>	Alignment	not modelled	50.7	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
36	<a href="#">c3aogA</a>	Alignment	not modelled	48.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
37	<a href="#">d1bvua1</a>	Alignment	not modelled	48.2	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
38	<a href="#">c3aoeC</a>	Alignment	not modelled	48.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
39	<a href="#">c2jvfA</a>	Alignment	not modelled	46.9	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo protein m7; <b>PDBTitle:</b> solution structure of m7, a computationally-designed2 artificial protein
40	<a href="#">c1qysA</a>	Alignment	not modelled	45.5	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> top7; <b>PDBTitle:</b> crystal structure of top7: a computationally designed2 protein with a novel fold
41	<a href="#">c4xgiA</a>	Alignment	not modelled	45.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
42	<a href="#">d1b26a1</a>	Alignment	not modelled	44.7	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
43	<a href="#">d2g82a1</a>	Alignment	not modelled	41.9	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	<a href="#">d1hwxal</a>	Alignment	not modelled	40.2	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
45	<a href="#">c5xviA</a>	Alignment	not modelled	40.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspergillus niger apo- glutamate dehydrogenase
46	<a href="#">d1vc2a1</a>	Alignment	not modelled	39.5	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	<a href="#">c1hrdA</a>	Alignment	not modelled	37.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> glutamate dehydrogenase
48	<a href="#">c3k8zD</a>	Alignment	not modelled	37.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-specific glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of gudb1 a decyptified secondary glutamate2 dehydrogenase from b. subtilis
49	<a href="#">d1ueha</a>	Alignment	not modelled	36.7	14	<b>Fold:</b> Undecaprenyl diphosphate synthase <b>Superfamily:</b> Undecaprenyl diphosphate synthase <b>Family:</b> Undecaprenyl diphosphate synthase
50	<a href="#">c3kijA</a>	Alignment	not modelled	28.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-dependent dehydrogenase, nirb-family (n-terminal) <b>PDBTitle:</b> crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
51	<a href="#">c3hq4R</a>	Alignment	not modelled	28.2	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
52	<a href="#">c3ga9S</a>	Alignment	not modelled	28.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> S: <b>PDB Molecule:</b> capsule biosynthesis protein capd; <b>PDBTitle:</b> crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii
53	<a href="#">c3iz5Q</a>	Alignment	not modelled	27.3	27	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l5 (l18p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

54	<a href="#">c1bvuf_</a>	Alignment	not modelled	27.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> glutamate dehydrogenase from thermococcus litoralis
55	<a href="#">c2e0yB_</a>	Alignment	not modelled	27.1	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
56	<a href="#">c2v36D_</a>	Alignment	not modelled	26.8	30	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase small chain; <b>PDBTitle:</b> crystal structure of gamma-glutamyl transferase from bacillus subtilis
57	<a href="#">c3r3jC_</a>	Alignment	not modelled	25.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
58	<a href="#">c2tmgD_</a>	Alignment	not modelled	24.2	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
59	<a href="#">c2yh5A_</a>	Alignment	not modelled	24.2	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dapx protein; <b>PDBTitle:</b> structure of the c-terminal domain of bamc
60	<a href="#">c2ep7B_</a>	Alignment	not modelled	23.7	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structural study of project id aq_1065 from aquifex aeolicus vf5
61	<a href="#">d2g3qa1</a>	Alignment	not modelled	22.1	25	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
62	<a href="#">c4qx6A_</a>	Alignment	not modelled	20.6	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution
63	<a href="#">c5ld5C_</a>	Alignment	not modelled	20.1	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution
64	<a href="#">c1jp3A_</a>	Alignment	not modelled	20.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthase; <b>PDBTitle:</b> structure of e.coli undecaprenyl pyrophosphate synthase
65	<a href="#">c1s7cA_</a>	Alignment	not modelled	19.3	26	<b>PDB header:</b> structural genomics, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
66	<a href="#">c4gdxB_</a>	Alignment	not modelled	19.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase 1 light chain; <b>PDBTitle:</b> crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
67	<a href="#">c1gv4A_</a>	Alignment	not modelled	18.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programed cell death protein 8; <b>PDBTitle:</b> murine apoptosis-inducing factor (aif)
68	<a href="#">d1u8fo1</a>	Alignment	not modelled	18.7	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
69	<a href="#">c5zjgD_</a>	Alignment	not modelled	18.6	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> gamma-glutamyltransferase 1 threonine peptidase. merops <b>PDBTitle:</b> gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
70	<a href="#">c1b7gO_</a>	Alignment	not modelled	18.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> protein (glyceraldehyde 3-phosphate dehydrogenase); <b>PDBTitle:</b> glyceraldehyde 3-phosphate dehydrogenase
71	<a href="#">c3h9eO_</a>	Alignment	not modelled	18.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase, testis-specific; <b>PDBTitle:</b> crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
72	<a href="#">c2nqoB_</a>	Alignment	not modelled	17.3	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
73	<a href="#">c3ur8A_</a>	Alignment	not modelled	17.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucan endo-1,3-beta-d-glucosidase; <b>PDBTitle:</b> lower-density crystal structure of potato endo-1,3-beta-glucanase
74	<a href="#">c2j3eA_</a>	Alignment	not modelled	17.0	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t7i23.11 protein; <b>PDBTitle:</b> dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
75	<a href="#">d1hpla2</a>	Alignment	not modelled	16.3	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
76	<a href="#">c3kwsB_</a>	Alignment	not modelled	14.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate

77	<a href="#">c3hjaB_</a>	Alignment	not modelled	14.5	21	dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>2 borrelia burgdorferi</i>
78	<a href="#">c1cerC_</a>	Alignment	not modelled	13.9	32	<b>PDB header:</b> oxidoreductase (aldehyde(d)-nad(a)) <b>Chain:</b> C; <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> determinants of enzyme thermostability observed in the 2 molecular structure of <i>thermus aquaticus</i> d-glyceraldehyde-3-phosphate dehydrogenase at 2.5 angstroms resolution
79	<a href="#">c3aamA_</a>	Alignment	not modelled	13.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endonuclease iv; <b>PDBTitle:</b> crystal structure of endonuclease iv from <i>thermus thermophilus</i> hb8
80	<a href="#">d1etha2</a>	Alignment	not modelled	13.5	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
81	<a href="#">c5zbiB_</a>	Alignment	not modelled	13.4	15	<b>PDB header:</b> plant protein <b>Chain:</b> B; <b>PDB Molecule:</b> peptide asparaginyl ligase; <b>PDBTitle:</b> crystal structure of asparaginyl endopeptidases from <i>viola canadensis</i>
82	<a href="#">d1htwa_</a>	Alignment	not modelled	13.2	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> YjeE-like
83	<a href="#">d2cyga1</a>	Alignment	not modelled	13.1	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
84	<a href="#">c2b4rQ_</a>	Alignment	not modelled	12.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q; <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>2 plasmodium falciparum</i> at 2.25 angstrom resolution reveals intriguing 3 extra electron density in the active site
85	<a href="#">c4y23A_</a>	Alignment	not modelled	11.9	35	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> gamma glutamyl transpeptidase, gamma-glutamyltranspeptidase; <b>PDBTitle:</b> crystal structure of t399a precursor mutant protein of gamma-glutamyl 2 transpeptidase from <i>bacillus licheniformis</i>
86	<a href="#">c2e0wA_</a>	Alignment	not modelled	11.5	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> gamma-glutamyltranspeptidase; <b>PDBTitle:</b> t391a precursor mutant protein of gamma-glutamyltranspeptidase from <i>2 escherichia coli</i>
87	<a href="#">c4ochA_</a>	Alignment	not modelled	11.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endonuclease muts2; <b>PDBTitle:</b> apo structure of smr domain of muts2 from <i>deinococcus radiodurans</i>
88	<a href="#">c5mvrA_</a>	Alignment	not modelled	10.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of <i>bacillus subtilis</i> ydib
89	<a href="#">d1aq0a_</a>	Alignment	not modelled	10.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
90	<a href="#">c4dibF_</a>	Alignment	not modelled	10.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>2 bacillus anthracis str. sterne</i>
91	<a href="#">d1jlx2</a>	Alignment	not modelled	10.1	33	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Agglutinin <b>Family:</b> Agglutinin
92	<a href="#">c2hcuA_</a>	Alignment	not modelled	10.1	43	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-isopropylmalate dehydratase small subunit; <b>PDBTitle:</b> crystal structure of smu.1381 (or leud) from <i>streptococcus mutans</i>
93	<a href="#">c2gd1P_</a>	Alignment	not modelled	10.0	35	<b>PDB header:</b> oxidoreductase(aldehyde(d)-nad(a)) <b>Chain:</b> P; <b>PDB Molecule:</b> apo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> coenzyme-induced conformational changes in glyceraldehyde-3-phosphate dehydrogenase from <i>bacillus stearothermophilus</i>
94	<a href="#">c3wqoB_</a>	Alignment	not modelled	10.0	9	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
95	<a href="#">c5ku5A_</a>	Alignment	not modelled	9.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> sensor kinase cuss; <b>PDBTitle:</b> crystal structure of cuss sensor domain with silver bound
96	<a href="#">c1hplB_</a>	Alignment	not modelled	9.9	15	<b>PDB header:</b> hydrolase(carboxylic esterase) <b>Chain:</b> B; <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> horse pancreatic lipase. the crystal structure at 2.3 angstroms 2 resolution
97	<a href="#">d1v7la_</a>	Alignment	not modelled	9.5	43	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IvD-like <b>Family:</b> LeuD-like
98	<a href="#">c3h5jA_</a>	Alignment	not modelled	9.4	43	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 3-isopropylmalate dehydratase small subunit; <b>PDBTitle:</b> leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from <i>2 mycobacterium tuberculosis</i>
99	<a href="#">c5h0iB_</a>	Alignment	not modelled	9.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> asparaginyl endopeptidase; <b>PDBTitle:</b> name to be released when published