Phyre^2

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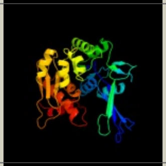
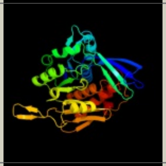
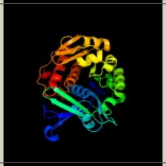
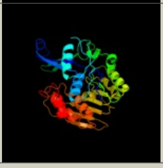
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cqdB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
2	c2jg1C_	Alignment		100.0	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tagatose-6-phosphate kinase; **PDBTitle:** structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
3	c2jg5B_	Alignment		100.0	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
4	d2abqa1	Alignment		100.0	31	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
5	d2f02a1	Alignment		100.0	26	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
6	d2ajra1	Alignment		100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
7	d1rkda_	Alignment		100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
8	c3julA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin2199 protein; **PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
9	d1vm7a_	Alignment		100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
10	d2fv7a1	Alignment		100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
11	c3kzhA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens

12	c2rbcA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
13	d2afba1	Alignment		100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
14	c2nwhA_	Alignment		100.0	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
15	c3go6B_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase rbsk; **PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
16	c2pkkA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine
17	c3pl2D_	Alignment		100.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sugar kinase, ribokinase family; **PDBTitle:** crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
18	c2c49A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase mj0406; **PDBTitle:** crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
19	d1bx4a_	Alignment		100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
20	c3i3yB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
21	d1v19a_	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
22	c3iq0B_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative ribokinase ii; **PDBTitle:** crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli
23	c2xtbA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
24	c3looC_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**anopheles gambiae adenosine kinase; **PDBTitle:** crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetraphosphate
25	c3ktnA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
26	c3b1qD_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
27	c2qcvA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 5-dehydro-2-deoxygluconokinase; **PDBTitle:** crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
28	c3in1A_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized sugar kinase ydjh; **PDBTitle:** crystal structure of a putative ribokinase in complex

						with2 adp from e.coli
29	c2absA_	Alignment	not modelled	100.0	20	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
30	d2absa1	Alignment	not modelled	100.0	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
31	c2varB_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
32	c3bf5A_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase related protein; **PDBTitle:** crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
33	d2dcna1	Alignment	not modelled	100.0	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
34	c3b3lC_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ketohexokinase; **PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase
35	c3gbuD_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized sugar kinase ph1459; **PDBTitle:** crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
36	d1tyya_	Alignment	not modelled	100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
37	c1tz6B_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sugar kinase; **PDBTitle:** crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog
38	c3lhxA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
39	c3lkiA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa
40	c2qhpA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
41	c3kd6B_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
42	d1vk4a_	Alignment	not modelled	100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
43	c3hj6B_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
44	c2ddmA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine kinase; **PDBTitle:** crystal structure of pyridoxal kinase from the escherichia2 coli pdxk gene at 2.1 a resolution
45	c2i5bC_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
46	d1ub0a_	Alignment	not modelled	99.7	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
47	c3mbjA_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphomethylpyrimidine kinase; **PDBTitle:** crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
48	d1vi9a_	Alignment	not modelled	99.6	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
49	c3ibqA_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
50	d1lhpa_	Alignment	not modelled	99.6	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
51	c3rm5B_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase **PDBTitle:** structure of trifunctional thi20 from yeast
52	c3dzvB_	Alignment	not modelled	99.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
						Fold: Ribokinase-like

53	d1jxha_	Alignment	not modelled	99.2	20	**Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
54	d1kyha_	Alignment	not modelled	99.2	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
55	d1v8aa_	Alignment	not modelled	99.1	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
56	d2ax3a1	Alignment	not modelled	98.9	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
57	c2ax3A_	Alignment	not modelled	98.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tm0922; **PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
58	d1ekqa_	Alignment	not modelled	98.7	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
59	c2r3bA_	Alignment	not modelled	98.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**yjef-related protein; **PDBTitle:** crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
60	d1gc5a_	Alignment	not modelled	98.7	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
61	d1l2la_	Alignment	not modelled	98.6	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
62	d1ua4a_	Alignment	not modelled	98.6	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
63	d1u2xa_	Alignment	not modelled	98.5	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
64	c3drwA_	Alignment	not modelled	98.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase; **PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
65	c3bgkA_	Alignment	not modelled	98.4	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
66	c3nm3D_	Alignment	not modelled	98.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
67	c3k5wA_	Alignment	not modelled	98.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
68	c2f00A_	Alignment	not modelled	89.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
69	c2vxyA_	Alignment	not modelled	84.5	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
70	d1p3da1	Alignment	not modelled	82.5	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
71	c3g5rA_	Alignment	not modelled	79.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
72	c2a87A_	Alignment	not modelled	76.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
73	c3kd9B_	Alignment	not modelled	71.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
74	c3dhnA_	Alignment	not modelled	69.2	27	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
75	c1gqqA_	Alignment	not modelled	67.4	22	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
76	c1vi2B_	Alignment	not modelled	67.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
77	d1djqa2	Alignment	not modelled	62.8	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
78	c3kpgA_	Alignment	not modelled	62.1	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative; **PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with

						decylubiquinone
79	c3d8xB_	Alignment	not modelled	59.2	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
80	c2r60A_	Alignment	not modelled	58.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
81	d1ofua1	Alignment	not modelled	58.1	12	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
82	c1gpjA_	Alignment	not modelled	58.0	15	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
83	d1hdoa_	Alignment	not modelled	57.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	d2afhe1	Alignment	not modelled	56.8	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
85	c3k96B_	Alignment	not modelled	56.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
86	d1j6ua1	Alignment	not modelled	56.3	19	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
87	c1xdiA_	Alignment	not modelled	55.0	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
88	c3ab1B_	Alignment	not modelled	53.9	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
89	d1ebda2	Alignment	not modelled	53.9	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
90	c1v59B_	Alignment	not modelled	53.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
91	c3c1oA_	Alignment	not modelled	50.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
92	d2d5ba2	Alignment	not modelled	49.5	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
93	c1i8tB_	Alignment	not modelled	49.3	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
94	d1uz5a3	Alignment	not modelled	48.3	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
95	d1w5fa1	Alignment	not modelled	48.0	14	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
96	c2q0lA_	Alignment	not modelled	46.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
97	c3rfxB_	Alignment	not modelled	46.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
98	d1n1ea2	Alignment	not modelled	45.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
99	d1rqga2	Alignment	not modelled	44.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
100	d1cp2a_	Alignment	not modelled	44.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
101	c3etjB_	Alignment	not modelled	44.4	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
102	d2ax3a2	Alignment	not modelled	44.0	19	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
103	c2eq8E_	Alignment	not modelled	41.9	33	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
104	c3tqoA	Alignment	not modelled	41.3	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase;

104	[illegible]	Alignment	not modelled	41.5	6	**PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
105	d1vi2a1	Alignment	not modelled	40.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
106	c3p19A_	Alignment	not modelled	40.6	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
107	d2vapa1	Alignment	not modelled	40.6	18	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
108	c2yx6C_	Alignment	not modelled	40.3	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
109	c3i3lA_	Alignment	not modelled	40.2	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
110	d1g3qa_	Alignment	not modelled	38.9	34	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
111	c1m67A_	Alignment	not modelled	38.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
112	c2f06B_	Alignment	not modelled	38.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
113	d1i8ta1	Alignment	not modelled	38.3	23	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
114	c3ghyA_	Alignment	not modelled	38.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
115	d2obba1	Alignment	not modelled	37.5	2	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
116	c2weuD_	Alignment	not modelled	37.1	17	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
117	d1wu2a3	Alignment	not modelled	37.1	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
118	c1w59B_	Alignment	not modelled	36.7	18	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
119	c2vawA_	Alignment	not modelled	35.7	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
120	c3allA_	Alignment	not modelled	34.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a