Phyre^2

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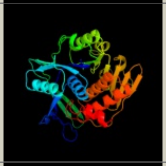
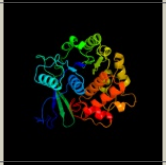
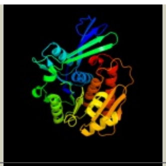
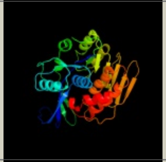
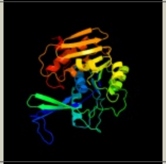
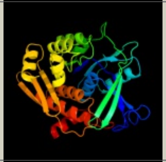
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rbcA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
2	d1rkda_	Alignment		100.0	28	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
3	d1vm7a_	Alignment		100.0	26	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
4	c2c49A_	Alignment		100.0	19	**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
5	c3pl2D_	Alignment		100.0	26	**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
6	c3iq0B_	Alignment		100.0	21	**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
7	d1v19a_	Alignment		100.0	23	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
8	c2nwhA_	Alignment		100.0	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
9	c3in1A_	Alignment		100.0	22	**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
10	c3kzhA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens
11	c2varB_	Alignment		100.0	21	**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

12	d2fv7a1	Alignment		100.0	28	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
13	c3i3yB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
14	c3go6B_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase rbsk; **PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
15	c2pkkA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine
16	d2dcna1	Alignment		100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
17	c3b1qD_	Alignment		100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
18	c3cqdB_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
19	c2qcvA_	Alignment		100.0	19	**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
20	d2afba1	Alignment		100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
21	d2abqa1	Alignment	not modelled	100.0	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
22	d2f02a1	Alignment	not modelled	100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
23	c3ktnA_	Alignment	not modelled	100.0	15	**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
24	d1tyya_	Alignment	not modelled	100.0	29	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
25	c2jg5B_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
26	c3b3lC_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ketohexokinase; **PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase
27	c2jg1C_	Alignment	not modelled	100.0	14	**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
28	c3gbuD_	Alignment	not modelled	100.0	22	**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
						PDB header:transferase

29	c2xtbA_	Alignment	not modelled	100.0	18	**Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
30	c3kd6B_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
31	c1tz6B_	Alignment	not modelled	100.0	28	**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
32	d1bx4a_	Alignment	not modelled	100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
33	c3lkiA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa
34	c3looC_	Alignment	not modelled	100.0	19	**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
35	c2absA_	Alignment	not modelled	100.0	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
36	d2absa1	Alignment	not modelled	100.0	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
37	c3bf5A_	Alignment	not modelled	100.0	18	**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
38	c3julA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin2199 protein; **PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
39	d2ajra1	Alignment	not modelled	100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
40	c3lhxA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
41	c2qhpA_	Alignment	not modelled	100.0	17	**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
42	c3hj6B_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
43	d1vk4a_	Alignment	not modelled	100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
44	c2ddmA_	Alignment	not modelled	99.8	20	**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	c3mbjA_	Alignment	not modelled	99.7	15	**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)
46	c2i5bC_	Alignment	not modelled	99.7	18	**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
47	d1ub0a_	Alignment	not modelled	99.6	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
48	c3ibqA_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
49	d1vi9a_	Alignment	not modelled	99.4	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
50	d1lhpa_	Alignment	not modelled	99.4	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
51	c3rm5B_	Alignment	not modelled	99.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase **PDBTitle:** structure of trifunctional thi20 from yeast
52	d1jxha_	Alignment	not modelled	99.1	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
53	d1kyha_	Alignment	not modelled	99.0	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
						PDB header:transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole

54	c3dzvB_	Alignment	not modelled	99.0	16	kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
55	d1v8aa_	Alignment	not modelled	98.7	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
56	d2ax3a1	Alignment	not modelled	98.6	11	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
57	d1ekqa_	Alignment	not modelled	98.3	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
58	c2r3bA_	Alignment	not modelled	98.3	14	**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
59	c2ax3A_	Alignment	not modelled	98.2	11	**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
60	c3k5wA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
61	d1l2la_	Alignment	not modelled	97.9	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
62	c3bgkA_	Alignment	not modelled	97.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
63	d1u2xa_	Alignment	not modelled	97.7	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
64	c3nm3D_	Alignment	not modelled	97.6	12	**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
65	d1gc5a_	Alignment	not modelled	97.5	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
66	c3drwA_	Alignment	not modelled	97.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase; **PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
67	d1ua4a_	Alignment	not modelled	97.1	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
68	c1i8tB_	Alignment	not modelled	73.4	41	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
69	c3dhnA_	Alignment	not modelled	72.7	19	**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.
70	c3g5rA_	Alignment	not modelled	66.7	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
71	d1hdoa_	Alignment	not modelled	62.2	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	c2f00A_	Alignment	not modelled	59.4	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
73	c3kd9B_	Alignment	not modelled	58.2	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
74	c3rfxB_	Alignment	not modelled	56.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
75	c3ghyA_	Alignment	not modelled	55.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
76	c2a87A_	Alignment	not modelled	54.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
77	c3etjB_	Alignment	not modelled	54.0	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
78	d1n1ea2	Alignment	not modelled	51.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
						PDB header:cell wall biosynthesis

79	c1gqqA_	Alignment	not modelled	51.1	24	**Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
80	d1gsoa2	Alignment	not modelled	50.4	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
81	c3i4fD_	Alignment	not modelled	44.9	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
82	d2c5aa1	Alignment	not modelled	43.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	c2rf4B_	Alignment	not modelled	42.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
84	c2r60A_	Alignment	not modelled	42.2	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
85	c3c1oA_	Alignment	not modelled	42.0	25	**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
86	d1p3da1	Alignment	not modelled	41.4	22	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
87	c3kpgA_	Alignment	not modelled	41.3	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
88	c3dojA_	Alignment	not modelled	39.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
89	d1rdua_	Alignment	not modelled	38.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
90	c3ay3C_	Alignment	not modelled	38.4	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
91	c3sc6F_	Alignment	not modelled	35.2	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
92	c3ab1B_	Alignment	not modelled	34.7	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
93	c3d3jA_	Alignment	not modelled	33.3	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
94	c1xdiA_	Alignment	not modelled	32.6	43	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
95	c2q0lA_	Alignment	not modelled	31.8	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
96	d1oc2a_	Alignment	not modelled	28.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
97	d2gtad1	Alignment	not modelled	27.3	22	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
98	c3plnA_	Alignment	not modelled	27.2	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
99	c1gsoA_	Alignment	not modelled	27.2	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
100	d2q46a1	Alignment	not modelled	27.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
101	c3crcB_	Alignment	not modelled	26.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
102	c3l6eA_	Alignment	not modelled	25.4	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, short-chain dehydrogenase/reductase family; **PDBTitle:** crystal structure of putative short chain dehydrogenase/reductase2 family oxidoreductase from aeromonas hydrophila subsp. hydrophila3 atcc 7966
103	d2afhe1	Alignment	not modelled	25.1	37	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like

104	d1ztda1	Alignment	not modelled	24.6	27	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
105	c2q1wC_	Alignment	not modelled	24.4	28	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
106	d1bxka_	Alignment	not modelled	24.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	c3ic9D_	Alignment	not modelled	23.7	43	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
108	c1su1A_	Alignment	not modelled	23.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
109	d1su1a_	Alignment	not modelled	23.3	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
110	c1v59B_	Alignment	not modelled	23.2	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
111	c2cduB_	Alignment	not modelled	22.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
112	c2eq8E_	Alignment	not modelled	21.5	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
113	c1nhqA_	Alignment	not modelled	21.0	21	**PDB header:**oxidoreductase (h2o2(a)) **Chain:** A: **PDB Molecule:**nadh peroxidase; **PDBTitle:** crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
114	d1wu2a3	Alignment	not modelled	20.6	10	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
115	c3d3kD_	Alignment	not modelled	20.6	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p