Phyre^2

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Description	Q6IFZ3
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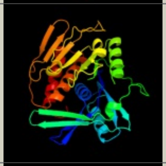
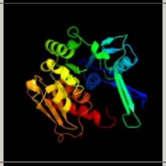
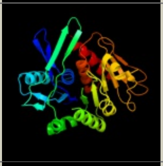
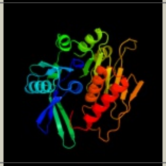
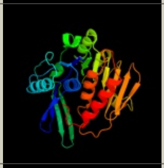
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v19a_	Alignment		100.0	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
2	c3iq0B_	Alignment		100.0	20	**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
3	c3pl2D_	Alignment		100.0	23	**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
4	c2xtbA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
5	d1bx4a_	Alignment		100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
6	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
7	c2nwhA_	Alignment		100.0	21	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
8	c3looC_	Alignment		100.0	21	**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
9	d2absa1	Alignment		100.0	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
10	c2absA_	Alignment		100.0	24	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
11	c2pkkA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine

12	d2afba1	Alignment		100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
13	c2qcvA_	Alignment		100.0	20	**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
14	c3go6B_	Alignment		100.0	21	**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	c3ktnA_	Alignment		100.0	22	**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
16	d1rkda_	Alignment		100.0	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
17	c2rbcA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
18	d2dcna1	Alignment		100.0	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
19	c2varB_	Alignment		100.0	16	**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
20	c3lhxA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
21	c3in1A_	Alignment	not modelled	100.0	24	**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
22	d1vm7a_	Alignment	not modelled	100.0	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
23	c2c49A_	Alignment	not modelled	100.0	18	**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
24	c2qhpA_	Alignment	not modelled	100.0	18	**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
25	c3i3yB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
26	d1tyya_	Alignment	not modelled	100.0	27	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
27	c3cqdB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
28	c3b1qD_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** crystal structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
						PDB header:transferase

29	c3gbuD_	Alignment	not modelled	100.0	25	**Chain:** D: **PDB Molecule:**uncharacterized sugar kinase ph1459; **PDBTitle:** crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
30	d2fv7a1	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
31	c1tz6B_	Alignment	not modelled	100.0	27	**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	c3lkiA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa
33	d2abqa1	Alignment	not modelled	100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
34	c3b3lC_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ketohexokinase; **PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase
35	c2jg1C_	Alignment	not modelled	100.0	16	**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
36	c3kd6B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
37	d2f02a1	Alignment	not modelled	100.0	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
38	c3hj6B_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
39	c2jg5B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
40	c3bf5A_	Alignment	not modelled	100.0	22	**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
41	c3julA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin2199 protein; **PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
42	d1vk4a_	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
43	d2ajra1	Alignment	not modelled	100.0	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
44	c2ddmA_	Alignment	not modelled	99.9	18	**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	19	**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	c3mbjA_	Alignment	not modelled	99.7	16	**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)
47	d1ub0a_	Alignment	not modelled	99.6	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
48	d1lhpa_	Alignment	not modelled	99.6	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
49	d1vi9a_	Alignment	not modelled	99.5	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
50	c3ibqA_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
51	c3rm5B_	Alignment	not modelled	99.2	19	**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	c3dzvB_	Alignment	not modelled	99.0	14	**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

54	d1v8aa_	Alignment	not modelled	98.9	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
55	d1kyha_	Alignment	not modelled	98.6	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
56	d2ax3a1	Alignment	not modelled	98.4	9	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
57	d1ekqa_	Alignment	not modelled	98.3	12	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
58	c3nm3D_	Alignment	not modelled	98.0	13	**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
59	c2ax3A_	Alignment	not modelled	97.9	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	c2r3bA_	Alignment	not modelled	97.8	10	**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
61	c3k5wA_	Alignment	not modelled	97.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
62	d1l2la_	Alignment	not modelled	97.2	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
63	d1gc5a_	Alignment	not modelled	97.1	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
64	c3bgkA_	Alignment	not modelled	96.9	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
65	d1u2xa_	Alignment	not modelled	96.9	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
66	c3drwA_	Alignment	not modelled	96.8	14	**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	94.9	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
68	c2f00A_	Alignment	not modelled	93.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
69	c3g5rA_	Alignment	not modelled	84.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
70	d1p3da1	Alignment	not modelled	83.8	22	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
71	c2a87A_	Alignment	not modelled	81.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
72	c3kd9B_	Alignment	not modelled	80.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
73	c3ab1B_	Alignment	not modelled	79.4	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
74	c1gqqA_	Alignment	not modelled	77.4	28	**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
75	c2q0lA_	Alignment	not modelled	76.5	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
76	c3dhnA_	Alignment	not modelled	75.1	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.
77	c3etjB_	Alignment	not modelled	74.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
78	c3fbsB_	Alignment	not modelled	72.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative;

79	c3kpgA_	Alignment	not modelled	69.6	20	**PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
80	c1xdiA_	Alignment	not modelled	66.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
81	c3d8xB_	Alignment	not modelled	65.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
82	c2i0zA_	Alignment	not modelled	64.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-utilizing dehydrogenases; **PDBTitle:** crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
83	d1hdoa_	Alignment	not modelled	62.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c2r60A_	Alignment	not modelled	61.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
85	d1n1ea2	Alignment	not modelled	59.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c3rfxB_	Alignment	not modelled	58.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
87	d1trba2	Alignment	not modelled	58.4	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
88	c2eq8E_	Alignment	not modelled	57.9	30	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
89	c3l8kB_	Alignment	not modelled	57.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
90	d1j6ua1	Alignment	not modelled	56.0	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
91	c2weuD_	Alignment	not modelled	55.4	17	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
92	c1lvlA_	Alignment	not modelled	54.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
93	c1i8tB_	Alignment	not modelled	53.5	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
94	d1f0ya2	Alignment	not modelled	52.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
95	d1i8ta1	Alignment	not modelled	52.4	20	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
96	c1v59B_	Alignment	not modelled	52.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
97	c3v76A_	Alignment	not modelled	51.2	21	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavoprotein; **PDBTitle:** the crystal structure of a flavoprotein from sinorhizobium meliloti
98	c1j6uA_	Alignment	not modelled	50.8	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
99	d1k0ia1	Alignment	not modelled	50.7	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
100	d1seza1	Alignment	not modelled	49.2	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
101	d1ebda1	Alignment	not modelled	49.0	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
102	c2bs3A_	Alignment	not modelled	48.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinol-fumarate reductase flavoprotein subunit a; **PDBTitle:** glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
103	c3lzxB_	Alignment	not modelled	47.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2; **PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
						PDB header:complex (oxidoreductase/transferase)

104	c1ebdB_	Alignment	not modelled	47.8	13	**Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
105	c1m67A_	Alignment	not modelled	47.2	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
106	d1h6va2	Alignment	not modelled	46.6	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
107	c3c1oA_	Alignment	not modelled	46.0	16	**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
108	d3grsa1	Alignment	not modelled	44.0	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
109	c3cp8C_	Alignment	not modelled	43.8	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
110	c3k96B_	Alignment	not modelled	43.3	23	**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
111	d1v59a1	Alignment	not modelled	42.6	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
112	c2eq7B_	Alignment	not modelled	42.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
113	c2e4gB_	Alignment	not modelled	41.9	13	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
114	c3l6eA_	Alignment	not modelled	41.6	13	**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
115	d2i0za1	Alignment	not modelled	40.2	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
116	c3ay3C_	Alignment	not modelled	40.2	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
117	c3ic9D_	Alignment	not modelled	40.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
118	c3lovA_	Alignment	not modelled	39.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
119	c2vdcI_	Alignment	not modelled	39.3	21	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
120	c1phhA_	Alignment	not modelled	39.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**p-hydroxybenzoate hydroxylase; **PDBTitle:** crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate