Phyre^2

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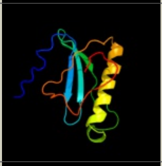
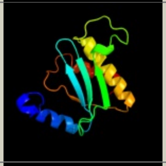
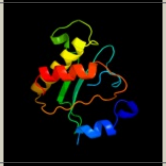
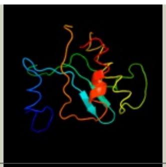
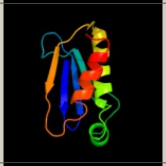
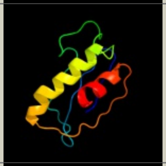
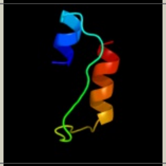
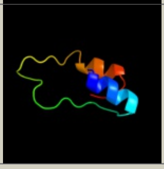
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gycm1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
2	c3bboQ_	Alignment		100.0	46	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein l18; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
3	d1ovya_	Alignment		100.0	57	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
4	c2jl8S_	Alignment		100.0	45	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**50s ribosomal protein l18; **PDBTitle:** insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
5	d2zjrl1	Alignment		100.0	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
6	d2j01s1	Alignment		100.0	47	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
7	d1vqon1	Alignment		100.0	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
8	c2zkrn_	Alignment		99.8	23	**PDB header:**ribosomal protein/rna **Chain:** N: **PDB Molecule:**rna expansion segment es27; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
9	c4a1aM_	Alignment		99.8	27	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** 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.
10	c3izcQ_	Alignment		99.8	29	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein rpl5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
11	c3iz5Q_	Alignment		99.7	27	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l5 (l18p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	c1s1iE_	Alignment		99.6	28	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
13	d2uubk1	Alignment		97.4	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
14	d2qalk1	Alignment		97.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
15	c3bbnK_	Alignment		96.8	18	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein s11; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
16	c2zkqk_	Alignment		96.5	16	**PDB header:**ribosomal protein/rna **Chain:** K: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
17	c3jyvK_	Alignment		95.1	20	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**40s ribosomal protein s14(a); **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
18	c2yfnA_	Alignment		70.6	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
19	c3mi6A_	Alignment		63.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
20	c2xn1B_	Alignment		61.1	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
21	c3gzaB_	Alignment	not modelled	59.5	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
22	c2pohA_	Alignment	not modelled	50.6	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head completion protein; **PDBTitle:** structure of phage p22 tail needle gp26
23	c3tevA_	Alignment	not modelled	45.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hyrolase, family 3; **PDBTitle:** the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
24	d1hl9a2	Alignment	not modelled	44.1	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
25	c1hl8B_	Alignment	not modelled	43.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
26	c2wvsD_	Alignment	not modelled	41.1	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
27	c3ff4A_	Alignment	not modelled	40.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
28	d1gtka2	Alignment	not modelled	37.1	18	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain

						Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
29	c3mo4B_	Alignment	not modelled	35.6	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
30	c3m0zD_	Alignment	not modelled	31.6	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
31	d1owla2	Alignment	not modelled	29.8	18	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
32	d1np7a2	Alignment	not modelled	28.6	14	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
33	c3eypB_	Alignment	not modelled	28.0	40	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
34	c3noyA_	Alignment	not modelled	27.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
35	d3cuma2	Alignment	not modelled	25.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
36	d1t35a_	Alignment	not modelled	24.8	36	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
37	c3qk7C_	Alignment	not modelled	23.4	28	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
38	c2juiA_	Alignment	not modelled	23.0	32	**PDB header:**toxin **Chain:** A: **PDB Molecule:**plne; **PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
39	d1zpda2	Alignment	not modelled	21.3	22	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
40	c3qhaB_	Alignment	not modelled	20.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
41	d1u3da2	Alignment	not modelled	19.9	12	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
42	c2cukC_	Alignment	not modelled	18.1	32	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
43	c2uyyD_	Alignment	not modelled	18.1	16	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
44	d1kjqa2	Alignment	not modelled	17.4	29	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
45	c2iz1C_	Alignment	not modelled	16.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
46	d1pdaa2	Alignment	not modelled	16.7	29	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
47	d2djia2	Alignment	not modelled	15.6	28	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
48	c1vpdA_	Alignment	not modelled	15.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
49	c2duwA_	Alignment	not modelled	15.5	36	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
50	c3gybB_	Alignment	not modelled	15.5	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulators (laci-family **PDBTitle:** crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
51	d1vpda2	Alignment	not modelled	15.2	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
52	d1y81a1	Alignment	not modelled	15.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
53	c3eywA_	Alignment	not modelled	15.0	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff

54	d1dosa_	Alignment	not modelled	14.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
55	c3qi7A_	Alignment	not modelled	14.1	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
56	d1np3a2	Alignment	not modelled	14.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
57	c2w4lC_	Alignment	not modelled	13.7	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** human dcmp deaminase
58	c2ypnA_	Alignment	not modelled	13.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
59	d1ktba2	Alignment	not modelled	13.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	d1hg3a_	Alignment	not modelled	13.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
61	c3toxG_	Alignment	not modelled	12.3	28	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
62	c2gf2B_	Alignment	not modelled	12.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
63	d1qyda_	Alignment	not modelled	12.1	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
64	d1w0ma_	Alignment	not modelled	12.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
65	c3muxB_	Alignment	not modelled	12.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
66	c3m6yA_	Alignment	not modelled	11.6	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
67	d1aopa1	Alignment	not modelled	11.4	25	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
68	c2yicC_	Alignment	not modelled	11.2	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
69	d1pjca1	Alignment	not modelled	11.2	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
70	c1ozhD_	Alignment	not modelled	11.1	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**acetolactate synthase, catabolic; **PDBTitle:** the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
71	c3l6dB_	Alignment	not modelled	10.8	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
72	d1ae1a_	Alignment	not modelled	10.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	c3u5in_	Alignment	not modelled	10.5	44	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l15-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
74	c3u5en_	Alignment	not modelled	10.5	44	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l15-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
75	c1tezB_	Alignment	not modelled	10.5	19	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans
76	c1zy9A_	Alignment	not modelled	10.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from thermotoga maritima at 2.34 a resolution
77	d1hjqa_	Alignment	not modelled	10.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
78	d1vq2a_	Alignment	not modelled	10.4	26	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
79	d1pgja2	Alignment	not modelled	10.3	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal

						domain
80	d2i9ua1	Alignment	not modelled	10.2	14	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
81	d2naca1	Alignment	not modelled	9.9	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
82	d1p5dx1	Alignment	not modelled	9.8	24	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
83	c3bmxB_	Alignment	not modelled	9.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis
84	c3lk6A_	Alignment	not modelled	9.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
85	d2d59a1	Alignment	not modelled	9.6	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	c3egcF_	Alignment	not modelled	9.6	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
87	c2rafC_	Alignment	not modelled	9.5	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase; **PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
88	d1gdha1	Alignment	not modelled	9.5	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
89	c3sjuA_	Alignment	not modelled	9.5	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
90	d1vp8a_	Alignment	not modelled	9.4	41	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
91	d1zj8a1	Alignment	not modelled	9.3	22	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
92	d1ebda2	Alignment	not modelled	9.2	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
93	d1leha1	Alignment	not modelled	9.2	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
94	d3coxa1	Alignment	not modelled	9.1	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
95	c2fpgA_	Alignment	not modelled	8.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
96	c3q94B_	Alignment	not modelled	8.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
97	c1zpdA_	Alignment	not modelled	8.8	26	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
98	c3uf0A_	Alignment	not modelled	8.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
99	c3jvdA_	Alignment	not modelled	8.6	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum