Phyre2

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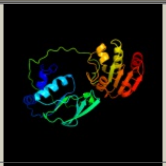
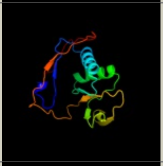
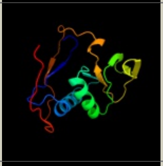
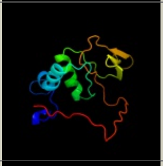
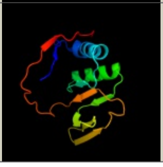
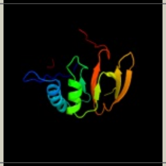
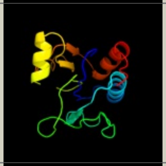
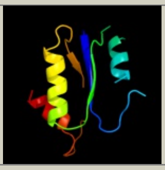
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1efpC_	Alignment		100.0	27	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
2	d1efva2	Alignment		100.0	38	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
3	d3clsd2	Alignment		100.0	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
4	d1efpa2	Alignment		100.0	42	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
5	d1efpa1	Alignment		99.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
6	d1efva1	Alignment		99.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
7	c1t9gR_	Alignment		99.8	16	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
8	c3ih5A_	Alignment		99.8	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
9	d3clsd1	Alignment		99.8	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
10	c1o94D_	Alignment		99.8	9	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
11	c3fetA_	Alignment		99.8	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein subunit alpha related **PDBTitle:** crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum

12	d1efpb_	Alignment		98.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
13	d1efvb_	Alignment		98.9	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
14	d3clsc1	Alignment		98.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
15	d1o94c_	Alignment		98.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
16	d1t9ba1	Alignment		98.6	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
17	d1ozha1	Alignment		98.5	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
18	d2ez9a1	Alignment		98.5	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
19	d2ji7a1	Alignment		98.2	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
20	d2ihta1	Alignment		98.0	29	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
21	d1ybha1	Alignment	not modelled	97.7	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
22	d2djia1	Alignment	not modelled	97.7	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
23	d1q6za1	Alignment	not modelled	97.5	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
24	c1powA_	Alignment	not modelled	97.5	20	**PDB header:**oxidoreductase(oxygen as acceptor) **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
25	c1ozhD_	Alignment	not modelled	97.4	20	**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.
26	c2djiA_	Alignment	not modelled	97.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
27	c2q27B_	Alignment	not modelled	97.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** crystal structure of oxalyl-coa decarboxylase from escherichia coli
28	c2pgnA_	Alignment	not modelled	97.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclohexane-1,2-dione hydrolase (cdh); **PDBTitle:** the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-

						1,2-dione
29	c1yi1A_	Alignment	not modelled	96.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase; **PDBTitle:** crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
30	c2x7jA_	Alignment	not modelled	96.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
31	c3eyaE_	Alignment	not modelled	96.8	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase [cytochrome]; **PDBTitle:** structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
32	c1t9dB_	Alignment	not modelled	96.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetolactate synthase, mitochondrial; **PDBTitle:** crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
33	c2ji6B_	Alignment	not modelled	96.7	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxalyl-coa decarboxylase; **PDBTitle:** x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
34	c3lq1A_	Alignment	not modelled	96.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene2 1-carboxylic acid synthase/2-oxoglutarate decarboxylase3 from listeria monocytogenes str. 4b f2365
35	c2ag1A_	Alignment	not modelled	96.2	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzaldehyde lyase; **PDBTitle:** crystal structure of benzaldehyde lyase (bal)- semet
36	c2panF_	Alignment	not modelled	95.9	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
37	d1pvda1	Alignment	not modelled	95.8	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
38	c1upaC_	Alignment	not modelled	95.7	28	**PDB header:**synthase **Chain:** C: **PDB Molecule:**carboxyethylarginine synthase; **PDBTitle:** carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
39	d1yc5a1	Alignment	not modelled	95.6	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
40	d1m2ka_	Alignment	not modelled	95.6	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
41	d2b4ya1	Alignment	not modelled	95.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
42	c2v3wC_	Alignment	not modelled	95.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
43	d1zpda1	Alignment	not modelled	95.0	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
44	c1jscA_	Alignment	not modelled	94.8	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
45	c3glsC_	Alignment	not modelled	94.1	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
46	c3k35D_	Alignment	not modelled	94.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
47	d1ma3a_	Alignment	not modelled	94.0	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
48	c2jlaD_	Alignment	not modelled	93.2	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase -semet3 protein
49	c3pkiF_	Alignment	not modelled	93.0	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
50	d1q1aa_	Alignment	not modelled	92.9	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
51	d1s5pa_	Alignment	not modelled	92.1	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
52	c2vbiF_	Alignment	not modelled	91.5	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
53	c3jwpA_	Alignment	not modelled	91.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein sir2 homologue;

						PDBTitle: crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
54	c1q14A_	Alignment	not modelled	90.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
55	c1zpdA_	Alignment	not modelled	90.1	16	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
56	d1j8fa_	Alignment	not modelled	86.6	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
57	c2hjhB_	Alignment	not modelled	86.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
58	c2w93A_	Alignment	not modelled	85.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pyruvate decarboxylase isozyme 1; **PDBTitle:** crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
59	d1l1qa_	Alignment	not modelled	84.7	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
60	c2dy0A_	Alignment	not modelled	82.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
61	c2vbgB_	Alignment	not modelled	78.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**branched-chain alpha-ketoacid decarboxylase; **PDBTitle:** the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
62	c3cf4G_	Alignment	not modelled	77.0	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
63	c2x3yA_	Alignment	not modelled	76.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
64	d1y5ea1	Alignment		74.5	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
65	d1x94a_	Alignment	not modelled	73.9	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
66	d1zn7a1	Alignment	not modelled	71.8	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
67	d1y0ba1	Alignment	not modelled	68.1	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1mkza_	Alignment	not modelled	67.0	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
69	d1o57a2	Alignment	not modelled	66.9	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
70	c1o57A_	Alignment	not modelled	66.4	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
71	d1mzva_	Alignment	not modelled	65.8	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
72	c2nxwB_	Alignment	not modelled	60.4	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phenyl-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
73	d1tk9a_	Alignment	not modelled	60.0	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
74	d1qb7a_	Alignment	not modelled	59.4	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
75	c2x5eA_	Alignment	not modelled	58.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
76	c3dezA_	Alignment	not modelled	55.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
77	d1moqa_	Alignment	not modelled	51.0	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
						PDB header:lyase

78	c1ovmC_	Alignment	not modelled	50.2	17	**Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
79	d1kjqa2	Alignment	not modelled	48.5	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
80	d1xw8a_	Alignment	not modelled	45.5	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
81	d1v6ta_	Alignment	not modelled	45.3	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
82	c2wnsB_	Alignment	not modelled	42.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
83	c2xhzC_	Alignment	not modelled	41.4	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
84	c2is8A_	Alignment	not modelled	41.0	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
85	c3d3qB_	Alignment	not modelled	38.4	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
86	d2dfaa1	Alignment	not modelled	38.3	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
87	c2p3wB_	Alignment	not modelled	37.9	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**probable serine protease htra3; **PDBTitle:** crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
88	d1jlja_	Alignment	not modelled	36.8	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
89	d3bzka5	Alignment	not modelled	36.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
90	c1nriA_	Alignment	not modelled	35.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
91	d1nria_	Alignment	not modelled	35.4	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
92	c3tbfA_	Alignment	not modelled	35.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
93	c2pn1A_	Alignment	not modelled	34.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
94	c3eplA_	Alignment	not modelled	33.1	27	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
95	d1a2za_	Alignment	not modelled	31.4	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
96	d1nt2a_	Alignment	not modelled	30.6	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
97	c2amlB_	Alignment	not modelled	30.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
98	c2ze5A_	Alignment	not modelled	30.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase; **PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
99	c3psiA_	Alignment	not modelled	30.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
100	c3fozB_	Alignment	not modelled	30.1	27	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
101	d1pama3	Alignment	not modelled	29.9	38	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain

102	c1kjjA_	Alignment	not modelled	29.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
103	c3uvzB_	Alignment	not modelled	28.1	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
104	d1g8sa_	Alignment	not modelled	28.0	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
105	d1g2qa_	Alignment	not modelled	26.9	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
106	c2p1zA_	Alignment	not modelled	26.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
107	d1auga_	Alignment	not modelled	26.3	27	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
108	d1di6a_	Alignment	not modelled	26.0	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
109	c3lacA_	Alignment	not modelled	25.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
110	d1qh8b_	Alignment	not modelled	25.2	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
111	d2iyva1	Alignment	not modelled	24.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
112	d2aeea1	Alignment	not modelled	24.7	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
113	d1iofa_	Alignment	not modelled	24.5	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
114	d1cxla3	Alignment	not modelled	24.2	31	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
115	d1w44a_	Alignment	not modelled	23.1	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
116	d1vcha1	Alignment	not modelled	22.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
117	c3imkA_	Alignment	not modelled	21.5	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
118	d1qhoa3	Alignment	not modelled	20.9	31	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
119	c2jtvA_	Alignment	not modelled	20.3	27	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
120	d1cgta3	Alignment	not modelled	20.3	38	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain