
































# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0018c_(ppp)_21637_23181
Date	Tue Jul 23 14:50:04 BST 2019
Unique Job ID	801715f783d151f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1txoa_</a>	 Alignment		100.0	97	<b>Fold:</b> PP2C-like <b>Superfamily:</b> PP2C-like <b>Family:</b> PP2C-like
2	<a href="#">c2cm1A_</a>	 Alignment		100.0	99	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine threonine protein phosphatase pstp; <b>PDBTitle:</b> crystal structure of the catalytic domain of serine2 threonine protein phosphatase pstp in complex with3 2 manganese ions.
3	<a href="#">c2jfsA_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ser-thr phosphatase mspp; <b>PDBTitle:</b> crystal structure of the ppm ser-thr phosphatase mspp from2 mycobacterium smegmatis in complex with cacodylate
4	<a href="#">c1a6qA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase 2c; <b>PDBTitle:</b> crystal structure of the protein serine/threonine phosphatase 2c at 22 a resolution
5	<a href="#">c4jndA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ca(2+)/calmodulin-dependent protein kinase phosphatase; <b>PDBTitle:</b> structure of a c.elegans sex determining protein
6	<a href="#">c5f1mA_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated protein phosphatase; <b>PDBTitle:</b> crystal structure of serine/threonine phosphatase stp1 from2 staphylococcus aureus
7	<a href="#">c6jkbB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pppa; <b>PDBTitle:</b> pppa, a key regulatory component of t6ss in pseudomonas aeruginosa
8	<a href="#">c2pk0C_</a>	 Alignment		100.0	35	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine protein phosphatase stp1; <b>PDBTitle:</b> structure of the s. agalactiae serine/threonine phosphatase at 2.652 resolution
9	<a href="#">c3ujgB_</a>	 Alignment		100.0	24	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein phosphatase 2c 16; <b>PDBTitle:</b> crystal structure of snrk2.6 in complex with hab1
10	<a href="#">c4yzhA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 2c 57; <b>PDBTitle:</b> structure of the arabidopsis tap38/pph1 in complex with plhcb12 phosphopeptide substrate
11	<a href="#">c4oicB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hormone receptor/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protein phosphatase 2c 6; <b>PDBTitle:</b> crystal structural of a soluble protein

12	<a href="#">c5gwpA</a>	Alignment		100.0	27	<b>PDB header:</b> hydrolase/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> probable protein phosphatase 2c 50; <b>PDBTitle:</b> crystal structure of rcar3:pp2c wild-type with (+)-aba
13	<a href="#">d1a6qa2</a>	Alignment		100.0	21	<b>Fold:</b> PP2C-like <b>Superfamily:</b> PP2C-like <b>Family:</b> PP2C-like
14	<a href="#">c2isnB</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nysgxc-8828z, phosphatase; <b>PDBTitle:</b> crystal structure of a phosphatase from a pathogenic strain toxoplasma2 gondii
15	<a href="#">c3kb3B</a>	Alignment		100.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein phosphatase 2c 16; <b>PDBTitle:</b> crystal structure of abscisic acid-bound pyl2 in complex with hab1
16	<a href="#">c4n0gB</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase/receptor <b>Chain:</b> B: <b>PDB Molecule:</b> protein phosphatase 2c 37; <b>PDBTitle:</b> crystal structure of pyl13-pp2ca complex
17	<a href="#">c3kdjB</a>	Alignment		100.0	26	<b>PDB header:</b> hydrolase/hormone receptor <b>Chain:</b> B: <b>PDB Molecule:</b> protein phosphatase 2c 56; <b>PDBTitle:</b> complex structure of (+)-aba-bound pyl1 and ab1
18	<a href="#">c2i44A</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine-threonine phosphatase 2c; <b>PDBTitle:</b> crystal structure of serine-threonine phosphatase 2c from2 toxoplasma gondii
19	<a href="#">c2i0oA</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ser/thr phosphatase; <b>PDBTitle:</b> crystal structure of anopheles gambiae ser/thr phosphatase complexed2 with zn2+
20	<a href="#">c2iq1A</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 2c kappa, ppm1k; <b>PDBTitle:</b> crystal structure of human ppm1k
21	<a href="#">c4da1A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein phosphatase 1k, mitochondrial; <b>PDBTitle:</b> crystal structure of branched-chain alpha-ketoacid dehydrogenase2 phosphatase with mg (ii) ions at the active site
22	<a href="#">c2pnaA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipamide]]-phosphatase <b>PDBTitle:</b> crystal structure of pyruvate dehydrogenase phosphatase 12 (pdp1)
23	<a href="#">c2j82A</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein serine-threonine phosphatase; <b>PDBTitle:</b> structural analysis of the pp2c family phosphatase tppha from2 thermosynechococcus elongatus
24	<a href="#">c3d8kD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein phosphatase 2c; <b>PDBTitle:</b> crystal structure of a phosphatase from a toxoplasma gondii
25	<a href="#">c5nzza</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tgf-beta-activated kinase 1 and map3k7-binding protein 1; <b>PDBTitle:</b> crystal structure of phosphorylated p38amapk in complex with tab1
26	<a href="#">c2irmA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 7 <b>PDBTitle:</b> crystal structure of mitogen-activated protein kinase kinase kinase 72 interacting protein 1 from anopheles gambiae
27	<a href="#">c3rnrB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation e family protein; <b>PDBTitle:</b> crystal structure of stage ii sporulation e family protein from2 thermanaerovibrio acidaminovorans
						<b>PDB header:</b> signaling protein/metal binding protein

28	<a href="#">c2pomA_</a>	Alignment	not modelled	100.0	18	<b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 7- <b>PDBTitle:</b> tab1 with manganese ion
29	<a href="#">c2j4oA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 7- <b>PDBTitle:</b> structure of tab1
30	<a href="#">c6ae9B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protein phosphatase 2c 1; <b>PDBTitle:</b> x-ray structure of the photosystem ii phosphatase pbcp
31	<a href="#">c3pu9A_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein serine/threonine phosphatase; <b>PDBTitle:</b> crystal structure of serine/threonine phosphatase sphaerobacter2 thermophilus dsm 20745
32	<a href="#">c3zt9A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine phosphatase; <b>PDBTitle:</b> the bacterial stressosome: a modular system that has been adapted to 2 control secondary messenger signaling
33	<a href="#">c5ucgE_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> stage ii sporulation protein e; <b>PDBTitle:</b> structure of the pp2c phosphatase domain and a fragment of the 2 regulatory domain of the cell fate determinant spoIIE from bacillus3 subtilis
34	<a href="#">c3w43A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine phosphatase rsbx; <b>PDBTitle:</b> crystal structure of rsbx in complex with manganese in space group p21
35	<a href="#">c3t9qB_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein e; <b>PDBTitle:</b> structure of the phosphatase domain of the cell fate determinant 2 spoIIE from bacillus subtilis (mn presoaked)
36	<a href="#">c6k4eB_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> hamp domain-containing protein; <b>PDBTitle:</b> siaa-pp2c domain of pseudomonas aeruginosa
37	<a href="#">c3ke6A_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein rv1364c/mt1410; <b>PDBTitle:</b> the crystal structure of the rsbu and rsbw domains of rv1364c from 2 mycobacterium tuberculosis
38	<a href="#">c3es2A_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> structure of the c-terminal phosphatase domain of p. aeruginosa rssb
39	<a href="#">c3eq2A_</a>	Alignment	not modelled	92.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> structure of hexagonal crystal form of pseudomonas aeruginosa rssb
40	<a href="#">c6od1A_</a>	Alignment	not modelled	79.3	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of rpos; <b>PDBTitle:</b> irad-bound to rssb d58p variant
41	<a href="#">c3e59A_</a>	Alignment	not modelled	54.8	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyoverdine biosynthesis protein pvca; <b>PDBTitle:</b> crystal structure of the pvca (pa2254) protein from pseudomonas aeruginosa
42	<a href="#">d1gpia_</a>	Alignment	not modelled	47.9	40	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
43	<a href="#">c2l9mA_</a>	Alignment	not modelled	42.9	25	<b>PDB header:</b> apoptosis inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 2; <b>PDBTitle:</b> structure of ciap1 card
44	<a href="#">c3nojA_</a>	Alignment	not modelled	42.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate <b>PDBTitle:</b> the structure of hmg/cha aldolase from the protocatechuate degradation 2 pathway of pseudomonas putida
45	<a href="#">c1p4vA_</a>	Alignment	not modelled	41.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n(4)-(beta-n-acetylglucosaminyI)-l-asparaginase <b>PDBTitle:</b> crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
46	<a href="#">c3k4iC_</a>	Alignment	not modelled	40.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein pspto_3204 from 2 pseudomonas syringae pv. tomato str. dc3000
47	<a href="#">d1q9ha_</a>	Alignment	not modelled	40.1	40	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
48	<a href="#">d1hq0a_</a>	Alignment	not modelled	39.0	25	<b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Family:</b> Type 1 cytotoxic necrotizing factor, catalytic domain
49	<a href="#">c5cx3F_</a>	Alignment	not modelled	35.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> fyve and coiled-coil domain-containing protein 1; <b>PDBTitle:</b> crystal structure of fyco1 lir in complex with lc3a
50	<a href="#">c2o90A_</a>	Alignment	not modelled	34.8	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroneopterin aldolase; <b>PDBTitle:</b> atomic resolution crystal structure of e.coli dihydroneopterin2 aldolase in complex with neopterin
51	<a href="#">d2b3ga1</a>	Alignment	not modelled	33.5	39	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
52	<a href="#">c5nygF_</a>	Alignment	not modelled	33.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> anbu; <b>PDBTitle:</b> anbu (gly-1) mutant from hypomicrobium sp. strain mc1 - sg p2(1)2(1)2 2(1) <b>Fold:</b> DsrEFH-like

53	<a href="#">d2d1pc1</a>	Alignment	not modelled	31.0	27	<b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrH-like
54	<a href="#">c5cx3G</a>	Alignment	not modelled	28.7	27	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> fyve and coiled-coil domain-containing protein 1; <b>PDBTitle:</b> crystal structure of fyco1 lir in complex with lc3a
55	<a href="#">c1k2xD</a>	Alignment	not modelled	28.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
56	<a href="#">c1k2xB</a>	Alignment	not modelled	28.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
57	<a href="#">c1jn9D</a>	Alignment	not modelled	28.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of putative asparaginase encoded by escherichia coli ybik2 gene
58	<a href="#">c4y4vB</a>	Alignment	not modelled	27.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical secreted protein; <b>PDBTitle:</b> structure of helicobacter pylori csd6 in the d-ala-bound state
59	<a href="#">d2hy5c1</a>	Alignment	not modelled	26.9	21	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrH-like
60	<a href="#">d1nbua</a>	Alignment	not modelled	26.8	17	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> DHN aldolase/epimerase
61	<a href="#">c2kn6A</a>	Alignment	not modelled	25.8	17	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis-associated speck-like protein containing a card; <b>PDBTitle:</b> structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card)
62	<a href="#">c3v9oA</a>	Alignment	not modelled	25.1	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroneopterin aldolase; <b>PDBTitle:</b> crystal structure of dihydroneopterin aldolase (bth_i0291) from2 burkholderia thailandensis bound to guanine.
63	<a href="#">c3vsjA</a>	Alignment	not modelled	24.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-5-chlorophenol 1,6-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
64	<a href="#">c2y9jt</a>	Alignment	not modelled	23.7	20	<b>PDB header:</b> protein transport <b>Chain:</b> T: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at subnanometer2 resolution
65	<a href="#">d1b9la</a>	Alignment	not modelled	23.2	10	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> DHN aldolase/epimerase
66	<a href="#">c1t3mD</a>	Alignment	not modelled	23.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
67	<a href="#">c1t3mB</a>	Alignment	not modelled	23.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
68	<a href="#">c1jn9B</a>	Alignment	not modelled	23.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of putative asparaginase encoded by escherichia coli ybik2 gene
69	<a href="#">d1dgna</a>	Alignment	not modelled	22.8	24	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> Caspase recruitment domain, CARD
70	<a href="#">d1dhna</a>	Alignment	not modelled	22.7	17	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> DHN aldolase/epimerase
71	<a href="#">c3vsjB</a>	Alignment	not modelled	22.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-amino-5-chlorophenol 1,6-dioxygenase beta subunit; <b>PDBTitle:</b> crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
72	<a href="#">c2m0oA</a>	Alignment	not modelled	21.9	31	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 1; <b>PDBTitle:</b> the solution structure of human phf1 in complex with h3k36me3
73	<a href="#">c6drpB</a>	Alignment	not modelled	21.6	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> cryo-em structures of asc and nlrc4 card filaments reveal a unified2 mechanism of nucleation and activation of caspase-1
74	<a href="#">c3ohgA</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein from duf2233 family; <b>PDBTitle:</b> crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
75	<a href="#">c3cqbB</a>	Alignment	not modelled	20.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protease htpx homolog; <b>PDBTitle:</b> crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
76	<a href="#">c2k2tA</a>	Alignment	not modelled	20.2	45	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> micronemal protein 6; <b>PDBTitle:</b> epidermal growth factor-like domain 2 from toxoplasma2 gondii microneme protein 6
77	<a href="#">c5fnaD</a>	Alignment	not modelled	19.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> caspase-1; <b>PDBTitle:</b> cryo-em reconstruction of caspase-1 card

78	<a href="#">d1sqa_</a>	Alignment	not modelled	19.4	23	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> DHN aldolase/epimerase
79	<a href="#">c4iikA_</a>	Alignment	not modelled	18.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine monophosphate-protein hydrolase sidd; <b>PDBTitle:</b> legionella pneumophila effector
80	<a href="#">c5bxyB_</a>	Alignment	not modelled	18.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rna methyltransferase; <b>PDBTitle:</b> crystal structure of rna methyltransferase from salinibacter ruber in2 complex with s-adenosyl-l-homocysteine
81	<a href="#">c5k7IA_</a>	Alignment	not modelled	17.9	4	<b>PDB header:</b> metal transport/calcium binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 1; <b>PDBTitle:</b> single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
82	<a href="#">c6qm8X_</a>	Alignment	not modelled	17.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> proteasome beta3 chain; <b>PDBTitle:</b> leishmania tarentolae proteasome 20s subunit apo structure
83	<a href="#">c2gacD_</a>	Alignment	not modelled	17.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosylasparaginase; <b>PDBTitle:</b> t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
84	<a href="#">c3katA_</a>	Alignment	not modelled	17.1	15	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> nacht, lrr and pyd domains-containing protein 1; <b>PDBTitle:</b> crystal structure of the card domain of the human nlrp1 protein,2 northeast structural genomics consortium target hr3486e
85	<a href="#">c5cx3E_</a>	Alignment	not modelled	17.1	27	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> fyve and coiled-coil domain-containing protein 1; <b>PDBTitle:</b> crystal structure of fyco1 lrr in complex with lc3a
86	<a href="#">c1sqIN_</a>	Alignment	not modelled	16.9	23	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> dihydroneopterin aldolase; <b>PDBTitle:</b> crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
87	<a href="#">d1npea_</a>	Alignment	not modelled	16.3	9	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> YWTD domain <b>Family:</b> YWTD domain
88	<a href="#">c5mq9A_</a>	Alignment	not modelled	16.2	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yacp; <b>PDBTitle:</b> crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
89	<a href="#">c4ebgA_</a>	Alignment	not modelled	16.0	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4467 family protein (sav0303) from2 staphylococcus aureus subsp. aureus mu50 at 1.35 a resolution
90	<a href="#">c6j52A_</a>	Alignment	not modelled	15.8	18	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> caspase recruitment domain-only protein; <b>PDBTitle:</b> crystal structure of card-only protein in frog virus 3
91	<a href="#">c4gduB_</a>	Alignment	not modelled	15.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of sulfate-bound human l-asparaginase protein
92	<a href="#">c3iddA_</a>	Alignment	not modelled	15.6	36	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent <b>PDBTitle:</b> cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
93	<a href="#">c1zglQ_</a>	Alignment	not modelled	15.6	24	<b>PDB header:</b> immune system <b>Chain:</b> Q: <b>PDB Molecule:</b> t cell receptor alpha chain; <b>PDBTitle:</b> crystal structure of 3a6 tcr bound to mbp/hla-dr2a
94	<a href="#">c2y9mB_</a>	Alignment	not modelled	15.4	18	<b>PDB header:</b> ligase/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisome assembly protein 22; <b>PDBTitle:</b> pex4p-pex22p structure
95	<a href="#">c2eqjA_</a>	Alignment	not modelled	15.3	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metal-response element-binding transcription <b>PDBTitle:</b> solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
96	<a href="#">c2n7zA_</a>	Alignment	not modelled	15.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-interacting serine/threonine-protein kinase 2; <b>PDBTitle:</b> solution structure of rip2 card
97	<a href="#">c4j0nA_</a>	Alignment	not modelled	15.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isatin hydrolase b; <b>PDBTitle:</b> crystal structure of a manganese dependent isatin hydrolase
98	<a href="#">c1nh2D_</a>	Alignment	not modelled	15.0	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcription initiation factor iia small chain; <b>PDBTitle:</b> crystal structure of a yeast tfiia/tbp/dna complex
99	<a href="#">c5l3xB_</a>	Alignment	not modelled	14.9	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> negative elongation factor c/d; <b>PDBTitle:</b> crystal structure of negative elongation factor subcomplex nelf-ac