Phyre²

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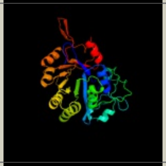
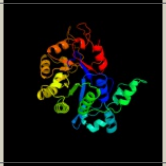
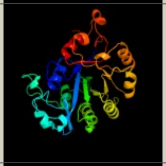
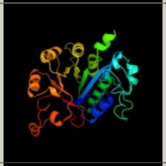
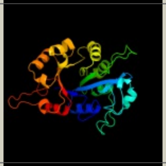
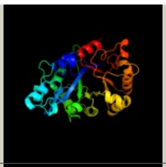
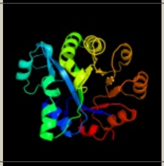
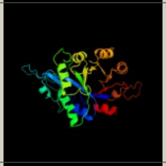
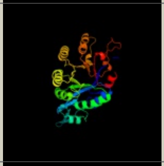
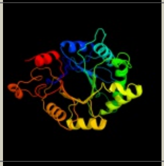
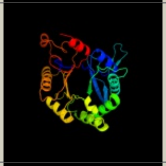
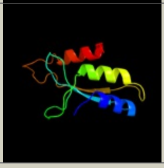
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ydyA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli
2	d1ydya1	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
3	c3l12A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
4	c2p76H_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
5	c2pz0B_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
6	c3mz2A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution
7	c3qvqB_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase olei02445; **PDBTitle:** the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
8	c2otdC_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
9	d1zcca1	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
10	c3ch0A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
11	c3no3A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution

12	c3ks6A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution
13	d1vd6a1	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
14	c3i10A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
15	c2o55A_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
16	d1o1za_	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
17	c3rlhA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
18	c3rlgA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
19	c2f9rC_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sphingomyelinase d 1; **PDBTitle:** crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom
20	c1djyB_	Alignment		98.0	16	**PDB header:**lipid degradation **Chain:** B: **PDB Molecule:**phosphoinositide-specific phospholipase c, **PDBTitle:** phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
21	d1qasa3	Alignment	not modelled	97.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
22	d2zkmx4	Alignment	not modelled	97.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
23	c3ohmB_	Alignment	not modelled	97.8	17	**PDB header:**signaling protein / hydrolase **Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase **PDBTitle:** crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
24	c3qr0A_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase c-beta (plc-beta); **PDBTitle:** crystal structure of s. officinalis plc21
25	c2fjuB_	Alignment	not modelled	97.2	13	**PDB header:**signaling protein,apoptosis/hydrolase **Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate **PDBTitle:** activated rac1 bound to its effector phospholipase c beta 2
26	d1vkfa_	Alignment	not modelled	93.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**GlpP-like **Family:**GlpP-like
27	c3ktsA_	Alignment	not modelled	93.0	12	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
28	c2zq0B_	Alignment	not modelled	92.6	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose

29	d2gjpa2	Alignment	not modelled	92.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
30	d1ob0a2	Alignment	not modelled	90.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	c3a24A_	Alignment	not modelled	89.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
32	d1pkla2	Alignment	not modelled	88.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
33	c1mwoA_	Alignment	not modelled	88.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrococus woesei alpha-amylase
34	d1e43a2	Alignment	not modelled	87.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
35	c2qpuB_	Alignment	not modelled	85.1	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
36	d1e0ta2	Alignment	not modelled	83.2	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
37	c1bplA_	Alignment	not modelled	83.0	13	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
38	c3h4wA_	Alignment	not modelled	82.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatidylinositol-specific phospholipase c1; **PDBTitle:** structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus
39	c1gcyA_	Alignment	not modelled	81.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
40	c3nvtA_	Alignment		80.4	24	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
41	c3hvbB_	Alignment	not modelled	79.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
42	c2r6oB_	Alignment	not modelled	78.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase (ggdef & eal **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
43	c1jdaA_	Alignment	not modelled	78.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
44	d1mxga2	Alignment	not modelled	77.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
45	d1ht6a2	Alignment	not modelled	77.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
46	c3thaB_	Alignment	not modelled	77.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
47	c3uk2B_	Alignment	not modelled	76.5	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
48	d1v8fa_	Alignment	not modelled	75.3	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
49	d1avaa2	Alignment	not modelled	75.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1ud2a2	Alignment	not modelled	75.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	c1uasA_	Alignment	not modelled	74.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
52	d1gcya2	Alignment	not modelled	72.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
53	c3pjwA_	Alignment	not modelled	72.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23

54	c3khdC_	Alignment	not modelled	72.1	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
55	c2ejcA_	Alignment	not modelled	72.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
56	c2qjhH_	Alignment	not modelled	71.0	10	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
57	c2p10D_	Alignment	not modelled	70.8	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
58	d2d3na2	Alignment	not modelled	70.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c3guzB_	Alignment	not modelled	67.6	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthetase (ps)provide insights into homotropic inhibition3 by pantoate in ps's
60	d1hvxa2	Alignment	not modelled	67.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	c3hv9A_	Alignment	not modelled	65.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
62	d2p10a1	Alignment	not modelled	65.5	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
63	c3s83A_	Alignment	not modelled	65.3	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
64	d1h7na_	Alignment	not modelled	64.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
65	c3n8hA_	Alignment	not modelled	64.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
66	c1aqfB_	Alignment	not modelled	58.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
67	c2dh3A_	Alignment	not modelled	57.8	24	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
68	c1t5aB_	Alignment	not modelled	54.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
69	c3blpX_	Alignment	not modelled	54.5	9	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
70	c3gndC_	Alignment	not modelled	54.3	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
71	d1ktba2	Alignment	not modelled	53.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	c3gfzB_	Alignment	not modelled	53.8	11	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
73	c3pfmA_	Alignment	not modelled	53.5	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
74	d1ujpa_	Alignment	not modelled	53.4	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
75	d2f06a2	Alignment	not modelled	53.3	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
76	c2vgbB_	Alignment	not modelled	53.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
77	d1ua7a2	Alignment	not modelled	52.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
78	d1pv8a_	Alignment	not modelled	51.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
79	d1jaea2	Alignment	not modelled	51.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
						PDB header:lyase

80	c2ekcA_	Alignment	not modelled	50.6	23	**Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
81	c1pklB_	Alignment	not modelled	50.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
82	d1hx0a2	Alignment	not modelled	49.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
83	c3kzpA_	Alignment	not modelled	48.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase; **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes
84	c3ma8A_	Alignment	not modelled	48.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
85	d1ihoa_	Alignment	not modelled	47.9	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
86	c3e0vB_	Alignment	not modelled	47.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
87	d1bxba_	Alignment	not modelled	47.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
88	d1rd5a_	Alignment	not modelled	46.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
89	c3mxtA_	Alignment	not modelled	46.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
90	d1r46a2	Alignment	not modelled	45.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d1qopa_	Alignment	not modelled	43.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
92	d1kjqa2	Alignment	not modelled	42.4	8	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
93	c3l2iB_	Alignment	not modelled	42.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
94	c3navB_	Alignment	not modelled	41.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
95	d2f6ua1	Alignment	not modelled	41.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
96	d2g50a2	Alignment	not modelled	41.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
97	c1ud8A_	Alignment	not modelled	41.1	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
98	d1tqxa_	Alignment	not modelled	41.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
99	d1a3xa2	Alignment	not modelled	40.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
100	c3t07D_	Alignment	not modelled	40.4	15	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
101	c3femB_	Alignment	not modelled	40.0	24	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
102	c3obkH_	Alignment	not modelled	40.0	16	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
103	c2nv2U_	Alignment	not modelled	39.8	27	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
104	d2ptda_	Alignment	not modelled	39.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Bacterial PLC
105	c3o6cA_	Alignment	not modelled	39.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
106	c2zbtB	Alignment	not modelled	38.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs;

106	c2zbtB_	Alignment	not modelled	38.9	20	**PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
107	c2htmB_	Alignment	not modelled	38.3	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
108	c1a3wB_	Alignment	not modelled	38.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
109	c2e28A_	Alignment	not modelled	38.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
110	d2basa1	Alignment	not modelled	37.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
111	c1kjjA_	Alignment	not modelled	37.7	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
112	d1ojxa_	Alignment	not modelled	36.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
113	c1jaeA_	Alignment	not modelled	36.0	13	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
114	c3a5vA_	Alignment	not modelled	35.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
115	c2w27A_	Alignment	not modelled	33.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ykui protein; **PDBTitle:** crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
116	d3dhpa2	Alignment	not modelled	33.4	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
117	d1gzga_	Alignment	not modelled	32.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
118	c1e0tD_	Alignment	not modelled	32.6	17	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
119	d1uasa2	Alignment	not modelled	32.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	c3eoeC_	Alignment	not modelled	32.4	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007