







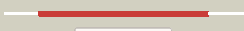













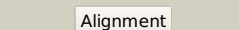

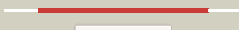



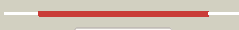















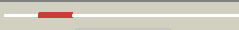

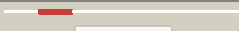





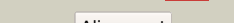
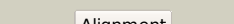
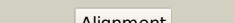

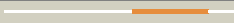



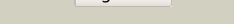

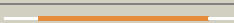


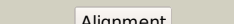
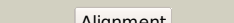


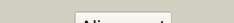

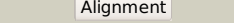
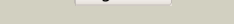


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0317c_glpQ2_385173_385943
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	f097d71a81eb844c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4oecD	 Alignment		100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase from2 thermococcus kodakarensis kod1
2	c4r7oE	 Alignment		100.0	20	PDB header: hydrolase Chain: E: PDB Molecule: glycerophosphoryl diester phosphodiesterase, putative; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterasefrom bacillus anthraci
3	c3i12A	 Alignment		100.0	26	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	c2pz0B	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
5	c5t91A	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of b. subtilis 168 glpQ in complex with bicine
6	c2p76H	 Alignment		100.0	22	PDB header: hydrolase Chain: H: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
7	c1ydyA	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli
8	d1ydyal	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
9	c3no3A	 Alignment		100.0	25	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
10	c2otdC	 Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
11	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

12	c3qvqB_	 Alignment		100.0	20	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
13	dlzcca1	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
14	c3ks6A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens str. c583 (dupont) at 1.80 a resolution
15	c2o55A_	 Alignment		100.0	20	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	c3i10A_	 Alignment		100.0	18	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
17	dlolza_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
18	dlvd6a1	 Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
19	c5vugA_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rv2277c; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 domain of uncharacterized protein rv2277c from mycobacterium3 tuberculosis
20	c3ch0A_	 Alignment		100.0	23	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
21	c3rlhA_	 Alignment	not modelled	100.0	15	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
22	c2f9rC_	 Alignment	not modelled	100.0	15	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
23	c3rlgA_	 Alignment	not modelled	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
24	c4q6xA_	 Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: phospholipase d stsictox-betaic1; PDBTitle: structure of phospholipase d beta1b1i from sicarius terrosus venom at2 2.14 a resolution
25	c1djyB_	 Alignment	not modelled	97.6	24	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
26	dlqasa3	 Alignment	not modelled	97.6	24	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
27	d2zkmx4	 Alignment	not modelled	97.6	21	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
28	c3qr0A_	 Alignment	not modelled	97.5	24	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase c-beta (plc-beta); PDBTitle: crystal structure of s. officinalis plc21

29	c3ohmB	 Alignment	not modelled	97.4	24	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
30	c2fjuB	 Alignment	not modelled	97.4	21	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
31	d1vkfa	 Alignment	not modelled	93.7	14	Fold: TIM beta/alpha-barrel Superfamily: GlpP-like Family: GlpP-like
32	c3ktsA	 Alignment	not modelled	93.1	22	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
33	d1rd5a	 Alignment	not modelled	90.9	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
34	c3h4wA	 Alignment	not modelled	90.1	21	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
35	d7rega2	 Alignment	not modelled	87.6	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
36	d1qopa	 Alignment	not modelled	86.5	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
37	c4s1aB	 Alignment	not modelled	85.5	20	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
38	c2zq0B	 Alignment	not modelled	85.4	8	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase subb); PDBTitle: crystal structure of subb complexed with acarbose
39	c1e1cA	 Alignment	not modelled	85.2	14	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
40	c4rnhA	 Alignment	not modelled	85.0	19	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
41	c3a24A	 Alignment	not modelled	84.9	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
42	c4nu7C	 Alignment	not modelled	84.7	12	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
43	c5d88A	 Alignment	not modelled	84.4	23	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
44	c5xgdA	 Alignment	not modelled	83.9	16	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
45	c3pjwA	 Alignment	not modelled	83.8	19	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
46	c2r6oB	 Alignment	not modelled	82.4	16	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
47	c5m3cB	 Alignment	not modelled	82.3	16	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
48	c5yrpB	 Alignment	not modelled	80.6	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa
49	c3hvbB	 Alignment	not modelled	80.1	15	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
50	c3gfbB	 Alignment	not modelled	79.5	19	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
51	d2cc0a1	 Alignment	not modelled	78.2	11	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
52	d1vc4a	 Alignment	not modelled	78.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
53	c2nv2U	 Alignment	not modelled	77.8	15	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
54	c5hqca_	Alignment	not modelled	76.8	15	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 97 enzyme; PDBTitle: a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8
55	c2p10D_	Alignment	not modelled	76.6	9	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
56	c2htmB_	Alignment	not modelled	76.4	6	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
57	c3pfmA_	Alignment	not modelled	75.4	17	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
58	c4lykB_	Alignment	not modelled	75.2	14	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
59	c5xfmD_	Alignment	not modelled	74.9	23	PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase
60	c4hu4B_	Alignment	not modelled	73.6	17	PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form
61	c2zbtB_	Alignment	not modelled	72.3	15	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
62	c3kzpA_	Alignment	not modelled	72.3	8	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
63	c4wca_	Alignment	not modelled	71.8	13	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structure of icab from ammonifex degensii
64	d2p10a1	Alignment	not modelled	71.5	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MI9387-like
65	c4q6jB_	Alignment	not modelled	71.4	23	PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e
66	c4y8eA_	Alignment	not modelled	71.1	20	PDB header: metal binding protein Chain: A: PDB Molecule: pa3825 eal; PDBTitle: pa3825-eal ca-apo structure
67	c3femB_	Alignment	not modelled	70.5	17	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
68	c4hjfa_	Alignment	not modelled	70.1	19	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
69	c5m1tB_	Alignment	not modelled	70.0	11	PDB header: signaling protein Chain: B: PDB Molecule: muCr phosphodiesterase; PDBTitle: pamuCr phosphodiesterase, c-di-gmp complex
70	d1xm3a_	Alignment	not modelled	69.9	19	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
71	c2c3zA_	Alignment	not modelled	69.7	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
72	c4f48A_	Alignment	not modelled	69.3	13	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimx-eal-c-di-gmp-pilz complexes from2 xanthomonas campestris
73	c3sy8C_	Alignment	not modelled	69.2	8	PDB header: transcription regulator Chain: C: PDB Molecule: rocr; PDBTitle: crystal structure of the response regulator rocr
74	c3bo9B_	Alignment	not modelled	68.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
75	c6bkaA_	Alignment	not modelled	68.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
76	c4fokA_	Alignment	not modelled	67.6	14	PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
77	d2basa1	Alignment	not modelled	67.1	3	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
78	d2g50a2	Alignment	not modelled	66.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
79	c3tlqB_	Alignment	not modelled	66.5	11	PDB header: transcription Chain: B: PDB Molecule: regulatory protein ydiv;

						PDBTitle: crystal structure of eal-like domain protein ydiv
80	d1pkla2	Alignment	not modelled	65.8	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
81	c6du6D	Alignment	not modelled	65.6	14	PDB header: transferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of the pyruvate kinase (pk1) from the mosquito aedes2 aegypti
82	c6hyeF	Alignment	not modelled	65.2	13	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a)
83	c3qz6A	Alignment	not modelled	64.8	8	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
84	c3inpA	Alignment	not modelled	64.7	13	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
85	c3t07D	Alignment	not modelled	63.8	14	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
86	d1ka9f	Alignment	not modelled	63.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
87	d2aama1	Alignment	not modelled	63.3	34	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: TM1410-like
88	c2aamA	Alignment	not modelled	63.3	34	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein tm1410; PDBTitle: crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
89	c5f56A	Alignment	not modelled	63.2	34	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
90	c3s83A	Alignment	not modelled	62.7	18	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea
91	d1h5ya	Alignment	not modelled	62.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
92	d2ptda	Alignment	not modelled	62.5	29	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Bacterial PLC
93	c4adsF	Alignment	not modelled	62.3	10	PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex
94	c5zjnB	Alignment	not modelled	61.5	8	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
95	c3ffsC	Alignment	not modelled	60.3	17	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
96	c2w27A	Alignment	not modelled	60.2	3	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium
97	c1t5aB	Alignment	not modelled	60.0	19	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
98	c1aqfB	Alignment	not modelled	60.0	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
99	c6dq3B	Alignment	not modelled	58.8	8	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate
100	c3e0vB	Alignment	not modelled	58.6	15	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
101	c3igsB	Alignment	not modelled	58.1	12	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
102	c3gndC	Alignment	not modelled	57.8	20	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
103	c2y8uA	Alignment	not modelled	57.7	10	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: a. nidulans chitin deacetylase
104	d1h7na	Alignment	not modelled	57.3	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
						PDB header: hydrolase

105	c4rnjA_	Alignment	not modelled	56.0	14	Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora phosphodiesterase domain, apo form
106	c1pkkB_	Alignment	not modelled	55.7	15	PDB header: transferase Chain: B: PDB Molecule: protein (pyruvate kinase); PDBTitle: the structure of leishmania pyruvate kinase
107	c5ws9C_	Alignment	not modelled	55.0	15	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase (pyk) from mycobacterium tuberculosis in complex with 2 oxalate, atp and allosteric activator amp
108	c2vgbB_	Alignment	not modelled	53.3	16	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes r/l; PDBTitle: human erythrocyte pyruvate kinase
109	c2gjlA_	Alignment	not modelled	53.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
110	c4iqkB_	Alignment	not modelled	53.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmn
111	d1wv2a_	Alignment	not modelled	53.0	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
112	d1rpxa_	Alignment	not modelled	50.6	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
113	c1a3wB_	Alignment	not modelled	50.0	15	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg, 2 mn2+ and k+
114	d1liua2	Alignment	not modelled	49.4	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
115	c6irtA_	Alignment	not modelled	49.4	17	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
116	d1ccwa_	Alignment	not modelled	49.0	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
117	d1thfd_	Alignment	not modelled	48.0	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
118	c3gk0H_	Alignment	not modelled	48.0	14	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
119	c1e0tD_	Alignment	not modelled	47.9	14	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
120	c3qtgA_	Alignment	not modelled	47.7	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum