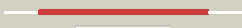























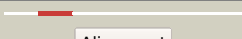


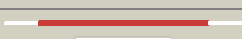
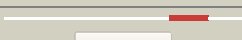






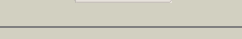

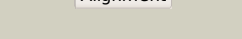
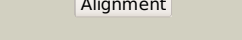
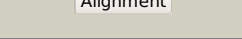
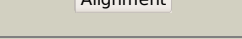
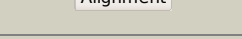
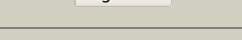






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2277c (- )_2549134_2550039
Date	Mon Aug 5 13:25:41 BST 2019
Unique Job ID	95440562cc21be68

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5vugA_</a>	 Alignment		100.0	98	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv2277c; <b>PDBTitle:</b> crystal structure of glycerophosphoryl diester phosphodiesterase2 domain of uncharacterized protein rv2277c from mycobacterium3 tuberculosis
2	<a href="#">c4r7oE_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase, putative; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterasefrom bacillus anthraci
3	<a href="#">c5t91A_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of b. subtilis 168 glpq in complex with bicine
4	<a href="#">c2p76H_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
5	<a href="#">c1ydyA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli
6	<a href="#">d1ydyal</a>	 Alignment		100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Glycerophosphoryl diester phosphodiesterase
7	<a href="#">c2pz0B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
8	<a href="#">c3l12A_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
9	<a href="#">d1zcca1</a>	 Alignment		100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Glycerophosphoryl diester phosphodiesterase
10	<a href="#">c3qvqB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase olei02445; <b>PDBTitle:</b> the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
11	<a href="#">c3mz2A_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution

12	<a href="#">c2otdC_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerophosphodiester phosphodiesterase; <b>PDBTitle:</b> the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
13	<a href="#">c4oecD_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of glycerophosphodiester phosphodiesterase from2 thermococcus kodakarensis kod1
14	<a href="#">c3ks6A_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens str. c583 (dupont) at 1.80 a resolution
15	<a href="#">c3no3A_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphodiester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution
16	<a href="#">d1vd6a1</a>	Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Glycerophosphoryl diester phosphodiesterase
17	<a href="#">d1o1za_</a>	Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Glycerophosphoryl diester phosphodiesterase
18	<a href="#">c3ch0A_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerophosphodiester phosphodiesterase; <b>PDBTitle:</b> crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
19	<a href="#">c3i10A_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphoryl diester phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
20	<a href="#">c2o55A_</a>	Alignment		100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphodiester phosphodiesterase; <b>PDBTitle:</b> crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
21	<a href="#">c3rlhA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sphingomyelin phosphodiesterase d lisictox-alphaia1a; <b>PDBTitle:</b> crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
22	<a href="#">c3rlgA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sphingomyelin phosphodiesterase d lisictox-alphaia1a; <b>PDBTitle:</b> crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
23	<a href="#">c2f9rC_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingomyelinase d 1; <b>PDBTitle:</b> crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom
24	<a href="#">c4q6xA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase d stsictox-betaic1; <b>PDBTitle:</b> structure of phospholipase d beta1b1i from sicarius terrosus venom at2 2.14 a resolution
25	<a href="#">c1djbB_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> lipid degradation <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoinositide-specific phospholipase c, <b>PDBTitle:</b> phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate
26	<a href="#">d1qasa3</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
27	<a href="#">d2zkmx4</a>	Alignment	not modelled	97.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Mammalian PLC
28	<a href="#">c3qr0A_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c-beta (plc-beta); <b>PDBTitle:</b> crystal structure of s. officinalis plc21

29	<a href="#">c2fjuB</a>	 Alignment	not modelled	97.3	11	<b>PDB header:</b> signaling protein,apoptosis/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate <b>PDBTitle:</b> activated rac1 bound to its effector phospholipase c beta 2
30	<a href="#">c3ohmB</a>	 Alignment	not modelled	97.3	16	<b>PDB header:</b> signaling protein / hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase <b>PDBTitle:</b> crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3
31	<a href="#">d1qopa</a>	 Alignment	not modelled	95.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
32	<a href="#">c3thaB</a>	 Alignment	not modelled	93.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
33	<a href="#">d1vkfa</a>	 Alignment	not modelled	92.4	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> GlpP-like <b>Family:</b> GlpP-like
34	<a href="#">c3ktsA</a>	 Alignment	not modelled	90.7	13	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol uptake operon antiterminator regulatory protein; <b>PDBTitle:</b> crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
35	<a href="#">c4rnhA</a>	 Alignment	not modelled	87.3	14	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> motility regulator; <b>PDBTitle:</b> pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
36	<a href="#">c3pjwA</a>	 Alignment	not modelled	85.7	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein; <b>PDBTitle:</b> structure of pseudomonas fluorescense lapd ggdef-eal dual domain, i23
37	<a href="#">c5xgdA</a>	 Alignment	not modelled	85.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa0861; <b>PDBTitle:</b> crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
38	<a href="#">c5m3cB</a>	 Alignment	not modelled	85.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> 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
39	<a href="#">c5k9xA</a>	 Alignment	not modelled	84.8	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
40	<a href="#">c3gzfB</a>	 Alignment	not modelled	82.7	22	<b>PDB header:</b> hydrolase, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> klebsiella pneumoniae blrp1; <b>PDBTitle:</b> klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
41	<a href="#">c2r6oB</a>	 Alignment	not modelled	81.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase (ggdef & eal) <b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
42	<a href="#">c4f48A</a>	 Alignment	not modelled	81.3	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the x-ray structural of fimxeal-c-di-gmp-pilz complexes from2 xanthomonas campestris
43	<a href="#">c2zbtB</a>	 Alignment	not modelled	81.3	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
44	<a href="#">c4fokA</a>	 Alignment	not modelled	80.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fimx; <b>PDBTitle:</b> 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
45	<a href="#">c3pfmA</a>	 Alignment	not modelled	80.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein; <b>PDBTitle:</b> crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
46	<a href="#">c6hq7B</a>	 Alignment	not modelled	80.0	8	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> eal enzyme bd1971; <b>PDBTitle:</b> structure of eal enzyme bd1971 - cgmp bound form
47	<a href="#">c4lykB</a>	 Alignment	not modelled	79.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic di-gmp phosphodiesterase yaha; <b>PDBTitle:</b> crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
48	<a href="#">c4hu4B</a>	 Alignment	not modelled	79.6	14	<b>PDB header:</b> signaling protein,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> oxygen sensor protein dosp; <b>PDBTitle:</b> crystal structure of eal domain of the e. coli dosp - dimeric form
49	<a href="#">c3hvbB</a>	 Alignment	not modelled	79.0	5	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein fimx; <b>PDBTitle:</b> crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
50	<a href="#">c2nv2U</a>	 Alignment	not modelled	78.3	29	<b>PDB header:</b> lyase/transferase <b>Chain:</b> U: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
51	<a href="#">c4y8eA</a>	 Alignment	not modelled	78.0	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pa3825 eal; <b>PDBTitle:</b> pa3825-eal ca-apo structure
52	<a href="#">c3femB</a>	 Alignment	not modelled	77.5	29	<b>PDB header:</b> biosynthetic protein, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine biosynthesis protein snz1; <b>PDBTitle:</b> structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
53	<a href="#">c4adsF</a>	 Alignment	not modelled	77.2	21	<b>PDB header:</b> transferase/transferase <b>Chain:</b> F: <b>PDB Molecule:</b> pyridoxine biosynthetic enzyme pdx1 homologue, putative; <b>PDBTitle:</b> crystal structure of plasmodial plp synthase complex

54	<a href="#">c6hyeF_</a>	Alignment	not modelled	76.5	31	<b>PDB header:</b> plant protein <b>Chain:</b> F; <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase subunit pdx1.3; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (pdx1.3:k97a)
55	<a href="#">c3s83A_</a>	Alignment	not modelled	76.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ggdef family protein; <b>PDBTitle:</b> eal domain of phosphodiesterase pdea
56	<a href="#">c3tlqB_</a>	Alignment	not modelled	76.3	8	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> regulatory protein ydiv; <b>PDBTitle:</b> crystal structure of eal-like domain protein ydiv
57	<a href="#">c6hxgE_</a>	Alignment	not modelled	76.2	28	<b>PDB header:</b> plant protein <b>Chain:</b> E; <b>PDB Molecule:</b> pyridoxal 5'-phosphate synthase-like subunit pdx1.2; <b>PDBTitle:</b> pdx1.2/pdx1.3 complex (intermediate)
58	<a href="#">c5m1tB_</a>	Alignment	not modelled	75.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> muacr phosphodiesterase; <b>PDBTitle:</b> pamucr phosphodiesterase, c-di-gmp complex
59	<a href="#">c3sy8C_</a>	Alignment	not modelled	75.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C; <b>PDB Molecule:</b> rocr; <b>PDBTitle:</b> crystal structure of the response regulator rocr
60	<a href="#">c4s1aB_</a>	Alignment	not modelled	75.4	28	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
61	<a href="#">c4rnjA_</a>	Alignment	not modelled	75.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> motility regulator; <b>PDBTitle:</b> pamora phosphodiesterase domain, apo form
62	<a href="#">c3h4wA_</a>	Alignment	not modelled	74.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphatidylinositol-specific phospholipase c1; <b>PDBTitle:</b> structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus
63	<a href="#">c3kzpA_</a>	Alignment	not modelled	74.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase; <b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listeria monocytigenes
64	<a href="#">c4q6jB_</a>	Alignment	not modelled	73.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> lmo0131 protein; <b>PDBTitle:</b> crystal structure of eal domain protein from listeria monocytogenes2 egd-e
65	<a href="#">c5yrpB_</a>	Alignment	not modelled	73.2	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> sensory box/response regulator; <b>PDBTitle:</b> crystal structure of the eal domain of mycobacterium smegmatis dcpa
66	<a href="#">c4hjfA_</a>	Alignment	not modelled	73.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ggdef family protein; <b>PDBTitle:</b> eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
67	<a href="#">c3a24A_</a>	Alignment	not modelled	72.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of bt1871 retaining glycosidase
68	<a href="#">c5d88A_</a>	Alignment	not modelled	72.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> predicted protease of the collagenase family; <b>PDBTitle:</b> the structure of the u32 peptidase mk0906
69	<a href="#">d2basa1</a>	Alignment	not modelled	72.2	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> EAL domain-like <b>Family:</b> EAL domain
70	<a href="#">c2w27A_</a>	Alignment	not modelled	69.8	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> ykui protein; <b>PDBTitle:</b> crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium
71	<a href="#">c2htmB_</a>	Alignment	not modelled	68.8	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> thiazole biosynthesis protein thig; <b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8
72	<a href="#">c3hv9A_</a>	Alignment	not modelled	67.8	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein fimx; <b>PDBTitle:</b> crystal structure of fimx eal domain from pseudomonas aeruginosa
73	<a href="#">c2zq0B_</a>	Alignment	not modelled	67.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> alpha-glucosidase (alpha-glucosidase sub); <b>PDBTitle:</b> crystal structure of sub complexed with acarbose
74	<a href="#">c5kzmA_</a>	Alignment	not modelled	67.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
75	<a href="#">c3bo9B_</a>	Alignment	not modelled	66.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> putative nitroalkan dioxygenase; <b>PDBTitle:</b> crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
76	<a href="#">c3vndD_</a>	Alignment	not modelled	64.8	18	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
77	<a href="#">c3gndC_</a>	Alignment	not modelled	64.6	17	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> aldolase lsrf; <b>PDBTitle:</b> crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
78	<a href="#">c3navB_</a>	Alignment	not modelled	62.5	13	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
79	<a href="#">c4iiaA_</a>	Alignment	not modelled	61.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> geranylgeranylglyceryl phosphate

79	<a href="#">c4tjA</a>	Alignment	not modelled	61.8	13	synthase; <b>PDBTitle:</b> gggps from flavobacterium johnsoniae
80	<a href="#">d2ptda</a>	Alignment	not modelled	61.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLC-like phosphodiesterases <b>Family:</b> Bacterial PLC
81	<a href="#">c2yztB</a>	Alignment	not modelled	60.8	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
82	<a href="#">c5hqCA</a>	Alignment	not modelled	60.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 97 enzyme; <b>PDBTitle:</b> a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8
83	<a href="#">c3vkbA</a>	Alignment	not modelled	57.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> moeo5; <b>PDBTitle:</b> crystal structure of moeo5 soaked with fspp overnight
84	<a href="#">c5xfmD</a>	Alignment	not modelled	57.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of beta-arabinopyranosidase
85	<a href="#">c2gjlA</a>	Alignment	not modelled	56.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1024; <b>PDBTitle:</b> crystal structure of 2-nitropropane dioxygenase
86	<a href="#">c4iqjB</a>	Alignment	not modelled	55.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase ii; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis enoyl-acp reductase ii2 (fabk) with cofactors nadph and fmh
87	<a href="#">d1xm3a</a>	Alignment	not modelled	53.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
88	<a href="#">c2qr6A</a>	Alignment	not modelled	51.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imp dehydrogenase/gmp reductase; <b>PDBTitle:</b> crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
89	<a href="#">c6nkeA</a>	Alignment	not modelled	51.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> wild-type gggps from thermoplasma volcanium
90	<a href="#">c4firB</a>	Alignment	not modelled	50.2	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal biosynthesis lyase pdxs; <b>PDBTitle:</b> crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus
91	<a href="#">c5hxgA</a>	Alignment	not modelled	49.3	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein stm1697; <b>PDBTitle:</b> stm1697-flhd complex
92	<a href="#">c3ffsC</a>	Alignment	not modelled	48.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
93	<a href="#">c4v1af</a>	Alignment	not modelled	46.9	44	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
94	<a href="#">c5tchG</a>	Alignment	not modelled	46.5	25	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
95	<a href="#">c2yw3E</a>	Alignment	not modelled	46.3	13	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- <b>PDBTitle:</b> crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
96	<a href="#">c2rbgB</a>	Alignment	not modelled	45.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein st0493; <b>PDBTitle:</b> crystal structure of hypothetical protein(st0493) from2 sulfobolus tokodaii
97	<a href="#">c2qjhH</a>	Alignment	not modelled	44.8	17	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
98	<a href="#">c4rk1F</a>	Alignment	not modelled	43.5	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> ribose transcriptional regulator; <b>PDBTitle:</b> crystal structure of laci family transcriptional regulator from2 enterococcus faecium, target efi-512930, with bound ribose
99	<a href="#">d2d13a1</a>	Alignment	not modelled	42.9	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
100	<a href="#">c5z9yB</a>	Alignment	not modelled	41.5	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole synthase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
101	<a href="#">c3o1hB</a>	Alignment	not modelled	41.2	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein tort; <b>PDBTitle:</b> crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
102	<a href="#">d1ru8a</a>	Alignment	not modelled	40.5	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
103	<a href="#">c5b69A</a>	Alignment	not modelled	39.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranylgeranyl phosphate synthase; <b>PDBTitle:</b> crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
104	<a href="#">d1wv2a</a>	Alignment	not modelled	39.8	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like <b>PDB header:</b> ribosome

105	<a href="#">c5ooma_</a>	Alignment	not modelled	37.3	44	<b>Chain:</b> A: <b>PDB Molecule:</b> 16s ribosomal rna; <b>PDBTitle:</b> structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rrna
106	<a href="#">c3qz6A_</a>	Alignment	not modelled	37.1	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfotobacterium2 hafniense dcb-2
107	<a href="#">c2ekcA_</a>	Alignment	not modelled	36.9	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
108	<a href="#">c2e77B_</a>	Alignment	not modelled	36.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate oxidase; <b>PDBTitle:</b> crystal structure of l-lactate oxidase with pyruvate complex
109	<a href="#">d1tqxa_</a>	Alignment	not modelled	36.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
110	<a href="#">c2zrvC_</a>	Alignment	not modelled	36.0	5	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase; <b>PDBTitle:</b> crystal structure of sulfobolus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
111	<a href="#">c5f56A_</a>	Alignment	not modelled	34.8	16	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease; <b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct
112	<a href="#">c5zknA_</a>	Alignment	not modelled	34.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
113	<a href="#">c4utwB_</a>	Alignment	not modelled	34.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structural characterisation of hane, mannac6p c2 epimerase,2 from clostridium perfringens
114	<a href="#">d1p4ca_</a>	Alignment	not modelled	34.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
115	<a href="#">c5kinC_</a>	Alignment	not modelled	33.1	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
116	<a href="#">c1fcbA_</a>	Alignment	not modelled	32.6	13	<b>PDB header:</b> oxidoreductase (ch-oh(d)-cytochrome(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome b2; <b>PDBTitle:</b> molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
117	<a href="#">c4mozC_</a>	Alignment	not modelled	32.0	27	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
118	<a href="#">c3v18A_</a>	Alignment	not modelled	31.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-phosphatidylinositol phosphodiesterase; <b>PDBTitle:</b> structure of the phosphatidylinositol-specific phospholipase c from2 staphylococcus aureus
119	<a href="#">c3nvtA_</a>	Alignment	not modelled	31.0	22	<b>PDB header:</b> transferase/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; <b>PDBTitle:</b> 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
120	<a href="#">c6fv5B_</a>	Alignment	not modelled	30.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> queuine trna-ribosyltransferase accessory subunit 2; <b>PDBTitle:</b> qtrt2, the non-catalytic subunit of murine trna-guanine2 transglycosylase