



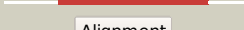
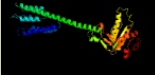
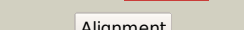

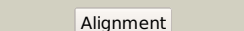





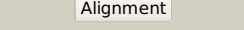

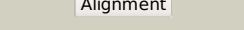

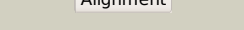

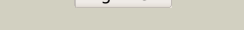








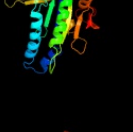



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1319c_(-)_1480900_1482507
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	8b563183e15e0132

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fhtB_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
2	<a href="#">c4yusA_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> family 3 adenylate cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
3	<a href="#">c6r4oA_</a>	 Alignment		100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a truncated adenyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
4	<a href="#">c5nbyA_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> beta subunit of photoactivated adenyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenyl cyclase
5	<a href="#">c4cliA_</a>	 Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase type 10; <b>PDBTitle:</b> crystal structure of human soluble adenyl cyclase in complex with2 bicarbonate
6	<a href="#">c5o5kC_</a>	 Alignment		100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> x-ray structure of a bacterial adenyl cyclase soluble domain
7	<a href="#">c1y10C_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
8	<a href="#">c6r4pA_</a>	 Alignment		100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a soluble domain of adenyl cyclase bound to an2 activated stimulatory g protein
9	<a href="#">c1wc6B_</a>	 Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
10	<a href="#">c2w01C_</a>	 Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of the guanylyl cyclase cya2
11	<a href="#">d1wc1a_</a>	 Alignment		100.0	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenyl and guanylyl cyclase catalytic domain

12	<a href="#">c1cjkA</a>	Alignment		100.0	19	<b>PDB header:</b> lyase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase, type v; <b>PDBTitle:</b> complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
13	<a href="#">c3r5gB</a>	Alignment		99.9	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenylyl cyclase cyab from p. aeruginosa
14	<a href="#">d1azsa</a>	Alignment		99.9	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
15	<a href="#">d1fx2a</a>	Alignment		99.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
16	<a href="#">c3uvjC</a>	Alignment		99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> guanylate cyclase soluble subunit alpha-3; <b>PDBTitle:</b> crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
17	<a href="#">d1fx4a</a>	Alignment		99.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
18	<a href="#">c3et6A</a>	Alignment		99.9	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble guanylyl cyclase beta; <b>PDBTitle:</b> the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
19	<a href="#">c2wz1B</a>	Alignment		99.9	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
20	<a href="#">c3mr7B</a>	Alignment		99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate/guanylate cyclase/hydrolase, alpha/beta fold <b>PDBTitle:</b> crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
21	<a href="#">d1azsb</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
22	<a href="#">c1ybuA</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
23	<a href="#">c1yk9A</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
24	<a href="#">c4wp3E</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> ma1120; <b>PDBTitle:</b> crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
25	<a href="#">c6aoaA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; <b>PDBTitle:</b> monomeric crystal structure of the e497/c566d double mutant of the2 guanylyl cyclase domain of the rhogc fusion protein from the aquatic3 fungus blastocladiella emersonii
26	<a href="#">c5jefA</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite sensor protein narq; <b>PDBTitle:</b> fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
27	<a href="#">c4gn0D</a>	Alignment	not modelled	98.7	10	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
28	<a href="#">c3lnrA</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2

29	<a href="#">c3zx6A</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
30	<a href="#">d2asxa1</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> HAMP domain-like <b>Superfamily:</b> HAMP domain-like <b>Family:</b> HAMP domain
31	<a href="#">c3zrwB</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
32	<a href="#">c4i5sA</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative histidine kinase covs; vick-like protein; <b>PDBTitle:</b> structure and function of sensor histidine kinase
33	<a href="#">c4ctiA</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> osmolarity sensor protein envz, af1503; <b>PDBTitle:</b> escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
34	<a href="#">c4biuB</a>	Alignment	not modelled	96.7	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (orthorhombic form 1)
35	<a href="#">c2qv6D</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase iii; <b>PDBTitle:</b> gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
36	<a href="#">c1w25B</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein; <b>PDBTitle:</b> response regulator pled in complex with c-digmp
37	<a href="#">c6d9mA</a>	Alignment	not modelled	95.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of endolysin,response receiver sensor <b>PDBTitle:</b> t4-lysozyme fusion to geobacter ggdef
38	<a href="#">c3ungC</a>	Alignment	not modelled	95.1	24	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> cmr2dhd; <b>PDBTitle:</b> structure of the cmr2 subunit of the crispr rna silencing complex
39	<a href="#">c4wxoA</a>	Alignment	not modelled	95.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> sadc (300-487) from pseudomonas aeruginosa pao1
40	<a href="#">c3i5cA</a>	Alignment	not modelled	95.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion of general control protein gcn4 and wspr response <b>PDBTitle:</b> crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
41	<a href="#">c4zmuD</a>	Alignment	not modelled	94.9	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
42	<a href="#">c3ezuA</a>	Alignment	not modelled	94.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein; <b>PDBTitle:</b> crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
43	<a href="#">c3i5aA</a>	Alignment	not modelled	94.4	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/ggdef domain protein; <b>PDBTitle:</b> crystal structure of full-length wpsr from pseudomonas syringae
44	<a href="#">c5llxB</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase (ggdef) domain-containing protein; <b>PDBTitle:</b> bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
45	<a href="#">c3breA</a>	Alignment	not modelled	93.9	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> crystal structure of p.aeruginosa pa3702
46	<a href="#">c2rm8A</a>	Alignment	not modelled	93.6	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory rhodopsin ii transducer; <b>PDBTitle:</b> the solution structure of phototactic transducer protein2 htiii linker region from natronomonas pharaonis
47	<a href="#">c3hvaA</a>	Alignment	not modelled	92.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fimx; <b>PDBTitle:</b> crystal structure of fimx ggdef domain from pseudomonas aeruginosa
48	<a href="#">c3mtkA</a>	Alignment	not modelled	92.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase/phosphodiesterase; <b>PDBTitle:</b> x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
49	<a href="#">c3i5bA</a>	Alignment	not modelled	92.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wpsr response regulator; <b>PDBTitle:</b> crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
50	<a href="#">d1w25a3</a>	Alignment	not modelled	91.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> GGDEF domain
51	<a href="#">c3ignA</a>	Alignment	not modelled	91.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
52	<a href="#">c3hvwA</a>	Alignment	not modelled	91.6	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate-cyclase (dgc); <b>PDBTitle:</b> crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural

						genomics consortium3 target par365c
53	<a href="#">c5euhA</a>	Alignment	not modelled	91.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative ggdef domain membrane protein; <b>PDBTitle:</b> crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbc
54	<a href="#">c4dmzB</a>	Alignment	not modelled	90.4	9	<b>PDB header:</b> nucleotide-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein peld; <b>PDBTitle:</b> peld 156-455 from pseudomonas aeruginosa pa14, apo form
55	<a href="#">c4zvH</a>	Alignment	not modelled	90.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase dosc; <b>PDBTitle:</b> crystal structure of ggdef domain of the e. coli dosc - form iv
56	<a href="#">c4iobA</a>	Alignment	not modelled	89.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase tpbb; <b>PDBTitle:</b> crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
57	<a href="#">c4ymeA</a>	Alignment	not modelled	88.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sensory box/ggdef family protein; <b>PDBTitle:</b> crystal structure of a sensory box/ggdef family protein (cc_0091) from2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
58	<a href="#">c5m3cB</a>	Alignment	not modelled	88.3	18	<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
59	<a href="#">c4h54B</a>	Alignment	not modelled	87.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase ydeh; <b>PDBTitle:</b> crystal structure of the diguanylate cyclase dgcz
60	<a href="#">c3pjwA</a>	Alignment	not modelled	84.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein; <b>PDBTitle:</b> structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
61	<a href="#">c3icIA</a>	Alignment	not modelled	84.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> eal/ggdef domain protein; <b>PDBTitle:</b> x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
62	<a href="#">c4zmmB</a>	Alignment	not modelled	84.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> ggdef domain of dcsbis complexed with c-di-gmp
63	<a href="#">c5xgdA</a>	Alignment	not modelled	82.6	15	<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
64	<a href="#">c6eibC</a>	Alignment	not modelled	81.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensory box/ggdef family protein; <b>PDBTitle:</b> structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
65	<a href="#">c3tvkA</a>	Alignment	not modelled	81.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase dgcz; <b>PDBTitle:</b> diguanylate cyclase domain of dgcz
66	<a href="#">c4urgB</a>	Alignment	not modelled	79.2	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> crystal structure of ggdef domain from t.maritima (active-like dimer)
67	<a href="#">c4euvA</a>	Alignment	not modelled	78.8	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> peld; <b>PDBTitle:</b> crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
68	<a href="#">c4rnhA</a>	Alignment	not modelled	77.2	19	<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
69	<a href="#">c4w8yA</a>	Alignment	not modelled	75.8	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr2; <b>PDBTitle:</b> structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
70	<a href="#">c3qyyB</a>	Alignment	not modelled	73.9	19	<b>PDB header:</b> signaling protein/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5 )-cyclic di-gmp
71	<a href="#">c5n9jB</a>	Alignment	not modelled	39.5	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 10; <b>PDBTitle:</b> core mediator of transcriptional regulation
72	<a href="#">c6ifnA</a>	Alignment	not modelled	35.7	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type iii-a crispr-associated protein csm1; <b>PDBTitle:</b> crystal structure of type iii-a crispr csm complex
73	<a href="#">d1v6ta</a>	Alignment	not modelled	33.4	5	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
74	<a href="#">c2x5eA</a>	Alignment	not modelled	33.0	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
75	<a href="#">d2dfaa1</a>	Alignment	not modelled	32.4	12	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
76	<a href="#">c2w6bA</a>	Alignment	not modelled	31.9	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 7; <b>PDBTitle:</b> crystal structure of the trimeric beta-pix coiled-coil2 domain
77	<a href="#">c5bw9G</a>	Alignment	not modelled	31.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> v-type proton atpase subunit d; <b>PDBTitle:</b> crystal structure of yeast v1-atpase in the autoinhibited form <b>PDB header:</b> hydrolase

78	<a href="#">c4rndC_</a>	Alignment	not modelled	30.3	18	<b>Chain:</b> C; <b>PDB Molecule:</b> v-type proton atpase subunit d; <b>PDBTitle:</b> crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
79	<a href="#">c4biyD_</a>	Alignment	not modelled	30.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpaxhc (monoclinic form 2)
80	<a href="#">d1q8ka2</a>	Alignment	not modelled	29.8	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
81	<a href="#">c3w3aO_</a>	Alignment	not modelled	28.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> O; <b>PDB Molecule:</b> v-type atp synthase subunit d; <b>PDBTitle:</b> crystal structure of v1-atpase at 3.9 angstrom resolution
82	<a href="#">c5buzC_</a>	Alignment	not modelled	27.8	19	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> snap receptor-like protein; <b>PDBTitle:</b> crystal structure of a complex between the snare vam3 and the hops2 vps33-vps16 subcomplex from chaetomium thermophilum
83	<a href="#">c3dcaC_</a>	Alignment	not modelled	26.4	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
84	<a href="#">c3j9vM_</a>	Alignment	not modelled	20.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> M; <b>PDB Molecule:</b> v-type proton atpase subunit d; <b>PDBTitle:</b> yeast v-atpase state 3
85	<a href="#">c3hlsE_</a>	Alignment	not modelled	18.5	19	<b>PDB header:</b> signaling protein <b>Chain:</b> E; <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> crystal structure of the signaling helix coiled-coil domain2 of the beta-1 subunit of the soluble guanylyl cyclase
86	<a href="#">c3a5dG_</a>	Alignment	not modelled	18.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> v-type atp synthase subunit d; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
87	<a href="#">c6iqwA_</a>	Alignment	not modelled	17.0	13	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> csm1; <b>PDBTitle:</b> cryo-em structure of csm effector complex
88	<a href="#">d1veha_</a>	Alignment	not modelled	16.7	15	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
89	<a href="#">d1ef5a_</a>	Alignment	not modelled	16.3	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
90	<a href="#">d1f6ga_</a>	Alignment	not modelled	15.9	8	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
91	<a href="#">c3q34A_</a>	Alignment	not modelled	15.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ycei-like family protein; <b>PDBTitle:</b> the crystal structure of ycei-like family protein from pseudomonas2 syringae
92	<a href="#">c5ixhB_</a>	Alignment	not modelled	15.7	11	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> ycei-like domain protein; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia bcna
93	<a href="#">c2x34A_</a>	Alignment	not modelled	15.2	9	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cellulose-binding protein, x158; <b>PDBTitle:</b> structure of a polyisoprenoid binding domain from saccharophagus2 degradans implicated in plant cell wall breakdown
94	<a href="#">c2xb2G_</a>	Alignment	not modelled	14.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> regulator of nonsense transcripts 3b; <b>PDBTitle:</b> crystal structure of the core mago-y14-eif4aiii-barentsz-2 upf3b assembly shows how the ejc is bridged to the nmd3 machinery
95	<a href="#">d1ttha_</a>	Alignment	not modelled	14.4	27	<b>Fold:</b> Anti-sigma factor AsiA <b>Superfamily:</b> Anti-sigma factor AsiA <b>Family:</b> Anti-sigma factor AsiA
96	<a href="#">c2mmbA_</a>	Alignment	not modelled	14.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr structure of the protein yp_001712342.1 from acinetobacter2 baumannii
97	<a href="#">c3vfvA_</a>	Alignment	not modelled	14.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> amino acid abc transporter, binding protein; <b>PDBTitle:</b> crystal structure of ttc0807 complexed with arginine
98	<a href="#">d2b3aa1</a>	Alignment	not modelled	13.6	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
99	<a href="#">d2ebfx1</a>	Alignment	not modelled	13.2	58	<b>Fold:</b> PMT central region-like <b>Superfamily:</b> PMT central region-like <b>Family:</b> PMT central region-like