
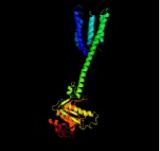
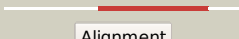












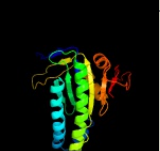











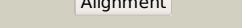
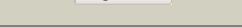




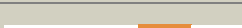

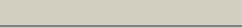




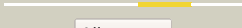
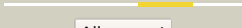

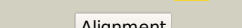

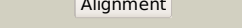
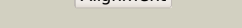

# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1625c\_cya\_1826621\_1827952  
 Date Fri Aug 2 13:30:21 BST 2019  
 Unique Job ID 4ee589b5a66987da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6r4oA_</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a truncated adenylyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
2	<a href="#">c6fhtB_</a>	 Alignment		100.0	24	<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 adenylyl/guanylyl cyclase in its dark adapted pr form
3	<a href="#">c6r4pA_</a>	 Alignment		100.0	36	<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 adenylyl cyclase bound to an2 activated stimulatory g protein
4	<a href="#">c5o5kC_</a>	 Alignment		100.0	85	<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 adenylyl cyclase soluble domain
5	<a href="#">c4yusA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> family 3 adenylyl cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaosillatoria acuminata in hexagonal form
6	<a href="#">c5nbyA_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> beta subunit of photoactivated adenylyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenylyl cyclase
7	<a href="#">c4cIIA_</a>	 Alignment		100.0	20	<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 adenylyl cyclase in complex with2 bicarbonate
8	<a href="#">c1cjkA_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase/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
9	<a href="#">dlazsa_</a>	 Alignment		100.0	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
10	<a href="#">dlazsb_</a>	 Alignment		100.0	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
11	<a href="#">c1y10C_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state

12	<a href="#">c2w01C_</a>	Alignment		100.0	24	<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
13	<a href="#">c1yk9A_</a>	Alignment		100.0	98	<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 adenyllyl cyclase rv1625c
14	<a href="#">c1wc6B_</a>	Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenyllyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
15	<a href="#">d1wc1a_</a>	Alignment		100.0	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
16	<a href="#">c3r5gB_</a>	Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenyllyl cyclase cyab from p. aeruginosa
17	<a href="#">c3uviC_</a>	Alignment		100.0	32	<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.
18	<a href="#">c6a0aA_</a>	Alignment		100.0	36	<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 blastocliadiella emersonii
19	<a href="#">d1fx2a_</a>	Alignment		100.0	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
20	<a href="#">c2wz1B_</a>	Alignment		100.0	39	<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.
21	<a href="#">d1fx4a_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
22	<a href="#">c3et6A_</a>	Alignment	not modelled	100.0	50	<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
23	<a href="#">c3mr7B_</a>	Alignment	not modelled	99.9	27	<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
24	<a href="#">c1ybuA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenyllyl cyclase rv1900c chd, in complex2 with a substrate analog.
25	<a href="#">c4wp3E_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> ma1120; <b>PDBTitle:</b> crystal structure of adenyllyl cyclase from mycobacterium avium ma11202 wild type
26	<a href="#">c2qv6D_</a>	Alignment	not modelled	97.2	13	<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
27	<a href="#">c3hlsE_</a>	Alignment	not modelled	96.3	15	<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 doimain2 of the beta-1 subunit of the soluble guanylyl cyclase
28	<a href="#">c3i5aA_</a>	Alignment	not modelled	94.9	12	<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

29	<a href="#">c3i5cA_</a>	 Alignment	not modelled	94.4	15	<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
30	<a href="#">c5llxB_</a>	 Alignment	not modelled	94.0	12	<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
31	<a href="#">c3breA_</a>	 Alignment	not modelled	93.2	14	<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
32	<a href="#">c4zmuD_</a>	 Alignment	not modelled	93.2	15	<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
33	<a href="#">c4h54B_</a>	 Alignment	not modelled	92.5	9	<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
34	<a href="#">c6d9mA_</a>	 Alignment	not modelled	92.2	15	<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
35	<a href="#">c1w25B_</a>	 Alignment	not modelled	89.5	13	<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
36	<a href="#">c3i5bA_</a>	 Alignment	not modelled	89.1	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wspr response regulator; <b>PDBTitle:</b> crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
37	<a href="#">c3ezuA_</a>	 Alignment	not modelled	87.4	16	<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
38	<a href="#">c5xgdA_</a>	 Alignment	not modelled	84.9	11	<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
39	<a href="#">c4ymeA_</a>	 Alignment	not modelled	84.5	16	<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)
40	<a href="#">c3ignA_</a>	 Alignment	not modelled	82.0	8	<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
41	<a href="#">c4urgB_</a>	 Alignment	not modelled	81.4	16	<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)
42	<a href="#">c4dmzB_</a>	 Alignment	not modelled	81.1	12	<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
43	<a href="#">c3hvwA_</a>	 Alignment	not modelled	79.7	4	<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
44	<a href="#">c4wxoA_</a>	 Alignment	not modelled	78.4	12	<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
45	<a href="#">d1w25a3</a>	 Alignment	not modelled	78.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> GGDEF domain
46	<a href="#">c4iobA_</a>	 Alignment	not modelled	78.1	18	<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.
47	<a href="#">c3mtkA_</a>	 Alignment	not modelled	76.6	9	<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
48	<a href="#">c5euhA_</a>	 Alignment	not modelled	75.2	15	<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
49	<a href="#">c5cupB_</a>	 Alignment	not modelled	74.7	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphate propanoyltransferase; <b>PDBTitle:</b> structure of rhodopseudomonas palustris pdul - phosphate bound form
50	<a href="#">c3tvkA_</a>	 Alignment	not modelled	74.1	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase dgcz; <b>PDBTitle:</b> diguanylate cyclase domain of dgcz
51	<a href="#">c4w8yA_</a>	 Alignment	not modelled	72.7	13	<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)
52	<a href="#">c3ungC_</a>	 Alignment	not modelled	72.4	11	<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

53	<a href="#">c3hvaA</a>	Alignment	not modelled	72.3	12	<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
54	<a href="#">c6eibC</a>	Alignment	not modelled	71.6	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.
55	<a href="#">c4zmmB</a>	Alignment	not modelled	68.7	11	<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
56	<a href="#">c4zvHb</a>	Alignment	not modelled	68.0	18	<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
57	<a href="#">c5m3cB</a>	Alignment	not modelled	63.1	13	<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
58	<a href="#">c6ifnA</a>	Alignment	not modelled	57.9	15	<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
59	<a href="#">c3pjwA</a>	Alignment	not modelled	55.2	8	<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
60	<a href="#">c3icIA</a>	Alignment	not modelled	54.4	14	<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
61	<a href="#">c2x5eA</a>	Alignment	not modelled	53.0	20	<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
62	<a href="#">d1v6ta</a>	Alignment	not modelled	52.4	22	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
63	<a href="#">c4euvA</a>	Alignment	not modelled	48.8	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
64	<a href="#">d2dfaa1</a>	Alignment	not modelled	48.5	24	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
65	<a href="#">c3qyvB</a>	Alignment	not modelled	48.5	12	<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
66	<a href="#">c4rnhA</a>	Alignment	not modelled	24.4	13	<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
67	<a href="#">c5buzC</a>	Alignment	not modelled	19.0	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
68	<a href="#">d1m9dc</a>	Alignment	not modelled	18.1	28	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
69	<a href="#">c2xgvA</a>	Alignment	not modelled	17.9	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> psiv capsid n-terminal domain; <b>PDBTitle:</b> structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
70	<a href="#">c5t4oA</a>	Alignment	not modelled	17.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1
71	<a href="#">c2pjhB</a>	Alignment	not modelled	17.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
72	<a href="#">d2eiaa2</a>	Alignment	not modelled	17.1	22	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
73	<a href="#">d1m9fd</a>	Alignment	not modelled	17.0	28	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
74	<a href="#">d2pxrc1</a>	Alignment	not modelled	16.3	28	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
75	<a href="#">c2wlvA</a>	Alignment	not modelled	16.1	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal capsid domain of hiv-2
76	<a href="#">c2n5IA</a>	Alignment	not modelled	15.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease zc3h12a; <b>PDBTitle:</b> regnase-1 c-terminal domain
77	<a href="#">c4axkB</a>	Alignment	not modelled	15.6	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of subhisa from the thermophile corynebacterium2 efficiens
78	<a href="#">c4rrfD</a>	Alignment	not modelled	15.0	19	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonine--trna ligase; <b>PDBTitle:</b> editing domain of threonyl-trna synthetase from

						methanococcus2 jannaschii with l-ser3aa
79	<a href="#">c5fa0B_</a>	Alignment	not modelled	14.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetyl glucosaminyl transferase; <b>PDBTitle:</b> the structure of the beta-3-deoxy-d-manno-oct-2-ulosonic acid2 transferase domain from wbbb
80	<a href="#">c6fkhA_</a>	Alignment	not modelled	13.9	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha, chloroplastic; <b>PDBTitle:</b> chloroplast fl1o conformation 2
81	<a href="#">c2kjaA_</a>	Alignment	not modelled	13.3	18	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> solution structure and backbone dynamics of the permutant p54-55
82	<a href="#">c1avoA_</a>	Alignment	not modelled	13.3	33	<b>PDB header:</b> proteasome activator <b>Chain:</b> A: <b>PDB Molecule:</b> 11s regulator; <b>PDBTitle:</b> proteasome activator reg(alpha)
83	<a href="#">c5ggoB_</a>	Alignment	not modelled	13.0	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein o-linked-mannose beta-1,2-n- <b>PDBTitle:</b> crystal structure of n-terminal domain of human protein o-mannose2 beta-1,2-n-acetylglucosaminyltransferase in complex with galnac-3 beta1,3-glcnac-beta-pnp
84	<a href="#">c2hl2A_</a>	Alignment	not modelled	12.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
85	<a href="#">c3dcaC_</a>	Alignment	not modelled	12.4	13	<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 rhodospseudomonas palustris- a structural3 genomics target
86	<a href="#">c6iqwA_</a>	Alignment	not modelled	12.3	16	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> csml1; <b>PDBTitle:</b> cryo-em structure of csm effector complex
87	<a href="#">c2y0fD_</a>	Alignment	not modelled	12.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> structure of gcpe (ispq) from thermus thermophilus hb27
88	<a href="#">c3a6mB_</a>	Alignment	not modelled	11.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein grpe; <b>PDBTitle:</b> crystal structure of grpe from thermus thermophilus hb8
89	<a href="#">c3nvbA_</a>	Alignment	not modelled	11.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
90	<a href="#">c2xgyA_</a>	Alignment	not modelled	11.1	17	<b>PDB header:</b> viral protein/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> relik capsid n-terminal domain; <b>PDBTitle:</b> complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a
91	<a href="#">d1v4ea_</a>	Alignment	not modelled	11.1	16	<b>Fold:</b> Terpenoid synthases <b>Superfamily:</b> Terpenoid synthases <b>Family:</b> Isoprenyl diphosphate synthases
92	<a href="#">c5dn6A_</a>	Alignment	not modelled	11.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> atp synthase from paracoccus denitrificans
93	<a href="#">c4aniA_</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein grpe; <b>PDBTitle:</b> structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
94	<a href="#">c4tt1A_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deneddyase; <b>PDBTitle:</b> crystal structure of fragment 1600-1733 of hsv1 ul36, native
95	<a href="#">d2gsva1</a>	Alignment	not modelled	10.6	16	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> YvfG-like <b>Family:</b> YvfG-like
96	<a href="#">c2vfwB_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain z-isoprenyl diphosphate synthetase; <b>PDBTitle:</b> rv1086 native
97	<a href="#">d2crua1</a>	Alignment	not modelled	10.2	15	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Double-stranded DNA-binding domain <b>Family:</b> Double-stranded DNA-binding domain
98	<a href="#">c1l6nA_</a>	Alignment	not modelled	10.2	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
99	<a href="#">d1k8ba_</a>	Alignment	not modelled	10.1	25	<b>Fold:</b> Ribosome binding domain-like <b>Superfamily:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain <b>Family:</b> Translation initiation factor 2 beta, aIF2beta, N-terminal domain