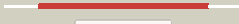

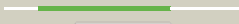

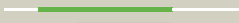
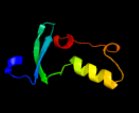

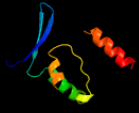

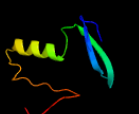


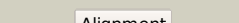
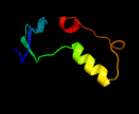


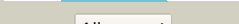
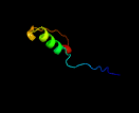
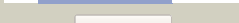




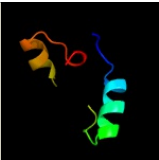

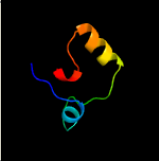
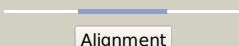

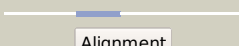
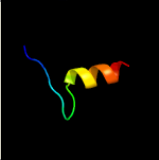
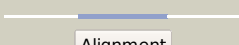
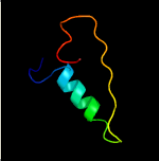
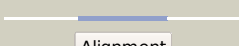
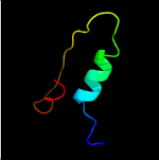
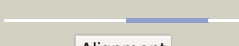

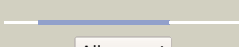


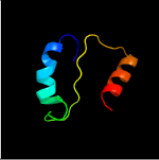
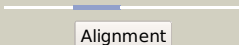

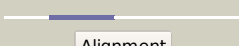



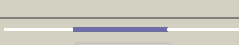


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2020c (- )_2266429_2266728
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	dc2bcfd847a5ead8

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xqkB_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> llabiii; <b>PDBTitle:</b> atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
2	<a href="#">c3pgvB_</a>	 Alignment		53.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
3	<a href="#">c3dnpA_</a>	 Alignment		51.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
4	<a href="#">c4bndB_</a>	 Alignment		45.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-phosphoglucomutase; <b>PDBTitle:</b> structure of an atypical alpha-phosphoglucomutase similar to2 eukaryotic phosphomannomutases
5	<a href="#">d1nrwa_</a>	 Alignment		37.6	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
6	<a href="#">d1nf2a_</a>	 Alignment		37.4	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
7	<a href="#">c3niwA_</a>	 Alignment		34.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
8	<a href="#">c3fzqA_</a>	 Alignment		31.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
9	<a href="#">c3gygA_</a>	 Alignment		30.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon putative hydrolase ntdb; <b>PDBTitle:</b> crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
10	<a href="#">d1s2oa1</a>	 Alignment		29.3	5	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
11	<a href="#">d2rbka1</a>	 Alignment		28.6	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof

12	<a href="#">c3ebnD</a>	 Alignment		24.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping
13	<a href="#">c3d23A</a>	 Alignment		23.9	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 3c-like proteinase; <b>PDBTitle:</b> main protease of hcov-hku1
14	<a href="#">c6cj0A</a>	 Alignment		23.9	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose phosphatase; <b>PDBTitle:</b> chromosomal trehalose-6-phosphate phosphatase from p. aeruginosa
15	<a href="#">c3tqdA</a>	 Alignment		22.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> structure of the 3-deoxy-d-manno-octulosonate cytidyltransferase2 (kdsb) from coxiella burnetii
16	<a href="#">c1xviA</a>	 Alignment		21.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
17	<a href="#">d1xvia</a>	 Alignment		21.9	26	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
18	<a href="#">d2duca1</a>	 Alignment		21.5	19	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
19	<a href="#">c2qyhD</a>	 Alignment		21.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical conserved protein, gk1056; <b>PDBTitle:</b> crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
20	<a href="#">c3nbmA</a>	 Alignment		20.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
21	<a href="#">c3polA</a>	 Alignment	not modelled	20.1	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-manno-octulosonate cytidyltransferase; <b>PDBTitle:</b> 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidyltransferase (kdsb) from acinetobacter baumannii.
22	<a href="#">c2d99A</a>	 Alignment	not modelled	19.6	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
23	<a href="#">c2dztA</a>	 Alignment	not modelled	19.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
24	<a href="#">c2ejeA</a>	 Alignment	not modelled	18.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
25	<a href="#">c2dn5A</a>	 Alignment	not modelled	18.7	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
26	<a href="#">c3okrC</a>	 Alignment	not modelled	18.4	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
27	<a href="#">d1h7ea</a>	 Alignment	not modelled	17.9	10	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases

						<b>Family:</b> Cytidylytransferase
28	<a href="#">c2e3IA_</a>	Alignment	not modelled	17.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor gtf2ird2 beta; <b>PDBTitle:</b> solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
29	<a href="#">c3zupB_</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
30	<a href="#">d1q60a_</a>	Alignment	not modelled	17.1	11	<b>Fold:</b> GTF2I-like repeat <b>Superfamily:</b> GTF2I-like repeat <b>Family:</b> GTF2I-like repeat
31	<a href="#">d1sv0c_</a>	Alignment	not modelled	16.9	38	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Pointed domain
32	<a href="#">c2ed2A_</a>	Alignment	not modelled	16.8	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
33	<a href="#">c4ys8B_</a>	Alignment	not modelled	16.3	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd) from burkholderia thailandensis
34	<a href="#">c2dn4A_</a>	Alignment	not modelled	15.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
35	<a href="#">c5wylC_</a>	Alignment	not modelled	15.9	45	<b>PDB header:</b> ribosomal protein/nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
36	<a href="#">c2dzqA_</a>	Alignment	not modelled	15.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
37	<a href="#">c3f1cB_</a>	Alignment	not modelled	15.1	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase from listeria monocytogenes
38	<a href="#">c5ubdB_</a>	Alignment	not modelled	14.6	60	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rctb replication initiator protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain (domain 1) of rctb, rctb-1-2 124-148m
39	<a href="#">c2n8pA_</a>	Alignment	not modelled	14.3	17	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> lactacin q; <b>PDBTitle:</b> solution structure of lactacin q
40	<a href="#">c4zexA_</a>	Alignment	not modelled	14.2	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pfhad1; <b>PDBTitle:</b> crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
41	<a href="#">c1vw3D_</a>	Alignment	not modelled	14.1	17	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 54s ribosomal protein yml6, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
42	<a href="#">c5e9oC_</a>	Alignment	not modelled	13.4	35	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cellulase, glycosyl hydrolase family 5, tps linker, domain <b>PDBTitle:</b> spirochaeta thermophila x module - cbm64 - mutant g504a
43	<a href="#">c6nd4M_</a>	Alignment	not modelled	13.3	27	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> utp10; <b>PDBTitle:</b> conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
44	<a href="#">d1vgwa_</a>	Alignment	not modelled	13.2	8	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylytransferase
45	<a href="#">c6hlwB_</a>	Alignment	not modelled	12.8	45	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
46	<a href="#">c2n8oA_</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin aureocin a53; <b>PDBTitle:</b> nmr solution structure of aureocin a53
47	<a href="#">c1ng7A_</a>	Alignment	not modelled	12.7	45	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> genome polyprotein [core protein p3a]; <b>PDBTitle:</b> the solution structure of the soluble domain of poliovirus2 3a protein
48	<a href="#">d1ng7a_</a>	Alignment	not modelled	12.7	45	<b>Fold:</b> Soluble domain of poliovirus core protein 3a <b>Superfamily:</b> Soluble domain of poliovirus core protein 3a <b>Family:</b> Soluble domain of poliovirus core protein 3a
49	<a href="#">c2q6fB_</a>	Alignment	not modelled	12.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> infectious bronchitis virus (ibv) main protease; <b>PDBTitle:</b> crystal structure of infectious bronchitis virus (ibv) main protease2 in complex with a michael acceptor inhibitor n3
50	<a href="#">c6hltD_</a>	Alignment	not modelled	12.2	55	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
51	<a href="#">d1eyra_</a>	Alignment	not modelled	12.1	26	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylytransferase

52	<a href="#">c3r4cA_</a>	Alignment	not modelled	12.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
53	<a href="#">c3u3iA_</a>	Alignment	not modelled	12.1	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> a rna binding protein from crimean-congo hemorrhagic fever virus
54	<a href="#">d1sxea_</a>	Alignment	not modelled	12.0	26	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Pointed domain
55	<a href="#">c3zljC_</a>	Alignment	not modelled	11.7	71	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
56	<a href="#">c3zljD_</a>	Alignment	not modelled	11.7	71	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
57	<a href="#">c4e6fB_</a>	Alignment	not modelled	11.1	31	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4468 family protein (bacova_04320) from2 bacteroides ovatus atcc 8483 at 1.49 a resolution
58	<a href="#">c3tloA_</a>	Alignment	not modelled	11.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3c-like proteinase; <b>PDBTitle:</b> crystal structure of hcov-nl63 3c-like protease
59	<a href="#">c3pnnA_</a>	Alignment	not modelled	11.1	0	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
60	<a href="#">c3bboG_</a>	Alignment	not modelled	10.9	23	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> ribosomal protein l4; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
61	<a href="#">d1qwja_</a>	Alignment	not modelled	10.8	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylytransferase
62	<a href="#">c5dxiB_</a>	Alignment	not modelled	10.7	5	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
63	<a href="#">c2kadA_</a>	Alignment	not modelled	10.6	43	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
64	<a href="#">c2kadD_</a>	Alignment	not modelled	10.6	43	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
65	<a href="#">c2kadB_</a>	Alignment	not modelled	10.6	43	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
66	<a href="#">c2kadC_</a>	Alignment	not modelled	10.6	43	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> transmembrane peptide of matrix protein 2; <b>PDBTitle:</b> magic-angle-spinning solid-state nmr structure of influenza2 a m2 transmembrane domain
67	<a href="#">c5i8jB_</a>	Alignment	not modelled	10.3	13	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> dmd discriminators of mrna degradation; <b>PDBTitle:</b> crystal structure of dmd from phage rb69
68	<a href="#">c6ifdD_</a>	Alignment	not modelled	10.1	17	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cmp-n-acetylneuraminase synthetase; <b>PDBTitle:</b> crystal structure of cmp-n-acetylneuraminase synthetase from vibrio2 cholerae in complex with cdp and mg2+
69	<a href="#">d1lvoa_</a>	Alignment	not modelled	9.9	22	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
70	<a href="#">c4mhvB_</a>	Alignment	not modelled	9.8	31	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein c-ets-2; <b>PDBTitle:</b> crystal structure of the pnt domain of human ets2
71	<a href="#">d1u02a_</a>	Alignment	not modelled	9.6	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Trehalose-phosphatase
72	<a href="#">d1sxda_</a>	Alignment	not modelled	9.5	31	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Pointed domain
73	<a href="#">d1rlma_</a>	Alignment	not modelled	9.4	9	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
74	<a href="#">d1uhwa_</a>	Alignment	not modelled	9.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
75	<a href="#">c2ynbA_</a>	Alignment	not modelled	9.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3c-like proteinase; <b>PDBTitle:</b> crystal structure of the main protease of coronavirus hku4 in complex2 with a michael acceptor sg85
76	<a href="#">c2crnA_</a>	Alignment	not modelled	9.1	43	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ubash3a protein; <b>PDBTitle:</b> solution structure of the uba domain of human ubash3a2

						protein
77	<a href="#">c6hmvB_</a>	Alignment	not modelled	9.0	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
78	<a href="#">d1wzca1</a>	Alignment	not modelled	8.9	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
79	<a href="#">c4aezC_</a>	Alignment	not modelled	8.7	23	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> mitotic spindle checkpoint component mad3; <b>PDBTitle:</b> crystal structure of mitotic checkpoint complex
80	<a href="#">c5jqmB_</a>	Alignment	not modelled	8.5	27	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein ups1, mitochondrial,mitochondrial distribution and <b>PDBTitle:</b> crystal structure of phosphatidic acid transporter ups1/mdm35 void of2 bound phospholipid from saccharomyces cerevisiae at 1.5 angstroms3 resolution
81	<a href="#">c4jisB_</a>	Alignment	not modelled	8.5	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribitol-5-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ribitol 5-phosphate cytidylyltransferase (tari)2 from bacillus subtilis
82	<a href="#">c2px7A_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
83	<a href="#">c6n9gB_</a>	Alignment	not modelled	8.2	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of g-protein signaling 7; <b>PDBTitle:</b> crystal structure of rgs7-gbeta5 dimer
84	<a href="#">c2vshB_</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate <b>PDBTitle:</b> synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
85	<a href="#">d2crna1</a>	Alignment	not modelled	8.1	38	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
86	<a href="#">d1vh3a_</a>	Alignment	not modelled	8.0	18	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
87	<a href="#">c6akIA_</a>	Alignment	not modelled	8.0	45	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of ikbke 1; <b>PDBTitle:</b> crystal structure of striatin3 in complex with sike1 coiled-coil2 domain
88	<a href="#">d1eexa_</a>	Alignment	not modelled	7.9	60	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Diol dehydratase, alpha subunit
89	<a href="#">c6akKA_</a>	Alignment	not modelled	7.6	45	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of ikbke 1; <b>PDBTitle:</b> crystal structure of the second coiled-coil domain of sike1
90	<a href="#">c4mybA_</a>	Alignment	not modelled	7.6	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of francisella tularensis 2-c-methyl-d-erythritol 4-2 phosphate cytidylyltransferase (ispd)
91	<a href="#">c4htjA_</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase n2; <b>PDBTitle:</b> crystallographic structure of the membrane-proximal ectodomain of the2 human receptor-type protein-tyrosine phosphatase phogrin at ph 4.6
92	<a href="#">d2cpwa1</a>	Alignment	not modelled	7.4	29	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
93	<a href="#">c2d10G_</a>	Alignment	not modelled	7.3	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> G: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
94	<a href="#">c2d10E_</a>	Alignment	not modelled	7.3	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> E: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
95	<a href="#">c2d10F_</a>	Alignment	not modelled	7.3	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> F: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
96	<a href="#">c2d10H_</a>	Alignment	not modelled	7.3	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> H: <b>PDB Molecule:</b> ezrin-radixin-moesin binding phosphoprotein 50; <b>PDBTitle:</b> crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
97	<a href="#">c2dagA_</a>	Alignment	not modelled	7.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5; <b>PDBTitle:</b> solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
98	<a href="#">d1bqva_</a>	Alignment	not modelled	7.1	46	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Pointed domain
99	<a href="#">d2ffta1</a>	Alignment	not modelled	7.0	17	<b>Fold:</b> Intrinsically disordered proteins <b>Superfamily:</b> TSP9-like <b>Family:</b> TSP9-like