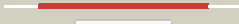



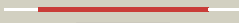

















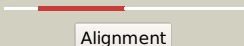













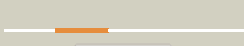


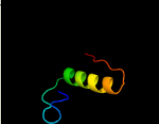
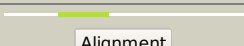

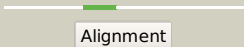
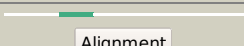
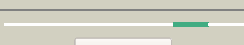






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3566c_nat_4007510_4008361
Date	Fri Aug 9 18:20:24 BST 2019
Unique Job ID	9794954004053ff7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vfbA_</a>	 Alignment		100.0	76	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylamine n-acetyltransferase; <b>PDBTitle:</b> the structure of mycobacterium marinum arylamine n-2 acetyltransferase
2	<a href="#">d1w5ra1</a>	 Alignment		100.0	60	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
3	<a href="#">d1w4ta1</a>	 Alignment		100.0	34	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
4	<a href="#">d1e2ta_</a>	 Alignment		100.0	35	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
5	<a href="#">d2bsza1</a>	 Alignment		100.0	43	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
6	<a href="#">c4guzA_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable arylamine n-acetyl transferase; <b>PDBTitle:</b> structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
7	<a href="#">c3d9wA_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase
8	<a href="#">c4dmoB_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-hydroxyarylamine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of the (baccr)nat3 arylamine n-acetyltransferase2 from bacillus cereus reveals a unique cys-his-glu catalytic triad
9	<a href="#">c3lnbA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase family protein; <b>PDBTitle:</b> crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
10	<a href="#">c2pfrB_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arylamine n-acetyltransferase 2; <b>PDBTitle:</b> human n-acetyltransferase 2
11	<a href="#">c3kd4A_</a>	 Alignment		97.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative protease; <b>PDBTitle:</b> crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution

12	<a href="#">c3lsrB_</a>	 Alignment		96.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transglutaminase-like enzymes, putative cysteine protease; <b>PDBTitle:</b> the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
13	<a href="#">c4u65F_</a>	 Alignment		95.9	13	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> putative cysteine protease; <b>PDBTitle:</b> structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
14	<a href="#">c4xz7A_</a>	 Alignment		93.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a tgase
15	<a href="#">c6g49A_</a>	 Alignment		92.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of the periplasmic domain of tgpa from pseudomonas2 aeruginosa
16	<a href="#">d2f4ma1</a>	 Alignment		90.2	24	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
17	<a href="#">c3eswA_</a>	 Alignment		88.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide-n(4)-(n-acetyl-beta-glucosaminy)l)asparagine <b>PDBTitle:</b> complex of yeast pngase with glcnac2-iac.
18	<a href="#">c4g29A_</a>	 Alignment		83.2	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> secreted effector protein ssei; <b>PDBTitle:</b> structure of the catalytic domain of the salmonella virulence factor2 ssei
19	<a href="#">d1x3za1</a>	 Alignment		81.5	24	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
20	<a href="#">d2q3za4</a>	 Alignment		66.8	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
21	<a href="#">c4fqpB_</a>	 Alignment	not modelled	62.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein; <b>PDBTitle:</b> legionella pneumophila lapg (egta-treated)
22	<a href="#">c2qshA_</a>	 Alignment	not modelled	57.4	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad4; <b>PDBTitle:</b> crystal structure of rad4-rad23 bound to a mismatch dna
23	<a href="#">c6j4nD_</a>	 Alignment	not modelled	52.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> metallo-beta-lactamases pngm-1; <b>PDBTitle:</b> structure of papua new guinea mbl-1(pngm-1) native
24	<a href="#">d1g0da4</a>	 Alignment	not modelled	49.5	27	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
25	<a href="#">d1jmx1</a>	 Alignment	not modelled	48.0	12	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
26	<a href="#">c2jq4A_</a>	 Alignment	not modelled	46.0	24	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu2571; <b>PDBTitle:</b> complete resonance assignments and solution structure calculation of2 atc2521 (nesg id: att6) from agrobacterium tumefaciens
27	<a href="#">d2jq4a1</a>	 Alignment	not modelled	46.0	24	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
28	<a href="#">c4a19F_</a>	 Alignment	not modelled	44.3	17	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl14; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
		 Alignment				<b>PDB header:</b> ribosome

29	<a href="#">c3j3bM_</a>	Alignment	not modelled	43.4	21	<b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
30	<a href="#">d1lcaa_</a>	Alignment	not modelled	43.3	60	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
31	<a href="#">d1pbya1</a>	Alignment	not modelled	43.1	14	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
32	<a href="#">c1wv9B_</a>	Alignment	not modelled	42.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
33	<a href="#">c3iacA_</a>	Alignment	not modelled	41.6	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronate isomerase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
34	<a href="#">d1ex0a4</a>	Alignment	not modelled	41.6	27	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
35	<a href="#">c3iz5N_</a>	Alignment	not modelled	40.1	14	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
36	<a href="#">c1boiA_</a>	Alignment	not modelled	39.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> n-terminally truncated rhodanese
37	<a href="#">c1zkpD_</a>	Alignment	not modelled	38.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ba1088; <b>PDBTitle:</b> 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homologue of bacillus anthracis, a putative3 ribonuclease
38	<a href="#">c4as2D_</a>	Alignment	not modelled	37.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
39	<a href="#">c3zwfA_</a>	Alignment	not modelled	35.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc phosphodiesterase elac protein 1; <b>PDBTitle:</b> crystal structure of human trnase z, short form (elac1).
40	<a href="#">c2nz3A_</a>	Alignment	not modelled	35.4	60	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin, mutant def-aaa; <b>PDBTitle:</b> nmr structure of def-aaa, a mutant of anopheles defensin2 def-aaa
41	<a href="#">c3izcN_</a>	Alignment	not modelled	34.6	20	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein rpl14 (l14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
42	<a href="#">d1s1ma2</a>	Alignment	not modelled	30.4	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
43	<a href="#">c2e3eA_</a>	Alignment	not modelled	30.4	70	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> defensin, mutant def-bbb; <b>PDBTitle:</b> nmr structure of def-bbb, a mutant of anopheles defensin2 def-aaa
44	<a href="#">c2lr5A_</a>	Alignment	not modelled	29.8	38	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> micasin; <b>PDBTitle:</b> 1h chemical shift assignments for micasin
45	<a href="#">c3bwwA_</a>	Alignment	not modelled	29.3	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf692/cog3220; <b>PDBTitle:</b> crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
46	<a href="#">c5xa6A_</a>	Alignment	not modelled	28.0	88	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bmkdfsin3; <b>PDBTitle:</b> ion channel modulation by scorpion haemolymph and its defensin2 ingredients uncovers origin of neurotoxins in telson formed in3 paleozoic scorpion
47	<a href="#">d1kkxa_</a>	Alignment	not modelled	27.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> ARID-like <b>Family:</b> ARID domain
48	<a href="#">d1vcoa2</a>	Alignment	not modelled	26.3	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
49	<a href="#">c3j39M_</a>	Alignment	not modelled	26.0	24	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
50	<a href="#">c3nvaB_</a>	Alignment	not modelled	24.8	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> dimeric form of ctp synthase from sulfolobus solfataricus
51	<a href="#">c5u03C_</a>	Alignment	not modelled	24.3	19	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament
52	<a href="#">d1zkpa1</a>	Alignment	not modelled	24.2	26	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> YhfI-like
53	<a href="#">c2ru0A_</a>	Alignment	not modelled	23.6	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> arthropod defensin; <b>PDBTitle:</b> solution structure of actinomycin
54	<a href="#">c3g5jA_</a>	Alignment	not modelled	23.4	27	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp/gtp binding protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630 <b>PDB header:</b> ligand binding protein

55	<a href="#">c3chgB</a>	Alignment	not modelled	22.3	33	<b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine-binding protein; <b>PDBTitle:</b> the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
56	<a href="#">d1rha1</a>	Alignment	not modelled	22.1	10	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
57	<a href="#">c3zuaA</a>	Alignment	not modelled	21.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-hemolysin translocation atp-binding protein hlyb; <b>PDBTitle:</b> a c39-like domain
58	<a href="#">c3h11A</a>	Alignment	not modelled	20.5	38	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> zymogen caspase-8:c-flipl protease domain complex
59	<a href="#">c1l9mB</a>	Alignment	not modelled	19.3	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein-glutamine glutamyltransferase e3; <b>PDBTitle:</b> three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
60	<a href="#">c2aivA</a>	Alignment	not modelled	19.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> fragment of nucleoporin nup116/nsp116; <b>PDBTitle:</b> multiple conformations in the ligand-binding site of the yeast nuclear2 pore targeting domain of nup116p
61	<a href="#">c3sirD</a>	Alignment	not modelled	18.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> caspase; <b>PDBTitle:</b> crystal structure of drice
62	<a href="#">c3x30A</a>	Alignment	not modelled	18.6	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0173 metal-dependent hydrolase tm_1162; <b>PDBTitle:</b> crystal structure of metallo-beta-lactamase from thermotoga maritima
63	<a href="#">c2jo7A</a>	Alignment	not modelled	18.2	29	<b>PDB header:</b> surface active protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycosylphosphatidylinositol-anchored merozoite <b>PDBTitle:</b> solution structure of the adhesion protein bd37 from2 babesia divergens
64	<a href="#">c5uoiA</a>	Alignment	not modelled	18.2	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> hhh_rd1_0142; <b>PDBTitle:</b> solution structure of the de novo mini protein hhh_rd1_0142
65	<a href="#">c3p45I</a>	Alignment	not modelled	17.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> caspase-6; <b>PDBTitle:</b> crystal structure of apo-caspase-6 at physiological ph
66	<a href="#">d2plia1</a>	Alignment	not modelled	17.6	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
67	<a href="#">c3k8uA</a>	Alignment	not modelled	17.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, atp-binding protein coma; <b>PDBTitle:</b> crystal structure of the peptidase domain of streptococcus coma, a bi-2 functional abc transporter involved in quorum sensing pathway
68	<a href="#">c3zf7P</a>	Alignment	not modelled	17.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> probable 60s ribosomal protein l14; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
69	<a href="#">c2ad5B</a>	Alignment	not modelled	17.3	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
70	<a href="#">d1yt8a4</a>	Alignment	not modelled	16.9	20	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
71	<a href="#">c2yqeA</a>	Alignment	not modelled	16.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> jumonji/arid domain-containing protein 1d; <b>PDBTitle:</b> solution structure of the arid domain of jarid1d protein
72	<a href="#">d2cbna1</a>	Alignment	not modelled	16.8	22	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
73	<a href="#">c1g0dA</a>	Alignment	not modelled	16.8	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of red sea bream transglutaminase
74	<a href="#">c1cjbB</a>	Alignment	not modelled	16.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (cytosolic phospholipase a2); <b>PDBTitle:</b> human cytosolic phospholipase a2
75	<a href="#">c4wfcF</a>	Alignment	not modelled	16.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> exosome complex protein lrp1; <b>PDBTitle:</b> structure of the rrp6-rrp47 interaction
76	<a href="#">c2lm1A</a>	Alignment	not modelled	16.1	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase lid; <b>PDBTitle:</b> solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics consortium3 target fr824d
77	<a href="#">c3llbA</a>	Alignment	not modelled	15.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
78	<a href="#">d1vfga2</a>	Alignment	not modelled	15.5	24	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
79	<a href="#">d3ci0k2</a>	Alignment	not modelled	15.0	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like

80	<a href="#">c2ql5A_</a>	Alignment	not modelled	14.8	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> caspase-7; <b>PDBTitle:</b> crystal structure of caspase-7 with inhibitor ac-dmqd-cho
81	<a href="#">c4ejyA_</a>	Alignment	not modelled	14.8	16	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> 3-methyladenine dna glycosylase; <b>PDBTitle:</b> structure of mbogg1 in complex with high affinity dna ligand
82	<a href="#">c4wfcB_</a>	Alignment	not modelled	14.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exosome complex protein lrp1; <b>PDBTitle:</b> structure of the rrp6-rrp47 interaction
83	<a href="#">d3deda1</a>	Alignment	not modelled	14.6	22	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
84	<a href="#">d1af7a1</a>	Alignment	not modelled	14.5	26	<b>Fold:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain <b>Superfamily:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain <b>Family:</b> Chemotaxis receptor methyltransferase CheR, N-terminal domain
85	<a href="#">d1vija4</a>	Alignment	not modelled	14.5	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
86	<a href="#">d1y44a1</a>	Alignment	not modelled	14.5	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
87	<a href="#">c5laaB_</a>	Alignment	not modelled	14.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tetrahydromethanopterin s-methyltransferase subunit a; <b>PDBTitle:</b> x-ray structure of the methyltransferase subunit a from methanothermus2 fervidus in complex with cobalamin
88	<a href="#">c4zdiE_</a>	Alignment	not modelled	14.4	24	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
89	<a href="#">c2ln4A_</a>	Alignment	not modelled	14.3	50	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> coprisin; <b>PDBTitle:</b> insight into the antimicrobial activities based on the structure-2 activity relationships of coprisin isolated from the dung beetle,3 copris tripartitus
90	<a href="#">c1f13A_</a>	Alignment	not modelled	13.7	29	<b>PDB header:</b> coagulation factor <b>Chain:</b> A: <b>PDB Molecule:</b> cellular coagulation factor xiii zymogen; <b>PDBTitle:</b> recombinant human cellular coagulation factor xiii
91	<a href="#">c2eg4B_</a>	Alignment	not modelled	13.4	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase
92	<a href="#">c5mz61_</a>	Alignment	not modelled	13.4	22	<b>PDB header:</b> cell cycle <b>Chain:</b> 1: <b>PDB Molecule:</b> separase; <b>PDBTitle:</b> cryo-em structure of a separase-securin complex from caenorhabditis2 elegans at 3.8 a resolution
93	<a href="#">c1kv3F_</a>	Alignment	not modelled	13.4	29	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> human tissue transglutaminase in gdp bound form
94	<a href="#">c6bugA_</a>	Alignment	not modelled	13.4	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl carrier protein; <b>PDBTitle:</b> crystal structure of a membrane protein, crystal form i
95	<a href="#">c2veqA_</a>	Alignment	not modelled	13.2	30	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> centromere dna-binding protein complex cbf3 subunit b; <b>PDBTitle:</b> insights into kinetochore-dna interactions from the structure of cep3p
96	<a href="#">d2rk5a1</a>	Alignment	not modelled	13.2	9	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
97	<a href="#">c1i3oC_</a>	Alignment	not modelled	13.0	27	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> caspase 3; <b>PDBTitle:</b> crystal structure of the complex of xiap-bir2 and caspase 3
98	<a href="#">c4gxtA_</a>	Alignment	not modelled	12.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a conserved functionally unknown protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
99	<a href="#">c4wv4B_</a>	Alignment	not modelled	12.5	8	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor tffiid subunit 8; <b>PDBTitle:</b> heterodimer of taf8/taf10