
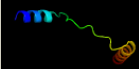
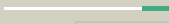






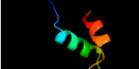









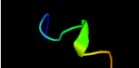

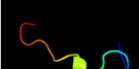

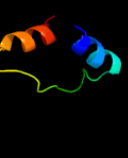
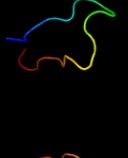
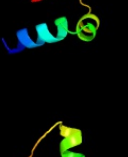


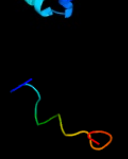

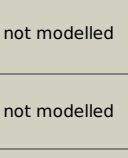


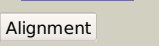
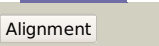
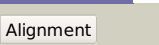
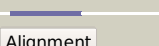
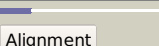
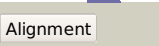
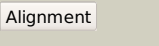
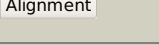
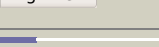
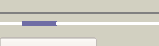
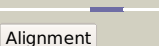
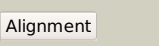
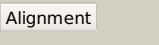
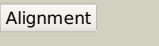
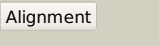
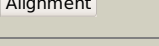

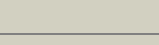


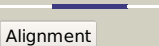
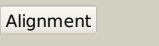
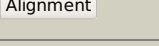


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2643A\_(RVBD2643A)\_2968420\_2968842  
 Date Wed Aug 7 12:50:29 BST 2019  
 Unique Job ID dd1cdbaa22ba8294

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ns5A_</a>	 Alignment		80.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidase glij; <b>PDBTitle:</b> cys-gly dipeptidase glij in complex with cu2+ and zn2+
2	<a href="#">c3iysA_</a>	 Alignment		44.1	45	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> homology model of avian polyomavirus asymmetric unit
3	<a href="#">d1vpsa_</a>	 Alignment		40.4	32	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Group I dsDNA viruses <b>Family:</b> Papovaviridae-like VP
4	<a href="#">c4fmiN_</a>	 Alignment		39.7	30	<b>PDB header:</b> viral protein <b>Chain:</b> N: <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> merkel cell polyomavirus vp1 in complex with 3'-sialyllactosamine
5	<a href="#">c2r18A_</a>	 Alignment		37.7	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly protein vp3; <b>PDBTitle:</b> structural insights into the multifunctional protein vp3 of 2 birnaviruses
6	<a href="#">d1sida_</a>	 Alignment		36.9	30	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Group I dsDNA viruses <b>Family:</b> Papovaviridae-like VP
7	<a href="#">d1tg7a5</a>	 Alignment		34.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Glycosyl hydrolases family 35 catalytic domain
8	<a href="#">c5jknA_</a>	 Alignment		34.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fam63a; <b>PDBTitle:</b> crystal structure of deubiquitinase mindy-1
9	<a href="#">c4pcgD_</a>	 Alignment		33.1	35	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> structure of human polyomavirus 6 (hpyv6) vp1 pentamer
10	<a href="#">c4mbyB_</a>	 Alignment		29.2	31	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose
11	<a href="#">c3bwrC_</a>	 Alignment		26.8	31	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> capsid protein vp1; <b>PDBTitle:</b> sv40 vp1 pentamer in complex with gm1 oligosaccharide

12	<a href="#">c4fe4C_</a>	Alignment		26.8	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> xylose operon regulatory protein; <b>PDBTitle:</b> crystal structure of apo e. coli xylr
13	<a href="#">c2wbnA_</a>	Alignment		26.6	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase large subunit; <b>PDBTitle:</b> crystal structure of the g2p (large terminase) nuclease2 domain from the bacteriophage spp1
14	<a href="#">d1sva1_</a>	Alignment		25.6	26	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Group I dsDNA viruses <b>Family:</b> Papovaviridae-like VP
15	<a href="#">c5oqm1_</a>	Alignment		25.3	52	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> general transcription and dna repair factor iih subunit <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
16	<a href="#">c6gym1_</a>	Alignment		24.6	52	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> general transcription and dna repair factor iih subunit <b>PDBTitle:</b> structure of a yeast closed complex with distorted dna (ccdist)
17	<a href="#">c5oqj1_</a>	Alignment		24.6	52	<b>PDB header:</b> transcription <b>Chain:</b> 1: <b>PDB Molecule:</b> rna polymerase ii transcription factor b subunit 1; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih
18	<a href="#">d1k1xa3</a>	Alignment		23.5	18	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> 4-alpha-glucanotransferase, N-terminal domain
19	<a href="#">c4u62D_</a>	Alignment		21.8	33	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> structural protein vp1; <b>PDBTitle:</b> trichodysplasia spinulosa-associated polyomavirus (tspyv) vp1 in2 complex with 3'-sialyllactose
20	<a href="#">c4pchE_</a>	Alignment		21.8	36	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> structure of human polyomavirus 7 (hpyv7) vp1 pentamer
21	<a href="#">c3s7xC_</a>	Alignment	not modelled	21.3	36	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> major capsid protein vp1; <b>PDBTitle:</b> unassembled washington university polyomavirus vp1 pentamer r198k2 mutant
22	<a href="#">c4ug1A_</a>	Alignment	not modelled	20.9	29	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> gpsb n-terminal domain
23	<a href="#">c2wukD_</a>	Alignment	not modelled	20.6	29	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> septum site-determining protein diviva; <b>PDBTitle:</b> diviva n-terminal domain, f17a mutant
24	<a href="#">c4ug3C_</a>	Alignment	not modelled	19.2	25	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> b. subtilis gpsb n-terminal domain
25	<a href="#">c6gqaD_</a>	Alignment	not modelled	18.2	25	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> cell division regulator s. pneumoniae gpsb
26	<a href="#">c6humN_</a>	Alignment	not modelled	17.4	28	<b>PDB header:</b> proton transport <b>Chain:</b> N: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit n; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
27	<a href="#">c5hyzA_</a>	Alignment	not modelled	15.1	10	<b>PDB header:</b> transcription factor <b>Chain:</b> A: <b>PDB Molecule:</b> gras family transcription factor containing protein, <b>PDBTitle:</b> crystal structure of scl7 in oryza sativa
28	<a href="#">c1fp2A_</a>	Alignment	not modelled	14.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoflavone o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of isoflavone o-methyltransferase

29	<a href="#">c4lbhA</a>	 Alignment	not modelled	13.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg); <b>PDBTitle:</b> 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg) from2 burkholderia phenoliruptrix ac1100: apo-form
30	<a href="#">c6d4oA</a>	 Alignment	not modelled	13.5	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> eubacterium eligens beta-glucuronidase bound to an amoxapine-2 glucuronide conjugate
31	<a href="#">c4lhdB</a>	 Alignment	not modelled	13.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine dehydrogenase [decarboxylating]; <b>PDBTitle:</b> crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
32	<a href="#">c6o7yA</a>	 Alignment	not modelled	13.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative eukaryotic translation initiation factor 4e type <b>PDBTitle:</b> trypanosoma cruzi eif4e5 translation initiation factor in complex with2 cap-4
33	<a href="#">c5lnkY</a>	 Alignment	not modelled	12.8	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Y: <b>PDB Molecule:</b> mitochondrial complex i, pgiv subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
34	<a href="#">c2gqcA</a>	 Alignment	not modelled	12.7	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rhomboid intramembrane protease; <b>PDBTitle:</b> solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
35	<a href="#">d2oola2</a>	 Alignment	not modelled	12.2	33	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> BphP N-terminal domain-like
36	<a href="#">c2yufA</a>	 Alignment	not modelled	12.0	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ngfi-a-binding protein 1; <b>PDBTitle:</b> solution structure of the ncd2 domain in human2 transcriptional repressor nab1 protein
37	<a href="#">d1cw0a</a>	 Alignment	not modelled	12.0	28	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Very short patch repair (VSR) endonuclease
38	<a href="#">d2veaa3</a>	 Alignment	not modelled	11.4	6	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> BphP N-terminal domain-like
39	<a href="#">d2j5wa1</a>	 Alignment	not modelled	11.3	57	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
40	<a href="#">c6dlmB</a>	 Alignment	not modelled	10.5	31	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> dhd127_b; <b>PDBTitle:</b> dhd127
41	<a href="#">c3nsnA</a>	 Alignment	not modelled	10.4	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosaminidase; <b>PDBTitle:</b> crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
42	<a href="#">c5b3hB</a>	 Alignment	not modelled	10.1	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein short-root; <b>PDBTitle:</b> the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex
43	<a href="#">d1j5ya2</a>	 Alignment	not modelled	9.9	29	<b>Fold:</b> HPr-like <b>Superfamily:</b> Putative transcriptional regulator TM1602, C-terminal domain <b>Family:</b> Putative transcriptional regulator TM1602, C-terminal domain
44	<a href="#">d1vsra</a>	 Alignment	not modelled	9.8	28	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Very short patch repair (VSR) endonuclease
45	<a href="#">d2j5wa3</a>	 Alignment	not modelled	9.1	31	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
46	<a href="#">d3c2wa3</a>	 Alignment	not modelled	9.0	36	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> BphP N-terminal domain-like
47	<a href="#">c1yf5L</a>	 Alignment	not modelled	8.5	28	<b>PDB header:</b> transport protein <b>Chain:</b> L: <b>PDB Molecule:</b> general secretion pathway protein I; <b>PDBTitle:</b> cyto-epsI: the cytoplasmic domain of epsI, an inner membrane component2 of the type ii secretion system of vibrio cholerae
48	<a href="#">c2i56A</a>	 Alignment	not modelled	8.2	21	<b>PDB header:</b> isomerase, metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose isomerase; <b>PDBTitle:</b> crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
49	<a href="#">d1luzxa</a>	 Alignment	not modelled	8.1	57	<b>Fold:</b> UBC-like <b>Superfamily:</b> UBC-like <b>Family:</b> UEV domain
50	<a href="#">d1rh9a1</a>	 Alignment	not modelled	7.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
51	<a href="#">d2vzsa5</a>	 Alignment	not modelled	7.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
52	<a href="#">d1w7ja1</a>	 Alignment	not modelled	7.7	43	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
53	<a href="#">c2ph7B</a>	 Alignment	not modelled	7.7	37	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein af_2093; <b>PDBTitle:</b> crystal structure of af2093 from archaeoglobus fulgidus
54	<a href="#">c2ketA</a>	Alignment	not modelled	7.7	58	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> cathelicidin-6;

						<b>PDBTitle:</b> solution structure of bmap-27
55	<a href="#">c3ketA</a>	Alignment	not modelled	7.4	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
56	<a href="#">c2k2wA</a>	Alignment	not modelled	7.4	42	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> recombination and dna repair protein; <b>PDBTitle:</b> second brct domain of nbs1
57	<a href="#">c5tkwA</a>	Alignment	not modelled	7.4	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii secretion system protein i; <b>PDBTitle:</b> 1.35 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (n-terminal fragment; residues 1-237) from klebsiella pneumoniae.
58	<a href="#">c4jkmB</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of clostridium perfringens beta-glucuronidase
59	<a href="#">d1sdda1</a>	Alignment	not modelled	7.3	35	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
60	<a href="#">d1jz8a5</a>	Alignment	not modelled	7.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
61	<a href="#">c2qzcB</a>	Alignment	not modelled	7.2	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional activator tena-1; <b>PDBTitle:</b> crystal structure of a putative tena-like thiaminase (tena-1, sso2206)2 from sulfolobus solfataricus p2 at 1.50 a resolution
62	<a href="#">c1kyzC</a>	Alignment	not modelled	7.2	6	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> caffeic acid 3-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
63	<a href="#">d2o9ca2</a>	Alignment	not modelled	7.0	42	<b>Fold:</b> Profilin-like <b>Superfamily:</b> PYP-like sensor domain (PAS domain) <b>Family:</b> BphP N-terminal domain-like
64	<a href="#">d1yq2a5</a>	Alignment	not modelled	6.7	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
65	<a href="#">c5b3hD</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> protein scarecrow; <b>PDBTitle:</b> the crystal structure of the jackdaw/idd10 bound to the heterodimeric2 shr-scr complex
66	<a href="#">c5gslB</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 778aa long hypothetical beta-galactosidase; <b>PDBTitle:</b> glycoside hydrolase a
67	<a href="#">c4jklA</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> crystal structure of streptococcus agalactiae beta-glucuronidase in2 space group p21212
68	<a href="#">d2obpa1</a>	Alignment	not modelled	6.0	60	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
69	<a href="#">d1s1qa</a>	Alignment	not modelled	6.0	44	<b>Fold:</b> UBC-like <b>Superfamily:</b> UBC-like <b>Family:</b> UEV domain
70	<a href="#">c3aicC</a>	Alignment	not modelled	5.9	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucosyltransferase-si; <b>PDBTitle:</b> crystal structure of glucansucrase from streptococcus mutans
71	<a href="#">c1us7B</a>	Alignment	not modelled	5.9	43	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> complex of hsp90 and p50
72	<a href="#">d1us7b</a>	Alignment	not modelled	5.9	43	<b>Fold:</b> Hsp90 co-chaperone CDC37 <b>Superfamily:</b> Hsp90 co-chaperone CDC37 <b>Family:</b> Hsp90 co-chaperone CDC37
73	<a href="#">d1lrza</a>	Alignment	not modelled	5.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> GARP response regulators
74	<a href="#">c3gwzB</a>	Alignment	not modelled	5.6	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mmcr; <b>PDBTitle:</b> structure of the mitomycin 7-o-methyltransferase mmcr
75	<a href="#">c5gsmB</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
76	<a href="#">c5jbfB</a>	Alignment	not modelled	5.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> inactive glucansucrase; <b>PDBTitle:</b> 4,6-alpha-glucanotransferase gtfb (d1015n mutant) from lactobacillus2 reuteri 121 complexed with maltopentaose
77	<a href="#">d1x4ka2</a>	Alignment	not modelled	5.5	67	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
78	<a href="#">c2w7nA</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
79	<a href="#">c6ecaA</a>	Alignment	not modelled	5.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> lactobacillus rhamnosus beta-glucuronidase
80	<a href="#">c1k1vA</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase;

80	<a href="#">c1k1yA_</a>	Alignment	not modelled	5.3	42	<b>PDBTitle:</b> crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
81	<a href="#">c4wwrE_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> transport protein <b>Chain:</b> E; <b>PDB Molecule:</b> large proline-rich protein bag6; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
82	<a href="#">c2m1aA_</a>	Alignment	not modelled	5.4	43	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> hiv-1 rev arginine-rich motif (arm); <b>PDBTitle:</b> hiv-1 rev arm peptide (residues t34-r50)
83	<a href="#">c2fe3B_</a>	Alignment	not modelled	5.4	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
84	<a href="#">c5lc5W_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> W; <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
85	<a href="#">d2je8a5</a>	Alignment	not modelled	5.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
86	<a href="#">c6iv7B_</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> methyltransferase lepi; <b>PDBTitle:</b> the crystal structure of a sam-dependent enzyme from aspergillus2 flavus
87	<a href="#">c6hvgA_</a>	Alignment	not modelled	5.2	34	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> alternansucrase; <b>PDBTitle:</b> crystal structure of truncated alternansucrase from leuconostoc2 mesenteroides nrri b-1355
88	<a href="#">c4phtY_</a>	Alignment	not modelled	5.2	24	<b>PDB header:</b> protein transport <b>Chain:</b> Y; <b>PDB Molecule:</b> type ii secretion system protein I; <b>PDBTitle:</b> atpase gspe in complex with the cytoplasmic domain of gspI from the2 vibrio vulnificus type ii secretion system
89	<a href="#">c3gabC_</a>	Alignment	not modelled	5.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dna mismatch repair protein mutI; <b>PDBTitle:</b> c-terminal domain of bacillus subtilis mutI crystal form i