

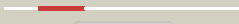












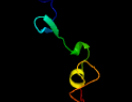

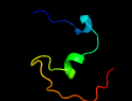


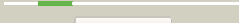

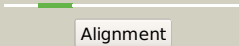


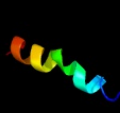


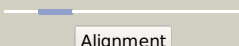

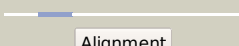

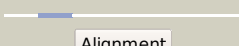

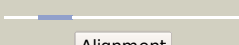
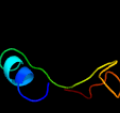





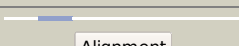



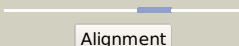
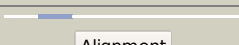




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3479_(- )_3895999_3899064
Date	Fri Aug 9 18:20:15 BST 2019
Unique Job ID	539b0444b476f5b2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5fyaA_</a>	 Alignment		99.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> patatin-like protein, plpd; <b>PDBTitle:</b> cubic crystal of the native plpd
2	<a href="#">c4akfA_</a>	 Alignment		99.7	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vipd; <b>PDBTitle:</b> crystal structure of vipd from legionella pneumophila
3	<a href="#">d1oxwa_</a>	 Alignment		99.5	15	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> Patatin
4	<a href="#">c4qmkB_</a>	 Alignment		99.5	28	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> type iii secretion system effector protein exou; <b>PDBTitle:</b> crystal structure of type iii effector protein exou (exou)
5	<a href="#">c4akxB_</a>	 Alignment		99.4	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> exou; <b>PDBTitle:</b> structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
6	<a href="#">c6aunB_</a>	 Alignment		99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pla2g6, ipla2beta; <b>PDBTitle:</b> calcium-independent phospholipase a2 beta
7	<a href="#">c3tu3B_</a>	 Alignment		99.3	34	<b>PDB header:</b> toxin/toxin chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> exou; <b>PDBTitle:</b> 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
8	<a href="#">c1cjbB_</a>	 Alignment		71.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (cytosolic phospholipase a2); <b>PDBTitle:</b> human cytosolic phospholipase a2
9	<a href="#">d1cja2</a>	 Alignment		64.2	30	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> Lysophospholipase
10	<a href="#">c4uzqA_</a>	 Alignment		55.2	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein notum homolog; <b>PDBTitle:</b> structure of the wnt deacylase notum in complex with2 o-palmitoleoyl serine - crystal form ix - 1.5a
11	<a href="#">c4uzjB_</a>	 Alignment		54.0	50	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> notum; <b>PDBTitle:</b> structure of the wnt deacylase notum from drosophila -2 crystal form i - 2.4a

12	<a href="#">d1hm6a_</a>	 Alignment		53.5	19	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
13	<a href="#">d2b5dx1</a>	 Alignment		39.2	21	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> AmyC C-terminal domain-like
14	<a href="#">c4o9pC_</a>	 Alignment		29.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha 2; <b>PDBTitle:</b> crystal structure of thermus thermophilis transhydrogeanse domain ii2 dimer semet derivative
15	<a href="#">c3chlA_</a>	 Alignment		28.5	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-14 giardin; <b>PDBTitle:</b> crystal structure of alpha-14 giardin with magnesium bound
16	<a href="#">c2cfmA_</a>	 Alignment		27.9	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable dna ligase; <b>PDBTitle:</b> atp-dependent dna ligase from pyrococcus furiosus
17	<a href="#">d1axna_</a>	 Alignment		27.9	14	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
18	<a href="#">c3e4dD_</a>	 Alignment		27.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
19	<a href="#">d1hvda_</a>	 Alignment		26.5	18	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
20	<a href="#">c5izrC_</a>	 Alignment		25.8	9	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> cytosolic phospholipase a2 delta; <b>PDBTitle:</b> human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride
21	<a href="#">c6a4tB_</a>	 Alignment	not modelled	25.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase e; <b>PDBTitle:</b> crystal structure of peptidase e from deinococcus radiodurans r1
22	<a href="#">d1fyea_</a>	 Alignment	not modelled	24.0	36	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Aspartyl dipeptidase PepE
23	<a href="#">d1avca1</a>	 Alignment	not modelled	23.8	21	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
24	<a href="#">c3en0A_</a>	 Alignment	not modelled	23.8	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
25	<a href="#">c3l4eA_</a>	 Alignment	not modelled	22.2	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
26	<a href="#">c5ip1A_</a>	 Alignment	not modelled	21.4	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> tomato spotted wilt tospovirus nucleocapsid protein
27	<a href="#">c6b3iB_</a>	 Alignment	not modelled	21.0	14	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> annexin; <b>PDBTitle:</b> annexin a13a
28	<a href="#">d2ie7a1</a>	 Alignment	not modelled	19.4	18	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
29	<a href="#">d1nu9c1</a>	 Alignment	not modelled	19.2	23	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Staphylocoagulase

						<b>Family:</b> Staphylocoagulase
30	<a href="#">c4b6gA_</a>	Alignment	not modelled	18.3	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> the crystal structure of the neisserial esterase d.
31	<a href="#">d1dqza_</a>	Alignment	not modelled	17.3	27	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
32	<a href="#">d1whva_</a>	Alignment	not modelled	16.9	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
33	<a href="#">d1r88a_</a>	Alignment	not modelled	16.2	34	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Mycobacterial antigens
34	<a href="#">c7ceiB_</a>	Alignment	not modelled	15.8	29	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> protein (colicin e7 immunity protein); <b>PDBTitle:</b> the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
35	<a href="#">d1aina_</a>	Alignment	not modelled	15.3	20	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
36	<a href="#">d2nr5a1</a>	Alignment	not modelled	15.3	80	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> SO2669-like <b>Family:</b> SO2669-like
37	<a href="#">d2jb0b1</a>	Alignment	not modelled	15.1	29	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNH-motif
38	<a href="#">c5ix1A_</a>	Alignment	not modelled	14.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> morc family cw-type zinc finger protein 3; <b>PDBTitle:</b> crystal structure of mouse morc3 atpase-cw cassette in complex with2 amppnp and h3k4me3 peptide
39	<a href="#">c3fcxA_</a>	Alignment	not modelled	14.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-formylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of human esterase d
40	<a href="#">c5m6gA_</a>	Alignment	not modelled	14.4	47	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of kutzneria albida transglutaminase
41	<a href="#">c4qkoH_</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> H: <b>PDB Molecule:</b> pyocin-s2; <b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
42	<a href="#">c1w3wA_</a>	Alignment	not modelled	14.3	16	<b>PDB header:</b> coagulation <b>Chain:</b> A: <b>PDB Molecule:</b> annexin a8; <b>PDBTitle:</b> the 2.1 angstroem resolution structure of annexin a8
43	<a href="#">d1m9ia1</a>	Alignment	not modelled	13.6	14	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
44	<a href="#">c4uhpA_</a>	Alignment	not modelled	13.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> large component of pyocin ap41; <b>PDBTitle:</b> crystal structure of the pyocin ap41 dnase-immunity complex
45	<a href="#">d1xu9a_</a>	Alignment	not modelled	13.0	33	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
46	<a href="#">c3bjrA_</a>	Alignment	not modelled	12.9	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
47	<a href="#">d1i4aa_</a>	Alignment	not modelled	12.5	16	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
48	<a href="#">d1alaa_</a>	Alignment	not modelled	12.3	19	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
49	<a href="#">c4as2D_</a>	Alignment	not modelled	11.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
50	<a href="#">c3sftA_</a>	Alignment	not modelled	11.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator protein-glutamate <b>PDBTitle:</b> crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
51	<a href="#">d1m9ia2</a>	Alignment	not modelled	11.4	19	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
52	<a href="#">d1ufaa1</a>	Alignment	not modelled	11.0	13	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Families 57/38 glycoside transferase middle domain <b>Family:</b> AmyC C-terminal domain-like
53	<a href="#">d1vkna2</a>	Alignment	not modelled	10.8	43	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
54	<a href="#">d1w7ba_</a>	Alignment	not modelled	10.4	20	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
55	<a href="#">c5ohcB_</a>	Alignment	not modelled	10.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> crystal structure of mycolicibacterium hassiacum glucosylglycerate2 hydrolase (mhggh) in complex with glycerol
						<b>Fold:</b> His-Me finger endonucleases

56	<a href="#">d2gykb1</a>	Alignment	not modelled	10.0	29	<b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> HNNH-motif
57	<a href="#">c5if3B_</a>	Alignment	not modelled	9.9	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of a short-chain dehydrogenase/reductase sdr from2 burkholderia vietnamiensis
58	<a href="#">c2hivA_</a>	Alignment	not modelled	9.8	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable dna ligase; <b>PDBTitle:</b> atp-dependent dna ligase from s. solfataricus
59	<a href="#">d1b93a_</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
60	<a href="#">c3ctrA_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a)-specific ribonuclease parn; <b>PDBTitle:</b> crystal structure of the rrm-domain of the poly(a)-specific2 ribonuclease parn bound to m7gtp
61	<a href="#">c6c4vA_</a>	Alignment	not modelled	9.5	60	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
62	<a href="#">c3gdeA_</a>	Alignment	not modelled	9.5	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> the closed conformation of atp-dependent dna ligase from archaeoglobus2 fulgidus
63	<a href="#">d1dk5a_</a>	Alignment	not modelled	9.4	20	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
64	<a href="#">c4jmqA_</a>	Alignment	not modelled	9.3	33	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage t5 distal tail protein; <b>PDBTitle:</b> crystal structure of pb9: the dit of bacteriophage t5.
65	<a href="#">d1jvna1</a>	Alignment	not modelled	9.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
66	<a href="#">d2g17a2</a>	Alignment	not modelled	9.3	25	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
67	<a href="#">d1chda_</a>	Alignment	not modelled	8.9	46	<b>Fold:</b> Methylesterase CheB, C-terminal domain <b>Superfamily:</b> Methylesterase CheB, C-terminal domain <b>Family:</b> Methylesterase CheB, C-terminal domain
68	<a href="#">d1avca2</a>	Alignment	not modelled	8.9	20	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
69	<a href="#">c6gcsq_</a>	Alignment	not modelled	8.6	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 30-kda protein (nugm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
70	<a href="#">c5ew5C_</a>	Alignment	not modelled	8.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
71	<a href="#">c1avcA_</a>	Alignment	not modelled	8.4	21	<b>PDB header:</b> calcium/phospholipid-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> annexin vi; <b>PDBTitle:</b> bovine annexin vi (calcium-bound)
72	<a href="#">d1b63a1</a>	Alignment	not modelled	8.4	13	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> DNA gyrase/MutL, second domain
73	<a href="#">c6pheA_</a>	Alignment	not modelled	8.3	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylglyoxal synthase; <b>PDBTitle:</b> crystal structure of methylglyoxal synthase from elizabethkingia2 anophelis nuhp1
74	<a href="#">d1dm5a_</a>	Alignment	not modelled	8.3	18	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
75	<a href="#">d1vqo21</a>	Alignment	not modelled	8.2	71	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Ribosomal protein L39e <b>Family:</b> Ribosomal protein L39e
76	<a href="#">c5n6yC_</a>	Alignment	not modelled	8.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitrogenase vanadium-iron protein delta chain; <b>PDBTitle:</b> azotobacter vinelandii vanadium nitrogenase
77	<a href="#">d1sbya1</a>	Alignment	not modelled	7.9	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
78	<a href="#">c4bmvH_</a>	Alignment	not modelled	7.8	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> short-chain dehydrogenase; <b>PDBTitle:</b> short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
79	<a href="#">c6cl5F_</a>	Alignment	not modelled	7.8	38	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> tail fiber protein; <b>PDBTitle:</b> structure of p. aeruginosa r1 pyocin fiber pales_06171 comprising c-2 terminal residues 323-701
80	<a href="#">c4h18D_</a>	Alignment	not modelled	7.7	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cmt1; <b>PDBTitle:</b> three dimensional structure of corynomycoloyl tranferase c
81	<a href="#">d1n00a_</a>	Alignment	not modelled	7.5	17	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin
82	<a href="#">c1yx5A_</a>	Alignment	not modelled	7.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 26s proteasome non-atpase regulatory subunit 4; <b>PDBTitle:</b> solution structure of s5a uim-1/ubiquitin complex

83	<a href="#">c2lzaA_</a>	Alignment	not modelled	7.4	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> ns2 peptide; <b>PDBTitle:</b> structure of ns2(32-57) gbvb protein
84	<a href="#">c4zqrD_</a>	Alignment	not modelled	7.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> inosine-5'-monophosphate dehydrogenase,inosine-5'- <b>PDBTitle:</b> crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
85	<a href="#">d1o5ia_</a>	Alignment	not modelled	7.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
86	<a href="#">c1nm3B_</a>	Alignment	not modelled	7.4	50	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein hi0572; <b>PDBTitle:</b> crystal structure of heamophilus influenza hybrid-prx5
87	<a href="#">d1e44b_</a>	Alignment	not modelled	7.3	24	<b>Fold:</b> Ribonuclease domain of colicin E3 <b>Superfamily:</b> Ribonuclease domain of colicin E3 <b>Family:</b> Ribonuclease domain of colicin E3
88	<a href="#">c3bxaA_</a>	Alignment	not modelled	7.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase/esterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution
89	<a href="#">d1y6xa1</a>	Alignment	not modelled	7.3	13	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)
90	<a href="#">c4mdvB_</a>	Alignment	not modelled	7.2	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> annexin; <b>PDBTitle:</b> crystal structure of calcium-bound annexin (sm)1
91	<a href="#">c3tjrA_</a>	Alignment	not modelled	7.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a rv0851c ortholog short chain dehydrogenase from2 mycobacterium paratuberculosis
92	<a href="#">d1x9na1</a>	Alignment	not modelled	7.1	23	<b>Fold:</b> ATP-dependent DNA ligase DNA-binding domain <b>Superfamily:</b> ATP-dependent DNA ligase DNA-binding domain <b>Family:</b> ATP-dependent DNA ligase DNA-binding domain
93	<a href="#">c3h7aC_</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase from rhodospseudomonas2 palustris
94	<a href="#">c5mrwL_</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
95	<a href="#">c5mrwD_</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
96	<a href="#">c6hraD_</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)
97	<a href="#">c5mrwH_</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
98	<a href="#">c6hrbD_</a>	Alignment	not modelled	6.9	60	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
99	<a href="#">d1mcxa_</a>	Alignment	not modelled	6.8	19	<b>Fold:</b> Annexin <b>Superfamily:</b> Annexin <b>Family:</b> Annexin