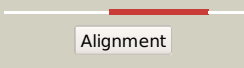

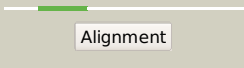

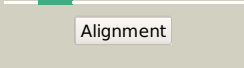
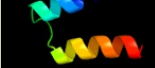
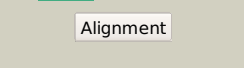

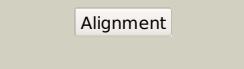
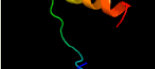
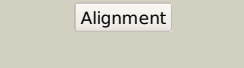

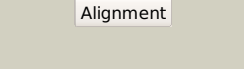

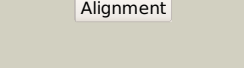

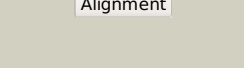

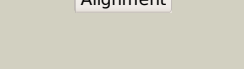

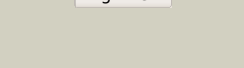


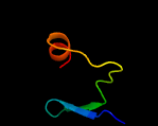


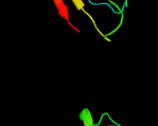






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2862c_(- )_3174069_3174653
Date	Wed Aug 7 12:50:53 BST 2019
Unique Job ID	227d87b91e48a957

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4qrkA_</a>	 Alignment		98.3	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative cell adhesion protein (clospo_03726)2 from clostridium sporogenes atcc 15579 at 1.95 a resolution
2	<a href="#">d2pp4a1</a>	 Alignment		53.4	14	<b>Fold:</b> TAFH domain-like <b>Superfamily:</b> TAFH domain-like <b>Family:</b> TAFH domain-like
3	<a href="#">d2p12a1</a>	 Alignment		45.2	25	<b>Fold:</b> FomD barrel-like <b>Superfamily:</b> FomD-like <b>Family:</b> FomD-like
4	<a href="#">d2p6va1</a>	 Alignment		40.0	19	<b>Fold:</b> TAFH domain-like <b>Superfamily:</b> TAFH domain-like <b>Family:</b> TAFH domain-like
5	<a href="#">d1khia2</a>	 Alignment		38.8	39	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
6	<a href="#">d2caza1</a>	 Alignment		37.5	19	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
7	<a href="#">c2cazD_</a>	 Alignment		37.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> D; <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> escrt-i core
8	<a href="#">d2f6ma1</a>	 Alignment		35.5	19	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
9	<a href="#">c4egeA_</a>	 Alignment		29.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidase pepe; <b>PDBTitle:</b> crystal structure of dipeptidase pepe from mycobacterium ulcerans
10	<a href="#">c2p22A_</a>	 Alignment		26.8	26	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> structure of the yeast escrt-i heterotetramer core
11	<a href="#">c3e56A_</a>	 Alignment		23.5	31	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme

12	<a href="#">c3vdoB_</a>	Alignment		21.4	18	<b>PDB header:</b> dna binding protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anti-sigma-k factor rska; <b>PDBTitle:</b> structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
13	<a href="#">c4nxiB_</a>	Alignment		21.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
14	<a href="#">c1ponB_</a>	Alignment		20.7	36	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> troponin c; <b>PDBTitle:</b> site iii-site iv troponin c heterodimer, nmr
15	<a href="#">c3nctC_</a>	Alignment		19.5	16	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> protein psib; <b>PDBTitle:</b> x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
16	<a href="#">c3i38K_</a>	Alignment		18.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
17	<a href="#">c6cumA_</a>	Alignment		17.6	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase; <b>PDBTitle:</b> crystal structure of a c-terminal proteolytic fragment of a protein2 annotated as an lao/ao transport system atpase but likely meab and3 mmaa-like gtpase from mycobacterium smegmatis
18	<a href="#">c3i38D_</a>	Alignment		17.3	16	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
19	<a href="#">c3i38B_</a>	Alignment		17.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
20	<a href="#">c3i38G_</a>	Alignment		16.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> G: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
21	<a href="#">c3i38A_</a>	Alignment	not modelled	16.6	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
22	<a href="#">d1x6oa2</a>	Alignment	not modelled	16.5	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
23	<a href="#">c5j73A_</a>	Alignment	not modelled	16.4	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein design 2l4hc2_9; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
24	<a href="#">d1xxfc_</a>	Alignment	not modelled	16.1	17	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
25	<a href="#">c3i38E_</a>	Alignment	not modelled	15.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
26	<a href="#">c3i38C_</a>	Alignment	not modelled	15.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
27	<a href="#">d2f6mb1</a>	Alignment	not modelled	15.9	11	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS28 N-terminal domain
28	<a href="#">d2cazb1</a>	Alignment	not modelled	15.8	11	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS28 N-terminal domain
29	<a href="#">c2cazB_</a>	Alignment	not modelled	15.8	11	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein vps28;

						<b>PDBTitle:</b> escrt-i core
30	<a href="#">c2y6tE_</a>	Alignment	not modelled	15.8	25	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> ecotin; <b>PDBTitle:</b> molecular recognition of chymotrypsin by the serine protease inhibitor2 ecotin from yersinia pestis
31	<a href="#">c2f7nA_</a>	Alignment	not modelled	15.8	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding stress response protein, dps family; <b>PDBTitle:</b> structure of d. radiodurans dps-1
32	<a href="#">d1kxpd3</a>	Alignment	not modelled	15.8	11	<b>Fold:</b> Serum albumin-like <b>Superfamily:</b> Serum albumin-like <b>Family:</b> Serum albumin-like
33	<a href="#">d1slua_</a>	Alignment	not modelled	15.3	17	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
34	<a href="#">d1ug3a1</a>	Alignment	not modelled	15.0	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
35	<a href="#">d3orca_</a>	Alignment	not modelled	14.5	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
36	<a href="#">c4n7vC_</a>	Alignment	not modelled	14.3	55	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> centrosomal protein of 152 kda; <b>PDBTitle:</b> crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment
37	<a href="#">c2kq1A_</a>	Alignment	not modelled	14.1	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh0266 protein; <b>PDBTitle:</b> solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
38	<a href="#">c3i38L_</a>	Alignment	not modelled	14.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> L: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
39	<a href="#">c3li6D_</a>	Alignment	not modelled	13.4	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> calcium-binding protein; <b>PDBTitle:</b> crystal structure and trimer-monomer transition of n-terminal domain2 of ehcap1 from entamoeba histolytica
40	<a href="#">c2bh1Y_</a>	Alignment	not modelled	13.4	27	<b>PDB header:</b> transport protein <b>Chain:</b> Y: <b>PDB Molecule:</b> general secretion pathway protein e.; <b>PDBTitle:</b> x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
41	<a href="#">d2bh1x1</a>	Alignment	not modelled	13.4	27	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> EspE N-terminal domain-like <b>Family:</b> GSPII protein E N-terminal domain-like
42	<a href="#">c6mi5X_</a>	Alignment	not modelled	13.0	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> lanmodulin; <b>PDBTitle:</b> nmr solution structure of lanmodulin (lanm) complexed with2 yttrium(iii) ions
43	<a href="#">c3i38F_</a>	Alignment	not modelled	12.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
44	<a href="#">c3sqlB_</a>	Alignment	not modelled	11.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3; <b>PDBTitle:</b> crystal structure of glycoside hydrolase from synechococcus
45	<a href="#">c2dhyA_</a>	Alignment	not modelled	11.9	14	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cue domain-containing protein 1; <b>PDBTitle:</b> solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
46	<a href="#">c3l6aA_</a>	Alignment	not modelled	11.5	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 4 gamma 2; <b>PDBTitle:</b> crystal structure of the c-terminal region of human p97
47	<a href="#">c6b2zd_</a>	Alignment	not modelled	11.3	44	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit c, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
48	<a href="#">c6qfjA_</a>	Alignment	not modelled	11.1	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> magnetosome membrane protein mamb, putative co/zn/cd cation <b>PDBTitle:</b> mamb ctd magnetosome protein [desulfamplus magnetovallimortis bw-1]
49	<a href="#">d1yfnal</a>	Alignment	not modelled	11.0	26	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
50	<a href="#">c3fpnA_</a>	Alignment	not modelled	10.9	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus stearothermophilus uvra interaction domain; <b>PDBTitle:</b> crystal structure of uvra-uvrb interaction domains
51	<a href="#">c5cuvB_</a>	Alignment	not modelled	10.9	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> acidocalcisomal pyrophosphatase; <b>PDBTitle:</b> crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
52	<a href="#">c2vrgA_</a>	Alignment	not modelled	10.9	40	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> multiple coagulation factor deficiency protein 2; <b>PDBTitle:</b> structure of human mcf2
53	<a href="#">c3i38H_</a>	Alignment	not modelled	10.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> H: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
54	<a href="#">d1ou9a_</a>	Alignment	not modelled	10.6	28	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
						<b>PDB header:</b> hydrolase/hydrolase regulator

55	<a href="#">c4v0xB_</a>	Alignment	not modelled	10.6	36	<b>Chain:</b> B: <b>PDB Molecule:</b> protein phosphatase 1 regulatory subunit 15b; <b>PDBTitle:</b> the crystal structure of mouse pp1g in complex with truncated human2 ppp1r15b (631-684)
56	<a href="#">c5hjhB_</a>	Alignment	not modelled	10.2	5	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferritin, dps family protein; <b>PDBTitle:</b> dps4 from nostoc punctiforme in complex with fe ions
57	<a href="#">c3i38J_</a>	Alignment	not modelled	10.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> J: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
58	<a href="#">c3fsdA_</a>	Alignment	not modelled	10.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like protein of unknown function in nutrient uptake; <b>PDBTitle:</b> crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution
59	<a href="#">c5euOB_</a>	Alignment	not modelled	9.9	20	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin 1; <b>PDBTitle:</b> fic domain of bep1 from bartonella rochalimae in complex with biao
60	<a href="#">c1ug3A_</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic protein synthesis initiation factor <b>PDBTitle:</b> c-terminal portion of human eif4gi
61	<a href="#">c3lsgD_</a>	Alignment	not modelled	9.6	0	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
62	<a href="#">d1jmx1</a>	Alignment	not modelled	9.6	28	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
63	<a href="#">c3iq1A_</a>	Alignment	not modelled	9.5	14	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> dps family protein; <b>PDBTitle:</b> crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
64	<a href="#">c2zyzA_</a>	Alignment	not modelled	9.3	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1012; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
65	<a href="#">c1wr2A_</a>	Alignment	not modelled	9.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1789; <b>PDBTitle:</b> crystal structure of ph1788 from pyrococcus horikoshii ot3
66	<a href="#">c6odmK_</a>	Alignment	not modelled	9.2	20	<b>PDB header:</b> viral protein <b>Chain:</b> K: <b>PDB Molecule:</b> capsid vertex component 2; <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
67	<a href="#">d1ctda_</a>	Alignment	not modelled	9.1	31	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
68	<a href="#">c5hqhA_</a>	Alignment	not modelled	9.0	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2119 protein; <b>PDBTitle:</b> 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.
69	<a href="#">d1ulza1</a>	Alignment	not modelled	8.7	11	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
70	<a href="#">c4il1A_</a>	Alignment	not modelled	8.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin, calcineurin subunit b type 1, serine/threonine- <b>PDBTitle:</b> crystal structure of the rat calcineurin
71	<a href="#">c6e5fA_</a>	Alignment	not modelled	8.6	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid binding protein lpqn; <b>PDBTitle:</b> crystal structure of lpqn involved in cell envelope biogenesis of2 mycobacterium tuberculosis
72	<a href="#">c4ol4A_</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
73	<a href="#">d1ezsa_</a>	Alignment	not modelled	8.6	13	<b>Fold:</b> Ecotin, trypsin inhibitor <b>Superfamily:</b> Ecotin, trypsin inhibitor <b>Family:</b> Ecotin, trypsin inhibitor
74	<a href="#">c5bzaA_</a>	Alignment	not modelled	8.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> crystal structure of cbsa from thermotoga neapolitana
75	<a href="#">c4r60A_</a>	Alignment	not modelled	8.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dipeptidase; <b>PDBTitle:</b> crystal structure of xaa-pro dipeptidase from xanthomonas campestris
76	<a href="#">c5wzeC_</a>	Alignment	not modelled	8.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> aminopeptidase p; <b>PDBTitle:</b> the structure of pseudomonas aeruginosa aminopeptidase pepp
77	<a href="#">c3h96B_</a>	Alignment	not modelled	8.4	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
78	<a href="#">c1t7IA_</a>	Alignment	not modelled	8.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of cobalamin-independent methionine synthase from t.2 maritima
79	<a href="#">c4xaeB_</a>	Alignment	not modelled	8.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> feruloyl coa ortho-hydroxylase 1; <b>PDBTitle:</b> structure of feruloyl-coa 6-hydroxylase (f6h) from

					arabidopsis2 thaliana
80	<a href="#">d1s6ja_</a>	Alignment	not modelled	8.2	30 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
81	<a href="#">d1pvaa_</a>	Alignment	not modelled	8.1	41 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Parvalbumin
82	<a href="#">c3es5A_</a>	Alignment	not modelled	8.0	17 <b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> putative capsid protein; <b>PDBTitle:</b> crystal structure of partitivirus (psv-f)
83	<a href="#">c5zx9A_</a>	Alignment	not modelled	7.9	24 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> alanine and proline-rich secreted protein apa; <b>PDBTitle:</b> crystal structure of a protein from mycobacterium
84	<a href="#">c3ndqA_</a>	Alignment	not modelled	7.9	25 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor a protein 1; <b>PDBTitle:</b> structure of human tfiis domain ii
85	<a href="#">c3ppgA_</a>	Alignment	not modelled	7.8	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
86	<a href="#">c2nszA_</a>	Alignment	not modelled	7.7	17 <b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> 1.15 angstrom crystal structure of the ma3 domain of pdcd4
87	<a href="#">c2ionA_</a>	Alignment	not modelled	7.7	17 <b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 4, pdcd4; <b>PDBTitle:</b> crystal structure of the c-terminal ma3 domain of pdcd4 (mouse); form2
88	<a href="#">d2nsza1</a>	Alignment	not modelled	7.7	17 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
89	<a href="#">c2mxtA_</a>	Alignment	not modelled	7.5	14 <b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein q; <b>PDBTitle:</b> nmr structure of the acidic domain of syncrip (hnrnpq)
90	<a href="#">d1tjoa_</a>	Alignment	not modelled	7.5	16 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ferritin
91	<a href="#">d1br1b_</a>	Alignment	not modelled	7.3	15 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
92	<a href="#">c6iieA_</a>	Alignment	not modelled	7.2	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol kinase alpha; <b>PDBTitle:</b> crystal structure of human diacylglycerol kinase alpha ef-hand domains2 bound to ca2+
93	<a href="#">c6a9vA_</a>	Alignment	not modelled	7.2	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> intermediate cleaving peptidase 55; <b>PDBTitle:</b> crystal structure of icp55 from saccharomyces cerevisiae (n-terminal2 42 residues deletion)
94	<a href="#">c2iosA_</a>	Alignment	not modelled	7.2	18 <b>PDB header:</b> antitumor protein <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 4, pdcd4; <b>PDBTitle:</b> crystal structure of the c-terminal ma3 domain of pdcd42 (mouse); form 3
95	<a href="#">d5pala_</a>	Alignment	not modelled	7.1	29 <b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Parvalbumin
96	<a href="#">d1x4pa1</a>	Alignment	not modelled	7.0	28 <b>Fold:</b> Surp module (SWAP domain) <b>Superfamily:</b> Surp module (SWAP domain) <b>Family:</b> Surp module (SWAP domain)
97	<a href="#">c2bpbB_</a>	Alignment	not modelled	7.0	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfite cytochrome c oxidoreductase subunit b; <b>PDBTitle:</b> sulfite dehydrogenase from starkeya novella
98	<a href="#">c5aooA_</a>	Alignment	not modelled	7.0	16 <b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> vp0; <b>PDBTitle:</b> x-ray structure of a human kobuvirus: aichi virus a (aiv)
99	<a href="#">c3lz8A_</a>	Alignment	not modelled	6.9	16 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative chaperone dnaj; <b>PDBTitle:</b> structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.