

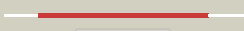












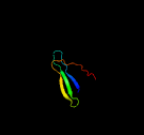






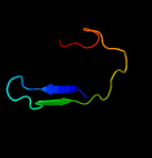
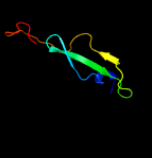
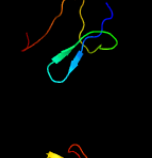
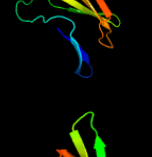
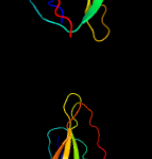


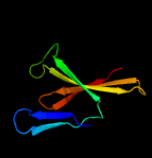
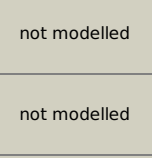


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0654 (-) _750003_751508
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	e710a3cebb44cd79

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3npeA_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; <b>PDBTitle:</b> structure of vp14 in complex with oxygen
2	<a href="#">c5v2dA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dioxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas brassicacearum lignostilbene2 dioxygenase
3	<a href="#">c5u90A_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> carotenoid oxygenase 1; <b>PDBTitle:</b> crystal structure of co-cao1 in complex with resveratrol
4	<a href="#">c5j54A_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> carotenoid oxygenase; <b>PDBTitle:</b> the structure and mechanism of nov1, a resveratrol-cleaving2 dioxygenase
5	<a href="#">c2biwC_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> apocarotenoid-cleaving oxygenase; <b>PDBTitle:</b> crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
6	<a href="#">c3fsnA_</a>	 Alignment		100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> retinal pigment epithelium-specific 65 kda protein; <b>PDBTitle:</b> crystal structure of rpe65 at 2.14 angstrom resolution
7	<a href="#">c1nnoA_</a>	 Alignment		72.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nitrite reductase; <b>PDBTitle:</b> conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
8	<a href="#">c1gq1B_</a>	 Alignment		70.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome cd1 nitrite reductase; <b>PDBTitle:</b> cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
9	<a href="#">c4cvcA_</a>	 Alignment		64.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of quinone-dependent alcohol dehydrogenase from2 pseudogluconobacter saccharoketogenenes with zinc in the active site
10	<a href="#">c6rteB_</a>	 Alignment		48.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome c; <b>PDBTitle:</b> dihydro-heme d1 dehydrogenase nirn in complex with dhe
11	<a href="#">c6damA_</a>	 Alignment		40.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> lanthanide-dependent methanol dehydrogenase xoxf; <b>PDBTitle:</b> crystal structure of lanthanide-dependent methanol dehydrogenase xoxf2 from methylomicrobium buryatense 5g

12	<a href="#">d1mdah_</a>	Alignment		36.6	24	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> YVTN repeat-like/Quinoprotein amine dehydrogenase <b>Family:</b> Methylamine dehydrogenase, H-chain
13	<a href="#">c3qc2A_</a>	Alignment		35.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a glycosyl hydrolase (bacova_03624) from <i>Bacteroides ovatus</i> at 2.30 Å resolution
14	<a href="#">c5c2mA_</a>	Alignment		32.7	25	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> the de novo evolutionary emergence of a symmetrical protein is shaped by folding constraints
15	<a href="#">c6cmkB_</a>	Alignment		22.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> aztd protein; <b>PDBTitle:</b> crystal structure of <i>Citrobacter koseri</i> aztd
16	<a href="#">c3metB_</a>	Alignment		22.3	10	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> saga-associated factor 29 homolog; <b>PDBTitle:</b> crystal structure of sgf29 in complex with h3k4me2
17	<a href="#">d1nira2</a>	Alignment		22.0	19	<b>Fold:</b> 8-bladed beta-propeller <b>Superfamily:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase <b>Family:</b> C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
18	<a href="#">c1hzhK_</a>	Alignment		21.6	17	<b>PDB header:</b> immune system <b>Chain:</b> K; <b>PDB Molecule:</b> immunoglobulin heavy chain; <b>PDBTitle:</b> crystal structure of the intact human igg b12 with broad and potent activity against primary hiv-1 isolates: a template for vaccine design
19	<a href="#">c2j57J_</a>	Alignment		20.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> methylamine dehydrogenase heavy chain; <b>PDBTitle:</b> x-ray reduced <i>Paracoccus denitrificans</i> methylamine dehydrogenase n-quinol in complex with amicyanin.
20	<a href="#">d1jmxB_</a>	Alignment		19.5	21	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> YVTN repeat-like/Quinoprotein amine dehydrogenase <b>Family:</b> Quinohemoprotein amine dehydrogenase B chain
21	<a href="#">c3mbrX_</a>	Alignment	not modelled	19.2	11	<b>PDB header:</b> transferase <b>Chain:</b> X; <b>PDB Molecule:</b> glutamine cyclotransferase; <b>PDBTitle:</b> crystal structure of the glutamyl cyclase from <i>Xanthomonas campestris</i>
22	<a href="#">c5i5iA_</a>	Alignment	not modelled	18.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> nitrous-oxide reductase; <b>PDBTitle:</b> <i>Shewanella denitrificans</i> nitrous oxide reductase, app form
23	<a href="#">c1yiqA_</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> molecular cloning and structural analysis of quinohemoprotein alcohol dehydrogenase adhig from <i>Pseudomonas putida</i> hk5. comparison to the other 4 quinohemoprotein alcohol dehydrogenase adhiib found in the same microorganism.
24	<a href="#">c1kb0A_</a>	Alignment	not modelled	17.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of quinohemoprotein alcohol dehydrogenase from <i>Comamonas testosteroni</i>
25	<a href="#">c1n7dA_</a>	Alignment	not modelled	17.6	16	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> low-density lipoprotein receptor; <b>PDBTitle:</b> extracellular domain of the ldl receptor
26	<a href="#">d1zaka2</a>	Alignment	not modelled	16.6	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain <b>Family:</b> Microbial and mitochondrial ADK, insert "zinc finger" domain
27	<a href="#">d1k91a_</a>	Alignment	not modelled	14.2	31	<b>Fold:</b> P-domain of calnexin/calreticulin <b>Superfamily:</b> P-domain of calnexin/calreticulin <b>Family:</b> P-domain of calnexin/calreticulin
						<b>Fold:</b> Immunoglobulin-like beta-sandwich

28	<a href="#">d1uvqb1</a>	Alignment	not modelled	12.8	23	<b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
29	<a href="#">d1m7ja2</a>	Alignment	not modelled	12.6	26	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> D-aminoacylase
30	<a href="#">d1mspa_</a>	Alignment	not modelled	12.2	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> MSP-like
31	<a href="#">c5v1dA_</a>	Alignment	not modelled	11.6	11	<b>PDB header:</b> transferase/substrate <b>Chain:</b> A: <b>PDB Molecule:</b> seif2ak3 protein; <b>PDBTitle:</b> complex structure of the bovine perk luminal domain and its substrate2 peptide
32	<a href="#">c4iiqC_</a>	Alignment	not modelled	11.5	19	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> beta-2-microglobulin, mhc class i-related protein; <b>PDBTitle:</b> crystal structure of a human mait tcr in complex with bovine mr1
33	<a href="#">c5aycA_</a>	Alignment	not modelled	11.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
34	<a href="#">d1es0a1</a>	Alignment	not modelled	10.6	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
35	<a href="#">c5f30B_</a>	Alignment	not modelled	10.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thiocyanate dehydrogenase; <b>PDBTitle:</b> thiocyanate dehydrogenase from thioalkalivibrio paradoxus
36	<a href="#">d1kb0a2</a>	Alignment	not modelled	10.6	13	<b>Fold:</b> 8-bladed beta-propeller <b>Superfamily:</b> Quinoprotein alcohol dehydrogenase-like <b>Family:</b> Quinoprotein alcohol dehydrogenase-like
37	<a href="#">d1bf2a1</a>	Alignment	not modelled	10.6	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
38	<a href="#">c3elqA_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfate sulfotransferase; <b>PDBTitle:</b> crystal structure of a bacterial arylsulfate2 sulfotransferase
39	<a href="#">c4ozuA_</a>	Alignment	not modelled	10.1	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> coronin; <b>PDBTitle:</b> crystal structure of wd40 domain from toxoplasma gondii coronin
40	<a href="#">d2oz4a1</a>	Alignment	not modelled	8.9	36	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
41	<a href="#">d2hu7a1</a>	Alignment	not modelled	8.6	19	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Peptidase/esterase 'gauge' domain <b>Family:</b> Acylamino-acid-releasing enzyme, N-terminal donain
42	<a href="#">c3pqyB_</a>	Alignment	not modelled	8.5	20	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224
43	<a href="#">c5c2wD_</a>	Alignment	not modelled	8.5	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hydrazine synthase alpha subunit; <b>PDBTitle:</b> kueningenia stuttgartiensis hydrazine synthase pressurized with 20 bar2 xenon
44	<a href="#">c3watA_</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc
45	<a href="#">d2q3za4</a>	Alignment	not modelled	8.3	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
46	<a href="#">d1c16a1</a>	Alignment	not modelled	7.8	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
47	<a href="#">c2vb6A_</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin vi; <b>PDBTitle:</b> myosin vi (md-insert2-cam, delta insert1) post-rigor state (2 crystal form 2)
48	<a href="#">c3ov6A_</a>	Alignment	not modelled	7.7	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin, t-cell surface glycoprotein cd1c, t- <b>PDBTitle:</b> cd1c in complex with mpm (mannosyl-beta1-phosphomycoketide)
49	<a href="#">c1qniE_</a>	Alignment	not modelled	7.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitrous-oxide reductase; <b>PDBTitle:</b> crystal structure of nitrous oxide reductase from pseudomonas nautica,2 at 2.4a resolution
50	<a href="#">d1qnia2</a>	Alignment	not modelled	7.5	12	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> Nitrous oxide reductase, N-terminal domain <b>Family:</b> Nitrous oxide reductase, N-terminal domain
51	<a href="#">d1qo3a1</a>	Alignment	not modelled	7.4	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
52	<a href="#">c2dzjA_</a>	Alignment	not modelled	7.3	31	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptic glycoprotein sc2; <b>PDBTitle:</b> 2dzj/solution structure of the n-terminal ubiquitin-like2 domain in human synaptic glycoprotein sc2
53	<a href="#">c2jroA_</a>	Alignment	not modelled	7.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of so0334 from shewanella

						oneidensis. northeast2 structural genomics target sor75
54	<a href="#">d2g50a1</a>	Alignment	not modelled	7.2	27	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
55	<a href="#">c2k8qA</a>	Alignment	not modelled	7.1	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein shq1; <b>PDBTitle:</b> nmr structure of shq1p n-terminal domain
56	<a href="#">d1liua1</a>	Alignment	not modelled	7.0	25	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
57	<a href="#">d1vija4</a>	Alignment	not modelled	7.0	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
58	<a href="#">d1iaka1</a>	Alignment	not modelled	7.0	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
59	<a href="#">d1w1ha</a>	Alignment	not modelled	6.9	21	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
60	<a href="#">c3pohA</a>	Alignment	not modelled	6.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase f1; <b>PDBTitle:</b> crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
61	<a href="#">c5sv7D</a>	Alignment	not modelled	6.8	4	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2-alpha kinase 3; <b>PDBTitle:</b> the crystal structure of a chaperone
62	<a href="#">d1flga</a>	Alignment	not modelled	6.7	13	<b>Fold:</b> 8-bladed beta-propeller <b>Superfamily:</b> Quinoprotein alcohol dehydrogenase-like <b>Family:</b> Quinoprotein alcohol dehydrogenase-like
63	<a href="#">d1muja1</a>	Alignment	not modelled	6.7	25	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
64	<a href="#">c1l9mB</a>	Alignment	not modelled	6.6	17	<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
65	<a href="#">d1xv2a</a>	Alignment	not modelled	6.6	26	<b>Fold:</b> AF0104/ALDC/Ptd012-like <b>Superfamily:</b> AF0104/ALDC/Ptd012-like <b>Family:</b> Alpha-acetolactate decarboxylase-like
66	<a href="#">d1hdmb1</a>	Alignment	not modelled	6.5	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
67	<a href="#">c4ozkA</a>	Alignment	not modelled	6.4	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> putative bacteriocin; <b>PDBTitle:</b> crystal structure of laterosporulin, a broad spectrum leaderless2 bacteriocin produced by brevivacillus laterosporus strain gi-9
68	<a href="#">d1fp5a2</a>	Alignment	not modelled	6.4	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
69	<a href="#">c4wndB</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ferm and pdz domain-containing protein 4; <b>PDBTitle:</b> crystal structure of the tpr domain of lgn in complex with2 frmpd4/preso1 at 1.5 angstrom resolution
70	<a href="#">d1uowa</a>	Alignment	not modelled	6.3	19	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
71	<a href="#">c4wneB</a>	Alignment	not modelled	6.3	13	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> peptide from ferm and pdz domain-containing protein 4; <b>PDBTitle:</b> crystal structure of the tpr domain of lgn in complex with2 frmpd4/preso1 at 2.0 angstrom resolution
72	<a href="#">c3pqyG</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> immune system <b>Chain:</b> G: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224
73	<a href="#">c2qrsA</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> h-2 class i histocompatibility antigen k-b alpha chain, <b>PDBTitle:</b> crystal structure of a single chain trimer composed of the mhc i heavy2 chain h-2kb y84a, beta-2microglobulin, and ovalbumin-derived peptide.
74	<a href="#">c3q54A</a>	Alignment	not modelled	6.2	11	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane assembly lipoprotein yfgl; <b>PDBTitle:</b> crystal structure of escherichia coli bamb
75	<a href="#">c2bkiA</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> motor protein/metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin; <b>PDBTitle:</b> myosin vi nucleotide-free (mdinsert2-iq) crystal structure
76	<a href="#">c2bc4C</a>	Alignment	not modelled	6.2	11	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> hla class ii histocompatibility antigen, dm alpha chain; <b>PDBTitle:</b> crystal structure of hla-dm
77	<a href="#">d1dqva2</a>	Alignment	not modelled	6.1	13	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
78	<a href="#">c3eudE</a>	Alignment	not modelled	6.1	7	<b>PDB header:</b> nuclear protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein shq1; <b>PDBTitle:</b> structure of the cs domain of the essential h/aca rnp assembly protein2 shq1p

79	<a href="#">c3e7hA</a>	Alignment	not modelled	6.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor
80	<a href="#">d1vgka1</a>	Alignment	not modelled	6.0	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
81	<a href="#">c2hyij</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> J: <b>PDB Molecule:</b> protein casc3; <b>PDBTitle:</b> structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
82	<a href="#">d1dl5a2</a>	Alignment	not modelled	5.9	38	<b>Fold:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain <b>Superfamily:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain <b>Family:</b> Protein-L-isoaspartyl O-methyltransferase, C-terminal domain
83	<a href="#">c2hlwA</a>	Alignment	not modelled	5.8	10	<b>PDB header:</b> ligase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 1; <b>PDBTitle:</b> solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
84	<a href="#">d1pkma1</a>	Alignment	not modelled	5.8	28	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
85	<a href="#">c2ypdB</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable jmjc domain-containing histone demethylation prot <b>PDBTitle:</b> crystal structure of the jumonji domain of human jumonji domain2 containing 1c protein
86	<a href="#">c2kyvA</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible atp-dependent dna helicase recg-related protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of putative atp-2 dependent dna helicase recg-related protein from nitrosomonas3 europaea, northeast structural genomics consortium target ner70a
87	<a href="#">c5j8tA</a>	Alignment	not modelled	5.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> choline binding protein; <b>PDBTitle:</b> nmr structure of excalibur domain of cbpl
88	<a href="#">c4mh1A</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbose dehydrogenase; <b>PDBTitle:</b> crystal structure and functional studies of quinoprotein l-sorbose2 dehydrogenase from ketogulonigenium vulgare y25
89	<a href="#">d1mdca</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
90	<a href="#">c3ex7I</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> I: <b>PDB Molecule:</b> protein casc3; <b>PDBTitle:</b> the crystal structure of ejc in its transition state
91	<a href="#">c4gioA</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of campylobacter jejuni cj0090
92	<a href="#">c2l92A</a>	Alignment	not modelled	5.6	38	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone family protein nucleoid-structuring protein h-ns; <b>PDBTitle:</b> solution structure of the c-terminal domain of h-ns like protein bv3f
93	<a href="#">c2bkhA</a>	Alignment	not modelled	5.6	29	<b>PDB header:</b> motor protein/metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin; <b>PDBTitle:</b> myosin vi nucleotide-free (mdinsert2) crystal structure
94	<a href="#">d1k8ib1</a>	Alignment	not modelled	5.5	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C1 set domains (antibody constant domain-like)
95	<a href="#">c6hygA</a>	Alignment	not modelled	5.5	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ighg1 and ighg4 hybrid; <b>PDBTitle:</b> heteromeric tandem igg4/igg1 fc
96	<a href="#">c4c8dA</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific demethylase 3b; <b>PDBTitle:</b> crystal structure of jmjc domain of human histone 3 lysine-specific2 demethylase 3b (kdm3b)
97	<a href="#">c4hdjA</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein assembly factor bamb; <b>PDBTitle:</b> crystal structure of bamb from pseudomonas aeruginosa
98	<a href="#">c6cebP</a>	Alignment	not modelled	5.5	86	<b>PDB header:</b> signaling protein <b>Chain:</b> P: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> insulin receptor ectodomain in complex with two insulin molecules - c12 symmetry
99	<a href="#">c3ilqD</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> beta-2 microglobulin; <b>PDBTitle:</b> structure of mcd1d with bound glycolipid bbg1-2c from2 borrelia burgdorferi