


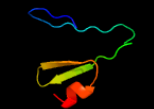

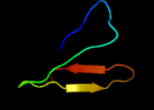


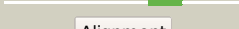
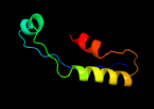
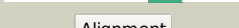


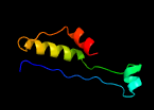


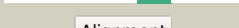
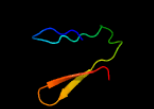
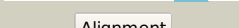

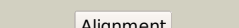





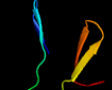
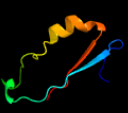


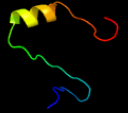


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3311 (-) _3698292_3699554
Date	Thu Aug 8 16:20:52 BST 2019
Unique Job ID	706e8020ac6b7116

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6dnmA</a>	 Alignment		100.0	100	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> export chaperone sats; <b>PDBTitle:</b> the crystal structure of sats c-terminal domain
2	<a href="#">d1gph12</a>	 Alignment		61.5	17	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
3	<a href="#">d1xffa</a>	 Alignment		56.0	15	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
4	<a href="#">d2a1ha1</a>	 Alignment		54.1	13	<b>Fold:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Superfamily:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes <b>Family:</b> D-aminoacid aminotransferase-like PLP-dependent enzymes
5	<a href="#">c3dtfB</a>	 Alignment		52.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> branched-chain amino acid aminotransferase; <b>PDBTitle:</b> structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
6	<a href="#">c4dqnA</a>	 Alignment		47.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative branched-chain amino acid aminotransferase ilve; <b>PDBTitle:</b> crystal structure of the branched-chain aminotransferase from2 streptococcus mutans
7	<a href="#">c2abjG</a>	 Alignment		42.7	15	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> branched-chain-amino-acid aminotransferase, cytosolic; <b>PDBTitle:</b> crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
8	<a href="#">c2vtwF</a>	 Alignment		41.8	19	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fiber protein 2; <b>PDBTitle:</b> structure of the c-terminal head domain of the fowl2 adenovirus type 1 short fibre
9	<a href="#">c1gph1</a>	 Alignment		40.6	21	<b>PDB header:</b> transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis
10	<a href="#">c2kuaA</a>	 Alignment		36.0	10	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-like protein 10; <b>PDBTitle:</b> solution structure of a divergent bcl-2 protein
11	<a href="#">c1wd6B</a>	 Alignment		32.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydhr; <b>PDBTitle:</b> crystal structure of jw1657 from escherichia coli

12	<a href="#">c6cfzC</a>	Alignment		31.5	42	<b>PDB header:</b> nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
13	<a href="#">c3uzbA</a>	Alignment		30.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structures of branched-chain aminotransferase from deinococcus2 radiodurans complexes with alpha-ketoisocaproate and l-glutamate3 suggest its radio-resistance for catalysis
14	<a href="#">c2hq3A</a>	Alignment		29.7	26	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nosl protein; <b>PDBTitle:</b> solution nmr structure of the apo-nosl protein from2 achromobacter cycloclastes
15	<a href="#">d2hpu1</a>	Alignment		29.7	26	<b>Fold:</b> NosL/MerB-like <b>Superfamily:</b> NosL/MerB-like <b>Family:</b> NosL-like
16	<a href="#">c1ecjB</a>	Alignment		28.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
17	<a href="#">c3l7mC</a>	Alignment		27.4	18	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f; <b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a
18	<a href="#">d1t0ha</a>	Alignment		25.4	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
19	<a href="#">c2vofA</a>	Alignment		24.3	19	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-related protein a1; <b>PDBTitle:</b> structure of mouse a1 bound to the puma bh3-domain
20	<a href="#">d2o2xa1</a>	Alignment		21.0	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Histidinol phosphatase-like
21	<a href="#">c1wrjA</a>	Alignment	not modelled	20.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine <b>PDBTitle:</b> crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
22	<a href="#">d1vyua1</a>	Alignment	not modelled	20.6	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
23	<a href="#">c5wddA</a>	Alignment	not modelled	20.2	10	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-related ovarian killer protein; <b>PDBTitle:</b> crystal structure of chicken bok
24	<a href="#">d1zxqa1</a>	Alignment	not modelled	20.2	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
25	<a href="#">c2yudA</a>	Alignment	not modelled	19.7	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> yth domain-containing protein 1; <b>PDBTitle:</b> solution structure of the yth domain in yth domain-2 containing protein 1 (putative splicing factor yt521)
26	<a href="#">c3oqlA</a>	Alignment	not modelled	19.7	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tena homolog; <b>PDBTitle:</b> crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
27	<a href="#">c5d5nA</a>	Alignment	not modelled	18.6	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> virion egress protein ul34 homolog; <b>PDBTitle:</b> crystal structure of the human cytomegalovirus pul50-pul53 complex
28	<a href="#">c6h1nA</a>	Alignment	not modelled	18.3	14	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2-like 10 (apoptosis facilitator); <b>PDBTitle:</b> crystal structure of a zebra-fish pro-survival protein nrz- apo
						<b>PDB header:</b> transcription

29	<a href="#">c3oqlB_</a>	Alignment	not modelled	18.1	33	<b>Chain:</b> B: <b>PDB Molecule:</b> tena homolog; <b>PDBTitle:</b> crystal structure of a tena homolog (pspto1738) from pseudomonas2 syringae pv. tomato str. dc3000 at 2.54 a resolution
30	<a href="#">c5e8jC_</a>	Alignment	not modelled	18.0	22	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> rnmt-activating mini protein; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
31	<a href="#">c3wofB_</a>	Alignment	not modelled	17.4	50	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of p23-45 gp39 (6-132) bound to thermus thermophilus2 rna polymerase beta-flap domain
32	<a href="#">d2bhua1</a>	Alignment	not modelled	17.4	40	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
33	<a href="#">c2h6oA_</a>	Alignment	not modelled	16.7	42	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> major outer envelope glycoprotein gp350; <b>PDBTitle:</b> epstein barr virus major envelope glycoprotein
34	<a href="#">c4b4sA_</a>	Alignment	not modelled	16.4	13	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-like protein 10; <b>PDBTitle:</b> crystal structure of a pro-survival bcl-2:bim bh3 complex
35	<a href="#">c2gk2B_</a>	Alignment	not modelled	16.3	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> carcinoembryonic antigen-related cell adhesion molecule 1; <b>PDBTitle:</b> crystal structure of the n terminal domain of human ceacam1
36	<a href="#">c2dskA_</a>	Alignment	not modelled	16.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> crystal structure of catalytic domain of hyperthermophilic chitinase2 from pyrococcus furiosus
37	<a href="#">d1pgja1</a>	Alignment	not modelled	15.8	21	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
38	<a href="#">c3wodG_</a>	Alignment	not modelled	15.6	50	<b>PDB header:</b> transferase/transcription <b>Chain:</b> G: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rna polymerase-gp39 complex
39	<a href="#">c5ua4A_</a>	Alignment	not modelled	15.3	11	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> 5-hl; <b>PDBTitle:</b> crystal structure of a179l:bid bh3 complex
40	<a href="#">d1o6aa_</a>	Alignment	not modelled	15.3	17	<b>Fold:</b> Surface presentation of antigens (SPOA) <b>Superfamily:</b> Surface presentation of antigens (SPOA) <b>Family:</b> Surface presentation of antigens (SPOA)
41	<a href="#">c2vm6A_</a>	Alignment	not modelled	15.0	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2-related protein a1; <b>PDBTitle:</b> human bcl-2-a1 in complex with bim-bh3 peptide
42	<a href="#">c1ezaA_</a>	Alignment	not modelled	15.0	16	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> enzyme i; <b>PDBTitle:</b> amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
43	<a href="#">d1uxja2</a>	Alignment	not modelled	13.6	19	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
44	<a href="#">d1hxna_</a>	Alignment	not modelled	13.4	20	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
45	<a href="#">d2oz4a2</a>	Alignment	not modelled	13.1	20	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
46	<a href="#">d1prtf_</a>	Alignment	not modelled	13.0	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
47	<a href="#">c3uepB_</a>	Alignment	not modelled	12.8	25	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yscq-c, type iii secretion protein; <b>PDBTitle:</b> crystal structure of yscq-c from yersinia pseudotuberculosis
48	<a href="#">c4azzB_</a>	Alignment	not modelled	12.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> levanase; <b>PDBTitle:</b> carbohydrate binding module cbm66 from bacillus subtilis
49	<a href="#">d1m7xa1</a>	Alignment	not modelled	12.6	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
50	<a href="#">c1zvtA_</a>	Alignment	not modelled	12.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase iv subunit a; <b>PDBTitle:</b> structure of the e. coli parc c-terminal domain
51	<a href="#">c4e8cA_</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 35; <b>PDBTitle:</b> crystal structure of streptococcal beta-galactosidase in complex with2 galactose
52	<a href="#">c4ifdH_</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> exosome complex component rrp4; <b>PDBTitle:</b> crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
53	<a href="#">c2k0mA_</a>	Alignment	not modelled	12.1	17	<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 the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
54	<a href="#">c4zyeA_</a>	Alignment	not modelled	11.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase

55	<a href="#">d1axxa_</a>	Alignment	not modelled	11.8	18	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
56	<a href="#">d1ofda2</a>	Alignment	not modelled	11.7	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
57	<a href="#">c4lubA_</a>	Alignment	not modelled	11.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative prephenate dehydratase; <b>PDBTitle:</b> x-ray structure of prephenate dehydratase from streptococcus mutans
58	<a href="#">d2plqa1</a>	Alignment	not modelled	11.3	24	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> TII0839-like
59	<a href="#">c4l4qA_</a>	Alignment	not modelled	11.2	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> methionine adenosyltransferase
60	<a href="#">c1x5eA_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain containing protein 1; <b>PDBTitle:</b> the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
61	<a href="#">c2xa0A_</a>	Alignment	not modelled	10.6	8	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis regulator bcl-2; <b>PDBTitle:</b> crystal structure of bcl-2 in complex with a bax bh32 peptide
62	<a href="#">d1qhua1</a>	Alignment	not modelled	10.6	27	<b>Fold:</b> 4-bladed beta-propeller <b>Superfamily:</b> Hemopexin-like domain <b>Family:</b> Hemopexin-like domain
63	<a href="#">c1mq8C_</a>	Alignment	not modelled	10.2	11	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> intercellular adhesion molecule-1; <b>PDBTitle:</b> crystal structure of alpha i domain in complex with icam-1
64	<a href="#">c1pgiA_</a>	Alignment	not modelled	10.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
65	<a href="#">d2hiqua1</a>	Alignment	not modelled	10.1	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdhR
66	<a href="#">d1ea0a2</a>	Alignment	not modelled	10.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
67	<a href="#">d1hyha2</a>	Alignment	not modelled	10.1	22	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
68	<a href="#">c5xrwD_</a>	Alignment	not modelled	9.8	28	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> flyi; <b>PDBTitle:</b> crystal structure of flagellar motor switch complex from h. pylori
69	<a href="#">c5a15A_</a>	Alignment	not modelled	9.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> btb/poz domain-containing protein kctd16; <b>PDBTitle:</b> crystal structure of the btb domain of human kctd16
70	<a href="#">d1pkxa2</a>	Alignment	not modelled	9.3	15	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
71	<a href="#">c3iykK_</a>	Alignment	not modelled	9.3	32	<b>PDB header:</b> virus <b>Chain:</b> K: <b>PDB Molecule:</b> vp2; <b>PDBTitle:</b> bluetongue virus structure reveals a sialic acid binding domain,2 amphipathic helices and a central coiled coil in the outer capsid3 proteins
72	<a href="#">d1gv0a2</a>	Alignment	not modelled	9.3	28	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
73	<a href="#">c3ushB_</a>	Alignment	not modelled	9.2	46	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
74	<a href="#">d1qhma_</a>	Alignment	not modelled	9.2	20	<b>Fold:</b> PFL-like glycol radical enzymes <b>Superfamily:</b> PFL-like glycol radical enzymes <b>Family:</b> PFL-like
75	<a href="#">c2ds2B_</a>	Alignment	not modelled	9.1	10	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain b; <b>PDBTitle:</b> crystal structure of mabinlin ii
76	<a href="#">c2l3gA_</a>	Alignment	not modelled	9.1	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 7; <b>PDBTitle:</b> solution nmr structure of ch domain of rho guanine nucleotide exchange2 factor 7 from homo sapiens, northeast structural genomics consortium3 target hr4495e
77	<a href="#">c4iohA_</a>	Alignment	not modelled	9.1	46	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tlI1086 protein; <b>PDBTitle:</b> crystal structure of the tlI1086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
78	<a href="#">c3fgrB_</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phospholipase b-like 2 40 kda form; <b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstroem
79	<a href="#">c2mwfA_</a>	Alignment	not modelled	9.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation regulator 1; <b>PDBTitle:</b> nmr structure of fbp28 ww2 mutant y438r dn
80	<a href="#">c4bzyC_</a>	Alignment	not modelled	8.8	40	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1,4-alpha-glucan-branching enzyme; <b>PDBTitle:</b> crystal structure of human glycogen branching enzyme (gbe1)

81	<a href="#">d1hkoa_</a>	Alignment	not modelled	8.8	18	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
82	<a href="#">c3drzE_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> btb/poz domain-containing protein kctd5; <b>PDBTitle:</b> x-ray crystal structure of the n-terminal btb domain of human kctd52 protein
83	<a href="#">c1bdsA_</a>	Alignment	not modelled	8.6	36	<b>PDB header:</b> anti-hypertensive, anti-viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> bds-i; <b>PDBTitle:</b> determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
84	<a href="#">d1bdsa_</a>	Alignment	not modelled	8.6	36	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
85	<a href="#">c1lm1A_</a>	Alignment	not modelled	8.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
86	<a href="#">c5vgiG_</a>	Alignment	not modelled	8.5	46	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> G: <b>PDB Molecule:</b> 1fd6-v1v2-wito; <b>PDBTitle:</b> crystal structure of the human fab vrc38.01, an hiv-1 v1v2-directed2 neutralizing antibody isolated from donor n90, bound to a scaffolded3 wito v1v2 domain
87	<a href="#">c1sfeA_</a>	Alignment	not modelled	8.4	17	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ada o6-methylguanine-dna methyltransferase; <b>PDBTitle:</b> ada o6-methylguanine-dna methyltransferase from escherichia coli
88	<a href="#">d1hc7a3</a>	Alignment	not modelled	8.3	25	<b>Fold:</b> IF3-like <b>Superfamily:</b> C-terminal domain of ProRS <b>Family:</b> C-terminal domain of ProRS
89	<a href="#">c2lpdA_</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
90	<a href="#">c1t39A_</a>	Alignment	not modelled	8.3	22	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine <b>PDBTitle:</b> human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
91	<a href="#">c2vdcF_</a>	Alignment	not modelled	8.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadh] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
92	<a href="#">c5azaA_</a>	Alignment	not modelled	8.2	18	<b>PDB header:</b> sugar binding protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,oligosaccharyl <b>PDBTitle:</b> crystal structure of mbp-saglb fusion protein with a 20-residue spacer2 in the connector helix
93	<a href="#">d1soxa2</a>	Alignment	not modelled	8.1	15	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
94	<a href="#">c5gquA_</a>	Alignment	not modelled	8.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme glgb; <b>PDBTitle:</b> crystal structure of branching enzyme from cyanothecce sp. atcc 51142
95	<a href="#">c4ht7G_</a>	Alignment	not modelled	8.0	32	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> co2 concentrating mechanism protein p; <b>PDBTitle:</b> co2 concentrating mechanism protein p, ccmp form 2
96	<a href="#">d1euea_</a>	Alignment	not modelled	8.0	13	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
97	<a href="#">c5czdB_</a>	Alignment	not modelled	7.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-carrier-protein; <b>PDBTitle:</b> the complex structure of vink with vinl
98	<a href="#">d1ldna2</a>	Alignment	not modelled	7.9	34	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
99	<a href="#">c5us5B_</a>	Alignment	not modelled	7.9	27	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> upf0297 protein ef_1202; <b>PDBTitle:</b> solution structure of the ireb homodimer