
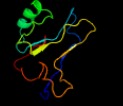
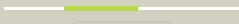


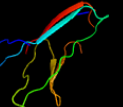

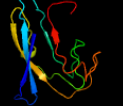

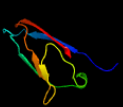

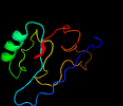

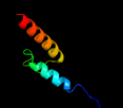



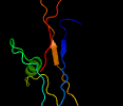


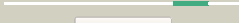

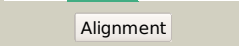








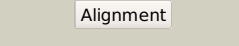
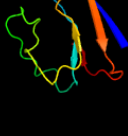
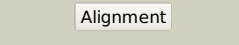

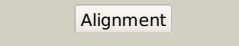



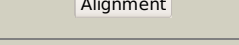
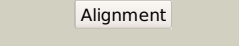
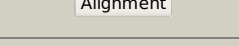


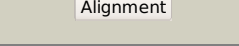




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0633c_(-)_729330_730169
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	deef0e63b6502fc8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2ccwa1</a>	 Alignment		67.9	15	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
2	<a href="#">d1azca_</a>	 Alignment		62.4	13	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
3	<a href="#">c2rtta_</a>	 Alignment		62.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> chic; <b>PDBTitle:</b> solution structure of the chitin-binding domain of chi18ac from2 streptomyces coelicolor
4	<a href="#">c5a1vG_</a>	 Alignment		62.2	20	<b>PDB header:</b> transport protein <b>Chain:</b> G; <b>PDB Molecule:</b> coatomer subunit beta'; <b>PDBTitle:</b> the structure of the copi coat linkage i
5	<a href="#">d1exha_</a>	 Alignment		62.1	12	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
6	<a href="#">d1rkra_</a>	 Alignment		60.4	10	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
7	<a href="#">d1nkpa_</a>	 Alignment		57.1	25	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
8	<a href="#">c4dtfA_</a>	 Alignment		51.5	36	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> vgrg protein; <b>PDBTitle:</b> structure of a vgrg vibrio cholerae toxin acd domain in complex with2 amp-pnp and mg++
9	<a href="#">c2kutA_</a>	 Alignment		51.2	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 gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
10	<a href="#">c2qj2D_</a>	 Alignment		51.0	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> D; <b>PDB Molecule:</b> neurogenic differentiation factor 1; <b>PDBTitle:</b> crystal structure of the basic-helix-loop-helix domains of2 the heterodimer e47/neurod1 bound to dna
11	<a href="#">d1nlwa_</a>	 Alignment		48.5	16	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain

12	<a href="#">c3ay2A_</a>	 Alignment		45.9	16	<b>PDB header:</b> antitumor protein, antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid modified azurin protein; <b>PDBTitle:</b> crystal structure of neisserial azurin
13	<a href="#">c119mB_</a>	 Alignment		42.8	14	<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
14	<a href="#">c2kl6A_</a>	 Alignment		42.4	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 cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
15	<a href="#">c3uekA_</a>	 Alignment		41.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(adp-ribose) glycohydrolase; <b>PDBTitle:</b> crystal structure of the catalytic domain of rat poly (adp-ribose)2 glycohydrolase
16	<a href="#">c2ypaA_</a>	 Alignment		39.5	19	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell acute lymphocytic leukemia protein 1; <b>PDBTitle:</b> structure of the scl:e47:lmo2:ldb1 complex bound to dna
17	<a href="#">d1cuoa_</a>	 Alignment		38.5	13	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
18	<a href="#">d1joia_</a>	 Alignment		37.8	12	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
19	<a href="#">c2l0dA_</a>	 Alignment		37.7	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
20	<a href="#">c6f7eA_</a>	 Alignment		37.6	10	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted cellulose binding protein; <b>PDBTitle:</b> nmr solution structure of the cellulose-binding family 2 carbohydrate2 binding domain (cbm2) from sclpmo9c
21	<a href="#">d1tzoa_</a>	 Alignment	not modelled	34.9	21	<b>Fold:</b> Anthrax protective antigen <b>Superfamily:</b> Anthrax protective antigen <b>Family:</b> Anthrax protective antigen
22	<a href="#">c3ndyG_</a>	 Alignment	not modelled	33.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
23	<a href="#">d1w8oa1</a>	 Alignment	not modelled	32.6	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
24	<a href="#">d1jzga_</a>	 Alignment	not modelled	31.7	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
25	<a href="#">c2yppB_</a>	 Alignment	not modelled	31.5	8	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor e2-alpha; <b>PDBTitle:</b> structure of the scl:e47 complex bound to dna
26	<a href="#">c5epwB_</a>	 Alignment	not modelled	31.3	23	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> c-terminal domain of human coronavirus nl63 nucleocapsid protein
27	<a href="#">d1cc3a_</a>	 Alignment	not modelled	29.9	7	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
28	<a href="#">c2h47C_</a>	 Alignment	not modelled	28.9	15	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> azurin; <b>PDBTitle:</b> crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)

29	<a href="#">d1jatb_</a>	Alignment	not modelled	28.2	6	<b>Fold:</b> UBC-like <b>Superfamily:</b> UBC-like <b>Family:</b> UBC-related
30	<a href="#">c5fj8C_</a>	Alignment	not modelled	28.1	30	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> dna-directed rna polymerases i and iii subunit rpac1; <b>PDBTitle:</b> cryo-em structure of yeast rna polymerase iii elongation complex at 3.2 9 a
31	<a href="#">d2cjr1_</a>	Alignment	not modelled	25.4	15	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
32	<a href="#">c3u5vA_</a>	Alignment	not modelled	24.9	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein max, transcription factor e2-alpha chimera; <b>PDBTitle:</b> crystal structure of max-e47
33	<a href="#">d1ef1c_</a>	Alignment	not modelled	24.0	31	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Moesin tail domain <b>Family:</b> Moesin tail domain
34	<a href="#">d2ge7a1</a>	Alignment	not modelled	23.3	17	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
35	<a href="#">d1bdya_</a>	Alignment	not modelled	22.3	14	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> PLC-like (P variant)
36	<a href="#">d2giba1</a>	Alignment	not modelled	22.3	15	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
37	<a href="#">c2lbwA_</a>	Alignment	not modelled	21.6	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 2; <b>PDBTitle:</b> solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
38	<a href="#">d1c4ka3</a>	Alignment	not modelled	21.1	30	<b>Fold:</b> Ornithine decarboxylase C-terminal domain <b>Superfamily:</b> Ornithine decarboxylase C-terminal domain <b>Family:</b> Ornithine decarboxylase C-terminal domain
39	<a href="#">d1etha1</a>	Alignment	not modelled	20.3	12	<b>Fold:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Superfamily:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Family:</b> Colipase-binding domain
40	<a href="#">c2enjA_</a>	Alignment	not modelled	20.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c theta type; <b>PDBTitle:</b> solution structure of the c2 domain from human protein2 kinase c theta
41	<a href="#">d1mdya_</a>	Alignment	not modelled	20.1	19	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
42	<a href="#">d2ca1a1</a>	Alignment	not modelled	20.0	17	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
43	<a href="#">c4atkB_</a>	Alignment	not modelled	18.9	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> microphthalmia-associated transcription factor; <b>PDBTitle:</b> mitf:e-box complex
44	<a href="#">d1g5aa1</a>	Alignment	not modelled	18.9	17	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
45	<a href="#">c4ayaA_</a>	Alignment	not modelled	18.6	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein inhibitor id-2; <b>PDBTitle:</b> crystal structure of id2 hlh homodimer at 2.1a resolution
46	<a href="#">d1hloa_</a>	Alignment	not modelled	18.1	13	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
47	<a href="#">c1ywke_</a>	Alignment	not modelled	17.5	29	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-1-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
48	<a href="#">d1nlwe_</a>	Alignment	not modelled	17.2	14	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
49	<a href="#">c2lfhA_</a>	Alignment	not modelled	16.7	16	<b>PDB header:</b> dna binding protein inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein inhibitor id-3; <b>PDBTitle:</b> solution nmr structure of the helix-loop-helix domain of human id32 protein, northeast structural genomics consortium target hr3111a
50	<a href="#">c1yueA_</a>	Alignment	not modelled	15.0	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> head vertex protein gp24; <b>PDBTitle:</b> bacteriophage t4 capsid vertex protein gp24
51	<a href="#">c3kfbB_</a>	Alignment	not modelled	14.8	29	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein ten1; <b>PDBTitle:</b> crystal structure of s. pombe stn1-ten1 complex
52	<a href="#">c1s1iG_</a>	Alignment	not modelled	14.4	16	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l8-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
53	<a href="#">d1gp1a1</a>	Alignment	not modelled	14.3	15	<b>Fold:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Superfamily:</b> Lipase/lipoxygenase domain (PLAT/LH2 domain) <b>Family:</b> Colipase-binding domain
54	<a href="#">d2hija1</a>	Alignment	not modelled	14.1	29	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain

						<b>Family:</b> Ykff-like
55	<a href="#">c2hijA_</a>	Alignment	not modelled	14.1	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ykff; <b>PDBTitle:</b> solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
56	<a href="#">c6hn9A_</a>	Alignment	not modelled	14.0	47	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> nicomicin-1; <b>PDBTitle:</b> nicomicin-1 -- novel antimicrobial peptides from the arctic polychaeta2 nicomache minor provide new molecular insight into biological role of3 the brichos domain
57	<a href="#">d1nwpa_</a>	Alignment	not modelled	13.0	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
58	<a href="#">d2bwqa1</a>	Alignment	not modelled	12.8	14	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)
59	<a href="#">c2x7IP_</a>	Alignment	not modelled	12.8	45	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> protein rev; <b>PDBTitle:</b> implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
60	<a href="#">c5bu3A_</a>	Alignment	not modelled	12.7	46	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pyri4; <b>PDBTitle:</b> crystal structure of diels-alderase pyri4 in complex with its product
61	<a href="#">d1si2a_</a>	Alignment	not modelled	12.2	29	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> PAZ domain <b>Family:</b> PAZ domain
62	<a href="#">c2aanA_</a>	Alignment	not modelled	12.0	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> auracyanin a; <b>PDBTitle:</b> auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium, chloroflexus aurantiacus
63	<a href="#">d1st6a3</a>	Alignment	not modelled	11.9	17	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
64	<a href="#">d1an2a_</a>	Alignment	not modelled	11.9	14	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
65	<a href="#">c2h2yA_</a>	Alignment	not modelled	11.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme; <b>PDBTitle:</b> crystal structure of ubiquitin conjugating enzyme e2 from2 plasmodium falciparum
66	<a href="#">c6b4hB_</a>	Alignment	not modelled	11.7	36	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin amo1; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum gle1 ctd-nup42 gbm-ip62 complex
67	<a href="#">c2x3bB_</a>	Alignment	not modelled	11.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
68	<a href="#">c5dfkA_</a>	Alignment	not modelled	11.5	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable fimbrial chaperone ecpb; <b>PDBTitle:</b> crystal structure of the escherichia coli common pilus chaperone, ecpb
69	<a href="#">c6g1IA_</a>	Alignment	not modelled	11.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> microphthalmia-associated transcription factor; <b>PDBTitle:</b> mitf/clearbox structure
70	<a href="#">d1wmda1</a>	Alignment	not modelled	11.0	18	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Protein convertase P-domain
71	<a href="#">d1e42a1</a>	Alignment	not modelled	10.8	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> Alpha-adaptin ear subdomain-like
72	<a href="#">d1twfc2</a>	Alignment	not modelled	10.6	33	<b>Fold:</b> Insert subdomain of RNA polymerase alpha subunit <b>Superfamily:</b> Insert subdomain of RNA polymerase alpha subunit <b>Family:</b> Insert subdomain of RNA polymerase alpha subunit
73	<a href="#">d2aifa1</a>	Alignment	not modelled	10.4	16	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
74	<a href="#">c5vwIA_</a>	Alignment	not modelled	10.3	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic tail of hiv-1 gp41 protein; <b>PDBTitle:</b> solution nmr structure of the membrane associated segment of hiv-12 gp41 cytoplasmic tail
75	<a href="#">c2m1aA_</a>	Alignment	not modelled	10.3	46	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 rev arginine-rich motif (arm); <b>PDBTitle:</b> hiv-1 rev arm peptide (residues t34-r50)
76	<a href="#">d1uuja_</a>	Alignment	not modelled	10.0	30	<b>Fold:</b> Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain <b>Superfamily:</b> Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain <b>Family:</b> Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain
77	<a href="#">c1etgB_</a>	Alignment	not modelled	10.0	46	<b>PDB header:</b> viral protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rev peptide; <b>PDBTitle:</b> rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures
78	<a href="#">c1etfB_</a>	Alignment	not modelled	10.0	46	<b>PDB header:</b> viral protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rev peptide; <b>PDBTitle:</b> rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure
79	<a href="#">d2ozba1</a>	Alignment	not modelled	9.8	20	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
						<b>Fold:</b> Bacillus chorismate mutase-like

80	<a href="#">d1xbia1</a>	Alignment	not modelled	9.7	10	<b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
81	<a href="#">d2vzsa2</a>	Alignment	not modelled	9.5	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
82	<a href="#">d1u2ca2</a>	Alignment	not modelled	9.4	40	<b>Fold:</b> Dystroglycan, domain 2 <b>Superfamily:</b> Dystroglycan, domain 2 <b>Family:</b> Dystroglycan, domain 2
83	<a href="#">d2czwa1</a>	Alignment	not modelled	9.3	17	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
84	<a href="#">c4ympC</a>	Alignment	not modelled	9.0	14	<b>PDB header:</b> heme-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> internalin; <b>PDBTitle:</b> crystal structure of the bacillus anthracis hal neat domain in complex2 with heme
85	<a href="#">c2p7vA</a>	Alignment	not modelled	9.0	42	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma d; <b>PDBTitle:</b> crystal structure of the escherichia coli regulator of sigma 70, rsd_2 in complex with sigma 70 domain 4
86	<a href="#">d1nkpB</a>	Alignment	not modelled	8.8	14	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
87	<a href="#">c2x3IA</a>	Alignment	not modelled	8.8	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orn/lys/arg decarboxylase family protein; <b>PDBTitle:</b> crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
88	<a href="#">c2q2eB</a>	Alignment	not modelled	8.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
89	<a href="#">c5hdwA</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fb-box only protein 3; <b>PDBTitle:</b> apag domain of fbxo3
90	<a href="#">c3os7D</a>	Alignment	not modelled	8.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> galactose mutarotase-like protein; <b>PDBTitle:</b> crystal structure of a galactose mutarotase-like protein (ca_c0697)2 from clostridium acetobutylicum at 1.80 a resolution
91	<a href="#">c3os7B</a>	Alignment	not modelled	8.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> galactose mutarotase-like protein; <b>PDBTitle:</b> crystal structure of a galactose mutarotase-like protein (ca_c0697)2 from clostridium acetobutylicum at 1.80 a resolution
92	<a href="#">c4h10B</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> circadian locomoter output cycles protein kaput; <b>PDBTitle:</b> intermolecular recognition revealed by the complex structure of human2 clock-bmal1 basic helix-loop-helix domains with e-box dna
93	<a href="#">d1an4a</a>	Alignment	not modelled	8.7	9	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
94	<a href="#">d2alea1</a>	Alignment	not modelled	8.6	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> L30e/L7ae ribosomal proteins
95	<a href="#">c4fc2C</a>	Alignment	not modelled	8.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> poly(adp-ribose) glycohydrolase; <b>PDBTitle:</b> crystal structure of mouse poly(adp-ribose) glycohydrolase (parg)2 catalytic domain
96	<a href="#">c4v193</a>	Alignment	not modelled	8.4	25	<b>PDB header:</b> ribosome <b>Chain:</b> 3: <b>PDB Molecule:</b> mitoribosomal protein ul30m, mrpl30; <b>PDB Fragment:</b> cca-3' end; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
97	<a href="#">c5udtD</a>	Alignment	not modelled	8.3	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
98	<a href="#">c5gnjI</a>	Alignment	not modelled	8.3	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> I: <b>PDB Molecule:</b> transcription factor myc2; <b>PDBTitle:</b> structure of a transcription factor and dna complex
99	<a href="#">d1v27a</a>	Alignment	not modelled	8.2	14	<b>Fold:</b> C2 domain-like <b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB) <b>Family:</b> Synaptotagmin-like (S variant)