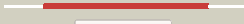

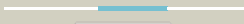
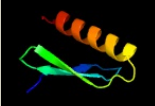

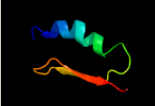



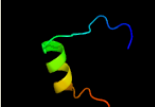





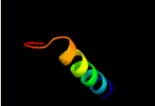

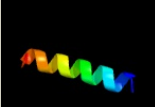



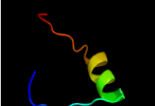
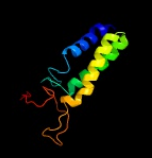
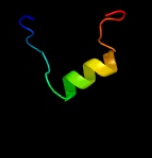

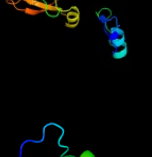

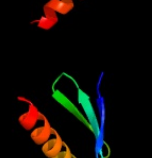

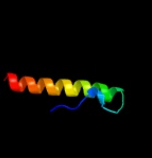
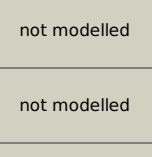


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2544_(lppB)_2867134_2867796
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	d683bfd05a77c1b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2v7sA_</a>	 Alignment		100.0	85	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
2	<a href="#">d1mp9a1</a>	 Alignment		37.7	20	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
3	<a href="#">c1wd6B_</a>	 Alignment		36.8	17	<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
4	<a href="#">c6bs7A_</a>	 Alignment		31.2	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
5	<a href="#">d1dj2a_</a>	 Alignment		31.2	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
6	<a href="#">c3r7tA_</a>	 Alignment		27.3	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
7	<a href="#">c2yufA_</a>	 Alignment		26.0	39	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ngfi-a-binding protein 1; <b>PDBTitle:</b> solution structure of the ncd2 domain in human2 transcriptional repressor nab1 protein
8	<a href="#">c6h3uA_</a>	 Alignment		25.4	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> schmallerberg virus glycoprotein gc head domain in complex with scfv2 4b6
9	<a href="#">d1nvmb2</a>	 Alignment		25.3	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
10	<a href="#">c5j34B_</a>	 Alignment		24.9	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
11	<a href="#">d1qf5a_</a>	 Alignment		24.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like

12	<a href="#">d1ulva1</a>	Alignment		24.6	18	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Bacterial glucoamylase C-terminal domain-like
13	<a href="#">c1iweB_</a>	Alignment		24.6	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> imp complex of the recombinant mouse-muscle adenylosuccinate2 synthetase
14	<a href="#">d1iwea_</a>	Alignment		24.2	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
15	<a href="#">c4xhiB_</a>	Alignment		24.1	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of native theosa assigna virus rna-dependent rna2 polymerase (rdrp) at 2.15 angstrom resolution
16	<a href="#">d1dj3a_</a>	Alignment		23.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
17	<a href="#">d1qnaa1</a>	Alignment		23.4	19	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
18	<a href="#">d1aisa1</a>	Alignment		22.2	22	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
19	<a href="#">c4ps2A_</a>	Alignment		22.0	19	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative type vi secretion protein; <b>PDBTitle:</b> structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
20	<a href="#">d1jl3a_</a>	Alignment		21.6	17	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
21	<a href="#">c2wylF_</a>	Alignment	not modelled	21.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> l-ascorbate-6-phosphate lactonase ulag; <b>PDBTitle:</b> apo structure of a metallo-b-lactamase
22	<a href="#">d2oqea2</a>	Alignment	not modelled	21.5	23	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
23	<a href="#">d1p9ba_</a>	Alignment	not modelled	21.2	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
24	<a href="#">c6h3xA_</a>	Alignment	not modelled	20.7	27	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> oropouche virus glycoprotein gc head domain
25	<a href="#">c4jn6B_</a>	Alignment	not modelled	20.4	29	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
26	<a href="#">d2hiqa1</a>	Alignment	not modelled	18.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdHR
27	<a href="#">c3k6gA_</a>	Alignment	not modelled	18.4	28	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> telomeric repeat-binding factor 2-interacting protein 1; <b>PDBTitle:</b> crystal structure of rap1 and trf2 complex
28	<a href="#">c6h3wA_</a>	Alignment	not modelled	18.3	9	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> la crosse virus glycoprotein gc head domain
29	<a href="#">c6h3sA_</a>	Alignment	not modelled	18.3	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein;

						<b>PDBTitle:</b> schmallerberg virus glycoprotein gc head/stalk domains
30	<a href="#">c4n6cB_</a>	Alignment	not modelled	18.0	6	<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 b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
31	<a href="#">c4m0gB_</a>	Alignment	not modelled	17.7	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> the crystal structure of an adenylosuccinate synthetase from bacillus2 anthracis str. ames ancestor.
32	<a href="#">c4f6oA_</a>	Alignment	not modelled	17.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase-1; <b>PDBTitle:</b> crystal structure of the yeast metacaspase yca1
33	<a href="#">d1nh2a1</a>	Alignment	not modelled	17.2	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
34	<a href="#">d1i7aa_</a>	Alignment	not modelled	17.1	24	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
35	<a href="#">c4dknB_</a>	Alignment	not modelled	16.6	39	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfpa1; <b>PDBTitle:</b> crystal structure of amphioxus green fluorescent protein, gfpa1
36	<a href="#">d1qnaa2</a>	Alignment	not modelled	15.7	13	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
37	<a href="#">c2mt3A_</a>	Alignment	not modelled	15.7	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> structure of -24 dna binding domain of sigma 54 from e.coli
38	<a href="#">c4clvB_</a>	Alignment	not modelled	15.0	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
39	<a href="#">c2ahqA_</a>	Alignment	not modelled	14.4	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
40	<a href="#">c3uoaB_</a>	Alignment	not modelled	14.3	36	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> smucosa-associated lymphoid tissue lymphoma translocation <b>PDBTitle:</b> crystal structure of the malt1 paracaspase (p21 form)
41	<a href="#">d1mp9a2</a>	Alignment	not modelled	14.0	12	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
42	<a href="#">d1cdwa1</a>	Alignment	not modelled	14.0	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
43	<a href="#">c3ls1A_</a>	Alignment	not modelled	13.6	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> sll1638 protein; <b>PDBTitle:</b> crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
44	<a href="#">c2o8kA_</a>	Alignment	not modelled	13.0	22	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
45	<a href="#">d1kgda_</a>	Alignment	not modelled	12.9	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
46	<a href="#">d1xbpg2</a>	Alignment	not modelled	12.8	53	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
47	<a href="#">c4mjgB_</a>	Alignment	not modelled	12.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4853 family protein (actodo_00621) from2 actinomyces odontolyticus atcc 17982 at 2.65 a resolution
48	<a href="#">d2gycg2</a>	Alignment	not modelled	11.8	41	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
49	<a href="#">c1nvmB_</a>	Alignment	not modelled	11.5	25	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase (acylating); <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
50	<a href="#">d1nh2a2</a>	Alignment	not modelled	11.3	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
51	<a href="#">c3bjjC_</a>	Alignment	not modelled	11.3	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein gsu0716; <b>PDBTitle:</b> crystal structure of protein gsu0716 from geobacter sulfurreducens.2 northeast structural genomics target gsr13
52	<a href="#">d1cdwa2</a>	Alignment	not modelled	11.0	15	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
53	<a href="#">d1fnna1</a>	Alignment	not modelled	10.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Helicase DNA-binding domain
54	<a href="#">c5ltrA_</a>	Alignment	not modelled	10.7	24	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> mneongreen; <b>PDBTitle:</b> structure of the yellow-green fluorescent protein mneongreen from2 branchiostoma lanceolatum at the near physiological ph 8.0

55	<a href="#">c4xhpA</a>	Alignment	not modelled	10.7	29	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm hybrid fusion protein; <b>PDBTitle:</b> bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
56	<a href="#">c4dkmH</a>	Alignment	not modelled	10.5	39	<b>PDB header:</b> fluorescent protein <b>Chain:</b> H: <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfp1a; <b>PDBTitle:</b> crystal structure of amphioxus gfp1a
57	<a href="#">d1lf6a1</a>	Alignment	not modelled	10.3	10	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Bacterial glucoamylase C-terminal domain-like
58	<a href="#">c6h3vA</a>	Alignment	not modelled	10.3	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> bunyamwera virus glycoprotein gc head domain
59	<a href="#">c2vdcF</a>	Alignment	not modelled	10.0	26	<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.
60	<a href="#">c5lnk2</a>	Alignment	not modelled	10.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 2: <b>PDB Molecule:</b> mitochondrial complex i, 24 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
61	<a href="#">c1lm1A</a>	Alignment	not modelled	9.6	22	<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
62	<a href="#">d1aisa2</a>	Alignment	not modelled	9.5	23	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
63	<a href="#">c5civA</a>	Alignment	not modelled	9.4	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
64	<a href="#">c3ue9A</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
65	<a href="#">c3v4oA</a>	Alignment	not modelled	9.2	36	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> mucosa-associated lymphoid tissue lymphoma translocation <b>PDBTitle:</b> human malt1 (caspase domain) in complex with an irreversible peptidic2 inhibitor
66	<a href="#">c4yk3B</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
67	<a href="#">c5itgA</a>	Alignment	not modelled	9.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sorbitol dehydrogenase; <b>PDBTitle:</b> crystal structure of d-sorbitol dehydrogenase in substrate-free form
68	<a href="#">d1ofda2</a>	Alignment	not modelled	9.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
69	<a href="#">d1smya1</a>	Alignment	not modelled	8.9	36	<b>Fold:</b> DCoH-like <b>Superfamily:</b> RBP11-like subunits of RNA polymerase <b>Family:</b> RNA polymerase alpha subunit dimerisation domain
70	<a href="#">d1d6za2</a>	Alignment	not modelled	8.6	18	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
71	<a href="#">d1ea0a2</a>	Alignment	not modelled	8.6	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
72	<a href="#">d1w2za2</a>	Alignment	not modelled	8.5	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
73	<a href="#">c5cogB</a>	Alignment	not modelled	8.3	8	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> irc4; <b>PDBTitle:</b> crystal structure of yeast irc4
74	<a href="#">d1ynja1</a>	Alignment	not modelled	8.3	32	<b>Fold:</b> DCoH-like <b>Superfamily:</b> RBP11-like subunits of RNA polymerase <b>Family:</b> RNA polymerase alpha subunit dimerisation domain
75	<a href="#">c2jp3A</a>	Alignment	not modelled	8.0	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fyxd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
76	<a href="#">d1mmsa2</a>	Alignment	not modelled	7.9	53	<b>Fold:</b> Ribosomal L11/L12e N-terminal domain <b>Superfamily:</b> Ribosomal L11/L12e N-terminal domain <b>Family:</b> Ribosomal L11/L12e N-terminal domain
77	<a href="#">d2i8da1</a>	Alignment	not modelled	7.5	10	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
78	<a href="#">d2pv4a1</a>	Alignment	not modelled	7.4	32	<b>Fold:</b> Sama2622-like <b>Superfamily:</b> Sama2622-like <b>Family:</b> Sama2622-like
79	<a href="#">c5y00A</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> acid-tolerant monomeric gfp, gamillus, fluorescence (on) state
80	<a href="#">d1w27a</a>	Alignment	not modelled	7.4	25	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> HAL/PAL-like
						<b>PDB header:</b> transferase

81	<a href="#">c4ffcD_</a>	Alignment	not modelled	7.2	13	<b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate aminotransferase (gabt); <b>PDBTitle:</b> crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
82	<a href="#">c3o6xC_</a>	Alignment	not modelled	7.2	17	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamine synthetase; <b>PDBTitle:</b> crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
83	<a href="#">c5xf9E_</a>	Alignment	not modelled	7.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
84	<a href="#">c4jeoB_</a>	Alignment	not modelled	7.0	44	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> red fluorescent protein blfp-r5; <b>PDBTitle:</b> crystal structure of red fluorescent protein lanrfdam exposed to2 prolonged x-ray irradiation
85	<a href="#">c4a8xB_</a>	Alignment	not modelled	7.0	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hook-like, isoform a; <b>PDBTitle:</b> structure of the core asap complex
86	<a href="#">c5cqVb_</a>	Alignment	not modelled	7.0	6	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
87	<a href="#">c1vqzA_</a>	Alignment	not modelled	6.7	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoate-protein ligase, putative; <b>PDBTitle:</b> crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
88	<a href="#">c4fk9A_</a>	Alignment	not modelled	6.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose-binding family ii; <b>PDBTitle:</b> high resolution structure of the catalytic domain of mannanase2 sacte_2347 from streptomyces sp. sirexaa-e
89	<a href="#">d1ddwa_</a>	Alignment	not modelled	6.5	20	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
90	<a href="#">c2mbgA_</a>	Alignment	not modelled	6.3	26	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rala-binding protein 1; <b>PDBTitle:</b> rlip76 (gap-gbd)
91	<a href="#">d1w6ga2</a>	Alignment	not modelled	6.2	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
92	<a href="#">c5mmi7_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> 50s ribosomal protein 6, chloroplastic; <b>PDBTitle:</b> structure of the large subunit of the chloroplast ribosome
93	<a href="#">c4yk1A_</a>	Alignment	not modelled	6.2	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep6 from bartonella rochalimae
94	<a href="#">c3n2xB_</a>	Alignment	not modelled	6.1	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
95	<a href="#">c4afpA_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metacaspase mca2; <b>PDBTitle:</b> the structure of metacaspase 2 from t. brucei determined in the2 presence of samarium
96	<a href="#">c4i7vD_</a>	Alignment	not modelled	6.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhdps with pyruvate
97	<a href="#">c6ht4A_</a>	Alignment	not modelled	6.0	60	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ns5a; <b>PDBTitle:</b> nmr structure of ns5a-d2 (jfh1) peptide (304-323)
98	<a href="#">c4omhA_</a>	Alignment	not modelled	5.9	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl diphosphate cyclase; <b>PDBTitle:</b> crystal structure of the bacterial diterpene cyclase cotb2 variant2 f149l
99	<a href="#">c5hopA_</a>	Alignment	not modelled	5.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0182 protein; <b>PDBTitle:</b> 1.65 angstrom resolution crystal structure of lmo0182 (residues 1-245)2 from listeria monocytogenes egd-e