



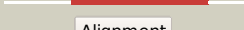

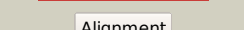







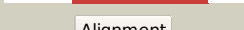

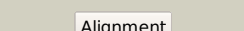

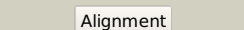


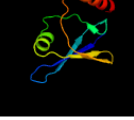
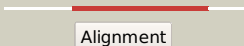


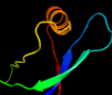
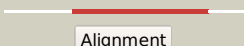


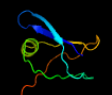
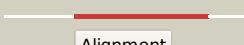

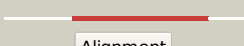


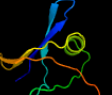




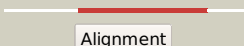

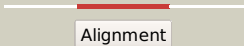
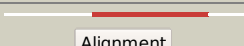
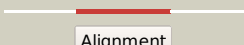
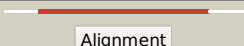

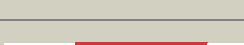


# Phyre2

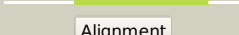
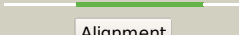
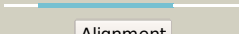
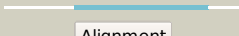
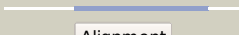
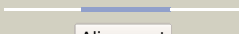

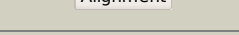
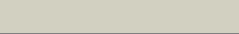



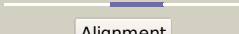
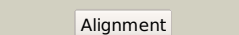
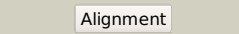



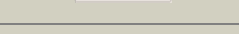
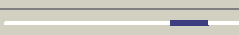



Email	mdejesus@rockefeller.edu
Description	RVBD1598c_(-)_1799080_1799490
Date	Fri Aug 2 13:30:19 BST 2019
Unique Job ID	ea11bab3f6653873

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r5zB_</a>	 Alignment		99.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
2	<a href="#">c3r5yC_</a>	 Alignment		99.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
3	<a href="#">c4y9iA_</a>	 Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
4	<a href="#">c3h96B_</a>	 Alignment		99.9	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
5	<a href="#">c3r5wO_</a>	 Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O; <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
6	<a href="#">c2iabB_</a>	 Alignment		97.7	16	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
7	<a href="#">c3f7eB_</a>	 Alignment		97.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn- <b>PDBTitle:</b> msmeg_3380 f420 reductase
8	<a href="#">d1rfea_</a>	 Alignment		97.4	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
9	<a href="#">d1w9aa_</a>	 Alignment		97.4	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
10	<a href="#">d2asfa1</a>	 Alignment		96.6	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
11	<a href="#">d2htia1</a>	 Alignment		96.4	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

12	<a href="#">c2htiA_</a>	 Alignment		96.4	9	<b>PDB header:</b> fmn-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bh0577 protein; <b>PDBTitle:</b> crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
13	<a href="#">c2q9kA_</a>	 Alignment		96.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
14	<a href="#">d2i02a1</a>	 Alignment		96.1	6	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
15	<a href="#">c2htdB_</a>	 Alignment		96.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted flavin-nucleotide-binding protein from cog3576 <b>PDBTitle:</b> crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
16	<a href="#">d2hq7a1</a>	 Alignment		96.0	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
17	<a href="#">c4zkyB_</a>	 Alignment		95.9	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5-phosphate oxidase; <b>PDBTitle:</b> structure of f420 binding protein, msmeq_6526, from mycobacterium2 smegmatis
18	<a href="#">c5escD_</a>	 Alignment		95.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hupz; <b>PDBTitle:</b> crystal structure of group a streptococcus hupz
19	<a href="#">d2hq9a1</a>	 Alignment		95.8	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
20	<a href="#">c3db0B_</a>	 Alignment		95.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lin2891 protein; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
21	<a href="#">c3tgvD_</a>	 Alignment	not modelled	95.6	10	<b>PDB header:</b> heme binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> heme-binding protein hutz; <b>PDBTitle:</b> crystal structure of hutz,the heme storsge protein from vibrio2 cholerae
22	<a href="#">d1vl7a_</a>	 Alignment	not modelled	95.5	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
23	<a href="#">c2hhzA_</a>	 Alignment	not modelled	95.3	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
24	<a href="#">d2fura1</a>	 Alignment	not modelled	95.3	6	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
25	<a href="#">c6eciQ_</a>	 Alignment	not modelled	95.1	6	<b>PDB header:</b> fad-binding protein <b>Chain:</b> Q: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding <b>PDBTitle:</b> structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis
26	<a href="#">d1t9ma_</a>	 Alignment	not modelled	94.8	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
27	<a href="#">c3dnhB_</a>	 Alignment	not modelled	94.7	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
						<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-binding, putative

28	<a href="#">c3u0IA</a>	Alignment	not modelled	94.5	10	uncharacterized protein; <b>PDBTitle:</b> crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
29	<a href="#">c2a2jA</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
30	<a href="#">d2a2ja1</a>	Alignment	not modelled	94.4	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
31	<a href="#">d2fg9a1</a>	Alignment	not modelled	94.3	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
32	<a href="#">d2arza1</a>	Alignment	not modelled	94.0	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
33	<a href="#">d2fhqa1</a>	Alignment	not modelled	93.9	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
34	<a href="#">c2re7A</a>	Alignment	not modelled	93.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
35	<a href="#">c3ec6A</a>	Alignment	not modelled	93.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 26; <b>PDBTitle:</b> crystal structure of the general stress protein 26 from bacillus2 anthracis str. sterne
36	<a href="#">c3fkhB</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
37	<a href="#">d1ty9a</a>	Alignment	not modelled	92.9	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
38	<a href="#">c2ig6B</a>	Alignment	not modelled	92.6	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nimc/nima family protein; <b>PDBTitle:</b> crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
39	<a href="#">c4ybnB</a>	Alignment	not modelled	92.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-nucleotide-binding protein; <b>PDBTitle:</b> structure of the fad and heme binding protein msmeg_4975 from2 mycobacterium smegmatis
40	<a href="#">c1nrgA</a>	Alignment	not modelled	91.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate oxidase; <b>PDBTitle:</b> structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
41	<a href="#">d1nrga</a>	Alignment	not modelled	91.7	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
42	<a href="#">c5bncB</a>	Alignment	not modelled	90.4	16	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeg_6519; <b>PDBTitle:</b> structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis
43	<a href="#">c3cp3A</a>	Alignment	not modelled	89.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
44	<a href="#">d2ptfa1</a>	Alignment	not modelled	88.0	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
45	<a href="#">d1ci0a</a>	Alignment	not modelled	87.7	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
46	<a href="#">c2ptfB</a>	Alignment	not modelled	87.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mth_863; <b>PDBTitle:</b> crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
47	<a href="#">c3gasA</a>	Alignment	not modelled	86.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heme oxygenase; <b>PDBTitle:</b> crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
48	<a href="#">d1dnla</a>	Alignment	not modelled	85.0	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
49	<a href="#">c4hmwB</a>	Alignment	not modelled	84.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of phzg from burkholderia lata 383
50	<a href="#">c2qeaB</a>	Alignment	not modelled	75.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative general stress protein 26; <b>PDBTitle:</b> crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
51	<a href="#">c6rk0A</a>	Alignment	not modelled	75.2	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the flavocytochrome anf3 from azotobacter vinelandii
52	<a href="#">c3u34D</a>	Alignment	not modelled	66.2	7	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> general stress protein; <b>PDBTitle:</b> crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
53	<a href="#">d2vpaa1</a>	Alignment	not modelled	65.0	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

54	<a href="#">c3dmbA_</a>	 Alignment	not modelled	60.3	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative general stress protein 26 with a pnp-oxidase like <b>PDBTitle:</b> crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
55	<a href="#">d1flma_</a>	 Alignment	not modelled	57.7	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
56	<a href="#">c2i51B_</a>	 Alignment	not modelled	38.3	9	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein of cog5135; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
57	<a href="#">d1xhna1</a>	 Alignment	not modelled	31.9	8	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
58	<a href="#">c2ou5B_</a>	 Alignment	not modelled	25.3	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
59	<a href="#">d2imla1</a>	 Alignment	not modelled	24.8	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
60	<a href="#">d2nr4a1</a>	 Alignment	not modelled	23.4	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
61	<a href="#">d2arca_</a>	 Alignment	not modelled	22.8	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Regulatory protein AraC <b>Family:</b> Regulatory protein AraC
62	<a href="#">c4n7rD_</a>	 Alignment	not modelled	19.9	11	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> genomic dna, chromosome 3, p1 clone: mxl8; <b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
63	<a href="#">c2ol5B_</a>	 Alignment	not modelled	12.5	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> pai 2 protein; <b>PDBTitle:</b> crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
64	<a href="#">c2o6pA_</a>	 Alignment	not modelled	11.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-regulated surface determinant protein c; <b>PDBTitle:</b> crystal structure of the heme-isdc complex
65	<a href="#">c2e7dA_</a>	 Alignment	not modelled	11.3	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein isdh; <b>PDBTitle:</b> crystal structure of a neat domain from staphylococcus aureus
66	<a href="#">c1ztnA_</a>	 Alignment	not modelled	10.3	100	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily c member 4; <b>PDBTitle:</b> inactivation gate of potassium channel raw3, nmr, 8 structures
67	<a href="#">d2o6pa1</a>	 Alignment	not modelled	10.0	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> NEAT domain-like <b>Family:</b> NEAT domain
68	<a href="#">c2x8nA_</a>	 Alignment	not modelled	9.8	18	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> cv0863; <b>PDBTitle:</b> solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. ocsb target cv0863.
69	<a href="#">c4wt5A_</a>	 Alignment	not modelled	9.6	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco accumulation factor 1, isoform 2; <b>PDBTitle:</b> the c-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana, crystal form ii
70	<a href="#">c2k78A_</a>	 Alignment	not modelled	9.5	16	<b>PDB header:</b> heme-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-regulated surface determinant protein c; <b>PDBTitle:</b> solution structure of the isdc neat domain bound to zinc2 protoporphyrin
71	<a href="#">c3rurB_</a>	 Alignment	not modelled	9.2	13	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> iron-regulated surface determinant protein b; <b>PDBTitle:</b> staphylococcus aureus heme-bound selenomethionine-labeled isdb-n2
72	<a href="#">d1ftaa_</a>	 Alignment	not modelled	8.5	13	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
73	<a href="#">d2itea1</a>	 Alignment	not modelled	8.4	4	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> NEAT domain-like <b>Family:</b> NEAT domain
74	<a href="#">c3ke2A_</a>	 Alignment	not modelled	8.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_928783.1; <b>PDBTitle:</b> crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
75	<a href="#">c3idwA_</a>	 Alignment	not modelled	8.3	30	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> actin cytoskeleton-regulatory complex protein sla1; <b>PDBTitle:</b> crystal structure of sla1 homology domain 2
76	<a href="#">c5e6fA_</a>	 Alignment	not modelled	8.0	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> cnpv261 holliday junction resolvase protein; <b>PDBTitle:</b> canarypox virus resolvase <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin reductase with split barrel

77	<a href="#">c3fgeA_</a>	Alignment	not modelled	7.9	15	domain; <b>PDBTitle:</b> crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
78	<a href="#">c3l48B_</a>	Alignment	not modelled	6.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane usher protein papc; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the papc usher
79	<a href="#">c4makA_</a>	Alignment	not modelled	5.8	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endoribonuclease cas2; <b>PDBTitle:</b> crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli
80	<a href="#">d1vhea1</a>	Alignment	not modelled	5.7	22	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminopeptidase/glucanase lid domain <b>Family:</b> Aminopeptidase/glucanase lid domain
81	<a href="#">d1ewfa1</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> Aha1/BPI domain-like <b>Superfamily:</b> Bactericidal permeability-increasing protein, BPI <b>Family:</b> Bactericidal permeability-increasing protein, BPI
82	<a href="#">c3zfnA_</a>	Alignment	not modelled	5.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-terminal protease npro; <b>PDBTitle:</b> crystal structure of product-like, processed n-terminal protease npro