


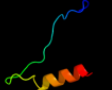




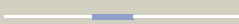













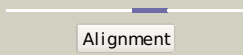
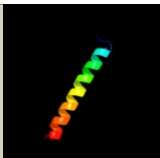
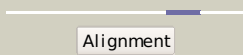
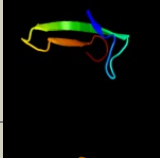

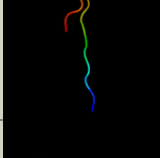
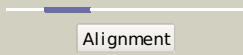

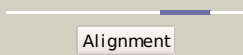
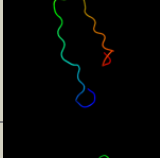
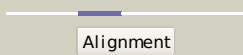
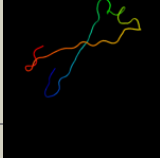
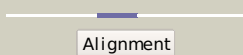
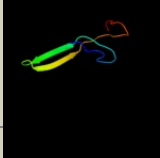
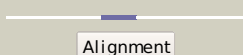
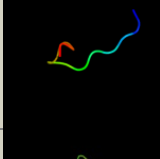


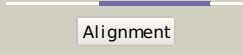
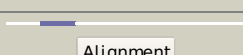
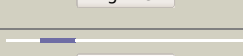
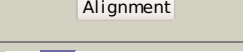
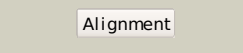


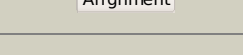
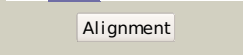


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P32681
Date	Thu Jan 5 11:50:07 GMT 2012
Unique Job ID	6739eb73e153c98d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ph0A_</a>	 Alignment		74.5	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the q6d2t7_ervct protein from erwinia2 carotovora. nesg target ewr41.
2	<a href="#">d2hqva1</a>	 Alignment		71.1	17	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> ChuX-like
3	<a href="#">c2oviA_</a>	 Alignment		70.6	17	<b>PDB header:</b> ligand binding protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein chux; <b>PDBTitle:</b> structure of the heme binding protein chux
4	<a href="#">c2k2tA_</a>	 Alignment		30.5	29	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> micronemal protein 6; <b>PDBTitle:</b> epidermal growth factor-like domain 2 from toxoplasma2 gondii microneme protein 6
5	<a href="#">c2k4vA_</a>	 Alignment		28.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1076; <b>PDBTitle:</b> solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
6	<a href="#">d1njha_</a>	 Alignment		22.1	12	<b>Fold:</b> Hypothetical protein YojF <b>Superfamily:</b> Hypothetical protein YojF <b>Family:</b> Hypothetical protein YojF
7	<a href="#">c3bq4G_</a>	 Alignment		21.6	38	<b>PDB header:</b> viral protein <b>Chain:</b> G: <b>PDB Molecule:</b> fiber; <b>PDBTitle:</b> crystal structure of ad35 fiber knob
8	<a href="#">c2vbeA_</a>	 Alignment		20.9	36	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tailspike-protein; <b>PDBTitle:</b> tailspike protein of bacteriophage sf6
9	<a href="#">c2zzfA_</a>	 Alignment		20.8	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of alanyl-trna synthetase without2 oligomerization domain
10	<a href="#">d2jl2a1</a>	 Alignment		19.8	21	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
11	<a href="#">c1yfsB_</a>	 Alignment		18.5	27	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> the crystal structure of alanyl-trna synthetase in complex2 with l-alanine

12	<a href="#">d1ydga_</a>		Alignment		17.7	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
13	<a href="#">c2e70A_</a>		Alignment		17.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the fifth kow motif of human2 transcription elongation factor spt5
14	<a href="#">d1h7za_</a>		Alignment		16.4	31	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
15	<a href="#">d2d9qb1</a>		Alignment		16.4	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> C2 set domains
16	<a href="#">c3n08A_</a>		Alignment		15.3	33	<b>PDB header:</b> phosphatidylethanolamine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphatidylethanolamine-binding protein (pebp); <b>PDBTitle:</b> crystal structure of a putative phosphatidylethanolamine-binding2 protein (pebp) homolog ct736 from chlamydia trachomatis d/uv-3/cx
17	<a href="#">d2j2ja1</a>		Alignment		15.2	15	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
18	<a href="#">d1riqa2</a>		Alignment		14.4	22	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
19	<a href="#">c2bzva_</a>		Alignment		14.4	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> fiber protein 2; <b>PDBTitle:</b> human enteric adenovirus serotype 41 short fiber head (ph8)
20	<a href="#">c3hxxA_</a>		Alignment		14.1	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
21	<a href="#">c3fduF_</a>		Alignment	not modelled	13.6	15	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
22	<a href="#">d2v3ia1</a>		Alignment	not modelled	13.1	27	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Glycosyl hydrolase family 7 catalytic core
23	<a href="#">c3dbxA_</a>		Alignment	not modelled	12.4	20	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cd1-2 antigen; <b>PDBTitle:</b> structure of chicken cd1-2 with bound fatty acid
24	<a href="#">d2imja1</a>		Alignment	not modelled	12.3	50	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PFL3262-like
25	<a href="#">d1knba_</a>		Alignment	not modelled	12.3	38	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
26	<a href="#">c3cncD_</a>		Alignment	not modelled	11.9	23	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> fiber protein; <b>PDBTitle:</b> crystal structure of ad16 fiber knob
27	<a href="#">c3hk4B_</a>		Alignment	not modelled	11.4	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mlr7391 protein; <b>PDBTitle:</b> crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
28	<a href="#">d1kaca_</a>		Alignment	not modelled	11.2	38	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
							<b>Fold:</b> RI 5-like

29	<a href="#">d2nrqa1</a>	Alignment	not modelled	11.1	27	<b>Superfamily:</b> RL5-like <b>Family:</b> SSO1042-like
30	<a href="#">d2ijra1</a>	Alignment	not modelled	11.0	23	<b>Fold:</b> Api92-like <b>Superfamily:</b> Api92-like <b>Family:</b> Api92-like
31	<a href="#">d1qhva_</a>	Alignment	not modelled	10.8	54	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
32	<a href="#">c2wstE_</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> putative fiber protein; <b>PDBTitle:</b> head domain of porcine adenovirus type 4 nadc-1 isolate2 fibre
33	<a href="#">c1yaxB_</a>	Alignment	not modelled	10.6	22	<b>PDB header:</b> transferase, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> virulence sensor protein phoq, sensor domain; <b>PDBTitle:</b> crystal structure analysis of s.typhimurium phoq sensor domain with2 calcium
34	<a href="#">c3ls1A_</a>	Alignment	not modelled	10.4	14	<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+
35	<a href="#">d2po6a2</a>	Alignment	not modelled	10.3	15	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
36	<a href="#">d2arka1</a>	Alignment	not modelled	9.7	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
37	<a href="#">d1rjlc_</a>	Alignment	not modelled	9.3	21	<b>Fold:</b> open-sided beta-meander <b>Superfamily:</b> Outer surface protein <b>Family:</b> Outer surface protein
38	<a href="#">c2rf4B_</a>	Alignment	not modelled	9.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna-directed rna polymerase i subunit rpa4; <b>PDBTitle:</b> crystal structure of the rna polymerase i subcomplex a14/43
39	<a href="#">d2o39a1</a>	Alignment	not modelled	9.0	31	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Adenovirus fiber protein "knob" domain
40	<a href="#">c1qiuC_</a>	Alignment	not modelled	8.3	54	<b>PDB header:</b> fibre protein <b>Chain:</b> C: <b>PDB Molecule:</b> adenovirus fibre; <b>PDBTitle:</b> a triple beta-spiral in the adenovirus fibre shaft reveals2 a new structural motif for biological fibres
41	<a href="#">d2f2ac1</a>	Alignment	not modelled	8.3	11	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Glu-tRNAGln amidotransferase C subunit <b>Family:</b> Glu-tRNAGln amidotransferase C subunit
42	<a href="#">d2dy7a1</a>	Alignment	not modelled	8.3	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo domain
43	<a href="#">d1fuxa_</a>	Alignment	not modelled	8.2	38	<b>Fold:</b> PEBP-like <b>Superfamily:</b> PEBP-like <b>Family:</b> Prokaryotic PEBP-like proteins
44	<a href="#">d1eyga_</a>	Alignment	not modelled	7.3	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
45	<a href="#">c3jvgB_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> t-cell surface glycoprotein cd1a1 antigen; <b>PDBTitle:</b> crystal structure of chicken cd1-1
46	<a href="#">c3tqyA_</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
47	<a href="#">d1a5za2</a>	Alignment	not modelled	7.2	8	<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
48	<a href="#">d1dmla1</a>	Alignment	not modelled	7.1	41	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
49	<a href="#">c1gzpA_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> glycoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd1b; <b>PDBTitle:</b> cd1b in complex with gm2 ganglioside
50	<a href="#">d1q42a_</a>	Alignment	not modelled	6.8	36	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> NTF2-like
51	<a href="#">d1pgxa_</a>	Alignment	not modelled	6.6	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
52	<a href="#">d1jmx5</a>	Alignment	not modelled	6.4	13	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3 <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3
53	<a href="#">c1f02T_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> T: <b>PDB Molecule:</b> translocated intimin receptor; <b>PDBTitle:</b> crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
54	<a href="#">c3pifD_</a>	Alignment	not modelled	6.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'->3' exoribonuclease (xrn1); <b>PDBTitle:</b> crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
55	<a href="#">d1xu2r_</a>	Alignment	not modelled	6.3	62	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like

						<b>Family:</b> BAFF receptor-like
56	<a href="#">c1xu2R_</a>	Alignment	not modelled	6.3	62	<b>PDB header:</b> cytokine, hormone/growth factor receptor <b>Chain:</b> R: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 17; <b>PDBTitle:</b> the crystal structure of april bound to bcma
57	<a href="#">c3qiiA_</a>	Alignment	not modelled	6.1	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20; <b>PDBTitle:</b> crystal structure of tudor domain 2 of human phd finger protein 20
58	<a href="#">d1o75a1</a>	Alignment	not modelled	5.9	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Tp47 lipoprotein, middle and C-terminal domains <b>Family:</b> Tp47 lipoprotein, middle and C-terminal domains
59	<a href="#">c1rpuA_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 19 kda protein; <b>PDBTitle:</b> crystal structure of cirv p19 bound to sirna
60	<a href="#">d1rpua_</a>	Alignment	not modelled	5.9	19	<b>Fold:</b> Tombusvirus P19 core protein, VP19 <b>Superfamily:</b> Tombusvirus P19 core protein, VP19 <b>Family:</b> Tombusvirus P19 core protein, VP19
61	<a href="#">d1s48a_</a>	Alignment	not modelled	5.9	16	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase
62	<a href="#">c3rf1B_</a>	Alignment	not modelled	5.8	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glycyl-trna synthetase alpha subunit; <b>PDBTitle:</b> the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
63	<a href="#">d1llda2</a>	Alignment	not modelled	5.8	8	<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
64	<a href="#">d1j5wa_</a>	Alignment	not modelled	5.8	5	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
65	<a href="#">d2j0pa1</a>	Alignment	not modelled	5.7	24	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> HemS/ChuS-like
66	<a href="#">c2xetB_</a>	Alignment	not modelled	5.7	7	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
67	<a href="#">c1q40C_</a>	Alignment	not modelled	5.7	36	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> mrna transport regulator mtr2; <b>PDBTitle:</b> crystal structure of the c. albicans mtr2-mex67 m domain complex
68	<a href="#">c3d2uE_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> immune system <b>Chain:</b> E: <b>PDB Molecule:</b> ul18 protein; <b>PDBTitle:</b> structure of ul18, a peptide-binding viral mhc mimic, bound to a host2 inhibitory receptor
69	<a href="#">d1f46a_</a>	Alignment	not modelled	5.6	7	<b>Fold:</b> TBP-like <b>Superfamily:</b> Cell-division protein ZipA, C-terminal domain <b>Family:</b> Cell-division protein ZipA, C-terminal domain
70	<a href="#">c1vibA_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> neurotoxin <b>Chain:</b> A: <b>PDB Molecule:</b> neurotoxin b-iv; <b>PDBTitle:</b> nmr solution structure of the neurotoxin b-iv, 20 structures
71	<a href="#">d1viba_</a>	Alignment	not modelled	5.5	33	<b>Fold:</b> Toxic hairpin <b>Superfamily:</b> Neurotoxin B-IV <b>Family:</b> Neurotoxin B-IV
72	<a href="#">d2ogka1</a>	Alignment	not modelled	5.5	18	<b>Fold:</b> RL5-like <b>Superfamily:</b> RL5-like <b>Family:</b> SSO1042-like
73	<a href="#">d2b2ya2</a>	Alignment	not modelled	5.4	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo domain
74	<a href="#">c2epbA_</a>	Alignment	not modelled	5.4	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 6; <b>PDBTitle:</b> solution structure of chromo domain 2 in chromodomain-2 helicase-dna-binding protein 6
75	<a href="#">c2e37B_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure of tt0471 protein from thermus thermophilus
76	<a href="#">d1oc4a2</a>	Alignment	not modelled	5.4	8	<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
77	<a href="#">c1l6jA_</a>	Alignment	not modelled	5.3	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
78	<a href="#">d1ywy1</a>	Alignment	not modelled	5.3	24	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PA2021-like <b>Family:</b> PA2021-like
79	<a href="#">c2lazA_</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
80	<a href="#">c2lb0A_</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
81	<a href="#">c3bmzA_</a>	Alignment	not modelled	5.2	28	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;

					<b>PDBTitle:</b> violacein biosynthetic enzyme vioe
82	<a href="#">c1r5mA_</a>	Alignment	not modelled	5.2	15
					<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> sir4-interacting protein sif2; <b>PDBTitle:</b> crystal structure of the c-terminal wd40 domain of sif2
83	<a href="#">c3h0mU_</a>	Alignment	not modelled	5.1	18
					<b>PDB header:</b> ligase <b>Chain:</b> U: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c; <b>PDBTitle:</b> structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus