




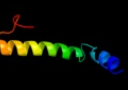





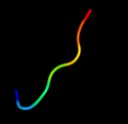
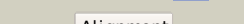
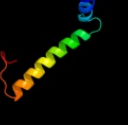

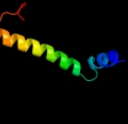

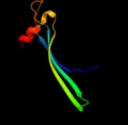


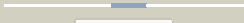

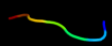










# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O13297
Date	Mon Jul 2 19:10:04 BST 2012
Unique Job ID	e0d02f148dc4d9b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1d8ia_</a>	 Alignment		100.0	100	<b>Fold:</b> CYTH-like phosphatases <b>Superfamily:</b> CYTH-like phosphatases <b>Family:</b> mRNA triphosphatase CET1
2	<a href="#">c3bgyA_</a>	 Alignment		91.8	29	<b>PDB header:</b> hydrolase, viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide 5'-triphosphatase; <b>PDBTitle:</b> triclinic structure of mimivirus capping enzyme2 triphosphatase at 1.65 a
3	<a href="#">d1bj4a_</a>	 Alignment		52.4	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
4	<a href="#">c3tleE_</a>	 Alignment		30.5	45	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> hemagglutinin-neuraminidase; <b>PDBTitle:</b> the structure of the newcastle disease virus hemagglutinin-2 neuraminidase (hn) ectodomain reveals a 4-helix bundle stalk
5	<a href="#">d2epqa1</a>	 Alignment		27.8	71	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
6	<a href="#">d1ylla1</a>	 Alignment		27.0	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> PA5104-like
7	<a href="#">d2a7va1</a>	 Alignment		25.4	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
8	<a href="#">c2a7vA_</a>	 Alignment		25.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> human mitochondrial serine hydroxymethyltransferase 2
9	<a href="#">c2gfgB_</a>	 Alignment		24.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> bh2851; <b>PDBTitle:</b> crystal structure of a putative adenylate cyclase (bh2851) from2 bacillus halodurans at 2.12 a resolution
10	<a href="#">c2rrhA_</a>	 Alignment		23.1	26	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> vip peptides; <b>PDBTitle:</b> nmr structure of vasoactive intestinal peptide in methanol
11	<a href="#">c3ebnD_</a>	 Alignment		22.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> replicase polyprotein 1ab; <b>PDBTitle:</b> a special dimerization of sars-cov main protease c-terminal2 domain due to domain-swapping

12	<a href="#">c3esgA</a>	Alignment		20.4	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of htdt from pseudomonas fluorescens sbw25
13	<a href="#">c1qloA</a>	Alignment		20.0	24	<b>PDB header:</b> membrane proteins <b>Chain:</b> A: <b>PDB Molecule:</b> herpes simplex virus protein icp47; <b>PDBTitle:</b> structure of the active domain of the herpes simplex virus2 protein icp47 in water/sodium dodecyl sulfate solution3 determined by nuclear magnetic resonance spectroscopy
14	<a href="#">d1ov9a</a>	Alignment		18.4	28	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
15	<a href="#">d1x9ba</a>	Alignment		18.4	30	<b>Fold:</b> Protozoan pheromone-like <b>Superfamily:</b> Hypothetical membrane protein Ta0354, soluble domain <b>Family:</b> Hypothetical membrane protein Ta0354, soluble domain
16	<a href="#">d1hs7a</a>	Alignment		17.8	25	<b>Fold:</b> STAT-like <b>Superfamily:</b> t-snare proteins <b>Family:</b> t-snare proteins
17	<a href="#">c2ee7A</a>	Alignment		17.5	26	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sperm flagellar protein 1; <b>PDBTitle:</b> solution structure of the ch domain from human sperm2 flagellar protein 1
18	<a href="#">c2ph5A</a>	Alignment		15.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
19	<a href="#">d1ejia</a>	Alignment		15.4	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
20	<a href="#">c3sy3D</a>	Alignment		15.2	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> gbaa_1210 protein; <b>PDBTitle:</b> gbaa_1210 protein, a putative adenylate cyclase, from bacillus2 anthracis
21	<a href="#">d3er7a1</a>	Alignment	not modelled	14.1	26	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Exig0174-like
22	<a href="#">d1yema</a>	Alignment	not modelled	13.7	18	<b>Fold:</b> CYTH-like phosphatases <b>Superfamily:</b> CYTH-like phosphatases <b>Family:</b> CYTH domain
23	<a href="#">c3i9wA</a>	Alignment	not modelled	12.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein tors; <b>PDBTitle:</b> crystal structure of the e. coli histidine kinase sensor2 tors sensor domain
24	<a href="#">d2p13a1</a>	Alignment	not modelled	12.6	11	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
25	<a href="#">c2kvsA</a>	Alignment	not modelled	12.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mw0776; <b>PDBTitle:</b> nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
26	<a href="#">d1u5tb1</a>	Alignment	not modelled	12.1	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
27	<a href="#">d2plia1</a>	Alignment	not modelled	12.0	10	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
28	<a href="#">d2rk5a1</a>	Alignment	not modelled	11.6	18	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
						<b>Fold:</b> Dimerisation interlock

29	<a href="#">d1b0na1</a>	Alignment	not modelled	11.0	22	<b>Superfamily:</b> SinR repressor dimerisation domain-like <b>Family:</b> SinR repressor dimerisation domain-like
30	<a href="#">c2q6fB</a>	Alignment	not modelled	11.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> infectious bronchitis virus (ibv) main protease; <b>PDBTitle:</b> crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
31	<a href="#">c3ic8D</a>	Alignment	not modelled	10.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized gst-like proteinprotein; <b>PDBTitle:</b> the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
32	<a href="#">d1lm7a</a>	Alignment	not modelled	10.5	29	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Plakin repeat <b>Family:</b> Plakin repeat
33	<a href="#">c4eiuA</a>	Alignment	not modelled	10.1	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hypothetical protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein (bacuni_03093) from2 bacteroides uniformis atcc 8492 at 1.90 a resolution
34	<a href="#">d1rv3a</a>	Alignment	not modelled	9.8	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
35	<a href="#">d2nqwa1</a>	Alignment	not modelled	9.7	8	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
36	<a href="#">d1lm5a</a>	Alignment	not modelled	9.6	21	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Plakin repeat <b>Family:</b> Plakin repeat
37	<a href="#">c2fjtA</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyl cyclase class iv; <b>PDBTitle:</b> adenylyl cyclase class iv from yersinia pestis
38	<a href="#">d2duca1</a>	Alignment	not modelled	9.1	33	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
39	<a href="#">d4ubpc1</a>	Alignment	not modelled	8.9	20	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
40	<a href="#">d2ddha1</a>	Alignment	not modelled	8.7	21	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> acyl-CoA oxidase C-terminal domains
41	<a href="#">d1lvoa</a>	Alignment	not modelled	8.7	20	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
42	<a href="#">d2d8ca1</a>	Alignment	not modelled	8.2	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain
43	<a href="#">c2vwaE</a>	Alignment	not modelled	8.1	15	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein pf13_0012; <b>PDBTitle:</b> crystal structure of a sporozoite protein essential for2 liver stage development of malaria parasite
44	<a href="#">c2vq5B</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> s-norococlaurine synthase; <b>PDBTitle:</b> x-ray structure of norococlaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde
45	<a href="#">c3d23A</a>	Alignment	not modelled	7.5	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3c-like proteinase; <b>PDBTitle:</b> main protease of hcov-hku1
46	<a href="#">d2oaia1</a>	Alignment	not modelled	7.3	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
47	<a href="#">d2o1ra1</a>	Alignment	not modelled	7.3	14	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
48	<a href="#">d1ic8a2</a>	Alignment	not modelled	7.1	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
49	<a href="#">d1gm5a2</a>	Alignment	not modelled	7.1	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> RecG "wedge" domain
50	<a href="#">d1zrua3</a>	Alignment	not modelled	6.9	53	<b>Fold:</b> Pseudo beta-prism <b>Superfamily:</b> Bacteriophage trimeric proteins domain <b>Family:</b> Lactophage receptor-binding protein N-terminal domain
51	<a href="#">c2d2pA</a>	Alignment	not modelled	6.9	19	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> pituitary adenylyl cyclase activating <b>PDBTitle:</b> the solution structure of micelle-bound peptide
52	<a href="#">d2p6ia1</a>	Alignment	not modelled	6.8	20	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> TM1646-like <b>Family:</b> TM1646-like
53	<a href="#">c2p61A</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm_1646; <b>PDBTitle:</b> crystal structure of protein tm1646 from thermotoga2 maritima, pfam duf327
54	<a href="#">c2dc4A</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 165aa long hypothetical protein; <b>PDBTitle:</b> structure of ph1012 protein from pyrococcus horikoshii ot3
55	<a href="#">d2r25a1</a>	Alignment	not modelled	6.5	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain

						<b>Family:</b> Phosphorelay protein-like
56	<a href="#">c2qw6A_</a>	Alignment	not modelled	6.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aaa atpase, central region; <b>PDBTitle:</b> crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do
57	<a href="#">d2qw6a1</a>	Alignment	not modelled	6.3	30	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
58	<a href="#">c3llbA_</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
59	<a href="#">d1v5sa_</a>	Alignment	not modelled	6.1	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> KA1-like <b>Family:</b> Kinase associated domain 1, KA1
60	<a href="#">c3c7tB_</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysteroid-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
61	<a href="#">c2a7uA_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase alpha chain; <b>PDBTitle:</b> nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
62	<a href="#">d2p3ha1</a>	Alignment	not modelled	6.0	6	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
63	<a href="#">d1w07a1</a>	Alignment	not modelled	5.9	14	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> acyl-CoA oxidase C-terminal domains
64	<a href="#">d2caza1</a>	Alignment	not modelled	5.9	29	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
65	<a href="#">d1ef5a_</a>	Alignment	not modelled	5.9	25	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
66	<a href="#">c3vejB_</a>	Alignment	not modelled	5.8	40	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein mdy2; <b>PDBTitle:</b> crystal structure of the get5 carboxyl domain from s. cerevisiae
67	<a href="#">c3dedB_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable hemolysin; <b>PDBTitle:</b> c-terminal domain of probable hemolysin from chromobacterium violaceum
68	<a href="#">d2gx8a1</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
69	<a href="#">c2cazD_</a>	Alignment	not modelled	5.7	29	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> suppressor protein stp22 of temperature- <b>PDBTitle:</b> escrt-i core
70	<a href="#">d3deda1</a>	Alignment	not modelled	5.6	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
71	<a href="#">d3ctda1</a>	Alignment	not modelled	5.6	23	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
72	<a href="#">d2f6ma1</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Endosomal sorting complex assembly domain <b>Family:</b> VPS23 C-terminal domain
73	<a href="#">d1y6xa1</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)
74	<a href="#">c2rmrA_</a>	Alignment	not modelled	5.6	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> paired amphipathic helix protein sin3a; <b>PDBTitle:</b> solution structure of msn3a pah1 domain
75	<a href="#">d2plsa1</a>	Alignment	not modelled	5.6	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
76	<a href="#">c2a7wF_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> phosphoribosyl-atp pyrophosphatase; <b>PDBTitle:</b> crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
77	<a href="#">d2a7wa1</a>	Alignment	not modelled	5.5	25	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)
78	<a href="#">d1x4ta1</a>	Alignment	not modelled	5.5	10	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> ISY1 domain-like <b>Family:</b> ISY1 N-terminal domain-like
79	<a href="#">c3myfB_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
80	<a href="#">c3qflA_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> m1a10; <b>PDBTitle:</b> coiled-coil domain-dependent homodimerization of intracellular m1a2 immune receptors defines a minimal functional module for triggering3 cell death
81	<a href="#">d1p9sa_</a>	Alignment	not modelled	5.2	33	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold

82	<a href="#">c3k44D_</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> purine-rich binding protein-alpha, isoform b; <b>PDBTitle:</b> crystal structure of drosophila melanogaster pur-alpha
83	<a href="#">dlyxba1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)
84	<a href="#">c3kjd_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
85	<a href="#">c3iqta_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction histidine-protein kinase bara; <b>PDBTitle:</b> structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
86	<a href="#">c3pl9A_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> chlorophyll a-b binding protein; <b>PDBTitle:</b> crystal structure of spinach minor light-harvesting complex cp29 at2 2.80 angstrom resolution
87	<a href="#">dly4oa1</a>	Alignment	not modelled	5.1	25	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Roadblock/LC7 domain <b>Family:</b> Roadblock/LC7 domain
88	<a href="#">c2gx8B_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal stucture of bacillus cereus protein related to nif3
89	<a href="#">d2o3ga1</a>	Alignment	not modelled	5.1	13	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
90	<a href="#">dlnmpa_</a>	Alignment	not modelled	5.0	15	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
91	<a href="#">dlyvwa1</a>	Alignment	not modelled	5.0	19	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> HisE-like (PRA-PH)