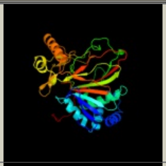
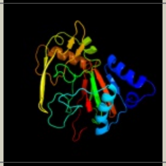
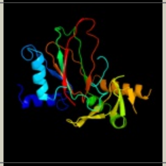
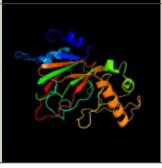
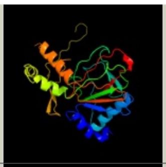
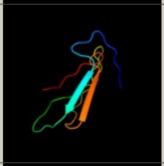
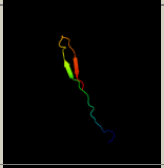
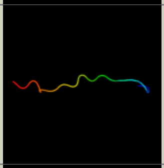
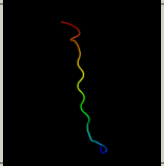
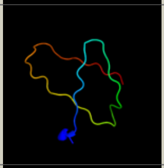
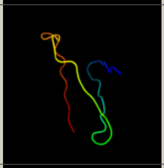
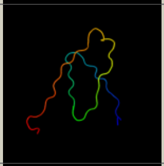
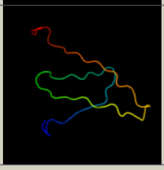
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76621
Date	Thu Jan 5 12:25:03 GMT 2012
Unique Job ID	1bf68732d3aaa2dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jr7a_	Alignment		100.0	99	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
2	c3ms5A_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
3	c2og5A_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
4	d1ds1a_	Alignment		100.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
5	c2wbqA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
6	d1oiha_	Alignment		100.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
7	d1otja_	Alignment		100.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
8	c3eatX_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
9	c3pvjB_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
10	c3r1jB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
11	d1nx4a_	Alignment		100.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase

12	d1y0za_	Alignment		99.9	21	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
13	c3pl0B_	Alignment		94.1	36	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution
14	d1wdia_	Alignment		92.5	17	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
15	c1yy3A_	Alignment		92.1	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
16	d1vkya_	Alignment		91.0	22	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
17	d2fcta1	Alignment		84.5	12	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
18	c2opwA_	Alignment		79.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
19	d2a1xa1	Alignment		73.1	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
20	c2rdsA_	Alignment		69.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- **PDBTitle:** crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
21	c3emrA_	Alignment	not modelled	68.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
22	c3gjbA_	Alignment	not modelled	67.9	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
23	c3nnlB_	Alignment	not modelled	54.2	16	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
24	c2fg0B_	Alignment	not modelled	50.5	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
25	d1v9la2	Alignment	not modelled	43.8	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
26	d2evra2	Alignment	not modelled	37.5	9	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
27	c3npfB_	Alignment	not modelled	32.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
28	d1dqua_	Alignment	not modelled	29.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like

29	c2xivA_	Alignment	not modelled	28.6	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
30	d1f61a_	Alignment	not modelled	27.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
31	d1ywka1	Alignment	not modelled	25.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
32	c3gt2A_	Alignment	not modelled	25.5	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
33	c2dbiA_	Alignment	not modelled	23.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
34	c1yo8A_	Alignment	not modelled	23.5	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-2; **PDBTitle:** structure of the c-terminal domain of human thrombospondin-2
35	d1xnea_	Alignment	not modelled	19.6	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
36	c3rcqA_	Alignment	not modelled	19.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase; **PDBTitle:** crystal structure of human aspartate beta-hydroxylase isoform a
37	d2axte1	Alignment	not modelled	18.7	36	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
38	d1fw8a_	Alignment	not modelled	18.4	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
39	d1s04a_	Alignment	not modelled	18.1	6	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
40	d16pka_	Alignment	not modelled	18.0	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
41	c3ndhA_	Alignment	not modelled	17.8	23	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**restriction endonuclease thai; **PDBTitle:** restriction endonuclease in complex with substrate dna
42	c2k1gA_	Alignment	not modelled	17.4	20	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
43	c3pbiA_	Alignment	not modelled	16.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
44	c1zmrA_	Alignment	not modelled	16.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
45	d1b26a2	Alignment	not modelled	16.7	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
46	d1te5a_	Alignment	not modelled	16.6	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
47	d1l1fa2	Alignment	not modelled	16.2	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
48	d1vpea_	Alignment	not modelled	16.1	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
49	d1e5ra_	Alignment	not modelled	15.5	6	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Type II Proline 3-hydroxylase (proline oxidase)
50	d1phpa_	Alignment	not modelled	14.9	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
51	d1hdia_	Alignment	not modelled	14.9	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
52	c1ywkE_	Alignment	not modelled	14.7	14	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**4-deoxy-l-threo-5-hexosulose-uronate ketol- **PDBTitle:** crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
53	d1v6sa_	Alignment	not modelled	14.6	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
54	d1qpga_	Alignment	not modelled	14.3	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
55	c3lvwA_	Alignment	not modelled	14.2	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase;

						PDBTitle: glutathione-inhibited scgcl
56	c3f1zF_	Alignment	not modelled	13.6	24	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**putative nucleic acid-binding lipoprotein; **PDBTitle:** crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
57	d1ltka_	Alignment	not modelled	13.6	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
58	c3uyjA_	Alignment	not modelled	13.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
59	c1ux6A_	Alignment	not modelled	13.4	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thrombospondin-1; **PDBTitle:** structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats
60	c2jijA_	Alignment	not modelled	13.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl-4 hydroxylase; **PDBTitle:** crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
61	c3i86A_	Alignment	not modelled	12.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
62	d1vjda_	Alignment	not modelled	12.8	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
63	c3itqB_	Alignment	not modelled	12.6	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit domain protein; **PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis
64	c3aicC_	Alignment	not modelled	11.8	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
65	c3al6A_	Alignment	not modelled	11.7	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
66	d2toda1	Alignment	not modelled	11.7	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
67	c1wtaA_	Alignment	not modelled	11.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
68	c3q3vA_	Alignment	not modelled	11.5	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
69	c2w8iG_	Alignment	not modelled	11.4	0	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
70	c3h41A_	Alignment	not modelled	11.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
71	d1bvua2	Alignment	not modelled	11.0	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
72	d1vrba1	Alignment	not modelled	10.9	23	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
73	d1njjb1	Alignment	not modelled	10.7	36	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
74	d1cb0a_	Alignment	not modelled	10.5	7	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
75	d1gtma2	Alignment	not modelled	10.4	17	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
76	c3cvoA_	Alignment	not modelled	10.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase-like protein of unknown function; **PDBTitle:** crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
77	d1h2ka_	Alignment	not modelled	10.3	31	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
78	c2cunA_	Alignment	not modelled	10.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
79	c3k2oB_	Alignment	not modelled	9.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
80	c2zpmA_	Alignment	not modelled	9.8	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
						Fold: Thioredoxin fold

81	d1n8ja_	Alignment	not modelled	9.4	15	**Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
82	c2x4iA_	Alignment	not modelled	9.2	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein 114; **PDBTitle:** orf 114a from sulfolobus islandicus rudivirus 1
83	c2bnoA_	Alignment	not modelled	9.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
84	d1euza2	Alignment	not modelled	9.0	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
85	d7odca1	Alignment	not modelled	8.9	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
86	d1gph12	Alignment	not modelled	8.9	29	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
87	d1v4na_	Alignment	not modelled	8.3	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
88	c2bf9A_	Alignment	not modelled	8.2	10	**PDB header:**hormone **Chain:** A: **PDB Molecule:**pancreatic hormone; **PDBTitle:** anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
89	c2p1gA_	Alignment	not modelled	8.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis
90	d1bgva2	Alignment	not modelled	8.0	9	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
91	c3e5bB_	Alignment	not modelled	7.8	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
92	c3bvcA_	Alignment	not modelled	7.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ism_01780; **PDBTitle:** crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
93	d1f3ta1	Alignment	not modelled	7.6	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
94	c3khsB_	Alignment	not modelled	7.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
95	c1xjvA_	Alignment	not modelled	7.4	43	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
96	c3kw0D_	Alignment	not modelled	7.4	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
97	c3dkqB_	Alignment	not modelled	7.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
98	c1ronA_	Alignment	not modelled	7.2	29	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide y; **PDBTitle:** nmr solution structure of human neuropeptide y
99	c1z7hA_	Alignment	not modelled	7.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tetanus toxin light chain; **PDBTitle:** 2.3 angstrom crystal structure of tetanus neurotoxin light2 chain