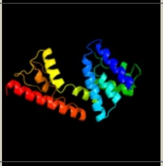
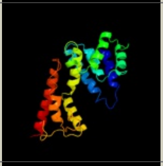
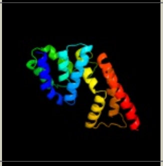
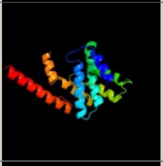
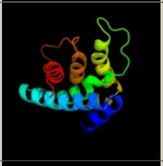
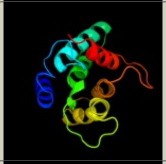
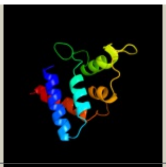
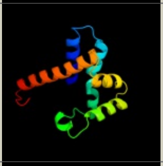
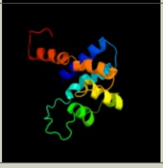
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P46144
Date	Thu Jan 5 12:04:11 GMT 2012
Unique Job ID	8c7bc51fddaf53ac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gw7A_	Alignment		100.0	96	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj; **PDBTitle:** crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
2	d2pjqa1	Alignment		100.0	31	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
3	d2qgsa1	Alignment		100.0	29	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
4	d3djba1	Alignment		100.0	34	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
5	d3dtoa1	Alignment		100.0	35	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
6	d3b57a1	Alignment		100.0	34	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
7	d2pq7a1	Alignment		100.0	32	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
8	c2o08B_	Alignment		99.4	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh1327 protein; **PDBTitle:** crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
9	c3ccgA_	Alignment		99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd superfamily hydrolase; **PDBTitle:** crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
10	c2ogiA_	Alignment		99.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein sag1661; **PDBTitle:** crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
11	c3mzoA_	Alignment		98.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lin2634 protein; **PDBTitle:** crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution

12	c2dqbB_	Alignment		98.7	16	**PDB header:**hydrolase, dna binding protein **Chain:** B: **PDB Molecule:**deoxyguanosinetriphosphate triphosphohydrolase, putative; **PDBTitle:** crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
13	c2cqzA_	Alignment		98.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
14	d2paqa1	Alignment		98.6	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
15	d1ynba1	Alignment		98.6	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	c2o6iA_	Alignment		98.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
17	d2o6ia1	Alignment		98.5	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
18	c2q14A_	Alignment		98.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
19	c3m1tA_	Alignment		98.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
20	d2heka1	Alignment		98.5	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
21	c2pgsA_	Alignment	not modelled	98.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
22	c3kh1B_	Alignment	not modelled	98.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
23	c2floA_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
24	d1xx7a_	Alignment	not modelled	98.2	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
25	c3u1nC_	Alignment	not modelled	98.1	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
26	d1u6za1	Alignment	not modelled	98.1	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**Ppx associated domain
27	c3hc1A_	Alignment	not modelled	98.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized hdod domain protein; **PDBTitle:** crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution

28	c3memA_	Alignment	not modelled	97.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
29	c3hi0B_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
30	c3i7aA_	Alignment	not modelled	97.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
31	c3bg2A_	Alignment	not modelled	97.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
32	d1vqra_	Alignment	not modelled	97.5	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
33	c3skdA_	Alignment	not modelled	97.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb187; **PDBTitle:** crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
34	c3m5fA_	Alignment	not modelled	97.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent phosphohydrolase; **PDBTitle:** structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
35	c1vj7B_	Alignment	not modelled	96.9	19	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
36	d2gz4a1	Alignment	not modelled	96.7	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
37	c3ljvA_	Alignment	not modelled	96.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mmoq response regulator; **PDBTitle:** crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
38	c3nr1A_	Alignment	not modelled	96.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain-containing protein 3; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
39	c3nqwB_	Alignment	not modelled	96.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
40	d1vj7a1	Alignment	not modelled	96.1	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
41	c1xozA_	Alignment	not modelled	95.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
42	d1tbfa_	Alignment	not modelled	95.5	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
43	c2ounA_	Alignment	not modelled	95.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp
44	d3dy8a1	Alignment	not modelled	95.4	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
45	c2o8hA_	Alignment	not modelled	95.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase-10a; **PDBTitle:** crystal structure of the catalytic domain of rat2 phosphodiesterase 10a
46	d2h44a1	Alignment	not modelled	95.3	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
47	d1y2ka1	Alignment	not modelled	95.3	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
48	c3qi4A_	Alignment	not modelled	95.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity cgmp-specific 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of pde9a(q453e) in complex with ibmx
49	c2r8qA_	Alignment	not modelled	95.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
50	c1z1lA_	Alignment	not modelled	95.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** the crystal structure of the phosphodiesterase 2a catalytic2 domain
51	c3ibjB_	Alignment	not modelled	95.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
52	c3kg5A	Alignment	not modelled	94.9	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical cytosolic protein;

						PDBTitle: crystal structure of an uncharacterized protein from coxiella burnetii
53	d1f0ja_	Alignment	not modelled	94.9	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
54	c3ecmA_	Alignment	not modelled	94.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific and ibmx-insensitive **PDBTitle:** crystal structure of the unliganded pde8a catalytic domain
55	c1xotB_	Alignment	not modelled	94.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**camp-specific 3',5'-cyclic phosphodiesterase 4b; **PDBTitle:** catalytic domain of human phosphodiesterase 4b in complex with2 vardenafil
56	c3bjcA_	Alignment	not modelled	94.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of the pde5a catalytic domain in complex2 with a novel inhibitor
57	c3g3nA_	Alignment	not modelled	94.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific 3',5'-cyclic **PDBTitle:** pde7a catalytic domain in complex with 3-(2,6-2 difluorophenyl)-2-(methylthio)quinazolin-4(3h)-one
58	c1zklA_	Alignment	not modelled	93.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high-affinity camp-specific 3',5'-cyclic **PDBTitle:** multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
59	d1taza_	Alignment	not modelled	93.4	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
60	d1so2a_	Alignment	not modelled	92.6	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
61	c3aqnA_	Alignment	not modelled	83.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
62	d3bxda1	Alignment	not modelled	82.7	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
63	c2huoA_	Alignment	not modelled	82.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
64	d2ibna1	Alignment	not modelled	70.2	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
65	d1g3wa2	Alignment	not modelled	64.6	12	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
66	c1g3wA_	Alignment	not modelled	57.7	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
67	c3hruA_	Alignment	not modelled	51.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
68	d2ev0a2	Alignment	not modelled	51.4	20	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
69	d1f5ta2	Alignment	not modelled	44.8	19	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
70	c1fx7C_	Alignment	not modelled	43.3	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
71	d2isya2	Alignment	not modelled	43.0	19	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
72	c3dptB_	Alignment	not modelled	41.4	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**rab family protein; **PDBTitle:** cor domain of rab family protein (roco)
73	d1jjcb1	Alignment	not modelled	33.8	52	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
74	c3pcoD_	Alignment	not modelled	31.5	32	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
75	c2ev5B_	Alignment	not modelled	24.4	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
76	d1s3ja_	Alignment	not modelled	24.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
77	c3nzpA_	Alignment	not modelled	23.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast

						structural genomics consortium target3 br53
78	c2akwB_	Alignment	not modelled	22.9	47	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
79	c2cxiA_	Alignment	not modelled	20.5	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
80	c3l4gL_	Alignment	not modelled	19.0	35	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
81	c3bjaA_	Alignment	not modelled	17.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
82	c3kp3B_	Alignment	not modelled	12.9	7	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
83	c3f3xA_	Alignment	not modelled	12.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
84	c2rhsB_	Alignment	not modelled	12.3	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
85	c2gxgA_	Alignment	not modelled	12.0	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
86	d2a61a1	Alignment	not modelled	11.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
87	c3nqoB_	Alignment	not modelled	11.5	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**marr-family transcriptional regulator; **PDBTitle:** crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
88	c3e6mD_	Alignment	not modelled	11.3	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
89	c3nrvC_	Alignment	not modelled	10.0	23	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**putative transcriptional regulator (marr/emrr family); **PDBTitle:** crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
90	c2w31A_	Alignment	not modelled	9.2	21	**PDB header:**oxygen transport **Chain:** A: **PDB Molecule:**globin; **PDBTitle:** globin domain of geobacter sulfurreducens globin-coupled2 sensor
91	d1ylea1	Alignment	not modelled	9.1	6	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
92	c3jw4C_	Alignment	not modelled	8.9	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
93	c2nnnB_	Alignment	not modelled	8.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
94	c2zycA_	Alignment	not modelled	8.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
95	c2ek0B_	Alignment	not modelled	8.4	45	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**stage v sporulation protein s (spovs) related protein; **PDBTitle:** stage v sporolation protein s (spovs) from thermus thermophilus zinc2 form
96	c2rdpA_	Alignment	not modelled	8.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
97	c2veeC_	Alignment	not modelled	8.0	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protoglobin; **PDBTitle:** structure of protoglobin from methanosarcina acetivorans2 c2a
98	c2l6pA_	Alignment	not modelled	7.9	19	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
99	c3g3zA_	Alignment	not modelled	7.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis