Phyre2

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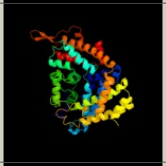
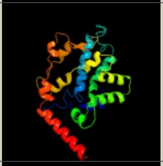
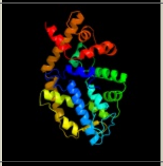
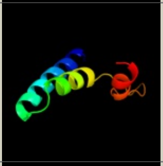
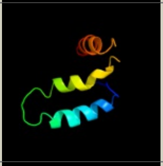
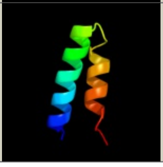
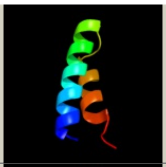
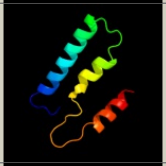
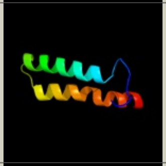
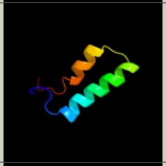
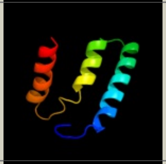
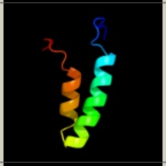
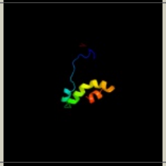
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bg2A_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
2	c2pgsA_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
3	c2dqbB_	Alignment		100.0	31	**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
4	d2heka1	Alignment		100.0	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
5	c2o6iA_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
6	d2o6ia1	Alignment		99.9	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
7	c3u1nC_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
8	c2q14A_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
9	c3ccgA_	Alignment		97.9	29	**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	c3gw7A_	Alignment		97.9	15	**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
11	c2ogiA_	Alignment		97.8	22	**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

12	c2o08B_	Alignment		97.7	25	**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
13	d2qgsa1	Alignment		97.5	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
14	d2pq7a1	Alignment		97.4	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
15	d3b57a1	Alignment		97.1	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	d3djba1	Alignment		97.0	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
17	c3m1tA_	Alignment		96.9	25	**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
18	d2pjqa1	Alignment		96.7	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
19	d3dtoa1	Alignment		96.6	19	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
20	c3skdA_	Alignment		95.7	20	**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+
21	c2ounA_	Alignment	not modelled	95.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp
22	d3dy8a1	Alignment	not modelled	95.1	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
23	c3ecmA_	Alignment	not modelled	95.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high affinity camp-specific and ibmx-insensitive **PDBTitle:** crystal structure of the unliganded pde8a catalytic domain
24	c3i7aA_	Alignment	not modelled	94.9	22	**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
25	c1z1lA_	Alignment	not modelled	94.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** the crystal structure of the phosphodiesterase 2a catalytic2 domain
26	c2o8hA_	Alignment	not modelled	94.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase-10a; **PDBTitle:** crystal structure of the catalytic domain of rat2 phosphodiesterase 10a
27	c3qi4A_	Alignment	not modelled	94.8	16	**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

28	c2r8qA_	Alignment	not modelled	94.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
29	c3ibjB_	Alignment	not modelled	94.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
30	c1zklA_	Alignment	not modelled	94.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high-affinity camp-specific 3',5'-cyclic **PDBTitle:** multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
31	c3g3nA_	Alignment	not modelled	94.6	23	**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
32	d1f0ja_	Alignment	not modelled	94.5	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
33	d1tbfa_	Alignment	not modelled	94.5	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
34	c1xozA_	Alignment	not modelled	94.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
35	c3hc1A_	Alignment	not modelled	94.4	29	**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
36	d1y2ka1	Alignment	not modelled	94.2	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
37	d2h44a1	Alignment	not modelled	94.2	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
38	c1xotB_	Alignment	not modelled	93.8	16	**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
39	c3bjcA_	Alignment	not modelled	93.7	18	**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
40	c2cqzA_	Alignment	not modelled	93.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
41	d1taza_	Alignment	not modelled	93.5	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
42	d1ynba1	Alignment	not modelled	93.3	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
43	c3kq5A_	Alignment	not modelled	93.2	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of an uncharacterized protein from coxiella burnetii
44	d2paqa1	Alignment	not modelled	92.5	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
45	c3memA_	Alignment	not modelled	92.3	15	**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
46	d1so2a_	Alignment	not modelled	92.0	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
47	c3mzoA_	Alignment	not modelled	91.3	15	**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
48	d1vqra_	Alignment	not modelled	90.8	11	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
49	d1u6za1	Alignment	not modelled	89.4	8	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**Ppx associated domain
50	d1xx7a_	Alignment	not modelled	87.0	26	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
51	c2floA_	Alignment	not modelled	84.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
52	c3m5fA_	Alignment	not modelled	83.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent phosphohydrolase; **PDBTitle:** structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
						PDB header:transcription **Chain:** A: **PDB Molecule:**mmoq response regulator;

53	c3ljvA_	Alignment	not modelled	81.7	18	**PDBTitle:** crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
54	c3kh1B_	Alignment	not modelled	79.6	25	**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
55	c3hi0B_	Alignment	not modelled	79.1	18	**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
56	d2gz4a1	Alignment	not modelled	69.0	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
57	c2zxqA_	Alignment	not modelled	60.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
58	c3ecqA_	Alignment	not modelled	57.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
59	d1vj7a1	Alignment	not modelled	53.5	38	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
60	c1aqjB_	Alignment	not modelled	47.6	71	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**adenine-n6-dna-methyltransferase taqi; **PDBTitle:** structure of adenine-n6-dna-methyltransferase taqi
61	d2ar0a1	Alignment	not modelled	46.6	71	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
62	c1vj7B_	Alignment	not modelled	45.6	39	**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.
63	d2okca1	Alignment	not modelled	42.6	71	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
64	c1g38A_	Alignment	not modelled	42.2	71	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**modification methylase taqi; **PDBTitle:** adenine-specific methyltransferase m. taq i/dna complex
65	c3khkA_	Alignment	not modelled	41.8	57	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**type i restriction-modification system **PDBTitle:** crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
66	d2f8la1	Alignment	not modelled	38.9	43	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
67	c3lkdB_	Alignment	not modelled	36.7	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type i restriction-modification system **PDBTitle:** crystal structure of the type i restriction-modification2 system methyltransferase subunit from streptococcus3 thermophilus, northeast structural genomics consortium4 target sur80
68	c3o5cA_	Alignment	not modelled	33.1	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
69	d1eb7a2	Alignment	not modelled	32.3	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
70	d1b4ub_	Alignment	not modelled	30.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
71	c3nr1A_	Alignment	not modelled	29.2	16	**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
72	c3nqwB_	Alignment	not modelled	28.7	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
73	d1iqca2	Alignment	not modelled	25.9	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
74	c3ldgA_	Alignment	not modelled	24.3	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah
75	c2c1uB_	Alignment	not modelled	23.5	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
76	c1nh1A_	Alignment	not modelled	23.2	27	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
77	d1nh1a_	Alignment	not modelled	23.2	27	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor

78	c3oa8B_	Alignment	not modelled	21.8	35	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
79	c2xzn3_	Alignment	not modelled	21.5	8	**PDB header:**ribosome **Chain:** 3: **PDB Molecule:**rps7e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
80	c3k0bA_	Alignment	not modelled	20.9	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted n6-adenine-specific dna methylase; **PDBTitle:** crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
81	c2jqqA_	Alignment	not modelled	20.6	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**conserved oligomeric golgi complex subunit 2; **PDBTitle:** solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit 2 protein (cog2p)
82	d1nmla2	Alignment	not modelled	17.8	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
83	c3lduA_	Alignment	not modelled	17.3	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methylase; **PDBTitle:** the crystal structure of a possible methylase from2 clostridium difficile 630.
84	c1iqcB_	Alignment	not modelled	17.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-heme peroxidase; **PDBTitle:** crystal structure of di-heme peroxidase from nitrosomonas europaea
85	c2kviA_	Alignment	not modelled	17.2	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nuclear polyadenylated rna-binding protein 3; **PDBTitle:** structure of nab3 rrm
86	c2vhdB_	Alignment	not modelled	16.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
87	c3p04B_	Alignment	not modelled	16.3	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
88	c3p04A_	Alignment	not modelled	16.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
89	c3zrgB_	Alignment	not modelled	15.8	55	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**pexrd2 family secreted rxlr effector peptide, putative; **PDBTitle:** crystal structure of rxlr effector pexrd2 from phytophthora infestans
90	c1ni3A_	Alignment	not modelled	15.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ychf gtp-binding protein; **PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase
91	d1wf2a_	Alignment	not modelled	15.2	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
92	c2huoA_	Alignment	not modelled	14.7	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
93	d3bxda1	Alignment	not modelled	14.7	33	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
94	d2ibna1	Alignment	not modelled	14.1	33	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
95	d1lghb_	Alignment	not modelled	13.5	22	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
96	c1nmlA_	Alignment	not modelled	13.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
97	d2ovra1	Alignment	not modelled	13.1	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
98	c3k6jA_	Alignment	not modelled	13.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
99	c3s1sA_	Alignment	not modelled	12.5	43	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi