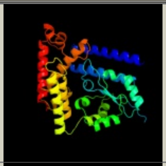
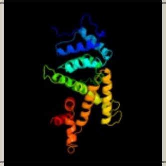
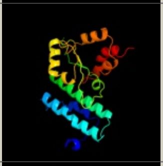
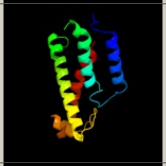
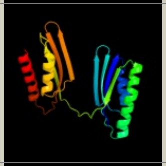
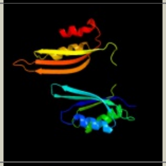
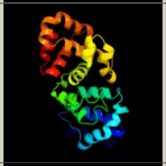
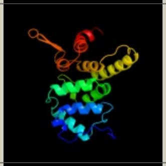
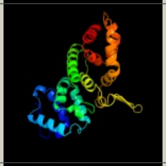
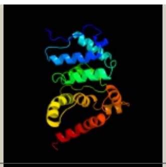
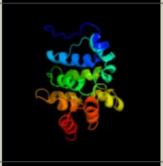
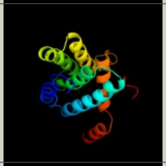
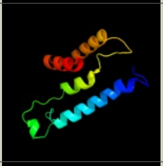
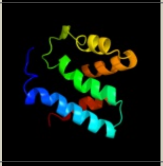
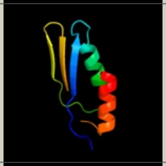
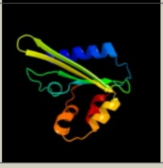
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P27249
Date	Thu Jan 5 11:43:29 GMT 2012
Unique Job ID	2ff26d4812459fb6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1v4aA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenylyltransferase
2	c3k7dA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenylyltransferase
3	c3aqnA_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
4	d1v4aa2	Alignment		100.0	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GlnE-like domain
5	d1v4aa1	Alignment		99.9	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Glutamine synthase adenylyltransferase GlnE, domain 2
6	c1u8sB_	Alignment		99.8	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
7	c2nyiB_	Alignment		99.8	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
8	c1miyB_	Alignment		99.7	16	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
9	c1vfgB_	Alignment		99.7	16	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**poly a polymerase; **PDBTitle:** crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
10	d1vfga1	Alignment		99.7	15	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
11	d1miwa1	Alignment		99.6	15	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like

12	c3h37B_	Alignment		99.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein; **PDBTitle:** the structure of cca-adding enzyme apo form i
13	c1ou5A_	Alignment		99.5	13	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
14	d1ou5a1	Alignment		99.3	13	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
15	d2pq7a1	Alignment		98.9	25	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	d2qgsa1	Alignment		98.7	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
17	d3djba1	Alignment		98.6	26	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
18	c2f06B_	Alignment		98.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
19	c3ibwA_	Alignment		98.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
20	d1knya2	Alignment		98.2	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
21	d1u8sa2	Alignment	not modelled	98.1	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
22	d3dtoa1	Alignment	not modelled	98.1	29	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
23	d3b57a1	Alignment	not modelled	98.0	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
24	d1zpva1	Alignment	not modelled	98.0	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
25	d1u8sa1	Alignment	not modelled	98.0	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
26	c3gw7A_	Alignment	not modelled	97.9	20	**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
27	c3p96A_	Alignment	not modelled	97.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
28	c3m5fA_	Alignment	not modelled	97.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent phosphohydrolase; **PDBTitle:** structure of mj0384, a cas3 protein from methanocaldococcus jannaschii

29	c2q14A_	Alignment	not modelled	97.9	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
30	c2o08B_	Alignment	not modelled	97.9	26	**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
31	c3ccgA_	Alignment		97.8	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
32	c3skdA_	Alignment	not modelled	97.8	15	**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+
33	c2ogiA_	Alignment	not modelled	97.6	25	**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
34	d2pjqa1	Alignment	not modelled	97.5	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
35	d1u6za1	Alignment	not modelled	97.5	25	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**Ppx associated domain
36	c3n0vD_	Alignment	not modelled	97.5	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
37	c3o1lB_	Alignment	not modelled	97.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
38	d2o6ia1	Alignment	not modelled	97.4	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
39	c2o6iA_	Alignment	not modelled	97.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
40	d1ygya3	Alignment	not modelled	97.4	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
41	c3obiC_	Alignment	not modelled	97.3	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
42	c2dqbB_	Alignment	not modelled	97.3	20	**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
43	c3nrbD_	Alignment	not modelled	97.2	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
44	d2heka1	Alignment	not modelled	97.2	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
45	c1knyA_	Alignment	not modelled	97.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kanamycin nucleotidyltransferase; **PDBTitle:** kanamycin nucleotidyltransferase
46	c2rffA_	Alignment	not modelled	97.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
47	c3hc1A_	Alignment	not modelled	97.0	14	**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
48	d1sc6a3	Alignment	not modelled	97.0	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
49	d2f1fa1	Alignment	not modelled	96.9	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
50	c3l76B_	Alignment		96.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
51	c2floA	Alignment	not modelled	96.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase;

51	[illegible]	Alignment	not modelled	96.9	20	**PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
52	d2pc6a2	Alignment	not modelled	96.8	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
53	d2gz4a1	Alignment	not modelled	96.8	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
54	c3m1tA_	Alignment	not modelled	96.8	15	**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
55	c3louB_	Alignment	not modelled	96.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
56	c3hi0B_	Alignment	not modelled	96.7	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
57	c3memA_	Alignment	not modelled	96.7	17	**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
58	d2f06a1	Alignment	not modelled	96.7	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
59	c1ygyA_	Alignment	not modelled	96.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
60	c3u1nC_	Alignment	not modelled	96.6	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
61	d1vqra_	Alignment	not modelled	96.6	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
62	d1no5a_	Alignment	not modelled	96.6	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
63	c2f1fA_	Alignment	not modelled	96.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
64	d1ylqa1	Alignment	not modelled	96.4	19	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
65	d1taza_	Alignment	not modelled	96.2	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
66	c2pc6C_	Alignment	not modelled	96.1	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
67	d2fgca2	Alignment	not modelled	96.1	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
68	c3ljvA_	Alignment	not modelled	95.8	10	**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
69	c2fgcA_	Alignment	not modelled	95.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
70	d2f06a2	Alignment	not modelled	95.8	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
71	c3i7aA_	Alignment	not modelled	95.7	7	**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
72	c2pgsA_	Alignment	not modelled	95.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
73	c1zklA_	Alignment	not modelled	95.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**high-affinity camp-specific 3',5'-cyclic **PDBTitle:** multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
74	d1wota_	Alignment	not modelled	95.5	26	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
						Fold:HD-domain/PDEase-like

75	d1so2a_	Alignment	not modelled	95.5	19	**Superfamily:**HD-domain/PDEase-like **Family:**PDEase
76	d1f0ja_	Alignment	not modelled	95.4	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
77	c3g3nA_	Alignment	not modelled	95.2	17	**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
78	c2zhoB_	Alignment	not modelled	95.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
79	c3qi4A_	Alignment	not modelled	94.8	15	**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
80	c2dtjA_	Alignment	not modelled	94.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
81	c3kq5A_	Alignment	not modelled	94.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of an uncharacterized protein from coxiella burnetii
82	d1phza1	Alignment	not modelled	93.7	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
83	c3c66B_	Alignment	not modelled	93.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
84	c1xotB_	Alignment	not modelled	93.3	19	**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
85	d2qmwa2	Alignment	not modelled	93.1	25	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
86	c2r8qA_	Alignment	not modelled	93.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
87	c3luyA_	Alignment	not modelled	92.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
88	c3mwbA_	Alignment	not modelled	92.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
89	c3bg2A_	Alignment	not modelled	92.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
90	c3mtjA_	Alignment	not modelled	92.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
91	d1q79a2	Alignment	not modelled	92.4	11	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
92	c2qmxB_	Alignment	not modelled	92.3	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
93	c2ounA_	Alignment	not modelled	92.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp
94	d1jmsa4	Alignment	not modelled	92.1	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
95	c1q78A_	Alignment	not modelled	92.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase alpha; **PDBTitle:** crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride
96	c1xozA_	Alignment	not modelled	91.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
97	c3ibjB_	Alignment	not modelled	91.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
98	d1y2ka1	Alignment	not modelled	91.5	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
99	d1tbfa_	Alignment	not modelled	91.1	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
100	d2q66a2	Alignment	not modelled	91.1	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly(A) polymerase, PAP, N-terminal domain
						PDB header:hydrolase

101	c1z1lA_	Alignment	not modelled	90.6	14	**Chain:** A: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** the crystal structure of the phosphodiesterase 2a catalytic2 domain
102	d3dy8a1	Alignment	not modelled	90.5	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
103	c1kdhA_	Alignment	not modelled	90.3	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
104	c2re1A_	Alignment	not modelled	90.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
105	c3mzoA_	Alignment	not modelled	89.7	20	**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
106	c3nqwB_	Alignment	not modelled	88.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
107	c2o8hA_	Alignment	not modelled	88.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase-10a; **PDBTitle:** crystal structure of the catalytic domain of rat2 phosphodiesterase 10a
108	c2cqzA_	Alignment	not modelled	88.2	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
109	d2h44a1	Alignment	not modelled	87.4	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
110	c3jz0B_	Alignment	not modelled	87.2	23	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**lincosamide nucleotidyltransferase; **PDBTitle:** linb complexed with clindamycin and ampcpp
111	c3bjcA_	Alignment	not modelled	87.0	15	**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
112	c2huoA_	Alignment	not modelled	85.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
113	d3bxda1	Alignment	not modelled	85.6	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
114	d2hmfa3	Alignment	not modelled	85.1	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
115	d1ynba1	Alignment	not modelled	84.6	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
116	c1sz1A_	Alignment	not modelled	83.2	19	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
117	d2ibna1	Alignment	not modelled	83.0	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
118	d2paqa1	Alignment	not modelled	81.8	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
119	c2qmwA_	Alignment	not modelled	81.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
120	d2fmpa3	Alignment	not modelled	80.6	13	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like