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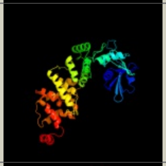
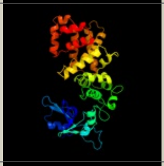
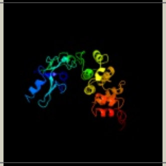
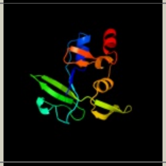
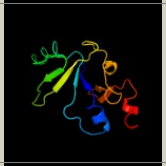
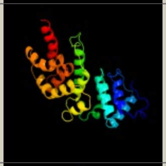
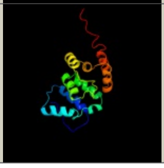
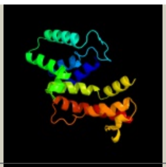
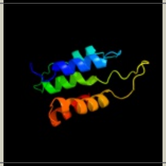
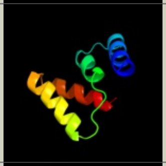
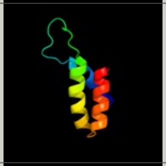
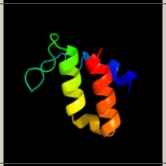
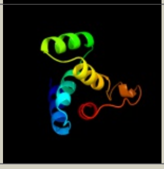
Description	P06961
Date	Thu Jan 5 10:59:31 GMT 2012
Unique Job ID	932a8cb9bad437bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1miyB_	Alignment		100.0	26	**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
2	c1vfgB_	Alignment		100.0	24	**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
3	c3h37B_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein; **PDBTitle:** the structure of cca-adding enzyme apo form i
4	c3aqnA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
5	c1ou5A_	Alignment		100.0	25	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
6	d1miwa1	Alignment		100.0	22	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
7	d1miwa2	Alignment		100.0	36	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
8	d1vfga2	Alignment		100.0	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
9	d1ou5a2	Alignment		100.0	29	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
10	d1vfga1	Alignment		100.0	18	**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	d1ou5a1	Alignment		99.9	23	**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	d2qgsa1	Alignment		97.3	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
13	d2pq7a1	Alignment		97.2	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
14	d3djba1	Alignment		96.6	22	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
15	d3b57a1	Alignment		95.5	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	c3m5fA_	Alignment		94.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent phosphohydrolase; **PDBTitle:** structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
17	d3dtoa1	Alignment		94.3	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
18	c2la3A_	Alignment		93.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
19	d1u6za1	Alignment		91.8	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**Ppx associated domain
20	d2pjqa1	Alignment		91.7	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
21	d2fcla1	Alignment	not modelled	91.4	19	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like
22	c2q14A_	Alignment	not modelled	90.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
23	c2o08B_	Alignment	not modelled	90.7	28	**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
24	c3ccgA_	Alignment	not modelled	88.9	32	**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
25	c3skdA_	Alignment	not modelled	87.7	18	**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+
26	c3u1nC_	Alignment	not modelled	86.6	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
27	c2ogiA_	Alignment	not modelled	85.9	28	**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
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj;

28	c3gw7A_	Alignment	not modelled	85.5	14	**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
29	c2floA_	Alignment	not modelled	84.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
30	d2o6ia1	Alignment	not modelled	82.9	23	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
31	c2o6iA_	Alignment	not modelled	82.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
32	d2gz4a1	Alignment	not modelled	70.6	12	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
33	c3kq5A_	Alignment	not modelled	66.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of an uncharacterized protein from coxiella burnetii
34	c3hi0B_	Alignment	not modelled	61.4	10	**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
35	c2dqbB_	Alignment	not modelled	61.3	22	**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
36	c2pgsA_	Alignment	not modelled	54.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
37	c3lmaC_	Alignment	not modelled	44.5	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
38	c3hc1A_	Alignment	not modelled	43.5	16	**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
39	c3m1tA_	Alignment	not modelled	41.1	14	**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
40	d1vqra_	Alignment	not modelled	40.9	12	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**modified HD domain
41	d1ylqa1	Alignment	not modelled	38.8	30	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
42	c2w9mB_	Alignment	not modelled	34.1	21	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
43	d2ibna1	Alignment	not modelled	31.2	16	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
44	d2heka1	Alignment	not modelled	30.7	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
45	c2huoA_	Alignment	not modelled	26.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol oxygenase; **PDBTitle:** crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
46	d3bxda1	Alignment	not modelled	26.1	26	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**MioX-like
47	d1jmsa4	Alignment	not modelled	21.1	17	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
48	d1wota_	Alignment	not modelled	20.1	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
49	c3bg2A_	Alignment	not modelled	19.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
50	c3k1rB_	Alignment	not modelled	19.4	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
51	d1r89a2	Alignment	not modelled	18.6	13	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Archaeal tRNA CCA-adding enzyme catalytic domain
52	d2bcqa3	Alignment	not modelled	17.2	10	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase

						Family:DNA polymerase beta-like
53	d2b7oa1	Alignment	not modelled	17.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
54	d1no5a_	Alignment	not modelled	15.8	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
55	d2dula1	Alignment	not modelled	15.1	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
56	d1bgfa_	Alignment	not modelled	12.8	22	**Fold:**Transcription factor STAT-4 N-domain **Superfamily:**Transcription factor STAT-4 N-domain **Family:**Transcription factor STAT-4 N-domain
57	c3riuC_	Alignment	not modelled	12.7	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**translin associated factor x, isoform b; **PDBTitle:** crystal structure of drosophila hexameric c3po formed by truncated2 translin and trax
58	c2bcuA_	Alignment	not modelled	12.2	14	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
59	c2ihmA_	Alignment	not modelled	11.8	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
60	d1vola2	Alignment	not modelled	11.4	17	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
61	d1es6a1	Alignment	not modelled	11.3	45	**Fold:**EV matrix protein **Superfamily:**EV matrix protein **Family:**EV matrix protein
62	d2gmwa1	Alignment	not modelled	11.0	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
63	c3esqA_	Alignment	not modelled	11.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d,d-heptose 1,7-bisphosphate phosphatase; **PDBTitle:** crystal structure of calcium-bound d,d-heptose 1.7-2 bisphosphate phosphatase from e. coli
64	c2r8qA_	Alignment	not modelled	10.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i phosphodiesterase pdeb1; **PDBTitle:** structure of lmjpdeb1 in complex with ibmx
65	d1t3ta4	Alignment	not modelled	9.3	44	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
66	d2fmpa3	Alignment	not modelled	9.2	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
67	c3ndcB_	Alignment	not modelled	9.2	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
68	d1vk3a1	Alignment	not modelled	9.1	67	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
69	c1h2dA_	Alignment	not modelled	9.1	45	**PDB header:**virus/viral protein **Chain:** A: **PDB Molecule:**matrix protein vp40; **PDBTitle:** ebola virus matrix protein vp40 n-terminal domain in2 complex with rna (low-resolution vp40[31-212] variant).
70	c2cqzA_	Alignment	not modelled	9.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long hypothetical protein; **PDBTitle:** crystal structure of ph0347 protein from pyrococcus horikoshii ot3
71	d1h2ca_	Alignment	not modelled	9.1	45	**Fold:**EV matrix protein **Superfamily:**EV matrix protein **Family:**EV matrix protein
72	d1jqra_	Alignment	not modelled	8.8	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
73	c2rffA_	Alignment	not modelled	8.6	26	**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
74	d1uqva_	Alignment	not modelled	8.6	4	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
75	c1b0nB_	Alignment	not modelled	7.8	32	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**protein (sini protein); **PDBTitle:** sinr protein/sini protein complex
76	d1b0nb_	Alignment	not modelled	7.8	32	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
77	d1g60a_	Alignment	not modelled	7.6	25	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
78	d1eg2a_	Alignment	not modelled	7.4	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Type II DNA methylase
						Fold: Cyclin-like

79	d1vola1	Alignment	not modelled	7.4	12	**Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
80	c3ljvA_	Alignment	not modelled	7.4	9	**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
81	c2zifB_	Alignment	not modelled	7.3	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative modification methylase; **PDBTitle:** crystal structure of ttha0409, putative dna modification2 methylase from thermus thermophilus hb8- complexed with s-3 adenosyl-l-methionine
82	d2vana2	Alignment	not modelled	7.1	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
83	c1xotB_	Alignment	not modelled	6.3	14	**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
84	c2w11B_	Alignment	not modelled	5.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2-haloalkanoic acid dehalogenase; **PDBTitle:** structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
85	c2ounA_	Alignment	not modelled	5.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp
86	c3i7aA_	Alignment	not modelled	5.8	9	**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
87	c1nw6A_	Alignment	not modelled	5.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
88	d1tbfa_	Alignment	not modelled	5.7	13	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
89	c1xozA_	Alignment	not modelled	5.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
90	c1es6A_	Alignment	not modelled	5.6	45	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein vp40; **PDBTitle:** crystal structure of the matrix protein of ebola virus
91	d1oxja1	Alignment	not modelled	5.6	12	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
92	d1sv0c_	Alignment	not modelled	5.5	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain
93	d1taza_	Alignment	not modelled	5.5	31	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
94	d1pv5a_	Alignment	not modelled	5.4	30	**Fold:**Hypothetical protein YwqG **Superfamily:**Hypothetical protein YwqG **Family:**Hypothetical protein YwqG
95	c2zq5A_	Alignment	not modelled	5.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)