Phyre2

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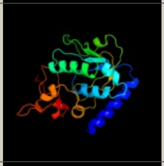
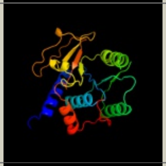
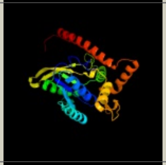
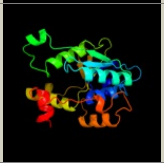
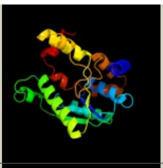
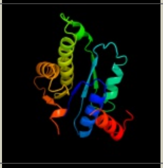
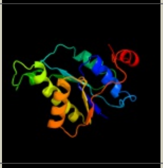
Description	P21156
Date	Thu Jan 5 11:37:52 GMT 2012
Unique Job ID	9bfbabc29201b47d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oq2B_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
2	c2goyC_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
3	c2o8vA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
4	c3g59A_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
5	c2wsiA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad
6	c1zunA_	Alignment		100.0	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
7	d1sura_	Alignment		100.0	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
8	d1zuna1	Alignment		100.0	79	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
9	c3a2kB_	Alignment		99.9	15	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
10	c2e21A_	Alignment		99.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with ampppnp from aquifex2 aeolicus.
11	c1ni5A_	Alignment		99.9	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli

12	d1wy5a1	Alignment		99.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
13	c3bl5E_	Alignment		99.9	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
14	d1ni5a1	Alignment		99.9	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
15	d1k92a1	Alignment		99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
16	d1j20a1	Alignment		99.8	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
17	c2dplA_	Alignment		99.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
18	d1vl2a1	Alignment		99.7	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
19	d1gpma1	Alignment		99.7	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
20	c3p52B_	Alignment		99.7	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
21	c3tqiB_	Alignment	not modelled	99.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
22	c1vl2C_	Alignment	not modelled	99.7	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
23	d2c5sa1	Alignment	not modelled	99.7	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
24	c1kh2D_	Alignment	not modelled	99.6	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
25	c2nz2A_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
26	c2e18B_	Alignment	not modelled	99.6	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
27	c3k32D_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
28	c2derA_	Alignment	not modelled	99.6	14	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
						PDB header:transferase

29	c2hmaA_	Alignment	not modelled	99.5	14	**Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
30	c2ywcC_	Alignment	not modelled	99.5	21	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
31	c1gpmD_	Alignment	not modelled	99.5	16	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
32	d1xnga1	Alignment	not modelled	99.5	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
33	c3fiuD_	Alignment	not modelled	99.5	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
34	c1k97A_	Alignment	not modelled	99.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
35	d2pg3a1	Alignment	not modelled	99.5	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
36	c3uowB_	Alignment	not modelled	99.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
37	c2c5sA_	Alignment	not modelled	99.4	14	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
38	c2vxoB_	Alignment	not modelled	99.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
39	d1vbka1	Alignment	not modelled	99.2	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
40	d1kqpa_	Alignment	not modelled	99.1	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
41	c3q4gA_	Alignment	not modelled	99.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
42	c3dpiA_	Alignment	not modelled	98.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
43	d1wxia1	Alignment	not modelled	98.7	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
44	d1ru8a_	Alignment	not modelled	98.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
45	c3n05B_	Alignment	not modelled	98.5	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
46	d2d13a1	Alignment	not modelled	98.2	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
47	c1ct9D_	Alignment	not modelled	98.0	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
48	d1jgta1	Alignment	not modelled	98.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
49	d1ct9a1	Alignment	not modelled	97.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
50	d1q15a1	Alignment	not modelled	97.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
51	c1m1zB_	Alignment	not modelled	97.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
52	c1q15A_	Alignment	not modelled	97.5	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
53	c3ilvA_	Alignment	not modelled	97.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
54	c1vbkA_	Alignment	not modelled	97.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3

55	c3dlaD_	Alignment	not modelled	95.2	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
56	c2pfsA_	Alignment	not modelled	91.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
57	d1tq8a_	Alignment	not modelled	91.3	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
58	c3loqA_	Alignment	not modelled	88.8	17	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
59	c3rhfB_	Alignment	not modelled	87.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
60	c3mt0A_	Alignment	not modelled	85.4	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
61	c2j0eA_	Alignment	not modelled	83.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
62	c3czpA_	Alignment	not modelled	81.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
63	c3nbmA_	Alignment	not modelled	80.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
64	c1y89B_	Alignment	not modelled	78.9	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
65	c3lwdA_	Alignment	not modelled	78.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
66	c3hgmD_	Alignment	not modelled	77.2	13	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
67	d2z3va1	Alignment	not modelled	69.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
68	c3lhiA_	Alignment	not modelled	68.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
69	c3nwpA_	Alignment	not modelled	66.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
70	c1pbtA_	Alignment	not modelled	64.2	7	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
71	c3dloC_	Alignment	not modelled	60.8	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
72	c3o1lB_	Alignment	not modelled	60.4	10	**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
73	c3s3tD_	Alignment	not modelled	58.2	16	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
74	c3hn6D_	Alignment	not modelled	58.0	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
75	d1q77a_	Alignment	not modelled	55.3	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
76	c2l2qA_	Alignment	not modelled	54.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
77	c2zxrA_	Alignment	not modelled	54.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj; **PDBTitle:** crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
						Fold:SAM domain-like

78	d1pk1c1	Alignment	not modelled	53.8	28	**Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
79	c3bq7A_	Alignment	not modelled	53.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
80	d1vl1a_	Alignment	not modelled	53.5	7	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
81	c1wozA_	Alignment	not modelled	52.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long conserved hypothetical protein (st1454); **PDBTitle:** crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
82	c3olqA_	Alignment	not modelled	51.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein e; **PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
83	c3n0vD_	Alignment	not modelled	50.8	11	**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
84	c2ah6B_	Alignment	not modelled	50.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
85	c2g2dA_	Alignment	not modelled	49.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase; **PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
86	c2d1fA_	Alignment	not modelled	49.7	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** structure of mycobacterium tuberculosis threonine synthase
87	d1ne7a_	Alignment	not modelled	45.2	10	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
88	d1fsfa_	Alignment	not modelled	44.7	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
89	c2afdA_	Alignment	not modelled	43.7	13	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**protein asl1650; **PDBTitle:** solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
90	c2dumD_	Alignment	not modelled	43.1	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
91	c3bs7A_	Alignment	not modelled	43.0	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
92	c3p9xB_	Alignment	not modelled	40.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
93	c1jbqD_	Alignment	not modelled	39.9	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cystathionine beta-synthase; **PDBTitle:** structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
94	d1jbqa_	Alignment	not modelled	39.6	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
95	c1nogA_	Alignment	not modelled	39.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein ta0546; **PDBTitle:** crystal structure of conserved protein 0546 from thermoplasma2 acidophilum
96	d1noga_	Alignment	not modelled	39.0	15	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
97	d1jmva_	Alignment	not modelled	37.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
98	c3oc6A_	Alignment	not modelled	37.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
99	c2nt8A_	Alignment	not modelled	37.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
100	c2px0D_	Alignment	not modelled	36.8	13	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
101	c1pk1A_	Alignment	not modelled	36.1	28	**PDB header:**transcription repression **Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein; **PDBTitle:** hetero sam domain structure of ph and scm.
102	c3ci1A_	Alignment	not modelled	35.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase pduo-like protein; **PDBTitle:** structure of the pduo-type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri complexed3 with

						four-coordinate cob(ii)alamin and atp
103	c3cssA_	Alignment	not modelled	35.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
104	d1xx6a1	Alignment	not modelled	34.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
105	c3bs5A_	Alignment	not modelled	34.8	17	**PDB header:**signaling protein/membrane protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex
106	d1v7ca_	Alignment	not modelled	34.7	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
107	d1wwva1	Alignment	not modelled	33.7	15	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
108	d1z7wa1	Alignment	not modelled	33.7	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
109	d1kw4a_	Alignment	not modelled	33.5	28	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
110	c3icoA_	Alignment	not modelled	32.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
111	c2zhzC_	Alignment	not modelled	32.4	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
112	c3czqA_	Alignment	not modelled	31.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
113	c2ju2A_	Alignment	not modelled	31.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase; **PDBTitle:** minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
114	c3ke4B_	Alignment	not modelled	31.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus
115	c1pk1B_	Alignment	not modelled	30.2	33	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
116	c1ir6A_	Alignment	not modelled	30.2	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
117	d1ir6a_	Alignment	not modelled	30.2	5	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
118	c2zsjB_	Alignment	not modelled	30.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase from aquifex aeolicus vf5
119	d1mjha_	Alignment	not modelled	28.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
120	d2zdra2	Alignment	not modelled	28.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like