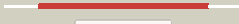



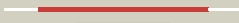









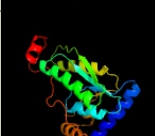








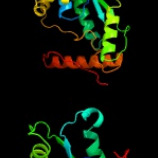
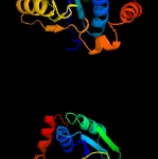
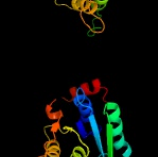
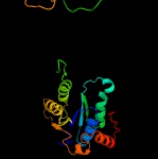

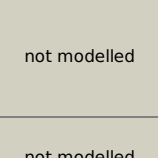


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3625c_mesj_4064080_4065051
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	79ad56bfa060e2be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3a2kB_</a>	 Alignment		100.0	31	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysidine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
2	<a href="#">c1ni5A_</a>	 Alignment		100.0	26	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
3	<a href="#">c2e21A_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysidine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
4	<a href="#">d1ni5a1</a>	 Alignment		100.0	29	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
5	<a href="#">d1wy5a1</a>	 Alignment		100.0	27	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
6	<a href="#">c3vrhA_</a>	 Alignment		100.0	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
7	<a href="#">c5ghaC_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sulfur transferase ttua; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
8	<a href="#">c5udwB_</a>	 Alignment		99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
9	<a href="#">c2nz2A_</a>	 Alignment		99.9	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
10	<a href="#">c1vj2C_</a>	 Alignment		99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
11	<a href="#">c3k32D_</a>	 Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mj0690; <b>PDBTitle:</b> the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm

12	<a href="#">c4nzpA</a>	Alignment		99.9	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
13	<a href="#">c1kh2D</a>	Alignment		99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> argininosuccinate synthetase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
14	<a href="#">d2c5sa1</a>	Alignment		99.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
15	<a href="#">c2dplA</a>	Alignment		99.9	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
16	<a href="#">c1k97A</a>	Alignment		99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
17	<a href="#">d1vl2a1</a>	Alignment		99.9	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
18	<a href="#">d1j20a1</a>	Alignment		99.8	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
19	<a href="#">d1k92a1</a>	Alignment		99.8	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
20	<a href="#">c4kr7A</a>	Alignment		99.8	16	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna sulfurtransferase; <b>PDBTitle:</b> crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
21	<a href="#">c2hmaA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna (5-methylaminomethyl-2-thiouridylate)- <b>PDBTitle:</b> the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
22	<a href="#">c2derA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
23	<a href="#">d1gpmA1</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
24	<a href="#">d1vbka1</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
25	<a href="#">c3tqiB</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
26	<a href="#">c2c5sA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable thiamine biosynthesis protein thii; <b>PDBTitle:</b> crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
27	<a href="#">c3p52B</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
						<b>Fold:</b> Adenine nucleotide alpha hydrolase-like

28	<a href="#">d1sura_</a>	Alignment	not modelled	99.7	10	<b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
29	<a href="#">d1zuna1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
30	<a href="#">d1xnga1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
31	<a href="#">c2ywcC_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
32	<a href="#">c3bl5E_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> queuosine biosynthesis protein quec; <b>PDBTitle:</b> crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
33	<a href="#">c2o8vA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> paps reductase in a covalent complex with thioredoxin c35a
34	<a href="#">c4u7jB_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
35	<a href="#">c3fiuD_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nmh synthetase from francisella tularensis
36	<a href="#">c3uowB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
37	<a href="#">c1gpmD_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
38	<a href="#">c1zunA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
39	<a href="#">c2goyC_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
40	<a href="#">c2vxob_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
41	<a href="#">c2e18B_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of project ph0182 from pyrococcus horikoshii ot3
42	<a href="#">d2pg3a1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
43	<a href="#">c5tw7E_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
44	<a href="#">c2oq2B_</a>	Alignment	not modelled	99.4	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
45	<a href="#">c4bwvB_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine-phosphosulphate reductase; <b>PDBTitle:</b> structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
46	<a href="#">c4xfda_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
47	<a href="#">c5hujB_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nade from streptococcus pyogenes
48	<a href="#">c3g59A_</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn adenylyltransferase; <b>PDBTitle:</b> crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
49	<a href="#">d1kqpa_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
50	<a href="#">c4q16C_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad+ synthetase from deinococcus radiodurans
51	<a href="#">c3q4gA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> structure of nad synthetase from vibrio cholerae
52	<a href="#">c3dpiA_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+ synthetase; <b>PDBTitle:</b> crystal structure of nad+ synthetase from burkholderia pseudomallei
53	<a href="#">d1wxia1</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases

54	<a href="#">c2wsiA</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fad synthetase; <b>PDBTitle:</b> crystal structure of yeast fad synthetase (fad1) in complex2 with fad
55	<a href="#">c5udtD</a>	Alignment	not modelled	98.9	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
56	<a href="#">d1ru8a</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
57	<a href="#">d1wy5a2</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> MesJ substrate recognition domain-like <b>Superfamily:</b> MesJ substrate recognition domain-like <b>Family:</b> MesJ substrate recognition domain-like
58	<a href="#">c5khaA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad+ synthetase; <b>PDBTitle:</b> structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
59	<a href="#">d1q15a1</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
60	<a href="#">c4f4hA</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine dependent nad+ synthetase; <b>PDBTitle:</b> crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
61	<a href="#">d1jgtA1</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
62	<a href="#">c1vbkA</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1313; <b>PDBTitle:</b> crystal structure of ph1313 from pyrococcus horikoshii ot3
63	<a href="#">c3n05B</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nh(3)-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
64	<a href="#">d1ct9a1</a>	Alignment	not modelled	98.4	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
65	<a href="#">c1ct9D</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> asparagine synthetase b; <b>PDBTitle:</b> crystal structure of asparagine synthetase b from2 escherichia coli
66	<a href="#">d2d13a1</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
67	<a href="#">c1q15A</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cara; <b>PDBTitle:</b> carbapenam synthetase
68	<a href="#">c1m1zB</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactam synthetase; <b>PDBTitle:</b> beta-lactam synthetase apo enzyme
69	<a href="#">c3ilvA</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
70	<a href="#">c3dlaD</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamine-dependent nad(+) synthetase; <b>PDBTitle:</b> x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
71	<a href="#">d1ni5a4</a>	Alignment	not modelled	96.8	21	<b>Fold:</b> MesJ substrate recognition domain-like <b>Superfamily:</b> MesJ substrate recognition domain-like <b>Family:</b> MesJ substrate recognition domain-like
72	<a href="#">c3lhiA</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase(yj_207848.1)2 from neisseria gonorrhoeae fa 1090 at 1.33 a resolution
73	<a href="#">d1tq8a</a>	Alignment	not modelled	89.3	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
74	<a href="#">c3nwpA</a>	Alignment	not modelled	88.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
75	<a href="#">c3oc6A</a>	Alignment	not modelled	86.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
76	<a href="#">d1vl1a</a>	Alignment	not modelled	85.5	14	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
77	<a href="#">c3lwdA</a>	Alignment	not modelled	85.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
78	<a href="#">c3o1lB</a>	Alignment	not modelled	83.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
						<b>PDB header:</b> hydrolase, oxidoreductase

79	<a href="#">c1pbtA</a>	Alignment	not modelled	83.2	14	<b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
80	<a href="#">c5ahwC</a>	Alignment	not modelled	81.5	18	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein msmeg_3811 in2 complex with camp
81	<a href="#">c2j0eA</a>	Alignment	not modelled	81.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
82	<a href="#">c2pfsA</a>	Alignment	not modelled	79.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea
83	<a href="#">c4r2lB</a>	Alignment	not modelled	79.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> universal stress protein f; <b>PDBTitle:</b> crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
84	<a href="#">d1fsfa</a>	Alignment	not modelled	77.2	10	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
85	<a href="#">c3hn6D</a>	Alignment	not modelled	76.0	6	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
86	<a href="#">d1ne7a</a>	Alignment	not modelled	71.4	9	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> NagB-like
87	<a href="#">c3cssA</a>	Alignment	not modelled	67.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
88	<a href="#">d2z3va1</a>	Alignment	not modelled	64.1	9	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
89	<a href="#">c4ponB</a>	Alignment	not modelled	61.3	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative rna methylase; <b>PDBTitle:</b> the crystal structure of a putative sam-dependent methyltransferase,2 ytgB, from bacillus subtilis
90	<a href="#">c3icoA</a>	Alignment	not modelled	61.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> crystal structure of 6-phosphogluconolactonase from mycobacterium2 tuberculosis
91	<a href="#">d1rz3a</a>	Alignment	not modelled	58.1	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
92	<a href="#">c3louB</a>	Alignment	not modelled	54.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
93	<a href="#">c3e15D</a>	Alignment	not modelled	51.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> 6-phosphogluconolactonase from plasmodium vivax
94	<a href="#">c1y89B</a>	Alignment	not modelled	50.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> devb protein; <b>PDBTitle:</b> crystal structure of devb protein
95	<a href="#">c3wisA</a>	Alignment	not modelled	48.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydromethanopterin reductase (afpa); <b>PDBTitle:</b> crystal structure of burkholderia xenovorans dmrB in complex with fmn:2 a cubic protein cage for redox transfer
96	<a href="#">c4wnyA</a>	Alignment	not modelled	47.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
97	<a href="#">c2bkxB</a>	Alignment	not modelled	46.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
98	<a href="#">c3lqkA</a>	Alignment	not modelled	46.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
99	<a href="#">c3w7bB</a>	Alignment	not modelled	46.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
100	<a href="#">d1pjqa3</a>	Alignment	not modelled	46.5	32	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
101	<a href="#">c3mcfF</a>	Alignment	not modelled	46.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
102	<a href="#">c3s3tD</a>	Alignment	not modelled	44.0	12	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> nucleotide-binding protein, universal stress protein uspa <b>PDBTitle:</b> universal stress protein uspa from lactobacillus plantarum
103	<a href="#">d1p3y1</a>	Alignment	not modelled	43.5	10	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc

104	<a href="#">c3nbmA_</a>	Alignment	not modelled	42.8	18	components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the 2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from <i>Streptococcus pneumoniae</i> .
105	<a href="#">d1odfa_</a>	Alignment	not modelled	42.0	6	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
106	<a href="#">c3n0vD_</a>	Alignment	not modelled	41.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from <i>Pseudomonas putida</i> kt2440 at 2.25 Å resolution
107	<a href="#">c4bphA_</a>	Alignment	not modelled	41.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 2; <b>PDBTitle:</b> high resolution crystal structure of <i>Bacillus subtilis</i> dltc
108	<a href="#">c6qlgD_</a>	Alignment	not modelled	41.5	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> flavin prenyltransferase pad1, mitochondrial; <b>PDBTitle:</b> crystal structure of anubix (pada1) in complex with fmn and 2 dimethylallyl pyrophosphate
109	<a href="#">c3vmmA_</a>	Alignment	not modelled	41.2	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine-anticapsin ligase bacd; <b>PDBTitle:</b> crystal structure of bacd, an L-amino acid dipeptide ligase from <i>Bacillus subtilis</i>
110	<a href="#">c3zquA_</a>	Alignment	not modelled	40.8	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
111	<a href="#">c3t7yB_</a>	Alignment	not modelled	38.5	11	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the <i>Yersinia enterocolitica</i> homologue of <i>Chlamydia trachomatis</i>
112	<a href="#">d3bzra1</a>	Alignment	not modelled	38.5	6	<b>Fold:</b> EscU C-terminal domain-like <b>Superfamily:</b> EscU C-terminal domain-like <b>Family:</b> EscU C-terminal domain-like
113	<a href="#">c3bzrA_</a>	Alignment	not modelled	38.5	6	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
114	<a href="#">c2jlhA_</a>	Alignment	not modelled	37.9	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of <i>Yersinia pestis</i> yscu n263a mutant
115	<a href="#">d1mjha_</a>	Alignment	not modelled	37.4	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
116	<a href="#">c3eeyL_</a>	Alignment	not modelled	35.4	11	<b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> putative rRNA methylase; <b>PDBTitle:</b> crystal structure of putative rRNA-methylase from <i>Clostridium thermocellum</i>
117	<a href="#">c4rheB_</a>	Alignment	not modelled	35.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-octaprenyl-4-hydroxybenzoate carboxylase; <b>PDBTitle:</b> crystal structure of ubix, an aromatic acid decarboxylase from <i>Theobacillus psychrophilus</i> 34h
118	<a href="#">c5h75B_</a>	Alignment	not modelled	35.0	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mersacidin decarboxylase, immunoglobulin G-binding protein <b>PDBTitle:</b> crystal structure of the mrsd-protein a fusion protein
119	<a href="#">c6jddA_</a>	Alignment	not modelled	34.9	6	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cypemycin cysteine dehydrogenase (decarboxylating); <b>PDBTitle:</b> crystal structure of the cypemycin decarboxylase cypd.
120	<a href="#">c2ejbA_</a>	Alignment	not modelled	34.0	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from <i>Aquifex aeolicus</i>