

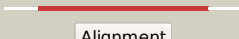

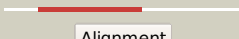




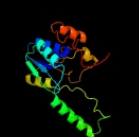






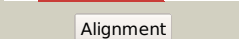
















Phyre2

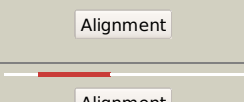
Email	mdejesus@rockefeller.edu
Description	RVBD3024c_trmU_3382796_3383899
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	c242c5b566dfa70

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hmaA_	 Alignment		100.0	36	PDB header: transferase 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
2	c2derA_	 Alignment		100.0	35	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
3	c2vx0B_	 Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
4	c4kr7A_	 Alignment		100.0	20	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
5	c3q4gA_	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
6	c2c5sA_	 Alignment		100.0	21	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
7	c5hujB_	 Alignment		99.9	21	PDB header: transferase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
8	c3fiuD_	 Alignment		99.9	19	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmn synthetase from francisella tularensis
9	c3k32D_	 Alignment		99.9	19	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
10	c5udwB_	 Alignment		99.9	24	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
11	c2e21A_	 Alignment		99.9	20	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.

12	d1wy5a1	Alignment		99.9	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
13	c3a2kB	Alignment		99.9	19	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
14	c1kh2D	Alignment		99.9	20	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
15	d2c5sa1	Alignment		99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
16	c2nz2A	Alignment		99.9	22	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
17	d1kqpa	Alignment		99.9	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
18	c4xfgA	Alignment		99.9	21	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
19	c2e18B	Alignment		99.9	25	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
20	c3vrhA	Alignment		99.9	25	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
21	c4nzpA	Alignment	not modelled	99.9	22	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
22	c3dpiA	Alignment	not modelled	99.9	25	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
23	d1wxia1	Alignment	not modelled	99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
24	d1j20a1	Alignment	not modelled	99.9	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
25	c5ghaC	Alignment	not modelled	99.9	27	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
26	c4q16C	Alignment	not modelled	99.9	22	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
27	c2ywcC	Alignment	not modelled	99.9	26	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
28	c3tqiB	Alignment	not modelled	99.9	20	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
						Fold: Adenine nucleotide alpha hydrolase-like

29	d1vl2a1	Alignment	not modelled	99.9	23	Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
30	d1gpm1	Alignment	not modelled	99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
31	c1vl2C_	Alignment	not modelled	99.9	19	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from <i>Thermotoga maritima</i> at 1.65 Å resolution
32	c2dplA_	Alignment	not modelled	99.9	27	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from <i>Pyrococcus horikoshii</i> ot3
33	c3p52B_	Alignment	not modelled	99.9	22	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168 in complex with the nitrate ion
34	c5tw7E_	Alignment	not modelled	99.9	27	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from <i>Neisseria gonorrhoeae</i>
35	c4u7jB_	Alignment	not modelled	99.9	26	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from <i>Mycobacterium thermoresistibile</i>
36	c1ni5A_	Alignment	not modelled	99.9	17	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from <i>Escherichia coli</i>
37	d1ni5a1	Alignment	not modelled	99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
38	c1gpmD_	Alignment	not modelled	99.9	19	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: <i>Escherichia coli</i> gmp synthetase complexed with amp and pyrophosphate
39	d1xnga1	Alignment	not modelled	99.9	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
40	d1k92a1	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
41	c1k97A_	Alignment	not modelled	99.9	18	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of <i>E. coli</i> argininosuccinate synthetase in complex2 with aspartate and citrulline
42	c3bl5E_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from <i>Bacillus subtilis</i> : an enzyme2 involved in preq1 biosynthesis
43	c3uowB_	Alignment	not modelled	99.9	23	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from <i>Plasmodium falciparum</i>
44	c5udtD_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp
45	d1vbk1	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
46	d2pg3a1	Alignment	not modelled	99.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
47	c5khaA_	Alignment	not modelled	99.8	21	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad+ synthetase; PDBTitle: structure of glutamine-dependent nad+ synthetase from <i>Acinetobacter baumannii</i> in complex with adenosine diphosphate (adp)
48	c4f4hA_	Alignment	not modelled	99.8	22	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from <i>Burkholderia thailandensis</i>
49	c3n05B_	Alignment	not modelled	99.8	28	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from <i>Streptomyces avermitilis</i>
50	d1sura_	Alignment	not modelled	99.7	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
51	c1vbkA_	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from <i>Pyrococcus horikoshii</i> ot3
52	c3ilvA_	Alignment	not modelled	99.6	18	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from <i>Cytophaga hutchinsonii</i>
53	d1ru8a_	Alignment	not modelled	99.6	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
54	c2o8vA_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a

55	c3dlaD	 Alignment	not modelled	99.5	22	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
56	c2goyC	 Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
57	dlzuna1	 Alignment	not modelled	99.3	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
58	c1zunA	 Alignment	not modelled	99.2	13	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
59	c2oq2B	 Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
60	c4bwvB	 Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulphate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
61	c1ct9D	 Alignment	not modelled	99.1	21	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
62	dlq15a1	 Alignment	not modelled	99.0	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	dlct9a1	 Alignment	not modelled	99.0	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
64	dljgta1	 Alignment	not modelled	98.9	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
65	c1q15A	 Alignment	not modelled	98.8	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
66	d2d13a1	 Alignment	not modelled	98.7	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
67	c3g59A	 Alignment	not modelled	98.7	15	PDB header: transferase Chain: A: PDB Molecule: fmn adenylyltransferase; PDBTitle: crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
68	c1m1zB	 Alignment	not modelled	98.6	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
69	c2wsiA	 Alignment	not modelled	98.2	16	PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
70	c3o1lB	 Alignment	not modelled	95.1	21	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
71	c3n0vD	 Alignment	not modelled	95.0	22	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
72	c2ys6A	 Alignment	not modelled	95.0	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
73	c2yyaB	 Alignment	not modelled	94.2	16	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
74	c3w7bB	 Alignment	not modelled	94.1	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
75	c1m6vE	Alignment	not modelled	94.0	17	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
76	c2xd4A	Alignment	not modelled	92.8	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
77	c2ywrA	Alignment	not modelled	92.3	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex aeolicus
78	c4dimA	Alignment	not modelled	91.4	7	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
79	c3k5lB	Alignment	not modelled	91.1	16	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase;

79	c3k3jB	Alignment	not modelled	91.1	10	PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
80	c3louB	Alignment	not modelled	90.1	20	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
81	c1gsoA	Alignment	not modelled	89.0	14	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
82	c2x7vA	Alignment	not modelled	88.5	15	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
83	d1fmta2	Alignment	not modelled	88.3	18	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
84	c3nbmA	Alignment	not modelled	87.6	18	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.
85	c3aufA	Alignment	not modelled	87.3	23	PDB header: transferase Chain: A: PDB Molecule: glycinamide ribonucleotide transformylase 1; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 symbiobacterium toebii
86	c3tqrA	Alignment	not modelled	87.1	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
87	c5cjjA	Alignment	not modelled	86.8	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from campylobacter jejuni subsp. jejuni nctc 11168
88	d1jkxa	Alignment	not modelled	84.8	18	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
89	c3obiC	Alignment	not modelled	84.7	22	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
90	d1meoa	Alignment	not modelled	82.9	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
91	d2blna2	Alignment	not modelled	82.5	24	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
92	c2dzdB	Alignment	not modelled	82.0	13	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
93	d2hy5a1	Alignment	not modelled	81.4	16	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
94	d1qtwa	Alignment	not modelled	80.4	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
95	c4r3uD	Alignment	not modelled	79.9	17	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
96	c4mgeB	Alignment	not modelled	77.4	22	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
97	c3kcgA	Alignment	not modelled	77.3	22	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
98	d2d1pa1	Alignment	not modelled	76.6	13	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
99	c3lp8A	Alignment	not modelled	76.5	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
100	c2l2qA	Alignment	not modelled	76.1	14	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
101	c1yrwA	Alignment	not modelled	74.6	24	PDB header: transferase Chain: A: PDB Molecule: protein arna; PDBTitle: crystal structure of e.coli arna transformylase domain

102	d1s3ia2	Alignment	not modelled	72.0	22	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
103	c5vevB	Alignment	not modelled	71.5	17	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
104	d1gsoa2	Alignment	not modelled	71.5	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
105	c2pk3B	Alignment	not modelled	70.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
106	d2bw0a2	Alignment	not modelled	70.6	23	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
107	c2ejbA	Alignment	not modelled	70.2	16	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
108	d1xp3a1	Alignment	not modelled	69.6	20	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
109	c1wv9B	Alignment	not modelled	68.4	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
110	c3foja	Alignment	not modelled	67.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
111	c1qzuB	Alignment	not modelled	67.3	27	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoylcysteine decarboxylase
112	c4ffnA	Alignment	not modelled	65.4	11	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
113	c1djinB	Alignment	not modelled	64.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
114	c4rheB	Alignment	not modelled	62.9	21	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
115	d1gy8a	Alignment	not modelled	61.4	37	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c3mcf	Alignment	not modelled	61.4	20	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
117	c3lwbA	Alignment	not modelled	61.2	25	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
118	c3nrbd	Alignment	not modelled	61.0	21	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
119	c4jgbB	Alignment	not modelled	61.0	30	PDB header: protein binding Chain: B: PDB Molecule: putative exported protein; PDBTitle: crystal structure of putative exported protein from burkholderia2 pseudomallei
120	c5uaiA	Alignment	not modelled	59.7	18	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa