Phyre2

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Description	RVBD1658_(argG)_1871370_1872566
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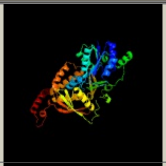
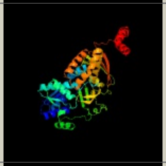
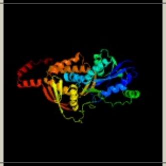
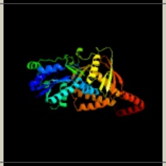
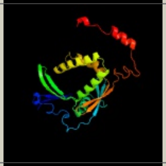
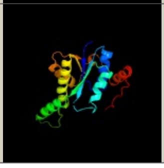
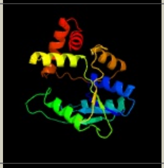
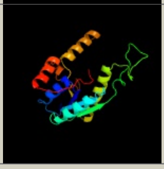
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4u7jB_	Alignment		100.0	88	**PDB header:**ligase **Chain:** B: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
2	c1vl2C_	Alignment		100.0	40	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
3	c1kh2D_	Alignment		100.0	42	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
4	c1k97A_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
5	c2nz2A_	Alignment		100.0	39	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
6	c4nzpA_	Alignment		100.0	39	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
7	d1j20a2	Alignment		100.0	39	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
8	d1vl2a2	Alignment		100.0	36	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
9	d1k92a2	Alignment		100.0	28	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
10	d1j20a1	Alignment		100.0	45	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
11	d1k92a1	Alignment		100.0	29	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases

12	d1vl2a1	Alignment		100.0	46	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
13	c3a2kB_	Alignment		100.0	16	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
14	c2e21A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
15	c1ni5A_	Alignment		100.0	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
16	c2hmaA_	Alignment		100.0	19	**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
17	c3vrhA_	Alignment		99.9	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0300; **PDBTitle:** crystal structure of ph0300
18	c5ghaC_	Alignment		99.9	24	**PDB header:**transferase/transport protein **Chain:** C: **PDB Molecule:**sulfur transferase ttua; **PDBTitle:** sulfur transferase ttua in complex with sulfur carrier ttub
19	d1ni5a1	Alignment		99.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
20	d1wy5a1	Alignment		99.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
21	d2c5sa1	Alignment	not modelled	99.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
22	c5udwB_	Alignment	not modelled	99.9	19	**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
23	c2derA_	Alignment	not modelled	99.9	18	**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
24	c2dplA_	Alignment	not modelled	99.9	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
25	d1gpma1	Alignment	not modelled	99.9	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
26	c3k32D_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
27	c4kr7A_	Alignment	not modelled	99.9	15	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**probable trna sulfurtransferase; **PDBTitle:** crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
28	c3tqiB_	Alignment	not modelled	99.9	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii

29	c2c5sA_	Alignment	not modelled	99.9	19	**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
30	c3p52B_	Alignment	not modelled	99.9	12	**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
31	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
32	c2vxoB_	Alignment	not modelled	99.9	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
33	c1gpmD_	Alignment	not modelled	99.8	23	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
34	c3bl5E_	Alignment	not modelled	99.8	18	**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
35	c3fiuD_	Alignment	not modelled	99.8	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
36	c2e18B_	Alignment	not modelled	99.8	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
37	c5tw7E_	Alignment	not modelled	99.8	28	**PDB header:**ligase **Chain:** E: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
38	d1sura_	Alignment	not modelled	99.8	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
39	d1xnga1	Alignment	not modelled	99.8	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
40	d2pg3a1	Alignment	not modelled	99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
41	d1vbka1	Alignment	not modelled	99.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
42	c4xfdA_	Alignment	not modelled	99.8	18	**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
43	c3uowB_	Alignment	not modelled	99.8	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
44	c2o8vA_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
45	d1ru8a_	Alignment	not modelled	99.7	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
46	d1kqpa_	Alignment	not modelled	99.7	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
47	c5hujB_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nade from streptococcus pyogenes
48	c3q4gA_	Alignment	not modelled	99.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
49	c4q16C_	Alignment	not modelled	99.7	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad+ synthetase from deinococcus radiodurans
50	c3dpiA_	Alignment	not modelled	99.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
51	d1wxia1	Alignment	not modelled	99.6	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
52	c2goyC_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
53	c5khaA_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad+ synthetase; **PDBTitle:** structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp)
54	c4f4hA_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine dependent nad+ synthetase;

54	c4f4hA_	Alignment	not modelled	99.6	16	**PDBTitle:** crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
55	d1zuna1	Alignment	not modelled	99.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
56	c2oq2B_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
57	d2d13a1	Alignment	not modelled	99.5	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
58	c1zunA_	Alignment	not modelled	99.5	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	c4bwvB_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine-phosphosulphate reductase; **PDBTitle:** structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
60	c3n05B_	Alignment	not modelled	99.4	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
61	c1vbkA_	Alignment	not modelled	99.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
62	c3g59A_	Alignment	not modelled	99.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
63	c3dlaD_	Alignment	not modelled	99.1	15	**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
64	c5udtD_	Alignment	not modelled	99.0	27	**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
65	c3ilvA_	Alignment	not modelled	98.9	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
66	c2wsiA_	Alignment	not modelled	98.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad
67	d1ct9a1	Alignment	not modelled	98.8	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
68	d1q15a1	Alignment	not modelled	98.7	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
69	c1ct9D_	Alignment	not modelled	98.7	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
70	d1jgta1	Alignment	not modelled	98.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
71	c1q15A_	Alignment	not modelled	98.2	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
72	c1m1zB_	Alignment	not modelled	98.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
73	c2gpwC_	Alignment	not modelled	93.8	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
74	d1q77a_	Alignment	not modelled	93.4	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
75	c3g8cB_	Alignment	not modelled	92.9	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion
76	c2pfsA_	Alignment	not modelled	90.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
77	c1ulzA_	Alignment	not modelled	90.4	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
78	c2dzdB_	Alignment	not modelled	88.7	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
79	c3jzfA_	Alignment	not modelled	88.1	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series

80	d1tq8a_	Alignment	not modelled	87.0	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
81	c2vpqA_	Alignment	not modelled	86.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
82	c3hgmD_	Alignment	not modelled	86.8	23	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
83	c5ahwC_	Alignment	not modelled	86.2	14	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein msmeg_3811 in2 complex with camp
84	c3ouzA_	Alignment	not modelled	84.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
85	d2z3va1	Alignment	not modelled	83.9	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
86	c4rheB_	Alignment	not modelled	83.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-octaprenyl-4-hydroxybenzoate carboxy-lyase; **PDBTitle:** crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
87	d1m1na_	Alignment	not modelled	81.2	20	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
88	c5mlkA_	Alignment	not modelled	81.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
89	c3o1lB_	Alignment	not modelled	80.8	14	**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
90	c3s3tD_	Alignment	not modelled	80.8	10	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
91	c4wnyA_	Alignment	not modelled	79.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
92	c2h9aA_	Alignment	not modelled	77.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron-sulfur **PDBTitle:** corrinoid iron-sulfur protein
93	c1vliA_	Alignment	not modelled	76.7	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
94	c4rxuA_	Alignment	not modelled	76.6	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
95	c1xjqA_	Alignment	not modelled	75.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** adp complex of human paps synthetase 1
96	d2zdra2	Alignment	not modelled	75.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
97	c4r2lB_	Alignment	not modelled	75.7	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**universal stress protein f; **PDBTitle:** crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
98	c3u9sA_	Alignment	not modelled	75.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
99	c6qlgD_	Alignment	not modelled	74.5	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**flavin prenyltransferase pad1, mitochondrial; **PDBTitle:** crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
100	c2dwcB_	Alignment	not modelled	74.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
101	d2gm3a1	Alignment	not modelled	73.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
102	c5h80A_	Alignment	not modelled	73.2	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carboxylase; **PDBTitle:** biotin carboxylase domain of single-chain bacterial carboxylase
103	c2iy3A_	Alignment	not modelled	72.3	23	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein,signal recognition **PDBTitle:** structure of the e. coli signal regognition particle

104	c3lqkA_	Alignment	not modelled	72.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
105	c3mcuF_	Alignment	not modelled	71.7	28	**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.
106	c5mlkB_	Alignment	not modelled	71.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
107	c3d3kD_	Alignment	not modelled	71.3	10	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
108	c3mt0A_	Alignment	not modelled	70.8	16	**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
109	c3n0vD_	Alignment	not modelled	70.8	16	**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
110	d1vlia2	Alignment	not modelled	70.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
111	c3zquA_	Alignment	not modelled	69.8	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
112	c1xuzA_	Alignment	not modelled	69.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
113	c5ks8B_	Alignment	not modelled	69.2	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase subunit alpha; **PDBTitle:** crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
114	c2yclA_	Alignment	not modelled	67.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron-sulfur **PDBTitle:** complete structure of the corrinoid,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
115	d1qzua_	Alignment	not modelled	67.5	22	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
116	c5n6yD_	Alignment	not modelled	67.2	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitrogenase vanadium-iron protein alpha chain; **PDBTitle:** azotobacter vinelandii vanadium nitrogenase
117	c3fz0C_	Alignment	not modelled	66.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nucleoside hydrolase, putative; **PDBTitle:** inosine-guanosine nucleoside hydrolase (ig-nh)
118	c3dloC_	Alignment	not modelled	66.2	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
119	c3uvzB_	Alignment	not modelled	65.7	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
120	d1g5qa_	Alignment	not modelled	65.0	15	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD