



















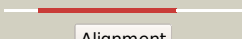










Phyre2

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Description	RVBD1285_(cysD)_1437915_1438913
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	e9d2083c49287603

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bwvB_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulfate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
2	c2oq2B_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
3	c3g59A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: fmn adenylyltransferase; PDBTitle: crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
4	c2wsiA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
5	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
6	c1zunA_	 Alignment		100.0	60	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	d1zuna1	 Alignment		100.0	59	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
8	c2govC_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
9	d1sura_	 Alignment		100.0	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
10	c3bl5E_	 Alignment		99.8	15	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
11	c3vrhA_	 Alignment		99.8	18	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300

12	d1wy5a1	Alignment		99.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
13	c5ghaC	Alignment		99.7	20	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
14	c3a2kB	Alignment		99.7	13	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
15	d1ni5a1	Alignment		99.7	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
16	c2e21A	Alignment		99.7	16	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
17	d1k92a1	Alignment		99.6	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
18	c5udwB	Alignment		99.6	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
19	d1j20a1	Alignment		99.6	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
20	c1ni5A	Alignment		99.6	17	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
21	c2dplA	Alignment	not modelled	99.6	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
22	c3p52B	Alignment	not modelled	99.5	14	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
23	d1gpma1	Alignment	not modelled	99.5	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
24	d1vl2a1	Alignment	not modelled	99.5	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
25	c2e18B	Alignment	not modelled	99.5	18	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
26	c3tqiB	Alignment	not modelled	99.4	17	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
27	d2pg3a1	Alignment	not modelled	99.3	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
28	c5tw7E	Alignment	not modelled	99.3	21	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae

29	c1kh2D	Alignment	not modelled	99.3	21	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
30	c1vl2C	Alignment	not modelled	99.3	15	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
31	c1gpmD	Alignment	not modelled	99.3	20	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
32	c3fiuD	Alignment	not modelled	99.3	19	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
33	c2nz2A	Alignment	not modelled	99.3	13	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
34	c2ywcC	Alignment	not modelled	99.2	19	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
35	d1xnga1	Alignment	not modelled	99.2	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
36	c2hmaA	Alignment	not modelled	99.2	14	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
37	c2derA	Alignment	not modelled	99.2	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
38	d2c5sa1	Alignment	not modelled	99.2	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
39	c2vx0B	Alignment	not modelled	99.2	17	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
40	c1k97A	Alignment	not modelled	99.2	16	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
41	c3uowB	Alignment	not modelled	99.1	11	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
42	c3k32D	Alignment	not modelled	99.1	16	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm
43	c4kr7A	Alignment	not modelled	99.0	16	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
44	c4nzpA	Alignment	not modelled	98.9	16	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
45	c2c5sA	Alignment	not modelled	98.9	15	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
46	c4xfDA	Alignment	not modelled	98.9	17	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
47	c4u7jB	Alignment	not modelled	98.9	22	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
48	d1kqpa	Alignment	not modelled	98.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
49	c5hujB	Alignment	not modelled	98.7	13	PDB header: transferase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
50	d1ru8a	Alignment	not modelled	98.6	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
51	d1vbka1	Alignment	not modelled	98.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
52	c3dpiA	Alignment	not modelled	98.6	16	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
53	c3q4gA	Alignment	not modelled	98.5	15	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
54	c4n16C	Alignment	not modelled	98.3	13	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase;

54	c4q10C	Alignment	not modelled	98.3	13	PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
55	d1wxia1	Alignment	not modelled	98.2	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
56	c3n05B	Alignment	not modelled	98.2	15	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
57	d2d13a1	Alignment	not modelled	98.2	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
58	c4f4hA	Alignment	not modelled	98.1	16	PDB header: ligase Chain: A: PDB Molecule: glutamine dependent nad+ synthetase; PDBTitle: crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis
59	c5khaA	Alignment	not modelled	97.9	23	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)
60	c5udtD	Alignment	not modelled	97.8	19	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
61	c1ct9D	Alignment	not modelled	97.6	15	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
62	d1jgtal	Alignment	not modelled	97.5	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	d1q15a1	Alignment	not modelled	97.4	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
64	d1ct9a1	Alignment	not modelled	97.2	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
65	c1m1zB	Alignment	not modelled	97.0	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
66	c1q15A	Alignment	not modelled	96.9	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: carA; PDBTitle: carbapenam synthetase
67	c1vbkA	Alignment	not modelled	95.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
68	c3ilvA	Alignment	not modelled	94.9	16	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
69	c3dlaD	Alignment	not modelled	94.5	20	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
70	c3loqA	Alignment	not modelled	89.5	17	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
71	d1tq8a	Alignment	not modelled	89.0	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
72	c2pfsA	Alignment	not modelled	88.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
73	d2z3va1	Alignment	not modelled	80.7	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
74	c3hgmD	Alignment	not modelled	80.3	19	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
75	c3mt0A	Alignment	not modelled	79.2	6	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
76	c2j0eA	Alignment	not modelled	69.1	7	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
77	c1y89B	Alignment	not modelled	61.5	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: devb protein; PDBTitle: crystal structure of devb protein
78	c4pfsA	Alignment	not modelled	60.8	20	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
79	c3bq7A	Alignment	not modelled	57.3	10	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
80	c3hn6D	Alignment	not modelled	56.7	16	PDB header: isomerase Chain: D: PDB Molecule: glucosamine-6-phosphate deaminase;

104	c1pbtA_	Alignment	not modelled	34.9	9	Chain: A; PDB Molecule: 6-phosphogluconolactonase; PDBTitle: the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
105	d1xx6a1	Alignment	not modelled	34.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
106	c3nwpA_	Alignment	not modelled	34.4	16	PDB header: hydrolase Chain: A; PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from shewanella baltica os155 at 1.40 a resolution
107	c1lt1G_	Alignment	not modelled	34.2	37	PDB header: de novo protein Chain: G; PDB Molecule: l13g-df1; PDBTitle: sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
108	c1xp8A_	Alignment	not modelled	34.1	19	PDB header: dna binding protein Chain: A; PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
109	c2nt8A_	Alignment	not modelled	32.5	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
110	c1pk1B_	Alignment	not modelled	32.2	30	PDB header: transcription repression Chain: B; PDB Molecule: ssex comb on midleg cg9495-pa; PDBTitle: hetero sam domain structure of ph and scm.
111	d1kw4a_	Alignment	not modelled	32.1	28	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
112	c3ke4B_	Alignment	not modelled	32.0	20	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
113	c4zjbG_	Alignment	not modelled	31.6	20	PDB header: lyase/biosynthetic protein Chain: G; PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) in complex with holo-acc from helicobacter pylori
114	c3dloC_	Alignment	not modelled	30.8	17	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
115	c2ah6B_	Alignment	not modelled	30.6	23	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
116	d2ctza1	Alignment	not modelled	30.5	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
117	c3b6nA_	Alignment	not modelled	29.4	21	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
118	c4oc9N_	Alignment	not modelled	28.8	13	PDB header: lyase Chain: N; PDB Molecule: putative o-acetylhomoserine (thiol)-lyase; PDBTitle: 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
119	c1v85A_	Alignment	not modelled	28.1	11	PDB header: apoptosis Chain: A; PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
120	c3fg9B_	Alignment	not modelled	27.7	22	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1