

Phyre2

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 Description RVBD2919c_glnB_3230748_3231086
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r25A_	Alignment		100.0	36	PDB header: transcription Chain: A: PDB Molecule: nitrogen regulatory pii-like protein; PDBTitle: structure of b. subtilis glnK
2	d2ns1b1	Alignment		100.0	54	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
3	c3mhyC_	Alignment		100.0	56	PDB header: signaling protein Chain: C: PDB Molecule: pii-like protein pz; PDBTitle: a new pii protein structure
4	d1vfja_	Alignment		100.0	44	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
5	d2piia_	Alignment		100.0	62	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
6	d1qy7a_	Alignment		100.0	62	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
7	c2rd5D_	Alignment		100.0	46	PDB header: protein binding Chain: D: PDB Molecule: pii protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
8	c3ncpD_	Alignment		100.0	51	PDB header: signaling protein Chain: D: PDB Molecule: nitrogen regulatory protein p-ii (glnB-2); PDBTitle: glnK2 from archaeoglobus fulgidus
9	d1hwua_	Alignment		100.0	63	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
10	d1ul3a_	Alignment		100.0	59	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
11	c4ozlA_	Alignment		100.0	44	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: glnK2 from haloferax mediterranei complexed with amp

12	c3bzqA_	Alignment		100.0	100	PDB header: signaling protein/transcription Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
13	c2j9dG_	Alignment		100.0	56	PDB header: membrane transport Chain: G: PDB Molecule: hypothetical nitrogen regulatory pii-like PDBTitle: structure of glnK1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
14	c3o8wA_	Alignment		100.0	50	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii (glnB-1); PDBTitle: archaeoglobus fulgidus glnK1
15	c4usiC_	Alignment		100.0	39	PDB header: signaling protein Chain: C: PDB Molecule: nitrogen regulatory protein pii; PDBTitle: nitrogen regulatory protein pii from chlamydomonas2 reinhardtii in complex with mgatp and 2-oxoglutarate
16	c3l7pA_	Alignment		99.9	48	PDB header: transcription Chain: A: PDB Molecule: putative nitrogen regulatory protein pii; PDBTitle: crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
17	d2cz4a1	Alignment		99.8	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
18	c5d4pA_	Alignment		99.7	21	PDB header: signaling protein Chain: A: PDB Molecule: putative nitrogen regulatory protein p-ii glnB; PDBTitle: structure of cpil bound to adp and bicarbonate, from thiomonas2 intermedia k12
19	c4wk1A_	Alignment		98.7	25	PDB header: signaling protein Chain: A: PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
20	c4rleA_	Alignment		98.6	30	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pii-like protein dara
21	c4rwwB_	Alignment	not modelled	98.5	24	PDB header: protein binding Chain: B: PDB Molecule: lmo2692 protein; PDBTitle: crystal structure of l. monocytogenes psta in complex with cyclic-di-2 amp
22	c3ce8A_	Alignment	not modelled	98.5	18	PDB header: unknown function Chain: A: PDB Molecule: putative pii-like nitrogen regulatory protein; PDBTitle: crystal structure of a duf3240 family protein (sba1_0098) from2 shewanella baltica os155 at 2.40 a resolution
23	c3m05A_	Alignment	not modelled	98.2	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein pepe_1480 from2 pediococcus pentosaceus atcc 25745
24	d1o51a_	Alignment	not modelled	96.6	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
25	c2dc1B_	Alignment	not modelled	95.1	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
26	c2gx8B_	Alignment	not modelled	93.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
27	d2gx8a1	Alignment	not modelled	91.7	26	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
28	c3hluA_	Alignment	not modelled	86.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein duf2179; PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum

29	c2nydB	Alignment	not modelled	85.0	18	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
30	d1nh8a2	Alignment	not modelled	83.9	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
31	c2vd3B	Alignment	not modelled	74.7	18	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
32	c4yb5B	Alignment	not modelled	72.7	15	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: adenosine triphosphate phosphoribosyltransferase from campylobacter2 jejuni in complex with the allosteric inhibitor histidine
33	c1nh7A	Alignment	not modelled	69.9	19	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
34	c3dfeA	Alignment	not modelled	65.6	25	PDB header: signaling protein Chain: A: PDB Molecule: putative pii-like signaling protein; PDBTitle: crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anaebaena variabilis atcc 29413 at 2.35 a3 resolution
35	c6czlA	Alignment	not modelled	60.1	24	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase catalytic subunit; PDBTitle: crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
36	d1h3da2	Alignment	not modelled	58.0	13	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
37	c3rrkA	Alignment	not modelled	50.5	20	PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase
38	c2cz9A	Alignment	not modelled	47.1	18	PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
39	c1q1kA	Alignment	not modelled	43.5	13	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
40	c2f06B	Alignment	not modelled	42.4	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
41	c2dtjA	Alignment	not modelled	37.5	17	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
42	c6bwqB	Alignment	not modelled	27.6	23	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
43	d1zhva2	Alignment	not modelled	23.4	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
44	c2hk3A	Alignment	not modelled	22.7	10	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
45	c6a4cA	Alignment	not modelled	22.3	41	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mxan_0049; PDBTitle: solution structure of mxan_0049
46	c3u7rB	Alignment	not modelled	21.1	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent fmh reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
47	c3s1tB	Alignment	not modelled	20.3	18	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
48	c3j9tb	Alignment	not modelled	17.6	20	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase state 1
49	d2j0wa3	Alignment	not modelled	16.9	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
50	d1v6za2	Alignment	not modelled	16.0	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
51	d2hmfa2	Alignment	not modelled	15.9	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
52	d1w1oa1	Alignment	not modelled	15.8	19	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
53	d2a5la1	Alignment	not modelled	15.2	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like

54	d2f06a2	Alignment	not modelled	14.9	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
55	c2zhoB	Alignment	not modelled	14.8	18	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
56	c3hulA	Alignment	not modelled	14.7	23	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: structure of putative homoserine kinase thrb from listeria2 monocytogenes
57	c5yeiF	Alignment	not modelled	14.2	16	PDB header: transferase Chain: F: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
58	c3nnqA	Alignment	not modelled	14.0	12	PDB header: viral protein Chain: A: PDB Molecule: n-terminal domain of moloney murine leukemia virus PDBTitle: crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
59	c3mahA	Alignment	not modelled	13.4	25	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
60	d1vi2a2	Alignment	not modelled	12.6	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
61	d1x8da1	Alignment	not modelled	12.5	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YiIL-like
62	c2gs8A	Alignment	not modelled	12.3	12	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
63	c4ur7B	Alignment	not modelled	12.2	11	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
64	c6hnnA	Alignment	not modelled	12.0	28	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
65	c2qlxA	Alignment	not modelled	11.4	11	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
66	c2qlwA	Alignment	not modelled	11.4	11	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
67	c2nuxB	Alignment	not modelled	11.1	21	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
68	d1nxza2	Alignment	not modelled	10.5	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
69	d1p77a2	Alignment	not modelled	10.2	8	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
70	d1nvtA2	Alignment	not modelled	10.0	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
71	c3fluD	Alignment	not modelled	9.9	17	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
72	d1oyia	Alignment	not modelled	9.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
73	c1oyiA	Alignment	not modelled	9.8	20	PDB header: viral protein Chain: A: PDB Molecule: double-stranded rna-binding protein; PDBTitle: solution structure of the z-dna binding domain of the2 vaccinia virus gene e3l
74	c4rpfA	Alignment	not modelled	9.5	21	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
75	c3n2xB	Alignment	not modelled	9.1	21	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
76	c4yiyA	Alignment	not modelled	9.1	19	PDB header: rna binding protein Chain: A: PDB Molecule: krna editing a6 specific protein; PDBTitle: structure of mrb1590 bound to amp-pnp
77	d1mwza	Alignment	not modelled	8.8	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
78	c1zhvA	Alignment	not modelled	8.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics

						consortium target atr8.
79	c4p52A_	Alignment	not modelled	8.8	29	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from cytophaga hutchinsonii2 atcc 33406, nysgrc target 032717.
80	d1nyta2	Alignment	not modelled	8.8	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
81	c2cx8A_	Alignment	not modelled	8.7	20	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
82	c4zhwA_	Alignment	not modelled	8.7	18	PDB header: signaling protein Chain: A: PDB Molecule: yfib; PDBTitle: crystal structure of a bacterial signalling protein (n-terminal2 truncation)
83	d1vhka2	Alignment	not modelled	8.6	10	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
84	c1z85B_	Alignment	not modelled	8.5	10	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
85	d1aopa2	Alignment	not modelled	8.3	22	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
86	c2cx8B_	Alignment	not modelled	8.2	20	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
87	c4xkyC_	Alignment	not modelled	8.1	17	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
88	c3d7aB_	Alignment	not modelled	8.0	11	PDB header: unknown function Chain: B: PDB Molecule: upf0201 protein ph1010; PDBTitle: crystal structure of duf54 family protein ph1010 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
89	d2cdqa3	Alignment	not modelled	7.9	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
90	d1fx0a2	Alignment	not modelled	7.9	21	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
91	c4i69A_	Alignment	not modelled	7.8	14	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
92	d1ny5a2	Alignment	not modelled	7.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	c4o9iA_	Alignment	not modelled	7.7	10	PDB header: antiviral protein Chain: A: PDB Molecule: mitochondrial antiviral signaling protein (mavs); PDBTitle: crystal structure of horse mavs card domain mutant e26r
94	c3dz1A_	Alignment	not modelled	7.6	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
95	c3lerA_	Alignment	not modelled	7.5	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
96	c4e8bA_	Alignment	not modelled	7.4	13	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
97	c5watB_	Alignment	not modelled	7.3	29	PDB header: transferase Chain: B: PDB Molecule: homoserine kinase; PDBTitle: corynebacterium glutamicum full length homoserine kinase
98	d1v7ra_	Alignment	not modelled	7.3	23	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
99	c2zvyB_	Alignment	not modelled	7.2	8	PDB header: membrane protein Chain: B: PDB Molecule: chemotaxis protein motb; PDBTitle: structure of the periplasmic domain of motb from salmonella2 (crystal form ii)