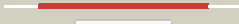



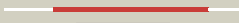
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1005c_(pabB)_1122226_1123602
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	b668d182453c10b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4penA_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component 1; PDBTitle: structure of anthranilate synthase component i (trpe) from2 mycobacterium tuberculosis with inhibitor bound
2	dli7qa_	 Alignment		100.0	24	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
3	dli1qa_	 Alignment		100.0	25	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
4	d1qdlA_	 Alignment		100.0	28	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
5	c5kckA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component i; PDBTitle: crystal structure of anthranilate synthase component i from2 streptococcus pneumoniae tigr4
6	c4grhA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: aminodeoxychorismate synthase; PDBTitle: crystal structure of pabb of stentrophomonas maltophilia
7	d2q5fa1	 Alignment		100.0	22	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
8	d1k0ga_	 Alignment		100.0	29	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
9	c2i6yA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component i, putative; PDBTitle: structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbt1
10	d2fn0a1	 Alignment		100.0	24	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
11	c3h9mA_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: p-aminobenzoate synthetase, component i; PDBTitle: crystal structure of para-aminobenzoate synthetase, component i from2 cytophaga hutchinsonii

12	c3os6A_	Alignment		100.0	24	PDB header: isomerase Chain: A: PDB Molecule: isochorismate synthase dhbc; PDBTitle: crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
13	c3r74B_	Alignment		100.0	22	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
14	c3hwoB_	Alignment		100.0	20	PDB header: isomerase Chain: B: PDB Molecule: isochorismate synthase entc; PDBTitle: crystal structure of escherichia coli enterobactin-specific2 isochorismate synthase entc in complex with isochorismate
15	d3bzna1	Alignment		100.0	23	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
16	c3gseA_	Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: menaquinone-specific isochorismate synthase; PDBTitle: crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
17	c3nqkA_	Alignment		26.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a structural genomics, unknown function2 (bacova_03322) from bacteroides ovatus at 2.61 a resolution
18	d1cvra1	Alignment		24.0	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Gingipain R (RgpB), C-terminal domain
19	d1rp3b_	Alignment		19.3	30	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Anti-sigma factor FlgM Family: Anti-sigma factor FlgM
20	c4k6nA_	Alignment		19.1	8	PDB header: lyase Chain: A: PDB Molecule: aminodeoxychorismate lyase; PDBTitle: crystal structure of yeast 4-amino-4-deoxychorismate lyase
21	c5jnoB_	Alignment	not modelled	16.1	24	PDB header: cell cycle Chain: B: PDB Molecule: dna excision repair protein ercc-6-like; PDBTitle: crystal structure of the bd1-ntrp complex from bend3 and pich
22	c2km1A_	Alignment	not modelled	14.0	22	PDB header: protein binding Chain: A: PDB Molecule: protein dre2; PDBTitle: solution structure of the n-terminal domain of the yeast protein dre2
23	c3vf0A_	Alignment	not modelled	13.2	17	PDB header: cell adhesion/protein binding Chain: A: PDB Molecule: vinculin; PDBTitle: raver1 in complex with metavinculin I954 deletion mutant
24	d1hxra_	Alignment	not modelled	12.6	22	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
25	d2fu5a1	Alignment	not modelled	12.0	22	Fold: Mss4-like Superfamily: Mss4-like Family: RabGEF Mss4
26	d1qkra_	Alignment	not modelled	11.6	17	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
27	c4w5xA_	Alignment	not modelled	11.2	18	PDB header: viral protein Chain: A: PDB Molecule: late protein h7; PDBTitle: the structure of vaccinia virus h7 protein displays a novel2 phosphoinositide binding fold required for membrane biogenesis
28	c4aq2l_	Alignment	not modelled	10.0	27	PDB header: oxidoreductase Chain: I: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: resting state of homogentisate 1,2-dioxygenase
						PDB header: hydrolase

29	c4oltA	Alignment	not modelled	9.4	36	Chain: A: PDB Molecule: chitosanase; PDBTitle: chitosanase complex structure
30	c2hlwA	Alignment	not modelled	8.9	17	PDB header: ligase, signaling protein Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 variant 1; PDBTitle: solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
31	d1xe7a	Alignment	not modelled	8.7	41	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
32	c5f5tD	Alignment	not modelled	8.2	62	PDB header: splicing Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum
33	d2obpa1	Alignment	not modelled	8.2	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
34	c2xt6B	Alignment	not modelled	8.1	29	PDB header: lyase Chain: B: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
35	c1wazA	Alignment	not modelled	7.9	57	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
36	c5foiB	Alignment	not modelled	7.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: mycinamicin viii c21 methyl hydroxylase; PDBTitle: crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii
37	c1wqkA	Alignment	not modelled	7.8	38	PDB header: toxin Chain: A: PDB Molecule: toxin apetx1; PDBTitle: solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
38	c2edgA	Alignment	not modelled	7.7	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
39	d2ffca1	Alignment	not modelled	7.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
40	c3dzaB	Alignment	not modelled	7.3	32	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized putative membrane protein; PDBTitle: crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
41	d1d5ta2	Alignment	not modelled	7.1	21	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
42	c2lt2A	Alignment	not modelled	6.4	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
43	c4nm0B	Alignment	not modelled	6.4	30	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of peptide inhibitor-free gsk-3/axin complex
44	c3c66B	Alignment	not modelled	6.3	30	PDB header: transferase Chain: B: PDB Molecule: poly(a) polymerase; PDBTitle: yeast poly(a) polymerase in complex with fip1 residues 80-105
45	c3oaiB	Alignment	not modelled	6.2	10	PDB header: membrane protein, cell adhesion Chain: B: PDB Molecule: maltose-binding periplasmic protein, myelin protein p0; PDBTitle: crystal structure of the extra-cellular domain of human myelin protein2 zero
46	c4nm7B	Alignment	not modelled	6.1	35	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated wnt2 receptor lrp6 e-motif
47	c4nm3B	Alignment	not modelled	6.1	35	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated n-2 terminal auto-inhibitory ps9 peptide
48	c4nu1B	Alignment	not modelled	6.1	35	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of a transition state mimic of the gsk-3/axin2 complex bound to phosphorylated n-terminal auto-inhibitory ps93 peptide
49	c4nm5B	Alignment	not modelled	6.1	35	PDB header: transferase/peptide Chain: B: PDB Molecule: axin-1; PDBTitle: crystal structure of gsk-3/axin complex bound to phosphorylated wnt2 receptor lrp6 c-motif
50	d1eyba	Alignment	not modelled	6.0	28	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Homogentisate dioxygenase
51	c1ey2A	Alignment	not modelled	6.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
52	c4anrA	Alignment	not modelled	5.6	19	PDB header: lyase Chain: A: PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
53	d1zofa1	Alignment	not modelled	5.6	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like

54	d1ofcx1	Alignment	not modelled	5.6	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
55	c6a2uA	Alignment	not modelled	5.5	24	PDB header: signaling protein/oxidoreductase Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
56	c6bkbE	Alignment	not modelled	5.3	25	PDB header: immune system Chain: E: PDB Molecule: polyprotein; PDBTitle: structure of hepatitis c virus envelope glycoprotein e2 core from2 genotype 6a bound to broadly neutralizing antibody ar3a
57	c5n81B	Alignment	not modelled	5.3	16	PDB header: ligase Chain: B: PDB Molecule: tyrocidine synthase 1; PDBTitle: crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
58	c5h1nB	Alignment	not modelled	5.3	11	PDB header: unknown function Chain: B: PDB Molecule: upf0253 protein yaep; PDBTitle: crystal structure of sf173 from shigella flexneri
59	d1ji8a	Alignment	not modelled	5.3	20	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
60	c2h3oA	Alignment	not modelled	5.3	57	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
61	c6mejC	Alignment	not modelled	5.2	27	PDB header: immune system Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: broadly neutralizing antibodies against hcv use a cdrh3 disulfide2 motif to recognize an e2 glycoprotein site that can be targeted for3 vaccine design
62	c6cg8A	Alignment	not modelled	5.2	25	PDB header: dna binding protein/dna Chain: A: PDB Molecule: upf0335 protein b7z12_12435; PDBTitle: structure of c. crescentus gapr-dna
63	d2v4jc1	Alignment	not modelled	5.1	18	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
64	c6od1B	Alignment	not modelled	5.1	16	PDB header: signaling protein Chain: B: PDB Molecule: anti-adapter protein irad; PDBTitle: irad-bound to rsb d58p variant