

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3224A (-) _3600632_3600820
Date	Thu Aug 8 16:20:42 BST 2019
Unique Job ID	6b2e59428d7b145a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3memA_	Alignment		37.6	23	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein; PDBTitle: crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
2	d1dcea2	Alignment		25.7	41	Fold: C2 domain-like Superfamily: Rab geranylgeranyltransferase alpha-subunit, insert domain Family: Rab geranylgeranyltransferase alpha-subunit, insert domain
3	c5ivaB_	Alignment		23.3	15	PDB header: transport protein Chain: B: PDB Molecule: lps-assembly lipoprotein lpte; PDBTitle: the lps transporter lptde from pseudomonas aeruginosa, core complex
4	c2d46A_	Alignment		20.9	100	PDB header: metal transport Chain: A: PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
5	c3okrC_	Alignment		15.5	42	PDB header: transferase Chain: C: PDB Molecule: 2-c-methyl-d-erythritol 4-phosphate cytidyltransferase; PDBTitle: structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
6	c3cxbA_	Alignment		13.3	57	PDB header: signaling protein Chain: A: PDB Molecule: protein sifa; PDBTitle: crystal structure of sifa and skip
7	d1vkia_	Alignment		11.6	22	Fold: YbaK/ProRS associated domain Superfamily: YbaK/ProRS associated domain Family: YbaK/ProRS associated domain
8	c4lm6A_	Alignment		9.2	42	PDB header: photosynthesis Chain: A: PDB Molecule: cryptophyte phycocyanin alpha chain; PDBTitle: light harvesting complex pc612 from the cryptophyte hemiselmis2 virescens m1635
9	c3ng3A_	Alignment		7.7	50	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
10	c6hm3B_	Alignment		7.5	54	PDB header: cell cycle Chain: B: PDB Molecule: dna replication regulator sld3; PDBTitle: crystal structure of rad4 brct1,2 in complex with a sld32 phosphopeptide
11	c5dbul_	Alignment		7.4	43	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis

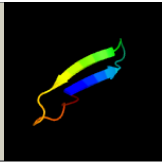
12	c3ngjC_	Alignment		7.0	57	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from <i>Entamoeba histolytica</i>
13	c4xbsA_	Alignment		6.6	43	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
14	c1yk0E_	Alignment		6.5	86	PDB header: hormone/growth factor receptor Chain: E: PDB Molecule: atrial natriuretic factor; PDBTitle: structure of natriuretic peptide receptor-c complexed with atrial2 natriuretic peptide
15	d1o0ya_	Alignment		6.0	43	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
16	d1mzha_	Alignment		5.9	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
17	c1t34H_	Alignment		5.7	86	PDB header: signaling protein,membrane protein Chain: H: PDB Molecule: atrial natriuretic peptide factor; PDBTitle: rotation mechanism for transmembrane signaling by the atrial2 natriuretic peptide receptor
18	d2glza1	Alignment		5.6	25	Fold: FwdE/GAPDH domain-like Superfamily: FwdE-like Family: FwdE-like
19	c4evuB_	Alignment		5.2	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative periplasmic protein ydgh; PDBTitle: crystal structure of c-terminal domain of putative periplasmic protein2 ydgh from <i>S. enterica</i>

20

[c2cx5B](#)



Alignment



5.2

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PDB header:translation

Chain: B: **PDB Molecule:**a putative trans-editing enzyme;

PDB Title: crystal structure of a putative trans-editing enzyme for2
prolyl trna synthetase