


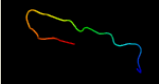



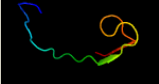





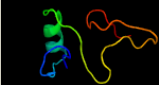



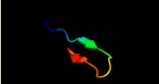






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1351_(-)_1518237_1518566
Date	Wed Jul 31 22:05:45 BST 2019
Unique Job ID	f81493cd761d5d01

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q32a2	 Alignment		22.6	26	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
2	c3lhnB_	 Alignment		11.0	50	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein; PDBTitle: crystal structure of putative lipoprotein (np_718719.1) from <i>Shewanella oneidensis</i> at 1.42 Å resolution
3	c2elnA_	 Alignment		9.6	45	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 11th c2h2 zinc finger of human 2 zinc finger protein 406
4	c3sq3C_	 Alignment		7.9	26	PDB header: hydrolase Chain: C: PDB Molecule: tyrosyl-dna phosphodiesterase 1; PDBTitle: crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
5	c4cmqB_	 Alignment		7.5	27	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound <i>S. pyogenes</i> cas9
6	c2mf8A_	 Alignment		7.1	50	PDB header: metal binding protein/dna Chain: A: PDB Molecule: myelin transcription factor 1; PDBTitle: haddock model of myt1 f4f5 - dna complex
7	c5wvpA_	 Alignment		6.9	27	PDB header: hydrolase Chain: A: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
8	c5vobC_	 Alignment		6.6	36	PDB header: viral protein/immune system Chain: C: PDB Molecule: envelope glycoprotein ul128; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 8i21
9	c5cffE_	 Alignment		6.1	40	PDB header: transcription/rna binding protein Chain: E: PDB Molecule: staufen; PDBTitle: crystal structure of miranda/staufen dsrbd5 complex
10	d1ebfa2	 Alignment		6.0	30	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
11	c2y8sE_	 Alignment		5.8	50	PDB header: membrane protein Chain: E: PDB Molecule: rhoptry neck protein 2; PDBTitle: co-structure of an ama1 mutant (y230a) with a surface exposed region2 of ron2 from <i>Toxoplasma gondii</i>

12	c2z4hB_	Alignment		5.7	35	PDB header: signaling protein activator Chain: B: PDB Molecule: copper homeostasis protein cutf; PDBTitle: crystal structure of the cpx pathway activator nlpe from2 escherichia coli
13	c4i21C_	Alignment		5.7	67	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: erbB receptor feedback inhibitor 1; PDBTitle: crystal structure of l858r + t790m egfr kinase domain in complex with2 mig6 peptide
14	c2y8tB_	Alignment		5.7	50	PDB header: membrane protein Chain: B: PDB Molecule: rhoptry neck protein 2; PDBTitle: co-structure of ama1 with a surface exposed region of ron2 from2 toxoplasma gondii
15	c3do5A_	Alignment		5.5	35	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
16	c4fvvA_	Alignment		5.5	37	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the n-terminal domain of the lon-like protease2 mtalonc
17	d1bndb_	Alignment		5.5	50	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin

18 [d2d8xa2](#)

Alignment



5.2

83

Fold:Glucocorticoid receptor-like (DNA-binding domain)
Superfamily:Glucocorticoid receptor-like (DNA-binding domain)
Family:LIM domain