


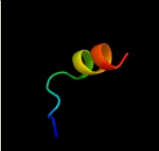

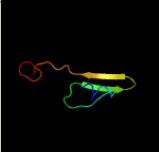

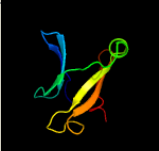

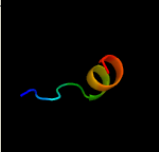

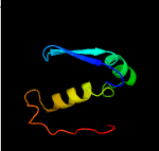

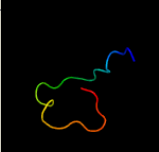







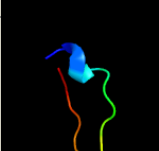








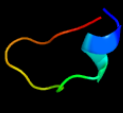


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3032A_(RVBD3032A)_3392823_3393212
 Date Thu Aug 8 16:20:20 BST 2019
 Unique Job ID f7ff7d68c0c697b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wj9a2	 Alignment		24.1	38	Fold: Ferredoxin-like Superfamily: CRISPR-associated protein Family: CRISPR-associated protein
2	c4dzdA_	 Alignment		15.3	20	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygch; PDBTitle: crystal structure of the crispr-associated protein cas6e from2 escherichia coli str. k-12
3	c4ld7N_	 Alignment		13.3	22	PDB header: transferase Chain: N: PDB Molecule: dimethylallyl tryptophan synthase; PDBTitle: crystal structure of anapt from neosartorya fischeri
4	c4whiA_	 Alignment		12.5	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of c-terminal domain of penicillin binding protein2 rv0907
5	c3qrgA_	 Alignment		12.4	43	PDB header: rna binding protein/rna Chain: A: PDB Molecule: putative uncharacterized protein tthb192; PDBTitle: structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
6	c1dl5A_	 Alignment		10.7	36	PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase
7	d1bhua_	 Alignment		8.6	42	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Streptomyces metalloproteinase inhibitor, SMPI
8	c1wj9A_	 Alignment		8.4	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of a crispr-associated protein from2 thermus thermophilus
9	c4y7IB_	 Alignment		8.3	21	PDB header: membrane protein Chain: B: PDB Molecule: type vi secretion protein icmf; PDBTitle: t6ss protein tssm c-terminal domain (869-1107) from eaec
10	c3oe3B_	 Alignment		8.2	23	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of plic-st, periplasmic lysozyme inhibitor of c-type2 lysozyme from salmonella typhimurium
11	c3tbdA_	 Alignment		7.7	24	PDB header: cell adhesion Chain: A: PDB Molecule: netrin-g2; PDBTitle: crystal structure of domain vi and le1 of human netrin-g2

12	d1hlca_	Alignment		7.6	9	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
13	c2bkdN_	Alignment		7.3	34	PDB header: nuclear protein Chain: N: PDB Molecule: fragile x mental retardation 1 protein; PDBTitle: structure of the n-terminal domain of fragile x mental retardation2 protein
14	c5u0aA_	Alignment		7.3	13	PDB header: immune system Chain: A: PDB Molecule: crispr-associated protein, cse3 family; PDBTitle: crispr rna-guided surveillance complex
15	d2csba2	Alignment		6.7	44	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
16	c4agtA_	Alignment		6.7	18	PDB header: cell adhesion Chain: A: PDB Molecule: laminin subunit gamma-1; PDBTitle: laminin gamma1 ln-le1-2 structure
17	c6ixhQ_	Alignment		6.7	14	PDB header: membrane protein Chain: Q: PDB Molecule: type vi secretion system tssm; PDBTitle: type vi secretion system membrane core complex
18	c3zyiB_	Alignment		6.7	24	PDB header: cell adhesion Chain: B: PDB Molecule: netrin-g2; PDBTitle: netring2 in complex with ngl2
19	d1w6na_	Alignment		6.5	11	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
20	c4wnxA_	Alignment		6.4	35	PDB header: laminin binding protein Chain: A: PDB Molecule: netrin-4; PDBTitle: netrin 4 lacking the c-terminal domain
21	d1qmja_	Alignment	not modelled	6.4	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
22	c3duiB_	Alignment	not modelled	6.1	21	PDB header: sugar binding protein Chain: B: PDB Molecule: beta-galactoside-binding lectin; PDBTitle: crystal structure of the oxidized cg-1b: an adhesion/growth-2 regulatory lectin from chicken
23	d1a78a_	Alignment	not modelled	5.8	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
24	c2o61A_	Alignment	not modelled	5.4	10	PDB header: transcription/dna Chain: A: PDB Molecule: transcription factor p65/interferon regulatory factor PDBTitle: crystal structure of nfkb, irf7, irf3 bound to the interferon-b2 enhancer
25	c4brwB_	Alignment	not modelled	5.4	56	PDB header: hydrolase Chain: B: PDB Molecule: dna topoisomerase 2-associated protein pat1; PDBTitle: crystal structure of the yeast dhh1-pat1 complex
26	c4e0uB_	Alignment	not modelled	5.4	40	PDB header: transferase Chain: B: PDB Molecule: cyclic dipeptide n-prenyltransferase; PDBTitle: crystal structure of cdpnpt in complex with thiolodiphosphate and (s)-2 benzodiazependione
27	c3i31A_	Alignment	not modelled	5.1	50	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: hera helicase rna binding domain is an rrm fold
28	c2yxsA_	Alignment	not modelled	5.0	13	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin-8 variant; PDBTitle: crystal structure of n-terminal domain of human galectin-8 with d-2 lactose