
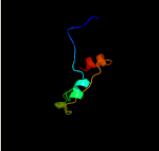
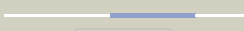
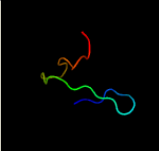



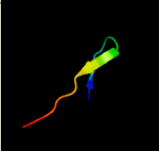

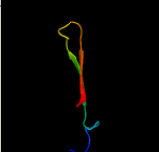

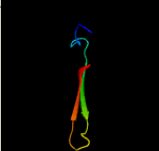

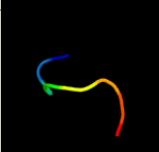

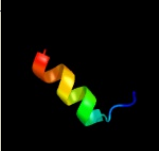

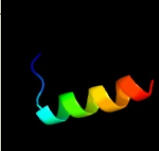




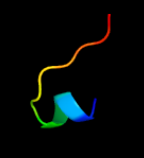

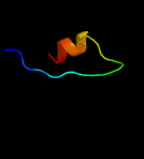

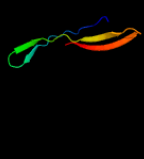





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1211_(-)_1354249_1354476
Date	Wed Jul 31 22:05:30 BST 2019
Unique Job ID	48c2bef2c97cf346

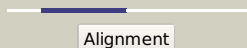
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xwna1	 Alignment		38.6	25	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: Cyclophilin (peptidylprolyl isomerase)
2	c2y9xG_	 Alignment		23.9	39	PDB header: oxidoreductase Chain: G: PDB Molecule: lectin-like fold protein; PDBTitle: crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
3	d2w0pa1	 Alignment		19.3	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
4	c2c4rL_	 Alignment		14.3	40	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e
5	d1dwka2	 Alignment		11.2	32	Fold: Cyanase C-terminal domain Superfamily: Cyanase C-terminal domain Family: Cyanase C-terminal domain
6	c2iv1J_	 Alignment		9.8	32	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
7	c5y88S_	 Alignment		9.3	75	PDB header: splicing Chain: S: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
8	c3obhA_	 Alignment		8.2	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
9	c2l3aA_	 Alignment		7.8	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
10	c2jorA_	 Alignment		6.5	67	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha chain; PDBTitle: nmr solution structure, stability, and interaction of the2 recombinant bovine fibrinogen alphac-domain fragment
11	c5t5iL_	 Alignment		6.1	23	PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwd; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a

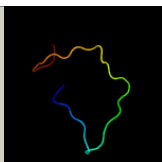
12	d1xdpa4	Alignment		6.0	31	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
13	c2kkeA_	Alignment		5.7	48	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
14	d1bvua2	Alignment		5.6	38	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
15	c4kqzA_	Alignment		5.6	89	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: structure of the receptor binding domain (rbd) of mers-cov spike
16	c2otbB_	Alignment		5.5	37	PDB header: fluorescent protein Chain: B: PDB Molecule: gfp-like fluorescent chromoprotein cfp484; PDBTitle: crystal structure of a monomeric cyan fluorescent protein in the2 fluorescent state
17	d1gtma2	Alignment		5.5	40	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
18	d1kqfa1	Alignment		5.4	46	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
19	c2kkeB_	Alignment		5.2	48	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5

20

[c2qdrA_](#)



Alignment



5.1

29

PDB header: unknown function
Chain: A: **PDB Molecule:** uncharacterized protein;
PDB Title: crystal structure of a putative dioxygenase (npun_f5605)
from nostoc2 punctiforme pcc 73102 at 2.60 a resolution