
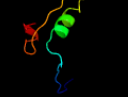


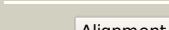

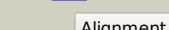




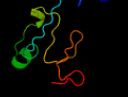


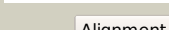

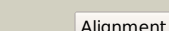
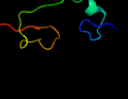

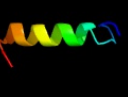

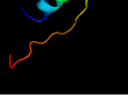

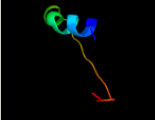

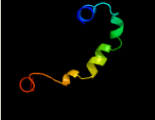


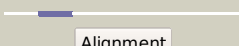

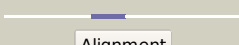

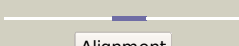

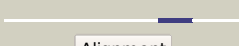
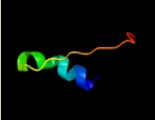

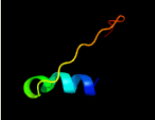


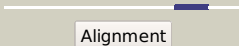
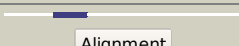


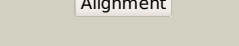


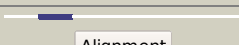


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3885c_(-)_4367086_4368699
Date	Sat Aug 10 22:05:07 BST 2019
Unique Job ID	2d2461fe5298c997

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fdfA_	 Alignment		65.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fr253; PDBTitle: crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
2	c3o2qB_	 Alignment		62.0	22	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
3	c3o2sB_	 Alignment		49.6	22	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72 complex
4	c2jsnA_	 Alignment		16.9	28	PDB header: protein transport Chain: A: PDB Molecule: trafficking protein particle complex subunit 4; PDBTitle: solution structure of the atypical pdz-like domain of2 synbindin
5	d1kjqA2	 Alignment		14.1	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
6	c2pe4A_	 Alignment		13.4	20	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
7	d1em8a_	 Alignment		13.2	10	Fold: DNA polymerase III chi subunit Superfamily: DNA polymerase III chi subunit Family: DNA polymerase III chi subunit
8	d2psba1	 Alignment		13.0	29	Fold: YerB-like Superfamily: YerB-like Family: YerB-like
9	c2psbA_	 Alignment		13.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yerb protein; PDBTitle: crystal structure of yerb protein from bacillus subtilis. northeast2 structural genomics target sr586
10	c6hwhX_	 Alignment		13.0	18	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
11	c3i0aA_	 Alignment		12.3	19	PDB header: transferase Chain: A: PDB Molecule: spectinomycin phosphotransferase; PDBTitle: crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomycin

12	c2iusB_			12.0	15	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
13	c3vxgA_			12.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: conjugated polyketone reductase c2; PDBTitle: crystal structure of conjugated polyketone reductase c2 from candida2 parapsilosis
14	c4pcvB_			11.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: bdca (yjgi); PDBTitle: the structure of bdca (yjgi) from e. coli
15	c2m0nA_			11.0	55	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
16	c4nimA_			10.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: versicolorin reductase; PDBTitle: crystal structure of a short chain dehydrogenase from brucella2 melitensis
17	d1pkha_			10.5	18	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
18	c2iuuE_			9.6	19	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
19	c2iutA_			9.6	19	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
20	c6jczL_			9.2	13	PDB header: isomerase Chain: L: PDB Molecule: putative ketol-acid reductoisomerase 2; PDBTitle: cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
21	c4kmhB_		not modelled	9.1	29	PDB header: protein binding Chain: B: PDB Molecule: suppressor of fused homolog; PDBTitle: crystal structure of suppressor of fused d20
22	c5tcsB_		not modelled	9.0	22	PDB header: replication Chain: B: PDB Molecule: kinetochore protein nuf2; PDBTitle: crystal structure of a dwarf ndc80 tetramer
23	d1bdba_		not modelled	8.8	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
24	c2wokA_		not modelled	8.6	10	PDB header: peptide binding protein/peptide Chain: A: PDB Molecule: clavulanic acid biosynthesis oligopeptide binding protein PDBTitle: clavulanic acid biosynthesis oligopeptide binding protein 2 complexed2 with bradykinin
25	c4qb0A_		not modelled	8.1	50	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: the crystal structure of the c-terminal domain of ebola (zaire)2 nucleoprotein
26	c5lnkq_		not modelled	7.5	31	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
27	c1oeiA_		not modelled	7.3	50	PDB header: prion protein Chain: A: PDB Molecule: major prion protein; PDBTitle: human prion protein 61-84
28	c2lkyA_		not modelled	7.2	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target

						mysma.17112.b
29	c2jz7A_	Alignment	not modelled	7.2	23	PDB header: selenium-binding protein Chain: A: PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vannielii
30	c2ki8A_	Alignment	not modelled	7.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
31	c5icqA_	Alignment	not modelled	7.0	13	PDB header: periplasmic binding protein Chain: A: PDB Molecule: methylocystis parvus obbp mbne; PDBTitle: methanobactin periplasmic binding protein
32	c6epzA_	Alignment	not modelled	6.8	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic alpha-galactoside-binding protein; PDBTitle: structure of the periplasmic binding protein melb (atu4661) in complex2 with melibiose from agrobacterium fabrum c58
33	d1m1la_	Alignment	not modelled	6.7	31	Fold: Suppressor of Fused, N-terminal domain Superfamily: Suppressor of Fused, N-terminal domain Family: Suppressor of Fused, N-terminal domain
34	c2m6oA_	Alignment	not modelled	5.8	30	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
35	c2k42B_	Alignment	not modelled	5.8	43	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
36	c3ftoA_	Alignment	not modelled	5.7	8	PDB header: peptide binding protein Chain: A: PDB Molecule: oligopeptide-binding protein oppa; PDBTitle: crystal structure of oppa in a open conformation
37	c1loiA_	Alignment	not modelled	5.6	57	PDB header: hydrolase Chain: A: PDB Molecule: cyclic 3',5'-amp specific phosphodiesterase rd1; PDBTitle: n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
38	d1uaxa_	Alignment	not modelled	5.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
39	d3ct6a1	Alignment	not modelled	5.4	14	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
40	c2kvcA_	Alignment	not modelled	5.3	45	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a