
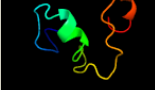






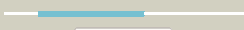


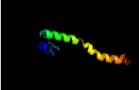



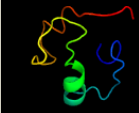



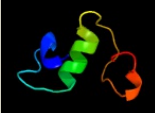



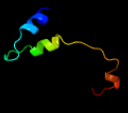





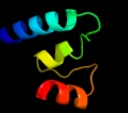
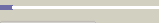



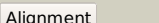

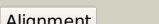

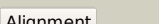

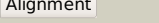

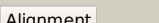
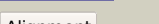
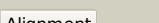
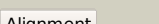

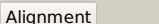



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3386_(-)_3800272_3800976
Date	Fri Aug 9 18:20:05 BST 2019
Unique Job ID	689b6065b7b22e7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1slma1	 Alignment		62.5	19	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
2	c1bg1A_	 Alignment		44.7	17	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
3	c3hefB_	 Alignment		44.2	15	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
4	c5wtnB_	 Alignment		42.6	19	PDB header: replication Chain: B: PDB Molecule: replication initiation and membrane attachment protein; PDBTitle: crystal structure analysis of primosome protein dnab (residues 1-300)2 from geobacillus stearothermophilus
5	c1yvlB_	 Alignment		36.5	13	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
6	c6raol_	 Alignment		35.3	13	PDB header: virus like particle Chain: I: PDB Molecule: afp11; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
7	d1bg1a2	 Alignment		27.8	18	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: STAT DNA-binding domain
8	d1leak1	 Alignment		25.5	21	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
9	c1bf5A_	 Alignment		24.7	18	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
10	d1su3a1	 Alignment		24.4	22	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
11	c6g4ww_	 Alignment		20.3	22	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a

12	c3nzbB	 Alignment		19.6	12	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
13	c1eakA	 Alignment		16.6	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 72 kda type iv collagenase; PDBTitle: catalytic domain of prommp-2 e404q mutant
14	c3iwfA	 Alignment		16.1	7	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
15	c2p06A	 Alignment		15.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
16	d2p06a1	 Alignment		15.9	18	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like
17	c3n2oA	 Alignment		15.9	16	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
18	c1slmA	 Alignment		15.0	14	PDB header: hydrolase Chain: A: PDB Molecule: stromelysin-1; PDBTitle: crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
19	c4fmoB	 Alignment		12.7	45	PDB header: hydrolase Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1
20	c3d3kD	 Alignment		12.5	24	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
21	d1q44a	 Alignment	not modelled	12.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAP5 sulfotransferase
22	d2v9va2	 Alignment	not modelled	11.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
23	d6paxa1	 Alignment	not modelled	11.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
24	d2d1ha1	 Alignment	not modelled	11.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
25	c4ql3A	 Alignment	not modelled	10.6	24	PDB header: hydrolase Chain: A: PDB Molecule: putative glucoamylase; PDBTitle: crystal structure of a putative glucoamylase (bacuni_03963) from2 bacteroides uniformis atcc 8492 at 2.01 a resolution
26	c6jnyA	 Alignment	not modelled	10.5	0	PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein
27	d2i52a1	 Alignment	not modelled	10.2	7	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
28	c2v7iA	 Alignment	not modelled	10.2	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: prnb; PDBTitle: prnb native
29	c3chwb	 Alignment	not modelled	9.9	5	PDB header: protein binding Chain: B: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide;

29	c30nwb	Alignment	not modelled	9.9	9	PDBTitle: x-ray structure of phycobilisome lcm core-membrane linker polypeptide 2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e
30	c3pruD	Alignment	not modelled	9.9	0	PDB header: photosynthesis Chain: D: PDB Molecule: phycobilisome 32.1 kda linker polypeptide, phycocyanin- PDBTitle: crystal structure of phycobilisome 32.1 kda linker polypeptide,2 phycocyanin-associated, rod 1 (fragment 14-158) from synechocystis3 sp. pcc 6803, northeast structural genomics consortium target sgr182a
31	d1s4ka	Alignment	not modelled	9.9	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
32	c3gabC	Alignment	not modelled	9.6	64	PDB header: hydrolase Chain: C: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: c-terminal domain of bacillus subtilis mutl crystal form i
33	c2kq5A	Alignment	not modelled	9.3	11	PDB header: unknown function Chain: A: PDB Molecule: avirulence protein; PDBTitle: solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
34	d1my6a2	Alignment	not modelled	9.3	8	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
35	c2ogfD	Alignment	not modelled	9.2	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
36	d1qaza	Alignment	not modelled	9.0	21	Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Alginate lyase A1-III
37	c3rnbB	Alignment	not modelled	8.8	21	PDB header: protein binding Chain: B: PDB Molecule: dna mismatch repair protein mlh1; PDBTitle: crystal structure of mutl protein homolog 1 isoform 1 [homo sapiens]
38	c2l06A	Alignment	not modelled	8.7	12	PDB header: protein binding Chain: A: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
39	c4xviA	Alignment	not modelled	8.5	13	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase nu; PDBTitle: binary complex of human polymerase nu and dna with the finger domain2 ajar
40	c2ky4A	Alignment	not modelled	8.5	10	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
41	c3dxeB	Alignment	not modelled	8.3	22	PDB header: protein binding Chain: B: PDB Molecule: amyloid beta a4 protein; PDBTitle: crystal structure of the intracellular domain of human app (t668a2 mutant) in complex with fe65-ptb2
42	c3ncvB	Alignment	not modelled	7.6	27	PDB header: hydrolase Chain: B: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: ngol
43	c3d3jA	Alignment	not modelled	7.5	24	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
44	d1prtd	Alignment	not modelled	7.5	43	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
45	c3b21A	Alignment	not modelled	7.3	27	PDB header: unknown function Chain: A: PDB Molecule: orf169b; PDBTitle: crystal structure of ospi from shigella flexineri
46	c4z38B	Alignment	not modelled	7.1	10	PDB header: transferase Chain: B: PDB Molecule: mlna; PDBTitle: crystal structure of enoyl reductase domain of mlna from the2 macrolactin biosynthesis cluster from bacillus amyloliquefaciens
47	c2qsrA	Alignment	not modelled	6.8	14	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
48	c5b42A	Alignment	not modelled	6.6	45	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
49	c5hubA	Alignment	not modelled	6.6	11	PDB header: isomerase Chain: A: PDB Molecule: chorismate mutase; PDBTitle: high-resolution structure of chorismate mutase from corynebacterium2 glutamicum
50	c2v9vA	Alignment	not modelled	6.5	28	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
51	d3e11a1	Alignment	not modelled	6.4	12	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
52	c2kebA	Alignment	not modelled	6.2	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
53	c4e2i3	Alignment	not modelled	6.2	19	PDB header: hydrolase/dna binding protein Chain: 3: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase

54	c2zw3B_	Alignment	not modelled	5.9	16	PDB header: cell adhesion Chain: B: PDB Molecule: gap junction beta-2 protein; PDBTitle: structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
55	d1puza_	Alignment	not modelled	5.8	13	Fold: YgfY-like Superfamily: YgfY-like Family: YgfY-like
56	c2ahqA_	Alignment	not modelled	5.7	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
57	c2y1hA_	Alignment	not modelled	5.6	12	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
58	c1xvlC_	Alignment	not modelled	5.6	5	PDB header: metal transport Chain: C: PDB Molecule: mn transporter; PDBTitle: the three-dimensional structure of mntc from synechocystis2 6803
59	c3cwgA_	Alignment	not modelled	5.6	20	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
60	d1unfx2_	Alignment	not modelled	5.5	16	Fold: Fe,Mn superoxide dismutase (SOD), C-terminal domain Superfamily: Fe,Mn superoxide dismutase (SOD), C-terminal domain Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
61	c3o0rC_	Alignment	not modelled	5.5	10	PDB header: immune system/oxidoreductase Chain: C: PDB Molecule: nitric oxide reductase subunit c; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
62	c2o8xA_	Alignment	not modelled	5.4	10	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
63	d1bwvs_	Alignment	not modelled	5.4	12	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
64	d1l6ja1_	Alignment	not modelled	5.4	16	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
65	c3nzpA_	Alignment	not modelled	5.3	24	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
66	c5z06A_	Alignment	not modelled	5.2	17	PDB header: hydrolase Chain: A: PDB Molecule: bdi_3064 protein; PDBTitle: crystal structure of beta-1,2-glucanase from parabacteroides2 distasonis
67	d1q8ha_	Alignment	not modelled	5.2	25	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
68	c1q8hA_	Alignment	not modelled	5.2	25	PDB header: metal binding protein Chain: A: PDB Molecule: osteocalcin; PDBTitle: crystal structure of porcine osteocalcin
69	c4ct4C_	Alignment	not modelled	5.1	8	PDB header: rna binding protein Chain: C: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: cnot1 mif4g domain - ddx6 complex
70	d1c06a_	Alignment	not modelled	5.1	12	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
71	c5ujcA_	Alignment	not modelled	5.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: mmachc-like protein; PDBTitle: crystal structure of a c.elegans b12-trafficking protein cbic, a human2 mmachc homologue