
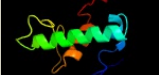
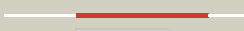


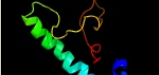



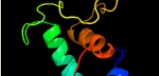



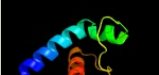



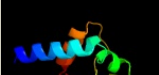










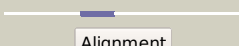

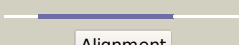

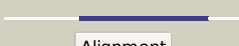

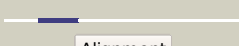
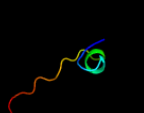







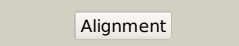


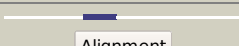



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1390_(rpoZ)_1565099_1565431
 Date Wed Jul 31 22:05:49 BST 2019
 Unique Job ID 0d8cfe86e8246b59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5tw1E_	 Alignment		100.0	96	PDB header: transcription activator/transferase/dna Chain: E; PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
2	c6asxK_	 Alignment		99.9	29	PDB header: transcription/dna/rna Chain: K; PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: cryoem structure of e.coli his pause elongation complex
3	c3iydE_	 Alignment		99.8	28	PDB header: transcription/dna Chain: E; PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
4	c6j9eE_	 Alignment		99.8	41	PDB header: transcription Chain: E; PDB Molecule: dna-directed rna polymerase subunit omega; PDBTitle: cryo-em structure of xanthomonas oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
5	d1ynjk1	 Alignment		98.7	30	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RNA polymerase omega subunit
6	d1smye_	 Alignment		98.7	33	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RNA polymerase omega subunit
7	d1twff_	 Alignment		96.9	27	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
8	c1twcF_	 Alignment		96.9	27	PDB header: transcription Chain: F; PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
9	c4qiwT_	 Alignment		96.9	22	PDB header: transcription Chain: T; PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
10	d1qkla_	 Alignment		96.8	31	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
11	c3h0qF_	 Alignment		96.7	29	PDB header: transcription Chain: F; PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc2; PDBTitle: rna polymerase ii from schizosaccharomyces pombe

12	c2pmzW_		Alignment		96.3	24	PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
13	c2kxhB_		Alignment		14.6	60	PDB header: protein binding Chain: B: PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
14	c6d6rL_		Alignment		14.4	23	PDB header: hydrolase Chain: L: PDB Molecule: m-phase phosphoprotein 6; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
15	c6d6qL_		Alignment		14.4	23	PDB header: hydrolase Chain: L: PDB Molecule: m-phase phosphoprotein 6; PDBTitle: human nuclear exosome-mtr4 rna complex - overall reconstruction
16	c6c05F_		Alignment		10.1	15	PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
17	d1gzsb_		Alignment		9.3	24	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
18	c1tjID_		Alignment		9.2	24	PDB header: transcription Chain: D: PDB Molecule: dnak suppressor protein; PDBTitle: crystal structure of transcription factor dkxa from e. coli
19	c6hlwB_		Alignment		8.7	42	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
20	c3m1rF_		Alignment		8.6	20	PDB header: hydrolase Chain: F: PDB Molecule: formimidoylglutamase; PDBTitle: the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
21	c4g3hC_		Alignment	not modelled	8.5	22	PDB header: hydrolase Chain: C: PDB Molecule: arginase (rocf); PDBTitle: crystal structure of helicobacter pylori arginase
22	d2jdid1		Alignment	not modelled	8.2	33	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
23	c3lhIA_		Alignment	not modelled	8.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile
24	c4x8kA_		Alignment	not modelled	7.3	29	PDB header: transcription activator Chain: A: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rbpa-sid in complex with sigmaa domain 2
25	c3ijeB_		Alignment	not modelled	7.0	29	PDB header: protein binding Chain: B: PDB Molecule: integrin beta-3; PDBTitle: crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
26	c6hltD_		Alignment	not modelled	6.7	42	PDB header: viral protein Chain: D: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
27	c6hmvB_		Alignment	not modelled	6.2	25	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
28	c5zeeA_		Alignment	not modelled	6.2	22	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: arginase; PDBTitle: crystal structure of entamoeba histolytica arginase in complex with2 n(omega)-hydroxy-l-arginine (noha) at 1.74 a

29	c4jicB_	Alignment	not modelled	6.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
30	c2eivH_	Alignment	not modelled	5.6	21	PDB header: hydrolase Chain: H: PDB Molecule: arginase; PDBTitle: crystal structure of the arginase from thermus thermophilus
31	c1ng7A_	Alignment	not modelled	5.4	42	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein [core protein p3a]; PDBTitle: the solution structure of the soluble domain of poliovirus2 3a protein
32	d1ng7a_	Alignment	not modelled	5.4	42	Fold: Soluble domain of poliovirus core protein 3a Superfamily: Soluble domain of poliovirus core protein 3a Family: Soluble domain of poliovirus core protein 3a
33	d1d3va_	Alignment	not modelled	5.4	19	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
34	c5uukB_	Alignment	not modelled	5.4	63	PDB header: apoptosis Chain: B: PDB Molecule: bfl-1-specific selected peptide; PDBTitle: human bfl-1 in complex with a bfl-1-specific selected peptide
35	c3pzlA_	Alignment	not modelled	5.3	29	PDB header: hydrolase Chain: A: PDB Molecule: agmatine ureohydrolase; PDBTitle: the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
36	c5uumC_	Alignment	not modelled	5.3	63	PDB header: apoptosis Chain: C: PDB Molecule: bfl-1 specific peptide fs2; PDBTitle: human mcl-1 in complex with a bfl-1-specific selected peptide
37	c5uumD_	Alignment	not modelled	5.3	63	PDB header: apoptosis Chain: D: PDB Molecule: bfl-1 specific peptide fs2; PDBTitle: human mcl-1 in complex with a bfl-1-specific selected peptide
38	c3j47P_	Alignment	not modelled	5.2	40	PDB header: protein binding Chain: P: PDB Molecule: 26s proteasome regulatory subunit rpn5; PDBTitle: formation of an intricate helical bundle dictates the assembly of the2 26s proteasome lid
39	c3mmrA_	Alignment	not modelled	5.2	19	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh