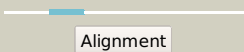
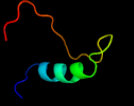
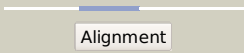



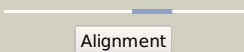

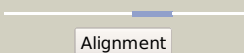

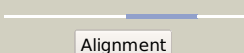



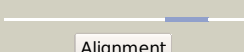
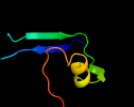
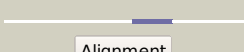

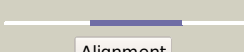

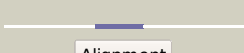



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1507c_(-)_1696733_1697428
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	938b67117cc4473d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fceB_	 Alignment		33.7	31	PDB header: cell adhesion Chain: B: PDB Molecule: lpxtg family cell surface protein fms2; PDBTitle: the crystal structure of the ligand binding region of serine-glutamate2 repeat protein a (sgra) of enterococcus faecium
2	c4ffbC_	 Alignment		29.7	8	PDB header: hydrolase Chain: C: PDB Molecule: protein stu2; PDBTitle: a tog:alpha/beta-tubulin complex structure reveals conformation-based2 mechanisms for a microtubule polymerase
3	c4j7hA_	 Alignment		28.7	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: evaa 2,3-dehydratase; PDBTitle: crystal structure of evaa, a 2,3-dehydratase in complex with dtdp-2 benzene and dtdp-rhamnose
4	c3f6wE_	 Alignment		24.4	7	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
5	c3eusB_	 Alignment		23.7	5	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
6	c1m6vE_	 Alignment		23.4	14	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
7	d1a9xa4	 Alignment		21.5	10	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
8	d2bs2b2	 Alignment		20.2	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
9	d1y7ya1	 Alignment		19.2	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
10	d1kkha2	 Alignment		18.5	14	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
11	c3p9aI_	 Alignment		18.1	13	PDB header: dna binding protein Chain: I: PDB Molecule: dna-packaging protein gp3; PDBTitle: an atomic view of the nonameric small terminase subunit of2 bacteriophage p22

12	d1lib_	Alignment		16.2	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
13	d1td6a_	Alignment		14.5	15	Fold: Hypothetical protein MPN330 Superfamily: Hypothetical protein MPN330 Family: Hypothetical protein MPN330
14	c3jb9c_	Alignment		14.4	9	PDB header: rna binding protein/rna Chain: C: PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
15	c2jvIA_	Alignment		14.4	10	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
16	d2cpwa1	Alignment		14.2	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
17	c3trbA_	Alignment		13.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii
18	c5fdkD_	Alignment		13.6	13	PDB header: hydrolase Chain: D: PDB Molecule: holliday junction resolvase recu; PDBTitle: crystal structure of recu(d88n) in complex with palindromic dna duplex
19	d1rioa_	Alignment		12.7	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
20	c3omtA_	Alignment		12.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xrc family from2 prevotella buccae.
21	c5lxIA_	Alignment	not modelled	12.5	21	PDB header: viral protein Chain: A: PDB Molecule: decoration protein; PDBTitle: nmr structure of the n-terminal domain of the bacteriophage t52 decoration protein pb10
22	c3f52A_	Alignment	not modelled	12.4	17	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
23	d1kf6b2	Alignment	not modelled	12.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
24	c2viaE_	Alignment	not modelled	11.7	16	PDB header: transferase Chain: E: PDB Molecule: rna-directed rna polymerase; PDBTitle: structure of the rna polymerase vp1 from infectious pancreatic2 necrosis virus
25	c2yibC_	Alignment	not modelled	11.5	16	PDB header: transferase Chain: C: PDB Molecule: rna-directed rna polymerase; PDBTitle: structure of the rna polymerase vp1 from infectious pancreatic2 necrosis virus
26	c2kpiA_	Alignment	not modelled	11.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
27	c2y27B_	Alignment	not modelled	11.3	15	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from burkholderia2 cenocepacia
28	c3mIfC_	Alignment	not modelled	10.6	10	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus

						aureus.
29	d1utxa_	Alignment	not modelled	10.3	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
30	c2yibD_	Alignment	not modelled	10.3	16	PDB header: transferase Chain: D: PDB Molecule: rna-directed rna polymerase; PDBTitle: structure of the rna polymerase vp1 from infectious pancreatic2 necrosis virus
31	c2ls01_	Alignment	not modelled	10.0	33	PDB header: hydrolase Chain: 1: PDB Molecule: zoozin a endopeptidase; PDB Fragment: unp residues 170-285; PDBTitle: solution structure of the target recognition domain of zoozin a
32	d1e3ha4	Alignment	not modelled	9.9	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
33	c1y6uA_	Alignment	not modelled	9.7	14	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
34	d3bexa1	Alignment	not modelled	9.7	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
35	c3ivpD_	Alignment	not modelled	9.2	10	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
36	c2ewtA_	Alignment	not modelled	9.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bidd
37	d1jqoa_	Alignment	not modelled	9.0	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
38	c1jqoA_	Alignment	not modelled	9.0	20	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
39	c1y9qA_	Alignment	not modelled	8.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
40	c3noeA_	Alignment	not modelled	8.5	30	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
41	c3bs3A_	Alignment	not modelled	8.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
42	c2cpwA_	Alignment	not modelled	8.3	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbl-interacting protein sts-1 variant; PDBTitle: solution structure of rsgi ruh-031, a uba domain from human2 cdna
43	c4wbdA_	Alignment	not modelled	8.3	13	PDB header: ligase Chain: A: PDB Molecule: bshc; PDBTitle: the crystal structure of bshc from bacillus subtilis complexed with2 citrate and adp
44	c1rznB_	Alignment	not modelled	8.3	14	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein u; PDBTitle: crystal structure of penicillin-binding protein-related2 factor a from bacillus subtilis.
45	c1k47F_	Alignment	not modelled	8.1	13	PDB header: transferase Chain: F: PDB Molecule: phosphomevalonate kinase; PDBTitle: crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
46	c3iz5t_	Alignment	not modelled	8.1	25	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
47	d1b0na2	Alignment	not modelled	8.0	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
48	c3clcC_	Alignment	not modelled	7.9	2	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
49	c3dnvB_	Alignment	not modelled	7.8	7	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
50	c6f8sA_	Alignment	not modelled	7.7	20	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
51	d1adra_	Alignment	not modelled	7.6	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c1y1oC_	Alignment	not modelled	7.6	11	PDB header: recombination Chain: C: PDB Molecule: penicillin-binding protein-related factor a; PDBTitle: x-ray crystal structure of penicillin-binding protein-2 related factor a from bacillus stearothermophilus
53	d1y1oa_	Alignment	not modelled	7.6	11	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: RecU-like
						Fold: lambda repressor-like DNA-binding domains

54	d1x57a1	Alignment	not modelled	7.5	5	Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
55	d2b5aa1	Alignment	not modelled	7.5	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
56	c3vk0B_	Alignment	not modelled	7.4	2	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
57	d1rzna_	Alignment	not modelled	7.4	14	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: RecU-like
58	c3skqA_	Alignment	not modelled	7.3	20	PDB header: metal transport Chain: A: PDB Molecule: mitochondrial distribution and morphology protein 38; PDBTitle: mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
59	d2gx8a1	Alignment	not modelled	7.1	15	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
60	c3t76A_	Alignment	not modelled	7.1	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
61	c6h56A_	Alignment	not modelled	7.0	11	PDB header: metal binding protein Chain: A: PDB Molecule: effector domain of pseudomonas aeruginosa vgrg2b; PDBTitle: effector domain of pseudomonas aeruginosa vgrg2b
62	c3op9A_	Alignment	not modelled	6.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
63	c4mcxE_	Alignment	not modelled	6.9	5	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
64	c1oheA_	Alignment	not modelled	6.8	14	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
65	c6bi7B_	Alignment	not modelled	6.8	21	PDB header: replication Chain: B: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-wt/rev3 as a monomer under high-salt2 conditions
66	d1edza2	Alignment	not modelled	6.8	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
67	c6mghB_	Alignment	not modelled	6.7	9	PDB header: fluorescent protein Chain: B: PDB Molecule: mirfp670nano; PDBTitle: x-ray structure of monomeric near-infrared fluorescent protein2 mirfp670nano
68	c5uk3J_	Alignment	not modelled	6.3	7	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
69	c3rn1A_	Alignment	not modelled	6.1	17	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius
70	c2mezA_	Alignment	not modelled	6.0	7	PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
71	d1sq8a_	Alignment	not modelled	5.9	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
72	c3n2xB_	Alignment	not modelled	5.8	22	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
73	d2r1j1	Alignment	not modelled	5.8	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
74	c2yxgD_	Alignment	not modelled	5.8	21	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
75	c2o38A_	Alignment	not modelled	5.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
76	d2o38a1	Alignment	not modelled	5.8	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
77	d2a6ca1	Alignment	not modelled	5.7	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
78	c2xxzA_	Alignment	not modelled	5.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 6b; PDBTitle: crystal structure of the human jmj3 jumonji domain
79	c2gx8B_	Alignment	not modelled	5.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
80	c4xd7G_	Alignment	not modelled	5.5	13	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of thermophilic f1-atpase inhibited by epsilon

					subunit
81	c3izbO_	Alignment	not modelled	5.5	32 PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein rps17 (s17e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
82	c4b0sA_	Alignment	not modelled	5.3	22 PDB header: hydrolase Chain: A: PDB Molecule: deamidase-depupylase dop; PDBTitle: structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp
83	c2ef8A_	Alignment	not modelled	5.2	15 PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
84	c3bdnB_	Alignment	not modelled	5.2	8 PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
85	c3eb2A_	Alignment	not modelled	5.2	29 PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
86	c5ocdD_	Alignment	not modelled	5.1	10 PDB header: rna binding protein Chain: D: PDB Molecule: cyclodipeptide synthase; PDBTitle: structure of a cdps from fluoribacter dumoffii
87	c6bi7D_	Alignment	not modelled	5.1	22 PDB header: replication Chain: D: PDB Molecule: dna polymerase zeta catalytic subunit; PDBTitle: crystal structure of rev7-wt/rev3 as a monomer under high-salt2 conditions
88	c3j3aR_	Alignment	not modelled	5.1	21 PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: structure of the human 40s ribosomal proteins