

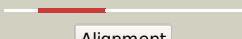








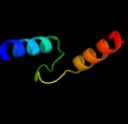




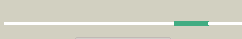




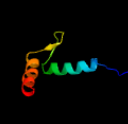


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1551_(plsB1)_1755451_1757316
 Date Fri Aug 2 13:30:14 BST 2019
 Unique Job ID 698f7676ebb46bc0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5kymA_	 Alignment		99.6	15	PDB header: transferase Chain: A: PDB Molecule: 1-acyl-sn-glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of the 1-acyl-sn-glycerophosphate (lpa)2 acyltransferase, plsc, from thermotoga maritima
2	c5f34A_	 Alignment		96.3	12	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannoside acyltransferase; PDBTitle: crystal structure of membrane associated pata from mycobacterium2 smegmatis in complex with s-hexadecyl coenzyme a - p21 space group
3	d1iuqa_	 Alignment		91.5	13	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
4	c5knkB_	 Alignment		85.7	4	PDB header: transferase Chain: B: PDB Molecule: lipid a biosynthesis lauroyl acyltransferase; PDBTitle: lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
5	d1t3la2	 Alignment		44.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
6	c6az1X_	 Alignment		42.9	19	PDB header: ribosome/antibiotic Chain: X: PDB Molecule: ribosomal protein s19e; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
7	d1m5wa_	 Alignment		41.6	29	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
8	c2jk1A_	 Alignment		41.2	10	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
9	c3zeyO_	 Alignment		40.1	22	PDB header: ribosome Chain: O: PDB Molecule: ribosomal protein s19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
10	c5xyiT_	 Alignment		39.8	16	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein s19e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
11	c3iz6S_	 Alignment		39.4	13	PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s19 (s19e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	c3j3aT_	Alignment		39.1	16	PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19; PDBTitle: structure of the human 40s ribosomal proteins
13	d1vyva2	Alignment		38.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
14	d1z67a1	Alignment		37.3	20	Fold: YidB-like Superfamily: YidB-like Family: YidB-like
15	d1vyua2	Alignment		37.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
16	d2dpwa1	Alignment		32.4	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: TTHA0179-like
17	d1wj5a_	Alignment		31.5	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: An Obfc1 domain
18	d2v7fa1	Alignment		30.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rps19E-like
19	c3jyvT_	Alignment		30.6	22	PDB header: ribosome Chain: T: PDB Molecule: s19e protein; PDBTitle: structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
20	c5xxuT_	Alignment		29.4	12	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein es19; PDBTitle: small subunit of toxoplasma gondii ribosome
21	d1rbla1	Alignment	not modelled	28.7	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
22	c3j38T_	Alignment	not modelled	28.5	22	PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
23	d1kcfaz	Alignment	not modelled	28.3	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
24	c3kcnA_	Alignment	not modelled	28.1	8	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodospirellula baltica
25	c4yyfC_	Alignment	not modelled	28.0	20	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
26	c2m4eA_	Alignment	not modelled	28.0	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution nmr structure of vv2_0175 from vibrio vulnificus, nesg target2 vnr1 and csgid target idp91333
27	d1t0hb_	Alignment	not modelled	26.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
28	c5g1mA_	Alignment	not modelled	26.2	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of nagz from pseudomonas aeruginosa
29	c3wz8B_	Alignment	not modelled	25.4	10	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylglucosaminidase;

29	c3w00B	Alignment	not modelled	23.4	19	PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima PDB header: hydrolase
30	c3tevA	Alignment	not modelled	25.0	19	Chain: A: PDB Molecule: glycosyl hyrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
31	c1sfeA	Alignment	not modelled	22.7	11	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
32	c30thB	Alignment	not modelled	22.4	28	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
33	c5m5iC	Alignment	not modelled	22.0	19	PDB header: motor protein Chain: C: PDB Molecule: kinesin-like protein cut7; PDBTitle: pseudo-atomic model of microtubule-bound s.pombe kinesin-5 motor2 domain in the amppnp state (based on cryo-electron microscopy3 experiment): the n-terminus conformation allows formation of a cover4 neck bundle.
34	c2xznT	Alignment	not modelled	21.5	13	PDB header: ribosome Chain: T: PDB Molecule: rps19e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
35	c4g6cA	Alignment	not modelled	21.3	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
36	c3hqdB	Alignment	not modelled	21.2	21	PDB header: motor protein Chain: B: PDB Molecule: kinesin-like protein kif11; PDBTitle: human kinesin eg5 motor domain in complex with amppnp and2 mg2+
37	c4zyeA	Alignment	not modelled	21.2	22	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
38	c3u6xU	Alignment	not modelled	20.5	50	PDB header: viral protein Chain: U: PDB Molecule: orf48; PDBTitle: phage tp901-1 baseplate tripod
39	d8ruca1	Alignment	not modelled	19.8	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
40	d1xl7a2	Alignment	not modelled	19.7	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
41	d1q42a	Alignment	not modelled	19.7	33	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
42	c2ctuA	Alignment	not modelled	19.5	60	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 483; PDBTitle: solution structure of zinc finger domain from human zn2 finger protein 483
43	c2fyuE	Alignment	not modelled	19.5	27	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
44	c1t39A	Alignment	not modelled	19.4	17	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
45	c5xcoB	Alignment	not modelled	19.4	40	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asn-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
46	c3tzeA	Alignment	not modelled	19.3	38	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of a tryptophanyl-trna synthetase from2 encephalitozoon cuniculi bound to tryptophan
47	c3nwrA	Alignment	not modelled	18.8	22	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
48	d1ej7l1	Alignment	not modelled	17.7	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
49	c1wrjA	Alignment	not modelled	17.6	22	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
50	c4bhCA	Alignment	not modelled	17.2	8	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r37l variant
51	c6hwhB	Alignment	not modelled	17.0	19	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
52	c1p84E	Alignment	not modelled	17.0	25	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex PDB header: metal binding protein

53	c6bwqB	Alignment	not modelled	16.9	15	Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometalase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
54	c2k9iB	Alignment	not modelled	16.6	23	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
55	d1vm6a3	Alignment	not modelled	16.5	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
56	d1t1ua2	Alignment	not modelled	16.4	28	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
57	c2wbeC	Alignment	not modelled	16.2	23	PDB header: structural protein Chain: C: PDB Molecule: bipolar kinesin krp-130; PDBTitle: kinesin-5-tubulin complex with amppnp
58	c2fynO	Alignment	not modelled	16.2	25	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
59	d1ndba2	Alignment	not modelled	15.8	22	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
60	c5nbcD	Alignment	not modelled	15.8	7	PDB header: dna binding protein Chain: D: PDB Molecule: ferric uptake regulation protein; PDBTitle: structure of prokaryotic transcription factors
61	c6bdeA	Alignment	not modelled	15.8	10	PDB header: signaling protein Chain: A: PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: crystal structure of fe(ii) unliganded h-nox protein mutant a71g from2 k. algicida
62	c3v32B	Alignment	not modelled	14.9	31	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcip1 n-terminal conserved domain
63	c2l25A	Alignment	not modelled	14.8	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: np_888769.1
64	d2hs5a1	Alignment	not modelled	14.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
65	d2bsqe1	Alignment	not modelled	14.2	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
66	d1svda1	Alignment	not modelled	14.0	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
67	c4r1hA	Alignment	not modelled	13.6	12	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0741 protein; PDBTitle: gntR family transcriptional regulator from listeria monocytogenes
68	d1j0aa	Alignment	not modelled	13.6	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	d3deua1	Alignment	not modelled	13.4	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
70	d1yfa1	Alignment	not modelled	13.1	7	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
71	c3cfyA	Alignment	not modelled	13.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo repressor2 protein from vibrio parahaemolyticus
72	d1sfea1	Alignment	not modelled	13.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
73	d1d7ka2	Alignment	not modelled	13.0	14	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
74	d1jm1a	Alignment	not modelled	12.8	21	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
75	c6b3yA	Alignment	not modelled	12.6	8	PDB header: transport protein Chain: A: PDB Molecule: denn domain-containing protein 3; PDBTitle: crystal structure of the ph-like domain from denn3
76	c3dcba	Alignment	not modelled	12.2	25	PDB header: motor protein Chain: A: PDB Molecule: kinesin-like protein nod; PDBTitle: crystal structure of the drosophila kinesin family member2 nod in complex with amppnp
77	d1tr9a	Alignment	not modelled	12.2	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
78	c2imgA	Alignment	not modelled	12.1	15	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2

						23 from homo sapiens in complex with ligand malate ion
79	d2fy9a1	Alignment	not modelled	12.0	7	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
80	d2doea1	Alignment	not modelled	12.0	19	Fold: Another 3-helical bundle Superfamily: FF domain Family: FF domain
81	d1whna_	Alignment	not modelled	11.9	18	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
82	c3ic7A_	Alignment	not modelled	11.7	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator of gnr family2 from bacteroides thetaiotaomicron
83	c5kvrA_	Alignment	not modelled	11.6	13	PDB header: translation Chain: A: PDB Molecule: pyruvate dehydrogenase complex repressor; PDBTitle: x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
84	c3rgqA_	Alignment	not modelled	11.6	15	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
85	d1riea_	Alignment	not modelled	11.6	27	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
86	c2kqA_	Alignment	not modelled	11.5	5	PDB header: transcription regulator Chain: A: PDB Molecule: transcription elongation regulator 1; PDBTitle: solution structure of the ff domain 2 of human transcription2 elongation factor ca150
87	c2zviB_	Alignment	not modelled	11.5	15	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
88	d2c6ya1	Alignment	not modelled	11.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
89	c1xl8B_	Alignment	not modelled	11.3	17	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
90	c2nvgA_	Alignment	not modelled	11.2	27	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
91	c2k5eA_	Alignment	not modelled	11.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nsg) target gsr195
92	c5z2hA_	Alignment	not modelled	11.2	13	PDB header: membrane protein Chain: A: PDB Molecule: dictyostelium discoideum mitochondrial calcium uniporter; PDBTitle: structure of dictyostelium discoideum mitochondrial calcium uniporter2 n-terminal domain(ddmdu-ntd)
93	c2vycA_	Alignment	not modelled	11.1	16	PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli
94	c5fkzE_	Alignment	not modelled	11.1	6	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, constitutive; PDBTitle: structure of e.coli constitutive lysine decarboxylase
95	d3cx5e1	Alignment	not modelled	11.0	27	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
96	d1qnta1	Alignment	not modelled	11.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
97	c3b1dD_	Alignment	not modelled	10.9	9	PDB header: lyase Chain: D: PDB Molecule: betac-s lyase; PDBTitle: crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form
98	c2du9A_	Alignment	not modelled	10.7	8	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
99	d3bwga1	Alignment	not modelled	10.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators