

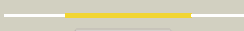


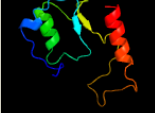







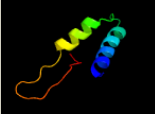

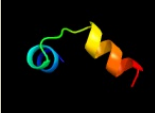








Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD1031_(kdpC)_1155857_1156426
 Date: Wed Jul 31 22:05:10 BST 2019
 Unique Job ID: c68f9fc010f74f44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mrwG	 Alignment		100.0	46	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpC subunit; PDBTitle: structure of the kdpfabC complex
2	c4oxqB	 Alignment		73.5	17	PDB header: metal binding protein Chain: B: PDB Molecule: manganese abc transporter, periplasmic-binding protein PDBTitle: structure of staphylococcus pseudintermedius metal-binding protein2 sita in complex with zinc
3	c4k3vA	 Alignment		58.7	15	PDB header: transport protein Chain: A: PDB Molecule: abc superfamily atp binding cassette transporter, binding PDBTitle: structure of staphylococcus aureus mntC
4	d1hq1a	 Alignment		55.4	25	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
5	d1dula	 Alignment		54.5	23	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
6	d1qb2a	 Alignment		53.3	33	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
7	c4aktB	 Alignment		53.1	22	PDB header: hydrolase/peptide Chain: B: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclase in complex with peptide
8	c4ue4C	 Alignment		51.8	27	PDB header: translation Chain: C: PDB Molecule: signal recognition particle protein; PDBTitle: structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
9	c2jqeA	 Alignment		51.4	21	PDB header: signaling protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: soutuion structure of af54 m-domain
10	c4xcoC	 Alignment		50.0	12	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle 54 kda protein,signal sequence; PDBTitle: signal-sequence induced conformational changes in the signal2 recognition particle
11	d2ffha2	 Alignment		49.1	27	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain

12	c3ipwA_	Alignment		47.0	11	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
13	d1qzxa2	Alignment		46.2	23	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
14	c3e2vA_	Alignment		43.6	14	PDB header: hydrolase Chain: A: PDB Molecule: 3'-5'-exonuclease; PDBTitle: crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
15	c3rcmA_	Alignment		43.5	11	PDB header: hydrolase Chain: A: PDB Molecule: tatd family hydrolase; PDBTitle: crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida
16	c3gg7A_	Alignment		41.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized metalloprotein; PDBTitle: crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
17	d1xwya1	Alignment		35.6	9	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
18	d1j6oa_	Alignment		35.4	13	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
19	d1zzma1	Alignment		28.3	7	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
20	c2y1hA_	Alignment		26.1	21	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn3; PDBTitle: crystal structure of the human tatd-domain protein 3 (tatdn3)
21	c3qllB_	Alignment	not modelled	25.0	18	PDB header: lyase Chain: B: PDB Molecule: citrate lyase; PDBTitle: crystal structure of ripc from yersinia pestis
22	c4cl2A_	Alignment	not modelled	23.4	29	PDB header: transport protein Chain: A: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of periplasmic metal binding protein from candidatus2 liberibacter asiaticus
23	c1toaA_	Alignment	not modelled	23.2	17	PDB header: binding protein Chain: A: PDB Molecule: protein (periplasmic binding protein troa); PDBTitle: periplasmic zinc binding protein troa from treponema pallidum
24	d1toaa_	Alignment	not modelled	23.2	17	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
25	c2xioA_	Alignment	not modelled	22.7	6	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyribonuclease tatdn1; PDBTitle: structure of putative deoxyribonuclease tatdn1 isoform a
26	c4ysnD_	Alignment	not modelled	22.5	41	PDB header: isomerase Chain: D: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp
27	d2jjob1	Alignment	not modelled	21.6	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
28	c3e90B_	Alignment	not modelled	21.0	33	PDB header: hydrolase Chain: B: PDB Molecule: ns3 protease; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kr-h PDB header: metal transport

29	c2ps3A_	Alignment	not modelled	21.0	17	Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
30	d1befa_	Alignment	not modelled	19.9	28	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
31	c2ordA_	Alignment	not modelled	19.8	19	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
32	c3lkwA_	Alignment	not modelled	19.8	28	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active site2 mutant
33	c2j37W_	Alignment	not modelled	19.2	33	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
34	c3mfqB_	Alignment	not modelled	19.1	19	PDB header: metal binding protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
35	c5nlaA_	Alignment	not modelled	18.8	20	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator transcription regulator PDBTitle: crystal structure of the arac-like transcriptional activator cuxr
36	d2phcb1	Alignment	not modelled	18.6	21	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
37	c4bjqB_	Alignment	not modelled	18.6	23	PDB header: transferase Chain: B: PDB Molecule: penicillin binding protein transpeptidase domain protein; PDBTitle: crystal structure of e. coli penicillin binding protein 3,2 domain v88-s165
38	d2fomb1	Alignment	not modelled	18.5	28	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
39	c2v3cC_	Alignment	not modelled	18.4	13	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
40	c5lc0B_	Alignment	not modelled	18.3	28	PDB header: hydrolase Chain: B: PDB Molecule: ns2b-ns3 protease,ns2b-ns3 protease; PDBTitle: crystal structure of zika virus ns2b-ns3 protease in complex with a2 boronate inhibitor
41	c4m9mA_	Alignment	not modelled	18.2	28	PDB header: viral protein Chain: A: PDB Molecule: ns2b-ns3 protease; PDBTitle: ns2b-ns3 protease from dengue virus at ph 8.5
42	d1vkoa1	Alignment	not modelled	18.2	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	c2gzxB_	Alignment	not modelled	18.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative tatd related dnase; PDBTitle: crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237.
44	c1gw4A_	Alignment	not modelled	17.6	22	PDB header: high density lipoproteins Chain: A: PDB Molecule: apoa-i; PDBTitle: the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
45	c2yolA_	Alignment	not modelled	17.5	28	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns2b, serine protease ns3; PDBTitle: west nile virus ns2b-ns3 protease in complex with 3,4-2 dichlorophenylacetyl-lys-lys-gcma
46	c3dxvA_	Alignment	not modelled	17.0	30	PDB header: isomerase Chain: A: PDB Molecule: alpha-amino-epsilon-caprolactam racemase; PDBTitle: the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
47	c3dm5A_	Alignment	not modelled	16.7	21	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
48	c5gafi_	Alignment	not modelled	16.6	23	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
49	c2iy3A_	Alignment	not modelled	16.5	21	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
50	c6arbA_	Alignment	not modelled	15.2	23	PDB header: lyase Chain: A: PDB Molecule: citrate lyase subunit beta-like protein; PDBTitle: crystal structure of protein cite from mycobacterium tuberculosis in2 complex with magnesium, pyruvate and coenzyme a
51	c4xrvB_	Alignment	not modelled	15.1	36	PDB header: metal binding protein Chain: B: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
52	c3zxxA_	Alignment	not modelled	14.6	20	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of self-cleaved protease domain of pata

53	c1qzwC	Alignment	not modelled	14.6	23	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
54	c2j289	Alignment	not modelled	14.5	23	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
55	c2zp2B	Alignment	not modelled	14.5	17	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
56	c5oqmk	Alignment	not modelled	14.3	14	PDB header: transcription Chain: K: PDB Molecule: dna-directed rna polymerase ii subunit rpb11; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
57	c1vkoA	Alignment	not modelled	14.2	24	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: crystal structure of inositol-3-phosphate synthase (ce21227) from2 caenorhabditis elegans at 2.30 a resolution
58	c1x3wB	Alignment	not modelled	14.1	5	PDB header: hydrolase Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: structure of a peptide:n-glycanase-rad23 complex
59	d1yixa1	Alignment	not modelled	14.1	16	Fold: TiM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
60	c5x3tA	Alignment	not modelled	14.1	33	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vappc from mycobacterium tuberculosis
61	d2fp7b1	Alignment	not modelled	14.0	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
62	c6n39A	Alignment	not modelled	13.9	12	PDB header: transferase Chain: A: PDB Molecule: dephospho-coa kinase; PDBTitle: crystal structure of an dephospho-coa kinase coae from mycobacterium2 paratuberculosis
63	d2pv4a1	Alignment	not modelled	13.9	32	Fold: Sama2622-like Superfamily: Sama2622-like Family: Sama2622-like
64	c2pb2B	Alignment	not modelled	13.8	22	PDB header: transferase Chain: B: PDB Molecule: acetylornithine/succinyl-diaminopimelate aminotransferase; PDBTitle: structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
65	c4aksA	Alignment	not modelled	13.3	23	PDB header: hydrolase Chain: A: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclyase domain
66	c5vxsF	Alignment	not modelled	13.2	21	PDB header: lyase Chain: F: PDB Molecule: citrate lyase subunit beta-like protein, mitochondrial; PDBTitle: crystal structure analysis of human clybl in apo form
67	c3hjtB	Alignment	not modelled	13.1	25	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
68	d1ohwa	Alignment	not modelled	13.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	c4cdiC	Alignment	not modelled	13.0	21	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex
70	d1oqya3	Alignment	not modelled	12.9	23	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
71	c2fvmA	Alignment	not modelled	12.9	19	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from saccharomyces kluveri2 in complex with the reaction product n-carbamyl-beta-alanine
72	c2ma3A	Alignment	not modelled	12.5	29	PDB header: replication Chain: A: PDB Molecule: dna replication initiator (cdc21/cdc54); PDBTitle: nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from methanothermobacter thermautotrophicus
73	c4v1ag	Alignment	not modelled	12.4	23	PDB header: ribosome Chain: G: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
74	c6gcsf	Alignment	not modelled	11.3	23	PDB header: oxidoreductase Chain: F: PDB Molecule: nufm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
75	c5n9jB	Alignment	not modelled	11.3	13	PDB header: transcription Chain: B: PDB Molecule: mediator of rna polymerase ii transcription subunit 10; PDBTitle: core mediator of transcriptional regulation
76	d2r6gf1	Alignment	not modelled	11.1	21	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
77	c1wnfA	Alignment	not modelled	11.1	16	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
						PDB header: transferase

78	c2kykB_	Alignment	not modelled	11.0	22	Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
79	d1e5pa_	Alignment	not modelled	10.6	14	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
80	d1afwa2	Alignment	not modelled	10.6	23	Fold: Thiolase-like Superfamily: Thiolase-like Family: Thiolase-related
81	c3thgA_	Alignment	not modelled	10.6	13	PDB header: protein binding Chain: A: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: crystal structure of the creosote rubisco activase c-domain
82	c1p1hD_	Alignment	not modelled	10.5	15	PDB header: isomerase Chain: D: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: crystal structure of the 1l-myo-inositol/nad+ complex
83	c3vs9F_	Alignment	not modelled	9.9	17	PDB header: transferase Chain: F: PDB Molecule: type iii polyketide synthase; PDBTitle: crystal structure of type iii pks arcs mutant
84	d1d8ca_	Alignment	not modelled	9.9	24	Fold: TIM beta/alpha-barrel Superfamily: Malate synthase G Family: Malate synthase G
85	c4oddB_	Alignment	not modelled	9.9	7	PDB header: allergen Chain: B: PDB Molecule: lipocalin allergen; PDBTitle: crystal structure of a dog lipocalin allergen
86	c3beyC_	Alignment	not modelled	9.8	8	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
87	c2k9sA_	Alignment	not modelled	9.7	23	PDB header: transcription Chain: A: PDB Molecule: arabinose operon regulatory protein; PDBTitle: solution structure of dna binding domain of e. coli arac
88	c5mmjw_	Alignment	not modelled	9.6	57	PDB header: ribosome Chain: W: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
89	c1u5vA_	Alignment	not modelled	9.6	23	PDB header: lyase Chain: A: PDB Molecule: cite; PDBTitle: structure of cite complexed with triphosphate group of atp form2 mycobacterium tuberculosis
90	d1gnsa_	Alignment	not modelled	9.5	21	Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases
91	c2as9B_	Alignment	not modelled	9.5	9	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
92	d1tw3a1	Alignment	not modelled	9.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Plant O-methyltransferase, N-terminal domain
93	c2ee7A_	Alignment	not modelled	9.3	14	PDB header: structural protein Chain: A: PDB Molecule: sperm flagellar protein 1; PDBTitle: solution structure of the ch domain from human sperm2 flagellar protein 1
94	c2ov3A_	Alignment	not modelled	9.3	33	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc type zinc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc bound
95	d1rp3a1	Alignment	not modelled	9.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
96	c3c19A_	Alignment	not modelled	9.2	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
97	c2mxBa_	Alignment	not modelled	9.2	50	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: structure of the transmembrane domain of the mouse erythropoietin2 receptor
98	c5xtdo_	Alignment	not modelled	9.1	23	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: cryo-em structure of human respiratory complex i
99	c2huoA_	Alignment	not modelled	9.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol oxygenase; PDBTitle: crystal structure of mouse myo-inositol oxygenase in complex with2 substrate