
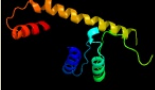


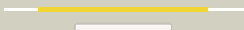

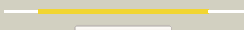



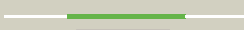






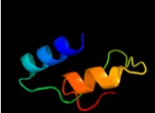



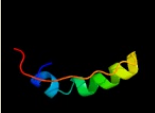
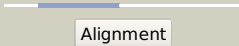



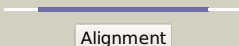
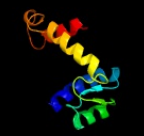
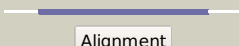

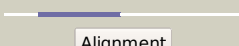
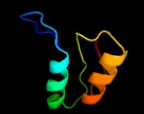
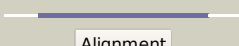

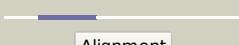
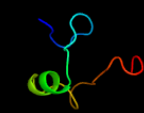

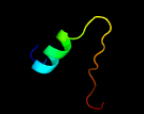





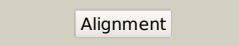

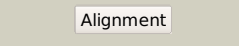

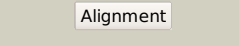


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1034c_(-)_1158922_1159311
Date	Wed Jul 31 22:05:10 BST 2019
Unique Job ID	ce676ae5f5053250

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	 Alignment		97.5	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	 Alignment		97.5	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
3	d1cxqa_	 Alignment		75.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
4	d1asua_	 Alignment		70.6	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c2b5dX_	 Alignment		52.9	18	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
6	c2etjA_	 Alignment		50.7	13	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution
7	d2etja1	 Alignment		50.7	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Ribonuclease H
8	c5cz1B_	 Alignment		49.8	14	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
9	d2b5dx2	 Alignment		40.2	18	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
10	c3nf9A_	 Alignment		25.6	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
11	c5my5A_	 Alignment		22.9	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic substrate-binding protein; PDBTitle: tungstate binding protein - tupa - from desulfovibrio alaskensis g20

12	d1ufaa2	 Alignment		22.9	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
13	c2qsrA	 Alignment		20.5	15	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
14	c4mq3A	 Alignment		19.7	17	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
15	c1k6yB	 Alignment		18.0	25	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
16	c3tsmB	 Alignment		16.4	18	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
17	d1c6va	 Alignment		16.2	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
18	c4zyaA	 Alignment		15.2	14	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the n-terminal extension domain of human asparaginyl-trna synthetase
19	c2wcvl	 Alignment		14.3	18	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
20	c3jcaE	 Alignment		13.5	15	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
21	d2eyqa6	 Alignment	not modelled	13.2	15	Fold: TRCF domain-like Superfamily: TRCF domain-like Family: TRCF domain
22	c3e7nB	 Alignment	not modelled	12.0	29	PDB header: transport protein Chain: B: PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
23	c4e38A	 Alignment	not modelled	11.9	11	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibriionales bacterium swat-3 (target efi-502156)
24	c1ufaA	 Alignment	not modelled	11.2	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
25	d1k1xa3	 Alignment	not modelled	10.6	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
26	d1lexqa	 Alignment	not modelled	10.5	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
27	c5yaaD	 Alignment	not modelled	10.5	17	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
28	c5ejkG	 Alignment	not modelled	10.3	11	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome

29	c3qjaA_	Alignment	not modelled	10.2	22	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
30	c5u1cD_	Alignment	not modelled	10.1	28	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
31	d1ogda_	Alignment	not modelled	9.1	29	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
32	d1ufza_	Alignment	not modelled	9.0	13	Fold: RuvA C-terminal domain-like Superfamily: HBS1-like domain Family: HBS1-like domain
33	c1k1yA_	Alignment	not modelled	8.9	15	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
34	c6bmaA_	Alignment	not modelled	8.5	20	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
35	c5tdyC_	Alignment	not modelled	8.5	17	PDB header: motor protein Chain: C: PDB Molecule: flagellar m-ring protein; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
36	c6nkeA_	Alignment	not modelled	8.5	13	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
37	d1b7go2	Alignment	not modelled	8.2	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
38	c3mvkA_	Alignment	not modelled	7.9	22	PDB header: isomerase Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
39	c2ekfA_	Alignment	not modelled	7.8	25	PDB header: ligase Chain: A: PDB Molecule: ancient ubiquitous protein 1; PDBTitle: solution structure of ruh-075, a human cue domain
40	c3lr1A_	Alignment	not modelled	7.6	12	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
41	c2oq2B_	Alignment	not modelled	7.0	8	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
42	c3kn3C_	Alignment	not modelled	6.9	18	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinella succinogenes
43	d1zuna1	Alignment	not modelled	6.9	5	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
44	c4a34L_	Alignment	not modelled	6.8	22	PDB header: isomerase Chain: L: PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with2 l-fucose from streptococcus pneumoniae
45	c1zunA_	Alignment	not modelled	6.7	5	PDB header: transferase Chain: A: PDB Molecule: sulfate adenyllyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
46	d1a53a_	Alignment	not modelled	6.7	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
47	c4v0hC_	Alignment	not modelled	6.4	26	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmblac1)
48	c3n92A_	Alignment	not modelled	6.3	27	PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
49	c3p13B_	Alignment	not modelled	6.3	16	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
50	d1h5ya_	Alignment	not modelled	6.0	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
51	c5tdyA_	Alignment	not modelled	5.9	16	PDB header: motor protein Chain: A: PDB Molecule: flagellar m-ring protein; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
52	c6hlwB_	Alignment	not modelled	5.9	31	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)
53	c2wcuB_	Alignment	not modelled	5.8	26	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
						Fold: Folate-binding domain

54	d1v5va2	Alignment	not modelled	5.6	19	Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
55	c1c0mA_	Alignment	not modelled	5.5	15	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
56	c3muqB_	Alignment	not modelled	5.5	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
57	c5wu7A_	Alignment	not modelled	5.4	22	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii
58	d2ob5a1	Alignment	not modelled	5.4	22	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
59	c5y9pA_	Alignment	not modelled	5.4	14	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease hii; PDBTitle: staphylococcus aureus rnase hii
60	c6ohiA_	Alignment	not modelled	5.3	32	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
61	c6n63A_	Alignment	not modelled	5.3	14	PDB header: metal binding protein Chain: A: PDB Molecule: encapsulin cargo protein; PDBTitle: crystal structure of an iron binding protein