

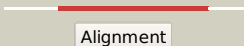



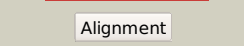

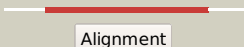







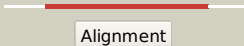



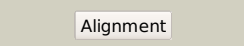


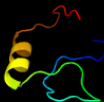




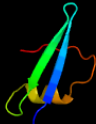
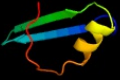
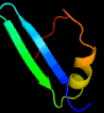


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0309 (-)_377931_378587
Date	Tue Jul 23 14:50:37 BST 2019
Unique Job ID	d2d3db324eb5f340

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4y4vB_	 Alignment		99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd6 in the d-ala-bound state
2	c4z7aA_	 Alignment		98.7	21	PDB header: transferase Chain: A: PDB Molecule: mycobacterium tuberculosis (3,3),d-transpeptidase type 5; PDBTitle: structural and biochemical characterization of a non-functionally2 redundant m. tuberculosis (3,3) l,d-transpeptidase, ldtmt5.
3	d1y7ma1	 Alignment		98.7	17	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
4	c4xvoB_	 Alignment		98.6	18	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from mycobacterium smegmatis
5	c3vynB_	 Alignment		98.6	13	PDB header: transferase Chain: B: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of mycobacterium tuberculosis l,d-transpeptidase2 ldtmt2 n55 truncation mutant (residue 55-408)
6	d1zata1	 Alignment		98.6	17	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
7	c4jmxA_	 Alignment		98.6	20	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase ldtmt1; PDBTitle: structure of ldtmt1 in complex with imipenem
8	c1y7mB_	 Alignment		98.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14040; PDBTitle: crystal structure of the b. subtilis ykud protein at 2 a2 resolution
9	c3u1qB_	 Alignment		98.4	12	PDB header: peptidoglycan binding protein Chain: B: PDB Molecule: mycobacteria tuberculosis ldtmt2; PDBTitle: crystal structure of m. tuberculosis ldtmt2 with 2-2 mercaptoethanol
10	c5bmqa_	 Alignment		98.4	18	PDB header: hydrolase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
11	c4k73A_	 Alignment		98.3	18	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an l,d-transpeptidase from mycobacterium2 tuberculosis h37rv

12	c2hkB_	Alignment		98.1	16	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
13	c4lzhA_	Alignment		97.6	18	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from klebsiella pneumoniae
14	c4xxtA_	Alignment		97.5	25	PDB header: hydrolase Chain: A: PDB Molecule: fusion of predicted zn-dependent amidase/peptidase (cell PDBTitle: crystal structure of fused zn-dependent2 amidase/peptidase/peptodoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
15	c4lpqA_	Alignment		96.1	15	PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894
16	c1wydB_	Alignment		42.1	20	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
17	c5groA_	Alignment		40.0	15	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna(asp/asn) ligase; PDBTitle: crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori
18	d1l0wa1	Alignment		38.0	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
19	c3i7fA_	Alignment		36.7	19	PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
20	d1b8aa1	Alignment		35.3	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
21	c4gn5A_	Alignment	not modelled	31.7	17	PDB header: de novo protein/hydrolase Chain: A: PDB Molecule: obody am3l15; PDBTitle: obody am3l15 bound to hen egg-white lysozyme
22	d1krta_	Alignment	not modelled	27.4	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
23	d1c0aa1	Alignment	not modelled	25.5	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
24	c4glaD_	Alignment	not modelled	19.2	20	PDB header: hydrolase/de novo protein Chain: D: PDB Molecule: obody n18; PDBTitle: obody n18 bound to hen egg-white lysozyme
25	d1e1oa1	Alignment	not modelled	17.7	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
26	c1u2zC_	Alignment	not modelled	17.0	17	PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 PDBTitle: crystal structure of histone k79 methyltransferase dot1p2 from yeast
27	d2nwua1	Alignment	not modelled	15.7	19	Fold: RL5-like Superfamily: RL5-like Family: SSO1042-like
28	c4wgkB_	Alignment	not modelled	15.4	15	PDB header: hydrolase Chain: B: PDB Molecule: neutral ceramidase; PDBTitle: crystal structure of human neutral ceramidase with zn-bound phosphate
						PDB header: virus

29	c3n7xA_	Alignment	not modelled	14.5	47	Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure of penaeus stylirostris densovirus capsid
30	c5elnC_	Alignment	not modelled	13.6	15	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
31	c5wy2D_	Alignment	not modelled	12.8	38	PDB header: transport protein/unknown function Chain: D: PDB Molecule: ince; PDBTitle: human snx5 px domain in complex with chlamydia ince c terminus
32	c5tgiD_	Alignment	not modelled	12.8	38	PDB header: protein transport Chain: D: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p212121
33	c5tghH_	Alignment	not modelled	12.8	38	PDB header: protein transport Chain: H: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p32
34	c5tghF_	Alignment	not modelled	12.8	38	PDB header: protein transport Chain: F: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p32
35	c5wy2B_	Alignment	not modelled	12.8	38	PDB header: transport protein/unknown function Chain: B: PDB Molecule: ince; PDBTitle: human snx5 px domain in complex with chlamydia ince c terminus
36	d1bbua1	Alignment	not modelled	12.7	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
37	c5tgiB_	Alignment	not modelled	12.3	38	PDB header: protein transport Chain: B: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group i2
38	c5tgiD_	Alignment	not modelled	12.3	38	PDB header: protein transport Chain: D: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group i2
39	c5tghD_	Alignment	not modelled	12.3	38	PDB header: protein transport Chain: D: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p32
40	c5tgiC_	Alignment	not modelled	11.9	38	PDB header: protein transport Chain: C: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p212121
41	c4wznB_	Alignment	not modelled	11.8	27	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of the 2b protein soluble domain from hepatitis a2 virus
42	c4j15A_	Alignment	not modelled	11.7	10	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna ligase, cytoplasmic; PDBTitle: crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
43	c2lq3A_	Alignment	not modelled	11.6	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of syc0711_d from synechococcus sp., northeast2 structural genomics consortium (nesg) target snr212
44	c1efwA_	Alignment	not modelled	11.6	20	PDB header: ligase/rna Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
45	c3ushB_	Alignment	not modelled	11.5	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
46	c2lxbB_	Alignment	not modelled	10.9	32	PDB header: transferase Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: spatial structure of the erbB4 dimeric tm domain
47	c2l2tA_	Alignment	not modelled	10.9	32	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: solution nmr structure of the erbB4 dimeric membrane domain
48	c5tghB_	Alignment	not modelled	10.2	38	PDB header: protein transport Chain: B: PDB Molecule: ince; PDBTitle: structure of the snx5 px domain in complex with chlamydial protein2 ince in space group p32
49	d1v3aa_	Alignment	not modelled	10.1	33	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
50	c3c9gB_	Alignment	not modelled	10.0	14	PDB header: nucleotide binding protein Chain: B: PDB Molecule: upf0200/upf0201 protein af_1395; PDBTitle: crystal structure of uncharacterized upf0201 protein af_135
51	c5xw4A_	Alignment	not modelled	10.0	26	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
52	c3s4oB_	Alignment	not modelled	10.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
53	c2imgA_	Alignment	not modelled	9.6	31	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
54	d1y02a1	Alignment	not modelled	9.2	25	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
						PDB header: transferase/transferase inhibitor

55	c6ntwA_	Alignment	not modelled	8.9	30	Chain: A: PDB Molecule: probable l,d-transpeptidase yccb; PDBTitle: crystal structure of e. coli yccb
56	d1ohea2	Alignment	not modelled	8.3	28	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
57	c1oheA_	Alignment	not modelled	8.2	28	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
58	c1b8aB_	Alignment	not modelled	7.7	27	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
59	c1yypA_	Alignment	not modelled	7.3	18	PDB header: replication/transferase Chain: A: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of cytomegalovirus ul44 bound to c-terminal peptide2 from cmv ul54
60	c1nw3A_	Alignment	not modelled	7.3	22	PDB header: transferase Chain: A: PDB Molecule: histone methyltransferase dot11; PDBTitle: structure of the catalytic domain of human dot11, a non-set domain2 nucleosomal histone methyltransferase
61	d1nw3a_	Alignment	not modelled	7.3	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Catalytic, N-terminal domain of histone methyltransferase Dot11
62	c4er3A_	Alignment	not modelled	7.0	22	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 specific; PDBTitle: crystal structure of human dot11 in complex with inhibitor epz004777
63	d1ju2a1	Alignment	not modelled	6.9	29	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	c6e8rC_	Alignment	not modelled	6.8	38	PDB header: protein transport Chain: C: PDB Molecule: ince; PDBTitle: structure of the snx32 px domain in complex with chlamydial protein2 ince in space group i121
65	c6e8rD_	Alignment	not modelled	6.8	38	PDB header: protein transport Chain: D: PDB Molecule: ince; PDBTitle: structure of the snx32 px domain in complex with chlamydial protein2 ince in space group i121
66	d1auga_	Alignment	not modelled	6.3	7	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
67	d1eova1	Alignment	not modelled	6.3	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
68	c2jtcA_	Alignment	not modelled	6.2	24	PDB header: hydrolase Chain: A: PDB Molecule: streptopain; PDBTitle: 3d structure and backbone dynamics of spe b
69	c3ckkA_	Alignment	not modelled	6.2	25	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(7)-)-methyltransferase; PDBTitle: crystal structure of human methyltransferase-like protein 1
70	c4o2dB_	Alignment	not modelled	6.1	18	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
71	c5gnnA_	Alignment	not modelled	6.1	19	PDB header: lipid binding protein Chain: A: PDB Molecule: lipid binding protein; PDBTitle: crystal structure of lipid binding protein nakanori at 1.6a
72	c3bjuB_	Alignment	not modelled	6.0	21	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase
73	d1we6a_	Alignment	not modelled	5.8	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
74	d1kfia4	Alignment	not modelled	5.8	17	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
75	c4iohA_	Alignment	not modelled	5.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tll1086 protein; PDBTitle: crystal structure of the tll1086 protein from thermosynechococcus2 elongatus, northeast structural genomics consortium target ter258
76	c4jqfA_	Alignment	not modelled	5.7	24	PDB header: dna binding protein Chain: A: PDB Molecule: csst complex subunit stn1; PDBTitle: structure of the c-terminal domain of human telomeric stn1
77	d1yb2a1	Alignment	not modelled	5.7	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
78	c1yb2A_	Alignment	not modelled	5.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum.
79	c1x55A_	Alignment	not modelled	5.7	13	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
80	c2rubA_	Alignment	not modelled	5.6	22	PDB header: peptide binding protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mdm2;

80	c2f0nA_	Alignment	not modelled	5.6	32	PDBTitle: chemical shift assignments for mip and mdm2 in bound state
81	d1f86a_	Alignment	not modelled	5.6	18	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
82	c3bbaB_	Alignment	not modelled	5.5	29	PDB header: hydrolase Chain: B: PDB Molecule: interpain a; PDBTitle: structure of active wild-type prevotella intermedia interpain a2 cysteine protease
83	d1mlaa2	Alignment	not modelled	5.5	20	Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
84	d2phcb1	Alignment	not modelled	5.3	11	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
85	c4ex5A_	Alignment	not modelled	5.3	22	PDB header: transferase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine