

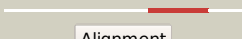

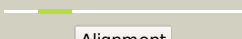
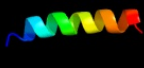



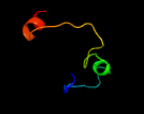



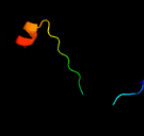

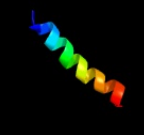
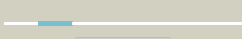


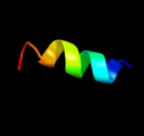




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0901 (-) _1003960_1004487
Date	Fri Jul 26 01:50:49 BST 2019
Unique Job ID	5d847966d2ae0702

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1eyfa_	 Alignment		97.7	17	Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10)
2	c1zgwA_	 Alignment		95.2	19	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
3	c2kncA_	 Alignment		69.6	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c2k1aA_	 Alignment		54.1	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
5	c5ze4A_	 Alignment		51.0	30	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
6	c5ym0A_	 Alignment		50.3	30	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
7	c3hfkB_	 Alignment		43.3	25	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
8	c3dinE_	 Alignment		42.7	19	PDB header: membrane protein, protein transport Chain: E: PDB Molecule: preprotein translocase subunit secg; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
9	c2l8sA_	 Alignment		36.3	29	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
10	c1z65A_	 Alignment		31.4	43	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide
11	c3dl8F_	 Alignment		27.1	25	PDB header: protein transport Chain: F: PDB Molecule: protein-export membrane protein secg; PDBTitle: structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca

12	c5j84A_	Alignment		25.0	14	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
13	d1d5ra1	Alignment		24.5	15	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
14	c2m1jA_	Alignment		23.9	35	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: ovine doppel signal peptide (1-30)
15	c2k1kA_	Alignment		22.0	25	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
16	c2k1lA_	Alignment		22.0	25	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
17	c2k1kB_	Alignment		22.0	25	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
18	c2k1lB_	Alignment		22.0	25	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
19	c3kdpH_	Alignment		19.2	38	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
20	c3kdpG_	Alignment		19.2	38	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
21	c4hqjG_	Alignment	not modelled	18.4	38	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
22	c4hqjE_	Alignment	not modelled	17.2	38	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
23	c2akiA_	Alignment	not modelled	15.6	33	PDB header: protein transport Chain: A: PDB Molecule: protein-export membrane protein secg; PDBTitle: normal mode-based flexible fitted coordinates of a translocating2 secyeg protein-conducting channel into the cryo-em map of a secyeg-3 nascent chain-70s ribosome complex from e. coli
24	d2pu9b1	Alignment	not modelled	14.0	32	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
25	d1h41a1	Alignment	not modelled	13.4	36	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
26	d1l8na1	Alignment	not modelled	13.0	36	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
27	c1mqrA_	Alignment	not modelled	12.9	36	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6
28	c5oynB_	Alignment	not modelled	12.9	10	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form

29	c1gqkB	Alignment	not modelled	12.4	36	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
30	c5j8tA	Alignment	not modelled	11.7	9	PDB header: hydrolase Chain: A: PDB Molecule: choline binding protein; PDBTitle: nmr structure of excalibur domain of cbpl
31	c5vcsB	Alignment	not modelled	11.3	50	PDB header: transferase Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor
32	c6fkip	Alignment	not modelled	10.4	12	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
33	d1tdha3	Alignment	not modelled	9.9	26	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
34	d2msta	Alignment	not modelled	9.8	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
35	c2m4iA	Alignment	not modelled	8.2	17	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: solution structure of bacillus subtilis minc n-terminal domain
36	d2cqca1	Alignment	not modelled	8.1	18	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
37	c2lcoA	Alignment	not modelled	7.5	25	PDB header: membrane protein Chain: A: PDB Molecule: walp19-p8 peptide; PDBTitle: 1h and 15n assignments of walp19-p8 peptide in sds micelles
38	c5vcmA	Alignment	not modelled	7.3	50	PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n- PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
39	c2na8A	Alignment	not modelled	7.3	28	PDB header: membrane protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
40	c2na9A	Alignment	not modelled	7.2	28	PDB header: signaling protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
41	d1nh1a	Alignment	not modelled	7.2	36	Fold: Antivirulence factor Superfamily: Antivirulence factor Family: Antivirulence factor
42	c1nh1A	Alignment	not modelled	7.2	36	PDB header: avirulence protein Chain: A: PDB Molecule: avirulence b protein; PDBTitle: crystal structure of the type iii effector avrb from2 pseudomonas syringae.
43	d1wela1	Alignment	not modelled	7.1	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
44	d1fxla2	Alignment	not modelled	6.9	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
45	d2ftra1	Alignment	not modelled	6.8	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
46	c2mj2A	Alignment	not modelled	6.3	40	PDB header: viral protein Chain: A: PDB Molecule: agnoprotein; PDBTitle: structure of the dimerization domain of the human polyoma, jc virus2 agnoprotein is an amphipathic alpha-helix.
47	d1gcca	Alignment	not modelled	6.2	50	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: GCC-box binding domain
48	d1b7fa2	Alignment	not modelled	6.1	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
49	c6bhpA	Alignment	not modelled	6.1	24	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein; PDBTitle: crystal structure of the chlamydomonas reinhardtii lci1 channel
50	c6bhpC	Alignment	not modelled	6.1	24	PDB header: membrane protein Chain: C: PDB Molecule: membrane protein; PDBTitle: crystal structure of the chlamydomonas reinhardtii lci1 channel
51	c2hacA	Alignment	not modelled	5.8	38	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
52	c2hacB	Alignment	not modelled	5.8	38	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
53	c3arcl	Alignment	not modelled	5.6	29	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
54	c4ardA	Alignment	not modelled	5.4	27	PDB header: viral protein Chain: A: PDB Molecule: capsid protein p27; PDBTitle: structure of the immature retroviral capsid at 8a resolution by cryo-2 electron microscopy
55	c2mdfA	Alignment	not modelled	5.2	9	PDB header: proton transport Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: nmr structure of a two-transmembrane segment tm vi-vii

						of nhe1
56	d2cqda1	Alignment	not modelled	5.2	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
57	c2lowA	Alignment	not modelled	5.2	36	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
58	c6az5A	Alignment	not modelled	5.2	28	PDB header: sugar binding protein Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k
59	d1hd0a	Alignment	not modelled	5.2	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
60	c5knwA	Alignment	not modelled	5.1	22	PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 7; PDBTitle: solution nmr structure of human larp7 xrrm2
61	c4a5uA	Alignment	not modelled	5.1	13	PDB header: transferase/rna binding protein Chain: A: PDB Molecule: rna replicase polyprotein; PDBTitle: turnip yellow mosaic virus proteinase and escherichia coli 30s2 ribosomal s15
62	c3awfC	Alignment	not modelled	5.0	21	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: voltage-sensor containing phosphatase; PDBTitle: crystal structure of pten-like domain of ci-vsp (236-576)
63	c2qksA	Alignment	not modelled	5.0	17	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera