






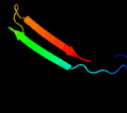

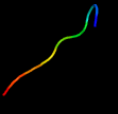

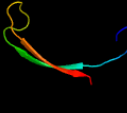

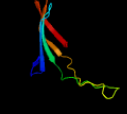



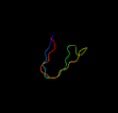



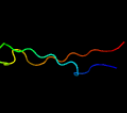


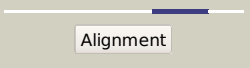
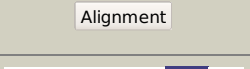
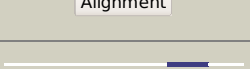
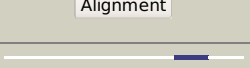
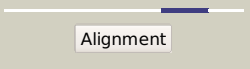
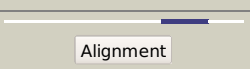
Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3763_(lpqH)_4209225_4209704
 Date Fri Aug 9 18:20:46 BST 2019
 Unique Job ID 290e532961e7abec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xinB_	 Alignment		100.0	34	PDB header: unknown function Chain: B; PDB Molecule: lpqH orthologue; PDBTitle: x-ray crystal structure of an lpqH orthologue from mycobacterium avium
2	c4zjmA_	 Alignment		100.0	90	PDB header: unknown function Chain: A; PDB Molecule: lipoprotein lpqH; PDBTitle: crystal structure of mycobacterium tuberculosis lpqH (rv3763)
3	c6qt9Y_	 Alignment		61.1	13	PDB header: virus Chain: Y; PDB Molecule: orf 31; PDBTitle: cryo-em structure of sh1 full particle.
4	c2g16A_	 Alignment		28.6	15	PDB header: luminescent protein Chain: A; PDB Molecule: green fluorescent protein; PDBTitle: structure of s65a y66s gfp variant after backbone2 fragmentation
5	d1wv3a1	 Alignment		25.5	44	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: EssC N-terminal domain-like
6	c2gw4C_	 Alignment		21.2	18	PDB header: luminescent protein Chain: C; PDB Molecule: kaede; PDBTitle: crystal structure of stony coral fluorescent protein kaede, red form
7	d2icha1	 Alignment		20.1	19	Fold: AtH-like Superfamily: AtH-like Family: AtH-like
8	c6fx6A_	 Alignment		19.5	11	PDB header: unknown function Chain: A; PDB Molecule: satie-ted; PDBTitle: thioester domain of the staphylococcus aureus tie protein
9	c6h9cb_	 Alignment		17.7	18	PDB header: virus Chain: B; PDB Molecule: vp4; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hcv-1) at 3.74 angstroms resolution.
10	c3najA_	 Alignment		17.3	19	PDB header: sugar binding protein Chain: A; PDB Molecule: galectin-8; PDBTitle: crystal structure of a protease-resistant mutant form of human2 galectin-8
11	c3ff7B_	 Alignment		16.5	18	PDB header: cell adhesion/immune system Chain: B; PDB Molecule: epithelial cadherin; PDBTitle: structure of nk cell receptor klrp1 bound to e-cadherin

12	c1vraA_	Alignment		15.6	19	PDB header: transferase Chain: A; PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
13	c2mraA_	Alignment		15.2	20	PDB header: de novo protein Chain: A; PDB Molecule: de novo designed protein or459; PDBTitle: solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or459
14	c3wp6A_	Alignment		14.4	24	PDB header: hydrolase Chain: A; PDB Molecule: cdbfv; PDBTitle: the complex structure of cdbfv e109a with xylotriase
15	c3lf4A_	Alignment		13.7	18	PDB header: fluorescent protein Chain: A; PDB Molecule: fluorescent timer precursor blue102; PDBTitle: crystal structure of fluorescent timer precursor blue102
16	c3mxnB_	Alignment		13.4	14	PDB header: replication Chain: B; PDB Molecule: recq-mediated genome instability protein 2; PDBTitle: crystal structure of the rmi core complex
17	c3c12A_	Alignment		12.8	17	PDB header: biosynthetic protein Chain: A; PDB Molecule: flagellar protein; PDBTitle: crystal structure of figd from xanthomonas campestris;2 insights into the hook capping essential for flagellar3 assembly
18	c2ovsB_	Alignment		12.7	4	PDB header: gene regulation, ligand binding protein Chain: B; PDB Molecule: i0044; PDBTitle: crystal structure of a type three secretion system protein
19	c4m02A_	Alignment		12.6	22	PDB header: calcium binding protein Chain: A; PDB Molecule: serine-rich adhesin for platelets; PDBTitle: middle fragment(residues 494-663) of the binding region of srap
20	d1mywa_	Alignment		11.4	11	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
21	c3rwaE_	Alignment	not modelled	9.9	21	PDB header: fluorescent protein Chain: E; PDB Molecule: fluorescent protein fp480; PDBTitle: crystal structure of circular-permuted mkate
22	d2go8a1	Alignment	not modelled	9.7	32	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
23	d1sgoa_	Alignment	not modelled	9.5	29	Fold: N domain of copper amine oxidase-like Superfamily: Hypothetical protein c14orf129, hspc210 Family: Hypothetical protein c14orf129, hspc210
24	d1kp5a_	Alignment	not modelled	9.4	15	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
25	c2l7yA_	Alignment	not modelled	9.1	20	PDB header: structural protein Chain: A; PDB Molecule: putative endo-beta-n-acetylglucosaminidase; PDBTitle: solution structure of a putative surface protein
26	c2a56A_	Alignment	not modelled	9.0	38	PDB header: luminescent protein Chain: A; PDB Molecule: gfp-like non-fluorescent chromoprotein fp595 chain 1; PDBTitle: fluorescent protein asfp595, a143s, on-state, 5min irradiation
27	c2ltyA_	Alignment	not modelled	8.5	24	PDB header: structural protein Chain: A; PDB Molecule: type-1 fimbrial protein, a chain; PDBTitle: self-complemented variant of fima, the main subunit of type 1 pilus
28	c5az3A_	Alignment	not modelled	8.1	21	PDB header: transport protein Chain: A; PDB Molecule: abc-type transporter, periplasmic component; PDBTitle: crystal structure of heme binding protein hmut

29	c2q9kA		Alignment	not modelled	8.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
30	c3akoG		Alignment	not modelled	8.0	11	PDB header: fluorescent protein Chain: G: PDB Molecule: venus; PDBTitle: crystal structure of the reassembled venus
31	c4p7hB		Alignment	not modelled	8.0	21	PDB header: motor/fluorescent protein Chain: B: PDB Molecule: myosin-7,green fluorescent protein; PDBTitle: structure of human beta-cardiac myosin motor domain::gfp chimera
32	c4gpvB		Alignment	not modelled	7.9	14	PDB header: cell adhesion Chain: B: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bacegg_00536)2 from bacteroides eggerthii dsm 20697 at 1.67 a resolution
33	c2mbIA		Alignment	not modelled	7.9	39	PDB header: de novo protein Chain: A: PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
34	c4uznA		Alignment	not modelled	7.7	35	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-glucanase (celulase b); PDBTitle: the native structure of the family 46 carbohydrate-binding2 module (cbm46) of endo-beta-1,4-glucanase b (cel5b) from3 bacillus halodurans
35	c3u0kA		Alignment	not modelled	7.5	25	PDB header: fluorescent protein Chain: A: PDB Molecule: rcamp; PDBTitle: crystal structure of the genetically encoded calcium indicator rcamp
36	d1rx0a2		Alignment	not modelled	7.1	50	Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
37	c5u75A		Alignment	not modelled	7.1	29	PDB header: toxin Chain: A: PDB Molecule: enterotoxin-like toxin x; PDBTitle: the structure of staphylococcal enterotoxin-like x (selx), a unique2 superantigen
38	c3t9gB		Alignment	not modelled	7.0	24	PDB header: lyase Chain: B: PDB Molecule: pectate lyase; PDBTitle: the crystal structure of family 3 pectate lyase from2 caldicellulosiruptor bescii
39	c4i2yB		Alignment	not modelled	6.9	18	PDB header: fluorescent protein Chain: B: PDB Molecule: rgeco1; PDBTitle: crystal structure of the genetically encoded calcium indicator rgeco1
40	c2m5sA		Alignment	not modelled	6.6	19	PDB header: viral protein Chain: A: PDB Molecule: coat protein; PDBTitle: high-resolution nmr structure and cryo-em imaging support multiple2 functional roles for the accessory i-domain of phage p22 coat protein
41	c2bgpA		Alignment	not modelled	6.5	12	PDB header: carbohydrate binding protein Chain: A: PDB Molecule: endo-b1,4-mannanase 5c; PDBTitle: mannan binding module from man5c in bound conformation
42	d2d29a2		Alignment	not modelled	6.5	26	Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
43	c4anjA		Alignment	not modelled	6.4	15	PDB header: motor protein/metal-binding protein Chain: A: PDB Molecule: unconventional myosin-vi, green fluorescent protein; PDBTitle: myosin vi (mdinsert2-gfp fusion) pre-powerstroke state (mg.adp.alf4)
44	c3evpA		Alignment	not modelled	6.3	14	PDB header: signaling protein Chain: A: PDB Molecule: green fluorescent protein,green fluorescent protein; PDBTitle: crystal structure of circular-permuted egfp
45	c3k25B		Alignment	not modelled	6.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: slr1438 protein; PDBTitle: crystal structure of slr1438 protein from synechocystis sp. pcc 6803,2 northeast structural genomics consortium target sgr112
46	c4l3aA		Alignment	not modelled	5.9	18	PDB header: cell invasion Chain: A: PDB Molecule: internalin k; PDBTitle: crystal structure of internalin k (inlk) from listeria monocytogenes
47	c3uv0B		Alignment	not modelled	5.7	17	PDB header: protein binding Chain: B: PDB Molecule: mutator 2, isoform b; PDBTitle: crystal structure of the drosophila mu2 fha domain
48	c3uv1B		Alignment	not modelled	5.6	13	PDB header: allergen Chain: B: PDB Molecule: der f 7 allergen; PDBTitle: crystal structure a major allergen from dust mite
49	c6efrA		Alignment	not modelled	5.3	18	PDB header: choline-binding protein Chain: A: PDB Molecule: inicsnfr 1.0, a genetically encoded nicotine biosensor, PDBTitle: crystal structure of inicsnfr 1.0
50	c3h3iA		Alignment	not modelled	5.3	56	PDB header: lipid binding protein Chain: A: PDB Molecule: putative lipid binding protein; PDBTitle: crystal structure of a putative lipid binding protein (bt_2261) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
51	c4ktoB		Alignment	not modelled	5.2	21	PDB header: oxidoreductase Chain: B: PDB Molecule: isovaleryl-coa dehydrogenase; PDBTitle: crystal structure of a putative isovaleryl-coa dehydrogenase (psi-2 nysgrc-012251) from sinorhizobium meliloti 1021
52	c6dgvA		Alignment	not modelled	5.1	18	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent gaba sensor precursor; PDBTitle: igabasnfr fluorescent gaba sensor precursor
							PDB header: fluorescent protein, de novo protein

53	c4ndkA_	Alignment	not modelled	5.1	14	Chain: A: PDB Molecule: e23p-yfp, gfp-like fluorescent chromoprotein fp506, PDBTitle: crystal structure of a computational designed engrailed homeodomain2 variant fused with yfp
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