
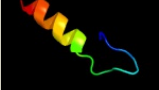
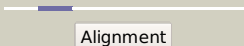

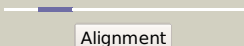

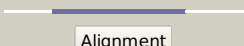

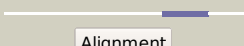

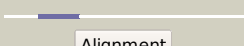
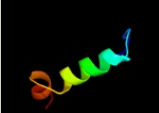
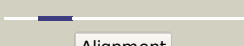




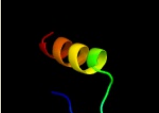

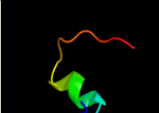




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0188 (-)_219484_219915
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	31da74e445ce9e5c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qgia_	 Alignment		26.0	41	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Chitosanase
2	c3kitB_	 Alignment		18.8	16	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
3	c2yy0D_	 Alignment		18.0	14	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
4	c6iu3A_	 Alignment		16.5	11	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
5	c2ks1B_	 Alignment		12.6	20	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
6	d2imha1	 Alignment		12.5	33	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: SPO2555-like
7	c4b1yM_	 Alignment		9.7	31	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-3 bound to g-actin
8	c2kmuA_	 Alignment		9.3	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase q4; PDBTitle: recq14 amino-terminal domain
9	c4ph6A_	 Alignment		9.2	9	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: structure of 3-dehydroquinate dehydratase from enterococcus faecalis
10	d2imra1	 Alignment		9.1	44	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: DR0824-like
11	c5kbhB_	 Alignment		8.4	27	PDB header: transcription Chain: B: PDB Molecule: mopr; PDBTitle: crystal structure of the aromatic sensor domain of mopr in complex2 with 3-chloro-phenol

12	c3js3C_	Alignment		8.3	13	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of type i 3-dehydroquinatase (arod) from2 clostridium difficile with covalent reaction intermediate
13	c2yr1B_	Alignment		7.4	22	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatase; PDBTitle: crystal structure of 3-dehydroquinatase from geobacillus2 kaustophilus hta426
14	c6b4gG_	Alignment		7.2	16	PDB header: transport protein Chain: G: PDB Molecule: nucleoporin gle1; PDBTitle: crystal structure of chaetomium thermophilum gle1 ctd-nup42 gbm2 complex
15	c3l2iB_	Alignment		7.2	9	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinatase dehydratase2 (arod) from salmonella typhimurium lt2.
16	c2mmuA_	Alignment		7.1	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein crga; PDBTitle: structure of crga, a cell division structural and regulatory protein2 from mycobacterium tuberculosis, in lipid bilayers
17	c3odmE_	Alignment		7.1	46	PDB header: lyase Chain: E: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: archaeal-type phosphoenolpyruvate carboxylase
18	d1sfla_	Alignment		6.9	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
19	c3sjrB_	Alignment		6.6	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
20	d2vv5a3	Alignment		6.5	20	Fold: Mechanosensitive channel protein MscS (YggB), transmembrane region Superfamily: Mechanosensitive channel protein MscS (YggB), transmembrane region Family: Mechanosensitive channel protein MscS (YggB), transmembrane region
21	c2n2aA_	Alignment	not modelled	6.3	27	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains
22	c4kunB_	Alignment	not modelled	6.2	0	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein lpp1115; PDBTitle: crystal structure of legionella pneumophila lpp1115 / kaib
23	c5wl0A_	Alignment	not modelled	5.8	8	PDB header: viral protein/inhibitor Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: co-crystal structure of influenza a h3n2 pb2 (241-741) bound to vx-787