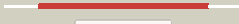
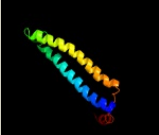


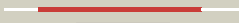










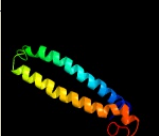



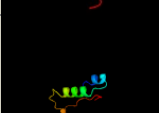




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3891c_(esxD)_4374227_4374550
 Date Sat Aug 10 22:05:07 BST 2019
 Unique Job ID 03c1db6f83c5d790

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8a1	 Alignment		96.6	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c2vs0B_	 Alignment		95.5	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
3	c4iogD_	 Alignment		94.1	12	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
4	c3zbcC_	 Alignment		93.3	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
5	c3gvmA_	 Alignment		91.4	20	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
6	c4lwsA_	 Alignment		86.2	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	c4lwsB_	 Alignment		26.8	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	d1wa8b1	 Alignment		26.5	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	d1st6a7	 Alignment		18.9	32	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
10	d1onra_	 Alignment		18.2	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
11	c2l92A_	 Alignment		17.7	42	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f

12	c3m16A_	Alignment		16.6	28	PDB header: transferase Chain: A: PDB Molecule: transaldolase; PDBTitle: structure of a transaldolase from oleispira antarctica
13	c2kg7B_	Alignment		16.1	8	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
14	c2jr1A_	Alignment		14.7	38	PDB header: dna binding protein Chain: A: PDB Molecule: virulence regulator; PDBTitle: solution structure of the dna binding domain of a nucleoid-associated2 protein, h-ns, from the phytopathogen xylella fastidiosa.
15	d2e1da1	Alignment		14.4	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
16	c3cq0B_	Alignment		10.6	31	PDB header: transferase Chain: B: PDB Molecule: putative transaldolase ygr043c; PDBTitle: crystal structure of tal2_yeast
17	d1f05a_	Alignment		9.9	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
18	c3hjaz_	Alignment		9.5	28	PDB header: transferase Chain: A: PDB Molecule: transaldolase b; PDBTitle: the structure of an aldolase from prochlorococcus marinus
19	c3phuA_	Alignment		9.1	10	PDB header: hydrolase Chain: A: PDB Molecule: rna-directed rna polymerase I; PDBTitle: otu domain of crimean congo hemorrhagic fever virus
20	c2khvA_	Alignment		8.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of protein nmu_a0922 from2 nitrospira multiformis. northeast structural genomics3 consortium target nmr38b.
21	d1mwwa_	Alignment	not modelled	7.2	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
22	d1hnra_	Alignment	not modelled	7.1	67	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
23	c5h5mA_	Alignment	not modelled	6.5	10	PDB header: cell adhesion Chain: A: PDB Molecule: alpha-catenin-like protein hmp-1; PDBTitle: crystal structure of hmp-1 m domain
24	c2levA_	Alignment	not modelled	5.9	83	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
25	c2i68B_	Alignment	not modelled	5.8	67	PDB header: transport protein Chain: B: PDB Molecule: protein emre; PDBTitle: cryo-em based theoretical model structure of transmembrane2 domain of the multidrug-resistance antiporter from e. coli3 emre
26	c4fazB_	Alignment	not modelled	5.8	20	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozyms from methylbium petroleiphilum
27	c2damA_	Alignment	not modelled	5.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: etea protein; PDBTitle: solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
						PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit;

28	c3mb2G_	Alignment	not modelled	5.5	12	PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
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