
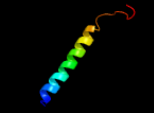

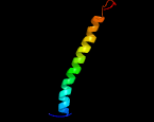

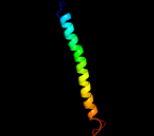

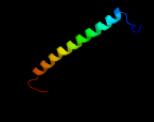
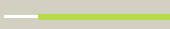
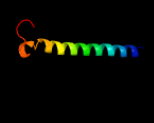

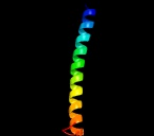

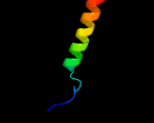

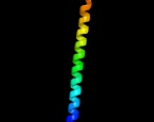

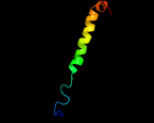






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1792_(RVBD1792)_2030354_2030530
 Date Fri Aug 2 13:30:40 BST 2019
 Unique Job ID 4f82ecc4498f6b90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ogiD_	 Alignment		99.6	85	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative esat-6-like protein 7; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
2	d1wa8a1	 Alignment		93.0	24	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
3	c4iogD_	 Alignment		82.8	23	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	c3gvmA_	 Alignment		70.7	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
5	c2vs0B_	 Alignment		65.4	17	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c3zbhC_	 Alignment		62.8	23	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
7	c2dw3A_	 Alignment		62.6	38	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
8	c4lwsB_	 Alignment		60.8	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	c2kg7B_	 Alignment		44.7	24	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
10	d1pqa2	 Alignment		31.9	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
11	d1wa8b1	 Alignment		30.9	12	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like

12	c4lwsA_	Alignment		29.9	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1t4ba2	Alignment		22.8	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
14	d1mb4a2	Alignment		22.8	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
15	d2gz1a2	Alignment		22.4	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
16	d1nlxa_	Alignment		20.2	62	Fold: Four-helical up-and-down bundle Superfamily: Group V grass pollen allergen Family: Group V grass pollen allergen
17	c4m70A_	Alignment		10.1	39	PDB header: plant protein Chain: A: PDB Molecule: rx protein; PDBTitle: crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
18	d2k49a2	Alignment		9.2	43	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
19	d2k8ea1	Alignment		8.9	71	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
20	c3l32B_	Alignment		8.1	35	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
21	c1i8tB_	Alignment	not modelled	7.9	40	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
22	d2hjsa2	Alignment	not modelled	7.5	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
23	c2ip6A_	Alignment	not modelled	6.4	29	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
24	c3nj2B_	Alignment	not modelled	5.9	18	PDB header: unknown function Chain: B: PDB Molecule: duf269-containing protein; PDBTitle: crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
25	c2k49A_	Alignment	not modelled	5.7	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0339 protein so_3888; PDBTitle: solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
26	d1w4xa1	Alignment	not modelled	5.5	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
27	c2vq7B_	Alignment	not modelled	5.4	53	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
28	c2bi8A_	Alignment	not modelled	5.3	47	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae

					with reduced fad
29	c1bzgA_	Alignment	not modelled	5.1	25
					PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
30	c5nmwA_	Alignment	not modelled	5.1	47
					PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of the pyrrolizidine alkaloid n-oxygenase from <i>Zonocerus variegatus</i> in complex with fad