
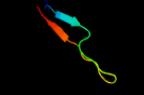
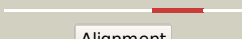
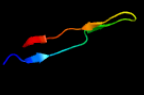
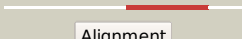
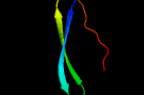

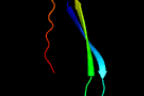
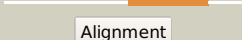
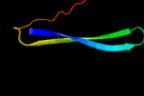

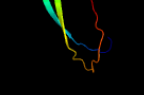



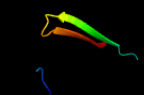
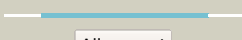


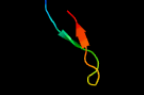
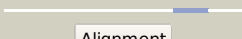



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1089\_(PE10)\_1214831\_1215136  
 Date Wed Jul 31 22:05:16 BST 2019  
 Unique Job ID 0a0fc2652792593f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1hehc_</a>	 Alignment		94.2	13	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
2	<a href="#">d1e5ba_</a>	 Alignment		94.0	26	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
3	<a href="#">c6f7eA_</a>	 Alignment		93.5	24	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted cellulose binding protein; <b>PDBTitle:</b> nmr solution structure of the cellulose-binding family 2 carbohydrate2 binding domain (cbm2) from sclpmo9c
4	<a href="#">c3ndyG_</a>	 Alignment		91.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
5	<a href="#">c2rttA_</a>	 Alignment		89.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chic; <b>PDBTitle:</b> solution structure of the chitin-binding domain of chi18ac from2 streptomyces coelicolor
6	<a href="#">d1exha_</a>	 Alignment		89.7	23	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family II
7	<a href="#">c2cwrA_</a>	 Alignment		73.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> crystal structure of chitin biding domain of chitinase from2 pyrococcus furiosus
8	<a href="#">c3icgD_</a>	 Alignment		56.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
9	<a href="#">c3hbzA_</a>	 Alignment		31.1	23	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bt_2081) from2 bacteroides thetaiotaomicron vpi-5482 at 2.05 a resolution
10	<a href="#">c1h2dA_</a>	 Alignment		23.0	44	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> ebola virus matrix protein vp40 n-terminal domain in complex with rna2 (low-resolution vp40[31-212] variant).
11	<a href="#">d1na6a1</a>	 Alignment		22.9	29	<b>Fold:</b> DNA-binding pseudobarrel domain <b>Superfamily:</b> DNA-binding pseudobarrel domain <b>Family:</b> Type II restriction endonuclease effector domain

12	<a href="#">d1h2ca_</a>	Alignment		22.9	44	<b>Fold:</b> EV matrix protein <b>Superfamily:</b> EV matrix protein <b>Family:</b> EV matrix protein
13	<a href="#">c3tcqA_</a>	Alignment		20.9	70	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> crystal structure of matrix protein vp40 from ebola virus sudan
14	<a href="#">c4hetA_</a>	Alignment		18.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bt3745) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
15	<a href="#">d1es6a1</a>	Alignment		16.8	44	<b>Fold:</b> EV matrix protein <b>Superfamily:</b> EV matrix protein <b>Family:</b> EV matrix protein
16	<a href="#">c1es6A_</a>	Alignment		13.3	44	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> crystal structure of the matrix protein of ebola virus
17	<a href="#">c6ekvA_</a>	Alignment		12.6	41	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> toxin complex component orf-x2; <b>PDBTitle:</b> structure of orfx2 from clostridium botulinum a2
18	<a href="#">c5jk2l_</a>	Alignment		10.6	63	<b>PDB header:</b> cell adhesion <b>Chain:</b> I: <b>PDB Molecule:</b> tp0751; <b>PDBTitle:</b> crystal structure of treponema pallidum tp0751 (pallilysin)
19	<a href="#">c5b0vA_</a>	Alignment		10.1	60	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein vp40; <b>PDBTitle:</b> crystal structure of marburg virus vp40 dimer

20

[c3ogiC\\_](#)

Alignment



6.9

75

**PDB header:** structural genomics, unknown function  
**Chain:** C: **PDB Molecule:** putative esat-6-like protein 6;  
**PDB Title:** crystal structure of the mycobacterium tuberculosis h37rv  
esxop2 complex (rv2346c-rv2347c)