

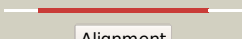







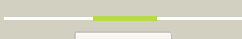
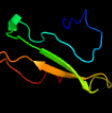



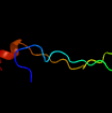
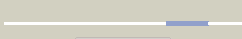




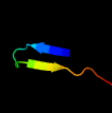


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3036c\_TB22.2\_3396469\_3397152  
 Date Thu Aug 8 16:20:21 BST 2019  
 Unique Job ID 0fee575ec01baf1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hhiA_</a>	 Alignment		100.0	48	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> immunogenic protein mpt64; <b>PDBTitle:</b> the solution structure of antigen mpt64 from mycobacterium2 tuberculosis defines a novel class of beta-grasp proteins
2	<a href="#">c3cygA_</a>	 Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from2 fervidobacterium nodosum rt17-b1
3	<a href="#">c5jenA_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase/hydrolase receptor <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-v factor rsiv; <b>PDBTitle:</b> crystal structure of the anti-sigma factor rsiv bound to lysozyme
4	<a href="#">c4e72A_</a>	 Alignment		100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3298 family protein (pa4972) from2 pseudomonas aeruginosa pao1 at 2.15 a resolution
5	<a href="#">c3s5tA_</a>	 Alignment		100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> duf3298 family protein; <b>PDBTitle:</b> crystal structure of a member of duf3298 family (bf2082) from2 bacteroides fragilis nctc. 9343 at 2.30 a resolution
6	<a href="#">c4qtqA_</a>	 Alignment		60.6	10	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> xac2610 protein; <b>PDBTitle:</b> structure of a xanthomonas type iv secretion system related protein
7	<a href="#">d2c1ia2</a>	 Alignment		44.2	20	<b>Fold:</b> Peptidoglycan deacetylase N-terminal noncatalytic region <b>Superfamily:</b> Peptidoglycan deacetylase N-terminal noncatalytic region <b>Family:</b> Peptidoglycan deacetylase N-terminal noncatalytic region
8	<a href="#">c3acqA_</a>	 Alignment		29.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,4-endoglucanase; <b>PDBTitle:</b> crystal structure of carbohydrate-binding module family 28 from2 clostridium josui cel5a in complex with cellobiose
9	<a href="#">c4ot1A_</a>	 Alignment		26.6	12	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> structural basis for the recognition of human cytomegalovirus2 glycoprotein b by the neutralizing human antibody sm5-1
10	<a href="#">d2g5gx1</a>	 Alignment		25.2	12	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> ChaN-like
11	<a href="#">d1hf2a2</a>	 Alignment		20.3	18	<b>Fold:</b> Cell-division inhibitor MinC, N-terminal domain <b>Superfamily:</b> Cell-division inhibitor MinC, N-terminal domain <b>Family:</b> Cell-division inhibitor MinC, N-terminal domain

12	<a href="#">c2lnzA_</a>	Alignment		19.7	31	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like protein mdy2; <b>PDBTitle:</b> solution structure of the get5 carboxyl domain from s. cerevisiae
13	<a href="#">c3e79A_</a>	Alignment		19.6	18	<b>PDB header:</b> tpb binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> high affinity transport system protein p37; <b>PDBTitle:</b> structure determination of the cancer-associated mycoplasma2 hyorhinis protein mh-p37
14	<a href="#">c6mjpC_</a>	Alignment		17.4	6	<b>PDB header:</b> lipid transport <b>Chain:</b> C: <b>PDB Molecule:</b> lipopolysaccharide export system protein lptc; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
15	<a href="#">d1uwwa_</a>	Alignment		16.0	5	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 28 carbohydrate binding module, CBM28
16	<a href="#">d2guma1</a>	Alignment		11.1	2	<b>Fold:</b> Viral glycoprotein ectodomain-like <b>Superfamily:</b> Viral glycoprotein ectodomain-like <b>Family:</b> Glycoprotein B-like
17	<a href="#">c3vejB_</a>	Alignment		10.9	29	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein mdy2; <b>PDBTitle:</b> crystal structure of the get5 carboxyl domain from s. cerevisiae
18	<a href="#">c6ax5A_</a>	Alignment		10.9	14	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> swi1/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> rpt1 region of ini1/snf5/smarcb1_human - swi/snf-related matrix-2 associated actin-dependent regulator of chromatin subfamily b member3 1.
19	<a href="#">c6bm8A_</a>	Alignment		10.5	2	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
20	<a href="#">c3nw8B_</a>	Alignment		10.5	2	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
21	<a href="#">c2amjD_</a>	Alignment	not modelled	9.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> modulator of drug activity b; <b>PDBTitle:</b> crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
22	<a href="#">c5v2sA_</a>	Alignment	not modelled	8.4	2	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
23	<a href="#">c2hp7A_</a>	Alignment	not modelled	8.2	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar motor switch protein flim; <b>PDBTitle:</b> structure of flim provides insight into assembly of the2 switch complex in the bacterial flagella motor
24	<a href="#">d1w6ga3</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
25	<a href="#">c3waiA_</a>	Alignment	not modelled	7.7	21	<b>PDB header:</b> transferase, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, transmembrane <b>PDBTitle:</b> crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
26	<a href="#">c5c6tA_</a>	Alignment	not modelled	7.6	9	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of hcmv glycoprotein b in complex with 1g2 fab
27	<a href="#">c2c1iA_</a>	Alignment	not modelled	7.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan glcnac deacetylase; <b>PDBTitle:</b> structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant. <b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplakin;

28	<a href="#">c4q28B_</a>	Alignment	not modelled	7.4	7	<b>PDBTitle:</b> crystal structure of the plectin 1 and 2 repeats of the human2 perioplakin. northeast structural genomics consortium (nesg) target3 hr9083a
29	<a href="#">c5yi8B_</a>	Alignment	not modelled	7.3	33	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> pon peptide from partner of numb; <b>PDBTitle:</b> crystal structure of drosophila numb ptb domain and pon peptide2 complex
30	<a href="#">d3c9fa1</a>	Alignment	not modelled	7.1	19	<b>Fold:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain <b>Superfamily:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
31	<a href="#">c4yk8A_</a>	Alignment	not modelled	6.7	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> meiotically up-regulated gene 66 protein; <b>PDBTitle:</b> crystal structure of the atg101-atg13 complex from fission yeast
32	<a href="#">d1w2za3</a>	Alignment	not modelled	6.3	14	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
33	<a href="#">c3fvcA_</a>	Alignment	not modelled	6.3	7	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycoprotein gp110; <b>PDBTitle:</b> crystal structure of a trimeric variant of the epstein-barr virus2 glycoprotein b
34	<a href="#">d1to0a_</a>	Alignment	not modelled	6.2	13	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
35	<a href="#">d2nysa1</a>	Alignment	not modelled	5.9	19	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> AGR C 3712p-like
36	<a href="#">c2nysA_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> agr_c_3712p; <b>PDBTitle:</b> x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
37	<a href="#">d1poia_</a>	Alignment	not modelled	5.4	47	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
38	<a href="#">c6escA_</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of pseudorabies virus glycoprotein b
39	<a href="#">c4bk8A_</a>	Alignment	not modelled	5.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> desulfoferrodoxin, ferrous iron-binding region; <b>PDBTitle:</b> superoxide reductase (neelaredoxin) from ignicoccus2 hospitalis
40	<a href="#">c3wajA_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase; <b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
41	<a href="#">d1u7ba1</a>	Alignment	not modelled	5.0	10	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor