




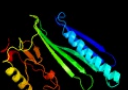


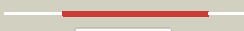
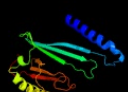





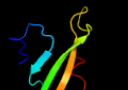








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1980c_(mpt64)_2223351_2224037
Date	Mon Aug 5 13:25:08 BST 2019
Unique Job ID	f927be7edccf2c59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hhiA_</a>	 Alignment		100.0	100	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> immunogenetic 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="#">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
3	<a href="#">c3cygA_</a>	 Alignment		100.0	16	<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
4	<a href="#">c4e72A_</a>	 Alignment		100.0	12	<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	15	<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="#">d2c1ia2</a>	 Alignment		55.4	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
7	<a href="#">c4ot1A_</a>	 Alignment		42.2	17	<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
8	<a href="#">c4qtqA_</a>	 Alignment		27.7	15	<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
9	<a href="#">d2g5qx1</a>	 Alignment		21.7	12	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> ChaN-like
10	<a href="#">d2guma1</a>	 Alignment		20.9	14	<b>Fold:</b> Viral glycoprotein ectodomain-like <b>Superfamily:</b> Viral glycoprotein ectodomain-like <b>Family:</b> Glycoprotein B-like
11	<a href="#">c3nw8B_</a>	 Alignment		20.3	14	<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

12	<a href="#">c2lnzA_</a>	Alignment		19.9	29	<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="#">c6bm8A_</a>	Alignment		19.9	14	<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
14	<a href="#">d1hf2a2</a>	Alignment		17.0	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
15	<a href="#">c5v2sA_</a>	Alignment		16.9	14	<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
16	<a href="#">c5c6tA_</a>	Alignment		15.8	16	<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
17	<a href="#">d3c9fa1</a>	Alignment		15.4	15	<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
18	<a href="#">c5efvC_</a>	Alignment		14.1	11	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> phi eta orf 56-like protein; <b>PDBTitle:</b> the host-recognition device of staphylococcus aureus phage phi11
19	<a href="#">c3fvcA_</a>	Alignment		13.6	10	<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
20	<a href="#">c2c1iA_</a>	Alignment		13.5	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.
21	<a href="#">d2czra1</a>	Alignment	not modelled	12.6	18	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> TBP-interacting protein-like <b>Family:</b> TBP-interacting protein-like
22	<a href="#">c5lngB_</a>	Alignment	not modelled	11.6	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> putative fml fimbrial adhesin fmlD; <b>PDBTitle:</b> lectin domain of e. coli f9 pilus adhesin fmlh
23	<a href="#">c3acgA_</a>	Alignment	not modelled	11.2	26	<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 ce15a in complex with cellobiose
24	<a href="#">c3vejB_</a>	Alignment	not modelled	9.9	33	<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
25	<a href="#">c6ax5A_</a>	Alignment	not modelled	9.4	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 - swi1/snf-related matrix-2 associated actin-dependent regulator of chromatin subfamily b member3 1.
26	<a href="#">c2amjD_</a>	Alignment	not modelled	9.2	12	<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
27	<a href="#">c3n1tE_</a>	Alignment	not modelled	8.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> hit-like protein hint; <b>PDBTitle:</b> crystal structure of the h101a mutant echint gmp complex
28	<a href="#">c6escA_</a>	Alignment	not modelled	7.8	16	<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

29	<a href="#">d2guya1</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
30	<a href="#">d2aaaa1</a>	Alignment	not modelled	7.1	50	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
31	<a href="#">c3c9fB</a>	Alignment	not modelled	7.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase from candida albicans sc5314
32	<a href="#">d1w6ga3</a>	Alignment	not modelled	6.9	13	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
33	<a href="#">d1w2za3</a>	Alignment	not modelled	6.9	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Amine oxidase N-terminal region <b>Family:</b> Amine oxidase N-terminal region
34	<a href="#">d1uwwa_</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 28 carbohydrate binding module, CBM28
35	<a href="#">c2qasA</a>	Alignment	not modelled	6.5	26	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of caulobacter crescentus sspb ortholog
36	<a href="#">d1poia_</a>	Alignment	not modelled	5.9	40	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
37	<a href="#">c2hp7A</a>	Alignment	not modelled	5.4	17	<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 the 2 switch complex in the bacterial flagella motor
38	<a href="#">d2hq4a1</a>	Alignment	not modelled	5.4	33	<b>Fold:</b> PH1570-like <b>Superfamily:</b> PH1570-like <b>Family:</b> PH1570-like
39	<a href="#">c5yi8B</a>	Alignment	not modelled	5.3	67	<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
40	<a href="#">c5mzyA</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaconate coa-transferase family, subunit a; <b>PDBTitle:</b> crystal structure of the decarboxylase aiba/aibb in complex with a2 possible transition state analog
41	<a href="#">c3waiA</a>	Alignment	not modelled	5.3	24	<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 of 2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion
42	<a href="#">c3e79A</a>	Alignment	not modelled	5.2	22	<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
43	<a href="#">d1ex0a2</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
44	<a href="#">d1u7ba1</a>	Alignment	not modelled	5.2	17	<b>Fold:</b> DNA clamp <b>Superfamily:</b> DNA clamp <b>Family:</b> DNA polymerase processivity factor
45	<a href="#">c4yk8A</a>	Alignment	not modelled	5.2	16	<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