






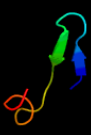

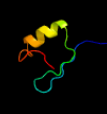







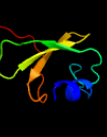

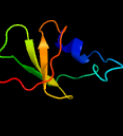




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2721c (-) _3032530_3034629
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	f91c4e305f9228cb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f3mB	 Alignment		96.9	18	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak-alpha; PDBTitle: crystal structure of human serine/threonine kinase pak1
2	c1e0aB	 Alignment		94.1	22	PDB header: signalling protein/kinase Chain: B: PDB Molecule: serine/threonine-protein kinase pak-alpha; PDBTitle: cdc42 complexed with the gtpase binding domain of p212 activated kinase
3	c2lnhA	 Alignment		83.0	12	PDB header: signaling protein/protein binding Chain: A: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
4	c2odbB	 Alignment		79.9	19	PDB header: protein binding Chain: B: PDB Molecule: serine/threonine-protein kinase pak 6; PDBTitle: the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
5	c1ceeB	 Alignment		77.7	15	PDB header: structural protein regulation Chain: B: PDB Molecule: wiskott-aldrich syndrome protein wasp; PDBTitle: solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
6	c2ov2O	 Alignment		76.3	19	PDB header: protein binding/transferase Chain: O: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
7	c2k42A	 Alignment		70.9	16	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
8	c6nbxG	 Alignment		58.5	14	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
9	c2ivjA	 Alignment		43.2	18	PDB header: isomerase Chain: A: PDB Molecule: thiol disulfide interchange protein dsbc; PDBTitle: crystal structure of the n-terminal dimer domain of e.coli2 dsbc
10	d1leej2	 Alignment		37.0	18	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
11	d1lodha	 Alignment		34.9	20	Fold: GCM domain Superfamily: GCM domain Family: GCM domain

12	c6hq8B_	Alignment		25.6	24	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,3-oligosaccharide phosphorylase; PDBTitle: bacterial beta-1,3-oligosaccharide phosphorylase from gh149 with 2 laminarihexaose bound at a surface site
13	d1f5ja_	Alignment		22.5	19	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
14	c2yh5A_	Alignment		21.6	26	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
15	c3hfkB_	Alignment		21.0	34	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in 2 complex with 4-methylmuconolactone
16	d1t3ba2	Alignment		20.8	12	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
17	d1lgoa_	Alignment		20.5	26	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
18	c2c1fA_	Alignment		19.3	13	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional endo-1,4-beta-xylanase a; PDBTitle: the structure of the family 11 xylanase from neocallimastix2 patriciarum
19	c2kncA_	Alignment		18.9	24	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
20	c2oruA_	Alignment		15.9	33	PDB header: de novo protein Chain: A: PDB Molecule: xtz1-peptide; PDBTitle: solution structure of xtz1-peptide, a beta-hairpin peptide2 with a structured extension
21	d1v58a2	Alignment	not modelled	13.3	20	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
22	c4ml1D_	Alignment	not modelled	11.8	21	PDB header: isomerase Chain: D: PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group) PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from 2 e. coli at 3.0 angstrom resolution
23	c3rkoF_	Alignment	not modelled	11.7	21	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from 2 e. coli at 3.0 angstrom resolution
24	d1mbma_	Alignment	not modelled	10.5	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
25	c1jzdA_	Alignment	not modelled	8.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
26	c3bnwA_	Alignment	not modelled	7.6	33	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase, putative; PDBTitle: crystal structure of riboflavin kinase from trypanosoma brucei
27	c5d0qC_	Alignment	not modelled	7.4	26	PDB header: protein transport Chain: C: PDB Molecule: outer membrane protein assembly factor bamc; PDBTitle: bamacde complex, outer membrane beta-barrel assembly machinery (bam)2 complex
28	d1eyfa_	Alignment	not modelled	7.0	19	Fold: Ada DNA repair protein, N-terminal domain (N-Ada 10) Superfamily: Ada DNA repair protein, N-terminal domain (N-Ada 10) Family: Ada DNA repair protein, N-terminal domain (N-Ada 10)

29	d1h4ga_	Alignment	not modelled	6.4	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
30	d1t6gc_	Alignment	not modelled	5.9	9	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
31	d1nb9a_	Alignment	not modelled	5.7	42	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
32	d1xyna_	Alignment	not modelled	5.6	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
33	c1m57H_	Alignment	not modelled	5.4	10	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
34	d1m4wa_	Alignment	not modelled	5.1	12	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12
35	c2zxcA_	Alignment	not modelled	5.1	22	PDB header: hydrolase Chain: A: PDB Molecule: neutral ceramidase; PDBTitle: ceramidase complexed with c2