











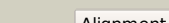








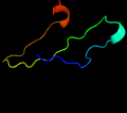
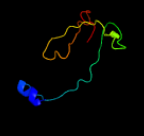
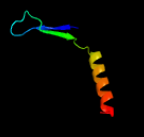
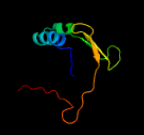

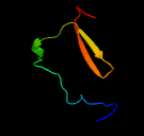
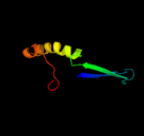
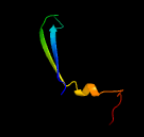


Phyre2

Email	mdejesus@rockefeller.edu
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Date	Wed Aug 7 12:50:30 BST 2019
Unique Job ID	28fedd3fdbceec39

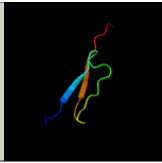
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pbka1	 Alignment		93.9	17	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
2	d1o6ea_	 Alignment		93.1	23	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
3	d1iega_	 Alignment		92.7	16	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
4	d1vzva_	 Alignment		90.3	17	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
5	c3njqB_	 Alignment		88.5	17	PDB header: viral protein/inhibitor Chain: B; PDB Molecule: orf 17; PDBTitle: crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
6	c4cx8B_	 Alignment		88.1	14	PDB header: viral protein Chain: B; PDB Molecule: pseudorabies virus protease; PDBTitle: monomeric pseudorabies virus protease pul26n at 2.5 a resolution
7	d1at3a_	 Alignment		86.7	18	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
8	d1jq6a_	 Alignment		64.3	18	Fold: Herpes virus serine proteinase, assemblin Superfamily: Herpes virus serine proteinase, assemblin Family: Herpes virus serine proteinase, assemblin
9	c4oy2D_	 Alignment		56.1	11	PDB header: transcription Chain: D; PDB Molecule: transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of taf1-taf7, a tfiid subcomplex
10	c5jblA_	 Alignment		51.8	14	PDB header: hydrolase Chain: A; PDB Molecule: prohead core protein protease; PDBTitle: structure of the bacteriophage t4 capsid assembly protease, gp21.
11	d2ed6a1	 Alignment		44.6	16	Fold: WSSV envelope protein-like Superfamily: WSSV envelope protein-like Family: WSSV envelope protein-like

12	c4x8rB_	Alignment		11.2	13	<p>PDB header:solute-binding protein Chain: B: PDB Molecule:trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_2138, target efi-510205) with3 bound glucuronate</p>
13	c5ur2C_	Alignment		10.6	10	<p>PDB header:oxidoreductase Chain: C: PDB Molecule:bifunctional protein puta; PDBTitle: crystal structure of proline utilization a (puta) from bdellovibrio2 bacteriovorus inactivated by n-propargylglycine</p>
14	c4rgwB_	Alignment		8.5	15	<p>PDB header:transferase/transcription Chain: B: PDB Molecule:transcription initiation factor tfiid subunit 7; PDBTitle: crystal structure of a taf1-taf7 complex in human transcription factor2 iid</p>
15	c4idmA_	Alignment		8.2	19	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:delta-1-pyrroline-5-carboxylate dehydrogenase; PDBTitle: crystal structure of the delta-pyrroline-5-carboxylate dehydrogenase2 from mycobacterium tuberculosis</p>
16	c2m4vA_	Alignment		6.4	16	<p>PDB header:transcription Chain: A: PDB Molecule:putative uncharacterized protein; PDBTitle: mycobacterium tuberculosis rna polymerase binding protein a (rbpa) and2 its interactions with sigma factors</p>
17	d2hjea1	Alignment		5.5	15	<p>Fold:Profilin-like Superfamily:Sensory domain-like Family:LuxQ-periplasmic domain-like</p>
18	c3caxA_	Alignment		5.5	12	<p>PDB header:structural genomics, unknown function Chain: A: PDB Molecule:uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695</p>

19 [c3m86B](#)

Alignment



5.2

9

PDB header:protein binding

Chain: B: **PDB Molecule:**amoebiasin-2;

PDBTitle: crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica