


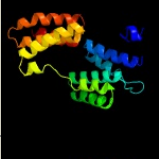



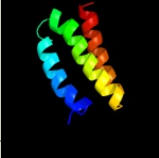


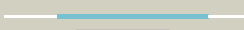




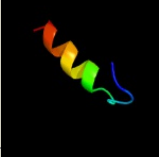

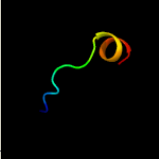

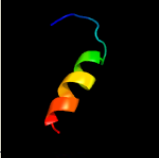


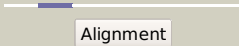


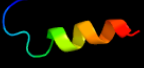


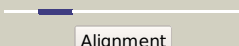

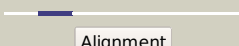
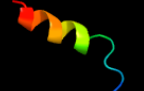
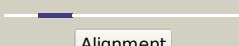

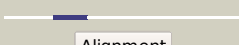
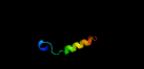


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3415c_(-)_3833874_3834701
Date	Fri Aug 9 18:20:08 BST 2019
Unique Job ID	a6ae10bd44c132ca

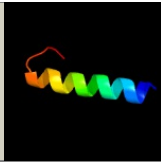
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6mfvC_</a>	 Alignment		96.4	12	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tetratricopeptide repeat sensor ph0952; <b>PDBTitle:</b> crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratricopeptide repeat sensor ph09523 from pyrococcus horikoshii
2	<a href="#">c5khrO_</a>	 Alignment		90.5	21	<b>PDB header:</b> cell cycle <b>Chain:</b> O: <b>PDB Molecule:</b> anaphase-promoting complex subunit 5; <b>PDBTitle:</b> model of human anaphase-promoting complex/cyclosome complex (apc152 deletion mutant) in complex with the e2 ube2c/ubch10 poised for3 ubiquitin ligation to substrate (apc/c-cdc20-substrate-ube2c)
3	<a href="#">d1hz4a_</a>	 Alignment		43.7	17	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Transcription factor MaT domain III
4	<a href="#">c2n8iA_</a>	 Alignment		42.1	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein da05; <b>PDBTitle:</b> solution nmr structure of designed protein da05, northeast structural2 genomics consortium (nesg) target or626
5	<a href="#">c3qkyA_</a>	 Alignment		32.4	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane assembly lipoprotein yfio; <b>PDBTitle:</b> crystal structure of rhodothermus marinus bamd
6	<a href="#">c4ui9O_</a>	 Alignment		31.8	18	<b>PDB header:</b> cell cycle <b>Chain:</b> O: <b>PDB Molecule:</b> anaphase-promoting complex subunit 5; <b>PDBTitle:</b> atomic structure of the human anaphase-promoting complex
7	<a href="#">c3gw4B_</a>	 Alignment		20.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
8	<a href="#">c3hmjB_</a>	 Alignment		14.5	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> saccharomyces cerevisiae fas type i
9	<a href="#">c3h87D_</a>	 Alignment		13.2	53	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
10	<a href="#">c2uv9B_</a>	 Alignment		10.9	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase alpha subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
11	<a href="#">c4b3yB_</a>	 Alignment		10.7	39	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase

12	<a href="#">c2uv8C_</a>	 Alignment		10.0	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha (fas2); <b>PDBTitle:</b> crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
13	<a href="#">c2vkzC_</a>	 Alignment		7.4	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
14	<a href="#">c4u4cB_</a>	 Alignment		6.0	67	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein air2,poly(a) rna polymerase protein 2; <b>PDBTitle:</b> the molecular architecture of the tramp complex reveals the2 organization and interplay of its two catalytic activities
15	<a href="#">c2pffD_</a>	 Alignment		6.0	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
16	<a href="#">c2pffG_</a>	 Alignment		6.0	33	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
17	<a href="#">c2pffA_</a>	 Alignment		6.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structural insights of yeast fatty acid synthase
18	<a href="#">d1gx5a_</a>	 Alignment		5.9	31	<b>Fold:</b> DNA/RNA polymerases <b>Superfamily:</b> DNA/RNA polymerases <b>Family:</b> RNA-dependent RNA-polymerase

19 [c2gbbA](#)

Alignment



5.3

17

**PDB header:** isomerase  
**Chain:** A: **PDB Molecule:** putative chorismate mutase;  
**PDB Title:** crystal structure of secreted chorismate mutase from yersinia pestis