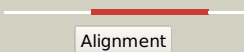

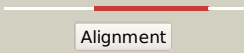

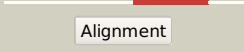
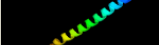
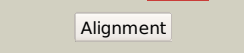



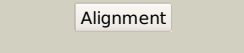

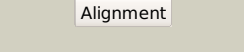



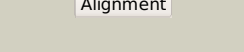
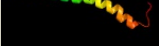
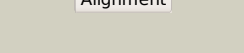

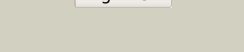

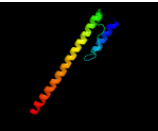

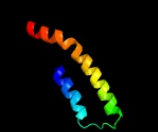
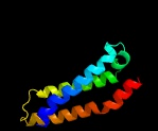
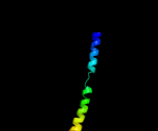
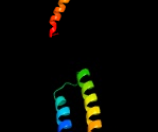

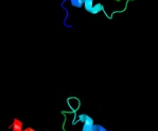
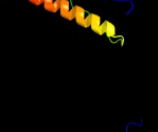


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0601c_(-)_698527_698997
Date	Fri Jul 26 01:50:16 BST 2019
Unique Job ID	def88cfa360277ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zrwB_	 Alignment		99.6	23	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
2	c4biuB_	 Alignment		99.2	27	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
3	c4mt8A_	 Alignment		99.2	21	PDB header: transferase Chain: A: PDB Molecule: ethylene response sensor 1; PDBTitle: structure of the ers1 dimerization and histidine phosphotransfer2 domain from arabidopsis thaliana
4	c5ukvA_	 Alignment		99.1	33	PDB header: transferase Chain: A: PDB Molecule: atp-binding protein; PDBTitle: dhp domain of phor of m. tuberculosis - semet
5	c4gn0D_	 Alignment		99.0	17	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
6	d1joya_	 Alignment		98.9	24	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
7	d2c2aa1	 Alignment		98.9	31	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
8	c5jefA_	 Alignment		98.8	17	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
9	c2c2aA_	 Alignment		98.6	31	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
10	c3lnrA_	 Alignment		98.3	14	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
11	c4ctiA_	 Alignment		98.1	25	PDB header: signaling protein Chain: A: PDB Molecule: osmolarity sensor protein envz, af1503; PDBTitle: escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain

12	c3zx6A_	Alignment		97.5	14	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
13	d2asxa1	Alignment		97.5	23	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
14	c2q8fA_	Alignment		97.2	6	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
15	c3d2rB_	Alignment		96.9	11	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
16	c3gieA_	Alignment		95.7	19	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase desk; PDBTitle: crystal structure of desk_h188e in complex with amp- pcp
17	c1y8oA_	Alignment		95.6	6	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
18	c3crlB_	Alignment		95.2	8	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.
19	c4i5sA_	Alignment		95.2	19	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
20	c2rm8A_	Alignment		92.5	21	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
21	c2bu8A_	Alignment	not modelled	91.9	8	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
22	c4gczB_	Alignment	not modelled	91.3	14	PDB header: signaling protein, de novo protein Chain: B: PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
23	c3tz5A_	Alignment	not modelled	87.4	16	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, PDBTitle: crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
24	c1gfvA_	Alignment	not modelled	86.1	16	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
25	c6e95A_	Alignment	not modelled	77.9	10	PDB header: signaling protein Chain: A: PDB Molecule: staphylococcus aureus agrc histidine kinase module fused to PDBTitle: chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hki2000)
26	c5c3lB_	Alignment	not modelled	22.7	20	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin nup58; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
27	c2oo4B_	Alignment	not modelled	17.5	23	PDB header: cell cycle,signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 2; PDBTitle: structure of Inr-hd (negative regulatory region) from human notch 2

28	c2n28A_	Alignment	not modelled	15.2	14	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
29	d1li5a1	Alignment	not modelled	13.8	30	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
30	c3i08C_	Alignment	not modelled	11.3	18	PDB header: signaling protein Chain: C: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
31	c3etoB_	Alignment	not modelled	10.9	18	PDB header: signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: 2 angstrom xray structure of the notch1 negative regulatory region2 (nrr)
32	c3rtyA_	Alignment	not modelled	10.8	8	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: structure of an enclosed dimer formed by the drosophila period protein
33	c2momC_	Alignment	not modelled	9.2	18	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
34	c2momB_	Alignment	not modelled	9.2	18	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
35	c4o9pC_	Alignment	not modelled	8.2	18	PDB header: membrane protein Chain: C: PDB Molecule: nad(p) transhydrogenase subunit alpha 2; PDBTitle: crystal structure of thermus thermophilis transhydrogenase domain ii2 dimer semet derivative
36	c5omdA_	Alignment	not modelled	7.9	17	PDB header: protein binding Chain: A: PDB Molecule: dna damage checkpoint protein lcd1; PDBTitle: crystal structure of s. cerevisiae ddc2 n-terminal coiled-coil domain
37	c2mi2A_	Alignment	not modelled	7.7	16	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
38	c4hj6A_	Alignment	not modelled	7.6	5	PDB header: signaling protein Chain: A: PDB Molecule: lov protein; PDBTitle: crystal structure of rhodobacter sphaeroides lov protein
39	c1zzaA_	Alignment	not modelled	7.4	23	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
40	c5v2sA_	Alignment	not modelled	7.4	12	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
41	c3qweA_	Alignment	not modelled	6.7	20	PDB header: protein binding Chain: A: PDB Molecule: gem-interacting protein; PDBTitle: crystal structure of the n-terminal domain of the gem interacting2 protein
42	c4zlpB_	Alignment	not modelled	6.7	32	PDB header: transcription Chain: B: PDB Molecule: neurogenic locus notch homolog protein 3; PDBTitle: crystal structure of notch3 negative regulatory region
43	c4o9rA_	Alignment	not modelled	6.6	10	PDB header: signaling protein Chain: A: PDB Molecule: smoothened homolog/soluble cytochrome b562 chimeric PDBTitle: human smoothened receptor structure in complex with cyclopamine