



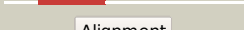











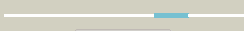
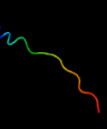





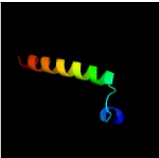



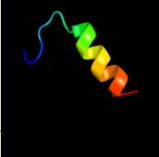
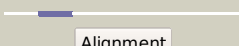
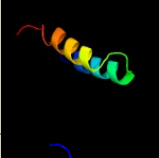
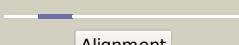
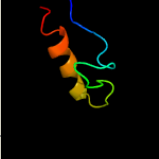
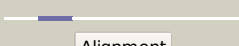
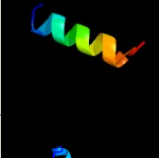
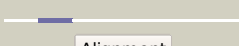
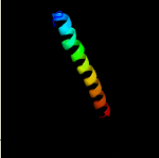





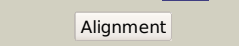
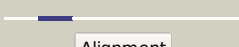
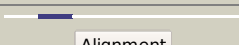

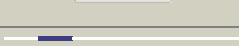
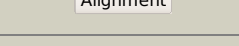




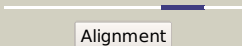


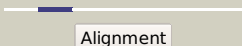
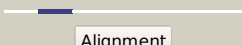
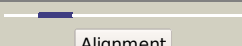
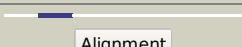
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0444c (-) _533094_533792
Date	Tue Jul 23 14:50:52 BST 2019
Unique Job ID	3cd8a218732f516b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vdoB_	 Alignment		99.6	100	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rska; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
2	c2z2sD_	 Alignment		99.3	12	PDB header: transcription Chain: D: PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
3	c5wuqD_	 Alignment		99.1	7	PDB header: metal binding protein Chain: D: PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
4	c5frhA_	 Alignment		98.9	7	PDB header: transcription Chain: A: PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra
5	c3hugJ_	 Alignment		98.8	16	PDB header: transcription/membrane protein Chain: J: PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
6	c5camC_	 Alignment		67.7	29	PDB header: transcription Chain: C: PDB Molecule: pupr protein; PDBTitle: crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
7	d1or7c_	 Alignment		34.4	13	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
8	c1or7C_	 Alignment		34.4	13	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
9	c5ee2A_	 Alignment		30.5	38	PDB header: metal transport Chain: A: PDB Molecule: hemoglobin-haptoglobin-utilization protein; PDBTitle: the crystal structure of the c-terminal beta-barrel of hpua from2 neisseria gonorrhoeae
10	c2mjlA_	 Alignment		22.5	15	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: solution structure of peptidyl-trna hyrolase from vibrio cholerae
11	c5j84A_	 Alignment		14.6	9	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form

12	d2ptha_	 Alignment		14.6	18	Fold: Phosphorylase/hydrolase-like Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
13	c5ze4A_	 Alignment		13.5	12	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
14	c4jd9B_	 Alignment		12.8	5	PDB header: protein binding Chain: B: PDB Molecule: 14.5 kda salivary protein; PDBTitle: contact pathway inhibitor from a sand fly
15	c5oynB_	 Alignment		11.4	18	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
16	d1j2na_	 Alignment		11.4	22	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17
17	c5ja9D_	 Alignment		11.2	22	PDB header: toxin Chain: D: PDB Molecule: toxin hlgb-2; PDBTitle: crystal structure of the hlgb2 toxin in complex with nb6
18	c5lbnD_	 Alignment		11.2	6	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor frmr; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
19	d1k5oa_	 Alignment		11.0	22	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17
20	d1wrda1	 Alignment		10.6	5	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
21	c4fopA_	 Alignment	not modelled	10.0	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from acinetobacter2 baumannii at 1.86 a resolution
22	d1sq4a_	 Alignment	not modelled	8.7	15	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YlbaA-like
23	c4dhwA_	 Alignment	not modelled	8.6	15	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from pseudomonas2 aeruginosa with adipic acid at 2.4 angstrom resolution
24	d2oqea3	 Alignment	not modelled	8.2	4	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
25	c4ynhA_	 Alignment	not modelled	7.9	15	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 5; PDBTitle: structure of the c. elegans sas-5 implico dimerization domain
26	c1soxB_	 Alignment	not modelled	7.6	32	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite oxidase; PDBTitle: sulfite oxidase from chicken liver
27	c5lcyD_	 Alignment	not modelled	7.2	6	PDB header: transcription Chain: D: PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
28	c5zx8A_	 Alignment	not modelled	7.1	21	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from thermus thermophilus

29	c2zxkB_	 Alignment	not modelled	6.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: red chlorophyll catabolite reductase, PDBTitle: crystal structure of semet-red chlorophyll catabolite2 reductase
30	c5n1tM_	 Alignment	not modelled	6.4	14	PDB header: oxidoreductase Chain: M: PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
31	c4adzA_	 Alignment	not modelled	6.3	6	PDB header: transcription Chain: A: PDB Molecule: csor; PDBTitle: crystal structure of the apo form of a copper-sensitive operon2 regulator (csor) protein from streptomyces lividans
32	d1rc6a_	 Alignment	not modelled	5.8	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YlbA-like
33	c5u1cA_	 Alignment	not modelled	5.6	13	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
34	c2hh7A_	 Alignment	not modelled	5.5	3	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
35	c2yreA_	 Alignment	not modelled	5.2	15	PDB header: protein binding Chain: A: PDB Molecule: f-box only protein 30; PDBTitle: solution structure of the zinc finger domains (1-87) from2 human f-box only protein
36	d1aqaa_	 Alignment	not modelled	5.1	21	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5