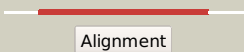

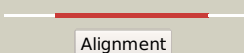
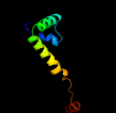
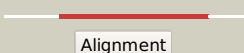

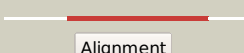





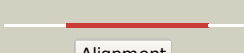

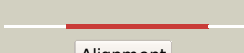

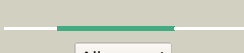



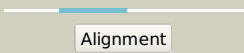

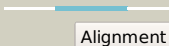
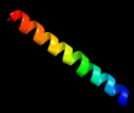
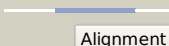

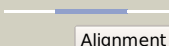

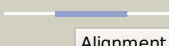

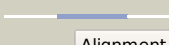

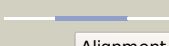

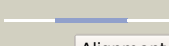

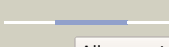





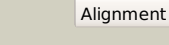
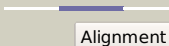
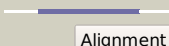
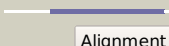
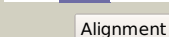


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3221A (-) _3598048_3598353
Date	Thu Aug 8 16:20:42 BST 2019
Unique Job ID	e8f6af54cbda1390

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5frhA_	 Alignment		99.7	22	PDB header: transcription Chain: A: PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra
2	c5wuqD_	 Alignment		99.4	26	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
3	c3vdoB_	 Alignment		99.3	13	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
4	c2z2sD_	 Alignment		98.9	14	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
5	c3hugJ_	 Alignment		98.9	20	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	c6in7A_	 Alignment		98.9	6	PDB header: transcription Chain: A: PDB Molecule: sigma factor algu negative regulatory protein; PDBTitle: crystal structure of algu in complex with muca(cyto)
7	d1or7c_	 Alignment		97.2	18	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		97.2	18	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	c5camC_	 Alignment		40.6	8	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)
10	c2xuvB_	 Alignment		40.1	27	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
11	d2db7a1	 Alignment		39.3	27	Fold: Orange domain-like Superfamily: Orange domain-like Family: Hairy Orange domain

12	c5fmnB	 Alignment		33.1	29	PDB header: dna binding protein Chain: B; PDB Molecule: inrs; PDBTitle: the nickel-responsive transcriptional regulator inrs
13	c5ze4A	 Alignment		28.9	21	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	c2hh7A	 Alignment		27.7	26	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
15	c5lcyD	 Alignment		27.3	16	PDB header: transcription Chain: D; PDB Molecule: frm; PDBTitle: formaldehyde-responsive regulator frm e64h variant from salmonella2 enterica serovar typhimurium
16	c3aaiB	 Alignment		26.2	23	PDB header: transcription Chain: B; PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
17	c5lbnD	 Alignment		24.5	16	PDB header: transcription Chain: D; PDB Molecule: transcriptional repressor frm; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frm from escherichia coli
18	c4m1pA	 Alignment		23.7	16	PDB header: transcription repressor Chain: A; PDB Molecule: copper-sensitive operon repressor (csor); PDBTitle: crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
19	c4adzA	 Alignment		23.1	19	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
20	c5oynB	 Alignment		22.9	14	PDB header: lyase Chain: B; PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
21	c4xvvB	 Alignment	not modelled	22.9	13	PDB header: chaperone Chain: B; PDB Molecule: acid stress chaperone hdeb; PDBTitle: crystal structure of an acid stress chaperone hdeb (kpn_03484) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a3 resolution
22	c2lkyA	 Alignment	not modelled	22.2	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
23	c5x56A	 Alignment	not modelled	16.8	10	PDB header: photosynthesis Chain: A; PDB Molecule: photosystem ii repair protein psb27-h1, chloroplastic; PDBTitle: crystal structure of psb27 from arabidopsis thaliana
24	d2elca1	 Alignment	not modelled	16.3	25	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
25	c5j84A	 Alignment	not modelled	15.8	7	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
26	d1khd1	 Alignment	not modelled	15.4	8	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
27	d1uoua1	 Alignment	not modelled	15.2	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain

						Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
28	c4jd9B_	Alignment	not modelled	15.2	20	PDB header: protein binding Chain: B: PDB Molecule: 14.5 kda salivary protein; PDBTitle: contact pathway inhibitor from a sand fly
29	c2kvcA_	Alignment	not modelled	15.2	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
30	c3mayE_	Alignment	not modelled	14.0	17	PDB header: heme-binding protein Chain: E: PDB Molecule: possible exported protein; PDBTitle: crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
31	c6gvkB_	Alignment	not modelled	14.0	80	PDB header: structural protein Chain: B: PDB Molecule: dystonin; PDBTitle: second pair of fibronectin type iii domains of integrin beta4 (t1663r2 mutant) bound to the bullous pemphigoid antigen bp230 (bpag1e)
32	c6gvlB_	Alignment	not modelled	13.9	80	PDB header: structural protein Chain: B: PDB Molecule: dystonin; PDBTitle: second pair of fibronectin type iii domains of integrin beta4 bound to2 the bullous pemphigoid antigen bp230 (bpag1e)
33	c2yreA_	Alignment	not modelled	13.3	50	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
34	d2pp4a1	Alignment	not modelled	12.7	26	Fold: TAFH domain-like Superfamily: TAFH domain-like Family: TAFH domain-like
35	d2hwna1	Alignment	not modelled	12.6	29	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
36	c2wfbA_	Alignment	not modelled	11.7	33	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
37	c5edvA_	Alignment	not modelled	11.4	17	PDB header: ligase/transferase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rnf31; PDBTitle: structure of the hoip-rbr/ubch5b~ubiquitin transfer complex
38	c3jb9j_	Alignment	not modelled	11.3	15	PDB header: rna binding protein/rna Chain: I: PDB Molecule: small nuclear ribonucleoprotein f; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
39	d1k8ia2	Alignment	not modelled	11.0	29	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
40	c5m45l_	Alignment	not modelled	10.7	13	PDB header: ligase Chain: I: PDB Molecule: acetone carboxylase gamma subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
41	c2lm4A_	Alignment	not modelled	10.7	13	PDB header: protein binding Chain: A: PDB Molecule: succinate dehydrogenase assembly factor 2, mitochondrial; PDBTitle: solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
42	d1wjva1	Alignment	not modelled	10.7	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: C2HC finger
43	d1puza_	Alignment	not modelled	10.4	11	Fold: YgfY-like Superfamily: YgfY-like Family: YgfY-like
44	c2kmfA_	Alignment	not modelled	10.3	17	PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii 11 kda protein; PDBTitle: solution structure of psb27 from cyanobacterial photosystem2 ii
45	d1r2aa_	Alignment	not modelled	9.9	23	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
46	d1k5oa_	Alignment	not modelled	9.7	24	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17
47	d1o17a1	Alignment	not modelled	9.2	14	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
48	d2b5ea3	Alignment	not modelled	9.2	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
49	d1v8ga1	Alignment	not modelled	9.1	22	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
50	d1j2na_	Alignment	not modelled	9.0	24	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17

51	d1jroa1	Alignment	not modelled	8.7	23	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
52	d2tpta1	Alignment	not modelled	8.6	7	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
53	d1ffva1	Alignment	not modelled	8.6	15	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
54	d1n62a1	Alignment	not modelled	8.4	20	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
55	c2qtdA	Alignment	not modelled	7.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
56	c2re2A	Alignment	not modelled	7.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein ta1041; PDBTitle: crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
57	d1brwa1	Alignment	not modelled	7.6	14	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
58	c2y6xA	Alignment	not modelled	7.4	16	PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii 11 kd protein; PDBTitle: structure of psb27 from thermosynechococcus elongatus
59	c3b73A	Alignment	not modelled	7.1	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phi11 repressor-like protein; PDBTitle: crystal structure of the phi11 repressor-like protein from haloarcula2 marismortui
60	c2c1bP	Alignment	not modelled	7.0	12	PDB header: metal binding protein Chain: P: PDB Molecule: dps-like protein; PDBTitle: the structure of the dps-like protein from sulfolobus2 solfataricus reveals a bacterioferritin-like di-metal3 binding site within a dps-like dodecameric assembly
61	d2f8aa1	Alignment	not modelled	7.0	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
62	c2zxkB	Alignment	not modelled	6.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: red chlorophyll catabolite reductase, PDBTitle: crystal structure of semet-red chlorophyll catabolite2 reductase
63	c5d6sB	Alignment	not modelled	6.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
64	c4a1qB	Alignment	not modelled	6.6	19	PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
65	c4aa1B	Alignment	not modelled	6.6	19	PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: thermostable protein from hyperthermophilic virus ssv-rh
66	d1t3va	Alignment	not modelled	6.5	27	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
67	d1e0ea	Alignment	not modelled	6.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
68	d1v58a1	Alignment	not modelled	6.5	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
69	c2rhfA	Alignment	not modelled	6.4	31	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase recq; PDBTitle: d. radiodurans recq hrdc domain 3
70	c3ol4B	Alignment	not modelled	6.4	16	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
71	c1nohB	Alignment	not modelled	6.0	15	PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
72	d1t3ba1	Alignment	not modelled	5.6	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
73	c3gv1A	Alignment	not modelled	5.4	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
74	d2di0a1	Alignment	not modelled	5.3	12	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
75	c4tr3A	Alignment	not modelled	5.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: type iii iodothyronine deiodinase; PDBTitle: mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
76	c2iyuA	Alignment	not modelled	5.2	7	PDB header: unknown function Chain: A: PDB Molecule: terb;

76	c2jauA_	Alignment	not modelled	5.2	7	PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae PDB header: transferase
77	c4gtnA_	Alignment	not modelled	5.2	15	Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
78	d1rdua_	Alignment	not modelled	5.2	13	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
79	d2ou3a1	Alignment	not modelled	5.2	19	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
80	d1k6ya1	Alignment	not modelled	5.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
81	d1wjfa_	Alignment	not modelled	5.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
82	c2yucA_	Alignment	not modelled	5.1	33	PDB header: signaling protein Chain: A: PDB Molecule: tnf receptor-associated factor 4; PDBTitle: solution structure of the traf-type zinc finger domains2 (102-164) from human tnf receptor associated factor 4 PDB header: ligase/transferase
83	c5edvB_	Alignment	not modelled	5.1	17	Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rnf31; PDBTitle: structure of the hoip-rbr/ubch5b~ubiquitin transfer complex