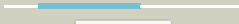

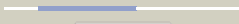
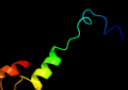


















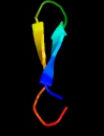


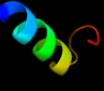


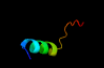




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2190Ac_(RVBD2190Ac)_2453466_2453744
Date	Mon Aug 5 13:25:31 BST 2019
Unique Job ID	2a8c2aa5f6c7dc0a

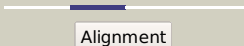

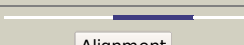

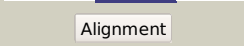
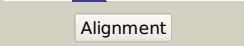
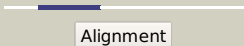


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6btmB_	 Alignment		34.8	28	PDB header: membrane protein Chain: B; PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
2	c6f0kB_	 Alignment		27.1	34	PDB header: membrane protein Chain: B; PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
3	c1ag7A_	 Alignment		26.2	46	PDB header: neurotoxin Chain: A; PDB Molecule: conotoxin gs; PDBTitle: conotoxin gs, nmr, 20 structures
4	d1ag7a_	 Alignment		26.2	46	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Conotoxin
5	c6jdpA_	 Alignment		25.9	32	PDB header: antitoxin Chain: A; PDB Molecule: imm52 family protein; PDBTitle: the imm52 family protein tsit (pa3908) from pseudomonas aeruginosa
6	d1jcea1	 Alignment		25.8	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
7	c4j3cB_	 Alignment		25.1	28	PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
8	c5frtC_	 Alignment		24.0	31	PDB header: oxidoreductase Chain: C; PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
9	c2e2zA_	 Alignment		21.1	38	PDB header: protein transport, chaperone regulator Chain: A; PDB Molecule: tim15; PDBTitle: solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
10	d2dextx1	 Alignment		19.1	33	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Peptidylarginine deiminase Pad4, middle domain Family: Peptidylarginine deiminase Pad4, middle domain
11	c2v51E_	 Alignment		18.8	35	PDB header: structural protein/contractile protein Chain: E; PDB Molecule: mk1/myocardin-like protein 1; PDBTitle: structure of mal-rpel1 complexed to actin

12	d1gl1i	Alignment		18.5	28	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
13	c2v51F	Alignment		17.8	35	PDB header: structural protein/contractile protein Chain: F; PDB Molecule: mk1/myocardin-like protein 1; PDBTitle: structure of mal-rpel1 complexed to actin
14	c3i38L	Alignment		17.6	28	PDB header: chaperone Chain: L; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
15	c2ckpB	Alignment		16.1	32	PDB header: transferase Chain: B; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha-2 in2 complex with adp
16	c3f2rB	Alignment		15.8	23	PDB header: transferase Chain: B; PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
17	c3i38K	Alignment		15.2	25	PDB header: chaperone Chain: K; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
18	c3h35B	Alignment		15.1	38	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein abo_0056; PDBTitle: structure of the uncharacterized protein abo_0056 from the2 hydrocarbon-degrading marine bacterium alcanivorax borkumensis sk2.
19	c4mo1B	Alignment		14.9	33	PDB header: transcription regulator Chain: B; PDB Molecule: antitermination protein q; PDBTitle: crystal structure of antitermination protein q from bacteriophage2 lambda. northeast structural genomics consortium target or18a.
20	d1bupa1	Alignment		14.6	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
21	c2oolA	Alignment	not modelled	14.5	28	PDB header: signaling protein Chain: A; PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbph3 from r. palustris
22	c3i38F	Alignment	not modelled	13.8	27	PDB header: chaperone Chain: F; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
23	c3kw2A	Alignment	not modelled	13.0	38	PDB header: transferase Chain: A; PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
24	c2egwB	Alignment	not modelled	12.0	20	PDB header: rna methyltransferase Chain: B; PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
25	c3eetA	Alignment	not modelled	12.0	41	PDB header: transcription regulator Chain: A; PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
26	d1dkgd1	Alignment	not modelled	11.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
27	c3dxqB	Alignment	not modelled	10.8	26	PDB header: transferase Chain: B; PDB Molecule: choline/ethanolamine kinase family protein; PDBTitle: crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
28	d1v6za2	Alignment	not modelled	10.6	19	Fold: alpha/beta knot Superfamily: alpha/beta knot

						Family:Yggj C-terminal domain-like
29	c4qxaB	Alignment	not modelled	10.6	25	PDB header: protein transport/protein binding Chain: B: PDB Molecule: small g protein signaling modulator 1; PDBTitle: crystal structure of the rab9a-rutbc2 rbd complex
30	c5e5bA	Alignment	not modelled	10.5	7	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of human spt16 n-terminal domain
31	c3i38G	Alignment	not modelled	10.5	25	PDB header: chaperone Chain: G: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
32	c3i38A	Alignment	not modelled	10.5	25	PDB header: chaperone Chain: A: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
33	d1vhka2	Alignment	not modelled	10.4	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
34	d1l5pa	Alignment	not modelled	10.3	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
35	d1kp0a2	Alignment	not modelled	10.2	10	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
36	c4uedB	Alignment	not modelled	10.2	40	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation factor 4e-binding protein 1; PDBTitle: complex of human eif4e with the 4e binding protein 4e-bp1
37	c3cb5A	Alignment	not modelled	10.0	14	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
38	d1wo9a	Alignment	not modelled	9.9	32	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
39	c5fvcF	Alignment	not modelled	9.7	38	PDB header: viral protein Chain: F: PDB Molecule: hmpv nucleoprotein; PDBTitle: structure of rna-bound decameric hmpv nucleoprotein
40	c5vm8A	Alignment	not modelled	9.4	12	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
41	c3tvjl	Alignment	not modelled	9.3	28	PDB header: hydrolase Chain: I: PDB Molecule: protease inhibitor sgpi-2; PDBTitle: catalytic fragment of masp-2 in complex with its specific inhibitor2 developed by directed evolution on sgci scaffold
42	c3i38I	Alignment	not modelled	9.3	23	PDB header: chaperone Chain: I: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
43	d1gl0i	Alignment	not modelled	9.2	32	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
44	d1vqow1	Alignment	not modelled	9.2	50	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
45	c5fmrC	Alignment	not modelled	9.0	24	PDB header: transport protein Chain: C: PDB Molecule: intraflagellar transport protein component ift52; PDBTitle: crift52 n-terminal domain
46	c4e8bA	Alignment	not modelled	9.0	38	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
47	c3i38D	Alignment	not modelled	8.9	25	PDB header: chaperone Chain: D: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
48	d1vaa3	Alignment	not modelled	8.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
49	c5ajaC	Alignment	not modelled	8.5	42	PDB header: viral protein Chain: C: PDB Molecule: sam domain and hd domain-containing protein; PDBTitle: crystal structure of mandrill samhd1 (amino acid residues 1-114)2 bound to vpx isolated from mandrill and human dcaf1 (amino3 acid residues 1058-1396)
50	c1k3rA	Alignment	not modelled	8.2	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
51	c6czaB	Alignment	not modelled	8.0	47	PDB header: oxidoreductase Chain: B: PDB Molecule: 4fe-4s ferredoxin, iron-sulfur binding domain protein; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate
52	c2hfvA	Alignment	not modelled	8.0	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90. PDB header: transcription

53	c5ce6A	Alignment	not modelled	7.6	19	Chain: A: PDB Molecule: fact-spt16; PDBTitle: n-terminal domain of fact complex subunit spt16 from cicer arietinum2 (chickpea)
54	c5cnxB	Alignment	not modelled	7.4	15	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase ypdf; PDBTitle: crystal structure of xaa-pro aminopeptidase from escherichia coli k12
55	c2xttA	Alignment	not modelled	7.3	32	PDB header: hydrolase Chain: A: PDB Molecule: protease inhibitor sgpi-1; PDBTitle: bovine trypsin in complex with evolutionary enhanced schistocerca2 gregaria protease inhibitor 1 (sgpi-1-p02)
56	d1kqfb1	Alignment	not modelled	7.3	44	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
57	c4phtC	Alignment	not modelled	7.2	64	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspi from the2 vibrio vulnificus type ii secretion system
58	c2o9bA	Alignment	not modelled	7.1	28	PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
59	c3d3kD	Alignment	not modelled	7.0	11	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
60	c5dbuL	Alignment	not modelled	7.0	30	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
61	c3m1mA	Alignment	not modelled	7.0	21	PDB header: replication Chain: A: PDB Molecule: orf904; PDBTitle: crystal structure of the primase-polymerase from sulfobolus islandicus
62	c5fmsA	Alignment	not modelled	7.0	21	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 52 homolog; PDBTitle: mmift52 n-terminal domain
63	c3ah7A	Alignment	not modelled	6.9	27	PDB header: metal binding protein Chain: A: PDB Molecule: [2fe-2s]ferredoxin; PDBTitle: crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
64	c3f2rA	Alignment	not modelled	6.9	32	PDB header: transferase Chain: A: PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
65	c2jm1A	Alignment	not modelled	6.7	33	PDB header: metal binding protein Chain: A: PDB Molecule: transcriptional regulator atrx; PDBTitle: structures and chemical shift assignments for the add domain of the2 atrx protein
66	c2f91B	Alignment	not modelled	6.6	32	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: serine protease inhibitor i/ii; PDBTitle: 1.2a resolution structure of a crayfish trypsin complexed2 with a peptide inhibitor, sgti
67	c3i38H	Alignment	not modelled	6.5	21	PDB header: chaperone Chain: H: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
68	c5laaB	Alignment	not modelled	6.4	26	PDB header: transferase Chain: B: PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of the methyltransferase subunit a from methanothermus2 fervidus in complex with cobalamin
69	d1d1da1	Alignment	not modelled	6.0	44	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
70	c5fzxA	Alignment	not modelled	5.9	45	PDB header: toxin Chain: A: PDB Molecule: u5-scytotoxin-sth1a; PDBTitle: high resolution solution nmr structure of the spider venom2 peptide u5-scytotoxin-sth1a
71	c4djzH	Alignment	not modelled	5.8	28	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: protease inhibitor sgpi-2; PDBTitle: catalytic fragment of masp-1 in complex with its specific inhibitor2 developed by directed evolution on sgci scaffold
72	c2a45H	Alignment	not modelled	5.8	30	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
73	c3edpB	Alignment	not modelled	5.8	38	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
74	d1i7ha	Alignment	not modelled	5.7	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
75	d2cjoa	Alignment	not modelled	5.7	34	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
76	c1yw7A	Alignment	not modelled	5.7	20	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase 2; PDBTitle: h-metap2 complexed with a444148
77	c2wj8N	Alignment	not modelled	5.6	30	PDB header: rna binding protein/rna Chain: N: PDB Molecule: nucleoprotein; PDBTitle: respiratory syncytial virus ribonucleoprotein
78	c2ivfB	Alignment	not modelled	5.5	42	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum

79	c1ti2F_	 Alignment	not modelled	5.5	32	PDB header: oxidoreductase Chain: F; PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
80	d2cu2a1	 Alignment	not modelled	5.4	22	Fold: Single-stranded left-handed beta-helix Superfamily: Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain Family: Guanosine diphospho-D-mannose pyrophosphorylase/mannose-6-phosphate isomerase linker domain
81	d1mzha_	 Alignment	not modelled	5.4	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
82	d2e8aa1	 Alignment	not modelled	5.4	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
83	c5uj5A_	 Alignment	not modelled	5.4	19	PDB header: electron transport Chain: A; PDB Molecule: adrenodoxin; PDBTitle: solution structure of the oxidized iron-sulfur protein adrenodoxin2 from encephalitozoon cuniculi. seattle structural genomics center for3 infectious disease target encua.00705.a
84	d1es6a2	 Alignment	not modelled	5.2	44	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
85	c2f5zK_	 Alignment	not modelled	5.1	41	PDB header: oxidoreductase/protein binding Chain: K; PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
86	c3i38C_	 Alignment	not modelled	5.1	20	PDB header: chaperone Chain: C; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
87	c3i38E_	 Alignment	not modelled	5.1	20	PDB header: chaperone Chain: E; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578