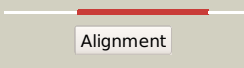

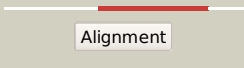

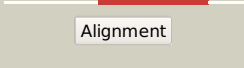

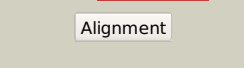

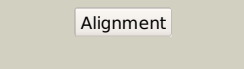

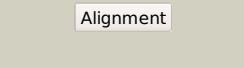

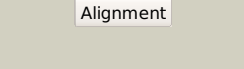

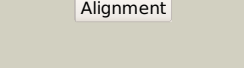

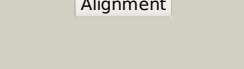

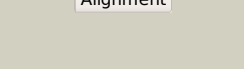

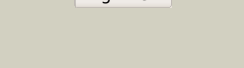



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3237C_(-)_3613118_3613600
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	8493d32786285e9e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bknA_	 Alignment		99.8	26	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein ph0236; PDBTitle: structure analysis of unknown function protein
2	d2fy8a2	 Alignment		99.7	20	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
3	d1vcta2	 Alignment		99.7	29	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
4	c4xttA_	 Alignment		99.7	22	PDB header: transport protein Chain: A: PDB Molecule: putative potassium transport protein; PDBTitle: structural studies of potassium transport protein ktra regulator of2 conductance of k+ (rck) c domain in complex with cyclic diadenosine3 monophosphate (c-di-amp)
5	c2fy8A_	 Alignment		99.6	17	PDB header: transport protein Chain: A: PDB Molecule: calcium-gated potassium channel mthk; PDBTitle: crystal structure of mthk rck domain in its ligand-free gating-ring2 form
6	c1lnqC_	 Alignment		99.6	17	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
7	c3jxoB_	 Alignment		99.5	24	PDB header: transport protein Chain: B: PDB Molecule: trka-n domain protein; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
8	c4gx2B_	 Alignment		99.5	27	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
9	c4g65A_	 Alignment		99.4	20	PDB header: transport protein Chain: A: PDB Molecule: trk system potassium uptake protein trka; PDBTitle: potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
10	c4j7cA_	 Alignment		99.4	21	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis
11	c4gvlB_	 Alignment		99.4	29	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: crystal structure of the gsuk rck domain

12	c4ys2A_	Alignment		99.4	23	PDB header: immune system Chain: A: PDB Molecule: na+/h+ antiporter-like protein; PDBTitle: rck domain with cda
13	c3l4bG_	Alignment		98.9	23	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
14	c3u6nC_	Alignment		98.7	17	PDB header: transport protein Chain: C: PDB Molecule: high-conductance ca2+-activated k+ channel protein; PDBTitle: open structure of the bk channel gating ring
15	c4hpfB_	Alignment		98.5	15	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: potassium channel subfamily u member 1; PDBTitle: structure of the human slo3 gating ring
16	c3mt5A_	Alignment		98.2	15	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium large conductance calcium-activated channel, PDBTitle: crystal structure of the human bk gating apparatus
17	c5u76A_	Alignment		98.0	20	PDB header: transport protein Chain: A: PDB Molecule: potassium channel subfamily t member 1; PDBTitle: chicken slo2.2 in a closed conformation vitrified in the presence of 2 300 mm nacl
18	c5a6eC_	Alignment		97.9	19	PDB header: transport Chain: C: PDB Molecule: gating ring of potassium channel subfamily t member 1; PDBTitle: cryo-em structure of the slo2.2 na-activated k channel
19	c5tj6A_	Alignment		97.8	17	PDB header: membrane protein Chain: A: PDB Molecule: high conductance calcium-activated potassium channel; PDBTitle: ca2+ bound aplysia slo1
20	c3nafA_	Alignment		97.4	17	PDB header: ion transport Chain: A: PDB Molecule: calcium-activated potassium channel subunit alpha-1, PDBTitle: structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
21	c5wwwA_	Alignment	not modelled	36.7	14	PDB header: rna binding protein/rna Chain: A: PDB Molecule: rna-binding e3 ubiquitin-protein ligase mex3c; PDBTitle: crystal structure of the kh1 domain of human rna-binding e3 ubiquitin-2 protein ligase mex-3c complex with rna
22	d2cu3a1	Alignment	not modelled	36.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
23	c1tuaA_	Alignment	not modelled	36.1	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ape0754; PDBTitle: 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
24	d1zud21	Alignment	not modelled	34.9	7	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
25	c5z1vB_	Alignment	not modelled	30.6	16	PDB header: unknown function Chain: B: PDB Molecule: avrpib protein; PDBTitle: crystal structure of avrpib
26	d1e5qa1	Alignment	not modelled	29.9	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	d1k25a2	Alignment	not modelled	27.6	2	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
28	c2qndA_	Alignment	not modelled	26.8	17	PDB header: rna binding protein Chain: A: PDB Molecule: fmr1 protein; PDBTitle: crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein

29	d1tuaa2	Alignment	not modelled	24.4	28	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
30	c2kl0A	Alignment	not modelled	22.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574.2 northeast structural genomics consortium (nesg) target rpr325
31	c2bjeA	Alignment	not modelled	21.5	22	PDB header: hydrolase Chain: A: PDB Molecule: acylphosphatase; PDBTitle: acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
32	c3cwiA	Alignment	not modelled	21.3	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
33	d1rp5a2	Alignment	not modelled	20.1	0	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
34	c3jcrK	Alignment	not modelled	18.3	18	PDB header: splicing Chain: K: PDB Molecule: hprp3; PDBTitle: 3d structure determination of the human*4/u6.u5* tri-snrrp complex
35	d1k25a1	Alignment	not modelled	18.2	13	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
36	c2kfwA	Alignment	not modelled	17.7	17	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
37	c5fwhA	Alignment	not modelled	16.4	32	PDB header: structural protein Chain: A: PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
38	c2dgrA	Alignment	not modelled	16.3	23	PDB header: rna binding protein Chain: A: PDB Molecule: ring finger and kh domain-containing protein 1; PDBTitle: solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
39	d1y7ma2	Alignment	not modelled	16.0	24	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
40	c6g18x	Alignment	not modelled	16.0	21	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state c
41	d1w2ia	Alignment	not modelled	15.7	15	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
42	c2e3uA	Alignment	not modelled	15.6	33	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein ph1566; PDBTitle: crystal structure analysis of dim2p from pyrococcus horikoshii ot3
43	d1tygb	Alignment	not modelled	15.0	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
44	c2y3mA	Alignment	not modelled	14.8	4	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein hofq; PDBTitle: structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
45	c4uw2C	Alignment	not modelled	14.5	25	PDB header: immune system Chain: C: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
46	c3rl4A	Alignment	not modelled	14.2	17	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
47	c3br8A	Alignment	not modelled	14.1	19	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis
48	c4dt4A	Alignment	not modelled	14.0	7	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
49	c2lxfA	Alignment	not modelled	13.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
50	c3ie4A	Alignment	not modelled	13.9	20	PDB header: immune system Chain: A: PDB Molecule: gram-negative binding protein 3; PDBTitle: b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor
51	d1pyya1	Alignment	not modelled	13.7	13	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
52	c4guaB	Alignment	not modelled	13.7	14	PDB header: hydrolase Chain: B: PDB Molecule: non-structural polyprotein; PDBTitle: alphavirus p23pro-zbd
53	c6emlp	Alignment	not modelled	12.7	23	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae PDB header: sugar binding protein

54	c2rqeA	Alignment	not modelled	12.6	15	Chain: A: PDB Molecule: beta-1,3-glucan-binding protein; PDBTitle: solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
55	c4hi2B	Alignment	not modelled	12.6	15	PDB header: hydrolase Chain: B: PDB Molecule: acylphosphatase; PDBTitle: crystal structure of an acylphosphatase protein cage
56	d1pyya2	Alignment	not modelled	12.3	0	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
57	c2hh2A	Alignment	not modelled	12.2	18	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the fourth kh domain of ksrp
58	d8ohma2	Alignment	not modelled	11.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
59	c2i5hA	Alignment	not modelled	11.2	63	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
60	d2i5ha1	Alignment	not modelled	11.2	63	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
61	c6b8wB	Alignment	not modelled	11.1	14	PDB header: transcription Chain: B: PDB Molecule: xre family transcriptional regulator; PDBTitle: 1.9 angstrom resolution crystal structure of cupin_2 domain (pfam2 07883) of xre family transcriptional regulator from enterobacter3 cloacae.
62	d1pn0a3	Alignment	not modelled	10.5	18	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: PHBH-like
63	d1zzka1	Alignment	not modelled	10.5	20	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
64	d2b9da1	Alignment	not modelled	10.1	22	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
65	d1sdwa2	Alignment	not modelled	10.1	12	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
66	d1zrra1	Alignment	not modelled	10.1	15	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acireductone dioxygenase
67	c1w78A	Alignment	not modelled	10.0	24	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
68	c4yhwa	Alignment	not modelled	9.9	33	PDB header: splicing Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: yeast prp3 (296-469) in complex with fragment of u4/u6 di-snrna
69	d1o5za1	Alignment	not modelled	9.9	16	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folylpolyglutamate synthetase, C-terminal domain
70	c2wkda	Alignment	not modelled	9.7	33	PDB header: dna binding protein Chain: A: PDB Molecule: orf34p2; PDBTitle: crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
71	c3gr5A	Alignment	not modelled	9.2	15	PDB header: membrane protein Chain: A: PDB Molecule: escsc; PDBTitle: periplasmic domain of the outer membrane secretin escsc from2 enteropathogenic e.coli (epec)
72	d1ulra	Alignment	not modelled	9.1	10	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
73	d1nm2a2	Alignment	not modelled	9.1	18	Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
74	c2gu9B	Alignment	not modelled	8.9	19	PDB header: immune system Chain: B: PDB Molecule: tetracenomycin polyketide synthesis protein; PDBTitle: crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
75	d2ewla1	Alignment	not modelled	8.8	17	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
76	d1dtja	Alignment	not modelled	8.8	14	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
77	c1tygG	Alignment	not modelled	8.7	18	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
78	c2hc8A	Alignment	not modelled	8.6	32	PDB header: transport protein Chain: A: PDB Molecule: cation-transporting atpase, p-type; PDBTitle: structure of the a. fulgidus copa a-domain
79	c2ki0A	Alignment	not modelled	8.4	19	PDB header: de novo protein Chain: A: PDB Molecule: ds119; PDBTitle: nmr structure of a de novo designed beta alpha beta

80	c2y9kG_	Alignment	not modelled	8.4	12	PDB header: protein transport Chain: G: PDB Molecule: protein invg; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
81	c1uheA_	Alignment	not modelled	8.4	14	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex
82	c5z2vB_	Alignment	not modelled	8.2	71	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
83	c2yqrA_	Alignment	not modelled	8.2	14	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
84	c2kr7A_	Alignment	not modelled	8.2	7	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase slyd; PDBTitle: solution structure of helicobacter pylori slyd
85	c3rykB_	Alignment	not modelled	8.2	27	PDB header: isomerase Chain: B: PDB Molecule: ddtp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
86	d1g7sa2	Alignment	not modelled	8.1	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
87	c2l8kA_	Alignment	not modelled	8.1	33	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 7; PDBTitle: nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
88	c4idiaA_	Alignment	not modelled	7.9	16	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
89	c1vddC_	Alignment	not modelled	7.9	57	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
90	c2z1eA_	Alignment	not modelled	7.9	19	PDB header: transferase Chain: A: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of hype from thermococcus kodakaraensis (outward2 form)
91	d1kjwa1	Alignment	not modelled	7.8	35	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
92	c2khaA_	Alignment	not modelled	7.8	16	PDB header: sugar binding protein Chain: A: PDB Molecule: beta-1,3-glucan-binding protein; PDBTitle: solution structure of a pathogen recognition domain from a2 lepidopteran insect, plodia interpunctella
93	c3fp9E_	Alignment	not modelled	7.8	31	PDB header: hydrolase Chain: E: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
94	c4zuaA_	Alignment	not modelled	7.7	21	PDB header: transcription Chain: A: PDB Molecule: exoenzyme s synthesis regulatory protein exsa; PDBTitle: crystal structure of the exsa regulatory domain
95	c5i65A_	Alignment	not modelled	7.7	27	PDB header: unknown function Chain: A: PDB Molecule: nonstructural proteins orf1a; PDBTitle: porcine reproductive and respiratory syndrome virus nonstructural2 protein 7 alpha (nsp7 alpha)
96	d2cta1	Alignment	not modelled	7.7	14	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
97	c5zvqA_	Alignment	not modelled	7.6	57	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
98	c3dwmA_	Alignment	not modelled	7.6	18	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
99	d1vdda_	Alignment	not modelled	7.5	57	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR