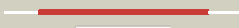










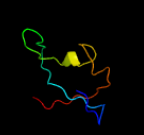









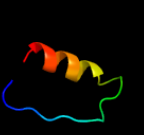


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1375 (-) _1547838_1549157
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	173a41c2b041028d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ci7A_	 Alignment		100.0	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: ycao; PDBTitle: the structure of ycao from methanopyrus kandleri bound with amppcp and 2 mg2+
2	c4bs9A_	 Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud
3	c4q86B_	 Alignment		100.0	19	PDB header: protein binding Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase accessory PDBTitle: ycao with amp bound
4	c6grgD_	 Alignment		100.0	13	PDB header: biosynthetic protein Chain: D: PDB Molecule: microcin b17-processing protein mcbbd; PDBTitle: e. coli microcin synthetase mcbbcd complex with promccb17, adp and 2 phosphate bound
5	c2mfzA_	 Alignment		58.4	42	PDB header: structural protein Chain: A: PDB Molecule: minor ampullate spidroin; PDBTitle: nmr structure of c-terminal domain from a. ventricosus minor ampullate 2 spidroin (misp)
6	c1oheA_	 Alignment		49.2	18	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
7	d1sr9a3	 Alignment		34.7	26	Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
8	d1lcka1	 Alignment		27.7	33	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
9	c5b16A_	 Alignment		25.9	33	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease 3, drosha, ribonuclease 3, drosha, ribonuclease 3; PDBTitle: x-ray structure of drosha in complex with the c-terminal tail of 2 dgcr8.
10	d1phta_	 Alignment		25.7	35	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
11	d1lxoa1	 Alignment		23.5	32	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like

12	c1cg2D_	Alignment		22.3	12	PDB header: metallocarboxypeptidase Chain: D: PDB Molecule: carboxypeptidase g2; PDBTitle: carboxypeptidase g2
13	c2o55A_	Alignment		22.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
14	d1fmka1	Alignment		21.8	38	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
15	d1shfa_	Alignment		21.1	38	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
16	c4afzC_	Alignment		20.6	38	PDB header: hydrolase/de novo protein Chain: C: PDB Molecule: fynomer; PDBTitle: human chymase - fynomer complex
17	d1jo8a_	Alignment		20.6	24	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
18	c3cqtA_	Alignment		19.5	33	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fyn; PDBTitle: n53i v55l mutant of fyn sh3 domain
19	c4jhdF_	Alignment		19.4	57	PDB header: structural protein/protein binding Chain: F: PDB Molecule: protein cordon-bleu; PDBTitle: crystal structure of an actin dimer in complex with the actin2 nucleator cordon-bleu
20	c6edfA_	Alignment		18.9	38	PDB header: transferase Chain: A: PDB Molecule: fyn; PDBTitle: fragment of a tyrosine-protein kinase
21	c2e5kA_	Alignment	not modelled	17.8	30	PDB header: protein binding Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: solution structure of sh3 domain in suppressor of t-cell2 receptor signaling 1
22	d1k1za_	Alignment	not modelled	17.6	24	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
23	d1efna_	Alignment	not modelled	17.3	38	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
24	c2j06B_	Alignment	not modelled	17.2	24	PDB header: signal transduction Chain: B: PDB Molecule: ras gtpase-activating protein 1; PDBTitle: crystal structure of the rasgap sh3 domain at 1.8 angstrom2 resolution
25	c2fpeB_	Alignment	not modelled	17.2	29	PDB header: signaling protein Chain: B: PDB Molecule: c-jun-amino-terminal kinase interacting protein 1; PDBTitle: conserved dimerization of the ib1 src-homology 3 domain
26	d1gcqc_	Alignment	not modelled	16.8	25	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
27	c2qyxB_	Alignment	not modelled	16.1	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein mj0159; PDBTitle: crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
28	c4yxaA_	Alignment	not modelled	16.0	58	PDB header: protein transport Chain: A: PDB Molecule: surface presentation of antigens protein spao; PDBTitle: complex of spao(spao1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein

29	c4wyqB	Alignment	not modelled	15.8	14	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: risc-loading complex subunit tarbp2; PDBTitle: crystal structure of the dicer-trbp interface
30	c2lj0A	Alignment	not modelled	15.1	29	PDB header: signaling protein Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: the third sh3 domain of r85fl
31	c2kt1A	Alignment	not modelled	15.1	35	PDB header: protein binding Chain: A: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit PDBTitle: solution nmr structure of the sh3 domain from the p85beta2 subunit of phosphatidylinositol 3-kinase from h.sapiens,3 northeast structural genomics consortium target hr5531e
32	d1y57a1	Alignment	not modelled	14.8	38	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
33	c2ct3A	Alignment	not modelled	14.3	24	PDB header: signaling protein Chain: A: PDB Molecule: vinexin; PDBTitle: solution structure of the sh3 domain of the vinexin protein
34	d2uube2	Alignment	not modelled	14.2	20	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
35	c2pokB	Alignment	not modelled	13.8	14	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
36	c4rksB	Alignment	not modelled	13.7	11	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein ta1305; PDBTitle: crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)
37	d1ojra	Alignment	not modelled	13.4	16	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
38	c1z9zA	Alignment	not modelled	13.4	24	PDB header: structural protein Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: crystal structure of yeast sla1 sh3 domain 3
39	d1uhza	Alignment	not modelled	13.2	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
40	d1f20a2	Alignment	not modelled	13.0	13	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
41	c5vaqC	Alignment	not modelled	12.4	37	PDB header: signaling protein Chain: C: PDB Molecule: fibroblast growth factor 21; PDBTitle: crystal structure of beta-klotho in complex with fgf21ct
42	c6gjeA	Alignment	not modelled	12.4	26	PDB header: protein transport Chain: A: PDB Molecule: protein amnionless; PDBTitle: structure of the amnionless(20-357)-cubilin(36-135) complex
43	d1ewqa4	Alignment	not modelled	12.2	25	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
44	c2cucA	Alignment	not modelled	12.1	40	PDB header: signaling protein Chain: A: PDB Molecule: sh3 domain containing ring finger 2; PDBTitle: solution structure of the sh3 domain of the mouse2 hypothetical protein sh3rf2
45	d1zbsa2	Alignment	not modelled	12.0	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
46	c4g6zA	Alignment	not modelled	12.0	28	PDB header: ligase Chain: A: PDB Molecule: glutamate-trna ligase; PDBTitle: crystal structure of a glutamyl-trna synthetase glurs from2 burkholderia thailandensis bound to l-glutamate
47	c1yn8E	Alignment	not modelled	11.8	29	PDB header: unknown function Chain: E: PDB Molecule: nap1-binding protein 2; PDBTitle: sh3 domain of yeast nbp2
48	c2zogA	Alignment	not modelled	11.5	13	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic non-specific dipeptidase; PDBTitle: crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
49	d1pkpa2	Alignment	not modelled	11.0	21	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
50	c5d6aA	Alignment	not modelled	11.0	24	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
51	c3rojD	Alignment	not modelled	10.6	21	PDB header: hydrolase Chain: D: PDB Molecule: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7- PDBTitle: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase2 of synechocystis sp. pcc 6803
52	c4yiyA	Alignment	not modelled	10.6	31	PDB header: rna binding protein Chain: A: PDB Molecule: krna editing a6 specific protein; PDBTitle: structure of mrb1590 bound to amp-pnp
53	d1qs0b1	Alignment	not modelled	10.5	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
54	c2lcsA	Alignment	not modelled	10.2	29	PDB header: transferase, signaling protein Chain: A: PDB Molecule: nap1-binding protein 2; PDBTitle: yeast nbp2p sh3 domain in complex with a peptide from

						ste20p
55	c2zkqe	Alignment	not modelled	10.1	17	PDB header: ribosomal protein/rna Chain: E: PDB Molecule: rna expansion segment es6 part ii; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
56	c2cudA	Alignment	not modelled	9.9	38	PDB header: signaling protein Chain: A: PDB Molecule: src-like-adapter; PDBTitle: solution structure of the sh3 domain of the human src-like2 adopter protein (slap)
57	c5kdmD	Alignment	not modelled	9.6	14	PDB header: chaperone / dna binding protein Chain: D: PDB Molecule: major tegument protein; PDBTitle: crystal structure of ebv tegument protein bnr1 in complex with2 histone chaperone daxx and histones h3.3-h4
58	d1tzza1	Alignment	not modelled	9.3	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
59	c6c4sA	Alignment	not modelled	9.0	38	PDB header: transferase, peptide binding protein Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src,csrc sh3 domain; PDBTitle: human csrc sh3 domain in complex with choline kinase fragment 60-69
60	c6c4sB	Alignment	not modelled	9.0	38	PDB header: transferase, peptide binding protein Chain: B: PDB Molecule: proto-oncogene tyrosine-protein kinase src,csrc sh3 domain; PDBTitle: human csrc sh3 domain in complex with choline kinase fragment 60-69
61	c2ecza	Alignment	not modelled	9.0	29	PDB header: signaling protein Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: solution structure of the sh3 domain of sorbin and sh32 domain-containing protein 1
62	c1x6bA	Alignment	not modelled	8.9	24	PDB header: signaling protein Chain: A: PDB Molecule: rho guanine exchange factor (gef) 16; PDBTitle: solution structures of the sh3 domain of human rho guanine2 exchange factor (gef) 16
63	c4dkkA	Alignment	not modelled	8.9	15	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein staufen homolog 1; PDBTitle: the x-ray crystal structure of the human stau1 ssm-'rbd'5 domain-2 swapped dimer
64	c3trjC	Alignment	not modelled	8.7	17	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
65	d1ohea2	Alignment	not modelled	8.4	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
66	c1x27F	Alignment	not modelled	8.3	33	PDB header: signaling protein Chain: F: PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: crystal structure of lck sh2-sh3 with sh2 binding site of2 p130cas
67	c6qssA	Alignment	not modelled	8.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ignicoccus islandicus malate dehydrogenase co-2 crystallized with 10 mm tb-xo4
68	c2xzmE	Alignment	not modelled	8.2	17	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein s5 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
69	d2qale2	Alignment	not modelled	8.2	17	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
70	c1s1hE	Alignment	not modelled	8.0	14	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s2; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
71	c2yt6A	Alignment	not modelled	8.0	33	PDB header: cell cycle Chain: A: PDB Molecule: adult male urinary bladder cdna, riken full- PDBTitle: solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1
72	c3bc1F	Alignment	not modelled	7.9	30	PDB header: signaling protein/transport protein Chain: F: PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a
73	c3rniA	Alignment	not modelled	7.5	25	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: crystal structure of the sh3 domain from irsp53 (baiap2)
74	c4x8wE	Alignment	not modelled	7.3	32	PDB header: gene regulation Chain: E: PDB Molecule: loquacious, isoform b; PDBTitle: dsrbd3 of loquacious
75	c3j20F	Alignment	not modelled	7.1	17	PDB header: ribosome Chain: F: PDB Molecule: 30s ribosomal protein s5p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
76	d1sp8a2	Alignment	not modelled	7.1	27	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
77	c4arpB	Alignment	not modelled	7.0	20	PDB header: hydrolase Chain: B: PDB Molecule: pesticin; PDBTitle: structure of the inactive pesticin e178a mutant

78	c5cffE_	Alignment	not modelled	7.0	14	PDB header: transcription/rna binding protein Chain: E; PDB Molecule: staufen; PDBTitle: crystal structure of miranda/staufen dsrbd5 complex
79	d2piaa2	Alignment	not modelled	6.9	9	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
80	c3zeyP_	Alignment	not modelled	6.9	14	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s2, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
81	c3pm7A_	Alignment	not modelled	6.9	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
82	c2l3aA_	Alignment	not modelled	6.8	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
83	c5uz9D_	Alignment	not modelled	6.5	19	PDB header: immune system/rna Chain: D; PDB Molecule: crispr-associated protein csy3; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
84	c6ayyB_	Alignment	not modelled	6.5	16	PDB header: hydrolase Chain: B; PDB Molecule: fructose-1,6-bisphosphatase class 2; PDBTitle: crystal structure of apo fructose-1,6-bisphosphatase from2 mycobacterium tuberculosis
85	c1sp8A_	Alignment	not modelled	6.5	27	PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: 4-hydroxyphenylpyruvate dioxygenase
86	c3j6vE_	Alignment	not modelled	6.5	11	PDB header: ribosome Chain: E; PDB Molecule: 28s ribosomal protein s5, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
87	d2iima1	Alignment	not modelled	6.5	33	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
88	d1j5ya2	Alignment	not modelled	6.5	30	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
89	c1x6gA_	Alignment	not modelled	6.4	14	PDB header: signaling protein Chain: A; PDB Molecule: megakaryocyte-associated tyrosine-protein kinase; PDBTitle: solution structures of the sh3 domain of human2 megakaryocyte-associated tyrosine-protein kinase.
90	c2khxA_	Alignment	not modelled	6.4	30	PDB header: gene regulation,nuclear protein Chain: A; PDB Molecule: ribonuclease 3; PDBTitle: drosha double-stranded rna binding motif
91	d1arka_	Alignment	not modelled	6.2	38	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
92	d1o98a1	Alignment	not modelled	6.1	19	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
93	c3pesA_	Alignment	not modelled	6.1	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein gp49; PDBTitle: crystal structure of uncharacterized protein from pseudomonas phage2 yua
94	c5o5jE_	Alignment	not modelled	6.1	17	PDB header: ribosome Chain: E; PDB Molecule: 30s ribosomal protein s5; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
95	c3qp9C_	Alignment	not modelled	6.0	25	PDB header: oxidoreductase Chain: C; PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase
96	c2rf0D_	Alignment	not modelled	5.9	30	PDB header: transferase Chain: D; PDB Molecule: mitogen-activated protein kinase kinase kinase 10; PDBTitle: crystal structure of human mixed lineage kinase map3k10 sh3 domain
97	d2hz5a1	Alignment	not modelled	5.5	42	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
98	c2p76H_	Alignment	not modelled	5.4	21	PDB header: hydrolase Chain: H; PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
99	d1c4ka1	Alignment	not modelled	5.3	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: Ornithine decarboxylase N-terminal "wing" domain