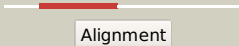


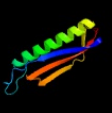




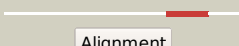
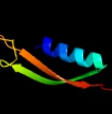
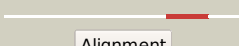
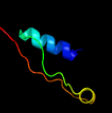
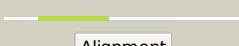

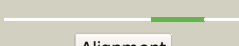


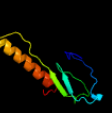

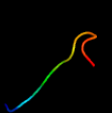







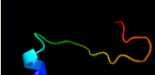
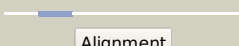

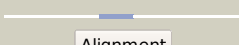

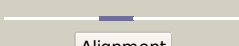
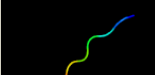
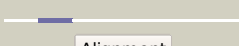
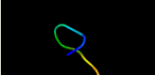
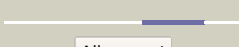


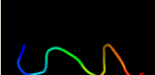



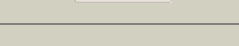
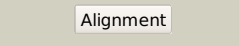


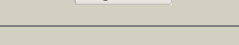


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1762c_(-)_1995061_1995849
Date	Fri Aug 2 13:30:36 BST 2019
Unique Job ID	db0ab4f90bd378f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y2iC_	 Alignment		99.9	27	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of mcsg target apc27401 from shigella flexneri
2	d1y2ia_	 Alignment		99.9	27	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
3	d1vr4a1	 Alignment		99.9	22	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
4	c3qkbB_	 Alignment		99.7	23	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
5	c2y1bA_	 Alignment		94.7	23	PDB header: membrane protein Chain: A; PDB Molecule: putative outer membrane protein, signal; PDBTitle: crystal structure of the e. coli outer membrane lipoprotein rcsf
6	c2jz7A_	 Alignment		93.9	19	PDB header: selenium-binding protein Chain: A; PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vannielii
7	c2odaB_	 Alignment		63.4	14	PDB header: protein binding Chain: B; PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
8	d1geqa_	 Alignment		53.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
9	c2qw5B_	 Alignment		51.0	11	PDB header: isomerase Chain: B; PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
10	c2nawA_	 Alignment		36.3	73	PDB header: toxin Chain: A; PDB Molecule: exendin-4, alpha/kappa-conotoxin pl14a chimera; PDBTitle: nmr solution structure of exendin-4/conotoxin chimera (ex-4[1-2 27]/pl14a)
11	c1d0rA_	 Alignment		32.4	73	PDB header: hormone/growth factor Chain: A; PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water

12	c6ge2A_	 Alignment		26.6	60	PDB header: hormone Chain: A: PDB Molecule: exendin-4; PDBTitle: exendin-4 based dual glp-1/glucagon receptor agonist
13	c1jrjA_	 Alignment		26.3	73	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
14	c4uc0A_	 Alignment		24.7	21	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
15	c2l64A_	 Alignment		21.9	36	PDB header: hormone Chain: A: PDB Molecule: glucagon-like peptide 2; PDBTitle: nmr solution structure of glp-2 in dhpc micelles
16	d1ejxb_	 Alignment		20.4	56	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
17	c4z42B_	 Alignment		19.7	33	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
18	d1p8ba_	 Alignment		19.6	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
19	c3ox4D_	 Alignment		19.4	13	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
20	c1bh0A_	 Alignment		19.3	55	PDB header: synthetic hormone Chain: A: PDB Molecule: glucagon; PDBTitle: structure of a glucagon analog
21	c3bfjK_	 Alignment	not modelled	19.1	9	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
22	d4ubpb_	 Alignment	not modelled	18.9	44	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
23	d1e9ya1	 Alignment	not modelled	18.2	56	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
24	c3zdrA_	 Alignment	not modelled	18.0	5	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
25	c2cx8B_	 Alignment	not modelled	17.8	17	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
26	d1rrma_	 Alignment	not modelled	17.0	9	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
27	c3bpkB_	 Alignment	not modelled	16.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase component b; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
28	d1ju8a_	 Alignment	not modelled	16.9	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like

				Family:Albumin 1		
29	d1vlja_	Alignment	not modelled	16.7	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
30	c2cx8A_	Alignment	not modelled	15.3	18	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
31	c1vliA_	Alignment	not modelled	14.9	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
32	c5yvma_	Alignment	not modelled	14.6	7	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
33	c2qf9B_	Alignment	not modelled	14.2	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative secreted protein; PDBTitle: crystal structure of putative secreted protein duf305 from2 streptomyces coelicolor
34	c1vhyB_	Alignment	not modelled	13.8	40	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
35	d1vliA2	Alignment	not modelled	13.7	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
36	c1vhkA_	Alignment	not modelled	13.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
37	c1e9zA_	Alignment	not modelled	13.2	56	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
38	c5ffbA_	Alignment	not modelled	12.7	10	PDB header: metal binding protein Chain: A: PDB Molecule: copm; PDBTitle: copm in the apo form
39	c3kw2A_	Alignment	not modelled	12.6	40	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
40	c1xuzA_	Alignment	not modelled	12.5	33	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
41	c3vgxD_	Alignment	not modelled	12.5	14	PDB header: membrane protein Chain: D: PDB Molecule: envelope glycoprotein gp160; PDBTitle: structure of gp41 t21/cp621-652
42	c6ncsB_	Alignment	not modelled	12.4	37	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminic acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminic acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with3 citrate
43	d1vhka2	Alignment	not modelled	12.3	7	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
44	c3qgaD_	Alignment	not modelled	12.3	33	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
45	c5o96F_	Alignment	not modelled	12.2	10	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
46	c6jkdD_	Alignment	not modelled	12.1	7	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
47	c2fh0A_	Alignment	not modelled	11.8	54	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-ch12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
48	c3fokH_	Alignment	not modelled	11.6	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
49	c4e8bA_	Alignment	not modelled	11.6	35	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rna methyltransferase rsme from e.coli
50	c4xvvB_	Alignment	not modelled	11.4	23	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
51	c1z85B_	Alignment	not modelled	11.1	17	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
						Fold: TIM beta/alpha-barrel

52	d2zdra2	Alignment	not modelled	11.0	33	Superfamily: Aldolase Family: NeuB-like
53	c4l69A_	Alignment	not modelled	10.6	10	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
54	d1nxza2	Alignment	not modelled	10.4	8	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
55	d1eija_	Alignment	not modelled	10.2	38	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
56	c2p4fA_	Alignment	not modelled	10.2	63	PDB header: chaperone Chain: A: PDB Molecule: similar to sp p32453 saccharomyces cerevisiae ynl315c
57	c2pd2A_	Alignment	not modelled	10.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
58	d1v6za2	Alignment	not modelled	10.0	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
59	c5i5iA_	Alignment	not modelled	9.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
60	c3bt5A_	Alignment	not modelled	9.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein duf305; PDBTitle: crystal structure of duf305 fragment from deinococcus radiodurans
61	c2m2qA_	Alignment	not modelled	9.6	60	PDB header: unknown function Chain: A: PDB Molecule: inhibitor cystine knot peptide mch-1; PDBTitle: solution structure of mch-1: a novel inhibitor cystine knot peptide2 from momordica charantia
62	c2xuvB_	Alignment	not modelled	9.3	27	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
63	d1y71a1	Alignment	not modelled	9.3	22	Fold: SH3-like barrel Superfamily: Kinase-associated protein B-like Family: Kinase-associated protein B-like
64	d1vaza_	Alignment	not modelled	9.0	19	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
65	d1gefa_	Alignment	not modelled	8.9	33	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
66	c3op1A_	Alignment	not modelled	8.6	26	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
67	c2zbaD_	Alignment	not modelled	8.4	24	PDB header: transferase Chain: D: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. sporotrichoides tri101 complexed with2 coenzyme a and t-2
68	d2fug71	Alignment	not modelled	8.4	23	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Nqo15-like
69	c2rbaB_	Alignment	not modelled	8.3	17	PDB header: hydrolase/dna Chain: B: PDB Molecule: g/t mismatch-specific thymine dna glycosylase; PDBTitle: structure of human thymine dna glycosylase bound to abasic and2 undamaged dna
70	c6c2uA_	Alignment	not modelled	8.2	50	PDB header: de novo protein Chain: A: PDB Molecule: phosphate-loop protein; PDBTitle: solution structure of a phosphate-loop protein
71	c1oyiA_	Alignment	not modelled	8.2	21	PDB header: viral protein Chain: A: PDB Molecule: double-stranded rna-binding protein; PDBTitle: solution structure of the z-dna binding domain of the2 vaccinia virus gene e3l
72	d1oyia_	Alignment	not modelled	8.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
73	d1to3a_	Alignment	not modelled	8.1	33	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
74	c6jx3B_	Alignment	not modelled	7.9	12	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
75	c2c2pA_	Alignment	not modelled	7.8	23	PDB header: hydrolase Chain: A: PDB Molecule: g/u mismatch-specific dna glycosylase; PDBTitle: the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
76	d1ss6a_	Alignment	not modelled	7.7	19	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
77	c6iqcA_	Alignment	not modelled	7.7	50	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein sso0352; PDBTitle: wild-type programmed cell death 5 protein from sulfolobus solfataricus
78	d1fiua_	Alignment	not modelled	7.7	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like

						Family:Restriction endonuclease NgoIV
79	d2g7oa1	Alignment	not modelled	7.6	15	Fold: TraM-like Superfamily: TraM-like Family: TraM-like
80	c2jxnA	Alignment	not modelled	7.6	54	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein ymr074c; PDBTitle: solution structure of s. cerevisiae pdcd5-like protein ymr074cp
81	d2crua1	Alignment	not modelled	7.4	60	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
82	c3okfA	Alignment	not modelled	7.4	13	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
83	c5vm8A	Alignment	not modelled	7.3	13	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
84	d3c8ya2	Alignment	not modelled	7.2	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
85	c5us5B	Alignment	not modelled	7.2	29	PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
86	c5hstB	Alignment	not modelled	7.1	13	PDB header: lyase Chain: B: PDB Molecule: polyketide synthase type i; PDBTitle: crystal structure of the dehydratase domain of mlNb from bacillus2 amyloliquefaciens
87	c4j3cB	Alignment	not modelled	6.8	11	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
88	d1w96a2	Alignment	not modelled	6.8	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
89	c3qi7A	Alignment	not modelled	6.7	10	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
90	c6n2fB	Alignment	not modelled	6.7	21	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase 2, chloroplastic; PDBTitle: meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
91	c5cwwC	Alignment	not modelled	6.7	30	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup159; PDBTitle: crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex
92	c1z4hA	Alignment	not modelled	6.6	19	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
93	c6hc2L	Alignment	not modelled	6.6	39	PDB header: cell cycle Chain: L: PDB Molecule: nuclear mitotic apparatus protein 1; PDBTitle: crystal structure of numa/Ign hetero-hexamers
94	c4ejqB	Alignment	not modelled	6.6	24	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
95	c2egwB	Alignment	not modelled	6.6	15	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
96	c2navA	Alignment	not modelled	6.6	64	PDB header: toxin Chain: A: PDB Molecule: exendin-4, alpha/kappa-conotoxin pl14a chimera; PDBTitle: nmr solution structure of ex-4[1-16]/pl14a
97	c6oawA	Alignment	not modelled	6.2	33	PDB header: immune system Chain: A: PDB Molecule: wyl1; PDBTitle: crystal structure of a crispr cas-related protein
98	c4z85A	Alignment	not modelled	6.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structure of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
99	c3iwpK	Alignment	not modelled	6.0	32	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc