


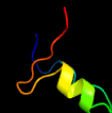

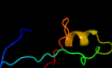

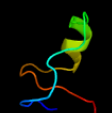



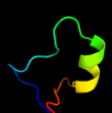



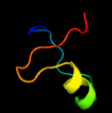







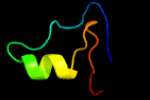



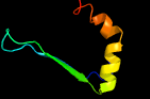
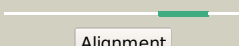

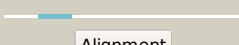
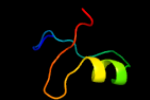
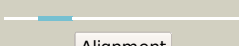




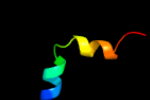





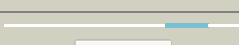

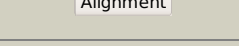
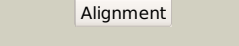



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0852_(fadD16)_948562_949398
 Date Fri Jul 26 01:50:44 BST 2019
 Unique Job ID dfe79a912dc9efbf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kngA_	 Alignment		72.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: snoab; PDBTitle: crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
2	c3tsyA_	 Alignment		72.1	53	PDB header: ligase, transferase Chain: A: PDB Molecule: fusion protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
3	c3qyaA_	 Alignment		67.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase; PDBTitle: crystal structure of a red-emitter mutant of lampyris turkestanicus2 luciferase
4	c3o82A_	 Alignment		64.5	22	PDB header: ligase Chain: A: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
5	c4dpoA_	 Alignment		63.0	17	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from methanosarcina2 mazeri go1
6	c3o82B_	 Alignment		62.1	22	PDB header: ligase Chain: B: PDB Molecule: peptide arylation enzyme; PDBTitle: structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
7	c5mssA_	 Alignment		59.4	34	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
8	c5mstA_	 Alignment		56.7	34	PDB header: oxidoreductase Chain: A: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from2 segniliparus rugosus in complex with amp and a co-purified carboxylic3 acid
9	d2omoa1	 Alignment		52.0	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
10	c3hx9B_	 Alignment		46.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: protein rv3592; PDBTitle: structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
11	c2omoC_	 Alignment		46.5	14	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea

12	c5n81B_	 Alignment		44.8	28	PDB header: ligase Chain: B: PDB Molecule: tyrocidine synthase 1; PDBTitle: crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
13	c5msdA_	 Alignment		44.2	34	PDB header: oxidoreductase Chain: A: PDB Molecule: carboxylic acid reductase; PDBTitle: structure of the a domain of carboxylic acid reductase (car) from <i>Nocardia iowensis</i> in complex with amp and benzoic acid
14	d1iuja_	 Alignment		40.3	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
15	c4zosA_	 Alignment		40.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ye0340 from <i>Yersinia enterocolitica</i> subsp. PDBTitle: 2.20 angstrom resolution crystal structure of protein ye0340 of 2 unidentified function from <i>Yersinia enterocolitica</i> subsp. 3 [enterocolitica 8081]
16	c3ivrA_	 Alignment		39.6	39	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from <i>Rhodopseudomonas palustris</i> cga009
17	d1v25a_	 Alignment		39.5	27	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
18	c2gffB_	 Alignment		39.3	5	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrG protein; PDBTitle: crystal structure of <i>Yersinia pestis</i> lsrG
19	c3l6gA_	 Alignment		39.0	33	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuAC in its open conformation
20	c3t5cA_	 Alignment		36.4	39	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadL13; PDBTitle: crystal structure of n-terminal domain of facl13 from <i>Mycobacterium tuberculosis</i> in different space group c2
21	c3tmgA_	 Alignment	not modelled	34.4	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter, 2 glycine/betaine/l-proline-binding protein (prox) from <i>Borrelia burgdorferi</i>
22	c5oe3C_	 Alignment	not modelled	33.8	26	PDB header: ligase Chain: C: PDB Molecule: anthranilate--coa ligase; PDBTitle: crystal structure of the n-terminal domain of ppsA in complex with 2 anthraniloyl-amp (crystal form 1)
23	c2bbeA_	 Alignment	not modelled	33.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so0527; PDBTitle: crystal structure of protein so0527 from <i>Shewanella oneidensis</i>
24	c4ae5C_	 Alignment	not modelled	30.9	15	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
25	c3e53A_	 Alignment	not modelled	30.9	22	PDB header: ligase Chain: A: PDB Molecule: fatty-acid-coa ligase fadL28; PDBTitle: crystal structure of n-terminal domain of a fatty acyl-amp2 ligase faal28 from <i>Mycobacterium tuberculosis</i>
26	d1x7va_	 Alignment	not modelled	29.9	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
27	c5jpbB_	 Alignment	not modelled	29.5	38	PDB header: ligase Chain: B: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
28	c2rejA_	 Alignment	not modelled	29.2	33	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded

						semi-2 closed conformation
29	c2fb0A_	Alignment	not modelled	28.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
30	c4w8oA_	Alignment	not modelled	27.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase-like enzymeamp-coa-ligase; PDBTitle: structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
31	c6xfxA_	Alignment	not modelled	26.8	14	PDB header: signaling protein Chain: A: PDB Molecule: sam and sh3 domain-containing protein 3; PDBTitle: crystal structure of the sam domain of murine sly1
32	c5burB_	Alignment	not modelled	26.6	23	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: o-succinylbenzoate coenzyme a synthetase (mene) from bacillus2 subtilis, in complex with atp and magnesium ion
33	c3bm7A_	Alignment	not modelled	25.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: protein of unknown function with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
34	c6gw6B_	Alignment	not modelled	25.6	24	PDB header: toxin Chain: B: PDB Molecule: xre antitoxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
35	c2lmrA_	Alignment	not modelled	24.6	19	PDB header: signaling protein Chain: A: PDB Molecule: ankyrin repeat and sam domain-containing protein 1a; PDBTitle: solution structure of the first sam domain of odin
36	c2yqpA_	Alignment	not modelled	24.4	33	PDB header: gene regulation, hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx59; PDBTitle: solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
37	c3fgvB_	Alignment	not modelled	23.5	7	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution
38	c2zdiC_	Alignment	not modelled	22.8	28	PDB header: chaperone Chain: C: PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
39	c3gz7B_	Alignment	not modelled	22.7	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 (np_888398.1) from bordetella bronchiseptica at 2.15 a resolution
40	c5zrzB_	Alignment	not modelled	21.8	24	PDB header: protein binding Chain: B: PDB Molecule: sterile alpha motif domain-containing protein 5; PDBTitle: crystal structure of epha5/samd5 complex
41	c5jipC_	Alignment	not modelled	21.5	38	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
42	c6d0hB_	Alignment	not modelled	21.5	24	PDB header: toxin Chain: B: PDB Molecule: pars: cog5642 (duf2384) antitoxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
43	c3k1rB_	Alignment	not modelled	21.4	5	PDB header: structural protein Chain: B: PDB Molecule: usher syndrome type-1g protein; PDBTitle: structure of harmonin npd21 in complex with the sam-pbm of2 sans
44	c3lo3E_	Alignment	not modelled	21.4	10	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
45	c2kg5A_	Alignment	not modelled	20.8	22	PDB header: signaling protein Chain: A: PDB Molecule: arf-gap, rho-gap domain, ank repeat and ph PDBTitle: nmr solution structure of arap3-sam
46	d1v38a_	Alignment	not modelled	20.8	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
47	c5jtiA_	Alignment	not modelled	20.7	12	PDB header: signaling protein Chain: A: PDB Molecule: tankyrase-1; PDBTitle: crystal structure of the human tankyrase 1 (tnks) sam domain (d1055r),2 crystal form 2
48	d1x8da1	Alignment	not modelled	20.4	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Yiil-like
49	c1cqtI_	Alignment	not modelled	19.8	69	PDB header: gene regulation/dna Chain: I: PDB Molecule: pou domain, class 2, associating factor 1; PDBTitle: crystal structure of a ternary complex containing an oca-b2 peptide, the oct-1 pou domain, and an octamer element
50	c3h8mB_	Alignment	not modelled	19.2	23	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 7; PDBTitle: sam domain of human ephrin type-a receptor 7 (epha7)
51	c4plaA_	Alignment	not modelled	19.0	39	PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein with ferredoxin-

52	c3e8oB_	Alignment	not modelled	18.9	14	like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monoxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
53	c2iutA_	Alignment	not modelled	18.7	27	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
54	c2iuuE_	Alignment	not modelled	18.7	27	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
55	d1ofcx2	Alignment	not modelled	17.8	46	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: SLIDE domain
56	c1cqtj_	Alignment	not modelled	17.8	69	PDB header: gene regulation/dna Chain: J: PDB Molecule: pou domain, class 2, associating factor 1; PDBTitle: crystal structure of a ternary complex containing an oca-b2 peptide, the oct-1 pou domain, and an octamer element
57	c3eabK_	Alignment	not modelled	17.6	73	PDB header: cell cycle Chain: K: PDB Molecule: chmp1b; PDBTitle: crystal structure of spastin mit in complex with escrt iii
58	c4rqmC_	Alignment	not modelled	17.3	35	PDB header: protein binding Chain: C: PDB Molecule: protein bicaudal c homolog 1; PDBTitle: crystal structure of the semet bicc1 sam domain r924e mutant
59	d1r9la_	Alignment	not modelled	17.2	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
60	c2qkqA_	Alignment	not modelled	17.0	29	PDB header: transferase Chain: A: PDB Molecule: ephrin type-b receptor 4; PDBTitle: structure of the sam domain of human ephrin type-b receptor2 4
61	d1b4fa_	Alignment	not modelled	16.9	23	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
62	c3chgB_	Alignment	not modelled	16.6	33	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
63	c2eseA_	Alignment	not modelled	16.0	9	PDB header: protein/rna complex Chain: A: PDB Molecule: vts1p; PDBTitle: structure of the sam domain of vts1p in complex with rna
64	c3tadB_	Alignment	not modelled	15.9	24	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
65	c5zrzA_	Alignment	not modelled	15.6	29	PDB header: protein binding Chain: A: PDB Molecule: ephrin type-a receptor 5; PDBTitle: crystal structure of epha5/samd5 complex
66	c4kf7A_	Alignment	not modelled	15.6	55	PDB header: structural protein Chain: A: PDB Molecule: nup188; PDBTitle: nup188(aa1-1160) from myceliophthora thermophila
67	c3rg2H_	Alignment	not modelled	15.1	25	PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
68	c4d56A_	Alignment	not modelled	15.1	28	PDB header: hydrolase Chain: A: PDB Molecule: apnaa1; PDBTitle: understanding bi-specificity of a-domains
69	d1hcfa_	Alignment	not modelled	15.0	33	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
70	c4n1aE_	Alignment	not modelled	15.0	18	PDB header: protein binding/protein binding Chain: E: PDB Molecule: cell divisionftskspoillee; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
71	c2ke7A_	Alignment	not modelled	14.8	18	PDB header: protein binding Chain: A: PDB Molecule: ankyrin repeat and sterile alpha motif domain- PDBTitle: nmr structure of the first sam domain from aida1
72	c5td8A_	Alignment	not modelled	14.8	33	PDB header: replication Chain: A: PDB Molecule: kinetochore protein ndc80; PDBTitle: crystal structure of an extended dwarf ndc80 complex
73	c5ey8D_	Alignment	not modelled	14.8	38	PDB header: ligase Chain: D: PDB Molecule: acyl-coa synthase; PDBTitle: structure of fadd32 from mycobacterium smegmatis complexed to ampc20
74	d1bh9b_	Alignment	not modelled	14.5	56	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
75	c3kkaD_	Alignment	not modelled	14.5	24	PDB header: transferase Chain: D: PDB Molecule: ephrin type-a receptor 2; PDBTitle: co-crystal structure of the sam domains of epha1 and epha2
76	c3senD_	Alignment	not modelled	14.2	32	PDB header: signaling protein Chain: D: PDB Molecule: caskin-1; PDBTitle: structure of caskin1 tandem sams
77	c2affB_	Alignment	not modelled	14.2	38	PDB header: cell cycle Chain: B: PDB Molecule: mki67 fha domain interacting nucleolar phosphoprotein; PDBTitle: the solution structure of the ki67fha/hnifk(226-269)3p complex

78	c2hi1A_	Alignment	not modelled	14.2	21	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
79	d1b8mb_	Alignment	not modelled	14.0	33	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
80	d1ow5a_	Alignment	not modelled	13.6	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
81	c1ow5A_	Alignment	not modelled	13.6	18	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase ste11; PDBTitle: nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
82	d1sgga_	Alignment	not modelled	13.6	20	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
83	c4dn9B_	Alignment	not modelled	13.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl
84	c4is7A_	Alignment	not modelled	12.9	26	PDB header: protein binding Chain: A: PDB Molecule: caskin-2; PDBTitle: crystal structure of the caskin2 sam domain tandem
85	c4gr5B_	Alignment	not modelled	12.7	22	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
86	d1ucva_	Alignment	not modelled	12.6	24	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
87	c5f3xB_	Alignment	not modelled	12.4	13	PDB header: structural protein/protein binding Chain: B: PDB Molecule: ankyrin repeat and sam domain-containing protein 4b; PDBTitle: crystal structure of harmonin npdz1 in complex with anks4b sam-pbm
88	c2eamA_	Alignment	not modelled	12.3	18	PDB header: signaling protein Chain: A: PDB Molecule: putative 47 kda protein; PDBTitle: solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
89	d1b0xa_	Alignment	not modelled	12.2	19	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
90	c1b0xA_	Alignment	not modelled	12.2	19	PDB header: transferase Chain: A: PDB Molecule: protein (epha4 receptor tyrosine kinase); PDBTitle: the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
91	d3b5ea1	Alignment	not modelled	12.1	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
92	c1gph1_	Alignment	not modelled	11.7	25	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
93	c3o0B_	Alignment	not modelled	11.6	40	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
94	d2zdpa1	Alignment	not modelled	11.2	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
95	c4gioA_	Alignment	not modelled	11.1	40	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of campylobacter jejuni cj0090
96	c2m3dA_	Alignment	not modelled	11.1	15	PDB header: hydrolase Chain: A: PDB Molecule: nucleolar rna helicase 2; PDBTitle: nmr structure of the guct domain from human dead box polypeptide 21
97	d2ooka1	Alignment	not modelled	11.1	31	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
98	c3da5A_	Alignment	not modelled	10.7	46	PDB header: rna binding protein Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of piwi/argonaute/zwiller(paz) domain from2 thermococcus thioreducens
99	d1ycqa_	Alignment	not modelled	10.6	31	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain