

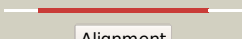

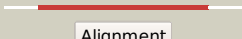

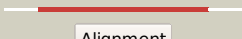










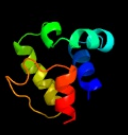






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0100_(-)_109780_110016
Date	Tue Jul 23 14:50:13 BST 2019
Unique Job ID	b21fc922d0c6f850

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2mf4A_	 Alignment		95.7	19	PDB header: transferase Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a
2	c2fq1A_	 Alignment		93.5	26	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
3	c4hkgB_	 Alignment		93.1	20	PDB header: phosphopantetheine binding protein Chain: B: PDB Molecule: phosphopantetheine attachment site family protein; PDBTitle: crystal structure of free-standing peptidyl carrier protein from2 uncharacterized acinetobacter baumannii secondary metabolic pathway
4	c2kr5A_	 Alignment		92.1	17	PDB header: transport protein Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase
5	c2ehtA_	 Alignment		91.4	19	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
6	c6gcsO_	 Alignment		91.3	21	PDB header: oxidoreductase Chain: Q: PDB Molecule: acpm2 subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
7	c2cgaA_	 Alignment		91.1	17	PDB header: protein transport Chain: A: PDB Molecule: acyl carrier protein acpa; PDBTitle: a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
8	c2n6yA_	 Alignment		91.1	20	PDB header: ligase Chain: A: PDB Molecule: hmwp2 nonribosomal peptide synthetase; PDBTitle: solution structure of holo arcp from yersiniabactin synthetase
9	c2n98A_	 Alignment		91.1	29	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein lipid from actinoplanes2 friuliensis
10	c4h2sD_	 Alignment		90.7	27	PDB header: ligase Chain: D: PDB Molecule: aminoacyl carrier protein 1; PDBTitle: crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and amp
11	d2gdwa1	 Alignment		90.6	22	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Peptidyl carrier domain

12	c6c4qA_	Alignment		90.6	16	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
13	c4ca3A_	Alignment		90.5	27	PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b
14	d1klpa_	Alignment		90.3	23	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
15	c2liuA_	Alignment		90.1	19	PDB header: transferase Chain: A: PDB Molecule: cura; PDBTitle: nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
16	c2afdA_	Alignment		90.1	21	PDB header: ligand binding protein Chain: A: PDB Molecule: protein asl1650; PDBTitle: solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
17	c2mr7A_	Alignment		89.9	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase
18	c2fq2A_	Alignment		88.5	21	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
19	c4zjbG_	Alignment		88.4	23	PDB header: lyase/biosynthetic protein Chain: G: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) in complex with holo-acp from helicobacter pylori
20	c2fvfA_	Alignment		88.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: structure of 10:0-acp (protein with docked fatty acid)
21	c4dxeH_	Alignment	not modelled	87.7	25	PDB header: transferase Chain: H: PDB Molecule: acyl carrier protein; PDBTitle: 2.52 angstrom resolution crystal structure of the acyl-carrier-protein2 synthase (acps)-acyl carrier protein (acp) protein-protein complex3 from staphylococcus aureus subsp. aureus col
22	d2af8a_	Alignment	not modelled	86.8	15	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
23	c2ju2A_	Alignment	not modelled	86.8	20	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
24	c5zk4D_	Alignment	not modelled	86.8	29	PDB header: transferase Chain: D: PDB Molecule: disa protein; PDBTitle: the structure of dszs acyltransferase with carrier protein
25	c5hvcA_	Alignment	not modelled	86.5	24	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: solution structure of the apo state of the acyl carrier protein from2 the mlsa2 subunit of the mycolactone polyketide synthase
26	c2lteA_	Alignment	not modelled	85.4	16	PDB header: transferase Chain: A: PDB Molecule: specialized acyl carrier protein; PDBTitle: solution nmr structure of the specialized acyl carrier protein pa33342 (apo) from pseudomonas aeruginosa, northeast structural genomics3 consortium target pat415
27	d1t8ka_	Alignment	not modelled	85.0	18	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
						PDB header: biosynthetic protein Chain: A: PDB Molecule: 4-hydroxy-2,2'-bipyrrrole-5-methanol

28	c5y08A	Alignment	not modelled	85.0	19	synthase pigh; PDBTitle: solution structure of the apo doublet acyl carrier protein from2 prodigiosin biosynthesis
29	c2kw1A	Alignment	not modelled	84.5	19	PDB header: lipid binding protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein from borrelia burgdorferi
30	c6gcsO	Alignment	not modelled	84.3	24	PDB header: oxidoreductase Chain: O; PDB Molecule: acpm1 subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
31	c5mtiA	Alignment	not modelled	83.5	16	PDB header: transport protein Chain: A; PDB Molecule: phosphopantetheine-binding protein; PDBTitle: bamb_5917 acyl-carrier protein
32	c2l9fA	Alignment	not modelled	83.2	18	PDB header: transferase Chain: A; PDB Molecule: scale8; PDBTitle: nmr solution structure of meacp
33	c2dnwA	Alignment	not modelled	82.6	25	PDB header: transport protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
34	d1vkua	Alignment	not modelled	82.5	16	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
35	c2cnrA	Alignment	not modelled	82.5	13	PDB header: lipid transport Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: structural studies on the interaction of scfas acp with2 acps
36	c2l4bA	Alignment	not modelled	81.5	24	PDB header: transferase Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
37	c3lmoA	Alignment	not modelled	80.5	23	PDB header: transferase Chain: A; PDB Molecule: specialized acyl carrier protein; PDBTitle: crystal structure of specialized acyl carrier protein (rpa2022) from2 rhodopseudomonas palustris, northeast structural genomics consortium3 target rpr324
38	c3ejbC	Alignment	not modelled	80.3	23	PDB header: oxidoreductase/lipid transport Chain: C; PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of p450bioi in complex with tetradecanoic acid2 ligated acyl carrier protein
39	c5kp8B	Alignment	not modelled	80.1	20	PDB header: transferase Chain: B; PDB Molecule: curb; PDBTitle: crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-acp
40	d2pnga1	Alignment	not modelled	80.1	30	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
41	c2m5rA	Alignment	not modelled	79.2	24	PDB header: lipid binding protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: solution structure of holo-acyl carrier protein of leishmania major
42	c5u3hA	Alignment	not modelled	78.9	25	PDB header: ligase Chain: A; PDB Molecule: hmwp2 nonribosomal peptide synthetase; PDBTitle: solution structure of apo pcp1 from yersiniabactin synthetase
43	c2l22A	Alignment	not modelled	78.7	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: mupirocin didomain acyl carrier protein; PDBTitle: mupirocin didomain acp
44	c4pxhF	Alignment	not modelled	78.0	19	PDB header: oxidoreductase/protein binding Chain: F; PDB Molecule: peptide synthetase; PDBTitle: structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
45	c5ejdK	Alignment	not modelled	78.0	13	PDB header: biosynthetic protein Chain: K; PDB Molecule: tqaa; PDBTitle: the crystal structure of holo t3ct
46	c2qnwA	Alignment	not modelled	77.6	24	PDB header: signaling protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: toxoplasma gondii apicoplast-targeted acyl carrier protein
47	c2jq4A	Alignment	not modelled	76.4	21	PDB header: structural genomics Chain: A; PDB Molecule: hypothetical protein atu2571; PDBTitle: complete resonance assignments and solution structure calculation of2 atc2521 (nesg id: att6) from agrobacterium tumefaciens
48	d2jq4a1	Alignment	not modelled	76.4	21	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
49	c4i4dA	Alignment	not modelled	73.4	21	PDB header: biosynthetic protein Chain: A; PDB Molecule: peptide synthetase nrps type ii-pcp; PDBTitle: structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
50	c2n50A	Alignment	not modelled	71.7	16	PDB header: biosynthetic protein Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: novel structural components contribute to the high thermal stability2 of acyl carrier protein from enterococcus faecalis
51	d1or5a	Alignment	not modelled	71.5	18	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
52	c2lola	Alignment	not modelled	70.4	20	PDB header: lipid transport Chain: A; PDB Molecule: acyl carrier protein; PDBTitle: nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
						Fold: Acyl carrier protein-like

53	d1nq4a_	Alignment	not modelled	70.4	13	Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
54	c6h0jA_	Alignment	not modelled	70.3	23	PDB header: protein binding Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: a1-type acp domain from module 5 of mlsA1
55	c4bphA_	Alignment	not modelled	69.8	16	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 2; PDBTitle: high resolution crystal structure of bacillus subtilis dltc
56	c4dg9A_	Alignment	not modelled	68.0	19	PDB header: ligase/inhibitor Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and 2 pcp domains bound to vinylsulfonamide inhibitor
57	c5mssA_	Alignment	not modelled	62.9	20	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
58	c1x3oA_	Alignment	not modelled	62.1	28	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
59	d1dv5a_	Alignment	not modelled	61.2	19	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: apo-D-alanyl carrier protein
60	c5czdB_	Alignment	not modelled	61.0	20	PDB header: transferase Chain: B: PDB Molecule: acyl-carrier-protein; PDBTitle: the complex structure of vink with vinl
61	c4r0mA_	Alignment	not modelled	51.8	25	PDB header: ligase Chain: A: PDB Molecule: mcgy protein; PDBTitle: structure of mcgy a-pcp complexed with phenylalanyl-adenylate
62	c2kciA_	Alignment	not modelled	49.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acyl carrier protein; PDBTitle: solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
63	c3ce7A_	Alignment	not modelled	48.1	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: specific mitochondrial acyl carrier protein; PDBTitle: crystal structure of toxoplasma specific mitochondrial acyl carrier2 protein, 59.m03510
64	c5msvB_	Alignment	not modelled	47.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: thioester reductase domain-containing protein; PDBTitle: structure of the phosphopantetheine modified pcp-r didomain of 2 carboxylic acid reductase (car) in complex with nadp
65	c4zxA_	Alignment	not modelled	39.9	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: crystal structure of holo-entf a nonribosomal peptide synthetase in 2 the thioester-forming conformation
66	c3rg2H_	Alignment	not modelled	39.3	26	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
67	c4is7A_	Alignment	not modelled	35.4	20	PDB header: protein binding Chain: A: PDB Molecule: caskin-2; PDBTitle: crystal structure of the caskin2 sam domain tandem
68	d1f80d_	Alignment	not modelled	34.6	26	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
69	c2roqA_	Alignment	not modelled	33.6	20	PDB header: transferase Chain: A: PDB Molecule: enterobactin synthetase component f; PDBTitle: solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
70	c2vsqA_	Alignment	not modelled	29.8	20	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
71	c6cxtA_	Alignment	not modelled	27.9	43	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of fad-dependent dehydrogenase
72	c4h2uC_	Alignment	not modelled	24.0	44	PDB header: ligase Chain: C: PDB Molecule: aminoacyl carrier protein 1; PDBTitle: crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and atp
73	c3m3gA_	Alignment	not modelled	19.2	23	PDB header: polysaccharide-binding protein Chain: A: PDB Molecule: ep11 protein; PDBTitle: crystal structure of sm1, an elicitor of plant defence responses from 2 trichoderma virens.
74	c2kivA_	Alignment	not modelled	18.2	20	PDB header: signaling protein Chain: A: PDB Molecule: ankyrin repeat and sterile alpha motif domain- PDBTitle: aida-1 sam domain tandem
75	c2my5A_	Alignment	not modelled	17.7	30	PDB header: transport protein Chain: A: PDB Molecule: peptidyl carrier protein; PDBTitle: solution structure of kstb-pcp in kosinostatin biosynthesis
76	c2n5iA_	Alignment	not modelled	17.3	24	PDB header: transport protein Chain: A: PDB Molecule: peptidyl carrier protein pltl; PDBTitle: pltl-pyrrolyl
77	c3senD_	Alignment	not modelled	16.1	20	PDB header: signaling protein Chain: D: PDB Molecule: caskin-1; PDBTitle: structure of caskin1 tandem sams
						PDB header: membrane protein

78	c6bugA	Alignment	not modelled	13.4	24	Chain: A: PDB Molecule: d-alanyl carrier protein; PDBTitle: crystal structure of a membrane protein, crystal form i
79	c3idwA	Alignment	not modelled	12.9	35	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
80	c2l3vA	Alignment	not modelled	11.9	29	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: nmr structure of acyl carrier protein from brucella melitensis
81	c2fjrB	Alignment	not modelled	11.8	11	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
82	d1oc4a2	Alignment	not modelled	11.4	26	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
83	d1tc3c	Alignment	not modelled	11.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
84	c1m1cB	Alignment	not modelled	11.3	50	PDB header: virus Chain: B: PDB Molecule: major coat protein; PDBTitle: structure of the I-a virus
85	d1m1ca	Alignment	not modelled	11.3	50	Fold: L-A virus major coat protein Superfamily: L-A virus major coat protein Family: L-A virus major coat protein
86	c3fzeA	Alignment	not modelled	10.9	38	PDB header: protein binding Chain: A: PDB Molecule: protein ste5; PDBTitle: structure of the 'minimal scaffold' (ms) domain of ste5 that2 cocatalyzes fus3 phosphorylation by ste7
87	d1o6za2	Alignment	not modelled	9.9	32	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
88	c2kkeA	Alignment	not modelled	9.5	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
89	d1llca2	Alignment	not modelled	9.4	32	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
90	c2kkeB	Alignment	not modelled	9.3	39	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
91	d1guza2	Alignment	not modelled	9.3	42	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
92	d1a5za2	Alignment	not modelled	9.0	32	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
93	c2cq8A	Alignment	not modelled	8.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: solution structure of rsgi ruh-033, a pp-binding domain of 2 10-ftfhdh from human cdna
94	d1pzga2	Alignment	not modelled	8.8	37	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
95	d5mdha2	Alignment	not modelled	8.7	32	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
96	c3okqA	Alignment	not modelled	8.7	55	PDB header: protein binding Chain: A: PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
97	d1ldma2	Alignment	not modelled	8.5	58	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
98	d1c99a	Alignment	not modelled	8.4	29	Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
99	c2jgpA	Alignment	not modelled	8.4	20	PDB header: ligase Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc