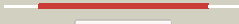



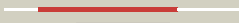


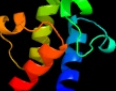

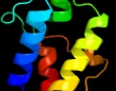














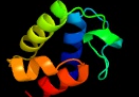








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2244_(acpP)_2517779_2518126
Date	Mon Aug 5 13:25:38 BST 2019
Unique Job ID	e3bae1059298aa85

Detailed template information

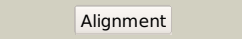
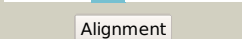
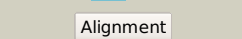
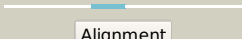
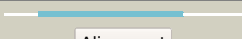


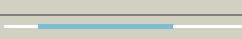







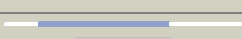

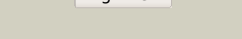
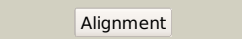
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1k1pa_</a>	 Alignment		99.9	99	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
2	<a href="#">c2dnwA</a>	 Alignment		99.7	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
3	<a href="#">c2cnrA</a>	 Alignment		99.7	53	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> structural studies on the interaction of scfas acp with2 acps
4	<a href="#">c1x3oA</a>	 Alignment		99.7	36	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
5	<a href="#">c2n50A</a>	 Alignment		99.7	37	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> novel structural components contribute to the high thermal stability2 of acyl carrier protein from enterococcus faecalis
6	<a href="#">c6gcsO</a>	 Alignment		99.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> acpm2 subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
7	<a href="#">c2kw1A</a>	 Alignment		99.7	35	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of acyl carrier protein from borrelia burgdorferi
8	<a href="#">c214bA</a>	 Alignment		99.7	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
9	<a href="#">c2lo1A</a>	 Alignment		99.7	33	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
10	<a href="#">c2qnwA</a>	 Alignment		99.7	35	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> toxoplasma gondii apicoplast-targeted acyl carrier protein
11	<a href="#">c2m5rA</a>	 Alignment		99.6	28	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of holo-acyl carrier protein of leishmania major

12	<a href="#">c2fvfA</a>	Alignment		99.6	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> structure of 10:0-acp (protein with docked fatty acid)
13	<a href="#">c2l9fA</a>	Alignment		99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cale8; <b>PDBTitle:</b> nmr solution structure of meacp
14	<a href="#">d1t8ka</a>	Alignment		99.6	35	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
15	<a href="#">c3ejbC</a>	Alignment		99.6	35	<b>PDB header:</b> oxidoreductase/lipid transport <b>Chain:</b> C: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of p450bioi in complex with tetradecanoic acid2 ligated acyl carrier protein
16	<a href="#">c6c4qA</a>	Alignment		99.6	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
17	<a href="#">c4zjbG</a>	Alignment		99.6	39	<b>PDB header:</b> lyase/biosynthetic protein <b>Chain:</b> G: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) in complex with holo-acp from helicobacter pylori
18	<a href="#">c2fq2A</a>	Alignment		99.6	32	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
19	<a href="#">c2afdA</a>	Alignment		99.6	18	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein asl1650; <b>PDBTitle:</b> solution structure of asl1650, an acyl carrier protein from anabaena2 sp. pcc 7120 with a variant phosphopantetheinylation-site sequence
20	<a href="#">c6gcsO</a>	Alignment		99.6	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> acpm1 subunit; <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
21	<a href="#">d1nq4a</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
22	<a href="#">c2kciA</a>	Alignment	not modelled	99.6	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl carrier protein; <b>PDBTitle:</b> solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
23	<a href="#">c2n98A</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> solution structure of acyl carrier protein lipd from actinoplanes2 friuliensis
24	<a href="#">d1vkua</a>	Alignment	not modelled	99.6	28	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
25	<a href="#">c4dxeH</a>	Alignment	not modelled	99.6	38	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> 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
26	<a href="#">d2af8a</a>	Alignment	not modelled	99.6	28	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
27	<a href="#">c5kp8B</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> curb; <b>PDBTitle:</b> crystal structure of the curacin biosynthetic pathway hmg synthase in2 complex with acetyl donor-acp
28	<a href="#">c2l3vA</a>	Alignment	not modelled	99.6	35	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> nmr structure of acyl carrier protein from brucella

						mellitensis
29	<a href="#">c2ehtA</a>	Alignment	not modelled	99.6	44	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein; <b>PDBTitle:</b> crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
30	<a href="#">c4hkgB</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> phosphopantetheine binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine attachment site family protein; <b>PDBTitle:</b> crystal structure of free-standing peptidyl carrier protein from2 uncharacterized acinetobacter baumannii secondary metabolic pathway
31	<a href="#">c2liuA</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cura; <b>PDBTitle:</b> nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
32	<a href="#">c2lteA</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> specialized acyl carrier protein; <b>PDBTitle:</b> solution nmr structure of the specialized acyl carrier protein pa33342 (apo) from pseudomonas aeruginosa, northeast structural genomics3 consortium target pat415
33	<a href="#">c3ce7A</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> specific mitochondrial acyl carrier protein; <b>PDBTitle:</b> crystal structure of toxoplasma specific mitochondrial acyl carrier2 protein, 59.m03510
34	<a href="#">c2mf4A</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hybrid polyketide synthase-non ribosomal peptide <b>PDBTitle:</b> 1h, 13c, 15n chemical shift assignments of streptomyces virginiae vira2 acp5a
35	<a href="#">c2ju2A</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> erythronolide synthase; <b>PDBTitle:</b> minimized mean solution structure of the acyl carrier2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
36	<a href="#">c4ca3A</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> hybrid polyketide synthase-non ribosomal peptide <b>PDBTitle:</b> solution structure of streptomyces virginiae vira acp5b
37	<a href="#">c4bphA</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 2; <b>PDBTitle:</b> high resolution crystal structure of bacillus subtilis dltc
38	<a href="#">d1f80d</a>	Alignment	not modelled	99.5	31	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
39	<a href="#">c5y08A</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2,2'-bipyrrole-5-methanol synthase pigh; <b>PDBTitle:</b> solution structure of the apo doublet acyl carrier protein from2 prodigiosin biosynthesis
40	<a href="#">d1dv5a</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> apo-D-alanyl carrier protein
41	<a href="#">c2kr5A</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> afлатoxin biosynthesis polyketide synthase; <b>PDBTitle:</b> solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase
42	<a href="#">c3lmoA</a>	Alignment	not modelled	99.5	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> specialized acyl carrier protein; <b>PDBTitle:</b> crystal structure of specialized acyl carrier protein (rpa2022) from2 rhodospseudomonas palustris, northeast structural genomics consortium3 target rpr324
43	<a href="#">c5hvcA</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> solution structure of the apo state of the acyl carrier protein from2 the mlsa2 subunit of the mycolactone polyketide synthase
44	<a href="#">c2n5iA</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl carrier protein pltl; <b>PDBTitle:</b> pltl-pyrrolyl
45	<a href="#">c2l22A</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> mupirocin didomain acyl carrier protein; <b>PDBTitle:</b> mupirocin didomain acp
46	<a href="#">c5mtiA</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine-binding protein; <b>PDBTitle:</b> bamb_5917 acyl-carrier protein
47	<a href="#">c6h0jA</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> type i modular polyketide synthase; <b>PDBTitle:</b> a1-type acp domain from module 5 of mlsa1
48	<a href="#">c2cggA</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> acyl carrier protein acpa; <b>PDBTitle:</b> a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
49	<a href="#">c2jgpA</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
50	<a href="#">c5msvB</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the phosphopantetheine modified pcp-r didomain of2 carboxylic acid reductase (car) in complex with nadp
51	<a href="#">c2cq8A</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 10-formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> solution structure of rsgi ruh-033, a pp-binding domain of2 10-ftfhfdh from human cdna
52	<a href="#">c2mr7A</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-ribosomal peptide synthetase; <b>PDBTitle:</b> apo structure of the peptidyl carrier protein domain 7 of

						the2 teicoplanin producing non-ribosomal peptide synthetase
53	<a href="#">c4pxhF_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> peptide synthetase; <b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
54	<a href="#">d1or5a_</a>	Alignment	not modelled	99.4	27	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
55	<a href="#">c2jq4A_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu2571; <b>PDBTitle:</b> complete resonance assignments and solution structure calculation of2 atc2521 (nesg id: att6) from agrobacterium tumefaciens
56	<a href="#">d2jq4a1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
57	<a href="#">c5zk4D_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> disa protein; <b>PDBTitle:</b> the structure of dszs acyltransferase with carrier protein
58	<a href="#">d2gdwa1</a>	Alignment	not modelled	99.3	27	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Peptidyl carrier domain
59	<a href="#">c5ejdK_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> K: <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of holo t3ct
60	<a href="#">c5u3hA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of apo pcp1 from yersiniabactin synthetase
61	<a href="#">c4zxiA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
62	<a href="#">c2roqA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthetase component f; <b>PDBTitle:</b> solution structure of the thiolation-thioesterase di-domain2 of enterobactin synthetase component f
63	<a href="#">c4i4dA_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide synthetase nrps type ii-pcp; <b>PDBTitle:</b> structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
64	<a href="#">c4r0mA_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> mcyg protein; <b>PDBTitle:</b> structure of mcyg a-pcp complexed with phenylalanyl-adenylate
65	<a href="#">c5es8A_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> linear gramicidin synthetase subunit a; <b>PDBTitle:</b> crystal structure of the initiation module of lgra in the thiolation2 state
66	<a href="#">c4h2sD_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and amp
67	<a href="#">c2my5A_</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl carrier protein; <b>PDBTitle:</b> solution structure of kstb-pcp in kosinostatin biosynthesis
68	<a href="#">c2fq1A_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isochorismatase; <b>PDBTitle:</b> crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
69	<a href="#">c2vsqA_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
70	<a href="#">c5mssA_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioester reductase domain-containing protein; <b>PDBTitle:</b> structure of the a-pcp didomain of carboxylic acid reductase (car)2 from segniliparus rugosus in complex with amp
71	<a href="#">c4zxiA_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
72	<a href="#">c2n6yA_</a>	Alignment	not modelled	99.1	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> hmwp2 nonribosomal peptide synthetase; <b>PDBTitle:</b> solution structure of holo arcp from yersiniabactin synthetase
73	<a href="#">c4dg9A_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> ligase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> pa1221; <b>PDBTitle:</b> structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
74	<a href="#">c3rg2H_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> ligase <b>Chain:</b> H: <b>PDB Molecule:</b> enterobactin synthase component e (ente), 2,3-dihydro-2,3- <b>PDBTitle:</b> structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
75	<a href="#">c5czdB_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-carrier-protein; <b>PDBTitle:</b> the complex structure of vink with vinl
76	<a href="#">c6cxtA_</a>	Alignment	not modelled	99.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> crystal structure of fad-dependent dehydrogenase
						<b>PDB header:</b> ligase

77	<a href="#">c5ja2A_</a>	Alignment	not modelled	99.0	18	<b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
78	<a href="#">d2pnga1</a>	Alignment	not modelled	99.0	24	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> ACP-like <b>Family:</b> Acyl-carrier protein (ACP)
79	<a href="#">c6bugA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl carrier protein; <b>PDBTitle:</b> crystal structure of a membrane protein, crystal form i
80	<a href="#">c6n8eA_</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
81	<a href="#">c5u89A_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid adenylation domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhhf
82	<a href="#">c2lkiA_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
83	<a href="#">c2amwA_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ne2163; <b>PDBTitle:</b> solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
84	<a href="#">c4v1am_</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
85	<a href="#">c6eqoB_</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a synthetase; <b>PDBTitle:</b> tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
86	<a href="#">c2vkzC_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha; <b>PDBTitle:</b> structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
87	<a href="#">c2uv8C_</a>	Alignment	not modelled	95.3	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> fatty acid synthase subunit alpha (fas2); <b>PDBTitle:</b> crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
88	<a href="#">c3s8mA_</a>	Alignment	not modelled	93.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acyl reductase; <b>PDBTitle:</b> the crystal structure of fabv
89	<a href="#">c2uv9B_</a>	Alignment	not modelled	93.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase alpha subunits; <b>PDBTitle:</b> crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
90	<a href="#">c4b3yB_</a>	Alignment	not modelled	90.6	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> cryo-em structure of the mycobacterial fatty acid synthase
91	<a href="#">c4h2uC_</a>	Alignment	not modelled	87.7	32	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and atp
92	<a href="#">c6c4vA_</a>	Alignment	not modelled	86.2	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
93	<a href="#">c5t81A_</a>	Alignment	not modelled	79.2	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> epob; <b>PDBTitle:</b> rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
94	<a href="#">c6cgoB_</a>	Alignment	not modelled	70.1	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> condensation domain protein; <b>PDBTitle:</b> molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
95	<a href="#">c2kztA_</a>	Alignment	not modelled	60.1	11	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> structure of the tandem ma-3 region of pdcd4
96	<a href="#">c5v6hC_</a>	Alignment	not modelled	58.6	22	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> pdz domain-containing protein gipc2; <b>PDBTitle:</b> crystal structure of myosin vi in complex with gh2 domain of gipc2
97	<a href="#">c2rg8A_</a>	Alignment	not modelled	52.6	13	<b>PDB header:</b> apoptosis, translation <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> crystal structure of programmed for cell death 4 middle ma3 domain
98	<a href="#">c4ggoA_</a>	Alignment	not modelled	49.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-2-enoyl-coa reductase; <b>PDBTitle:</b> crystal structure of trans-2-enoyl-coa reductase from treponema2 denticola
99	<a href="#">c5watB_</a>	Alignment	not modelled	46.7	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> corynebacterium glutamicum full length homoserine kinase
100	<a href="#">c4h2tC_</a>	Alignment	not modelled	39.1	24	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> aminoacyl carrier protein 1; <b>PDBTitle:</b> crystal structure of bradyrhizobium japonicum glycine:[carrier2 protein] ligase complexed with cognate carrier protein and an3 analogue of glycyl adenylate

101	<a href="#">d2gyc31</a>	 Alignment	not modelled	38.7	25	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
102	<a href="#">c1rqtB_</a>	 Alignment	not modelled	38.1	35	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
103	<a href="#">c1rqtA_</a>	 Alignment	not modelled	38.1	35	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
104	<a href="#">d1rqta_</a>	 Alignment	not modelled	38.1	35	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
105	<a href="#">c1zunA_</a>	 Alignment	not modelled	35.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
106	<a href="#">c3b64A_</a>	 Alignment	not modelled	33.1	15	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like <b>PDBTitle:</b> macrophage migration inhibitory factor (mif) from2 /leishmania major
107	<a href="#">c3ry0A_</a>	 Alignment	not modelled	31.6	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tautomerase; <b>PDBTitle:</b> crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
108	<a href="#">c5gxtA_</a>	 Alignment	not modelled	30.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> smaltose-binding periplasmic protein,pigg; <b>PDBTitle:</b> crystal structure of pigg
109	<a href="#">c4fazB_</a>	 Alignment	not modelled	30.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate isomerase protein; <b>PDBTitle:</b> kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
110	<a href="#">d1bjpa_</a>	 Alignment	not modelled	30.5	17	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
111	<a href="#">d1otfa_</a>	 Alignment	not modelled	30.3	13	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
112	<a href="#">c4fdxB_</a>	 Alignment	not modelled	29.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonase tautomerase isozyme; <b>PDBTitle:</b> kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
113	<a href="#">d2dt5a1</a>	 Alignment	not modelled	28.8	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional repressor Rex, N-terminal domain
114	<a href="#">c3fwtA_</a>	 Alignment	not modelled	28.2	18	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage migration inhibitory factor-like <b>PDBTitle:</b> crystal structure of leishmania major mif2
115	<a href="#">c3m20A_</a>	 Alignment	not modelled	28.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase, putative; <b>PDBTitle:</b> crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
116	<a href="#">c2op8A_</a>	 Alignment	not modelled	27.6	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase ywhb; <b>PDBTitle:</b> crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
117	<a href="#">d1q1va_</a>	 Alignment	not modelled	27.3	18	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> DEK C-terminal domain <b>Family:</b> DEK C-terminal domain
118	<a href="#">c3mb2G_</a>	 Alignment	not modelled	25.6	9	<b>PDB header:</b> isomerase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase family enzyme - alpha subunit; <b>PDBTitle:</b> kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
119	<a href="#">c3abfB_</a>	 Alignment	not modelled	25.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalocrotonate tautomerase; <b>PDBTitle:</b> crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
120	<a href="#">d1zuna1</a>	 Alignment	not modelled	25.1	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like