

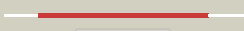





















# Phyre2

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Description	RVBD3088 (-)_3454337_3455761
Date	Thu Aug 8 16:20:26 BST 2019
Unique Job ID	96d5f732e0dfd0c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6chjB_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> diacylglycerol o-acyltransferase; <b>PDBTitle:</b> wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	<a href="#">c6n8eA_</a>	 Alignment		100.0	12	<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
3	<a href="#">c2vsqA_</a>	 Alignment		100.0	10	<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
4	<a href="#">c6aefB_</a>	 Alignment		100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase associated protein papa2; <b>PDBTitle:</b> papa2 acyl transferase
5	<a href="#">c5t81A_</a>	 Alignment		100.0	10	<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
6	<a href="#">c5u89A_</a>	 Alignment		100.0	11	<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 dhbf
7	<a href="#">c5m6pB_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> tyrocidine synthase 2; <b>PDBTitle:</b> crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
8	<a href="#">c5t3eA_</a>	 Alignment		100.0	10	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> bacillamide synthetase heterocyclization domain; <b>PDBTitle:</b> crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
9	<a href="#">c4zxiA_</a>	 Alignment		100.0	13	<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
10	<a href="#">c6ad3A_</a>	 Alignment		100.0	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> lovastatin nonaketide synthase moka; <b>PDBTitle:</b> structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
11	<a href="#">c2xhgA_</a>	 Alignment		100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrocidine synthetase a; <b>PDBTitle:</b> crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis

12	<a href="#">c6p1jA_</a>	Alignment		100.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> txo2; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
13	<a href="#">c4znmB_</a>	Alignment		100.0	10	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> c-domain type ii peptide synthetase; <b>PDBTitle:</b> crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
14	<a href="#">c6cgoB_</a>	Alignment		100.0	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
15	<a href="#">c4jn3B_</a>	Alignment		100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> cda peptide synthetase i; <b>PDBTitle:</b> crystal structures of the first condensation domain of the cda2 synthetase
16	<a href="#">c6m7lB_</a>	Alignment		100.0	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative non-ribosomal peptide synthetase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
17	<a href="#">c4zxiA_</a>	Alignment		100.0	14	<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
18	<a href="#">c2jgpA_</a>	Alignment		100.0	12	<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
19	<a href="#">c4tx3B_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> peptide synthetase, module 7; <b>PDBTitle:</b> complex of the x-domain and oxyb from teicoplanin biosynthesis
20	<a href="#">c5ja2A_</a>	Alignment		100.0	15	<b>PDB header:</b> ligase <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
21	<a href="#">c1l5aA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> amide synthase; <b>PDBTitle:</b> crystal structure of vibh, an nrps condensation enzyme
22	<a href="#">c6ozvA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> txo1; <b>PDBTitle:</b> the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
23	<a href="#">c5dijA_</a>	Alignment	not modelled	100.0	8	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> tqaa; <b>PDBTitle:</b> the crystal structure of ct
24	<a href="#">c1q9jA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> polyketide synthase associated protein 5; <b>PDBTitle:</b> structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
25	<a href="#">c4hvmC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C; <b>PDB Molecule:</b> tlmii; <b>PDBTitle:</b> crystal structure of tallysomycin biosynthesis protein tlmii
26	<a href="#">c3fotA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 15-o-acetyltransferase; <b>PDBTitle:</b> structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
27	<a href="#">c6dd2A_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable hydroxycinnamoyl transferase; <b>PDBTitle:</b> crystal structure of selaginella moellendorffii hct
28	<a href="#">d1l5aa1</a>	Alignment	not modelled	99.9	8	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
						<b>PDB header:</b> transferase

29	<a href="#">c4g0bA</a>	Alignment	not modelled	99.9	11	<b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa shikimate/quinate <b>PDBTitle:</b> structure of native hct from coffea canephora
30	<a href="#">d1q9ja1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
31	<a href="#">d1l5aa2</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
32	<a href="#">c2e1uA</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl transferase; <b>PDBTitle:</b> crystal structure of dendranthema morifolium dmat
33	<a href="#">d1q9ja2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
34	<a href="#">c2bghA</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vinorine synthase; <b>PDBTitle:</b> crystal structure of vinorine synthase
35	<a href="#">c2xr7A</a>	Alignment	not modelled	99.6	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> malonyltransferase; <b>PDBTitle:</b> crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
36	<a href="#">c4ke4A</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl <b>PDBTitle:</b> elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
37	<a href="#">c3b2sA</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
38	<a href="#">c2zbaD</a>	Alignment	not modelled	98.7	9	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trichothecene 3-o-acetyltransferase; <b>PDBTitle:</b> crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
39	<a href="#">c6eqoB</a>	Alignment	not modelled	98.2	11	<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
40	<a href="#">d1q23a</a>	Alignment	not modelled	88.2	22	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
41	<a href="#">d3claa</a>	Alignment	not modelled	85.1	24	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
42	<a href="#">c5es8A</a>	Alignment	not modelled	82.0	7	<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
43	<a href="#">c3maeA</a>	Alignment	not modelled	80.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-oxoisovalerate dehydrogenase e2 component, <b>PDBTitle:</b> crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
44	<a href="#">d1ndba2</a>	Alignment	not modelled	80.6	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
45	<a href="#">c3rqcB</a>	Alignment	not modelled	77.2	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable lipoamide acyltransferase; <b>PDBTitle:</b> crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
46	<a href="#">c2i9dC</a>	Alignment	not modelled	77.0	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> chloramphenicol acetyltransferase; <b>PDBTitle:</b> chloramphenicol acetyltransferase
47	<a href="#">d1nm8a2</a>	Alignment	not modelled	75.7	12	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
48	<a href="#">c2h4tB</a>	Alignment	not modelled	73.5	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase ii
49	<a href="#">c2fy2A</a>	Alignment	not modelled	71.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
50	<a href="#">d1scza</a>	Alignment	not modelled	70.9	27	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
51	<a href="#">d1b5sa</a>	Alignment	not modelled	68.0	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
52	<a href="#">c1t7qA</a>	Alignment	not modelled	64.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine acetyltransferase; <b>PDBTitle:</b> crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
53	<a href="#">c3b8kA</a>	Alignment	not modelled	62.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase; <b>PDBTitle:</b> structure of the truncated human dihydrolipoyl acetyltransferase (e2)
						<b>Fold:</b> CoA-dependent acyltransferases

54	<a href="#">d1dpba_</a>	Alignment	not modelled	61.5	12	<b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> CAT-like
55	<a href="#">c4n72B_</a>	Alignment	not modelled	54.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase (dihydrolipoyltransacetylase <b>PDBTitle:</b> catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
56	<a href="#">d1xl7a2</a>	Alignment	not modelled	50.5	11	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
57	<a href="#">c2fy0A_</a>	Alignment	not modelled	49.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, mitochondrial; <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
58	<a href="#">c3l60A_</a>	Alignment	not modelled	37.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain alpha-keto acid dehydrogenase; <b>PDBTitle:</b> crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis
59	<a href="#">c6h60A_</a>	Alignment	not modelled	35.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component, mitochondrial; <b>PDBTitle:</b> pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
60	<a href="#">c1q6xA_</a>	Alignment	not modelled	34.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> crystal structure of rat choline acetyltransferase
61	<a href="#">c2ii4C_</a>	Alignment	not modelled	27.9	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> lipoamide acyltransferase component of branched-chain <b>PDBTitle:</b> crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
62	<a href="#">c1x18B_</a>	Alignment	not modelled	24.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal carnitine o-octanoyltransferase; <b>PDBTitle:</b> crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
63	<a href="#">d1t1ua2</a>	Alignment	not modelled	19.1	14	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
64	<a href="#">c5wmmA_</a>	Alignment	not modelled	13.0	7	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> nrps; <b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
65	<a href="#">d1ry9a_</a>	Alignment	not modelled	9.9	15	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone
66	<a href="#">d2fm8a1</a>	Alignment	not modelled	8.8	10	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Type III secretory system chaperone-like <b>Family:</b> Type III secretory system chaperone
67	<a href="#">d2hh6a1</a>	Alignment	not modelled	6.5	8	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> BH3980-like <b>Family:</b> BH3980-like
68	<a href="#">c2k9iB_</a>	Alignment	not modelled	6.0	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein orf56; <b>PDBTitle:</b> nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
69	<a href="#">c2rr1A_</a>	Alignment	not modelled	5.7	5	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-length control protein; <b>PDBTitle:</b> solution structure of the c-terminal domain of the fliik
70	<a href="#">c2h0uA_</a>	Alignment	not modelled	5.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori