Phyre2

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Description	RVBD2484c_(-)_2791029_2792504
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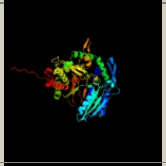
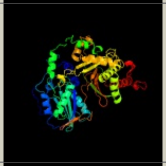
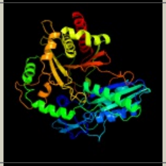
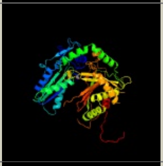
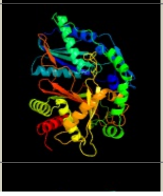
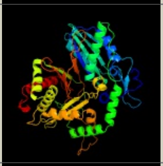
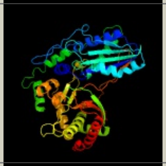
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6chjB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diacylglycerol o-acyltransferase; **PDBTitle:** wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8
2	c6n8eA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holo-obif1; **PDBTitle:** crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
3	c4zxiA_	Alignment		100.0	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
4	c2vsqA_	Alignment		100.0	10	**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
5	c5m6pB_	Alignment		100.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**tyrocidine synthase 2; **PDBTitle:** crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
6	c5u89A_	Alignment		100.0	12	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**amino acid adenylation domain protein; **PDBTitle:** crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
7	c6ad3A_	Alignment		100.0	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**lovastatin nonaketide synthase moka; **PDBTitle:** structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
8	c6cgoB_	Alignment		100.0	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**condensation domain protein; **PDBTitle:** molecular basis for condensation domain-mediated chain release from2 the enacyloxin polyketide synthase
9	c5t81A_	Alignment		100.0	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**epob; **PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
10	c2xhgA_	Alignment		100.0	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
11	c4znmB_	Alignment		100.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**c-domain type ii peptide synthetase; **PDBTitle:** crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)

12	c5t3eA_	Alignment		100.0	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bacillamide synthetase heterocyclization domain; **PDBTitle:** crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
13	c2jgpA_	Alignment		100.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
14	c6aefB_	Alignment		100.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyketide synthase associated protein papa2; **PDBTitle:** papa2 acyl transferase
15	c6p1jA_	Alignment		100.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**txo2; **PDBTitle:** the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo2 serine module
16	c4jn3B_	Alignment		100.0	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cda peptide synthetase i; **PDBTitle:** crystal structures of the first condensation domain of the cda2 synthetase
17	c6m7lB_	Alignment		100.0	14	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative non-ribosomal peptide synthetase; **PDBTitle:** complex of oxya with the x-domain from gpa biosynthesis
18	c4zxjA_	Alignment		100.0	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**enterobactin synthase component f; **PDBTitle:** crystal structure of holo-entf a nonribosomal peptide synthetase in2 the thioester-forming conformation
19	c1l5aA_	Alignment		100.0	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**amide synthase; **PDBTitle:** crystal structure of vibh, an nrps condensation enzyme
20	c5ja2A_	Alignment		100.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**enterobactin synthase component f; **PDBTitle:** entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
21	c4tx3B_	Alignment	not modelled	100.0	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide synthetase, module 7; **PDBTitle:** complex of the x-domain and oxyb from teicoplanin biosynthesis
22	c6ozvA_	Alignment	not modelled	100.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**txo1; **PDBTitle:** the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
23	c5dijA_	Alignment	not modelled	100.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tqaa; **PDBTitle:** the crystal structure of ct
24	c4hvmC_	Alignment	not modelled	100.0	10	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**tlmii; **PDBTitle:** crystal structure of tallysomycin biosynthesis protein tlmii
25	c1q9jA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**polyketide synthase associated protein 5; **PDBTitle:** structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
26	c3fotA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
27	c6dd2A_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable hydroxycinnamoyl transferase; **PDBTitle:** crystal structure of selaginella moellendorffii hct
28	c4g0bA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa shikimate/quinate **PDBTitle:** structure of native hct from coffea canephora
						Fold: CoA-dependent acyltransferases

29	d1l5aa1	Alignment	not modelled	99.9	12	**Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
30	d1q9ja1	Alignment	not modelled	99.9	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
31	c2e1uA_	Alignment	not modelled	99.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl transferase; **PDBTitle:** crystal structure of dendranthema morifolium dmat
32	d1l5aa2	Alignment	not modelled	99.8	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
33	c2bghA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vinorine synthase; **PDBTitle:** crystal structure of vinorine synthase
34	c2xr7A_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyltransferase; **PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
35	d1q9ja2	Alignment	not modelled	99.6	12	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
36	c4ke4A_	Alignment	not modelled	99.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxycinnamoyl-coa:shikimate hydroxycinnamoyl **PDBTitle:** elucidation of the structure and reaction mechanism of sorghum bicolor2 hydroxycinnamoyltransferase and its structural relationship to other3 coa-dependent transferases and synthases
37	c3b2sA_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol
38	c2zbaD_	Alignment	not modelled	99.2	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal structure of f. sporotrichioides tri101 complexed with2 coenzyme a and t-2
39	c6eqoB_	Alignment	not modelled	98.4	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a synthetase; **PDBTitle:** tri-functional propionyl-coa synthase of erythrobacter sp. nap1 with2 bound nadp+ and phosphomethylphosphonic acid adenylate ester
40	c5es8A_	Alignment	not modelled	97.6	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**linear gramicidin synthetase subunit a; **PDBTitle:** crystal structure of the initiation module of lgra in the thiolation2 state
41	d1ndba2	Alignment	not modelled	95.8	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
42	d1nm8a2	Alignment	not modelled	95.7	14	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
43	c1t7qA_	Alignment	not modelled	95.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine acetyltransferase; **PDBTitle:** crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
44	c2fy2A_	Alignment	not modelled	94.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** structures of ligand bound human choline acetyltransferase provide2 insight into regulation of acetylcholine synthesis
45	c1q6xA_	Alignment	not modelled	92.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** crystal structure of rat choline acetyltransferase
46	d1t1ua2	Alignment	not modelled	91.6	11	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
47	c2fyoA_	Alignment	not modelled	91.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212
48	c1xl8B_	Alignment	not modelled	90.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**peroxisomal carnitine o-octanoyltransferase; **PDBTitle:** crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
49	d1xl7a2	Alignment	not modelled	86.3	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
50	c2h4tB_	Alignment	not modelled	83.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, mitochondrial; **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
51	c3maeA_	Alignment	not modelled	74.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-oxoisovalerate dehydrogenase e2 component, **PDBTitle:** crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
52	d1q23a_	Alignment	not modelled	72.1	11	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
53	c3rqcB_	Alignment	not modelled	71.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable lipoamide acyltransferase; **PDBTitle:** crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum

54	d3claa_	Alignment	not modelled	70.4	9	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
55	d1scza_	Alignment	not modelled	61.9	30	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
56	c3b8kA_	Alignment	not modelled	41.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase; **PDBTitle:** structure of the truncated human dihydrolipoyl acetyltransferase (e2)
57	c6h60A_	Alignment	not modelled	38.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component, mitochondrial; **PDBTitle:** pseudo-atomic structural model of the e3bp component of the human2 pyruvate dehydrogenase multienzyme complex
58	d1f16a_	Alignment	not modelled	34.6	30	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
59	d1nija2	Alignment	not modelled	20.5	17	**Fold:**Hypothetical protein YjiA, C-terminal domain **Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain
60	c2i9dC_	Alignment	not modelled	19.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** chloramphenicol acetyltransferase
61	d1dpba_	Alignment	not modelled	16.7	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
62	c4n72B_	Alignment	not modelled	12.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate dehydrogenase (dihydrolipoyltransacetylase **PDBTitle:** catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli
63	c5wmmA_	Alignment	not modelled	12.1	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**nrps; **PDBTitle:** crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
64	d1b5sa_	Alignment	not modelled	8.8	18	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
65	d1ry9a_	Alignment	not modelled	8.1	18	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
66	d1ffva1	Alignment	not modelled	7.5	11	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
67	d1p94a_	Alignment	not modelled	7.3	15	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
68	c2ii4C_	Alignment	not modelled	6.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**lipoamide acyltransferase component of branched-chain **PDBTitle:** 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
69	d1zxia1	Alignment	not modelled	6.6	12	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
70	d2fm8a1	Alignment	not modelled	6.5	15	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
71	c4y01B_	Alignment	not modelled	6.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase s46; **PDBTitle:** crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
72	d1t3qa1	Alignment	not modelled	6.1	14	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
73	c3f42A_	Alignment	not modelled	6.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
74	d1v97a1	Alignment	not modelled	6.0	16	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
75	c5jxfA_	Alignment	not modelled	6.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**asp/glu-specific dipeptidyl-peptidase; **PDBTitle:** crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
76	c2k9iB_	Alignment	not modelled	5.9	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein orf56; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
77	d1rm6c1	Alignment	not modelled	5.9	17	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
78	c5jxpA_	Alignment	not modelled	5.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**asp/glu-specific dipeptidyl-peptidase; **PDBTitle:** crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
79	c2p0vA	Alignment	not modelled	5.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780;

79	c2p0yA_	Alignment	not modelled	5.7	20	**PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
80	d1n62a1	Alignment	not modelled	5.6	12	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
81	c1nijA_	Alignment	not modelled	5.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein
82	c5hypB_	Alignment	not modelled	5.4	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**m28 protein; **PDBTitle:** structure of human c4b-binding protein alpha cain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m283 protein
83	d1vlba1	Alignment	not modelled	5.4	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
84	d1e8ga1	Alignment	not modelled	5.4	9	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like