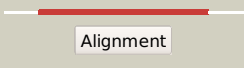

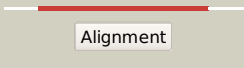

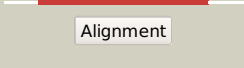

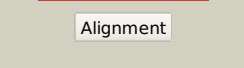

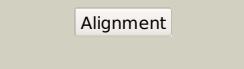

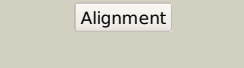

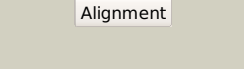
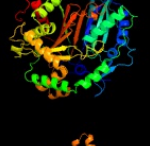
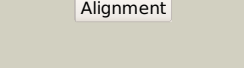

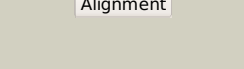
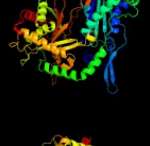
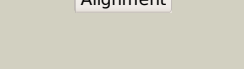

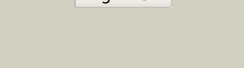



Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0895 (-) _997785_999302 |
| Date | Fri Jul 26 01:50:48 BST 2019 |
| Unique Job ID | 35bee40585cd2c59 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6chjB_ |  |  | 100.0 | 38 | PDB header: transferase Chain: B: PDB Molecule: diacylglycerol o-acyltransferase; PDBTitle: wax ester synthase/diacylglycerol acyltransferase from marinobacter2 aquaeolei vt8 |
| 2 | c4zxiA_ |  |  | 100.0 | 12 | 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 |
| 3 | c2vsqA_ |  |  | 100.0 | 11 | 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 |
| 4 | c5t81A_ |  |  | 100.0 | 14 | PDB header: biosynthetic protein Chain: A: PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulorum |
| 5 | c5m6pB_ |  |  | 100.0 | 13 | 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_ |  |  | 100.0 | 15 | 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 | c5t3eA_ |  |  | 100.0 | 14 | PDB header: ligase Chain: A: PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain. |
| 8 | c2xhgA_ |  |  | 100.0 | 11 | PDB header: isomerase Chain: A: PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis |
| 9 | c6p1iA_ |  |  | 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 |
| 10 | c6aefB_ |  |  | 100.0 | 12 | PDB header: transferase Chain: B: PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase |
| 11 | c2jgpA_ |  |  | 100.0 | 12 | PDB header: ligase Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tyc5-6 pcp-c bidomain of the tyrocidine synthetase2 tyc5 |

| | | | | | | |
|---|-------------------------|-----------|--------------|-------|----|---|
| 12 | c6ad3A_ | Alignment | | 100.0 | 11 | 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 |
| 13 | 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 |
| 14 | c4znmB_ | Alignment | | 100.0 | 12 | PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form) |
| 15 | c4jn3B_ | Alignment | | 100.0 | 17 | PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase |
| 16 | c4zxa_ | Alignment | | 100.0 | 13 | 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 |
| 17 | c5ja2A_ | Alignment | | 100.0 | 14 | 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 |
| 18 | c6m7IB_ | Alignment | | 100.0 | 15 | PDB header: biosynthetic protein Chain: B; PDB Molecule: putative non-ribosomal peptide synthetase; PDBTitle: complex of oxya with the x-domain from gpa biosynthesis |
| 19 | c4tx3B_ | Alignment | | 100.0 | 14 | PDB header: oxidoreductase Chain: B; PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis |
| 20 | c6ozvA_ | Alignment | | 100.0 | 15 | 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 |
| 21 | c1l5aA_ | Alignment | not modelled | 100.0 | 14 | PDB header: biosynthetic protein Chain: A; PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme |
| 22 | c5dijA_ | Alignment | not modelled | 100.0 | 12 | PDB header: unknown function Chain: A; PDB Molecule: tqaa; PDBTitle: the crystal structure of ct |
| 23 | c1q9jA_ | Alignment | not modelled | 100.0 | 15 | PDB header: ligase Chain: A; PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis |
| 24 | c4hvmC_ | Alignment | not modelled | 100.0 | 12 | PDB header: biosynthetic protein Chain: C; PDB Molecule: tlmii; PDBTitle: crystal structure of tallysomycin biosynthesis protein tlmii |
| 25 | c3fotA_ | Alignment | not modelled | 100.0 | 9 | 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 |
| 26 | c6dd2A_ | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: A; PDB Molecule: probable hydroxycinnamoyl transferase; PDBTitle: crystal structure of selaginella moellendorffii hct |
| 27 | c4g0bA_ | Alignment | not modelled | 99.9 | 12 | PDB header: transferase Chain: A; PDB Molecule: hydroxycinnamoyl-coa shikimate/quinate PDBTitle: structure of native hct from coffea canephora |
| 28 | c2e1uA_ | Alignment | not modelled | 99.8 | 11 | PDB header: transferase Chain: A; PDB Molecule: acyl transferase; PDBTitle: crystal structure of dendranthema morifolium dmat |
| Fold: CoA-dependent acyltransferases | | | | | | |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | d1q9ja2 | Alignment | not modelled | 99.8 | 14 | Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase) |
| 30 | d1l5aa1 | Alignment | not modelled | 99.8 | 14 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase) |
| 31 | d1l5aa2 | Alignment | not modelled | 99.8 | 14 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase) |
| 32 | c2bghA | Alignment | not modelled | 99.8 | 12 | PDB header: transferase Chain: A: PDB Molecule: vinorine synthase; PDBTitle: crystal structure of vinorine synthase |
| 33 | c2xr7A | Alignment | not modelled | 99.8 | 11 | PDB header: transferase Chain: A: PDB Molecule: malonyltransferase; PDBTitle: crystal structure of nicotiana tabacum malonyltransferase (ntrmat1)2 complexed with malonyl-coa |
| 34 | d1q9ja1 | Alignment | not modelled | 99.6 | 14 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase) |
| 35 | c4ke4A | Alignment | not modelled | 99.6 | 13 | 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 |
| 36 | c3b2sA | Alignment | not modelled | 99.5 | 11 | PDB header: transferase Chain: A: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. graminearum tri101 complexed with coenzyme a2 and deoxynivalenol |
| 37 | c2zbaD | Alignment | not modelled | 99.0 | 10 | PDB header: transferase Chain: D: PDB Molecule: trichothecene 3-o-acetyltransferase; PDBTitle: crystal structure of f. sporotrichoides tri101 complexed with2 coenzyme a and t-2 |
| 38 | c5es8A | Alignment | not modelled | 98.5 | 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 |
| 39 | c6eqoB | Alignment | not modelled | 98.3 | 12 | 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 | d3claa | Alignment | not modelled | 95.8 | 9 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like |
| 41 | d1q23a | Alignment | not modelled | 94.7 | 12 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like |
| 42 | d1b5sa | Alignment | not modelled | 93.4 | 11 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like |
| 43 | c3b8kA | Alignment | not modelled | 93.3 | 15 | PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase; PDBTitle: structure of the truncated human dihydrolipoyl acetyltransferase (e2) |
| 44 | d1dpba | Alignment | not modelled | 91.9 | 14 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like |
| 45 | c1xl8B | Alignment | not modelled | 91.2 | 11 | PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine |
| 46 | c2h4tB | Alignment | not modelled | 89.2 | 15 | PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii |
| 47 | d1ndba2 | Alignment | not modelled | 86.4 | 13 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase |
| 48 | c3l60A | Alignment | not modelled | 82.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: branched-chain alpha-keto acid dehydrogenase; PDBTitle: crystal structure of branched-chain alpha-keto acid dehydrogenase2 subunit e2 from mycobacterium tuberculosis |
| 49 | c2fyoA | Alignment | not modelled | 81.9 | 16 | PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, mitochondrial; PDBTitle: crystal structure of rat carnitine palmitoyltransferase 2 in space2 group p43212 |
| 50 | c3maeA | Alignment | not modelled | 80.4 | 10 | PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365 |
| 51 | c2fy2A | Alignment | not modelled | 79.7 | 14 | 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 |
| 52 | c2ii4C | Alignment | not modelled | 79.0 | 12 | 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 |

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|----|-------------------------|-----------|--------------|------|----|--|
| 53 | d1scza_ | Alignment | not modelled | 70.7 | 12 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: CAT-like |
| 54 | c3rqcB_ | Alignment | not modelled | 70.6 | 10 | 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 |
| 55 | c1t7qA_ | Alignment | not modelled | 69.3 | 15 | 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 |
| 56 | c4n72B_ | Alignment | not modelled | 68.9 | 10 | PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: catalytic domain from dihydrolipoamide acetyltransferase of pyruvate2 dehydrogenase from escherichia coli |
| 57 | c6h60A_ | Alignment | not modelled | 68.7 | 15 | 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 | c2i9dC_ | Alignment | not modelled | 65.5 | 16 | PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: chloramphenicol acetyltransferase |
| 59 | d1xl7a2 | Alignment | not modelled | 61.6 | 10 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase |
| 60 | d1nm8a2 | Alignment | not modelled | 61.4 | 13 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase |
| 61 | c1q6xA_ | Alignment | not modelled | 59.0 | 13 | PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase |
| 62 | d1t1ua2 | Alignment | not modelled | 51.7 | 12 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase |
| 63 | c6d9mA_ | Alignment | not modelled | 27.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef |
| 64 | c1w25B_ | Alignment | not modelled | 11.5 | 16 | PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp |
| 65 | c4dweA_ | Alignment | not modelled | 6.6 | 8 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative polysaccharide deacetylase2 (bacova_03992) from bacteroides ovatus atcc 8483 at 2.01 a resolution |
| 66 | d1mylb_ | Alignment | not modelled | 5.9 | 21 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors |
| 67 | d1myla_ | Alignment | not modelled | 5.5 | 15 | Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors |
| 68 | c2owyB_ | Alignment | not modelled | 5.4 | 14 | PDB header: dna binding protein Chain: B: PDB Molecule: recombination-associated protein rdgc; PDBTitle: the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding |