Phyre2

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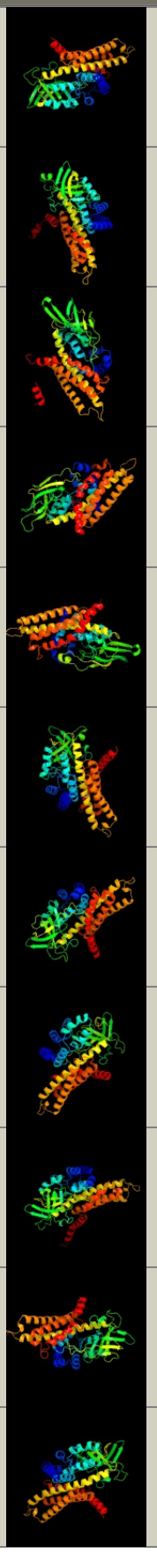
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1346_(fadE14)_1510852_1512012 |
| Date | Wed Jul 31 22:05:44 BST 2019 |
| Unique Job ID | 9fa3e62c8e780c8d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c6es9A_ | Alignment |  | 100.0 | 19 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** methylsuccinyl-coa dehydrogenase of paracoccus denitrificans with2 bound flavin adenine dinucleotide |
| 2 | c4m6zB_ | Alignment | | 100.0 | 99 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-[acyl-carrier-protein] dehydrogenase mbtn;<br>**PDBTitle:** crystal structure of an acyl-acp dehydrogenase |
| 3 | c2z1qA_ | Alignment | | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of acyl coa dehydrogenase |
| 4 | c2ix5A_ | Alignment | | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coenzyme a oxidase 4, peroxisomal;<br>**PDBTitle:** short chain specific acyl-coa oxidase from arabidopsis thaliana, acx42 in complex with acetoacetyl-coa |
| 5 | c3owaC_ | Alignment | | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of acyl-coa dehydrogenase complexed with fad from2 bacillus anthracis |
| 6 | c2a1tC_ | Alignment | | 100.0 | 18 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase, medium-chain specific,<br>**PDBTitle:** structure of the human mcad:etf e165betaa complex |
| 7 | c1rx0B_ | Alignment | | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 8, mitochondrial;<br>**PDBTitle:** crystal structure of isobutyryl-coa dehydrogenase complexed with2 substrate/ligand. |
| 8 | c2pg0B_ | Alignment | | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of acyl-coa dehydrogenase from geobacillus2 kaustophilus |
| 9 | c2uxwA_ | Alignment | | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**very-long-chain specific acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of human very long chain acyl-coa dehydrogenase2 (acadvl) |
| 10 | c5zw2A_ | Alignment | | 100.0 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**l-prolyl-[peptidyl-carrier protein] dehydrogenase;<br>**PDBTitle:** fad complex of piga |
| 11 | c2jifA_ | Alignment | | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**short/branched chain specific acyl-coa dehydrogenase;<br>**PDBTitle:** structure of human short-branched chain acyl-coa dehydrogenase2 (acadsb) |

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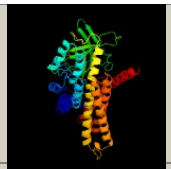
| 12 | c1egcB_ | Alignment |  | 100.0 | 19 | **PDB header:**electron transfer<br>**Chain:** B: **PDB Molecule:**medium chain acyl-coa dehydrogenase;<br>**PDBTitle:** structure of t255e, e376g mutant of human medium chain acyl-2 coa dehydrogenase complexed with octanoyl-coa |
| 13 | c4n5fA_ | Alignment |  | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase with bound2 fadh2 from burkholderia cenocepacia j2315 |
| 14 | c1ivhD_ | Alignment |  | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**isovaleryl-coa dehydrogenase;<br>**PDBTitle:** structure of human isovaleryl-coa dehydrogenase at 2.62 angstroms resolution: structural basis for substrate3 specificity |
| 15 | c5ol2F_ | Alignment |  | 100.0 | 21 | **PDB header:**flavoprotein<br>**Chain:** F: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile |
| 16 | c3swoA_ | Alignment |  | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of a glutaryl-coa dehydrogenase from mycobacterium2 smegmatis in complex with fadh2 |
| 17 | c4irnF_ | Alignment |  | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**prolyl-acp dehydrogenase;<br>**PDBTitle:** crystal structure of the prolyl acyl carrier protein oxidase anab |
| 18 | c2cx9C_ | Alignment |  | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of acyl-coa dehydrogenase |
| 19 | c2vigC_ | Alignment |  | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**short-chain specific acyl-coa dehydrogenase,;<br>**PDBTitle:** crystal structure of human short-chain acyl coa dehydrogenase |
| 20 | c4iv6A_ | Alignment |  | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase fade3;<br>**PDBTitle:** x-ray crystal structure of an isovaleryl-coa dehydrogenase from2 mycobacterium smegmatis |
| 21 | c3oibB_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak |
| 22 | c3r7kB_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable acyl coa dehydrogenase;<br>**PDBTitle:** crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196 |
| 23 | c6fahD_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**flavoprotein<br>**Chain:** D: **PDB Molecule:**caffeyl-coa reductase-etf complex subunit carc;<br>**PDBTitle:** molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction |
| 24 | c3sf6A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of glutaryl-coa dehydrogenase from mycobacterium2 smegmatis |
| 25 | c1ukwA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of medium-chain acyl-coa dehydrogenase2 from thermus thermophilus hb8 |
| 26 | c4l1fB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase domain protein;<br>**PDBTitle:** electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation |
| 27 | c1siqA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutaryl-coa dehydrogenase;<br>**PDBTitle:** the crystal structure and mechanism of human glutaryl-coa2 dehydrogenase |
| | | | | | | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; |

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| 28 | c3pfdB_ | Alignment | not modelled | 100.0 | 19 | **PDBTitle:** crystal structure of an acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to reduced flavin adenine dinucleotide solved3 by combined iodide ion sad mr |
| 29 | c6ijcA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase family protein;<br>**PDBTitle:** structure of mmpa-coa dehydrogenase from roseovarius nubinhibens ism |
| 30 | c5ahsB_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** 3-sulfinopropionyl-coenzyme a (3sp-coa) desulfinase from advenella2 mimgardefordensis dpn7t: holo crystal structure with the substrate3 analog succinyl-coa |
| 31 | c4hr3A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative acyl-coa dehydrogenase;<br>**PDBTitle:** structure of a putative acyl-coa dehydrogenase from mycobacterium2 abscessus |
| 32 | c2dvlB_ | Alignment | not modelled | 100.0 | 25 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of project tt0160 from thermus thermophilus hb8 |
| 33 | c3eomD_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**glutaryl-coa dehydrogenase;<br>**PDBTitle:** 2.4 a crystal structure of native glutaryl-coa dehydrogenase from2 burkholderia pseudomallei |
| 34 | c2ebaI_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** I: **PDB Molecule:**putative glutaryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus |
| 35 | c3nf4B_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to flavin adenine dinucleotide |
| 36 | c5iduB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase domain protein;<br>**PDBTitle:** crystal structure of an acyl-coa dehydrogenase domain protein from2 burkholderia phymatum bound to fad |
| 37 | c3mkhC_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nitroalkane oxidase;<br>**PDBTitle:** podospora anserina nitroalkane oxidase |
| 38 | c4u83A_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** structure of brucella abortus butyryl-coa dehydrogenase |
| 39 | c1bucB_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**butyryl-coa dehydrogenase;<br>**PDBTitle:** three-dimensional structure of butyryl-coa dehydrogenase from2 megasphaera elsdenii |
| 40 | c1r2jA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein fkbi;<br>**PDBTitle:** fkbi for biosynthesis of methoxymalonyl extender unit of fk5202 polyketide immunosuppresant |
| 41 | c6cy8B_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**butyryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of fad-dependent dehydrogenase |
| 42 | c4ktoB_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**isovaleryl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of a putative isovaleryl-coa dehydrogenase (psi-2 nysgrc-012251) from sinorhizobium meliloti 1021 |
| 43 | c5lnxC_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of mmgc, an acyl-coa dehydrogenase from bacillus2 subtilis. |
| 44 | c4x28B_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of the chse4-chse5 complex from mycobacterium2 tuberculosis |
| 45 | c3mpjG_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**glutaryl-coa dehydrogenase;<br>**PDBTitle:** structure of the glutaryl-coenzyme a dehydrogenase |
| 46 | c4w9uD_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of an acyl-coa dehydrogenase from brucella2 melitensis |
| 47 | c2rehD_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**nitroalkane oxidase;<br>**PDBTitle:** mechanistic and structural analyses of the roles of arg4092 and asp402 in the reaction of the flavoprotein nitroalkane3 oxidase |
| 48 | c4rm7A_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** the crystal structure of acyl-coa dehydrogenase from slackia2 heliotrinireducens dsm 20476 |
| 49 | c2wbiB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase family member 11;<br>**PDBTitle:** crystal structure of human acyl-coa dehydrogenase 11 |
| 50 | c4doyE_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**dibenzothiophene desulfurization enzyme c;<br>**PDBTitle:** crystal structure of dibenzothiophene desulfurization enzyme c |
| 51 | c5xdcB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thermophilic dibenzothiophene desulfurization enzyme c;<br>**PDBTitle:** crystal structure of indole-bound tdsc from paenibacillus sp. a11-2 |
| 52 | c5ez3B_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure acyl-coa dehydrogenase from brucella |

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| | | | | | | melitensis in2 complex with fad |
| 53 | c5gj7A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa dehydrogenase type 2 domain protein;<br>**PDBTitle:** putative acyl-coa dehydrogenase |
| 54 | c3m9vA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fad-dependent oxidoreductase;<br>**PDBTitle:** x-ray structure of a kijd3 in complex with dtdp |
| 55 | c2jbtA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**p-hydroxyphenylacetate hydroxylase c2\:oxygenase<br>**PDBTitle:** structure of the monooxygenase component of p-2 hydroxyphenylacetate hydroxylase from acinetobacter3 baumannii |
| 56 | c4x28D_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**acyl-coa dehydrogenase;<br>**PDBTitle:** crystal structure of the chse4-chse5 complex from mycobacterium2 tuberculosis |
| 57 | c5mr6R_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** R: **PDB Molecule:**xiaf protein;<br>**PDBTitle:** xiaf from streptomyces sp. in complex with fadh2 and glycerol |
| 58 | c4y9lB_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**protein acdh-11, isoform b;<br>**PDBTitle:** crystal structure of caenorhabditis elegans acdh-11 |
| 59 | c3djlA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein aidb;<br>**PDBTitle:** crystal structure of alkylation response protein e. coli aidb |
| 60 | c2rfqA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**3-hsa hydroxylase, oxygenase;<br>**PDBTitle:** crystal structure of 3-hsa hydroxylase from rhodococcus sp. rha1 |
| 61 | c4zxvB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dnmz;<br>**PDBTitle:** streptomyces peucetius nitrososynthase dnmz in ligand-free state |
| 62 | c2or0B_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**hydroxylase;<br>**PDBTitle:** structural genomics, the crystal structure of a putative hydroxylase2 from rhodococcus sp. rha1 |
| 63 | c2ddhA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa oxidase;<br>**PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate |
| 64 | c1w07A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa oxidase;<br>**PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1 |
| 65 | c2fonA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**peroxisomal acyl-coa oxidase 1a;<br>**PDBTitle:** x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato) |
| 66 | c5k3jA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coenzyme a oxidase;<br>**PDBTitle:** crystals structure of acyl-coa oxidase-2 in caenorhabditis elegans2 bound with fad, ascaroside-coa, and atp |
| 67 | c3mxlB_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nitrososynthase;<br>**PDBTitle:** crystal structure of nitrososynthase from micromonospora carbonacea2 var. africana |
| 68 | c5k3iH_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** H: **PDB Molecule:**acyl-coenzyme a oxidase;<br>**PDBTitle:** crystal structure of acyl-coa oxidase-1 in caenorhabditis elegans2 complexed with fad and atp |
| 69 | c5y9dA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coenzyme a oxidase 1;<br>**PDBTitle:** crystal structure of acyl-coa oxidase1 from yarrowia lipolytica |
| 70 | c5ys9A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coenzyme a oxidase 3;<br>**PDBTitle:** crystal structure of acyl-coa oxidase3 from yarrowia lipolytica |
| 71 | d1rx0a2 | Alignment | not modelled | 100.0 | 18 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 72 | d2d29a2 | Alignment | not modelled | 100.0 | 19 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 73 | d3mdea2 | Alignment | not modelled | 100.0 | 14 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 74 | d1jqia2 | Alignment | not modelled | 100.0 | 16 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 75 | d1ukwa2 | Alignment | not modelled | 100.0 | 17 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 76 | d1egda2 | Alignment | not modelled | 100.0 | 14 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 77 | d2c12a2 | Alignment | not modelled | 100.0 | 15 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 78 | d1r2ja2 | Alignment | not modelled | 100.0 | 25 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like |

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| 78 | d1r2ja2 | Alignment | not modelled | 100.0 | 25 | **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 79 | d1ivha2 | Alignment | not modelled | 100.0 | 19 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 80 | d1buca2 | Alignment | not modelled | 100.0 | 17 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 81 | d1siqa2 | Alignment | not modelled | 100.0 | 19 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| 82 | d2ddha3 | Alignment | not modelled | 100.0 | 13 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**acyl-CoA oxidase N-terminal domains |
| 83 | c3hwcD_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**chlorophenol-4-monooxygenase component 2;<br>**PDBTitle:** crystal structure of chlorophenol 4-monooxygenase (tftd) of2 burkholderia cepacia ac1100 |
| 84 | d1w07a3 | Alignment | not modelled | 100.0 | 14 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**acyl-CoA oxidase N-terminal domains |
| 85 | d3mdea1 | Alignment | not modelled | 100.0 | 25 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 86 | d1egda1 | Alignment | not modelled | 100.0 | 26 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 87 | c4g5eD_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**2,4,6-trichlorophenol 4-monooxygenase;<br>**PDBTitle:** 2,4,6-trichlorophenol 4-monooxygenase |
| 88 | c2yyjA_ | Alignment | not modelled | 100.0 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxyphenylacetate-3-hydroxylase;<br>**PDBTitle:** crystal structure of the oxygenase component (hpab) of 4-2 hydroxyphenylacetate 3-monooxygenase complexed with fad and 4-3 hydroxyphenylacetate |
| 89 | d1ivha1 | Alignment | not modelled | 100.0 | 28 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 90 | d1jqia1 | Alignment | not modelled | 100.0 | 21 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 91 | d1siqa1 | Alignment | not modelled | 100.0 | 17 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 92 | d1rx0a1 | Alignment | not modelled | 100.0 | 23 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 93 | d1buca1 | Alignment | not modelled | 100.0 | 26 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 94 | c1u8vA_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**lyase, isomerase<br>**Chain:** A: **PDB Molecule:**gamma-aminobutyrate metabolism dehydratase/isomerase;<br>**PDBTitle:** crystal structure of 4-hydroxybutyryl-coa dehydratase from clostridium2 aminobutyricum: radical catalysis involving a [4fe-4s] cluster and3 flavin |
| 95 | d2d29a1 | Alignment | not modelled | 100.0 | 28 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 96 | d1ukwa1 | Alignment | not modelled | 100.0 | 26 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 97 | d2c12a1 | Alignment | not modelled | 100.0 | 16 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 98 | d2ddha1 | Alignment | not modelled | 99.9 | 19 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**acyl-CoA oxidase C-terminal domains |
| 99 | d1r2ja1 | Alignment | not modelled | 99.9 | 20 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |
| 100 | d1w07a1 | Alignment | not modelled | 99.9 | 23 | **Fold:**Bromodomain-like<br>**Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like<br>**Family:**acyl-CoA oxidase C-terminal domains |
| 101 | c6eb0A_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit;<br>**PDBTitle:** structure of 4-hydroxyphenylacetate 3-monooxygenase (hpab), oxygenase2 component from escherichia coli |
| 102 | d1u8va2 | Alignment | not modelled | 99.8 | 13 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains |
| | | | | | | **PDB header:**oxidoreductase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 103 | c4oo2D_ | Alignment | not modelled | 99.3 | 12 | **Chain:** D: **PDB Molecule:**chlorophenol-4-monooxygenase; **PDBTitle:** streptomyces globisporus c-1027 fad dependent (s)-3-chloro-β-2 tyrosine-s-sgcc2 c-5 hydroxylase sgcc apo form |
| 104 | d1u8va1 | Alignment | not modelled | 92.8 | 13 | **Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain |