# Phyre²

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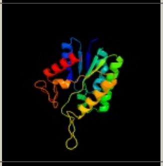
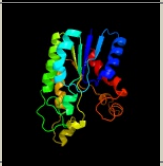
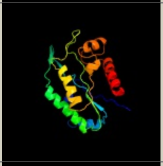
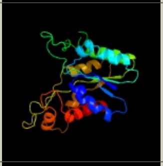
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0111_(-)_133948_136005 |
| Date | Tue Jul 23 14:50:15 BST 2019 |
| Unique Job ID | 65a1c169eb53a840 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c4iyjA_ | Alignment |  | 99.3 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gdsl-like protein;<br>**PDBTitle:** crystal structure of a putative acylhydrolase (bacuni_03406) from2 bacteroides uniformis atcc 8492 at 1.37 a resolution |
| 2 | c3p94A_ | Alignment |  | 99.3 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gdsl-like lipase;<br>**PDBTitle:** crystal structure of a gdsl-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution |
| 3 | c2o14A_ | Alignment |  | 99.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein yxim;<br>**PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr595 |
| 4 | c4rshB_ | Alignment |  | 99.2 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**lipolytic protein g-d-s-l family;<br>**PDBTitle:** structure of a putative lipolytic protein of g-d-s-l family from2 desulfitobacterium hafniense dcb-2 |
| 5 | c5ufyA_ | Alignment |  | 99.2 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acyltransferase;<br>**PDBTitle:** structure of streptococcus pneumoniae peptidoglycan o-2 acetyltransferase a (oata) c-terminal catalytic domain |
| 6 | c4h08A_ | Alignment |  | 99.2 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative hydrolase;<br>**PDBTitle:** crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution |
| 7 | c3milA_ | Alignment |  | 99.1 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**isoamyl acetate-hydrolyzing esterase;<br>**PDBTitle:** crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae |
| 8 | c4jggB_ | Alignment |  | 99.1 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**esterase tesa;<br>**PDBTitle:** crystal structure of tesa |
| 9 | c4k40B_ | Alignment |  | 99.1 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**gdsl-like lipase/acylhydrolase family protein;<br>**PDBTitle:** peptidoglycan o-acetylesterase in action, 0 min |
| 10 | d1k7ca_ | Alignment |  | 99.1 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Rhamnogalacturonan acetylesterase |
| 11 | d1jrla_ | Alignment |  | 99.1 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**TAP-like |

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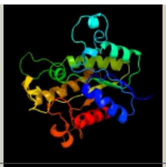
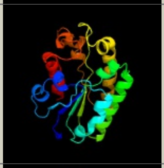
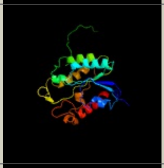
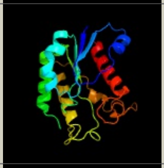
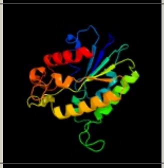
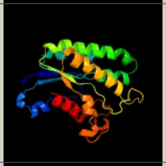
| 12 | c4s1pA_ | Alignment |  | 99.1 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** shel_16390 protein, a putative sgnh hydrolase from slackia2 heliotrinireducens |
| 13 | c6njcB_ | Alignment |  | 99.0 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**sialate o-acetylesterase;<br>**PDBTitle:** crystal structure of the sialate o-acetylesterase from bacteroides2 vulgatus |
| 14 | c4jhlA_ | Alignment |  | 99.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acetyl xylan esterase;<br>**PDBTitle:** crystal structure of of axe2, an acetylxylan esterase from geobacillus2 stearothermophilus |
| 15 | c3bzwA_ | Alignment |  | 99.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative lipase;<br>**PDBTitle:** crystal structure of a putative lipase from bacteroides2 thetaiotaomicron |
| 16 | d3bzwa1 | Alignment |  | 99.0 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**BT2961-like |
| 17 | d1yzfa1 | Alignment |  | 99.0 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**TAP-like |
| 18 | d2hsja1 | Alignment |  | 99.0 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Acetylhydrolase |
| 19 | c5jd3A_ | Alignment |  | 99.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lae5;<br>**PDBTitle:** crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain |
| 20 | c6iqbA_ | Alignment |  | 99.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sgnh-hydrolase family esterase;<br>**PDBTitle:** esterase aline4 mutant-s13a |
| 21 | c3hp4A_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gdsl-esterase;<br>**PDBTitle:** crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate |
| 22 | c3dc7B_ | Alignment | not modelled | 99.0 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein lp_3323;<br>**PDBTitle:** crystal structure of the protein q88sr8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109. |
| 23 | c4hf7A_ | Alignment | not modelled | 99.0 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative acylhydrolase;<br>**PDBTitle:** crystal structure of a gdsl-like lipase (bt0569) from bacteroides2 thetaiotaomicron vpi-5482 at 1.77 a resolution |
| 24 | c4lhsA_ | Alignment | not modelled | 99.0 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative gdsl-like lipase (bacova_00914) from2 bacteroides ovatus atcc 8483 at 1.40 a resolution |
| 25 | d2o14a2 | Alignment | not modelled | 99.0 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**YxiM C-terminal domain-like |
| 26 | c4rw0B_ | Alignment | not modelled | 99.0 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**lipolytic protein g-d-s-l family;<br>**PDBTitle:** crystal structure of a member of the lipolytic protein g-d-s-l family2 from veillonella parvula dsm 2008 |
| 27 | d1fxwf_ | Alignment | not modelled | 99.0 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Acetylhydrolase |
| 28 | d1es9a_ | Alignment | not modelled | 98.9 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Acetylhydrolase |

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| 29 | d3dc7a1 | Alignment | not modelled | 98.9 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**BT2961-like |
| 30 | c6iq8B_ | Alignment | not modelled | 98.9 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**carboxylesterase;<br>**PDBTitle:** esterase crme10 mutant-d178a |
| 31 | c3rjtA_ | Alignment | not modelled | 98.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lipolytic protein g-d-s-l family;<br>**PDBTitle:** crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446 |
| 32 | c2vptA_ | Alignment | not modelled | 98.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lipolytic enzyme;<br>**PDBTitle:** clostridium thermocellum family 3 carbohydrate esterase |
| 33 | c4q7qA_ | Alignment | not modelled | 98.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lipolytic protein g-d-s-l family;<br>**PDBTitle:** the crystal structure of a possible lipase from chitinophaga pinensis2 dsm 2588 |
| 34 | c5hoeB_ | Alignment | not modelled | 98.8 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hydrolase;<br>**PDBTitle:** crystal structrue of est24, a carbohydrate acetylesterase from2 sinorhizobium meliloti |
| 35 | c4c1bC_ | Alignment | not modelled | 98.7 | 17 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**orf1-encoded protein;<br>**PDBTitle:** esterase domain of the zfl2-1 orf1 protein from the zebrafish zfl2-12 retrotransposon |
| 36 | c4nrdA_ | Alignment | not modelled | 98.7 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative gdsl-like lipase (bacova_04955) from2 bacteroides ovatus atcc 8483 at 2.10 a resolution |
| 37 | c2waoA_ | Alignment | not modelled | 98.7 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endoglucanase e;<br>**PDBTitle:** structure of a family two carbohydrate esterase from clostridium2 thermocellum in complex with cellohexaose |
| 38 | d1esca_ | Alignment | not modelled | 98.7 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Esterase |
| 39 | c4q9aA_ | Alignment | not modelled | 98.7 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tat pathway signal sequence domain protein;<br>**PDBTitle:** crystal structure of a putative gdsl-like lipase (parmer_00689) from2 parabacteroides merdae atcc 43184 at 2.86 a resolution |
| 40 | c3x0hA_ | Alignment | not modelled | 98.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**carbohydrate esterase 1;<br>**PDBTitle:** crystal structure of a carbohydrate esterase family 1 from talaromyces2 cellulolyticus |
| 41 | c3dciB_ | Alignment | not modelled | 98.6 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**arylesterase;<br>**PDBTitle:** the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58 |
| 42 | c4devE_ | Alignment | not modelled | 98.6 | 12 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**acetyl-xylan esterase est2a;<br>**PDBTitle:** an acetyl xylan esterase (est2a) from the rumen bacterium butyrivibrio2 proteoclasticus. |
| 43 | c4tx1C_ | Alignment | not modelled | 98.6 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**esterase;<br>**PDBTitle:** the crystal structure of carbohydrate acetylesterase family member2 from sinorhizobium meliloti |
| 44 | d1vjga_ | Alignment | not modelled | 98.6 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Hypothetical protein alr1529 |
| 45 | c2q0qC_ | Alignment | not modelled | 98.6 | 16 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**aryl esterase;<br>**PDBTitle:** structure of the native m. smegmatis aryl esterase |
| 46 | c4m8kA_ | Alignment | not modelled | 98.6 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hypothetical protein, gdsl-like lipase/acylhydrolase family<br>**PDBTitle:** crystal structure of a putative gdsl-like lipase (bacuni_00748) from2 bacteroides uniformis atcc 8492 at 1.90 a resolution |
| 47 | c4xvhA_ | Alignment | not modelled | 98.5 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**carbohydrate esterase family 2 (ce2);<br>**PDBTitle:** crystal structure of a corynascus thermopiles (myceliophthora2 fergusii) carbohydrate esterase family 2 (ce2) enzyme plus3 carbohydrate binding domain (cbd) |
| 48 | c2waaA_ | Alignment | not modelled | 98.5 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**xylan esterase, putative, axe2c;<br>**PDBTitle:** structure of a family two carbohydrate esterase from2 cellvibrio japonicus |
| 49 | c2w9xA_ | Alignment | not modelled | 98.5 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative acetyl xylan esterase;<br>**PDBTitle:** the active site of a carbohydrate esterase displays2 divergent3 catalytic and non-catalytic binding functions |
| 50 | c5malA_ | Alignment | not modelled | 98.1 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lipase;<br>**PDBTitle:** crystal structure of extracelular lipase from streptomyces rimosus at2 1.7a resolution |
| 51 | c4hyqA_ | Alignment | not modelled | 98.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phospholipase a1;<br>**PDBTitle:** crystal structure of phospholipase a1 from streptomyces albidoflavus2 na297 |
| 52 | c6jl1A_ | Alignment | not modelled | 97.8 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**thermolabile hemolysin;<br>**PDBTitle:** crystal structure of vvplpa g389d from vibrio vulnificus |
| 53 | c4kncA_ | Alignment | not modelled | 97.5 | 12 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**alginate biosynthesis protein algx;<br>**PDBTitle:** structural and functional characterization of |

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|  |  |  |  |  |  | pseudomonas aeruginosa2 algx |
| 54 | c4o8vA_ | Alignment | not modelled | 97.3 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**alginate biosynthesis protein algj;<br>**PDBTitle:** o-acetyltransferase domain of pseudomonas putida algj |
| 55 | c5xtuA_ | Alignment | not modelled | 97.2 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gdsl-family esterase;<br>**PDBTitle:** crystal structure of gdsl esterase of photobacterium sp. j15 |
| 56 | c4i8iA_ | Alignment | not modelled | 96.7 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of a duf4886 family protein (bacuni_01406) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution |
| 57 | c4nzkA_ | Alignment | not modelled | 95.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a dhhw family protein (eubsir_00411) from2 eubacterium siraeum dsm 15702 at 1.49 a resolution |
| 58 | c3kvnA_ | Alignment | not modelled | 95.8 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase esta;<br>**PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa |
| 59 | d1zmba1 | Alignment | not modelled | 94.5 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Putative acetylxylan esterase-like |
| 60 | c5v8eB_ | Alignment | not modelled | 94.2 | 10 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**bacillus cereus patb1;<br>**PDBTitle:** structure of bacillus cereus patb1 |
| 61 | c6o93A_ | Alignment | not modelled | 91.9 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**d-alanyl transferase dltd;<br>**PDBTitle:** d-alanyl transferase dltd from enterococcus faecalis |
| 62 | c6pfxB_ | Alignment | not modelled | 91.6 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**d-alanyl transferase dltd;<br>**PDBTitle:** d-alanyl transferase dltd from enterococcus faecium |
| 63 | c3bmaC_ | Alignment | not modelled | 89.4 | 13 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase;<br>**PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6 |
| 64 | d2apja1 | Alignment | not modelled | 89.2 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Putative acetylxylan esterase-like |
| 65 | c3nvbA_ | Alignment | not modelled | 88.1 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate |
| 66 | c5w78B_ | Alignment | not modelled | 57.0 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**acyloxyacyl hydrolase;<br>**PDBTitle:** human acyloxyacyl hydrolase (aoah), proteolytically processed |
| 67 | d2gc6a1 | Alignment | not modelled | 53.5 | 24 | **Fold:**MurD-like peptide ligases, peptide-binding domain<br>**Superfamily:**MurD-like peptide ligases, peptide-binding domain<br>**Family:**Folylpolyglutamate synthetase, C-terminal domain |
| 68 | c2wwbB_ | Alignment | not modelled | 46.7 | 39 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma;<br>**PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome |
| 69 | c3eywA_ | Alignment | not modelled | 31.4 | 11 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux<br>**PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff |
| 70 | d3bypa1 | Alignment | not modelled | 27.9 | 10 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Cation efflux protein cytoplasmic domain-like<br>**Family:**Cation efflux protein cytoplasmic domain-like |
| 71 | d1rhzb_ | Alignment | not modelled | 26.9 | 28 | **Fold:**Single transmembrane helix<br>**Superfamily:**Preprotein translocase SecE subunit<br>**Family:**Preprotein translocase SecE subunit |
| 72 | c4s3hD_ | Alignment | not modelled | 23.7 | 24 | **PDB header:**unknown function<br>**Chain:** D: **PDB Molecule:**mdb1;<br>**PDBTitle:** crystal structure of s. pombe mdb1 fha domain |
| 73 | c4aghA_ | Alignment | not modelled | 20.5 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**mosub1, transcription cofactor;<br>**PDBTitle:** structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae |
| 74 | d1u1ia1 | Alignment | not modelled | 19.4 | 7 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 75 | c5fgnA_ | Alignment | not modelled | 19.3 | 10 | **PDB header:**transferase,hydrolase<br>**Chain:** A: **PDB Molecule:**lipooligosaccharide phosphoethanolamine transferase a;<br>**PDBTitle:** integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis |
| 76 | c5a4aA_ | Alignment | not modelled | 18.9 | 10 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**maternal effect protein oskar;<br>**PDBTitle:** crystal structure of the osk domain of drosophila oskar |
| 77 | c3pt5A_ | Alignment | not modelled | 18.8 | 8 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase;<br>**PDBTitle:** crystal structure of nans |
| 78 | c3vsjA_ | Alignment | not modelled | 17.2 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-amino-5-chlorophenol 1,6-dioxygenase alpha subunit; |

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| | | | | | | **PDBTitle:** crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products |
| 79 | d1y6ia2 | Alignment | not modelled | 15.9 | 33 | **Fold:**GUN4-like<br>**Superfamily:**GUN4-like<br>**Family:**GUN4-like |
| 80 | c3wrbB_ | Alignment | not modelled | 15.2 | 9 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**gallate dioxygenase;<br>**PDBTitle:** crystal structure of the anaerobic h124f desb-gallate complex |
| 81 | d1jmkc_ | Alignment | not modelled | 15.1 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 82 | d1k4ta3 | Alignment | not modelled | 13.8 | 12 | **Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment<br>**Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment<br>**Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment |
| 83 | c4oc8D_ | Alignment | not modelled | 11.5 | 22 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**restriction endonuclease aspbhi;<br>**PDBTitle:** dna modification-dependent restriction endonuclease aspbhi |
| 84 | c6odmK_ | Alignment | not modelled | 11.3 | 24 | **PDB header:**viral protein<br>**Chain:** K: **PDB Molecule:**capsid vertex component 2;<br>**PDBTitle:** herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit |
| 85 | c4rzlA_ | Alignment | not modelled | 11.1 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**restriction endonuclease lpnpi;<br>**PDBTitle:** dna recognition domain of the cytosine modification-dependent2 restriction endonuclease lpnpi |
| 86 | d1pcfa_ | Alignment | not modelled | 10.9 | 22 | **Fold:**ssDNA-binding transcriptional regulator domain<br>**Superfamily:**ssDNA-binding transcriptional regulator domain<br>**Family:**Transcriptional coactivator PC4 C-terminal domain |
| 87 | d1j6ua2 | Alignment | not modelled | 10.8 | 24 | **Fold:**MurD-like peptide ligases, peptide-binding domain<br>**Superfamily:**MurD-like peptide ligases, peptide-binding domain<br>**Family:**MurCDEF C-terminal domain |
| 88 | c5xj6A_ | Alignment | not modelled | 10.1 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycerol-3-phosphate acyltransferase;<br>**PDBTitle:** crystal structure of plsy (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form |
| 89 | c3mduA_ | Alignment | not modelled | 9.7 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-formimino-l-glutamate iminohydrolase;<br>**PDBTitle:** the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate |
| 90 | c4jxpA_ | Alignment | not modelled | 9.7 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-l-iduronidase;<br>**PDBTitle:** crystal structure of human alpha-l-iduronidase, monoclinic form |
| 91 | c6gvbC_ | Alignment | not modelled | 9.4 | 8 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**exo-beta-1,4-mannosidase;<br>**PDBTitle:** crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase |
| 92 | c3odmE_ | Alignment | not modelled | 9.1 | 9 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase;<br>**PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase |
| 93 | c2vr2A_ | Alignment | not modelled | 9.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydropyrimidinase;<br>**PDBTitle:** human dihydropyrimidinase |
| 94 | c5ho5D_ | Alignment | not modelled | 8.9 | 12 | **PDB header:**metal transport<br>**Chain:** D: **PDB Molecule:**magnetosome protein mamb;<br>**PDBTitle:** mamb |
| 95 | c1b9xC_ | Alignment | not modelled | 8.8 | 15 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**protein (phosducin);<br>**PDBTitle:** structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin |
| 96 | c4gn0D_ | Alignment | not modelled | 8.7 | 18 | **PDB header:**signaling protein<br>**Chain:** D: **PDB Molecule:**hamp domain of af1503;<br>**PDBTitle:** de novo phasing of a hamp-complex using an improved arcimboldo method |
| 97 | c5w7dA_ | Alignment | not modelled | 8.6 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acyloxyacyl hydrolase;<br>**PDBTitle:** murine acyloxyacyl hydrolase (aoah), s262a mutant |
| 98 | c2jq5A_ | Alignment | not modelled | 8.4 | 29 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**sec-c motif;<br>**PDBTitle:** solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097 |
| 99 | c6cciA_ | Alignment | not modelled | 8.3 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein eskimo 1;<br>**PDBTitle:** the crystal structure of xoat1 |