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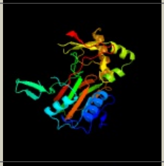
|---|---|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3406_(-)_3825510_3826397 |
| Date | Fri Aug 9 18:20:07 BST 2019 |
| Unique Job ID | 3908a605cf52cdeb |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3r1jB_ | Alignment |  | 100.0 | 83 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase;<br>**PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form |
| 2 | c5hsxB_ | Alignment |  | 100.0 | 45 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative alpha-ketoglutarate-dependent taurine dioxygenase;<br>**PDBTitle:** crystal structure of a putative alpha-ketoglutarate-dependent taurine2 dioxygenase from burkholderia xenovorans |
| 3 | c4y0eB_ | Alignment |  | 100.0 | 56 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative dioxygenase;<br>**PDBTitle:** x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus |
| 4 | d1oiha_ | Alignment |  | 100.0 | 56 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**TauD/TfdA-like |
| 5 | d1otja_ | Alignment |  | 100.0 | 36 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**TauD/TfdA-like |
| 6 | c4j5iH_ | Alignment |  | 100.0 | 67 | **PDB header:**oxidoreductase<br>**Chain:** H: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase;<br>**PDBTitle:** crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis |
| 7 | c3pvjB_ | Alignment |  | 100.0 | 37 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase;<br>**PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440 |
| 8 | c6d1oD_ | Alignment |  | 100.0 | 32 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**(r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase;<br>**PDBTitle:** ft_5 dioxygenase apoenzyme |
| 9 | c5j92B_ | Alignment |  | 100.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative alpha kg dependent 2,4-d dioxygenase;<br>**PDBTitle:** crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans |
| 10 | c5bkeF_ | Alignment |  | 100.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate<br>**PDBTitle:** crystal structure of aad-2 in complex with mn(ii) and n-oxalylglycine |
| 11 | c5vn6B_ | Alignment |  | 100.0 | 38 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**taurine dioxygenase;<br>**PDBTitle:** crystal structure of taurine dioxygenase from burkholderia ambifaria |

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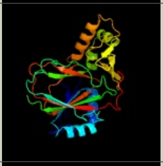
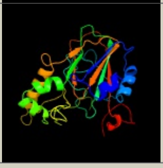
| 12 | c6dchA_ | Alignment |  | 100.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**scoe protein;<br>**PDBTitle:** structure of isonitrile biosynthesis enzyme scoe |
| 13 | c3eatX_ | Alignment |  | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb;<br>**PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa |
| 14 | d1nx4a_ | Alignment |  | 100.0 | 21 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**gamma-Butyrobetaine hydroxylase |
| 15 | d1y0za_ | Alignment |  | 100.0 | 13 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**gamma-Butyrobetaine hydroxylase |
| 16 | c3ms5A_ | Alignment |  | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase;<br>**PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1) |
| 17 | c6npcB_ | Alignment |  | 100.0 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**tmpa, 2-trimethylaminoethylphosphonate hydroxylase;<br>**PDBTitle:** x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate |
| 18 | c6f6jC_ | Alignment |  | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**l-lysine 3-hydroxylase;<br>**PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo1 with fe(ii)/succinate/(3s)-3-hydroxy-l-lysine |
| 19 | d1ds1a_ | Alignment |  | 100.0 | 18 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Clavaminate synthase |
| 20 | c2og5A_ | Alignment |  | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxygenase;<br>**PDBTitle:** crystal structure of asparagine oxygenase (asno) |
| 21 | d1jr7a_ | Alignment | not modelled | 100.0 | 15 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Gab protein (hypothetical protein YgaT) |
| 22 | c4ne0A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase;<br>**PDBTitle:** crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg |
| 23 | c2wbqA_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase;<br>**PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine |
| 24 | c4ne0B_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**l-arginine beta-hydroxylase;<br>**PDBTitle:** crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg |
| 25 | c6dawA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**non-heme iron hydroxylase;<br>**PDBTitle:** x-ray crystal structure of napi l-arginine desaturase bound to fe(ii),2 l-arginine, and acetate |
| 26 | c5eqnA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**frbj;<br>**PDBTitle:** structure of phosphonate hydroxylase |
| 27 | c6exhA_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-lysine 4-hydroxylase;<br>**PDBTitle:** crystal structure of the complex fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo5 with fe(ii)/succinate/(4r)-4-hydroxy-l-lysine |
| 28 | c2opwA_ | Alignment | not modelled | 97.9 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**phyhd1 protein;<br>**PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo) |

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| 29 | c4xaaA_ | Alignment | not modelled | 97.8 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxygenase;<br>**PDBTitle:** crystal structure of avio1 from streptomyces viridochromogenes tue57 |
| 30 | c5zm4B_ | Alignment | not modelled | 97.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dioxygenase anda;<br>**PDBTitle:** fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c |
| 31 | c4zonB_ | Alignment | not modelled | 97.7 | 23 | **PDB header:**oxidoreductase/oxidoreductase inhibitor<br>**Chain:** B: **PDB Molecule:**verruculogen synthase;<br>**PDBTitle:** structure of ftmox1 with fumitremorgen b complex |
| 32 | c5m0tA_ | Alignment | not modelled | 97.6 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alpha-ketoglutarate-dependent non-heme iron oxygenase eash;<br>**PDBTitle:** alpha-ketoglutarate-dependent non-heme iron oxygenase eash |
| 33 | c5erlD_ | Alignment | not modelled | 97.6 | 20 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**snon,snon;<br>**PDBTitle:** crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro |
| 34 | c4naoA_ | Alignment | not modelled | 97.6 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative oxygenase;<br>**PDBTitle:** crystal structure of eash |
| 35 | c5epaE_ | Alignment | not modelled | 97.2 | 18 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**snok;<br>**PDBTitle:** crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis |
| 36 | c5ncjB_ | Alignment | not modelled | 97.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**leucine hydroxylase;<br>**PDBTitle:** grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine |
| 37 | c2rdsA_ | Alignment | not modelled | 97.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha-<br>**PDBTitle:** crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound |
| 38 | d2a1xa1 | Alignment | not modelled | 96.7 | 11 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**PhyH-like |
| 39 | c4xabA_ | Alignment | not modelled | 96.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**evdo2;<br>**PDBTitle:** crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca |
| 40 | c5daqA_ | Alignment | not modelled | 96.6 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**phytanoyl-coa dioxygenase family protein (afu_orthologue<br>**PDBTitle:** fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycyclopeptin |
| 41 | c3emrA_ | Alignment | not modelled | 96.4 | 8 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ectd;<br>**PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens |
| 42 | c3gjbA_ | Alignment | not modelled | 96.3 | 14 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**cytc3;<br>**PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate |
| 43 | c4xbzB_ | Alignment | not modelled | 96.2 | 28 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**evdo1;<br>**PDBTitle:** crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca |
| 44 | c3nnlB_ | Alignment | not modelled | 95.5 | 11 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**cura;<br>**PDBTitle:** halogenase domain from cura module (crystal form iii) |
| 45 | c6ec3C_ | Alignment | not modelled | 95.3 | 16 | **PDB header:**transferase, oxidoreductase<br>**Chain:** C: **PDB Molecule:**methyltransferase domain-containing protein;<br>**PDBTitle:** crystal structure of evdmo1 |
| 46 | c5yboA_ | Alignment | not modelled | 95.2 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**prha;<br>**PDBTitle:** fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1 |
| 47 | c4mhuB_ | Alignment | not modelled | 95.2 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ectoine hydroxylase;<br>**PDBTitle:** crystal structure of ectd from s. alaskensis with bound fe |
| 48 | c4xc9B_ | Alignment | not modelled | 95.1 | 14 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**oxidase/hydroxylase;<br>**PDBTitle:** crystal structure of apo hygx from streptomyces hygroscopicus |
| 49 | c4iw3J_ | Alignment | not modelled | 94.8 | 14 | **PDB header:**metal binding protein/translation<br>**Chain:** J: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of a pseudomonas putida prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu) |
| 50 | c5c5tB_ | Alignment | not modelled | 92.5 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase;<br>**PDBTitle:** the crystal structure of viral collagen prolyl hydroxylase vcph from2 paramecium bursaria chlorella virus-1 - 2og complex |
| 51 | d2fcta1 | Alignment | not modelled | 89.9 | 16 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**PhyH-like |
| 52 | c6f0wA_ | Alignment | not modelled | 87.1 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hif prolyl hydroxylase;<br>**PDBTitle:** prolyl hydroxylase in complex with hypoxia inducible factor oxygen2 degradation domain peptide fragment from trichoplax adhaerens |
| 53 | d1wdia_ | Alignment | not modelled | 82.0 | 22 | **Fold:**QueA-like<br>**Superfamily:**QueA-like<br>**Family:**QueA-like |
| | | | | | | **PDB header:**isomerase |

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| 54 | c1yy3A_ | Alignment | not modelled | 81.4 | 17 | **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase-<br>**PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea) |
| 55 | c3itqB_ | Alignment | not modelled | 81.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**prolyl 4-hydroxylase, alpha subunit domain protein;<br>**PDBTitle:** crystal structure of a prolyl 4-hydroxylase from bacillus anthracis |
| 56 | d1vkya_ | Alignment | not modelled | 79.2 | 17 | **Fold:**QueA-like<br>**Superfamily:**QueA-like<br>**Family:**QueA-like |
| 57 | c2jijA_ | Alignment | not modelled | 65.4 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**prolyl-4 hydroxylase;<br>**PDBTitle:** crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i |
| 58 | c3pl0B_ | Alignment | not modelled | 58.8 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution |
| 59 | c2g19A_ | Alignment | not modelled | 50.6 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**egl nine homolog 1;<br>**PDBTitle:** cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2) |
| 60 | c3ghfA_ | Alignment | not modelled | 44.0 | 16 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**septum site-determining protein minc;<br>**PDBTitle:** crystal structure of the septum site-determining protein minc from2 salmonella typhimurium |
| 61 | c3ouiA_ | Alignment | not modelled | 41.4 | 9 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**egl nine homolog 1;<br>**PDBTitle:** phd2-r717 with 40787422 |
| 62 | d2csga1 | Alignment | not modelled | 41.3 | 11 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**YbiU-like |
| 63 | d1gp6a_ | Alignment | not modelled | 40.2 | 14 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Penicillin synthase-like |
| 64 | d1odma_ | Alignment | not modelled | 39.1 | 12 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Penicillin synthase-like |
| 65 | d1dcsa_ | Alignment | not modelled | 36.4 | 16 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Penicillin synthase-like |
| 66 | c2a5hC_ | Alignment | not modelled | 36.0 | 14 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase;<br>**PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate). |
| 67 | d2evra2 | Alignment | not modelled | 29.2 | 18 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**NlpC/P60 |
| 68 | c3on7C_ | Alignment | not modelled | 28.0 | 4 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**oxidoreductase, iron/ascorbate family;<br>**PDBTitle:** crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution |
| 69 | c5c3qB_ | Alignment | not modelled | 27.0 | 8 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**thymine dioxygenase;<br>**PDBTitle:** crystal structure of the full-length neurospora crassa t7h in complex2 with alpha-kg and thymine (t) |
| 70 | c4xaeB_ | Alignment | not modelled | 24.5 | 6 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**feruloyl coa ortho-hydroxylase 1;<br>**PDBTitle:** structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana |
| 71 | d16pka_ | Alignment | not modelled | 24.4 | 33 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 72 | c3lfjB_ | Alignment | not modelled | 24.1 | 7 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n-<br>**PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis |
| 73 | c2xivA_ | Alignment | not modelled | 23.8 | 31 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**hypothetical invasion protein;<br>**PDBTitle:** structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis |
| 74 | c3gt2A_ | Alignment | not modelled | 22.9 | 25 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c |
| 75 | c4i66A_ | Alignment | not modelled | 22.3 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein hoch_4089;<br>**PDBTitle:** crystal structure of hoch_4089 protein from haliangium ochraceum |
| 76 | c2fg0B_ | Alignment | not modelled | 21.0 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion-<br>**PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution |
| 77 | c2dbiA_ | Alignment | not modelled | 20.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ybiu;<br>**PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli |
| 78 | d1bvp12 | Alignment | not modelled | 20.2 | 21 | **Fold:**Viral protein domain<br>**Superfamily:**Viral protein domain<br>**Family:**Top domain of virus capsid protein |

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| 79 | c5gj9A_ | Alignment | not modelled | 20.1 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**1-aminocyclopropane-1-carboxylate oxidase 2;<br>**PDBTitle:** crystal structure of arabidopsis thaliana aco2 in complex with poa |
| 80 | c1zmrA_ | Alignment | not modelled | 19.8 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoglycerate kinase;<br>**PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase |
| 81 | c2nnzA_ | Alignment | not modelled | 19.6 | 28 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus |
| 82 | d1phpa_ | Alignment | not modelled | 18.6 | 27 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 83 | c4rgkA_ | Alignment | not modelled | 18.3 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of putative phytanoyl-coa dioxygenase family protein2 ybiu from yersinia pestis |
| 84 | d1hdia_ | Alignment | not modelled | 18.1 | 27 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 85 | d2if6a1 | Alignment | not modelled | 18.0 | 29 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**YiiX-like |
| 86 | d1e5ra_ | Alignment | not modelled | 17.3 | 25 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**Clavaminate synthase-like<br>**Family:**Type II Proline 3-hydroxylase (proline oxidase) |
| 87 | c3pbiA_ | Alignment | not modelled | 17.3 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**invasion protein;<br>**PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution |
| 88 | d1ltka_ | Alignment | not modelled | 16.9 | 13 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 89 | c3rcqA_ | Alignment | not modelled | 16.8 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase;<br>**PDBTitle:** crystal structure of human aspartate beta-hydroxylase isoform a |
| 90 | d1un7a2 | Alignment | not modelled | 16.8 | 8 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 91 | d1dt9a3 | Alignment | not modelled | 16.5 | 12 | **Fold:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br>**Superfamily:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br>**Family:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 |
| 92 | c3zlbA_ | Alignment | not modelled | 16.4 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoglycerate kinase;<br>**PDBTitle:** crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae |
| 93 | d1vpea_ | Alignment | not modelled | 15.7 | 20 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 94 | d1fw8a_ | Alignment | not modelled | 15.2 | 38 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 95 | c2cunA_ | Alignment | not modelled | 15.2 | 38 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoglycerate kinase;<br>**PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3 |
| 96 | d1v6sa_ | Alignment | not modelled | 15.2 | 31 | **Fold:**Phosphoglycerate kinase<br>**Superfamily:**Phosphoglycerate kinase<br>**Family:**Phosphoglycerate kinase |
| 97 | c4lvnP_ | Alignment | not modelled | 15.0 | 12 | **PDB header:**hydrolase/inhibitor/immune system<br>**Chain:** P: **PDB Molecule:**subtilisin-like serine protease;<br>**PDBTitle:** crystal structure of pfsub1-prodomain-nimp.m7 fab complex |
| 98 | c6ax6B_ | Alignment | not modelled | 14.8 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**procollagen lysyl hydroxylase and glycosyltransferase;<br>**PDBTitle:** the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus |
| 99 | c5buvC_ | Alignment | not modelled | 14.8 | 33 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**putative epimerase;<br>**PDBTitle:** x-ray structure of wbca from yersinia enterocolitica |