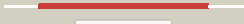



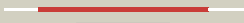







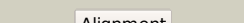











Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0097 (-) _106731_107600 |
| Date | Tue Jul 23 14:50:13 BST 2019 |
| Unique Job ID | f2fcba00809b7601 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6dchA_ |  Alignment |  | 100.0 | 45 | PDB header: oxidoreductase Chain: A: PDB Molecule: scoe protein; PDBTitle: structure of isonitrile biosynthesis enzyme scoe |
| 2 | c3pvjB_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440 |
| 3 | d1otja_ |  Alignment |  | 100.0 | 22 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like |
| 4 | c5hsxB_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of a putative alpha-ketoglutarate-dependent taurine2 dioxygenase from burkholderia xenovorans |
| 5 | c6d1oD_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: D: PDB Molecule: (r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; PDBTitle: ft_5 dioxygenase apoenzyme |
| 6 | c5vn6B_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: taurine dioxygenase; PDBTitle: crystal structure of taurine dioxygenase from burkholderia ambifaria |
| 7 | c4y0eB_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: x-ray crystal structure of a putative dioxygenase from mycobacterium2 abscessus |
| 8 | c5bkeF_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: F: PDB Molecule: alpha-ketoglutarate-dependent 2,4-dichlorophenoxyacetate PDBTitle: crystal structure of aad-2 in complex with mn(ii) and n-oxalyglycine |
| 9 | c3r1jB_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form |
| 10 | c5j92B_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative alpha kg dependent 2,4-d dioxygenase; PDBTitle: crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans |
| 11 | d1oiha_ |  Alignment |  | 100.0 | 20 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c4j5iH_ | Alignment | | 100.0 | 20 | PDB header: oxidoreductase Chain: H: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis |
| 13 | c3eatX_ | Alignment | | 100.0 | 18 | PDB header: oxidoreductase Chain: X: PDB Molecule: pyoverdine biosynthesis protein pvcb; PDBTitle: crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa |
| 14 | d1nx4a_ | Alignment | | 100.0 | 17 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: gamma-Butyrobetaine hydroxylase |
| 15 | d1y0za_ | Alignment | | 100.0 | 13 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: gamma-Butyrobetaine hydroxylase |
| 16 | c3ms5A_ | Alignment | | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-butyrobetaine dioxygenase; PDBTitle: crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1) |
| 17 | c6npcB_ | Alignment | | 100.0 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: tmpa, 2-trimethylaminoethylphosphonate hydroxylase; PDBTitle: x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate |
| 18 | c6f6jC_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: l-lysine 3-hydroxylase; 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 | 15 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Clavaminatase synthase |
| 20 | c2og5A_ | Alignment | | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno) |
| 21 | d1jr7a_ | Alignment | not modelled | 100.0 | 13 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Gab protein (hypothetical protein YgaT) |
| 22 | c4ne0A_ | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; 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 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine |
| 24 | c6dawA_ | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: non-heme iron hydroxylase; PDBTitle: x-ray crystal structure of napi l-arginine desaturase bound to fe(ii),2 l-arginine, and acetate |
| 25 | c4ne0B_ | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of non-heme iron oxygenase orfp d157a mutant in2 complex with (3s)-hydroxy-l-arg |
| 26 | c5eqnA_ | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: frbj; PDBTitle: structure of phosphonate hydroxylase |
| 27 | c6exhA_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-lysine 4-hydroxylase; 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 | 98.1 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo) PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c4xaaA | Alignment | not modelled | 97.8 | 23 | Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of avio1 from streptomyces viridochromogenes tue57 |
| 30 | c5erID | Alignment | not modelled | 97.7 | 23 | PDB header: isomerase Chain: D: PDB Molecule: snon,snon; PDBTitle: crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro |
| 31 | c4xabA | Alignment | not modelled | 97.7 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: evdo2; PDBTitle: crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca |
| 32 | c4naoA | Alignment | not modelled | 97.6 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of eash |
| 33 | c5m0tA | Alignment | not modelled | 97.5 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-ketoglutarate-dependent non-heme iron oxygenase eash; PDBTitle: alpha-ketoglutarate-dependent non-heme iron oxygenase eash |
| 34 | c5zm4B | Alignment | not modelled | 97.3 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: dioxygenase anda; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c |
| 35 | c5yboA | Alignment | not modelled | 97.2 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: prha; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase prha in complex with2 preaustinoid a1 |
| 36 | c2rdsA | Alignment | not modelled | 97.2 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)alpha- PDBTitle: crystal structure of pthl with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound |
| 37 | c4zonB | Alignment | not modelled | 97.2 | 22 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: verruculogen synthase; PDBTitle: structure of ftmox1 with fumitremorgen b complex |
| 38 | c5daqA | Alignment | not modelled | 97.2 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: phytanoyl-coa dioxygenase family protein (afu_orthologue PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycyclopeptin |
| 39 | c5epaE | Alignment | not modelled | 96.8 | 11 | PDB header: lyase Chain: E: PDB Molecule: snok; PDBTitle: crystal structure of non-heme alpha ketoglutarate dependent2 carbocyclase snok from nogalamycin biosynthesis |
| 40 | d2a1xa1 | Alignment | not modelled | 96.5 | 11 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like |
| 41 | c4xbzB | Alignment | not modelled | 95.7 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: evdo1; PDBTitle: crystal structure of evdo1 from micromonospora carbonacea var.2 aurantiaca |
| 42 | c3emrA | Alignment | not modelled | 94.9 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens |
| 43 | c4xc9B | Alignment | not modelled | 94.3 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidase/hydroxylase; PDBTitle: crystal structure of apo hygx from streptomyces hygrosopicus |
| 44 | c3gjbA | Alignment | not modelled | 93.3 | 14 | PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate |
| 45 | c5ncjB | Alignment | not modelled | 91.3 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: leucine hydroxylase; PDBTitle: grie in complex with manganese, succinate and (2s,4r)-5-hydroxyleucine |
| 46 | c3nnlB | Alignment | not modelled | 90.6 | 12 | PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii) |
| 47 | d2fcta1 | Alignment | not modelled | 88.3 | 18 | Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like |
| 48 | c4mhuB | Alignment | not modelled | 86.6 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: ectoine hydroxylase; PDBTitle: crystal structure of ectd from s. alaskensis with bound fe |
| 49 | c1yy3A | Alignment | not modelled | 80.1 | 16 | PDB header: isomerase Chain: A: PDB Molecule: s-adenosylmethionine:trna ribosyltransferase- PDBTitle: structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea) |
| 50 | c4iw3J | Alignment | not modelled | 78.2 | 14 | PDB header: metal binding protein(translation Chain: J: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a pseudomonas putida prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu) |
| 51 | d1wdia | Alignment | not modelled | 75.6 | 11 | Fold: QueA-like Superfamily: QueA-like Family: QueA-like |
| 52 | d1vkya | Alignment | not modelled | 72.7 | 11 | Fold: QueA-like Superfamily: QueA-like Family: QueA-like |
| 53 | c6ec3C | Alignment | not modelled | 68.1 | 23 | PDB header: transferase, oxidoreductase Chain: C: PDB Molecule: methyltransferase domain-containing protein; PDBTitle: crystal structure of evdm01 |
| 54 | c6ax6B | Alignment | not modelled | 58.1 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: procollagen lysyl hydroxylase and glycosyltransferase; |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | PDBTitle: the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus |
| 55 | c3rcqA_ | Alignment | not modelled | 56.8 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: crystal structure of human aspartate beta-hydroxylase isoform a |
| 56 | c2g19A_ | Alignment | not modelled | 51.4 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2) |
| 57 | c3pl0B_ | Alignment | not modelled | 44.7 | 22 | PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a bsma homolog (mpe_a2762) from methylobium2 petroleophilum pm1 at 1.91 a resolution |
| 58 | c3ouiA_ | Alignment | not modelled | 44.4 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422 |
| 59 | d1e5ra_ | Alignment | not modelled | 43.2 | 20 | Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase) |
| 60 | c3dkqB_ | Alignment | not modelled | 41.8 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sba1_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution |
| 61 | c5jqvA_ | Alignment | not modelled | 37.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph) oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser) |
| 62 | c3itqB_ | Alignment | not modelled | 35.5 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase, alpha subunit domain protein; PDBTitle: crystal structure of a prolyl 4-hydroxylase from bacillus anthracis |
| 63 | d2evra2 | Alignment | not modelled | 35.3 | 18 | Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60 |
| 64 | c4p7xA_ | Alignment | not modelled | 32.3 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase |
| 65 | c6f0wA_ | Alignment | not modelled | 32.0 | 9 | PDB header: oxidoreductase Chain: A: PDB Molecule: shif prolyl hydroxylase; PDBTitle: prolyl hydroxylase in complex with hypoxia inducible factor oxygen2 degradation domain peptide fragment from trichoplax adhaerens |
| 66 | d1w9ya1 | Alignment | not modelled | 28.8 | 10 | Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like |
| 67 | c4xaeB_ | Alignment | not modelled | 27.1 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: feruloyl coa ortho-hydroxylase 1; PDBTitle: structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana |
| 68 | c2xivA_ | Alignment | not modelled | 26.3 | 25 | PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis |
| 69 | d16pka_ | Alignment | not modelled | 25.6 | 27 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 70 | c3gt2A_ | Alignment | not modelled | 25.1 | 19 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c |
| 71 | c3on7C_ | Alignment | not modelled | 24.3 | 13 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, iron/ascorbate family; PDBTitle: crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution |
| 72 | c3nplB_ | Alignment | not modelled | 22.8 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution |
| 73 | c3pbiA_ | Alignment | not modelled | 21.2 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution |
| 74 | c1zmrA_ | Alignment | not modelled | 20.6 | 14 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase |
| 75 | c5c5tB_ | Alignment | not modelled | 20.3 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: the crystal structure of viral collagen prolyl hydroxylase vcph from2 paramecium bursaria chlorella virus-1 - 2og complex |
| 76 | c2c5sA_ | Alignment | not modelled | 20.1 | 23 | PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain |
| 77 | d1hdia_ | Alignment | not modelled | 20.1 | 27 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 78 | d1phpa_ | Alignment | not modelled | 19.9 | 27 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 79 | c6b8cA_ | Alignment | not modelled | 19.1 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlp/p60 domain of peptidoglycan |

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|----|--------------------------|-----------|--------------|------|----|---|
| | | | | | | hydrolase saga |
| 80 | d1ftra2 | Alignment | not modelled | 19.0 | 10 | Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase |
| 81 | d1gp6a_ | Alignment | not modelled | 18.7 | 6 | Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like |
| 82 | d1ltka_ | Alignment | not modelled | 18.5 | 20 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 83 | c6biqA_ | Alignment | not modelled | 18.2 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: clan ca, family c40, nlpc/p60 superfamily cysteine PDBTitle: structure of nlpc2 from trichomonas vaginalis |
| 84 | d1vpea_ | Alignment | not modelled | 18.2 | 20 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 85 | d1lodma_ | Alignment | not modelled | 18.1 | 3 | Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like |
| 86 | c3ghfA_ | Alignment | not modelled | 17.9 | 14 | PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium |
| 87 | c3zlbA_ | Alignment | not modelled | 17.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae |
| 88 | c1vbka_ | Alignment | not modelled | 17.4 | 12 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3 |
| 89 | d1fw8a_ | Alignment | not modelled | 16.7 | 29 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 90 | d1f1ja_ | Alignment | not modelled | 16.3 | 11 | Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain |
| 91 | c2cunA_ | Alignment | not modelled | 15.8 | 15 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3 |
| 92 | d1v6sa_ | Alignment | not modelled | 15.8 | 21 | Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase |
| 93 | d1m5sa2 | Alignment | not modelled | 15.4 | 13 | Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase |
| 94 | c2fg0B_ | Alignment | not modelled | 15.0 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- 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 |
| 95 | c4dg5A_ | Alignment | not modelled | 14.7 | 29 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of staphylococcal phosphoglycerate kinase |
| 96 | c3q3vA_ | Alignment | not modelled | 14.6 | 27 | PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni. |
| 97 | d1un7a2 | Alignment | not modelled | 14.0 | 15 | Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 98 | c4hpeA_ | Alignment | not modelled | 13.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: putative cell wall hydrolase tn916-like,ctn1-orf17; PDBTitle: crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution |
| 99 | c3bu7A_ | Alignment | not modelled | 13.8 | 9 | PDB header: oxidoreductase Chain: A: PDB Molecule: gentisate 1,2-dioxygenase; PDBTitle: crystal structure and biochemical characterization of gdisp, a2 gentisate 1,2-dioxygenase from silicibacter pomeroyi |