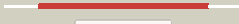

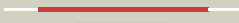



















Phyre2

| | |
|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3842c_glpQ1_4314916_4315740 |
| Date | Sat Aug 10 22:05:02 BST 2019 |
| Unique Job ID | 0909193cf873be25 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|----------|------------|--------|---|
| 1 | c2p76H_ |  Alignment | | 100.0 | 27 | PDB header: hydrolase Chain: H: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus |
| 2 | c2pz0B_ |  Alignment | | 100.0 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis |
| 3 | c3qvqB_ |  Alignment | | 100.0 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase olei02445; PDBTitle: the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate |
| 4 | c5t91A_ |  Alignment | | 100.0 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of b. subtilis 168 glpQ in complex with bicine |
| 5 | c4r7oE_ |  Alignment | | 100.0 | 31 | PDB header: hydrolase Chain: E: PDB Molecule: glycerophosphoryl diester phosphodiesterase, putative; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterasefrom bacillus anthraci |
| 6 | c3i12A_ |  Alignment | | 100.0 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: putative glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution |
| 7 | c2otdC_ |  Alignment | | 100.0 | 24 | PDB header: hydrolase Chain: C: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a |
| 8 | d1ydyal |  Alignment | | 100.0 | 26 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase |
| 9 | c1ydyA_ |  Alignment | | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli |
| 10 | d1zcca1 |  Alignment | | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase |
| 11 | c3ks6A_ |  Alignment | | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens str. c583 (dupont) at 1.80 a resolution |

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|----|-------------------------|-----------|---|-------|----|---|
| 12 | c40ecD | Alignment |  | 100.0 | 27 | PDB header: hydrolase Chain: D: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase from2 thermococcus kodakarensis kod1 |
| 13 | c3no3A | Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution |
| 14 | c2o55A | Alignment |  | 100.0 | 22 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria |
| 15 | c3mz2A | Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis atcc 8503 at 1.55 a3 resolution |
| 16 | c3ch0A | Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution |
| 17 | d1vd6a1 | Alignment |  | 100.0 | 30 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase |
| 18 | d1o1za | Alignment |  | 100.0 | 24 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase |
| 19 | c5vugA | Alignment |  | 100.0 | 22 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rv2277c; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 domain of uncharacterized protein rv2277c from mycobacterium3 tuberculosis |
| 20 | c3i10A | Alignment |  | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: putative glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution |
| 21 | c3rlhA | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alphaia1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom |
| 22 | c2f9rC | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: sphingomyelinase d 1; PDBTitle: crystal structure of the inactive state of the smase i, a2 sphingomyelinase d from loxosceles laeta venom |
| 23 | c3rlgA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alphaia1a; PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant |
| 24 | c4q6xA | Alignment | not modelled | 100.0 | 15 | PDB header: lyase Chain: A: PDB Molecule: phospholipase d stsictox-betaic1; PDBTitle: structure of phospholipase d beta1b1i from sicarius terrosus venom at2 2.14 a resolution |
| 25 | c1djyB | Alignment | not modelled | 98.0 | 24 | PDB header: lipid degradation Chain: B: PDB Molecule: phosphoinositide-specific phospholipase c, PDBTitle: phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate |
| 26 | c3qr0A | Alignment | not modelled | 97.8 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase c-beta (plc-beta); PDBTitle: crystal structure of s. officinalis plc21 |
| 27 | d2zkmx4 | Alignment | not modelled | 97.7 | 20 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC |
| 28 | d1qasa3 | Alignment | not modelled | 97.7 | 18 | Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC |
| | | | | | | PDB header: signaling protein,apoptosis/hydrolase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c2fjuB_ | Alignment | not modelled | 97.5 | 20 | Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate PDBTitle: activated rac1 bound to its effector phospholipase c beta 2 |
| 30 | c3ohmB_ | Alignment | not modelled | 97.4 | 23 | PDB header: signaling protein / hydrolase Chain: B: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase PDBTitle: crystal structure of activated g alpha q bound to its effector2 phospholipase c beta 3 |
| 31 | c3vndD_ | Alignment | not modelled | 97.3 | 16 | PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2 |
| 32 | c5kzmA_ | Alignment | not modelled | 97.1 | 12 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis |
| 33 | c3thaB_ | Alignment | not modelled | 97.0 | 9 | PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni. |
| 34 | c2ekcA_ | Alignment | not modelled | 96.8 | 11 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5 |
| 35 | c5k9xA_ | Alignment | not modelled | 96.5 | 15 | PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila |
| 36 | c3navB_ | Alignment | not modelled | 96.3 | 15 | PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961 |
| 37 | d1qopa_ | Alignment | not modelled | 96.2 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 38 | c5kinC_ | Alignment | not modelled | 95.2 | 15 | PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae |
| 39 | d1vkfa_ | Alignment | not modelled | 95.1 | 18 | Fold: TIM beta/alpha-barrel Superfamily: GlpP-like Family: GlpP-like |
| 40 | c3ktsA_ | Alignment | not modelled | 94.9 | 15 | PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365 |
| 41 | c5ey5A_ | Alignment | not modelled | 94.8 | 15 | PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats |
| 42 | d1ujpa_ | Alignment | not modelled | 94.8 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 43 | d1geqa_ | Alignment | not modelled | 93.8 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes |
| 44 | c2r6oB_ | Alignment | not modelled | 93.0 | 10 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal) PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans |
| 45 | c4rnhA_ | Alignment | not modelled | 92.0 | 11 | PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex |
| 46 | c5tchG_ | Alignment | not modelled | 91.3 | 16 | PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant |
| 47 | c3hvbB_ | Alignment | not modelled | 91.1 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa |
| 48 | c4hjfA_ | Alignment | not modelled | 90.6 | 14 | PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++ |
| 49 | d7reqa2 | Alignment | not modelled | 90.2 | 25 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 50 | c5xgdA_ | Alignment | not modelled | 90.2 | 11 | PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp |
| 51 | c3a24A_ | Alignment | not modelled | 89.7 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase |
| 52 | c4f48A_ | Alignment | not modelled | 89.1 | 8 | PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimxeal-c-di-gmp-pilz complexes from2 xanthomonas campestris |
| 53 | c3pjwA_ | Alignment | not modelled | 88.4 | 13 | PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23 |
| 54 | c5m3cB_ | Alignment | not modelled | 87.5 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 |

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| | | | | | | from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain |
| 55 | c4rnjA_ | Alignment | not modelled | 86.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora phosphodiesterase domain, apo form |
| 56 | c5m1tB_ | Alignment | not modelled | 86.0 | 13 | PDB header: signaling protein Chain: B: PDB Molecule: muclr phosphodiesterase; PDBTitle: pamuclr phosphodiesterase, c-di-gmp complex |
| 57 | c3gfbB_ | Alignment | not modelled | 85.9 | 17 | PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex |
| 58 | c5zjnB_ | Alignment | not modelled | 84.9 | 16 | PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate |
| 59 | c2zq0B_ | Alignment | not modelled | 84.7 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase subb); PDBTitle: crystal structure of subb complexed with acarbose |
| 60 | c4fokA_ | Alignment | not modelled | 83.9 | 8 | PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp |
| 61 | d1vhca_ | Alignment | not modelled | 83.7 | 19 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 62 | c4q6jB_ | Alignment | not modelled | 83.4 | 11 | PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e |
| 63 | c4lykB_ | Alignment | not modelled | 82.8 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++ |
| 64 | c2zbtB_ | Alignment | not modelled | 82.7 | 14 | PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 |
| 65 | c3h4wA_ | Alignment | not modelled | 82.4 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylinositol-specific phospholipase c1; PDBTitle: structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus |
| 66 | c2c3zA_ | Alignment | not modelled | 82.1 | 13 | PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus |
| 67 | c6oviA_ | Alignment | not modelled | 81.5 | 11 | PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate |
| 68 | c5xfmD_ | Alignment | not modelled | 80.9 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase |
| 69 | d1wbha1 | Alignment | not modelled | 80.8 | 13 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 70 | c3femB_ | Alignment | not modelled | 80.5 | 14 | PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae |
| 71 | d1mxsa_ | Alignment | not modelled | 80.4 | 17 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 72 | c2nv2U_ | Alignment | not modelled | 79.7 | 16 | PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis |
| 73 | c5d88A_ | Alignment | not modelled | 79.4 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906 |
| 74 | c6hq7B_ | Alignment | not modelled | 79.3 | 9 | PDB header: signaling protein Chain: B: PDB Molecule: eal enzyme bd1971; PDBTitle: structure of eal enzyme bd1971 - cgmp bound form |
| 75 | c4s1aB_ | Alignment | not modelled | 79.0 | 18 | PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405 |
| 76 | c3qjaA_ | Alignment | not modelled | 79.0 | 12 | PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form |
| 77 | c5yrpB_ | Alignment | not modelled | 78.9 | 8 | PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa |
| 78 | c6hyeF_ | Alignment | not modelled | 77.6 | 18 | PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a) |
| 79 | c2v82A_ | Alignment | not modelled | 77.0 | 14 | PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 79 | c2v62A | Alignment | not modelled | 77.0 | 14 | aldolase; PDBTitle: kdpgal complexed to kdpgal |
| 80 | c2gjlA | Alignment | not modelled | 76.6 | 14 | PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase |
| 81 | d1qapa1 | Alignment | not modelled | 76.5 | 22 | Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like |
| 82 | c4adsF | Alignment | not modelled | 76.1 | 14 | PDB header: transferase/transferase Chain: F; PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex |
| 83 | d2basa1 | Alignment | not modelled | 75.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain |
| 84 | d1vc4a | Alignment | not modelled | 75.9 | 21 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 85 | c2htmB | Alignment | not modelled | 75.9 | 11 | PDB header: biosynthetic protein Chain: B; PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8 |
| 86 | c3pfmA | Alignment | not modelled | 75.7 | 11 | PDB header: signaling protein Chain: A; PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from <i>2 pseudomonas fluorescens pf</i> |
| 87 | c6hxgE | Alignment | not modelled | 74.1 | 14 | PDB header: plant protein Chain: E; PDB Molecule: pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate) |
| 88 | d1a53a | Alignment | not modelled | 73.5 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 89 | c3sy8C | Alignment | not modelled | 73.4 | 12 | PDB header: transcription regulator Chain: C; PDB Molecule: rocr; PDBTitle: crystal structure of the response regulator rocr |
| 90 | c3gndC | Alignment | not modelled | 73.0 | 19 | PDB header: lyase Chain: C; PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 91 | d2gja2 | Alignment | not modelled | 72.2 | 10 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain |
| 92 | d2flia1 | Alignment | not modelled | 71.1 | 16 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase |
| 93 | c2p10D | Alignment | not modelled | 71.0 | 9 | PDB header: hydrolase Chain: D; PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution |
| 94 | d1pia2 | Alignment | not modelled | 70.4 | 18 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 95 | c3bo9B | Alignment | not modelled | 70.4 | 8 | PDB header: oxidoreductase Chain: B; PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from <i>2 thermotoga maritima</i> at 2.71 a resolution |
| 96 | d1xm3a | Alignment | not modelled | 69.5 | 19 | Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like |
| 97 | c4e38A | Alignment | not modelled | 69.3 | 21 | PDB header: lyase Chain: A; PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from <i>2 vibrionales bacterium swat-3 (target efi-502156)</i> |
| 98 | c5hxgA | Alignment | not modelled | 68.9 | 10 | PDB header: transcription Chain: A; PDB Molecule: uncharacterized protein stm1697; PDBTitle: stm1697-flhd complex |
| 99 | d2p10a1 | Alignment | not modelled | 67.4 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MII9387-like |
| 100 | d1avaa2 | Alignment | not modelled | 67.3 | 14 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain |
| 101 | c4fxsA | Alignment | not modelled | 67.2 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid |
| 102 | c3q58A | Alignment | not modelled | 66.7 | 10 | PDB header: isomerase Chain: A; PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 103 | c4hu4B | Alignment | not modelled | 66.5 | 14 | PDB header: signaling protein, hydrolase Chain: B; PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form |
| 104 | c3kzpA | Alignment | not modelled | 65.8 | 5 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative diguanylate cyclase/phosphodiesterase; PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes |

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| 105 | c5hqcA | Alignment | not modelled | 65.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 97 enzyme; PDBTitle: a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8 |
| 106 | c3inpA | Alignment | not modelled | 64.6 | 16 | PDB header: isomerase Chain: A: PDB Molecule: d-ribose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribose-phosphate 3-2 epimerase from francisella tularensis. |
| 107 | d1wa3a1 | Alignment | not modelled | 61.9 | 10 | Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase |
| 108 | c4utwB | Alignment | not modelled | 61.8 | 13 | PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens |
| 109 | c3tlqB | Alignment | not modelled | 61.7 | 11 | PDB header: transcription Chain: B: PDB Molecule: regulatory protein ydiv; PDBTitle: crystal structure of eal-like domain protein ydiv |
| 110 | c4qccA | Alignment | not modelled | 61.6 | 14 | PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains |
| 111 | c2w27A | Alignment | not modelled | 61.2 | 10 | PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium |
| 112 | c1e1cA | Alignment | not modelled | 60.1 | 26 | PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant |
| 113 | d1xcfa | Alignment | not modelled | 60.0 | 14 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 114 | c4firB | Alignment | not modelled | 59.7 | 14 | PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus |
| 115 | d1rd5a | Alignment | not modelled | 59.4 | 30 | Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes |
| 116 | c3hv9A | Alignment | not modelled | 58.7 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa |
| 117 | c2qpuB | Alignment | not modelled | 58.7 | 8 | PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose |
| 118 | c3ct7E | Alignment | not modelled | 58.5 | 15 | PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12 |
| 119 | c4j29A | Alignment | not modelled | 58.4 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: engineered protein or258; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or258. |
| 120 | c5zxbB | Alignment | not modelled | 58.2 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form |