Phyre2

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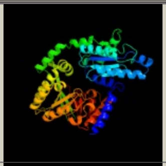
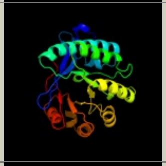
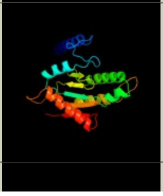
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77172 |
| Date | Thu Jan 5 12:25:57 GMT 2012 |
| Unique Job ID | 69cb39503e698f80 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3pjwA_ | Alignment |  | 100.0 | 22 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein;<br>**PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23 |
| 2 | c3gfzB_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase, signaling protein<br>**Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1;<br>**PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex |
| 3 | c3hvbB_ | Alignment |  | 100.0 | 30 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa |
| 4 | c3hv9A_ | Alignment |  | 100.0 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa |
| 5 | c3s83A_ | Alignment |  | 100.0 | 28 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef family protein;<br>**PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15 |
| 6 | c3pfmA_ | Alignment |  | 100.0 | 27 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef domain protein;<br>**PDBTitle:** crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf |
| 7 | c2w27A_ | Alignment |  | 100.0 | 22 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ykui protein;<br>**PDBTitle:** crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium |
| 8 | c2r6oB_ | Alignment |  | 100.0 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase (ggdef & eal<br>**PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans |
| 9 | d2basa1 | Alignment |  | 100.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**EAL domain-like<br>**Family:**EAL domain |
| 10 | c3kzpA_ | Alignment |  | 100.0 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase;<br>**PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes |
| 11 | c1w25B_ | Alignment |  | 100.0 | 10 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein;<br>**PDBTitle:** response regulator pled in complex with c-digmp |

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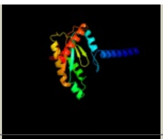
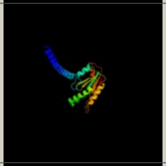
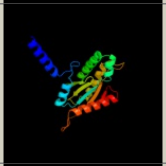
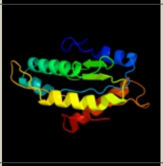
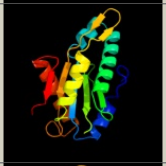
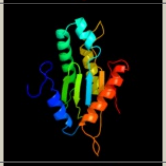
|---|---|---|---|---|---|---|
| 12 | c3ezuA_ | Alignment |  | 100.0 | 7 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef domain protein;<br>**PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution |
| 13 | c3mtkA_ | Alignment |  | 99.9 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase;<br>**PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c |
| 14 | c3breA_ | Alignment |  | 99.9 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**probable two-component response regulator;<br>**PDBTitle:** crystal structure of p.aeruginosa pa3702 |
| 15 | c3i5cA_ | Alignment |  | 99.9 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response<br>**PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa |
| 16 | c3ignA_ | Alignment |  | 99.9 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diguanylate cyclase;<br>**PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a |
| 17 | c3iclA_ | Alignment |  | 99.9 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**eal/ggdef domain protein;<br>**PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c |
| 18 | c3hvaA_ | Alignment |  | 99.9 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa |
| 19 | c3i5bA_ | Alignment |  | 99.9 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**wspr response regulator;<br>**PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa |
| 20 | c3qyyB_ | Alignment |  | 99.9 | 13 | **PDB header:**signaling protein/inhibitor<br>**Chain:** B: **PDB Molecule:**response regulator;<br>**PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5 )-cyclic di-gmp |
| 21 | c3i5aA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein;<br>**PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae |
| 22 | d1w25a3 | Alignment | not modelled | 99.9 | 9 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**GGDEF domain |
| 23 | c3hvwA_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc);<br>**PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c |
| 24 | c3p7nB_ | Alignment | not modelled | 97.7 | 15 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**sensor histidine kinase;<br>**PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis |
| 25 | c3khtA_ | Alignment | not modelled | 96.2 | 11 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator;<br>**PDBTitle:** crystal structure of response regulator from hahella chejuensis |
| 26 | d1mvoa_ | Alignment | not modelled | 95.5 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 27 | c2zayA_ | Alignment | not modelled | 95.2 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator receiver protein;<br>**PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans |
| 28 | d1p6qa_ | Alignment | not modelled | 94.6 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| | | | | | | **PDB header:**transcription regulator |

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|---|---|---|---|---|---|---|
| 29 | c3hebB_ | Alignment | not modelled | 94.6 | 18 | **Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey);<br>**PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum |
| 30 | c2qv6D_ | Alignment | not modelled | 94.5 | 9 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii;<br>**PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions |
| 31 | d1krwa_ | Alignment | not modelled | 94.4 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 32 | c2jk1A_ | Alignment | not modelled | 94.3 | 11 | **PDB header:**dna-binding<br>**Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1;<br>**PDBTitle:** crystal structure of the wild-type hupr receiver domain |
| 33 | d1w25a1 | Alignment | not modelled | 94.2 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 34 | d1jbea_ | Alignment | not modelled | 93.9 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 35 | c2pz0B_ | Alignment | not modelled | 93.7 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis |
| 36 | d1a53a_ | Alignment | not modelled | 93.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 37 | c3nhzA_ | Alignment | not modelled | 93.3 | 16 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra;<br>**PDBTitle:** structure of n-terminal domain of mtra |
| 38 | c3eulB_ | Alignment | not modelled | 93.2 | 12 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional<br>**PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis |
| 39 | c3q58A_ | Alignment | not modelled | 93.2 | 10 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase;<br>**PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica |
| 40 | c2c3zA_ | Alignment | not modelled | 93.2 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus |
| 41 | d1ua7a2 | Alignment | not modelled | 93.1 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 42 | d1dz3a_ | Alignment | not modelled | 93.1 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 43 | c3gt7A_ | Alignment | not modelled | 92.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus |
| 44 | c2rjnA_ | Alignment | not modelled | 92.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent<br>**PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis |
| 45 | d1u0sy_ | Alignment | not modelled | 92.9 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 46 | c2qr3A_ | Alignment | not modelled | 92.9 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**two-component system response regulator;<br>**PDBTitle:** crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis |
| 47 | c3b2nA_ | Alignment | not modelled | 92.6 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4;<br>**PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus |
| 48 | d1yioa2 | Alignment | not modelled | 92.5 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 49 | d1gjwa2 | Alignment | not modelled | 92.5 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 50 | d1dbwa_ | Alignment | not modelled | 92.4 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 51 | c3c97A_ | Alignment | not modelled | 92.2 | 11 | **PDB header:**signaling protein, transferase<br>**Chain:** A: **PDB Molecule:**signal transduction histidine kinase;<br>**PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae |
| 52 | c3i42A_ | Alignment | not modelled | 92.1 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-<br>**PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus |
| 53 | d1ys7a2 | Alignment | not modelled | 92.1 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like |

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| | | | | | | **Family:**CheY-related |
| 54 | d1qkka_ | Alignment | not modelled | 91.9 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 55 | c3crnA_ | Alignment | not modelled | 91.8 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like;<br>**PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1 |
| 56 | d1ny5a1 | Alignment | not modelled | 91.7 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 57 | d1xm3a_ | Alignment | not modelled | 91.5 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**ThiG-like<br>**Family:**ThiG-like |
| 58 | d1k68a_ | Alignment | not modelled | 91.5 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 59 | c2zwmA_ | Alignment | not modelled | 91.4 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf;<br>**PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis |
| 60 | c3gl9B_ | Alignment | not modelled | 91.3 | 18 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**response regulator;<br>**PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism |
| 61 | d1a04a2 | Alignment | not modelled | 91.1 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 62 | c1qhoA_ | Alignment | not modelled | 91.1 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-amylase;<br>**PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex |
| 63 | d1heya_ | Alignment | not modelled | 90.9 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 64 | d1vhna_ | Alignment | not modelled | 90.8 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**FMN-linked oxidoreductases<br>**Family:**FMN-linked oxidoreductases |
| 65 | d1nvma2 | Alignment | not modelled | 90.8 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**HMGL-like |
| 66 | c2p0oA_ | Alignment | not modelled | 90.7 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein duf871;<br>**PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function |
| 67 | c1gjuA_ | Alignment | not modelled | 90.6 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase;<br>**PDBTitle:** maltosyltransferase from thermotoga maritima |
| 68 | d1y0ea_ | Alignment | not modelled | 90.5 | 7 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 69 | d1kgsa2 | Alignment | not modelled | 90.4 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 70 | d2r25b1 | Alignment | not modelled | 90.0 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 71 | c3qvqB_ | Alignment | not modelled | 89.9 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**phosphodiesterase olei02445;<br>**PDBTitle:** the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate |
| 72 | c3cg0A_ | Alignment | not modelled | 89.8 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase<br>**PDBTitle:** crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding |
| 73 | c1cygA_ | Alignment | not modelled | 89.8 | 15 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase;<br>**PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase) |
| 74 | c2yxbA_ | Alignment | not modelled | 89.6 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase;<br>**PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix |
| 75 | d2pl1a1 | Alignment | not modelled | 89.6 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 76 | c3ucqA_ | Alignment | not modelled | 89.5 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**amylosucrase;<br>**PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis |
| 77 | d1xhfa1 | Alignment | not modelled | 89.3 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 78 | c3kruC_ | Alignment | not modelled | 89.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh:flavin oxidoreductase/nadh oxidase;<br>**PDBTitle:** crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39 |

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| 79 | d1k66a_ | Alignment | not modelled | 89.2 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 80 | d1zh2a1 | Alignment | not modelled | 89.1 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 81 | c2ayxA_ | Alignment | not modelled | 89.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor kinase protein rcsc;<br>**PDBTitle:** solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain |
| 82 | c3f6cB_ | Alignment | not modelled | 88.8 | 15 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**positive transcription regulator evga;<br>**PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli |
| 83 | c3gr7A_ | Alignment | not modelled | 88.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadph dehydrogenase;<br>**PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form |
| 84 | c3hv2B_ | Alignment | not modelled | 88.7 | 14 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**response regulator/hd domain protein;<br>**PDBTitle:** crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5 |
| 85 | c3cu5B_ | Alignment | not modelled | 88.5 | 11 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family;<br>**PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg |
| 86 | d2ayxa1 | Alignment | not modelled | 88.5 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 87 | c3a47A_ | Alignment | not modelled | 88.4 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase;<br>**PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae |
| 88 | c1m53A_ | Alignment | not modelled | 88.2 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**isomaltulose synthase;<br>**PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3 |
| 89 | c3edeB_ | Alignment | not modelled | 88.2 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cyclomaltodextrinase;<br>**PDBTitle:** structural base for cyclodextrin hydrolysis |
| 90 | c2h6rG_ | Alignment | not modelled | 88.1 | 19 | **PDB header:**isomerase<br>**Chain:** G: **PDB Molecule:**triosephosphate isomerase;<br>**PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii |
| 91 | c3igsB_ | Alignment | not modelled | 87.8 | 9 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2;<br>**PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase |
| 92 | d2guya2 | Alignment | not modelled | 87.5 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 93 | c2j48A_ | Alignment | not modelled | 87.4 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**two-component sensor kinase;<br>**PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein. |
| 94 | d1h3ga3 | Alignment | not modelled | 87.3 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 95 | c1bagA_ | Alignment | not modelled | 87.2 | 12 | **PDB header:**alpha-amylase<br>**Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase;<br>**PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose |
| 96 | c2ze0A_ | Alignment | not modelled | 87.1 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-glucosidase;<br>**PDBTitle:** alpha-glucosidase gsj |
| 97 | d1qhoa4 | Alignment | not modelled | 87.0 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 98 | c3t6kB_ | Alignment | not modelled | 86.9 | 14 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**response regulator receiver;<br>**PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution |
| 99 | c3t8yA_ | Alignment | not modelled | 86.8 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate<br>**PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb |
| 100 | d1mb3a_ | Alignment | not modelled | 86.7 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 101 | d2aaaa2 | Alignment | not modelled | 86.6 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 102 | c3hdgE_ | Alignment | not modelled | 86.6 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** E: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes |
| 103 | c2jrlA_ | Alignment | not modelled | 86.4 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer |
|  |  |  |  |  |  | **PDB header:**structural genomics, unknown function |

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| 104 | c3cfyA_ | Alignment | not modelled | 86.3 | 11 | **Chain:** A: **PDB Molecule:**putative luxo repressor protein;<br>**PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus |
| 105 | c2wcsA_ | Alignment | not modelled | 86.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha amylase, catalytic region;<br>**PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde) |
| 106 | d1i4na_ | Alignment | not modelled | 85.8 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 107 | d1lwha2 | Alignment | not modelled | 85.7 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 108 | d1tz9a_ | Alignment | not modelled | 85.5 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**UxuA-like |
| 109 | c1cjkA_ | Alignment | not modelled | 85.5 | 8 | **PDB header:**lyase/lyase/signaling protein<br>**Chain:** A: **PDB Molecule:**adenylate cyclase, type v;<br>**PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn |
| 110 | c1jibA_ | Alignment | not modelled | 85.2 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**neopullulanase;<br>**PDBTitle:** complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose. |
| 111 | d2a9pa1 | Alignment | not modelled | 85.0 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 112 | d1w0ma_ | Alignment | not modelled | 85.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Triosephosphate isomerase (TIM)<br>**Family:**Triosephosphate isomerase (TIM) |
| 113 | c1tcmB_ | Alignment | not modelled | 84.9 | 12 | **PDB header:**glycosyltransferase<br>**Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase;<br>**PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251 |
| 114 | c3rqiA_ | Alignment | not modelled | 84.8 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**response regulator protein;<br>**PDBTitle:** crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate |
| 115 | d1fmfa_ | Alignment | not modelled | 84.8 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 116 | d1eh9a3 | Alignment | not modelled | 84.8 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 117 | d1m53a2 | Alignment | not modelled | 84.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 118 | d1i3ca_ | Alignment | not modelled | 84.5 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 119 | c3uvjC_ | Alignment | not modelled | 84.4 | 7 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3;<br>**PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1. |
| 120 | c2otdC_ | Alignment | not modelled | 84.4 | 9 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a |