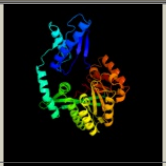
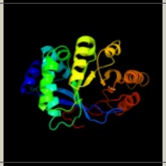
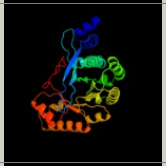
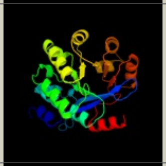
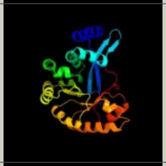
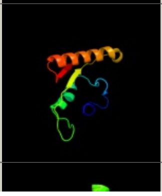
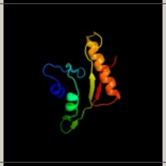
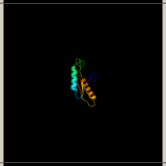
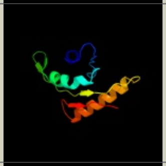
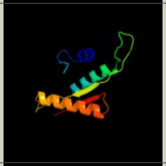
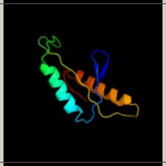
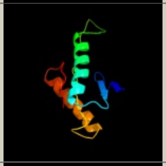
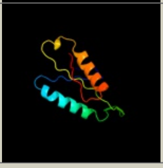
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q9JMT8 |
| Date | Thu Jan 5 12:38:13 GMT 2012 |
| Unique Job ID | 6f93e95dcb3cc3a6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3pjwA_ | Alignment |  | 100.0 | 12 | **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 | 15 | **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 | 11 | **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 | 11 | **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 | 17 | **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 | 16 | **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 | 16 | **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 | 24 | **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 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**EAL domain-like<br>**Family:**EAL domain |
| 10 | c3kzpA_ | Alignment |  | 100.0 | 13 | **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 |  | 99.0 | 13 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein;<br>**PDBTitle:** response regulator pled in complex with c-digmp |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c3ezuA_ | Alignment |  | 98.6 | 19 | **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 | c3iclA_ | Alignment |  | 98.4 | 17 | **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 |
| 14 | c3breA_ | Alignment |  | 98.4 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**probable two-component response regulator;<br>**PDBTitle:** crystal structure of p.aeruginosa pa3702 |
| 15 | c3mtkA_ | Alignment |  | 98.3 | 26 | **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 |
| 16 | d1w25a3 | Alignment |  | 98.2 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**GGDEF domain |
| 17 | c3hvaA_ | Alignment |  | 98.2 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa |
| 18 | c3i5aA_ | Alignment |  | 98.1 | 11 | **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 |
| 19 | c3ignA_ | Alignment |  | 98.1 | 10 | **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 |
| 20 | c3hvwA_ | Alignment |  | 97.9 | 6 | **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 |
| 21 | c3i5bA_ | Alignment | not modelled | 97.6 | 13 | **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 |
| 22 | c3i5cA_ | Alignment | not modelled | 97.5 | 10 | **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 |
| 23 | c3qyyB_ | Alignment | not modelled | 97.2 | 19 | **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 |
| 24 | d1mvoa_ | Alignment | not modelled | 96.2 | 8 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 25 | c3khtA_ | Alignment | not modelled | 96.1 | 11 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator;<br>**PDBTitle:** crystal structure of response regulator from hahella chejuensis |
| 26 | d1p6qa_ | Alignment | not modelled | 95.6 | 9 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 27 | d1zesa1 | Alignment | not modelled | 95.5 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 28 | d1w25a1 | Alignment | not modelled | 95.5 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| | | | | | | **PDB header:**signaling protein |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 29 | c2zayA_ | Alignment | not modelled | 95.3 | 14 | **Chain:** A: **PDB Molecule:**response regulator receiver protein;<br>**PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans |
| 30 | d1krwa_ | Alignment | not modelled | 94.7 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 31 | d1jbea_ | Alignment | not modelled | 94.7 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 32 | c3q58A_ | Alignment | not modelled | 94.7 | 18 | **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 |
| 33 | d1heya_ | Alignment | not modelled | 94.5 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 34 | c3eulB_ | Alignment | not modelled | 94.3 | 10 | **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 |
| 35 | c3gt7A_ | Alignment | not modelled | 94.1 | 10 | **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 |
| 36 | c3gl9B_ | Alignment | not modelled | 94.1 | 11 | **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 |
| 37 | c2jk1A_ | Alignment | not modelled | 93.9 | 7 | **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 |
| 38 | d1dbwa_ | Alignment | not modelled | 93.9 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 39 | c3hebB_ | Alignment | not modelled | 93.9 | 13 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey);<br>**PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum |
| 40 | c2ayxA_ | Alignment | not modelled | 93.6 | 14 | **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 |
| 41 | d1yioa2 | Alignment | not modelled | 93.2 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 42 | d1kgsa2 | Alignment | not modelled | 93.2 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 43 | c3nhzA_ | Alignment | not modelled | 93.1 | 12 | **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 |
| 44 | d1ua7a2 | Alignment | not modelled | 93.1 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 45 | c3crnA_ | Alignment | not modelled | 93.0 | 10 | **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 |
| 46 | d1xhfa1 | Alignment | not modelled | 92.8 | 8 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 47 | c2p0oA_ | Alignment | not modelled | 92.8 | 15 | **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 |
| 48 | d2pl1a1 | Alignment | not modelled | 92.8 | 8 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 49 | c2zwmA_ | Alignment | not modelled | 92.6 | 9 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf;<br>**PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis |
| 50 | c2rjnA_ | Alignment | not modelled | 92.6 | 12 | **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 |
| 51 | d1y0ea_ | Alignment | not modelled | 92.6 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**NanE-like |
| 52 | d1dz3a_ | Alignment | not modelled | 92.6 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 53 | d2a9pa1 | Alignment | not modelled | 92.5 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
|  |  |  |  |  |  | **PDB header:**transcription |

| | | | | | | |
|---|---|---|---|---|---|---|
| 54 | c2qr3A_ | Alignment | not modelled | 92.5 | 14 | **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 |
| 55 | d1zh2a1 | Alignment | not modelled | 92.3 | 9 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 56 | c3cu5B_ | Alignment | not modelled | 92.3 | 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 |
| 57 | d2ayxa1 | Alignment | not modelled | 92.2 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 58 | d1zgza1 | Alignment | not modelled | 92.1 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 59 | d1qkka_ | Alignment | not modelled | 92.1 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 60 | c3cnbC_ | Alignment | not modelled | 92.1 | 16 | **PDB header:**dna binding protein<br>**Chain:** C: **PDB Molecule:**dna-binding response regulator, merr family;<br>**PDBTitle:** crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h |
| 61 | d1ny5a1 | Alignment | not modelled | 91.9 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 62 | d1ys7a2 | Alignment | not modelled | 91.9 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 63 | c3edeB_ | Alignment | not modelled | 91.9 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cyclomaltodextrinase;<br>**PDBTitle:** structural base for cyclodextrin hydrolysis |
| 64 | d1kkoa1 | Alignment | not modelled | 91.5 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**D-glucarate dehydratase-like |
| 65 | d1k66a_ | Alignment | not modelled | 91.1 | 14 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 66 | d2r25b1 | Alignment | not modelled | 91.0 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 67 | c3i42A_ | Alignment | not modelled | 90.9 | 9 | **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 |
| 68 | c2pz0B_ | Alignment | not modelled | 90.9 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase;<br>**PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis |
| 69 | c1qhoA_ | Alignment | not modelled | 90.2 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-amylase;<br>**PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex |
| 70 | d1gjwa2 | Alignment | not modelled | 90.1 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 71 | d1a53a_ | Alignment | not modelled | 90.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 72 | c2c3zA_ | Alignment | not modelled | 89.7 | 15 | **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 |
| 73 | d1k68a_ | Alignment | not modelled | 89.6 | 7 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 74 | c3rqiA_ | Alignment | not modelled | 89.4 | 12 | **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 |
| 75 | c3hv2B_ | Alignment | not modelled | 89.3 | 13 | **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 |
| 76 | d1u0sy_ | Alignment | not modelled | 89.2 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 77 | d1a04a2 | Alignment | not modelled | 89.1 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 78 | c3t6kB_ | Alignment | not modelled | 89.0 | 8 | **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 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 79 | d1mb3a_ | Alignment | not modelled | 89.0 | 13 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 80 | c3nhmA_ | Alignment | not modelled | 89.0 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator;<br>**PDBTitle:** crystal structure of a response regulator from myxococcus xanthus |
| 81 | c3ucqA_ | Alignment | not modelled | 88.9 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**amylosucrase;<br>**PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis |
| 82 | c2yxbA_ | Alignment | not modelled | 88.8 | 8 | **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 |
| 83 | c1jdaA_ | Alignment | not modelled | 88.6 | 8 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase;<br>**PDBTitle:** maltotetraose-forming exo-amylase |
| 84 | c3b2nA_ | Alignment | not modelled | 88.6 | 11 | **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 |
| 85 | c1gcyA_ | Alignment | not modelled | 88.4 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase;<br>**PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase |
| 86 | c1bagA_ | Alignment | not modelled | 88.3 | 15 | **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 |
| 87 | d1gcya2 | Alignment | not modelled | 88.2 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 88 | c3dzdA_ | Alignment | not modelled | 88.2 | 11 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state |
| 89 | c3cfyA_ | Alignment | not modelled | 87.9 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative luxo repressor protein;<br>**PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus |
| 90 | d1h3ga3 | Alignment | not modelled | 87.7 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 91 | d1tz9a_ | Alignment | not modelled | 87.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**UxuA-like |
| 92 | c2jrlA_ | Alignment | not modelled | 87.5 | 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 |
| 93 | c3grcD_ | Alignment | not modelled | 86.9 | 6 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**sensor protein, kinase;<br>**PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666 |
| 94 | d2guya2 | Alignment | not modelled | 86.7 | 7 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 95 | d1g5aa2 | Alignment | not modelled | 86.5 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 96 | d1xrsb1 | Alignment | not modelled | 86.4 | 12 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 97 | d1i3ca_ | Alignment | not modelled | 86.4 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 98 | c3t8yA_ | Alignment | not modelled | 86.3 | 12 | **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 |
| 99 | c3bw2A_ | Alignment | not modelled | 85.8 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase;<br>**PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes |
| 100 | c3gr7A_ | Alignment | not modelled | 85.8 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadph dehydrogenase;<br>**PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form |
| 101 | d1peya_ | Alignment | not modelled | 85.6 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 102 | c1cygA_ | Alignment | not modelled | 85.5 | 12 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase;<br>**PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase) |
| 103 | c3c3mA_ | Alignment | not modelled | 85.4 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator receiver protein;<br>**PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1 |
| 104 | d1xi3a_ | Alignment | not modelled | 85.4 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Thiamin phosphate synthase<br>**Family:**Thiamin phosphate synthase |
| | | | | | | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2- |

| | | | | | | |
|---|---|---|---|---|---|---|
| 105 | c3igsB_ | Alignment | not modelled | 85.4 | 12 | epimerase 2;<br>**PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase |
| 106 | c3czkA_ | Alignment | not modelled | 85.0 | 8 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sucrose hydrolase;<br>**PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex |
| 107 | c1jgiA_ | Alignment | not modelled | 84.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**amylosucrase;<br>**PDBTitle:** crystal structure of the active site mutant glu328gln of2 amylosucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose |
| 108 | c1jibA_ | Alignment | not modelled | 84.5 | 19 | **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. |
| 109 | c1tcmB_ | Alignment | not modelled | 84.3 | 11 | **PDB header:**glycosyltransferase<br>**Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase;<br>**PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251 |
| 110 | d2aaaa2 | Alignment | not modelled | 84.0 | 8 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 111 | c3bmwA_ | Alignment | not modelled | 83.5 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase;<br>**PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor |
| 112 | d1rd5a_ | Alignment | not modelled | 83.4 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 113 | c3bdkB_ | Alignment | not modelled | 83.4 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**d-mannonate dehydratase;<br>**PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue |
| 114 | c3ilhA_ | Alignment | not modelled | 83.4 | 14 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**two component response regulator;<br>**PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii |
| 115 | c2wcsA_ | Alignment | not modelled | 83.3 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha amylase, catalytic region;<br>**PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde) |
| 116 | d1lwha2 | Alignment | not modelled | 83.2 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 117 | c2j48A_ | Alignment | not modelled | 83.1 | 8 | **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. |
| 118 | d1bf2a3 | Alignment | not modelled | 82.9 | 8 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 119 | c3f6cB_ | Alignment | not modelled | 82.8 | 11 | **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 |
| 120 | d1qhoa4 | Alignment | not modelled | 82.8 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |