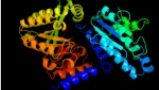
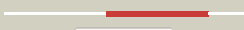
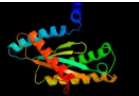
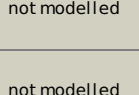
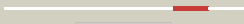
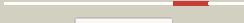
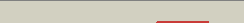
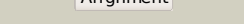
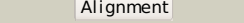
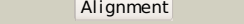
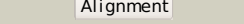
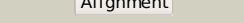
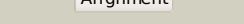
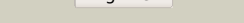
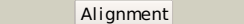
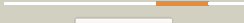
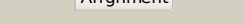
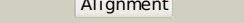
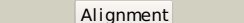


| #  | Template                 | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                    |
|----|--------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3pjwA_</a>  | <br>Alignment   |    | 100.0      | 18     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein;<br><b>PDBTitle:</b> structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23                                                                                         |
| 2  | <a href="#">c3gfbB_</a>  | <br>Alignment   |    | 100.0      | 21     | <b>PDB header:</b> hydrolase, signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> klebsiella pneumoniae blrp1;<br><b>PDBTitle:</b> klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex                                                                                   |
| 3  | <a href="#">c3hvbB_</a>  | <br>Alignment   |    | 100.0      | 22     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein fimx;<br><b>PDBTitle:</b> crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa                                                                                      |
| 4  | <a href="#">c3hvf9A_</a> | <br>Alignment   |    | 100.0      | 22     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein fimx;<br><b>PDBTitle:</b> crystal structure of fimx eal domain from pseudomonas aeruginosa                                                                                                                |
| 5  | <a href="#">c3s83A_</a>  | <br>Alignment |  | 100.0      | 32     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ggdef family protein;<br><b>PDBTitle:</b> crystal structure of eal domain from caulobacter crescentus cb15                                                                                                |
| 6  | <a href="#">c3pfmA_</a>  | <br>Alignment |  | 100.0      | 25     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein;<br><b>PDBTitle:</b> crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf                                                                      |
| 7  | <a href="#">c2w27A_</a>  | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ykui protein;<br><b>PDBTitle:</b> crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium                                           |
| 8  | <a href="#">c2r6oB_</a>  | <br>Alignment |  | 100.0      | 31     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase (ggdef & eal)<br><b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans |
| 9  | <a href="#">d2basa1</a>  | <br>Alignment |  | 100.0      | 22     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> EAL domain-like<br><b>Family:</b> EAL domain                                                                                                                                                                                  |
| 10 | <a href="#">c3kzpA_</a>  | <br>Alignment |  | 100.0      | 18     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative diguanylate cyclase/phosphodiesterase;<br><b>PDBTitle:</b> crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listeria monocytigenes                  |
| 11 | <a href="#">c1w25B_</a>  | <br>Alignment |  | 99.7       | 7      | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein;<br><b>PDBTitle:</b> response regulator pled in complex with c-digmp                                                                                     |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c3ezuA</a>  | Alignment |     | 99.5 | 8  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ggdef domain protein;<br><b>PDBTitle:</b> crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution                        |
| 13 | <a href="#">c3breA</a>  | Alignment |    | 99.4 | 7  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator;<br><b>PDBTitle:</b> crystal structure of p.aeruginosa pa3702                                                                                                            |
| 14 | <a href="#">c3i5cA</a>  | Alignment |    | 99.2 | 9  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> fusion of general control protein gcn4 and wspr response<br><b>PDBTitle:</b> crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa |
| 15 | <a href="#">d1w25a3</a> | Alignment |    | 99.2 | 6  | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Nucleotide cyclase<br><b>Family:</b> GGDEF domain                                                                                                                                                                                            |
| 16 | <a href="#">c3ic1A</a>  | Alignment |    | 99.2 | 6  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> eal/ggdef domain protein;<br><b>PDBTitle:</b> x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c               |
| 17 | <a href="#">c3ignA</a>  | Alignment |   | 99.2 | 4  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase;<br><b>PDBTitle:</b> crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a        |
| 18 | <a href="#">c3i5aA</a>  | Alignment |  | 99.2 | 8  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/ggdef domain protein;<br><b>PDBTitle:</b> crystal structure of full-length wspr from pseudomonas syringae                                                                                       |
| 19 | <a href="#">c3i5bA</a>  | Alignment |  | 99.2 | 9  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> wspr response regulator;<br><b>PDBTitle:</b> crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa                                                                                   |
| 20 | <a href="#">c3mtkA</a>  | Alignment |  | 99.1 | 6  | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase/phosphodiesterase;<br><b>PDBTitle:</b> x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c  |
| 21 | <a href="#">c3hvaA</a>  | Alignment | not modelled                                                                        | 99.1 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein fimx;<br><b>PDBTitle:</b> crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa                                                                                                                    |
| 22 | <a href="#">c3qyyB</a>  | Alignment | not modelled                                                                        | 99.1 | 4  | <b>PDB header:</b> signaling protein/inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> response regulator;<br><b>PDBTitle:</b> a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5 )-cyclic di-gmp                                                                    |
| 23 | <a href="#">c3hvwA</a>  | Alignment | not modelled                                                                        | 98.6 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate-cyclase (dgc);<br><b>PDBTitle:</b> crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c                              |
| 24 | <a href="#">c3khtA</a>  | Alignment | not modelled                                                                        | 95.2 | 12 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator;<br><b>PDBTitle:</b> crystal structure of response regulator from hahella chejuensis                                                                                                            |
| 25 | <a href="#">d1mvoa</a>  | Alignment | not modelled                                                                        | 95.2 | 12 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                     |
| 26 | <a href="#">d1ua7a2</a> | Alignment | not modelled                                                                        | 94.7 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                                        |
| 27 | <a href="#">d1p6ga</a>  | Alignment | not modelled                                                                        | 94.5 | 13 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                     |
| 28 | <a href="#">c3hebB</a>  | Alignment | not modelled                                                                        | 94.5 | 17 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver domain protein (chey);<br><b>PDBTitle:</b> crystal structure of response regulator receiver domain from2 rhodospirillum rubrum                                                   |
|    |                         |           |                                                                                     |      |    | <b>PDB header:</b> signaling protein                                                                                                                                                                                                                                                             |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c2zayA</a>  | Alignment | not modelled | 94.2 | 19 | <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein;<br><b>PDBTitle:</b> crystal structure of response regulator from desulfuromonas2 acetoxidans                                                                                                   |
| 30 | <a href="#">dlgwa2</a>  | Alignment | not modelled | 94.1 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                 |
| 31 | <a href="#">dla53a</a>  | Alignment | not modelled | 93.9 | 12 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Tryptophan biosynthesis enzymes                                                                                                                             |
| 32 | <a href="#">dlw25a1</a> | Alignment | not modelled | 93.7 | 12 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 33 | <a href="#">c2jk1A</a>  | Alignment | not modelled | 93.6 | 12 | <b>PDB header:</b> dna-binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1;<br><b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain                                                                 |
| 34 | <a href="#">c3edeB</a>  | Alignment | not modelled | 93.4 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyclomalto-dextrinase;<br><b>PDBTitle:</b> structural base for cyclodextrin hydrolysis                                                                                                              |
| 35 | <a href="#">dljbea</a>  | Alignment | not modelled | 93.0 | 19 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 36 | <a href="#">dlkrwa</a>  | Alignment | not modelled | 92.9 | 16 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 37 | <a href="#">clqhoA</a>  | Alignment | not modelled | 92.6 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase;<br><b>PDBTitle:</b> five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex                                                                            |
| 38 | <a href="#">c3q58A</a>  | Alignment | not modelled | 92.4 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase;<br><b>PDBTitle:</b> structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica                                                   |
| 39 | <a href="#">c2c3zA</a>  | Alignment | not modelled | 92.3 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase;<br><b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus                               |
| 40 | <a href="#">dly0ea</a>  | Alignment | not modelled | 92.2 | 10 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> NanE-like                                                                                                                                                   |
| 41 | <a href="#">c3qt7A</a>  | Alignment | not modelled | 92.1 | 12 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein;<br><b>PDBTitle:</b> crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus                                            |
| 42 | <a href="#">c2ayxA</a>  | Alignment | not modelled | 92.0 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase protein rcsc;<br><b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain                         |
| 43 | <a href="#">dlheya</a>  | Alignment | not modelled | 92.0 | 20 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 44 | <a href="#">c3eulB</a>  | Alignment | not modelled | 91.9 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> possible nitrate/nitrite response transcriptional<br><b>PDBTitle:</b> structure of the signal receiver domain of the putative2 response regulator narI from mycobacterium tuberculosis          |
| 45 | <a href="#">c2p0aA</a>  | Alignment | not modelled | 91.3 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871;<br><b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function         |
| 46 | <a href="#">cljdaA</a>  | Alignment | not modelled | 91.2 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha maltotetrahydrolase;<br><b>PDBTitle:</b> maltotetraose-forming exo-amylase                                                                                                                |
| 47 | <a href="#">c3hdgE</a>  | Alignment | not modelled | 91.0 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinetla3 succinogenes            |
| 48 | <a href="#">dlyioa2</a> | Alignment | not modelled | 91.0 | 11 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 49 | <a href="#">dlny5a1</a> | Alignment | not modelled | 91.0 | 15 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 50 | <a href="#">c3rqia</a>  | Alignment | not modelled | 90.8 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein;<br><b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate |
| 51 | <a href="#">clcygA</a>  | Alignment | not modelled | 90.8 | 16 | <b>PDB header:</b> glycosyltransferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase;<br><b>PDBTitle:</b> cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgase)                                                                               |
| 52 | <a href="#">dlqkka</a>  | Alignment | not modelled | 90.7 | 17 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                              |
| 53 | <a href="#">cljibA</a>  | Alignment | not modelled | 90.7 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> neopullulanase;<br><b>PDBTitle:</b> complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.                     |
| 54 | <a href="#">d2guya2</a> | Alignment | not modelled | 90.7 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                 |

|    |                         |                                                                                               |              |      |    |                                                                                                                                                                                                                                                                                                      |
|----|-------------------------|-----------------------------------------------------------------------------------------------|--------------|------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 55 | <a href="#">c1bagA</a>  |  Alignment    | not modelled | 90.5 | 14 | <b>PDB header:</b> alpha-amylase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase;<br><b>PDBTitle:</b> alpha-amylase from bacillus subtilis complexed with2 maltopentaose                                                                                                |
| 56 | <a href="#">c3ucqA</a>  |  Alignment   | not modelled | 90.5 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase;<br><b>PDBTitle:</b> crystal structure of amylsucrase from deinococcus geothermalis                                                                                                                              |
| 57 | <a href="#">d1h3ga3</a> |  Alignment   | not modelled | 90.2 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                                            |
| 58 | <a href="#">d1zesal</a> |  Alignment   | not modelled | 90.2 | 17 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 59 | <a href="#">c2wcsA</a>  |  Alignment   | not modelled | 90.1 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region;<br><b>PDBTitle:</b> crystal structure of debranching enzyme from nostoc2 punctiforme (npde)                                                                                                   |
| 60 | <a href="#">c2h6rG</a>  |  Alignment   | not modelled | 90.1 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> G: <b>PDB Molecule:</b> triosephosphate isomerase;<br><b>PDBTitle:</b> crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii                                                                                        |
| 61 | <a href="#">c1tcmB</a>  |  Alignment   | not modelled | 90.1 | 14 | <b>PDB header:</b> glycosyltransferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyclodextrin glycosyltransferase;<br><b>PDBTitle:</b> cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251                                                                              |
| 62 | <a href="#">c3czkA</a>  |  Alignment   | not modelled | 90.1 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> sucrose hydrolase;<br><b>PDBTitle:</b> crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex                                                                                                            |
| 63 | <a href="#">c3gl9B</a>  |  Alignment   | not modelled | 90.0 | 15 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> response regulator;<br><b>PDBTitle:</b> the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism                |
| 64 | <a href="#">c3crnA</a>  |  Alignment   | not modelled | 90.0 | 21 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, chey-like;<br><b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1                           |
| 65 | <a href="#">d1k68a</a>  |  Alignment   | not modelled | 89.8 | 10 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 66 | <a href="#">c3nhzA</a>  |  Alignment   | not modelled | 89.8 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> two component system transcriptional regulator mtra;<br><b>PDBTitle:</b> structure of n-terminal domain of mtra                                                                                                      |
| 67 | <a href="#">c1gjuA</a>  |  Alignment | not modelled | 89.7 | 18 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltodextrin glycosyltransferase;<br><b>PDBTitle:</b> maltosyltransferase from thermotoga maritima                                                                                                                           |
| 68 | <a href="#">d1qhoa4</a> |  Alignment | not modelled | 89.7 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                                            |
| 69 | <a href="#">d1kgsa2</a> |  Alignment | not modelled | 89.7 | 13 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 70 | <a href="#">d1lwah2</a> |  Alignment | not modelled | 89.7 | 17 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                                            |
| 71 | <a href="#">c3cg0A</a>  |  Alignment | not modelled | 89.7 | 20 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver modulated diguanylate cyclase<br><b>PDBTitle:</b> crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding |
| 72 | <a href="#">d2r25b1</a> |  Alignment | not modelled | 89.6 | 10 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 73 | <a href="#">c2rjnA</a>  |  Alignment | not modelled | 89.6 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver:metal-dependent<br><b>PDBTitle:</b> crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis                                                                       |
| 74 | <a href="#">c3i42A</a>  |  Alignment | not modelled | 89.4 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein (chey-<br><b>PDBTitle:</b> structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus                                |
| 75 | <a href="#">d1ys7a2</a> |  Alignment | not modelled | 89.1 | 14 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 76 | <a href="#">c2pz0B</a>  |  Alignment | not modelled | 89.0 | 9  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycerophosphoryl diester phosphodiesterase;<br><b>PDBTitle:</b> crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis                                                                    |
| 77 | <a href="#">d2aaaa2</a> |  Alignment | not modelled | 89.0 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                                            |
| 78 | <a href="#">d2ayxa1</a> |  Alignment | not modelled | 89.0 | 17 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                                         |
| 79 | <a href="#">c3bmwA</a>  |  Alignment | not modelled | 88.9 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclomalto dextrin glucanotransferase;<br><b>PDBTitle:</b> cyclodextrin glycosyl transferase from                                                                                                                            |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                          |
|-----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      |    | thermoanrobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor                                                                                                                                                                        |
| 80  | <a href="#">d1dz3a_</a> | Alignment | not modelled | 88.7 | 12 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 81  | <a href="#">c2zwmA_</a> | Alignment | not modelled | 88.5 | 12 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein yycf;<br><b>PDBTitle:</b> crystal structure of yycf receiver domain from bacillus2 subtilis                                                                 |
| 82  | <a href="#">c3b2nA_</a> | Alignment | not modelled | 88.4 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4;<br><b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus                                              |
| 83  | <a href="#">d1xhfa1</a> | Alignment | not modelled | 88.4 | 10 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 84  | <a href="#">d1g5aa2</a> | Alignment | not modelled | 88.4 | 13 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                |
| 85  | <a href="#">c2qr3A_</a> | Alignment | not modelled | 88.2 | 13 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator;<br><b>PDBTitle:</b> crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis |
| 86  | <a href="#">c3hv2B_</a> | Alignment | not modelled | 88.2 | 12 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> response regulator/hd domain protein;<br><b>PDBTitle:</b> crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5                  |
| 87  | <a href="#">d1a04a2</a> | Alignment | not modelled | 87.7 | 16 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 88  | <a href="#">c3k8kB_</a> | Alignment | not modelled | 87.7 | 17 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase, susg;<br><b>PDBTitle:</b> crystal structure of susg                                                                                                                          |
| 89  | <a href="#">d1h5ya_</a> | Alignment | not modelled | 87.5 | 10 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Ribulose-phosphate binding barrel<br><b>Family:</b> Histidine biosynthesis enzymes                                                                                                                             |
| 90  | <a href="#">c3igsB_</a> | Alignment | not modelled | 87.4 | 10 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2;<br><b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase                                               |
| 91  | <a href="#">d1i3ca_</a> | Alignment | not modelled | 87.3 | 13 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 92  | <a href="#">c3cz5B_</a> | Alignment | not modelled | 87.1 | 12 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> two-component response regulator, luxr family;<br><b>PDBTitle:</b> crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1               |
| 93  | <a href="#">d1dbwa_</a> | Alignment | not modelled | 87.1 | 18 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 94  | <a href="#">c1jgiA_</a> | Alignment | not modelled | 86.9 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase;<br><b>PDBTitle:</b> crystal structure of the active site mutant glu328gln of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose               |
| 95  | <a href="#">c3a47A_</a> | Alignment | not modelled | 86.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase;<br><b>PDBTitle:</b> crystal structure of isomaltase from saccharomyces cerevisiae                                                                                           |
| 96  | <a href="#">c2ya0A_</a> | Alignment | not modelled | 86.6 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase;<br><b>PDBTitle:</b> catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua                                               |
| 97  | <a href="#">c3cu5B_</a> | Alignment | not modelled | 86.5 | 12 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulator, arac family;<br><b>PDBTitle:</b> crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg |
| 98  | <a href="#">d1k66a_</a> | Alignment | not modelled | 86.5 | 16 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 99  | <a href="#">c3dhuC_</a> | Alignment | not modelled | 86.5 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> alpha-amylase;<br><b>PDBTitle:</b> crystal structure of an alpha-amylase from lactobacillus2 plantarum                                                                                             |
| 100 | <a href="#">d2pl1a1</a> | Alignment | not modelled | 86.4 | 13 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                             |
| 101 | <a href="#">d2bhua3</a> | Alignment | not modelled | 86.3 | 22 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                |
| 102 | <a href="#">c3c3mA_</a> | Alignment | not modelled | 86.3 | 16 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1             |
| 103 | <a href="#">c2yxba_</a> | Alignment | not modelled | 86.2 | 17 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase;<br><b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix                                                          |
|     |                         |           |              |      |    | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> dna-binding response regulator, merr                                                                                                                                                     |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                      |
|-----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 104 | <a href="#">c3cnbC_</a> | Alignment | not modelled | 86.2 | 18 | family;<br><b>PDBTitle:</b> crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h                                                                                                                         |
| 105 | <a href="#">d2d3na2</a> | Alignment | not modelled | 85.7 | 25 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                            |
| 106 | <a href="#">c2ze0A_</a> | Alignment | not modelled | 85.5 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase;<br><b>PDBTitle:</b> alpha-glucosidase gsj                                                                                                                                                   |
| 107 | <a href="#">c1gviA_</a> | Alignment | not modelled | 85.2 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltogenic amylase;<br><b>PDBTitle:</b> thermus maltogenic amylase in complex with beta-cd                                                                                                                     |
| 108 | <a href="#">d1eh9a3</a> | Alignment | not modelled | 85.2 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                            |
| 109 | <a href="#">d1zh2a1</a> | Alignment | not modelled | 84.9 | 15 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                         |
| 110 | <a href="#">d1u0sy_</a> | Alignment | not modelled | 84.9 | 10 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                         |
| 111 | <a href="#">c2iswB_</a> | Alignment | not modelled | 84.8 | 18 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-1,6-bisphosphate aldolase;<br><b>PDBTitle:</b> structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolhydroxamate                                                  |
| 112 | <a href="#">c3c97A_</a> | Alignment | not modelled | 84.4 | 17 | <b>PDB header:</b> signaling protein, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction histidine kinase;<br><b>PDBTitle:</b> crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae |
| 113 | <a href="#">d1hvxa2</a> | Alignment | not modelled | 84.3 | 24 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> (Trans)glycosidases<br><b>Family:</b> Amylase, catalytic domain                                                                                                                                                            |
| 114 | <a href="#">c3cfyA_</a> | Alignment | not modelled | 84.2 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative luxo repressor protein;<br><b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus                  |
| 115 | <a href="#">c2qpuB_</a> | Alignment | not modelled | 84.0 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase type a isozyme;<br><b>PDBTitle:</b> sugar tongs mutant s378p in complex with acarbose                                                                                                            |
| 116 | <a href="#">d1w0ma_</a> | Alignment | not modelled | 83.9 | 13 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Triosephosphate isomerase (TIM)<br><b>Family:</b> Triosephosphate isomerase (TIM)                                                                                                                                          |
| 117 | <a href="#">c3blpX_</a> | Alignment | not modelled | 83.9 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> alpha-amylase 1;<br><b>PDBTitle:</b> role of aromatic residues in human salivary alpha-amylase                                                                                                                 |
| 118 | <a href="#">d1zgza1</a> | Alignment | not modelled | 83.8 | 13 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> CheY-like<br><b>Family:</b> CheY-related                                                                                                                                                                                         |
| 119 | <a href="#">c2z1kA_</a> | Alignment | not modelled | 83.6 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> (neo)pullulanase;<br><b>PDBTitle:</b> crystal structure of ttha1563 from thermus thermophilus hb8                                                                                                              |
| 120 | <a href="#">c1zjaB_</a> | Alignment | not modelled | 83.6 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> trehalulose synthase;<br><b>PDBTitle:</b> crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)                                                           |