# Phyre$^2$

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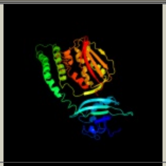
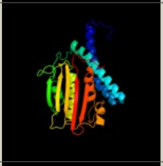
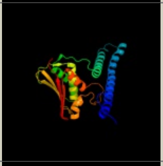
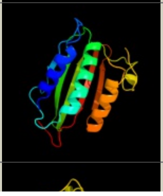
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q06067 |
| Date | Thu Jan 5 12:33:25 GMT 2012 |
| Unique Job ID | e476e983d4dea314 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3a0rA_ | Alignment |  | 100.0 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360) |
| 2 | c3d36B_ | Alignment |  | 100.0 | 28 | **PDB header:**transferase/transferase inhibitor<br>**Chain:** B: **PDB Molecule:**sporulation kinase b;<br>**PDBTitle:** how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda |
| 3 | c2q8fA_ | Alignment |  | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1;<br>**PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1 |
| 4 | c2bu8A_ | Alignment |  | 100.0 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate dehydrogenase kinase isoenzyme 2;<br>**PDBTitle:** crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands |
| 5 | c3d2rB_ | Alignment |  | 100.0 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4;<br>**PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp |
| 6 | c2c2aA_ | Alignment |  | 100.0 | 29 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor histidine kinase;<br>**PDBTitle:** structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein |
| 7 | c1gjvA_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[3-methyl-2-oxobutanoate dehydrogenase<br>**PDBTitle:** branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complxed with atp-gamma-s |
| 8 | c1y8oA_ | Alignment |  | 100.0 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3;<br>**PDBTitle:** crystal structure of the pdk3-l2 complex |
| 9 | c3a0tA_ | Alignment |  | 100.0 | 35 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal) |
| 10 | d2c2aa2 | Alignment |  | 100.0 | 29 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 11 | d1gkza2 | Alignment |  | 100.0 | 21 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |

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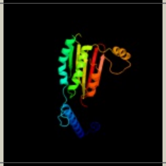
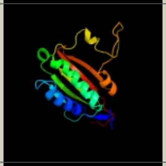
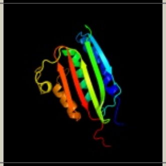
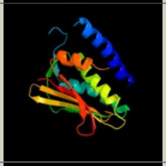
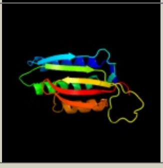
| 12 | d1jm6a2 | Alignment |  | 100.0 | 19 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 13 | d1id0a_ | Alignment |  | 100.0 | 24 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 14 | c1b3qA_ | Alignment |  | 100.0 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea);<br>**PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase |
| 15 | d1bxda_ | Alignment |  | 100.0 | 26 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 16 | c2ch4A_ | Alignment |  | 100.0 | 27 | **PDB header:**transferase/chemotaxis<br>**Chain:** A: **PDB Molecule:**chemotaxis protein chea;<br>**PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew |
| 17 | d1i58a_ | Alignment |  | 99.9 | 27 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 18 | d1ysra1 | Alignment |  | 99.9 | 23 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 19 | c3jz3B_ | Alignment |  | 99.9 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**sensor protein qsec;<br>**PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec |
| 20 | d1r62a_ | Alignment |  | 99.9 | 28 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 21 | d2hkja3 | Alignment | not modelled | 99.8 | 24 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 22 | c3ehgA_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor kinase (yocf protein);<br>**PDBTitle:** crystal structure of the atp-binding domain of desk in complex with2 atp |
| 23 | c3zxqA_ | Alignment | not modelled | 99.8 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypoxia sensor histidine kinase response regulator dost;<br>**PDBTitle:** crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost |
| 24 | c2zbkB_ | Alignment | not modelled | 99.7 | 24 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;<br>**PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms |
| 25 | c3gieA_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor histidine kinase desk;<br>**PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp |
| 26 | c1mx0D_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b;<br>**PDBTitle:** structure of topoisomerase subunit |
| 27 | c3zxoB_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**redox sensor histidine kinase response regulator devs;<br>**PDBTitle:** crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss |
| 28 | c2q2eB_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;<br>**PDBTitle:** crystal structure of the topoisomerase vi holoenzyme |

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| 29 | d1h7sa2 | Alignment | not modelled | 99.6 | 16 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 30 | d1th8a_ | Alignment | not modelled | 99.5 | 19 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Histidine kinase |
| 31 | d1bkna2 | Alignment | not modelled | 99.4 | 18 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 32 | d1ixma_ | Alignment | not modelled | 99.4 | 17 | **Fold:**Sporulation response regulatory protein Spo0B<br>**Superfamily:**Sporulation response regulatory protein Spo0B<br>**Family:**Sporulation response regulatory protein Spo0B |
| 33 | d1b63a2 | Alignment | not modelled | 99.4 | 23 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 34 | d1y8oa2 | Alignment | not modelled | 99.4 | 15 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 35 | c3na3A_ | Alignment | not modelled | 99.1 | 22 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1;<br>**PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens |
| 36 | c3h4lB_ | Alignment | not modelled | 98.8 | 27 | **PDB header:**dna binding protein, protein binding<br>**Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1;<br>**PDBTitle:** crystal structure of n terminal domain of a dna repair protein |
| 37 | c1bknA_ | Alignment | not modelled | 98.5 | 27 | **PDB header:**dna repair<br>**Chain:** A: **PDB Molecule:**mutl;<br>**PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl |
| 38 | c1kijB_ | Alignment | not modelled | 98.5 | 22 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit b;<br>**PDBTitle:** crystal structure of the 43k atpase domain of thermus thermophilus2 gyrase b in complex with novobiocin |
| 39 | c1ei1B_ | Alignment | not modelled | 98.4 | 18 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase b;<br>**PDBTitle:** dimerization of e. coli dna gyrase b provides a structural mechanism2 for activating the atpase catalytic center |
| 40 | c2v1bA_ | Alignment | not modelled | 98.4 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nph1-1;<br>**PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546)) |
| 41 | d1kija2 | Alignment | not modelled | 98.4 | 23 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 42 | d1pvga2 | Alignment | not modelled | 98.3 | 20 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 43 | c1ea6A_ | Alignment | not modelled | 98.3 | 18 | **PDB header:**dna repair<br>**Chain:** A: **PDB Molecule:**pms1 protein homolog 2;<br>**PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp |
| 44 | c2wkqA_ | Alignment | not modelled | 98.3 | 13 | **PDB header:**transferase, cell adhesion<br>**Chain:** A: **PDB Molecule:**nph1-1, ras-related c3 botulinum toxin substrate<br>**PDBTitle:** structure of a photoactivatable rac1 containing the lov22 c450a mutant |
| 45 | c3lyxA_ | Alignment | not modelled | 98.3 | 24 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**sensory box/ggdef domain protein;<br>**PDBTitle:** crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b |
| 46 | d1s16a2 | Alignment | not modelled | 98.3 | 16 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 47 | c2gj3A_ | Alignment | not modelled | 98.3 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nitrogen fixation regulatory protein;<br>**PDBTitle:** crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii. |
| 48 | d1ei1a2 | Alignment | not modelled | 98.3 | 18 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 49 | c3luqC_ | Alignment | not modelled | 98.3 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**sensor protein;<br>**PDBTitle:** the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a |
| 50 | c1y4sA_ | Alignment | not modelled | 98.2 | 24 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**chaperone protein htpg;<br>**PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding |
| | | | | | | **PDB header:**unknown function |

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| 51 | c3ke6A_ | Alignment | not modelled | 98.2 | 25 | **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410;<br>**PDBTitle:** the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis |
| 52 | d1bywa_ | Alignment | not modelled | 98.1 | 16 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Flavin-binding PAS domain |
| 53 | c1s16B_ | Alignment | not modelled | 98.1 | 15 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**topoisomerase iv subunit b;<br>**PDBTitle:** crystal structure of e. coli topoisomerase iv pare 43kda subunit2 complexed with adpnp |
| 54 | d1n9la_ | Alignment | not modelled | 98.1 | 14 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Flavin-binding PAS domain |
| 55 | c3caxA_ | Alignment | not modelled | 98.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pf0695;<br>**PDBTitle:** crystal structure of uncharacterized protein pf0695 |
| 56 | c2cg9A_ | Alignment | not modelled | 98.0 | 24 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82;<br>**PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex |
| 57 | c2iopD_ | Alignment | not modelled | 98.0 | 25 | **PDB header:**chaperone<br>**Chain:** D: **PDB Molecule:**chaperone protein htpg;<br>**PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp |
| 58 | c3b33A_ | Alignment | not modelled | 98.0 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus |
| 59 | c2o1wB_ | Alignment | not modelled | 98.0 | 22 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**endoplasmin;<br>**PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94 |
| 60 | c3g7bB_ | Alignment | not modelled | 98.0 | 21 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit b;<br>**PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor |
| 61 | c3mqoB_ | Alignment | not modelled | 98.0 | 15 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family;<br>**PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a |
| 62 | c2l4rA_ | Alignment | not modelled | 98.0 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h member 2;<br>**PDBTitle:** nmr solution structure of the n-terminal pas domain of herg |
| 63 | c1zxnB_ | Alignment | not modelled | 97.9 | 31 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme;<br>**PDBTitle:** human dna topoisomerase iia atpase/adp |
| 64 | c3iedA_ | Alignment | not modelled | 97.9 | 28 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**heat shock protein;<br>**PDBTitle:** crystal structure of n-terminal domain of plasmodium falciparum hsp902 (pf14_0417) in complex with amppn |
| 65 | d1jnua_ | Alignment | not modelled | 97.9 | 10 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Flavin-binding PAS domain |
| 66 | c2fwyA_ | Alignment | not modelled | 97.9 | 13 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**heat shock protein hsp 90-alpha;<br>**PDBTitle:** structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64 |
| 67 | c3pehB_ | Alignment | not modelled | 97.9 | 22 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**endoplasmin homolog;<br>**PDBTitle:** crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative |
| 68 | d1uyla_ | Alignment | not modelled | 97.9 | 16 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Heat shock protein 90, HSP90, N-terminal domain |
| 69 | c2vlgD_ | Alignment | not modelled | 97.9 | 6 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**sporulation kinase a;<br>**PDBTitle:** kina pas-a domain, homodimer |
| 70 | c2z6dB_ | Alignment | not modelled | 97.9 | 14 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phototropin-2;<br>**PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana |
| 71 | c3mxqC_ | Alignment | not modelled | 97.9 | 13 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae |
| 72 | c3mfxA_ | Alignment | not modelled | 97.8 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**sensory box/ggdef family protein;<br>**PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b |
| 73 | c2iorA_ | Alignment | not modelled | 97.8 | 23 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**chaperone protein htpg;<br>**PDBTitle:** crystal structure of the n-terminal domain of htpg, the2 escherichia coli hsp90, bound to adp |
| 74 | c2akpA_ | Alignment | not modelled | 97.8 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82;<br>**PDBTitle:** hsp90 delta24-n210 mutant |
| 75 | c3a0vA_ | Alignment | not modelled | 97.8 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m) |

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| 76 | c3f1oB_ | Alignment | not modelled | 97.8 | 10 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator;<br>**PDBTitle:** crystal structure of the high affinity heterodimer of hif22 alpha and arnt c-terminal pas domains, with an internally-3 bound artificial ligand |
| 77 | c1qzrA_ | Alignment | not modelled | 97.8 | 21 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**dna topoisomerase ii;<br>**PDBTitle:** crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane) |
| 78 | d2iwxa1 | Alignment | not modelled | 97.8 | 16 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Heat shock protein 90, HSP90, N-terminal domain |
| 79 | d2gqpa1 | Alignment | not modelled | 97.8 | 14 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Heat shock protein 90, HSP90, N-terminal domain |
| 80 | c1zwhA_ | Alignment | not modelled | 97.7 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82;<br>**PDBTitle:** yeast hsp82 in complex with the novel hsp90 inhibitor radester amine |
| 81 | d1v9ya_ | Alignment | not modelled | 97.7 | 20 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Heme-binding PAS domain |
| 82 | c1v9yA_ | Alignment | not modelled | 97.7 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**heme pas sensor protein;<br>**PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form) |
| 83 | c3fg8B_ | Alignment | not modelled | 97.7 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein rha05790;<br>**PDBTitle:** crystal structure of pas domain of rha05790 |
| 84 | d1s14a_ | Alignment | not modelled | 97.7 | 22 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**DNA gyrase/MutL, N-terminal domain |
| 85 | d1p97a_ | Alignment | not modelled | 97.7 | 10 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Hypoxia-inducible factor Hif2a, C-terminal domain |
| 86 | c2pr6A_ | Alignment | not modelled | 97.7 | 13 | **PDB header:**flavoprotein, signaling protein<br>**Chain:** A: **PDB Molecule:**blue-light photoreceptor;<br>**PDBTitle:** structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure) |
| 87 | c2qkpD_ | Alignment | not modelled | 97.7 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans |
| 88 | c3k3dA_ | Alignment | not modelled | 97.6 | 9 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein rv1364c/mt1410;<br>**PDBTitle:** the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom |
| 89 | c3mjqB_ | Alignment | not modelled | 97.6 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c. |
| 90 | c3eehA_ | Alignment | not modelled | 97.6 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative light and redox sensing histidine kinase;<br>**PDBTitle:** the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui |
| 91 | c2kdkA_ | Alignment | not modelled | 97.6 | 15 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator-like protein<br>**PDBTitle:** structure of human circadian clock protein bmal2 c-terminal pas domain |
| 92 | c3kx0X_ | Alignment | not modelled | 97.6 | 12 | **PDB header:**signaling protein<br>**Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410;<br>**PDBTitle:** crystal structure of the pas domain of rv1364c |
| 93 | c3h9wA_ | Alignment | not modelled | 97.5 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**diguanylate cyclase with pas/pac sensor;<br>**PDBTitle:** crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c |
| 94 | c3mr0B_ | Alignment | not modelled | 97.5 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**sensory box histidine kinase/response regulator;<br>**PDBTitle:** crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264 |
| 95 | d1uyma_ | Alignment | not modelled | 97.5 | 16 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Heat shock protein 90, HSP90, N-terminal domain |
| 96 | c1wa9A_ | Alignment | not modelled | 97.4 | 10 | **PDB header:**circadian rhythm<br>**Chain:** A: **PDB Molecule:**period circadian protein;<br>**PDBTitle:** crystal structure of the pas repeat region of the2 drosophila clock protein period |
| 97 | c3oloB_ | Alignment | not modelled | 97.4 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**two-component sensor histidine kinase;<br>**PDBTitle:** crystal structure of a pas domain from two-component sensor histidine2 kinase |
| 98 | d1y28a_ | Alignment | not modelled | 97.4 | 20 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Heme-binding PAS domain |

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| 99 | c2r78D_ | Alignment | not modelled | 97.4 | 18 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens |
| 100 | d1xj3a1 | Alignment | not modelled | 97.4 | 19 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Heme-binding PAS domain |
| 101 | c2o1uA_ | Alignment | not modelled | 97.4 | 21 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**endoplasmin;<br>**PDBTitle:** structure of full length grp94 with amp-pnp bound |
| 102 | d1ew0a_ | Alignment | not modelled | 97.4 | 14 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**Heme-binding PAS domain |
| 103 | d1qy5a_ | Alignment | not modelled | 97.4 | 18 | **Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase<br>**Family:**Heat shock protein 90, HSP90, N-terminal domain |
| 104 | c3fc7B_ | Alignment | not modelled | 97.4 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**htr-like protein;<br>**PDBTitle:** the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049 |
| 105 | c3lnuA_ | Alignment | not modelled | 97.3 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase iv subunit b;<br>**PDBTitle:** crystal structure of pare subunit |
| 106 | d1nwza_ | Alignment | not modelled | 97.3 | 21 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**PYP-like |
| 107 | d1mzua_ | Alignment | not modelled | 97.3 | 13 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**PYP-like |
| 108 | d1otda_ | Alignment | not modelled | 97.2 | 20 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**PYP-like |
| 109 | c2pdtD_ | Alignment | not modelled | 97.2 | 14 | **PDB header:**circadian clock protein<br>**Chain:** D: **PDB Molecule:**vivid pas protein vvd;<br>**PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid |
| 110 | c3p7nB_ | Alignment | not modelled | 97.2 | 12 | **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 |
| 111 | c3bwlA_ | Alignment | not modelled | 97.2 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui |
| 112 | c3rtyA_ | Alignment | not modelled | 97.1 | 13 | **PDB header:**circadian clock protein<br>**Chain:** A: **PDB Molecule:**period circadian protein;<br>**PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein |
| 113 | c2jheB_ | Alignment | not modelled | 96.9 | 14 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**transcription regulator tyrr;<br>**PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190) |
| 114 | c3njaC_ | Alignment | not modelled | 96.9 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**probable ggdef family protein;<br>**PDBTitle:** the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472. |
| 115 | c3ewkA_ | Alignment | not modelled | 96.8 | 21 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**sensor protein;<br>**PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos |
| 116 | c2w0nA_ | Alignment | not modelled | 96.7 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein dcus;<br>**PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus |
| 117 | d1xfna1 | Alignment | not modelled | 96.7 | 20 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**PYP-like |
| 118 | c3icyB_ | Alignment | not modelled | 96.7 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**sensor protein;<br>**PDBTitle:** the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 tls |
| 119 | d1oj5a_ | Alignment | not modelled | 96.6 | 9 | **Fold:**Profilin-like<br>**Superfamily:**PYP-like sensor domain (PAS domain)<br>**Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1 |
| 120 | c3gecA_ | Alignment | not modelled | 96.6 | 11 | **PDB header:**circadian clock protein<br>**Chain:** A: **PDB Molecule:**period circadian protein;<br>**PDBTitle:** crystal structure of a tandem pas domain fragment of2 drosophila period |