# Phyre$^2$

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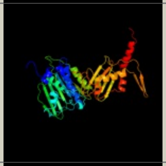
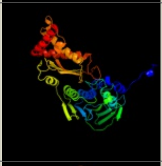
| Description | P0AES6 |
| Date | Thu Jan 5 11:24:06 GMT 2012 |
| Unique Job ID | 722f501f08c2a3c1 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3nuhB_ | Alignment |  | 100.0 | 98 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit b;<br>**PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function |
| 2 | c3lnuA_ | Alignment |  | 100.0 | 36 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase iv subunit b;<br>**PDBTitle:** crystal structure of pare subunit |
| 3 | c1zxnB_ | Alignment |  | 100.0 | 23 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna topoisomerase ii, alpha isozyme;<br>**PDBTitle:** human dna topoisomerase iia atpase/adp |
| 4 | c1ei1B_ | Alignment |  | 100.0 | 99 | **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 |
| 5 | c1qzrA_ | Alignment |  | 100.0 | 27 | **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) |
| 6 | c1s16B_ | Alignment |  | 100.0 | 37 | **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 |
| 7 | c3cwvB_ | Alignment |  | 100.0 | 31 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase, b subunit, truncated;<br>**PDBTitle:** crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus |
| 8 | c1kijB_ | Alignment |  | 100.0 | 47 | **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 |
| 9 | c2xkjE_ | Alignment |  | 100.0 | 47 | **PDB header:**isomerase<br>**Chain:** E: **PDB Molecule:**topoisomerase iv;<br>**PDBTitle:** crystal structure of catalytic core of a. baumannii topo iv2 (pare-parc fusion truncate) |
| 10 | c2xcqA_ | Alignment |  | 100.0 | 71 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a;<br>**PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase |
| 11 | c2xcsD_ | Alignment |  | 100.0 | 71 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a;<br>**PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna |

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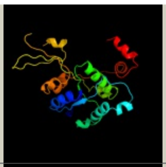
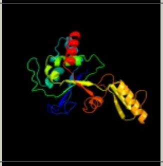
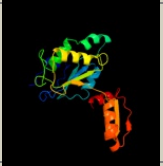
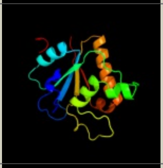
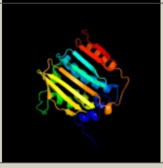
| 12 | c3fofD_ | Alignment |  | 100.0 | 66 | **PDB header:**isomerase/dna<br>**Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit b;<br>**PDBTitle:** structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases |
| 13 | c2zjtB_ | Alignment |  | 100.0 | 57 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit b;<br>**PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation |
| 14 | d1pvga2 | Alignment |  | 100.0 | 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:**DNA gyrase/MutL, N-terminal domain |
| 15 | d1bjta_ | Alignment |  | 100.0 | 34 | **Fold:**Type II DNA topoisomerase<br>**Superfamily:**Type II DNA topoisomerase<br>**Family:**Type II DNA topoisomerase |
| 16 | c1bjtA_ | Alignment |  | 100.0 | 34 | **PDB header:**topoisomerase<br>**Chain:** A: **PDB Molecule:**topoisomerase ii;<br>**PDBTitle:** topoisomerase ii residues 409-1201 |
| 17 | c3qx3B_ | Alignment |  | 100.0 | 35 | **PDB header:**isomerase/dna/isomerase inhibitor<br>**Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta;<br>**PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide |
| 18 | d1ei1a2 | Alignment |  | 100.0 | 99 | **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 |
| 19 | d1s16a2 | Alignment |  | 100.0 | 47 | **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 |
| 20 | d1kija2 | Alignment |  | 100.0 | 51 | **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 |
| 21 | d1kija1 | Alignment | not modelled | 100.0 | 44 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**DNA gyrase/MutL, second domain |
| 22 | d1ei1a1 | Alignment | not modelled | 100.0 | 100 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**DNA gyrase/MutL, second domain |
| 23 | c3g7bB_ | Alignment | not modelled | 100.0 | 57 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**dna gyrase subunit b;<br>**PDBTitle:** staphylococcus aureus gyrase b co-complex with inhibitor |
| 24 | d1s16a1 | Alignment | not modelled | 100.0 | 24 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**DNA gyrase/MutL, second domain |
| 25 | d1s14a_ | Alignment | not modelled | 100.0 | 44 | **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 |
| 26 | d1pvga1 | Alignment | not modelled | 100.0 | 23 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**DNA gyrase/MutL, second domain |
| 27 | c2q2eB_ | Alignment | not modelled | 99.9 | 20 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b;<br>**PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei |
| 28 | c2zbkB_ | Alignment | not modelled | 99.8 | 19 | **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 |

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| 29 | c3h4lB_ | Alignment | not modelled | 99.8 | 17 | **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 |
| 30 | d2hkja3 | Alignment | not modelled | 99.7 | 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:**DNA gyrase/MutL, N-terminal domain |
| 31 | c1mx0D_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b;<br>**PDBTitle:** structure of topoisomerase subunit |
| 32 | c3na3A_ | Alignment | not modelled | 99.6 | 16 | **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 |
| 33 | d1b63a2 | Alignment | not modelled | 99.5 | 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 |
| 34 | c1bknA_ | Alignment | not modelled | 99.4 | 16 | **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 |
| 35 | d1h7sa2 | Alignment | not modelled | 99.4 | 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 |
| 36 | d1bkna2 | Alignment | not modelled | 99.3 | 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:**DNA gyrase/MutL, N-terminal domain |
| 37 | c1ea6A_ | Alignment | not modelled | 99.1 | 24 | **PDB header:**dna repair<br>**Chain:** A: **PDB Molecule:**pms1 protein homolog 2;<br>**PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp |
| 38 | c2akpA_ | Alignment | not modelled | 98.9 | 17 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82;<br>**PDBTitle:** hsp90 delta24-n210 mutant |
| 39 | c3iedA_ | Alignment | not modelled | 98.8 | 23 | **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 |
| 40 | d2iwxa1 | Alignment | not modelled | 98.7 | 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 |
| 41 | c2fwyA_ | Alignment | not modelled | 98.7 | 19 | **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 |
| 42 | d1uyla_ | Alignment | not modelled | 98.7 | 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 |
| 43 | c1zwhA_ | Alignment | not modelled | 98.7 | 18 | **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 |
| 44 | d1uyma_ | Alignment | not modelled | 98.7 | 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 |
| 45 | c2cg9A_ | Alignment | not modelled | 98.4 | 17 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82;<br>**PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex |
| 46 | c2iorA_ | Alignment | not modelled | 98.4 | 20 | **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 |
| 47 | d1qy5a_ | 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:**Heat shock protein 90, HSP90, N-terminal domain |
| 48 | d2gqpa1 | Alignment | not modelled | 98.2 | 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:**Heat shock protein 90, HSP90, N-terminal domain |
| 49 | c2o1wB_ | Alignment | not modelled | 98.2 | 21 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**endoplasmin;<br>**PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94 |
| 50 | c3pehB_ | Alignment | not modelled | 98.2 | 19 | **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 |
| 51 | c1y4sA_ | Alignment | not modelled | 98.0 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**chaperone protein htpg;<br>**PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding |

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| 52 | c1gjvA_ | Alignment | not modelled | 97.8 | 22 | **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 |
| 53 | c2bu8A_ | Alignment | not modelled | 97.8 | 26 | **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 |
| 54 | c1y8oA_ | Alignment | not modelled | 97.7 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 3;<br>**PDBTitle:** crystal structure of the pdk3-l2 complex |
| 55 | c2iopD_ | Alignment | not modelled | 97.7 | 14 | **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 |
| 56 | c3d2rB_ | Alignment | not modelled | 97.7 | 22 | **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 |
| 57 | c2q8fA_ | Alignment | not modelled | 97.4 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1;<br>**PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1 |
| 58 | c3d36B_ | Alignment | not modelled | 97.2 | 19 | **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 |
| 59 | d1jm6a2 | Alignment | not modelled | 97.1 | 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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 60 | c2c2aA_ | Alignment | not modelled | 97.1 | 18 | **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 |
| 61 | d1gkza2 | Alignment | not modelled | 96.7 | 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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 62 | c2o1uA_ | Alignment | not modelled | 96.5 | 21 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**endoplasmin;<br>**PDBTitle:** structure of full length grp94 with amp-pnp bound |
| 63 | c3a0rA_ | Alignment | not modelled | 96.4 | 27 | **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) |
| 64 | c1b3qA_ | Alignment | not modelled | 96.3 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (chemotaxis protein chea);<br>**PDBTitle:** crystal structure of chea-289, a signal transducing histidine kinase |
| 65 | d1th8a_ | Alignment | not modelled | 96.2 | 17 | **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 |
| 66 | d1y8oa2 | Alignment | not modelled | 96.1 | 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:**alpha-ketoacid dehydrogenase kinase, C-terminal domain |
| 67 | d1bxda_ | Alignment | not modelled | 96.0 | 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 |
| 68 | c3a0tA_ | Alignment | not modelled | 95.8 | 23 | **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) |
| 69 | d2c2aa2 | Alignment | not modelled | 95.8 | 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:**Histidine kinase |
| 70 | c2ch4A_ | Alignment | not modelled | 95.7 | 32 | **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 |
| 71 | c3jz3B_ | Alignment | not modelled | 95.2 | 36 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**sensor protein qsec;<br>**PDBTitle:** structure of the cytoplasmic segment of histidine kinase qsec |
| 72 | d1ysra1 | Alignment | not modelled | 95.0 | 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 |
| 73 | c3ehgA_ | Alignment | not modelled | 94.4 | 24 | **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 |
| 74 | d1id0a_ | Alignment | not modelled | 94.3 | 31 | **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 |
| | | | | | | **PDB header:**unknown function |

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| 75 | c3ke6A_ | Alignment | not modelled | 92.4 | 28 | **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410;<br>**PDBTitle:** the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis |
| 76 | d1i58a_ | Alignment | not modelled | 90.5 | 34 | **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 |
| 77 | d1ixma_ | Alignment | not modelled | 89.8 | 9 | **Fold:**Sporulation response regulatory protein Spo0B<br>**Superfamily:**Sporulation response regulatory protein Spo0B<br>**Family:**Sporulation response regulatory protein Spo0B |
| 78 | c3gieA_ | Alignment | not modelled | 86.7 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor histidine kinase desk;<br>**PDBTitle:** crystal structure of deskc_h188e in complex with amp-pcp |
| 79 | c3zxqA_ | Alignment | not modelled | 85.1 | 32 | **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 |
| 80 | c3zxoB_ | Alignment | not modelled | 80.6 | 39 | **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 |
| 81 | d1vdda_ | Alignment | not modelled | 77.4 | 18 | **Fold:**Recombination protein RecR<br>**Superfamily:**Recombination protein RecR<br>**Family:**Recombination protein RecR |
| 82 | c3ssoE_ | Alignment | not modelled | 64.3 | 38 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2 |
| 83 | d2fcja1 | Alignment | not modelled | 52.7 | 20 | **Fold:**Toprim domain<br>**Superfamily:**Toprim domain<br>**Family:**Toprim domain |
| 84 | c1vddC_ | Alignment | not modelled | 51.4 | 20 | **PDB header:**recombination<br>**Chain:** C: **PDB Molecule:**recombination protein recr;<br>**PDBTitle:** crystal structure of recombinational repair protein recr |
| 85 | d2hkja2 | Alignment | not modelled | 47.8 | 15 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**DNA gyrase/MutL, second domain |
| 86 | c3dmaA_ | Alignment | not modelled | 45.4 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein;<br>**PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192 |
| 87 | c3ggqA_ | Alignment | not modelled | 45.1 | 46 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**capsid protein;<br>**PDBTitle:** dimerization of hepatitis e virus capsid protein e2s domain is2 essential for virus-host interaction |
| 88 | c1yo8A_ | Alignment | not modelled | 40.4 | 32 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**thrombospondin-2;<br>**PDBTitle:** structure of the c-terminal domain of human thrombospondin-2 |
| 89 | d1mw9x_ | Alignment | not modelled | 39.7 | 27 | **Fold:**Prokaryotic type I DNA topoisomerase<br>**Superfamily:**Prokaryotic type I DNA topoisomerase<br>**Family:**Prokaryotic type I DNA topoisomerase |
| 90 | d1wvha1 | Alignment | not modelled | 38.8 | 18 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Phosphotyrosine-binding domain (PTB) |
| 91 | d1ecwa_ | Alignment | not modelled | 34.6 | 42 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**Immunodeficiency virus matrix proteins |
| 92 | d1hiwa_ | Alignment | not modelled | 34.5 | 42 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**Immunodeficiency virus matrix proteins |
| 93 | c3devB_ | Alignment | not modelled | 34.3 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**sh1221;<br>**PDBTitle:** crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87 |
| 94 | d2gola1 | Alignment | not modelled | 34.1 | 42 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**Immunodeficiency virus matrix proteins |
| 95 | d1l6na1 | Alignment | not modelled | 32.0 | 42 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**Immunodeficiency virus matrix proteins |
| 96 | d2dkqa1 | Alignment | not modelled | 32.0 | 18 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Phosphotyrosine-binding domain (PTB) |
| 97 | d1tama_ | Alignment | not modelled | 30.5 | 29 | **Fold:**Retroviral matrix proteins<br>**Superfamily:**Retroviral matrix proteins<br>**Family:**Immunodeficiency virus matrix proteins |
| 98 | c2gajA_ | Alignment | not modelled | 27.6 | 23 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**dna topoisomerase i;<br>**PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form |
| 99 | d1ddma_ | Alignment | not modelled | 26.4 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Phosphotyrosine-binding domain (PTB) |
| 100 | d1ux6a1 | Alignment | not modelled | 26.2 | 35 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Thrombospondin C-terminal domain |

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|---|---|---|---|---|---|---|
| 101 | c1ux6A_ | Alignment | not modelled | 26.1 | 35 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**thrombospondin-1;<br>**PDBTitle:** structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats |
| 102 | d1i7da_ | Alignment | not modelled | 25.6 | 20 | **Fold:**Prokaryotic type I DNA topoisomerase<br>**Superfamily:**Prokaryotic type I DNA topoisomerase<br>**Family:**Prokaryotic type I DNA topoisomerase |
| 103 | d1vkza1 | Alignment | not modelled | 25.4 | 23 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**BC C-terminal domain-like |
| 104 | c3bq9A_ | Alignment | not modelled | 25.1 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain-<br>**PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145 |
| 105 | d1gkub3 | Alignment | not modelled | 24.1 | 29 | **Fold:**Prokaryotic type I DNA topoisomerase<br>**Superfamily:**Prokaryotic type I DNA topoisomerase<br>**Family:**Prokaryotic type I DNA topoisomerase |
| 106 | c1ir6A_ | Alignment | not modelled | 23.9 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exonuclease recj;<br>**PDBTitle:** crystal structure of exonuclease recj bound to manganese |
| 107 | d1ir6a_ | Alignment | not modelled | 23.9 | 24 | **Fold:**DHH phosphoesterases<br>**Superfamily:**DHH phosphoesterases<br>**Family:**Exonuclease RecJ |
| 108 | c2ccaA_ | Alignment | not modelled | 23.7 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**peroxidase/catalase t;<br>**PDBTitle:** crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis |
| 109 | d1h72c1 | Alignment | not modelled | 23.6 | 18 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**GHMP Kinase, N-terminal domain |
| 110 | c3fbyC_ | Alignment | not modelled | 22.7 | 26 | **PDB header:**cell adhesion<br>**Chain:** C: **PDB Molecule:**cartilage oligomeric matrix protein;<br>**PDBTitle:** the crystal structure of the signature domain of cartilage oligomeric2 matrix protein. |
| 111 | c2o59B_ | Alignment | not modelled | 22.3 | 21 | **PDB header:**isomerase/dna<br>**Chain:** B: **PDB Molecule:**dna topoisomerase 3;<br>**PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0 |
| 112 | d1jmca1 | Alignment | not modelled | 22.1 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 113 | d1wj1a_ | Alignment | not modelled | 21.2 | 18 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Phosphotyrosine-binding domain (PTB) |
| 114 | d2idba2 | Alignment | not modelled | 21.0 | 21 | **Fold:**UbiD C-terminal domain-like<br>**Superfamily:**UbiD C-terminal domain-like<br>**Family:**UbiD C-terminal domain-like |
| 115 | d1nuia1 | Alignment | not modelled | 20.6 | 22 | **Fold:**DNA primase core<br>**Superfamily:**DNA primase core<br>**Family:**Primase fragment of primase-helicase protein |
| 116 | c1zc1A_ | Alignment | not modelled | 20.4 | 23 | **PDB header:**protein turnover<br>**Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1;<br>**PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites |