# Phyre²

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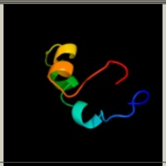
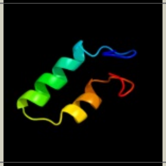
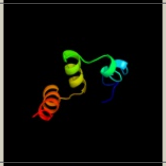
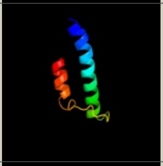
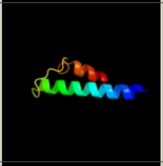
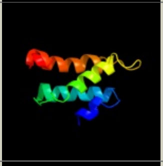
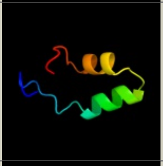
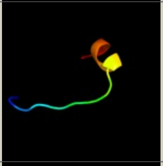
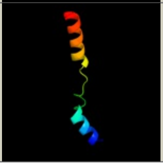
| Email | l.a.kelley@imperial.ac.uk |
| Description | P23840 |
| Date | Thu Jan 5 11:39:46 GMT 2012 |
| Unique Job ID | 5793eb893a5cb6aa |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2pmzN_ | Alignment |  | 33.6 | 31 | **PDB header:**translation, transferase<br>**Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 2 | d1ef4a_ | Alignment |  | 26.8 | 33 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**RNA polymerase subunit RPB10<br>**Family:**RNA polymerase subunit RPB10 |
| 3 | c3f6wE_ | Alignment |  | 26.3 | 13 | **PDB header:**dna binding protein<br>**Chain:** E: **PDB Molecule:**xre-family like protein;<br>**PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000 |
| 4 | d2qkwa1 | Alignment |  | 21.4 | 17 | **Fold:**immunoglobulin/albumin-binding domain-like<br>**Superfamily:**Avirulence protein AvrPto<br>**Family:**Avirulence protein AvrPto |
| 5 | c2qkwA_ | Alignment |  | 21.4 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**avirulence protein;<br>**PDBTitle:** structural basis for activation of plant immunity by2 bacterial effector protein avrpto |
| 6 | d1qi9a_ | Alignment |  | 17.1 | 23 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 7 | d1gw5b_ | Alignment |  | 17.1 | 16 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**ARM repeat<br>**Family:**Clathrin adaptor core protein |
| 8 | c2zopA_ | Alignment |  | 15.8 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb164;<br>**PDBTitle:** x-ray crystal structure of a crispr-associated cmr5 family2 protein from thermus thermophilus hb8 |
| 9 | d1twfj_ | Alignment |  | 15.7 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**RNA polymerase subunit RPB10<br>**Family:**RNA polymerase subunit RPB10 |
| 10 | d2bosa_ | Alignment |  | 13.5 | 47 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Bacterial AB5 toxins, B-subunits |
| 11 | c1m5iA_ | Alignment |  | 13.4 | 24 | **PDB header:**antitumor protein<br>**Chain:** A: **PDB Molecule:**apc protein;<br>**PDBTitle:** crystal structure of the coiled coil region 129-250 of the2 tumor suppressor gene product apc |

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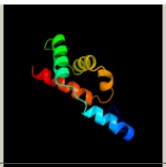
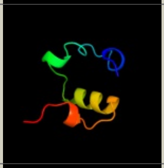
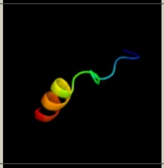
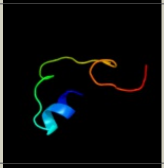
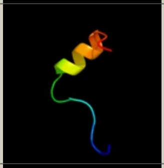
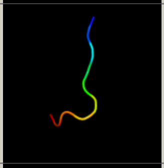
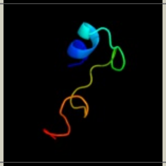
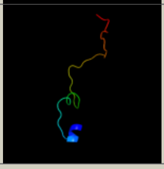
|---|---|---|---|---|---|---|
| 12 | c3ol4B_ | Alignment |  | 13.1 | 21 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c |
| 13 | c3omtA_ | Alignment |  | 13.0 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae. |
| 14 | d1qhba_ | Alignment |  | 12.7 | 21 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 15 | c3k2hA_ | Alignment |  | 11.9 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dihydrofolate reductase/thymidylate synthase;<br>**PDBTitle:** co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp |
| 16 | d1utxa_ | Alignment |  | 11.7 | 23 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 17 | d1up8a_ | Alignment |  | 11.7 | 19 | **Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase<br>**Family:**Haloperoxidase (bromoperoxidase) |
| 18 | c3fm8A_ | Alignment |  | 11.2 | 60 | **PDB header:**transport protein/hydrolase activator<br>**Chain:** A: **PDB Molecule:**kinesin-like protein kif13b;<br>**PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target) |
| 19 | c3jsuA_ | Alignment |  | 11.0 | 28 | **PDB header:**oxidoreductase, transferase<br>**Chain:** A: **PDB Molecule:**dihydrofolate reductase-thymidylate synthase;<br>**PDBTitle:** quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump |
| 20 | c2dunA_ | Alignment |  | 10.7 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase mu;<br>**PDBTitle:** solution structure of brct domain of dna polymerase mu |
| 21 | d2coba1 | Alignment | not modelled | 10.0 | 9 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Psq domain |
| 22 | d1biaa1 | Alignment | not modelled | 9.7 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Biotin repressor-like |
| 23 | c2of3A_ | Alignment | not modelled | 9.4 | 10 | **PDB header:**structural protein, cell cycle<br>**Chain:** A: **PDB Molecule:**zyg-9;<br>**PDBTitle:** tog domain structure from c.elegans zyg9 |
| 24 | d1r4pb_ | Alignment | not modelled | 9.2 | 47 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Bacterial AB5 toxins, B-subunits |
| 25 | c1yn3A_ | Alignment | not modelled | 9.1 | 19 | **PDB header:**toxin, protein binding<br>**Chain:** A: **PDB Molecule:**truncated cell surface protein map-w;<br>**PDBTitle:** crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens |
| 26 | c2kygC_ | Alignment | not modelled | 9.0 | 19 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**protein cbfa2t1;<br>**PDBTitle:** structure of the aml1-eto nervy domain - pka(riia) complex and its2 contribution to aml1-eto activity |
| 27 | d2dk5a1 | Alignment | not modelled | 8.7 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**RPO3F domain-like |
| 28 | d1mhyd_ | Alignment | not modelled | 8.6 | 14 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**Ribonucleotide reductase-like |
| 29 | d1ktba2 | Alignment | not modelled | 8.5 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases |

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|  |  |  |  |  |  | **Family:**Amylase, catalytic domain |
| 30 | c1yn5B_ | Alignment | not modelled | 8.2 | 28 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**eaph2;<br>**PDBTitle:** crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens |
| 31 | c2jspA_ | Alignment | not modelled | 8.2 | 5 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein ros;<br>**PDBTitle:** the prokaryotic cys2his2 zinc finger adopts a novel fold as2 revealed by the nmr structure of a. tumefaciens ros dna3 binding domain |
| 32 | c1yn4A_ | Alignment | not modelled | 8.2 | 20 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**eaph1;<br>**PDBTitle:** crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens |
| 33 | c2yu3A_ | Alignment | not modelled | 7.5 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii 39 kda<br>**PDBTitle:** solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide |
| 34 | c3clbA_ | Alignment | not modelled | 7.3 | 34 | **PDB header:**oxidoreductase, transferase<br>**Chain:** A: **PDB Molecule:**dhfr-ts;<br>**PDBTitle:** structure of bifunctional tcdhfr-ts in complex with tmq |
| 35 | c2ewtA_ | Alignment | not modelled | 7.1 | 16 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative dna-binding protein;<br>**PDBTitle:** crystal structure of the dna-binding domain of bldd |
| 36 | c3e7lD_ | Alignment | not modelled | 6.6 | 20 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family);<br>**PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain |
| 37 | c3mklB_ | Alignment | not modelled | 6.6 | 14 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx;<br>**PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12 |
| 38 | c2yujA_ | Alignment | not modelled | 6.6 | 19 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like;<br>**PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1 |
| 39 | c2k1gA_ | Alignment | not modelled | 6.6 | 13 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**lipoprotein spr;<br>**PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162 |
| 40 | c3q9dB_ | Alignment | not modelled | 6.3 | 32 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**protein cpn_0803/cp_1068/cpj0803/cpb0832;<br>**PDBTitle:** crystal structure of cpn0803 from c. pneumoniae. |
| 41 | d1c4qa_ | Alignment | not modelled | 6.1 | 33 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Bacterial AB5 toxins, B-subunits |
| 42 | d2ixna1 | Alignment | not modelled | 5.7 | 22 | **Fold:**PTPA-like<br>**Superfamily:**PTPA-like<br>**Family:**PTPA-like |
| 43 | d2huha1 | Alignment | not modelled | 5.5 | 38 | **Fold:**C2 domain-like<br>**Superfamily:**Smr-associated domain-like<br>**Family:**Smr-associated domain |
| 44 | d2nrac2 | Alignment | not modelled | 5.4 | 35 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Replication initiation protein |
| 45 | d1tkna_ | Alignment | not modelled | 5.4 | 19 | **Fold:**STAT-like<br>**Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein<br>**Family:**CAPPD, an extracellular domain of amyloid beta A4 protein |
| 46 | c2nogA_ | Alignment | not modelled | 5.4 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**iswi protein;<br>**PDBTitle:** sant domain structure of xenopus remodeling factor iswi |
| 47 | c1ktbA_ | Alignment | not modelled | 5.2 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase;<br>**PDBTitle:** the structure of alpha-n-acetylgalactosaminidase |
| 48 | c1w9zB_ | Alignment | not modelled | 5.2 | 45 | **PDB header:**virus coat protein<br>**Chain:** B: **PDB Molecule:**vp9;<br>**PDBTitle:** structure of bannavirus vp9 |
| 49 | c2zb9A_ | Alignment | not modelled | 5.2 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of tetr family transcription regulator2 sco0332 |
| 50 | c2qw6A_ | Alignment | not modelled | 5.2 | 26 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aaa atpase, central region;<br>**PDBTitle:** crystal structure of the c-terminal domain of an aaa atpase from2 enterococcus faecium do |
| 51 | d2qw6a1 | Alignment | not modelled | 5.2 | 26 | **Fold:**post-AAA+ oligomerization domain-like<br>**Superfamily:**post-AAA+ oligomerization domain-like<br>**Family:**MgsA/YrvN C-terminal domain-like |
| 52 | d1sr9a3 | Alignment | not modelled | 5.1 | 13 | **Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain<br>**Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain<br>**Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain |