# Phyre$^2$

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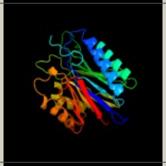
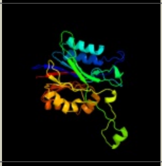
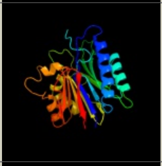
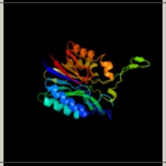
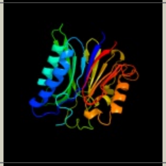
| Email | l.a.kelley@imperial.ac.uk |
| Description | P23930 |
| Date | Thu Jan 5 11:40:39 GMT 2012 |
| Unique Job ID | 3a98b0592725910e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1uf5a_ | Alignment |  | 100.0 | 18 | **Fold:**Carbon-nitrogen hydrolase<br>**Superfamily:**Carbon-nitrogen hydrolase<br>**Family:**Carbamilase |
| 2 | c2plqA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aliphatic amidase;<br>**PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8 |
| 3 | c2vhiG_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**cg3027-pa;<br>**PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster |
| 4 | c1emsB_ | Alignment |  | 100.0 | 17 | **PDB header:**antitumor protein<br>**Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein;<br>**PDBTitle:** crystal structure of the c. elegans nitfhit protein |
| 5 | c2e2kC_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**formamidase;<br>**PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad |
| 6 | c2w1vA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nitrilase homolog 2;<br>**PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution |
| 7 | d1emsa2 | Alignment |  | 100.0 | 17 | **Fold:**Carbon-nitrogen hydrolase<br>**Superfamily:**Carbon-nitrogen hydrolase<br>**Family:**Nitrilase |
| 8 | c3hkxA_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidase;<br>**PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp. |
| 9 | d1f89a_ | Alignment |  | 100.0 | 22 | **Fold:**Carbon-nitrogen hydrolase<br>**Superfamily:**Carbon-nitrogen hydrolase<br>**Family:**Nitrilase |
| 10 | c2e11B_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hydrolase;<br>**PDBTitle:** the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site |
| 11 | d1j31a_ | Alignment |  | 100.0 | 17 | **Fold:**Carbon-nitrogen hydrolase<br>**Superfamily:**Carbon-nitrogen hydrolase<br>**Family:**Carbamilase |

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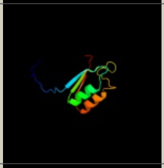
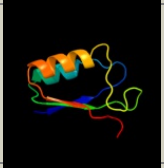
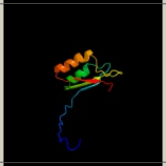
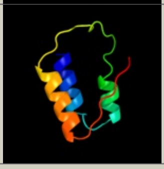
| 12 | c3n05B_ | Alignment |  | 100.0 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis |
| 13 | c3dlaD_ | Alignment |  | 100.0 | 17 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase;<br>**PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don |
| 14 | c3ilvA_ | Alignment |  | 100.0 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase;<br>**PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii |
| 15 | d1sgva1 | Alignment |  | 74.4 | 19 | **Fold:**PUA domain-like<br>**Superfamily:**PUA domain-like<br>**Family:**PUA domain |
| 16 | d4pgaa_ | Alignment |  | 58.7 | 13 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 17 | d1zq1a2 | Alignment |  | 47.0 | 12 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 18 | c2wltA_ | Alignment |  | 45.4 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**l-asparaginase;<br>**PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution |
| 19 | d2d6fa2 | Alignment |  | 43.1 | 10 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 20 | c1xf1A_ | Alignment |  | 42.3 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**c5a peptidase;<br>**PDBTitle:** structure of c5a peptidase- a key virulence factor from2 streptococcus |
| 21 | d1o7ja_ | Alignment | not modelled | 40.0 | 16 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 22 | c1zq1B_ | Alignment | not modelled | 39.9 | 13 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d;<br>**PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi |
| 23 | d3dhwc1 | Alignment | not modelled | 38.7 | 12 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 24 | d1nnsa_ | Alignment | not modelled | 36.4 | 11 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 25 | d2ocda1 | Alignment | not modelled | 32.3 | 16 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 26 | c2d6fA_ | Alignment | not modelled | 29.9 | 10 | **PDB header:**ligase/rna<br>**Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d;<br>**PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln) |
| 27 | d1agxa_ | Alignment | not modelled | 29.8 | 10 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 28 | c3qjaA_ | Alignment | not modelled | 28.3 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase;<br>**PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form |

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| 29 | c1wnfA_ | Alignment | not modelled | 26.8 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**l-asparaginase;<br>**PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii |
| 30 | c3cwcB_ | Alignment | not modelled | 26.6 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**putative glycerate kinase 2;<br>**PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2 |
| 31 | d1vc4a_ | Alignment | not modelled | 24.3 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 32 | c3k2qA_ | Alignment | not modelled | 22.7 | 34 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase;<br>**PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88 |
| 33 | c3gfoA_ | Alignment | not modelled | 22.2 | 14 | **PDB header:**atp binding protein<br>**Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1;<br>**PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq. |
| 34 | c2nydB_ | Alignment | not modelled | 22.0 | 7 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**upf0135 protein sa1388;<br>**PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388 |
| 35 | d1wsaa_ | Alignment | not modelled | 21.0 | 15 | **Fold:**Glutaminase/Asparaginase<br>**Superfamily:**Glutaminase/Asparaginase<br>**Family:**Glutaminase/Asparaginase |
| 36 | c2higA_ | Alignment | not modelled | 20.4 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase;<br>**PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei. |
| 37 | d2axto1 | Alignment | not modelled | 19.9 | 14 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**PsbO-like |
| 38 | c2x24B_ | Alignment | not modelled | 19.4 | 29 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**acetyl-coa carboxylase;<br>**PDBTitle:** bovine acc2 ct domain in complex with inhibitor |
| 39 | c3o3cD_ | Alignment | not modelled | 19.4 | 12 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2;<br>**PDBTitle:** glycogen synthase basal state udp complex |
| 40 | d1g2912 | Alignment | not modelled | 18.3 | 10 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 41 | d1js3a_ | Alignment | not modelled | 18.2 | 9 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Pyridoxal-dependent decarboxylase |
| 42 | c1pixB_ | Alignment | not modelled | 16.6 | 21 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glutaconyl-coa decarboxylase a subunit;<br>**PDBTitle:** crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase |
| 43 | d1jj7a_ | Alignment | not modelled | 16.6 | 12 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 44 | d3d31a2 | Alignment | not modelled | 15.4 | 10 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 45 | c3n6rF_ | Alignment | not modelled | 15.2 | 20 | **PDB header:**ligase<br>**Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit;<br>**PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) |
| 46 | c2yvaB_ | Alignment | not modelled | 14.9 | 19 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa;<br>**PDBTitle:** crystal structure of escherichia coli diaa |
| 47 | d1v43a3 | Alignment | not modelled | 14.6 | 2 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 48 | c3o8oC_ | Alignment | not modelled | 14.3 | 10 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha;<br>**PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae |
| 49 | d1oxxk2 | Alignment | not modelled | 14.0 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 50 | c3glmD_ | Alignment | not modelled | 14.0 | 19 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**glutaconyl-coa decarboxylase subunit a;<br>**PDBTitle:** glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa |
| 51 | c1f0xA_ | Alignment | not modelled | 13.9 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**d-lactate dehydrogenase;<br>**PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme. |
| 52 | d1pfka_ | Alignment | not modelled | 13.9 | 9 | **Fold:**Phosphofructokinase<br>**Superfamily:**Phosphofructokinase<br>**Family:**Phosphofructokinase |
| 53 | d1uyra1 | Alignment | not modelled | 13.8 | 21 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 54 | c1vrgE_ | Alignment | not modelled | 13.4 | 22 | **PDB header:**ligase<br>**Chain:** E: **PDB Molecule:**propionyl-coa carboxylase, beta subunit;<br>**PDBTitle:** crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution |

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| 55 | d2zcta1 | Alignment | not modelled | 13.1 | 14 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Glutathione peroxidase-like |
| 56 | d1i4na_ | Alignment | not modelled | 13.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 57 | c2f9yB_ | Alignment | not modelled | 12.8 | 27 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit<br>**PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli |
| 58 | d2f9yb1 | Alignment | not modelled | 12.8 | 27 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 59 | d1sffa_ | Alignment | not modelled | 12.5 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 60 | c1x0uB_ | Alignment | not modelled | 12.2 | 22 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit;<br>**PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii |
| 61 | c3eurA_ | Alignment | not modelled | 12.0 | 0 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343 |
| 62 | d2acfa1 | Alignment | not modelled | 11.8 | 10 | **Fold:**Macro domain-like<br>**Superfamily:**Macro domain-like<br>**Family:**Macro domain |
| 63 | c1drwA_ | Alignment | not modelled | 11.8 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase;<br>**PDBTitle:** escherichia coli dhpr/nhdh complex |
| 64 | c3ogfA_ | Alignment | not modelled | 11.6 | 22 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which<br>**PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly |
| 65 | c3u9rB_ | Alignment | not modelled | 11.6 | 26 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**methylcrotonyl-coa carboxylase, beta-subunit;<br>**PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit |
| 66 | d4pfka_ | Alignment | not modelled | 11.5 | 20 | **Fold:**Phosphofructokinase<br>**Superfamily:**Phosphofructokinase<br>**Family:**Phosphofructokinase |
| 67 | c1xnwD_ | Alignment | not modelled | 11.5 | 24 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**propionyl-coa carboxylase complex b subunit;<br>**PDBTitle:** acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i |
| 68 | c3trjC_ | Alignment | not modelled | 11.4 | 20 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**phosphoheptose isomerase;<br>**PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis |
| 69 | d1l2ta_ | Alignment | not modelled | 11.3 | 10 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 70 | d1vrga1 | Alignment | not modelled | 11.1 | 22 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 71 | c2a7sD_ | Alignment | not modelled | 11.1 | 27 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**probable propionyl-coa carboxylase beta chain 5;<br>**PDBTitle:** crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis |
| 72 | c2yyzA_ | Alignment | not modelled | 10.9 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein;<br>**PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein |
| 73 | c1od4C_ | Alignment | not modelled | 10.7 | 21 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase;<br>**PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain |
| 74 | c3fvqB_ | Alignment | not modelled | 10.4 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc;<br>**PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp |
| 75 | d1xnya1 | Alignment | not modelled | 10.3 | 24 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 76 | c3ewlA_ | Alignment | not modelled | 10.3 | 0 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized conserved protein bf1870;<br>**PDBTitle:** crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis |
| 77 | c2nq2C_ | Alignment | not modelled | 10.2 | 16 | **PDB header:**metal transport<br>**Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein<br>**PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter. |
| 78 | c1z47B | Alignment | not modelled | 10.2 | 7 | **PDB header:**ligand binding protein<br>**Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; |

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| 78 | c1z47B_ | Alignment | not modelled | 10.2 | 7 | **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius |
| 79 | d1nmpa_ | Alignment | not modelled | 10.0 | 12 | **Fold:**NIF3 (NGG1p interacting factor 3)-like<br>**Superfamily:**NIF3 (NGG1p interacting factor 3)-like<br>**Family:**NIF3 (NGG1p interacting factor 3)-like |
| 80 | d1on3a1 | Alignment | not modelled | 10.0 | 29 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 81 | c2d62A_ | Alignment | not modelled | 9.9 | 9 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding<br>**PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein |
| 82 | c3d34A_ | Alignment | not modelled | 9.8 | 44 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**spondin-2;<br>**PDBTitle:** structure of the f-spondin domain of mindin |
| 83 | c3opyH_ | Alignment | not modelled | 9.2 | 20 | **PDB header:**transferase<br>**Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit;<br>**PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 84 | c3opyB_ | Alignment | not modelled | 9.2 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit;<br>**PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 85 | d1sgwa_ | Alignment | not modelled | 9.0 | 14 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 86 | d2b7ka1 | Alignment | not modelled | 9.0 | 9 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Glutathione peroxidase-like |
| 87 | c1m56G_ | Alignment | not modelled | 8.8 | 7 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**cytochrome c oxidase;<br>**PDBTitle:** structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type) |
| 88 | c3dhwC_ | Alignment | not modelled | 8.8 | 14 | **PDB header:**membrane protein/hydrolase<br>**Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn;<br>**PDBTitle:** crystal structure of methionine importer metni |
| 89 | c1uytC_ | Alignment | not modelled | 8.7 | 21 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**acetyl-coa carboxylase;<br>**PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain |
| 90 | c1piiA_ | Alignment | not modelled | 8.5 | 10 | **PDB header:**bifunctional(isomerase and synthase)<br>**Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase;<br>**PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution |
| 91 | c3h0jA_ | Alignment | not modelled | 8.5 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetyl-coa carboxylase;<br>**PDBTitle:** crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2 |
| 92 | c3opyG_ | Alignment | not modelled | 8.3 | 10 | **PDB header:**transferase<br>**Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit;<br>**PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 93 | d1ohwa_ | Alignment | not modelled | 8.3 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 94 | c3ff6D_ | Alignment | not modelled | 8.3 | 26 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2;<br>**PDBTitle:** human acc2 ct domain with cp-640186 |
| 95 | d1xrsa_ | Alignment | not modelled | 8.1 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Cobalamin (vitamin B12)-dependent enzymes<br>**Family:**D-lysine 5,6-aminomutase alpha subunit, KamD |
| 96 | d2awna2 | Alignment | not modelled | 8.0 | 10 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**ABC transporter ATPase domain-like |
| 97 | c2p31B_ | Alignment | not modelled | 8.0 | 11 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glutathione peroxidase 7;<br>**PDBTitle:** crystal structure of human glutathione peroxidase 7 |
| 98 | c2it1B_ | Alignment | not modelled | 8.0 | 10 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin<br>**PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii |
| 99 | d1prxa_ | Alignment | not modelled | 7.8 | 23 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Glutathione peroxidase-like |