Phyre$^2$

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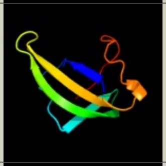
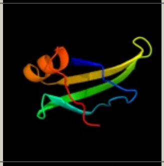
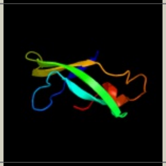
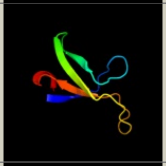
| Description | P76272 |
| Date | Thu Jan 5 12:21:28 GMT 2012 |
| Unique Job ID | a224dc802c7002a2 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1pj5a1 | Alignment |  | 93.3 | 16 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**Aminomethyltransferase beta-barrel domain<br>**Family:**Aminomethyltransferase beta-barrel domain |
| 2 | d1v5va1 | Alignment |  | 91.2 | 22 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**Aminomethyltransferase beta-barrel domain<br>**Family:**Aminomethyltransferase beta-barrel domain |
| 3 | c2j5uB_ | Alignment |  | 90.8 | 20 | **PDB header:**cell shape regulation<br>**Chain:** B: **PDB Molecule:**mrec protein;<br>**PDBTitle:** mrec lysteria monocytogenes |
| 4 | d1wosa1 | Alignment |  | 88.2 | 15 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**Aminomethyltransferase beta-barrel domain<br>**Family:**Aminomethyltransferase beta-barrel domain |
| 5 | c1v5vA_ | Alignment |  | 88.1 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution |
| 6 | d1vloa1 | Alignment |  | 78.9 | 20 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**Aminomethyltransferase beta-barrel domain<br>**Family:**Aminomethyltransferase beta-barrel domain |
| 7 | c1yx2B_ | Alignment |  | 76.7 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of the probable aminomethyltransferase2 from bacillus subtilis |
| 8 | c1worA_ | Alignment |  | 70.4 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system |
| 9 | c2qf4A_ | Alignment |  | 65.5 | 15 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**cell shape determining protein mrec;<br>**PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form) |
| 10 | c3girA_ | Alignment |  | 60.8 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae |
| 11 | c3tfhB_ | Alignment |  | 59.5 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**gcvt-like aminomethyltransferase protein;<br>**PDBTitle:** dmsp-dependent demethylase from p. ubique - apo |

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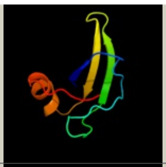
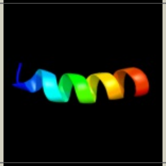
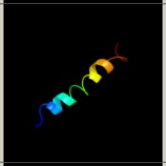
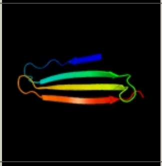
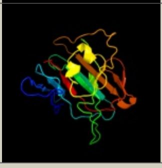
|---|---|---|---|---|---|---|
| 12 | c1wsrA_ | Alignment |  | 58.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of human t-protein of glycine cleavage2 system |
| 13 | d1c99a_ | Alignment |  | 47.9 | 17 | **Fold:**Transmembrane helix hairpin<br>**Superfamily:**F1F0 ATP synthase subunit C<br>**Family:**F1F0 ATP synthase subunit C |
| 14 | c1pj6A_ | Alignment |  | 46.5 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase;<br>**PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid |
| 15 | d1fftb2 | Alignment |  | 36.9 | 15 | **Fold:**Transmembrane helix hairpin<br>**Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region<br>**Family:**Cytochrome c oxidase subunit II-like, transmembrane region |
| 16 | c1txkA_ | Alignment |  | 35.2 | 25 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**glucans biosynthesis protein g;<br>**PDBTitle:** crystal structure of escherichia coli opgg |
| 17 | d1jz8a3 | Alignment |  | 33.6 | 17 | **Fold:**Galactose-binding domain-like<br>**Superfamily:**Galactose-binding domain-like<br>**Family:**beta-Galactosidase/glucuronidase, N-terminal domain |
| 18 | d1txka2 | Alignment |  | 33.2 | 23 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**MdoG-like |
| 19 | c1vloA_ | Alignment |  | 32.2 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aminomethyltransferase;<br>**PDBTitle:** crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution |
| 20 | c1yo8A_ | Alignment |  | 27.1 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**thrombospondin-2;<br>**PDBTitle:** structure of the c-terminal domain of human thrombospondin-2 |
| 21 | c3o0lB_ | Alignment | not modelled | 26.7 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution |
| 22 | d1yq2a3 | Alignment | not modelled | 26.1 | 13 | **Fold:**Galactose-binding domain-like<br>**Superfamily:**Galactose-binding domain-like<br>**Family:**beta-Galactosidase/glucuronidase, N-terminal domain |
| 23 | c1kqsA_ | Alignment | not modelled | 24.8 | 23 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**ribosomal protein l2;<br>**PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis |
| 24 | c3cb0B_ | Alignment | not modelled | 24.5 | 15 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**4-hydroxyphenylacetate 3-monooxygenase;<br>**PDBTitle:** cobr |
| 25 | c1vlyA_ | Alignment | not modelled | 24.2 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**unknown protein from 2d-page;<br>**PDBTitle:** crystal structure of a putative aminomethyltransferase (ygfz) from2 escherichia coli at 1.30 a resolution |
| 26 | d1wgba_ | Alignment | not modelled | 22.2 | 15 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**NADH:FMN oxidoreductase-like |
| 27 | d1kkga_ | Alignment | not modelled | 19.9 | 38 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Ribosome-binding factor A, RbfA<br>**Family:**Ribosome-binding factor A, RbfA |
| 28 | c2c1lA_ | Alignment | not modelled | 18.8 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**restriction endonuclease;<br>**PDBTitle:** structure of the bfii restriction endonuclease |
| | | | | | | **Fold:**Alpha-lytic protease prodomain-like |

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| 29 | d1pa4a_ | Alignment | not modelled | 18.2 | 44 | **Superfamily:**Ribosome-binding factor A, RbfA<br>**Family:**Ribosome-binding factor A, RbfA |
| 30 | c2kzfA_ | Alignment | not modelled | 18.1 | 38 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**ribosome-binding factor a;<br>**PDBTitle:** solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a |
| 31 | c2r6vA_ | Alignment | not modelled | 18.0 | 15 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ph0856;<br>**PDBTitle:** crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution |
| 32 | c2r39A_ | Alignment | not modelled | 17.2 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**fixg-related protein;<br>**PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus |
| 33 | c2r0xA_ | Alignment | not modelled | 16.9 | 10 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**possible flavin reductase;<br>**PDBTitle:** crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution |
| 34 | d2dyja1 | Alignment | not modelled | 16.6 | 34 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Ribosome-binding factor A, RbfA<br>**Family:**Ribosome-binding factor A, RbfA |
| 35 | d1bhua_ | Alignment | not modelled | 15.8 | 20 | **Fold:**gamma-Crystallin-like<br>**Superfamily:**gamma-Crystallin-like<br>**Family:**Streptomyces metalloproteinase inhibitor, SMPI |
| 36 | d1v58a2 | Alignment | not modelled | 15.2 | 21 | **Fold:**Cystatin-like<br>**Superfamily:**DsbC/DsbG N-terminal domain-like<br>**Family:**DsbC/DsbG N-terminal domain-like |
| 37 | c3fljA_ | Alignment | not modelled | 14.8 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a<br>**PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution |
| 38 | c1w2tE_ | Alignment | not modelled | 14.4 | 10 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**beta fructosidase;<br>**PDBTitle:** beta-fructosidase from thermotoga maritima in complex with2 raffinose |
| 39 | c2kebA_ | Alignment | not modelled | 14.4 | 11 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b;<br>**PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit |
| 40 | c2zjbB_ | Alignment | not modelled | 13.3 | 35 | **PDB header:**recombination<br>**Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog;<br>**PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant |
| 41 | d1josa_ | Alignment | not modelled | 12.4 | 35 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Ribosome-binding factor A, RbfA<br>**Family:**Ribosome-binding factor A, RbfA |
| 42 | c3o5aB_ | Alignment | not modelled | 12.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**diheme cytochrome c napb;<br>**PDBTitle:** crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids |
| 43 | c2p0yA_ | Alignment | not modelled | 12.1 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein lp_0780;<br>**PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6 |
| 44 | c2d38A_ | Alignment | not modelled | 11.8 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical nadh-dependent fmn oxidoreductase;<br>**PDBTitle:** the crystal structure of flavin reductase hpac complexed with nadp+ |
| 45 | d1whva_ | Alignment | not modelled | 11.6 | 30 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 46 | d1v5wa_ | Alignment | not modelled | 11.1 | 35 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 47 | c1pznG_ | Alignment | not modelled | 10.9 | 43 | **PDB header:**recombination<br>**Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51;<br>**PDBTitle:** rad51 (rada) |
| 48 | d1pzna2 | Alignment | not modelled | 10.6 | 43 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 49 | d2e7ga1 | Alignment | not modelled | 10.6 | 19 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Ribosome-binding factor A, RbfA<br>**Family:**Ribosome-binding factor A, RbfA |
| 50 | c2w0mA_ | Alignment | not modelled | 10.5 | 43 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**sso2452;<br>**PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2 |
| 51 | d1rz0a_ | Alignment | not modelled | 10.4 | 18 | **Fold:**Split barrel-like<br>**Superfamily:**FMN-binding split barrel<br>**Family:**NADH:FMN oxidoreductase-like |
| 52 | c3nmbA_ | Alignment | not modelled | 10.3 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative sugar hydrolase;<br>**PDBTitle:** crystal structure of a putative sugar hydrolase (bacova_03189) from2 bacteroides ovatus at 2.40 a resolution |
| 53 | d2axte1 | Alignment | not modelled | 9.8 | 30 | **Fold:**Single transmembrane helix<br>**Superfamily:**Cytochrome b559 subunits<br>**Family:**Cytochrome b559 subunits |
| 54 | c3hbkA_ | Alignment | not modelled | 9.7 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycosyl hydrolase;<br>**PDBTitle:** crystal structure of putative glycosyl hydrolase, was |

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| | | | | | | domain of2 unknown function (duf1080) (yp_001302580.1) from parabacteroides3 distasonis atcc 8503 at 2.36 a resolution |
| 55 | c3uaiA_ | Alignment | not modelled | 9.7 | 18 | **PDB header:**isomerase/chaperone<br>**Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4;<br>**PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae |
| 56 | c3izcN_ | Alignment | not modelled | 9.6 | 22 | **PDB header:**ribosome<br>**Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 57 | c2jqoA_ | Alignment | not modelled | 9.6 | 13 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**hypothetical protein yoba;<br>**PDBTitle:** nmr solution structure of bacillus subtilis yoba 21-120:2 northeast structural genomics consortium target sr547 |
| 58 | c1pkvB_ | Alignment | not modelled | 9.4 | 22 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain;<br>**PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin |
| 59 | c1pkvA_ | Alignment | not modelled | 9.4 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**riboflavin synthase alpha chain;<br>**PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin |
| 60 | c3h3lB_ | Alignment | not modelled | 9.2 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative sugar hydrolase;<br>**PDBTitle:** crystal structure of putative sugar hydrolase (yp_001304206.1) from2 parabacteroides distasonis atcc 8503 at 1.59 a resolution |
| 61 | d1mvqa_ | Alignment | not modelled | 9.1 | 23 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Legume lectins |
| 62 | d2evra1 | Alignment | not modelled | 8.6 | 25 | **Fold:**SH3-like barrel<br>**Superfamily:**Prokaryotic SH3-related domain<br>**Family:**Spr N-terminal domain-like |
| 63 | d1i8da1 | Alignment | not modelled | 8.6 | 22 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Riboflavin synthase |
| 64 | d2cp6a1 | Alignment | not modelled | 8.5 | 15 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 65 | d2i00a1 | Alignment | not modelled | 8.5 | 11 | **Fold:**SCP-like<br>**Superfamily:**SCP-like<br>**Family:**EF1021 C-terminal domain-like |
| 66 | d1h9wa_ | Alignment | not modelled | 8.4 | 20 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Legume lectins |
| 67 | d2i1qa2 | Alignment | not modelled | 8.3 | 39 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 68 | d2cu6a1 | Alignment | not modelled | 8.3 | 14 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Fe-S cluster assembly (FSCA) domain-like<br>**Family:**PaaD-like |
| 69 | d1zy9a1 | Alignment | not modelled | 8.3 | 43 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**YicI N-terminal domain-like |
| 70 | d1zq1a1 | Alignment | not modelled | 8.3 | 21 | **Fold:**Sm-like fold<br>**Superfamily:**GatD N-terminal domain-like<br>**Family:**GatD N-terminal domain-like |
| 71 | d2hv2a1 | Alignment | not modelled | 8.2 | 12 | **Fold:**SCP-like<br>**Superfamily:**SCP-like<br>**Family:**EF1021 C-terminal domain-like |
| 72 | c1icfB_ | Alignment | not modelled | 8.1 | 38 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein (cathepsin l: light chain);<br>**PDBTitle:** crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin l |
| 73 | d2pmaa1 | Alignment | not modelled | 8.0 | 16 | **Fold:**Acid proteases<br>**Superfamily:**Acid proteases<br>**Family:**LPG0085-like |
| 74 | d2cb2a1 | Alignment | not modelled | 7.9 | 25 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**SOR-like |
| 75 | c3k87B_ | Alignment | not modelled | 7.9 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**chlorophenol-4-monooxygenase component 1;<br>**PDBTitle:** crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex |
| 76 | c3u1xA_ | Alignment | not modelled | 7.8 | 27 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycosyl hydrolase;<br>**PDBTitle:** crystal structure of a putative glycosyl hydrolase (bdi_1869) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution |
| 77 | c3khsB_ | Alignment | not modelled | 7.8 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase;<br>**PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase |
| 78 | d1vm8a_ | Alignment | not modelled | 7.6 | 26 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**UDP-glucose pyrophosphorylase |
| 79 | c2z8nB_ | Alignment | not modelled | 7.6 | 25 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**27.5 kda virulence protein;<br>**PDBTitle:** structural basis for the catalytic mechanism of phosphothreonine lyase |

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|---|---|---|---|---|---|---|
| 80 | d2cnaa_ | Alignment | not modelled | 7.5 | 22 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Legume lectins |
| 81 | d1mzaa_ | Alignment | not modelled | 7.5 | 22 | **Fold:**Trypsin-like serine proteases<br>**Superfamily:**Trypsin-like serine proteases<br>**Family:**Eukaryotic proteases |
| 82 | d1tf7a2 | Alignment | not modelled | 7.5 | 43 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 83 | c2l66B_ | Alignment | not modelled | 7.4 | 17 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family;<br>**PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea. |
| 84 | c3nfgG_ | Alignment | not modelled | 7.4 | 10 | **PDB header:**transcription<br>**Chain:** G: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49;<br>**PDBTitle:** crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5 |
| 85 | d1g7sa1 | Alignment | not modelled | 7.3 | 16 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Translation proteins<br>**Family:**Elongation factors |
| 86 | d1o7ia_ | Alignment | not modelled | 7.3 | 23 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 87 | c1x31A_ | Alignment | not modelled | 7.3 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit;<br>**PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96 |
| 88 | c2v31A_ | Alignment | not modelled | 7.3 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1 x;<br>**PDBTitle:** structure of first catalytic cysteine half-domain of mouse2 ubiquitin-activating enzyme |
| 89 | d1eu3a1 | Alignment | not modelled | 7.2 | 19 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Superantigen toxins, N-terminal domain |
| 90 | d2uubq1 | Alignment | not modelled | 7.2 | 7 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 91 | c2xlfA_ | Alignment | not modelled | 7.2 | 12 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**sll1785 protein;<br>**PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet) |
| 92 | c2eqnA_ | Alignment | not modelled | 7.0 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**hypothetical protein loc92345;<br>**PDBTitle:** solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens] |
| 93 | c4a19F_ | Alignment | not modelled | 7.0 | 19 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**rpl14;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2. |
| 94 | c2kncA_ | Alignment | not modelled | 6.9 | 19 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 95 | c1jniA_ | Alignment | not modelled | 6.8 | 0 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**diheme cytochrome c napb;<br>**PDBTitle:** structure of the napb subunit of the periplasmic nitrate2 reductase from haemophilus influenzae. |
| 96 | d1jnia_ | Alignment | not modelled | 6.8 | 0 | **Fold:**Multiheme cytochromes<br>**Superfamily:**Multiheme cytochromes<br>**Family:**Di-heme elbow motif |
| 97 | c1cn3F_ | Alignment | not modelled | 6.8 | 43 | **PDB header:**viral protein<br>**Chain:** F: **PDB Molecule:**fragment of coat protein vp2;<br>**PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry |
| 98 | c2ztsB_ | Alignment | not modelled | 6.7 | 43 | **PDB header:**atp-binding protein<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186;<br>**PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3 |
| 99 | d1iaua_ | Alignment | not modelled | 6.7 | 14 | **Fold:**Trypsin-like serine proteases<br>**Superfamily:**Trypsin-like serine proteases<br>**Family:**Eukaryotic proteases |