
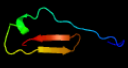

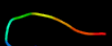





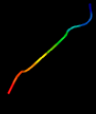



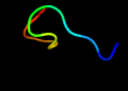










# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0061c\_(RVBD0061c)\_65009\_65347  
 Date Tue Jul 23 14:50:09 BST 2019  
 Unique Job ID 9f3d59ea841b8b5f

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2uurA_</a> |  Alignment   |    | 43.5       | 21     | <b>PDB header:</b> structural protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> collagen alpha-1(ix) chain;<br><b>PDBTitle:</b> n-terminal nc4 domain of collagen ix  |
| 2  | <a href="#">d1hn0a1</a> |  Alignment   |    | 30.4       | 50     | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Chondroitin AC/alginate lyase<br><b>Family:</b> Hyaluronate lyase-like catalytic, N-terminal domain   |
| 3  | <a href="#">c2vtcB_</a> |  Alignment   |    | 28.4       | 39     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B; <b>PDB Molecule:</b> cel61b;<br><b>PDBTitle:</b> the structure of a glycoside hydrolase family 61 member,2 cel61b from the hypocrea jecorina.   |
| 4  | <a href="#">d1fjra_</a> |  Alignment   |    | 26.3       | 19     | <b>Fold:</b> Methuselah ectodomain<br><b>Superfamily:</b> Methuselah ectodomain<br><b>Family:</b> Methuselah ectodomain  |
| 5  | <a href="#">c5nltD_</a> |  Alignment |  | 23.5       | 67     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D; <b>PDB Molecule:</b> cvaa9a;<br><b>PDBTitle:</b> cvaa9a  |
| 6  | <a href="#">c2q1fA_</a> |  Alignment |  | 23.4       | 33     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> chondroitinase;<br><b>PDBTitle:</b> crystal structure of chondroitin sulfate lyase abc from bacteroides2 thetaiotaomicron wal2926  |
| 7  | <a href="#">d1cwva5</a> |  Alignment |  | 23.2       | 43     | <b>Fold:</b> C-type lectin-like<br><b>Superfamily:</b> C-type lectin-like<br><b>Family:</b> Invasin/intimin cell-adhesion fragment, C-terminal domain  |
| 8  | <a href="#">c5ufvE_</a> |  Alignment |  | 22.5       | 31     | <b>PDB header:</b> hydrolase/oxidoreductase<br><b>Chain:</b> E; <b>PDB Molecule:</b> glycoside hydrolase family 61 protein;<br><b>PDBTitle:</b> crystal structure of a cellulose-active polysaccharide monoxygenase2 from m. thermophila (mtpmo3*) |
| 9  | <a href="#">c1hn0A_</a> |  Alignment |  | 22.4       | 50     | <b>PDB header:</b> lyase<br><b>Chain:</b> A; <b>PDB Molecule:</b> chondroitin abc lyase i;<br><b>PDBTitle:</b> crystal structure of chondroitin abc lyase i from proteus2 vulgaris at 1.9 angstroms resolution                                     |
| 10 | <a href="#">c5o2xA_</a> |  Alignment |  | 21.2       | 44     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A; <b>PDB Molecule:</b> glycoside hydrolase family 61;<br><b>PDBTitle:</b> extended catalytic domain of h. jecorina lpmo9a a.k.a eg4  |
| 11 | <a href="#">d8i1ba_</a> |  Alignment |  | 20.9       | 35     | <b>Fold:</b> beta-Trefoil<br><b>Superfamily:</b> Cytokine<br><b>Family:</b> Interleukin-1 (IL-1)   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c5fohA_</a> | Alignment |              | 20.7 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide monooxygenase;<br><b>PDBTitle:</b> crystal structure of the catalytic domain of nclpmo9a   |
| 13 | <a href="#">c1vi7A_</a> | Alignment |              | 20.0 | 25 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yigz;<br><b>PDBTitle:</b> crystal structure of an hypothetical protein  |
| 14 | <a href="#">c3ejaB_</a> | Alignment |              | 19.1 | 33 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein gh61e;<br><b>PDBTitle:</b> magnesium-bound glycoside hydrolase 61 isoform e from thielavia2 terrestris  |
| 15 | <a href="#">c2yetB_</a> | Alignment |              | 19.1 | 44 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> gh61 isozyme a;<br><b>PDBTitle:</b> thermoascus gh61 isozyme a   |
| 16 | <a href="#">d1a0ia1</a> | Alignment |              | 18.8 | 60 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain  |
| 17 | <a href="#">d1l2ha_</a> | Alignment |              | 18.6 | 24 | <b>Fold:</b> beta-Trefoil<br><b>Superfamily:</b> Cytokine<br><b>Family:</b> Interleukin-1 (IL-1)   |
| 18 | <a href="#">d2erfa1</a> | Alignment |              | 18.5 | 25 | <b>Fold:</b> Concanavalin A-like lectins/glucanases<br><b>Superfamily:</b> Concanavalin A-like lectins/glucanases<br><b>Family:</b> Laminin G-like module  |
| 19 | <a href="#">c4pkfB_</a> | Alignment |              | 17.5 | 45 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tutg;<br><b>PDBTitle:</b> benzylsuccinate synthase alpha-beta-gamma complex  |
| 20 | <a href="#">c2qieA_</a> | Alignment |              | 17.4 | 56 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2;<br><b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z                                     |
| 21 | <a href="#">d2hrva_</a> | Alignment | not modelled | 17.0 | 35 | <b>Fold:</b> Trypsin-like serine proteases<br><b>Superfamily:</b> Trypsin-like serine proteases<br><b>Family:</b> Viral cysteine protease of trypsin fold  |
| 22 | <a href="#">c4gafA_</a> | Alignment | not modelled | 16.7 | 24 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ebi-005;<br><b>PDBTitle:</b> crystal structure of ebi-005, a chimera of human il-1beta and il-1ra,2 bound to human interleukin-1 receptor type 1                       |
| 23 | <a href="#">c4b5qA_</a> | Alignment | not modelled | 16.5 | 27 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 61 protein d;<br><b>PDBTitle:</b> the lytic polysaccharide monooxygenase gh61d structure from the2 basidiomycota fungus phanerochaete chrysosporium |
| 24 | <a href="#">c5nnsB_</a> | Alignment | not modelled | 16.3 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 61, 2 protein;<br><b>PDBTitle:</b> crystal structure of hilpmo9b  |
| 25 | <a href="#">c2cveA_</a> | Alignment | not modelled | 15.4 | 24 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1053;<br><b>PDBTitle:</b> crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8     |
| 26 | <a href="#">c4d7uB_</a> | Alignment | not modelled | 14.8 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase ii;<br><b>PDBTitle:</b> the structure of the catalytic domain of nclpmo9c from the filamentous2 fungus neurospora crassa                                    |
| 27 | <a href="#">d1ilr1_</a> | Alignment | not modelled | 14.1 | 35 | <b>Fold:</b> beta-Trefoil<br><b>Superfamily:</b> Cytokine<br><b>Family:</b> Interleukin-1 (IL-1)   |
| 28 | <a href="#">d1uzdc1</a> | Alignment | not modelled | 13.9 | 50 | <b>Fold:</b> RuBisCO, small subunit<br><b>Superfamily:</b> RuBisCO, small subunit<br><b>Family:</b> RuBisCO, small subunit   |
|    |                         |           |              |      |    | <b>PDB header:</b> oxidoreductase  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c4eirB</a>  | Alignment | not modelled | 13.8 | 30 | <b>Chain:</b> B: <b>PDB Molecule:</b> polysaccharide monoxygenase-2;<br><b>PDBTitle:</b> structural basis for substrate targeting and catalysis by fungal2 polysaccharide monoxygenases (pmo-2)  |
| 30 | <a href="#">c4izeA</a>  | Alignment | not modelled | 13.5 | 24 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-36 gamma;<br><b>PDBTitle:</b> crystal structure of il-36gamma  |
| 31 | <a href="#">c2wryA</a>  | Alignment | not modelled | 13.3 | 47 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-1beta;<br><b>PDBTitle:</b> crystal structure of chicken cytokine interleukin 1 beta  |
| 32 | <a href="#">c1u5mA</a>  | Alignment | not modelled | 12.8 | 42 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha 1 type ii collagen isoform 1;<br><b>PDBTitle:</b> structure of a chordin-like cysteine-rich repeat (vwc2 module) from collagen iia  |
| 33 | <a href="#">d1u5ma</a>  | Alignment | not modelled | 12.8 | 42 | <b>Fold:</b> Fnl-like domain<br><b>Superfamily:</b> Fnl-like domain<br><b>Family:</b> VWC domain   |
| 34 | <a href="#">c1z8rA</a>  | Alignment | not modelled | 12.4 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cox sackievirus b4 polyprotein;<br><b>PDBTitle:</b> 2a cysteine proteinase from human cox sackievirus b4 (strain2 jvb / benschoten / new york / 51)  |
| 35 | <a href="#">d1fm0e</a>  | Alignment | not modelled | 12.3 | 44 | <b>Fold:</b> alpha/beta-Hammerhead<br><b>Superfamily:</b> Molybdopterin synthase subunit MoaE<br><b>Family:</b> Molybdopterin synthase subunit MoaE  |
| 36 | <a href="#">c2fl8N</a>  | Alignment | not modelled | 12.1 | 33 | <b>PDB header:</b> virus/viral protein<br><b>Chain:</b> N: <b>PDB Molecule:</b> baseplate structural protein gp10;<br><b>PDBTitle:</b> fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.  |
| 37 | <a href="#">d8rucj</a>  | Alignment | not modelled | 12.0 | 50 | <b>Fold:</b> RuBisCO, small subunit<br><b>Superfamily:</b> RuBisCO, small subunit<br><b>Family:</b> RuBisCO, small subunit   |
| 38 | <a href="#">c4e4fD</a>  | Alignment | not modelled | 11.9 | 38 | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> mannonate dehydratase;<br><b>PDBTitle:</b> crystal structure of enolase pc1_0802 (target efi-502240) from2 pectobacterium carotovorum subsp. carotovorum pc1   |
| 39 | <a href="#">d1pgsa2</a> | Alignment | not modelled | 11.9 | 29 | <b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins)<br><b>Superfamily:</b> PHM/PNGase F<br><b>Family:</b> Glycosyl-asparaginase  |
| 40 | <a href="#">d1cw0a</a>  | Alignment | not modelled | 11.5 | 40 | <b>Fold:</b> Restriction endonuclease-like<br><b>Superfamily:</b> Restriction endonuclease-like<br><b>Family:</b> Very short patch repair (VSR) endonuclease   |
| 41 | <a href="#">c1cb8A</a>  | Alignment | not modelled | 11.3 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (chondroitinase ac);<br><b>PDBTitle:</b> chondroitinase ac lyase from flavobacterium heparinum   |
| 42 | <a href="#">c4maiA</a>  | Alignment | not modelled | 11.2 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aa11 lytic polysaccharide monoxygenase;<br><b>PDBTitle:</b> structure of aspergillus oryzae aa11 lytic polysaccharide2 monoxygenase with cu(i)  |
| 43 | <a href="#">d1vsra</a>  | Alignment | not modelled | 11.1 | 44 | <b>Fold:</b> Restriction endonuclease-like<br><b>Superfamily:</b> Restriction endonuclease-like<br><b>Family:</b> Very short patch repair (VSR) endonuclease   |
| 44 | <a href="#">c6f2pA</a>  | Alignment | not modelled | 10.9 | 33 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> paenibacillus xanthan lyase;<br><b>PDBTitle:</b> structure of paenibacillus xanthan lyase to 2.6 a resolution  |
| 45 | <a href="#">c2m5tA</a>  | Alignment | not modelled | 10.9 | 60 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> human rhinovirus 2a proteinase;<br><b>PDBTitle:</b> solution structure of the 2a proteinase from a common cold agent,2 human rhinovirus rv-c02, strain w12   |
| 46 | <a href="#">c2k7rA</a>  | Alignment | not modelled | 10.8 | 24 | <b>PDB header:</b> replication<br><b>Chain:</b> A: <b>PDB Molecule:</b> primosomal protein dnaI;<br><b>PDBTitle:</b> n-terminal domain of the bacillus subtilis helicase-loading2 protein dnaI   |
| 47 | <a href="#">d1hg7a</a>  | Alignment | not modelled | 10.7 | 38 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> AFP III-like domain<br><b>Family:</b> AFP III-like domain  |
| 48 | <a href="#">d1ej7s</a>  | Alignment | not modelled | 10.5 | 50 | <b>Fold:</b> RuBisCO, small subunit<br><b>Superfamily:</b> RuBisCO, small subunit<br><b>Family:</b> RuBisCO, small subunit   |
| 49 | <a href="#">c1bdsA</a>  | Alignment | not modelled | 10.4 | 45 | <b>PDB header:</b> anti-hypertensive, anti-viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bds-i;<br><b>PDBTitle:</b> determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemonia sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing |
| 50 | <a href="#">d1bdsa</a>  | Alignment | not modelled | 10.4 | 45 | <b>Fold:</b> Defensin-like<br><b>Superfamily:</b> Defensin-like<br><b>Family:</b> Defensin   |
| 51 | <a href="#">c3v3wA</a>  | Alignment | not modelled | 10.4 | 44 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> starvation sensing protein rspa;<br><b>PDBTitle:</b> crystal structure of an enolase from the soil bacterium cellvibrio2 japonicus (target efi-502161) with bound mg and glycerol  |
| 52 | <a href="#">d1x4ka2</a> | Alignment | not modelled | 10.3 | 67 | <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Family:</b> LIM domain   |
| 53 | <a href="#">c1z0gA</a>  | Alignment | not modelled | 10.3 | 24 | <b>PDB header:</b> transcription/transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> interferon regulatory factor 3;<br><b>PDBTitle:</b> irf3-cbp complex   |
| 54 | <a href="#">c5bowA</a>  | Alignment | not modelled | 9.8  | 24 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> interleukin-1 family member 10;<br><b>PDBTitle:</b> crystal structure of il-38   |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 55 | <a href="#">d2l1aa_</a> | Alignment | not modelled | 9.7 | 20 | <b>Fold:</b> beta-Trefoil<br><b>Superfamily:</b> Cytokine<br><b>Family:</b> Interleukin-1 (IL-1)   |
| 56 | <a href="#">c2xfeA_</a> | Alignment | not modelled | 8.9 | 25 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding module;<br><b>PDBTitle:</b> vcbm60 in complex with galactobiose   |
| 57 | <a href="#">c2l61A_</a> | Alignment | not modelled | 8.7 | 67 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ec protein i/ii;<br><b>PDBTitle:</b> protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle.                 |
| 58 | <a href="#">c2l62A_</a> | Alignment | not modelled | 8.6 | 67 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ec protein i/ii;<br><b>PDBTitle:</b> protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle.                 |
| 59 | <a href="#">c5aciA_</a> | Alignment | not modelled | 8.5 | 41 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lytic polysaccharide monoxygenase;<br><b>PDBTitle:</b> x-ray structure of lpmo  |
| 60 | <a href="#">c3pmmA_</a> | Alignment | not modelled | 8.4 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein;<br><b>PDBTitle:</b> the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578             |
| 61 | <a href="#">d1x1ia1</a> | Alignment | not modelled | 8.4 | 33 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Chondroitin AC/alginate lyase<br><b>Family:</b> Hyaluronate lyase-like catalytic, N-terminal domain   |
| 62 | <a href="#">d1qwta_</a> | Alignment | not modelled | 8.4 | 24 | <b>Fold:</b> SMAD/FHA domain<br><b>Superfamily:</b> SMAD/FHA domain<br><b>Family:</b> Interferon regulatory factor 3 (IRF3), transactivation domain  |
| 63 | <a href="#">c2h1eB_</a> | Alignment | not modelled | 8.3 | 36 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> chromo domain protein 1;<br><b>PDBTitle:</b> tandem chromodomains of budding yeast chd1  |
| 64 | <a href="#">c6jzbC_</a> | Alignment | not modelled | 8.1 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein e;<br><b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens                                |
| 65 | <a href="#">d1biha2</a> | Alignment | not modelled | 8.1 | 33 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Immunoglobulin<br><b>Family:</b> I set domains   |
| 66 | <a href="#">c2wdaA_</a> | Alignment | not modelled | 7.8 | 33 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted lyase;<br><b>PDBTitle:</b> the x-ray structure of the streptomyces coelicolor a32 chondroitin ac lyase in complex with chondroitin sulphate                        |
| 67 | <a href="#">c1rwcA_</a> | Alignment | not modelled | 7.5 | 27 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chondroitin ac lyase;<br><b>PDBTitle:</b> crystal structure of arthrobacter aurescens chondroitin ac lyase   |
| 68 | <a href="#">d2oz4a3</a> | Alignment | not modelled | 7.4 | 38 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Immunoglobulin<br><b>Family:</b> I set domains   |
| 69 | <a href="#">c2wseE_</a> | Alignment | not modelled | 7.4 | 22 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> photosystem i reaction center subunit iv a, chloroplastic;<br><b>PDBTitle:</b> improved model of plant photosystem i  |
| 70 | <a href="#">c3k11A_</a> | Alignment | not modelled | 7.4 | 27 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyl hydrolase;<br><b>PDBTitle:</b> crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution |
| 71 | <a href="#">d1m9ma_</a> | Alignment | not modelled | 7.2 | 38 | <b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Family:</b> Nitric oxide (NO) synthase oxygenase domain  |
| 72 | <a href="#">c4eisA_</a> | Alignment | not modelled | 7.2 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide monoxygenase-3;<br><b>PDBTitle:</b> structural basis for substrate targeting and catalysis by fungal2 polysaccharide monoxygenases (pmo-3)                   |
| 73 | <a href="#">c2mfpA_</a> | Alignment | not modelled | 7.2 | 67 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ec protein i/ii;<br><b>PDBTitle:</b> solution structure of the circular g-domain analog from the wheat2 metallothionein ec-1   |
| 74 | <a href="#">d1cr5a1</a> | Alignment | not modelled | 6.9 | 14 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Cdc48 N-terminal domain-like   |
| 75 | <a href="#">c4wtrA_</a> | Alignment | not modelled | 6.8 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-glucanosyltransferase;<br><b>PDBTitle:</b> active-site mutant of rhizomucor miehei beta-1,3-glucanosyltransferase2 in complex with laminaribiose                      |
| 76 | <a href="#">c1x1jA_</a> | Alignment | not modelled | 6.8 | 33 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> xanthan lyase;<br><b>PDBTitle:</b> crystal structure of xanthan lyase (n194a) with a substrate.  |
| 77 | <a href="#">c1za4A_</a> | Alignment | not modelled | 6.8 | 24 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> thrombospondin 1;<br><b>PDBTitle:</b> crystal structure of the thrombospondin-1 n-terminal domain2 in complex with arixtra   |
| 78 | <a href="#">d1opsa_</a> | Alignment | not modelled | 6.7 | 33 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> AFP III-like domain<br><b>Family:</b> AFP III-like domain  |
| 79 | <a href="#">c4s3nA_</a> | Alignment | not modelled | 6.7 | 38 | <b>PDB header:</b> transferase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2'-5'-oligoadenylate synthase 3;<br><b>PDBTitle:</b> crystal structure of human oas3 domain i in complex with dsrna  |
| 80 | <a href="#">c3fgrA_</a> | Alignment | not modelled | 6.6 | 50 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative phospholipase b-like 2 28 kda form;<br><b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstrom<br><b>PDB header:</b> dna binding protein                |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 81 | <a href="#">c3dshA_</a> | Alignment | not modelled | 6.3 | 24 | <b>Chain:</b> A: <b>PDB Molecule:</b> interferon regulatory factor 5;<br><b>PDBTitle:</b> crystal structure of dimeric interferon regulatory factor 5 (irf-5)2 transactivation domain  |
| 82 | <a href="#">d1g40a4</a> | Alignment | not modelled | 6.3 | 15 | <b>Fold:</b> Complement control module/SCR domain<br><b>Superfamily:</b> Complement control module/SCR domain<br><b>Family:</b> Complement control module/SCR domain   |
| 83 | <a href="#">c3mi6A_</a> | Alignment | not modelled | 6.2 | 47 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase;<br><b>PDBTitle:</b> crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11. |
| 84 | <a href="#">d1vj1a1</a> | Alignment | not modelled | 6.0 | 25 | <b>Fold:</b> GroES-like<br><b>Superfamily:</b> GroES-like<br><b>Family:</b> Alcohol dehydrogenase-like, N-terminal domain  |
| 85 | <a href="#">c6imfB_</a> | Alignment | not modelled | 6.0 | 36 | <b>PDB header:</b> toxin/antitoxin<br><b>Chain:</b> B: <b>PDB Molecule:</b> small serum protein 2;<br><b>PDBTitle:</b> crystal structure of toxin/antitoxin complex  |
| 86 | <a href="#">d1mjta</a>  | Alignment | not modelled | 5.8 | 19 | <b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Family:</b> Nitric oxide (NO) synthase oxygenase domain  |
| 87 | <a href="#">d1ir1s_</a> | Alignment | not modelled | 5.8 | 50 | <b>Fold:</b> RuBisCO, small subunit<br><b>Superfamily:</b> RuBisCO, small subunit<br><b>Family:</b> RuBisCO, small subunit   |
| 88 | <a href="#">d2cvea1</a> | Alignment | not modelled | 5.7 | 27 | <b>Fold:</b> Ribosomal protein S5 domain 2-like<br><b>Superfamily:</b> Ribosomal protein S5 domain 2-like<br><b>Family:</b> YigZ N-terminal domain-like  |
| 89 | <a href="#">c2m7tA_</a> | Alignment | not modelled | 5.7 | 50 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> cystine knot protein 2.5d;<br><b>PDBTitle:</b> solution nmr structure of engineered cystine knot protein 2.5d  |
| 90 | <a href="#">c3fy4C_</a> | Alignment | not modelled | 5.7 | 40 | <b>PDB header:</b> lyase<br><b>Chain:</b> C: <b>PDB Molecule:</b> 6-4 photolyase;<br><b>PDBTitle:</b> (6-4) photolyase crystal structure   |
| 91 | <a href="#">c5wlxA_</a> | Alignment | not modelled | 5.7 | 60 | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> kappa-theraphotoxin-aa1a;<br><b>PDBTitle:</b> solution structure of kappa-theraphotoxin-aa1a   |
| 92 | <a href="#">c6igzE_</a> | Alignment | not modelled | 5.7 | 22 | <b>PDB header:</b> plant protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> psae;<br><b>PDBTitle:</b> structure of psi-lhci  |
| 93 | <a href="#">d1om4a_</a> | Alignment | not modelled | 5.6 | 31 | <b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain<br><b>Family:</b> Nitric oxide (NO) synthase oxygenase domain  |
| 94 | <a href="#">d2fyia1</a> | Alignment | not modelled | 5.6 | 15 | <b>Fold:</b> FdhE-like<br><b>Superfamily:</b> FdhE-like<br><b>Family:</b> FdhE-like  |
| 95 | <a href="#">c2n9oA_</a> | Alignment | not modelled | 5.5 | 31 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf126;<br><b>PDBTitle:</b> solution structure of rnf126 n-terminal zinc finger domain  |
| 96 | <a href="#">d1uzhc1</a> | Alignment | not modelled | 5.4 | 25 | <b>Fold:</b> RuBisCO, small subunit<br><b>Superfamily:</b> RuBisCO, small subunit<br><b>Family:</b> RuBisCO, small subunit   |
| 97 | <a href="#">d1k8kd2</a> | Alignment | not modelled | 5.4 | 25 | <b>Fold:</b> Secretion chaperone-like<br><b>Superfamily:</b> Arp2/3 complex subunits<br><b>Family:</b> Arp2/3 complex subunits   |
| 98 | <a href="#">c2iz3A_</a> | Alignment | not modelled | 5.3 | 45 | <b>PDB header:</b> inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-microseminoprotein;<br><b>PDBTitle:</b> solution structure of human and porcine beta-2 microseminoprotein   |
| 99 | <a href="#">c4o9iX_</a> | Alignment | not modelled | 5.3 | 36 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 4;<br><b>PDBTitle:</b> structure of chd4 double chromodomains depicts cooperative folding for2 dna binding                     |