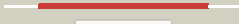



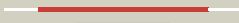




























# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD2778c_(-)_3085723_3086193 |
| Date          | Wed Aug 7 12:50:43 BST 2019   |
| Unique Job ID | 67e508996c5d7dac              |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2m47A_</a> |  Alignment   |    | 99.9       | 23     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein cgl2373;<br><b>PDBTitle:</b> solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160 |
| 2  | <a href="#">c2kf2A_</a> |  Alignment   |    | 99.9       | 14     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide cyclase;<br><b>PDBTitle:</b> solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365                        |
| 3  | <a href="#">d2d4ra1</a> |  Alignment   |    | 99.9       | 17     | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> oligoketide cyclase/dehydrase-like  |
| 4  | <a href="#">d2rera1</a> |  Alignment   |    | 99.9       | 15     | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> oligoketide cyclase/dehydrase-like  |
| 5  | <a href="#">c3tfzB_</a> |  Alignment |  | 99.9       | 17     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cyclase;<br><b>PDBTitle:</b> crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128   |
| 6  | <a href="#">c4xrwA_</a> |  Alignment |  | 99.9       | 13     | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bex1;<br><b>PDBTitle:</b> crystal structure of the di-domain aro/cyc bex1 from the be-7585a2 biosynthetic pathway  |
| 7  | <a href="#">d2b79a1</a> |  Alignment |  | 99.8       | 10     | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Smu440-like   |
| 8  | <a href="#">c5z8oA_</a> |  Alignment |  | 99.8       | 15     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclase/dehydrase;<br><b>PDBTitle:</b> structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis   |
| 9  | <a href="#">d1t17a_</a> |  Alignment |  | 99.8       | 13     | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> oligoketide cyclase/dehydrase-like  |
| 10 | <a href="#">d2ns9a1</a> |  Alignment |  | 99.8       | 10     | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> CoxG-like   |
| 11 | <a href="#">c5woxA_</a> |  Alignment |  | 99.8       | 18     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> nmr solution structure of kany protein (ms6282) using two 4d-spectra   |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">c4xrtB</a>  | Alignment |    | 99.8 | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> stfq aromatase/cyclase;<br><b>PDBTitle:</b> crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway  |
| 13 | <a href="#">d2pcsa1</a> | Alignment |    | 99.7 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> CoxG-like  |
| 14 | <a href="#">c2lf2A</a>  | Alignment |    | 99.7 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152                      |
| 15 | <a href="#">c2kczA</a>  | Alignment |    | 99.7 | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein dr_a0006;<br><b>PDBTitle:</b> solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d |
| 16 | <a href="#">c2lghA</a>  | Alignment |    | 99.7 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99.   |
| 17 | <a href="#">c3p9vA</a>  | Alignment |   | 99.7 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mqr197                         |
| 18 | <a href="#">d1xuva</a>  | Alignment |  | 99.7 | 16 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 19 | <a href="#">c2lcgA</a>  | Alignment |  | 99.7 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115                                    |
| 20 | <a href="#">c2l9pA</a>  | Alignment |  | 99.7 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of q5hli9 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147  |
| 21 | <a href="#">c2leqA</a>  | Alignment | not modelled  | 99.7 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145                     |
| 22 | <a href="#">c2l8oA</a>  | Alignment | not modelled  | 99.7 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148  |
| 23 | <a href="#">c2le1A</a>  | Alignment | not modelled  | 99.7 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a  |
| 24 | <a href="#">d1z94a1</a> | Alignment | not modelled  | 99.7 | 14 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 25 | <a href="#">d1xfsa</a>  | Alignment | not modelled  | 99.7 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 26 | <a href="#">c3uidA</a>  | Alignment | not modelled  | 99.7 | 19 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of protein ms6760 from mycobacterium smegmatis   |
| 27 | <a href="#">c3pu2G</a>  | Alignment | not modelled  | 99.7 | 16 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> G: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.                                  |
| 28 | <a href="#">c2ldkA</a>  | Alignment | not modelled  | 99.7 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of protein aaur_3427 from   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
|    |                         |           |              |      |    | arthrobacter2 aureus, northeast structural genomics consortium target aar96   |
| 29 | <a href="#">d2qpva1</a> | Alignment | not modelled | 99.7 | 14 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Atu1531-like   |
| 30 | <a href="#">c2m89A_</a> | Alignment | not modelled | 99.7 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> aha1 domain protein;<br><b>PDBTitle:</b> solution structure of the aha1 dimer from colwellia psychrerythraea  |
| 31 | <a href="#">c4n0gC_</a> | Alignment | not modelled | 99.7 | 15 | <b>PDB header:</b> hydrolase/receptor<br><b>Chain:</b> C: <b>PDB Molecule:</b> abscisic acid receptor pyl13;<br><b>PDBTitle:</b> crystal structure of pyl13-pp2ca complex   |
| 32 | <a href="#">d3cnwa1</a> | Alignment | not modelled | 99.7 | 15 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Atu1531-like   |
| 33 | <a href="#">c3q63F_</a> | Alignment | not modelled | 99.6 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> F: <b>PDB Molecule:</b> mll2253 protein;<br><b>PDBTitle:</b> x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404.   |
| 34 | <a href="#">c5vglA_</a> | Alignment | not modelled | 99.6 | 14 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lachrymatory-factor synthase;<br><b>PDBTitle:</b> crystal structure of lachrymatory factor synthase from allium cepa  |
| 35 | <a href="#">c4r7kA_</a> | Alignment | not modelled | 99.6 | 8  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein jhp0584;<br><b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori.   |
| 36 | <a href="#">d1xn5a_</a> | Alignment | not modelled | 99.6 | 17 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 37 | <a href="#">c3q6aH_</a> | Alignment | not modelled | 99.6 | 15 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116   |
| 38 | <a href="#">c3otiA_</a> | Alignment | not modelled | 99.6 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261 |
| 39 | <a href="#">c2nn5A_</a> | Alignment | not modelled | 99.6 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ef_2215;<br><b>PDBTitle:</b> structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis   |
| 40 | <a href="#">c3k90C_</a> | Alignment | not modelled | 99.6 | 17 | <b>PDB header:</b> hormone receptor, hydrolase regulator<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> the abscisic acid receptor pyr1 in complex with abscisic acid   |
| 41 | <a href="#">d2il5a1</a> | Alignment | not modelled | 99.6 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 42 | <a href="#">c3q64A_</a> | Alignment | not modelled | 99.6 | 15 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> mll3774 protein;<br><b>PDBTitle:</b> x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405.  |
| 43 | <a href="#">c3rd6A_</a> | Alignment | not modelled | 99.6 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> mll3558 protein;<br><b>PDBTitle:</b> crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403   |
| 44 | <a href="#">c3p51A_</a> | Alignment | not modelled | 99.5 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118   |
| 45 | <a href="#">d2nn5a1</a> | Alignment | not modelled | 99.5 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 46 | <a href="#">c2lakA_</a> | Alignment | not modelled | 99.5 | 18 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> ahsa1-like protein rhe_ch02687;<br><b>PDBTitle:</b> solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242                                   |
| 47 | <a href="#">c3oquB_</a> | Alignment | not modelled | 99.5 | 10 | <b>PDB header:</b> hormone receptor<br><b>Chain:</b> B: <b>PDB Molecule:</b> abscisic acid receptor pyl9;<br><b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl9 with aba  |
| 48 | <a href="#">d1xn6a_</a> | Alignment | not modelled | 99.5 | 12 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 49 | <a href="#">c4oicA_</a> | Alignment | not modelled | 99.5 | 17 | <b>PDB header:</b> hormone receptor/hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bet v i allergen-like;<br><b>PDBTitle:</b> crystal structural of a soluble protein   |
| 50 | <a href="#">c3qtjA_</a> | Alignment | not modelled | 99.5 | 16 | <b>PDB header:</b> hormone receptor<br><b>Chain:</b> A: <b>PDB Molecule:</b> abscisic acid receptor pyl10;<br><b>PDBTitle:</b> crystal structure of aba receptor pyl10 (apo)  |
| 51 | <a href="#">c3klxB_</a> | Alignment | not modelled | 99.5 | 15 | <b>PDB header:</b> hormone receptor<br><b>Chain:</b> B: <b>PDB Molecule:</b> f3n23.20 protein;<br><b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl3  |
| 52 | <a href="#">c2kewA_</a> | Alignment | not modelled | 99.5 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yndb;<br><b>PDBTitle:</b> the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy<br><b>PDB header:</b> structural genomics, unknown function                                       |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c2luzA_</a> | Alignment | not modelled | 99.5 | 17 | <b>Chain:</b> A: <b>PDB Molecule:</b> calu16;<br><b>PDBTitle:</b> solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12   |
| 54 | <a href="#">c3oh8A_</a> | Alignment | not modelled | 99.4 | 16 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate sugar epimerase (sula family);<br><b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91                          |
| 55 | <a href="#">c5e4bB_</a> | Alignment | not modelled | 99.4 | 10 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hydroxynitrile lyase;<br><b>PDBTitle:</b> hydroxynitrile lyase from the fern davallia tyermanii in complex with2 (r)-mandelonitrile / benzaldehyde  |
| 56 | <a href="#">d2k5ga1</a> | Alignment | not modelled | 99.4 | 14 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 57 | <a href="#">c3kdiA_</a> | Alignment | not modelled | 99.4 | 18 | <b>PDB header:</b> hormone receptor<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein at2g26040;<br><b>PDBTitle:</b> structure of (+)-aba bound pyl2  |
| 58 | <a href="#">d3elia1</a> | Alignment | not modelled | 99.4 | 15 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 59 | <a href="#">c5ujvA_</a> | Alignment | not modelled | 99.4 | 16 | <b>PDB header:</b> abscisic acid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyr1;<br><b>PDBTitle:</b> crystal structure of fepyr1 in complex with abscisic acid   |
| 60 | <a href="#">d1zxfa1</a> | Alignment | not modelled | 99.3 | 11 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 61 | <a href="#">d1x53a1</a> | Alignment | not modelled | 99.3 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> AHSA1 domain   |
| 62 | <a href="#">c4igyB_</a> | Alignment | not modelled | 99.3 | 13 | <b>PDB header:</b> allergen<br><b>Chain:</b> B: <b>PDB Molecule:</b> kirola;<br><b>PDBTitle:</b> crystal structure of kirola (act d 11) - triclinic form  |
| 63 | <a href="#">c5z4eA_</a> | Alignment | not modelled | 99.1 | 17 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> txno9;<br><b>PDBTitle:</b> an anthrahydroquino-gama-pyrone synthase txn09  |
| 64 | <a href="#">c3ni8A_</a> | Alignment | not modelled | 99.1 | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> pfc0360w protein;<br><b>PDBTitle:</b> crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum  |
| 65 | <a href="#">d1ifva_</a> | Alignment | not modelled | 99.1 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 66 | <a href="#">c4rejA_</a> | Alignment | not modelled | 99.0 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> major latex-like protein;<br><b>PDBTitle:</b> crystal structure of ginseng major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3)  |
| 67 | <a href="#">c2k7hA_</a> | Alignment | not modelled | 99.0 | 13 | <b>PDB header:</b> allergen<br><b>Chain:</b> A: <b>PDB Molecule:</b> stress-induced protein sam22;<br><b>PDBTitle:</b> nmr solution structure of soybean allergen gly m 4   |
| 68 | <a href="#">d1icxa_</a> | Alignment | not modelled | 99.0 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 69 | <a href="#">c2vq5B_</a> | Alignment | not modelled | 99.0 | 12 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> s-norcochlorine synthase;<br><b>PDBTitle:</b> x-ray structure of norcochlorine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde  |
| 70 | <a href="#">c3c0vC_</a> | Alignment | not modelled | 99.0 | 9  | <b>PDB header:</b> plant protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> cytokinin-specific binding protein;<br><b>PDBTitle:</b> crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12  |
| 71 | <a href="#">c3ie5A_</a> | Alignment | not modelled | 98.9 | 10 | <b>PDB header:</b> plant protein, biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenolic oxidative coupling protein hyp-1;<br><b>PDBTitle:</b> crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis  |
| 72 | <a href="#">d2bk0a1</a> | Alignment | not modelled | 98.9 | 16 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 73 | <a href="#">d1e09a_</a> | Alignment | not modelled | 98.9 | 11 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 74 | <a href="#">c3qszB_</a> | Alignment | not modelled | 98.9 | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> star-related lipid transfer protein;<br><b>PDBTitle:</b> crystal structure of the star-related lipid transfer protein (fragment2 25-204) from xanthomonas axonopodis at the resolution 2.4a, northeast3 structural genomics consortium target xar342 |
| 75 | <a href="#">d1xdfa1</a> | Alignment | not modelled | 98.9 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 76 | <a href="#">d1fm4a_</a> | Alignment | not modelled | 98.9 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 77 | <a href="#">c6gq9A_</a> | Alignment | not modelled | 98.8 | 10 | <b>PDB header:</b> allergen<br><b>Chain:</b> A: <b>PDB Molecule:</b> major allergen cor a 1.0401;<br><b>PDBTitle:</b> solution structure of the hazel allergen cor a 1.0401   |
| 78 | <a href="#">d1qmra_</a> | Alignment | not modelled | 98.8 | 14 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 79 | <a href="#">c2i9yA_</a> | Alignment | not modelled | 98.8 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> major latex protein-like protein 28 or mlp-like<br><b>PDBTitle:</b> solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family |
| 80 | <a href="#">c3rwsA_</a> | Alignment | not modelled | 98.7 | 14 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> mtn13 protein;<br><b>PDBTitle:</b> crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin  |
| 81 | <a href="#">d1txca1</a> | Alignment | not modelled | 98.6 | 12 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 82 | <a href="#">c2r55B_</a> | Alignment | not modelled | 98.0 | 7  | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> star-related lipid transfer protein 5;<br><b>PDBTitle:</b> human star-related lipid transfer protein 5  |
| 83 | <a href="#">c3fo5A_</a> | Alignment | not modelled | 98.0 | 12 | <b>PDB header:</b> lipid transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioesterase, adipose associated, isoform bfit2;<br><b>PDBTitle:</b> human start domain of acyl-coenzyme a thioesterase 11 (acot11)   |
| 84 | <a href="#">c3p0lC_</a> | Alignment | not modelled | 97.7 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> steroidogenic acute regulatory protein, mitochondrial;<br><b>PDBTitle:</b> human steroidogenic acute regulatory protein   |
| 85 | <a href="#">d1em2a_</a> | Alignment | not modelled | 97.6 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> STAR domain  |
| 86 | <a href="#">c2mouA_</a> | Alignment | not modelled | 97.2 | 5  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> star-related lipid transfer protein 6;<br><b>PDBTitle:</b> solution structure of star-related lipid transfer domain protein 62 (stard6)   |
| 87 | <a href="#">c1jssB_</a> | Alignment | not modelled | 97.1 | 8  | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cholesterol-regulated start protein 4;<br><b>PDBTitle:</b> crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4).   |
| 88 | <a href="#">d1jssa_</a> | Alignment | not modelled | 96.9 | 9  | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> STAR domain  |
| 89 | <a href="#">d1vjha_</a> | Alignment | not modelled | 93.2 | 9  | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Pathogenesis-related protein 10 (PR10)-like  |
| 90 | <a href="#">d1ln1a_</a> | Alignment | not modelled | 92.3 | 10 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> STAR domain  |
| 91 | <a href="#">c2e3rB_</a> | Alignment | not modelled | 87.7 | 11 | <b>PDB header:</b> lipid transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> lipid-transfer protein cert;<br><b>PDBTitle:</b> crystal structure of cert start domain in complex with c18-2 ceramide (p1)   |
| 92 | <a href="#">d2psoa1</a> | Alignment | not modelled | 86.9 | 13 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> STAR domain  |
| 93 | <a href="#">c2lioA_</a> | Alignment | not modelled | 85.6 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322              |
| 94 | <a href="#">c2ejxA_</a> | Alignment | not modelled | 79.9 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> stk_08120;<br><b>PDBTitle:</b> crystal structure of the hypothetical protein stk_08120 from2 sulfolobus tokodaii  |
| 95 | <a href="#">c3qzC_</a>  | Alignment | not modelled | 48.0 | 27 | <b>PDB header:</b> hormone receptor<br><b>Chain:</b> C: <b>PDB Molecule:</b> abscisic acid receptor pyl5;<br><b>PDBTitle:</b> crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom  |
| 96 | <a href="#">c2lafA_</a> | Alignment | not modelled | 46.8 | 6  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein 34;<br><b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc   |
| 97 | <a href="#">c5ys0A_</a> | Alignment | not modelled | 22.6 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> membrane-anchored lipid-binding protein ysp2;<br><b>PDBTitle:</b> crystal structure of the second starkin domain of lam2 in complex with2 ergosterol  |
| 98 | <a href="#">c2oqgA_</a> | Alignment | not modelled | 20.3 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein;<br><b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1  |
| 99 | <a href="#">c6gqfC_</a> | Alignment | not modelled | 20.3 | 16 | <b>PDB header:</b> lipid transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> gram domain-containing protein 1a;<br><b>PDBTitle:</b> the structure of mouse astera (gramd1a) with 25-hydroxy cholesterol  |