



























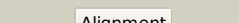
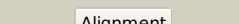
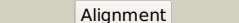



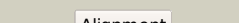
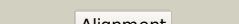
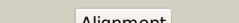
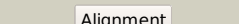

Phyre2

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|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1060_(-)_1183513_1183986 |
| Date | Wed Jul 31 22:05:13 BST 2019 |
| Unique Job ID | e4e445ab64c42467 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c4n0gC_ |  Alignment |  | 99.8 | 12 | PDB header: hydrolase/receptor Chain: C: PDB Molecule: abscisic acid receptor pyl13; PDBTitle: crystal structure of pyl13-pp2ca complex |
| 2 | c5e4bB_ |  Alignment |  | 99.8 | 12 | PDB header: lyase Chain: B: PDB Molecule: hydroxynitrile lyase; PDBTitle: hydroxynitrile lyase from the fern davallia tyermanii in complex with 2 (r)-mandelonitrile / benzaldehyde |
| 3 | c2le1A_ |  Alignment |  | 99.8 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of tfu_2981 from thermobifida fusca, northeast2 structural genomics consortium target tfr85a |
| 4 | c3p51A_ |  Alignment |  | 99.8 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein q2y8n9_nitmu from nitrosospira2 multiformis, northeast structural genomics consortium target nmr118 |
| 5 | d2ns9a1 |  Alignment |  | 99.8 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like |
| 6 | c5woxA_ |  Alignment |  | 99.8 | 19 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of kany protein (ms6282) using two 4d-spectra |
| 7 | c5vglA_ |  Alignment |  | 99.8 | 14 | PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa |
| 8 | c2kf2A_ |  Alignment |  | 99.8 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: solution nmr structure of of streptomyces coelicolor2 polyketide cyclase sco5315. northeast structural genomics3 consortium target rr365 |
| 9 | c2m47A_ |  Alignment |  | 99.8 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cgl2373; PDBTitle: solution nmr structure of the polyketide_cyc-like protein cgl2372 from2 corynebacterium glutamicum, northeast structural genomics consortium3 target cgr160 |
| 10 | d3cnwa1 |  Alignment |  | 99.8 | 19 | Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like |
| 11 | c3qtjA_ |  Alignment |  | 99.8 | 15 | PDB header: hormone receptor Chain: A: PDB Molecule: abscisic acid receptor pyl10; PDBTitle: crystal structure of aba receptor pyl10 (apo) |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c4oicA | Alignment |  | 99.8 | 15 | PDB header: hormone receptor/hydrolase Chain: A: PDB Molecule: bet v i allergen-like; PDBTitle: crystal structural of a soluble protein |
| 13 | d2d4ra1 | Alignment |  | 99.8 | 17 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |
| 14 | d2rera1 | Alignment |  | 99.8 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |
| 15 | c3oquB | Alignment |  | 99.8 | 12 | PDB header: hormone receptor Chain: B: PDB Molecule: abscisic acid receptor pyl9; PDBTitle: crystal structure of native abscisic acid receptor pyl9 with aba |
| 16 | c3tfzB | Alignment |  | 99.8 | 12 | PDB header: biosynthetic protein Chain: B: PDB Molecule: cyclase; PDBTitle: crystal structure of zhui aromatase/cyclase from streptomcyes sp.2 r1128 |
| 17 | d1t17a | Alignment |  | 99.8 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like |
| 18 | d2b79a1 | Alignment |  | 99.8 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like |
| 19 | c4xrwA | Alignment |  | 99.8 | 13 | PDB header: lyase Chain: A: PDB Molecule: bexl; PDBTitle: crystal structure of the di-domain aro/cyc bexl from the be-7585a2 biosynthetic pathway |
| 20 | c3klxB | Alignment |  | 99.7 | 14 | PDB header: hormone receptor Chain: B: PDB Molecule: f3n23.20 protein; PDBTitle: crystal structure of native abscisic acid receptor pyl3 |
| 21 | d2pcsa1 | Alignment | not modelled | 99.7 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like |
| 22 | c3kdiA | Alignment | not modelled | 99.7 | 18 | PDB header: hormone receptor Chain: A: PDB Molecule: putative uncharacterized protein at2g26040; PDBTitle: structure of (+)-aba bound pyl2 |
| 23 | c5ujvA | Alignment | not modelled | 99.7 | 17 | PDB header: abscisic acid binding protein Chain: A: PDB Molecule: pyr1; PDBTitle: crystal structure of fepyr1 in complex with abscisic acid |
| 24 | c5z8oA | Alignment | not modelled | 99.7 | 12 | PDB header: unknown function Chain: A: PDB Molecule: cyclase/dehydrase; PDBTitle: structural of start superfamily protein msmeg_0129 from mycobacterium2 smegmatis |
| 25 | c3k90C | Alignment | not modelled | 99.7 | 14 | PDB header: hormone receptor, hydrolase regulator Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the abscisic acid receptor pyr1 in complex with abscisic acid |
| 26 | d1ifva | Alignment | not modelled | 99.6 | 16 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 27 | c4xrtB | Alignment | not modelled | 99.6 | 17 | PDB header: lyase Chain: B: PDB Molecule: stfq aromatase/cyclase; PDBTitle: crystal structure of the di-domain aro/cyc stfq from the steffimycin2 biosynthetic pathway |
| 28 | c3pu2G | Alignment | not modelled | 99.6 | 13 | PDB header: structure genomics, unknown function Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263. |

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|----|-------------------------|---|--------------|------|----|---|
| 29 | c3p9vA |  Alignment | not modelled | 99.6 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: high resolution crystal structure of protein maqu_3174 from2 marinobacter aquaeolei, northeast structural genomics consortium3 target mgr197 |
| 30 | c2kczA |  Alignment | not modelled | 99.6 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein dr_a0006; PDBTitle: solution nmr structure of the c-terminal domain of protein2 dr_a0006 from deinococcus radiodurans. northeast3 structural genomics consortium target drr147d |
| 31 | c2l9pA |  Alignment | not modelled | 99.6 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of q5hl19 from staphylococcus epidermidis,2 northeast structural genomics consortium target ser147 |
| 32 | c2lf2A |  Alignment | not modelled | 99.6 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein chu_1110 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr152 |
| 33 | c3uidA |  Alignment | not modelled | 99.6 | 16 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of protein ms6760 from mycobacterium smegmatis |
| 34 | d1xfsa |  Alignment | not modelled | 99.6 | 12 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 35 | c2ldkA |  Alignment | not modelled | 99.6 | 9 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein aaur_3427 from arthrobacter2 aureus, northeast structural genomics consortium target aar96 |
| 36 | c4igyB |  Alignment | not modelled | 99.6 | 13 | PDB header: allergen Chain: B: PDB Molecule: kirola; PDBTitle: crystal structure of kirola (act d 11) - triclinic form |
| 37 | c2leqA |  Alignment | not modelled | 99.6 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: chemical shift assignment and solution structure of chr145 from2 cytophaga hutchinsonii, northeast structural genomics consortium3 target chr145 |
| 38 | d2bk0a1 |  Alignment | not modelled | 99.5 | 17 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 39 | c3c0vC |  Alignment | not modelled | 99.5 | 15 | PDB header: plant protein Chain: C: PDB Molecule: cytokinin-specific binding protein; PDBTitle: crystal structure of cytokinin-specific binding protein in complex2 with cytokinin and ta6br12 |
| 40 | c2k7hA |  Alignment | not modelled | 99.5 | 15 | PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4 |
| 41 | c4rejA |  Alignment | not modelled | 99.5 | 12 | PDB header: protein binding Chain: A: PDB Molecule: major latex-like protein; PDBTitle: crystal structure of ginseng major latex-like protein 151 (glp) from2 panax ginseng. (crystal-3) |
| 42 | d1e09a |  Alignment | not modelled | 99.5 | 18 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 43 | d1icxa |  Alignment | not modelled | 99.5 | 17 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 44 | c2vq5B |  Alignment | not modelled | 99.5 | 15 | PDB header: lyase Chain: B: PDB Molecule: s-norococlaurine synthase; PDBTitle: x-ray structure of norococlaurine synthase from thalictrum2 flavum in complex with dopamine and hydroxybenzaldehyde |
| 45 | d1qmra |  Alignment | not modelled | 99.5 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 46 | d1fm4a |  Alignment | not modelled | 99.5 | 15 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 47 | c3rd6A |  Alignment | not modelled | 99.5 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mll3558 protein; PDBTitle: crystal structure of mll3558 protein from rhizobium loti. northeast2 structural genomics consortium target id mlr403 |
| 48 | d1xuva |  Alignment | not modelled | 99.5 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 49 | d1z94a1 |  Alignment | not modelled | 99.5 | 15 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 50 | c3ie5A |  Alignment | not modelled | 99.5 | 17 | PDB header: plant protein, biosynthetic protein Chain: A: PDB Molecule: phenolic oxidative coupling protein hyp-1; PDBTitle: crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis |
| 51 | c2lakA |  Alignment | not modelled | 99.5 | 16 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: ahsa1-like protein rhe_ch02687; PDBTitle: solution nmr structure of the ahsa1-like protein rhe_ch02687 (1-152)2 from rhizobium etli, northeast structural genomics consortium target3 rer242 |
| 52 | c3otlA |  Alignment | not modelled | 99.5 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: three-dimensional structure of the putative uncharacterized protein2 from rhizobium leguminosarum at the resolution 1.9a, northeast3 structural genomics consortium target rlr261 |

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|----|-------------------------|-----------|--------------|------|----|---|
| 53 | c3q64A | Alignment | not modelled | 99.5 | 13 | PDB header: structure genomics, unknown function Chain: A: PDB Molecule: mll3774 protein; PDBTitle: x-ray crystal structure of protein mll3774 from mesorhizobium loti,2 northeast structural genomics consortium target mlr405. |
| 54 | c2i9yA | Alignment | not modelled | 99.5 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: major latex protein-like protein 28 or mlp-like PDBTitle: solution structure of arabidopsis thaliana protein2 at1g70830, a member of the major latex protein family |
| 55 | d2qpva1 | Alignment | not modelled | 99.5 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: Atu1531-like |
| 56 | c6ggq9A | Alignment | not modelled | 99.4 | 15 | PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401 |
| 57 | d1xdfa1 | Alignment | not modelled | 99.4 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 58 | c3rwsA | Alignment | not modelled | 99.4 | 12 | PDB header: plant protein Chain: A: PDB Molecule: mtn13 protein; PDBTitle: crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin |
| 59 | c3q63F | Alignment | not modelled | 99.4 | 19 | PDB header: structural genomics, unknown function Chain: F: PDB Molecule: mll2253 protein; PDBTitle: x-ray crystal structure of protein mll2253 from mesorhizobium loti,2 northeast structural genomics consortium target mlr404. |
| 60 | c2lghA | Alignment | not modelled | 99.4 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99. |
| 61 | c2lcgA | Alignment | not modelled | 99.4 | 12 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein rmet_5065 from ralstonia2 metallidurans, northeast structural genomics consortium target crr115 |
| 62 | d1txca1 | Alignment | not modelled | 99.4 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 63 | c2l8oA | Alignment | not modelled | 99.3 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of chr148 from cytophaga hutchinsonii, northeast2 structural genomics consortium target chr148 |
| 64 | d1xn5a | Alignment | not modelled | 99.3 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 65 | c2m89A | Alignment | not modelled | 99.3 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea |
| 66 | d2il5a1 | Alignment | not modelled | 99.2 | 9 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 67 | c2nn5A | Alignment | not modelled | 99.1 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ef_2215; PDBTitle: structure of conserved protein of unknown function ef2215 from2 enterococcus faecalis |
| 68 | d3elia1 | Alignment | not modelled | 99.1 | 18 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 69 | d1zxfa1 | Alignment | not modelled | 99.1 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 70 | d2nn5a1 | Alignment | not modelled | 99.1 | 10 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 71 | d2k5ga1 | Alignment | not modelled | 99.1 | 17 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 72 | c2kewA | Alignment | not modelled | 99.1 | 8 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yndb; PDBTitle: the solution structure of bacillus subtilis sr211 start domain by nmr2 spectroscopy |
| 73 | c4r7kA | Alignment | not modelled | 99.1 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein jhp0584; PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori. |
| 74 | c3q6aH | Alignment | not modelled | 99.1 | 12 | PDB header: structure genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of the protein ssp2350 from staphylococcus2 saprophyticus, northeast structural genomics consortium target syr116 |
| 75 | c2luzA | Alignment | not modelled | 99.1 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: calu16; PDBTitle: solution nmr structure of calu16 from micromonospora echinospora,2 northeast structural genomics consortium (nesg) target mir12 |
| 76 | d1xn6a | Alignment | not modelled | 99.0 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |
| 77 | d1x53a1 | Alignment | not modelled | 98.9 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: AHSA1 domain |

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|----|-------------------------|-----------|--------------|------|----|---|
| 78 | c5z4eA_ | Alignment | not modelled | 98.9 | 13 | PDB header: biosynthetic protein Chain: A: PDB Molecule: txno9; PDBTitle: an anthrahydroquino-gama-pyrone synthase txn09 |
| 79 | c3oh8A_ | Alignment | not modelled | 98.7 | 15 | PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91 |
| 80 | c3ni8A_ | Alignment | not modelled | 98.6 | 17 | PDB header: unknown function Chain: A: PDB Molecule: pfc0360w protein; PDBTitle: crystal structure of pfc0360w, an hsp90 activator from plasmodium2 falciparum |
| 81 | c3qszB_ | Alignment | not modelled | 98.1 | 13 | PDB header: unknown function Chain: B: PDB Molecule: star-related lipid transfer protein; PDBTitle: 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 |
| 82 | d1vjha_ | Alignment | not modelled | 97.9 | 14 | Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like |
| 83 | c3p0lC_ | Alignment | not modelled | 97.1 | 10 | PDB header: transport protein Chain: C: PDB Molecule: steroidogenic acute regulatory protein, mitochondrial; PDBTitle: human steroidogenic acute regulatory protein |
| 84 | c3fo5A_ | Alignment | not modelled | 97.1 | 10 | PDB header: lipid transport Chain: A: PDB Molecule: thioesterase, adipose associated, isoform bfit2; PDBTitle: human start domain of acyl-coenzyme a thioesterase 11 (acot11) |
| 85 | d2psoa1 | Alignment | not modelled | 96.7 | 11 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 86 | c2r55B_ | Alignment | not modelled | 96.6 | 12 | PDB header: transport protein Chain: B: PDB Molecule: star-related lipid transfer protein 5; PDBTitle: human star-related lipid transfer protein 5 |
| 87 | c2mouA_ | Alignment | not modelled | 95.7 | 9 | PDB header: transport protein Chain: A: PDB Molecule: star-related lipid transfer protein 6; PDBTitle: solution structure of star-related lipid transfer domain protein 62 (stard6) |
| 88 | c1jssB_ | Alignment | not modelled | 93.6 | 8 | PDB header: lipid binding protein Chain: B: PDB Molecule: cholesterol-regulated start protein 4; PDBTitle: crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4). |
| 89 | d1jssa_ | Alignment | not modelled | 93.1 | 8 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 90 | d1em2a_ | Alignment | not modelled | 92.0 | 10 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 91 | c2e3rB_ | Alignment | not modelled | 87.9 | 12 | PDB header: lipid transport Chain: B: PDB Molecule: lipid-transfer protein cert; PDBTitle: crystal structure of cert start domain in complex with c18-2 ceramide (p1) |
| 92 | d1ln1a_ | Alignment | not modelled | 78.7 | 8 | Fold: TBP-like Superfamily: Bet v1-like Family: STAR domain |
| 93 | c3qzrC_ | Alignment | not modelled | 76.3 | 15 | PDB header: hormone receptor Chain: C: PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom |
| 94 | d2ffsa1 | Alignment | not modelled | 75.7 | 13 | Fold: TBP-like Superfamily: Bet v1-like Family: PA1206-like |
| 95 | c2lafA_ | Alignment | not modelled | 42.5 | 0 | PDB header: membrane protein Chain: A: PDB Molecule: lipoprotein 34; PDBTitle: nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc |
| 96 | c2psoC_ | Alignment | not modelled | 39.6 | 11 | PDB header: structural genomics, unknown function Chain: C: PDB Molecule: star-related lipid transfer protein 13; PDBTitle: human stard13 (dlc2) lipid transfer and protein localization domain |
| 97 | c3x0tA_ | Alignment | not modelled | 19.3 | 21 | PDB header: toxin Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pira |
| 98 | c5ys0A_ | Alignment | not modelled | 15.7 | 16 | PDB header: transport protein Chain: A: PDB Molecule: membrane-anchored lipid-binding protein ysp2; PDBTitle: crystal structure of the second starkin domain of lam2 in complex with2 ergosterol |
| 99 | c3i3fB_ | Alignment | not modelled | 12.2 | 13 | PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from giardia lamblia gl50803_14299 |