# Phyre$^2$

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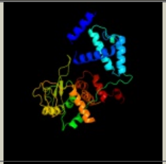
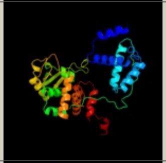
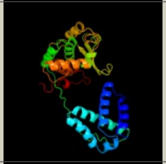
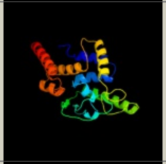
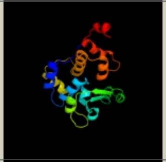
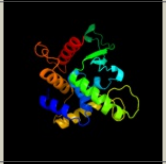
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76168 |
| Date | Thu Jan 5 12:20:01 GMT 2012 |
| Unique Job ID | e1e7c72ce2517992 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ma7A_ | Alignment |  | 100.0 | 13 | **PDB header:**hydrolase, ligase/dna<br>**Chain:** A: **PDB Molecule:**cre recombinase;<br>**PDBTitle:** crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27 |
| 2 | c1z1bA_ | Alignment |  | 100.0 | 16 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of a lambda integrase dimer bound to a2 coc' core site |
| 3 | c1crxA_ | Alignment |  | 100.0 | 13 | **PDB header:**replication/dna<br>**Chain:** A: **PDB Molecule:**cre recombinase;<br>**PDBTitle:** cre recombinase/dna complex reaction intermediate i |
| 4 | c2a3vA_ | Alignment |  | 100.0 | 15 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**site-specific recombinase inti4;<br>**PDBTitle:** structural basis for broad dna-specificity in integron2 recombination |
| 5 | d1p7da_ | Alignment |  | 100.0 | 16 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |
| 6 | c3nkhB_ | Alignment |  | 100.0 | 19 | **PDB header:**recombination<br>**Chain:** B: **PDB Molecule:**integrase;<br>**PDBTitle:** crystal structure of integrase from mrsa strain staphylococcus aureus |
| 7 | c1a0pA_ | Alignment |  | 100.0 | 19 | **PDB header:**dna recombination<br>**Chain:** A: **PDB Molecule:**site-specific recombinase xerd;<br>**PDBTitle:** site-specific recombinase, xerd |
| 8 | d1aiha_ | Alignment |  | 99.8 | 19 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |
| 9 | d1f44a2 | Alignment |  | 99.8 | 15 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |
| 10 | d1a0pa2 | Alignment |  | 99.7 | 20 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |
| 11 | d1ae9a_ | Alignment |  | 99.7 | 18 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |

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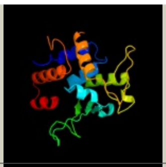
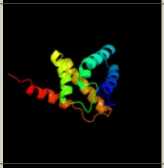
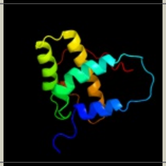
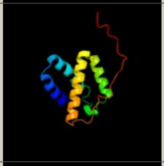
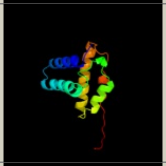
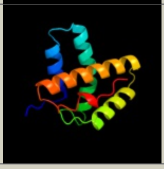
| 12 | d5crxb2_ | Alignment |  | 99.6 | 13 | **Fold:**DNA breaking-rejoining enzymes<br>**Superfamily:**DNA breaking-rejoining enzymes<br>**Family:**Lambda integrase-like, catalytic core |
| 13 | c2kd1A_ | Alignment |  | 99.6 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein;<br>**PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f |
| 14 | c2kj8A_ | Alignment |  | 99.5 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase;<br>**PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2 |
| 15 | c2kkpA_ | Alignment |  | 99.5 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**phage integrase;<br>**PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171). |
| 16 | c2kiwA_ | Alignment |  | 99.5 | 19 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**int protein;<br>**PDBTitle:** solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166). |
| 17 | c2khqA_ | Alignment |  | 99.5 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b |
| 18 | c3lysC_ | Alignment |  | 99.4 | 14 | **PDB header:**recombination<br>**Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase;<br>**PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f |
| 19 | c2kobA_ | Alignment |  | 99.4 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a |
| 20 | c3nrwA_ | Alignment |  | 99.4 | 17 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase;<br>**PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a |
| 21 | c2kj9A_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** nmr structure of intb phage-integrase-like protein fragment2 90-199 from erwinia carotova subsp. atroseptica: northeast3 structural genomics consortium target ewr217e |
| 22 | c2oxoA_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase |
| 23 | c2keyA_ | Alignment | not modelled | 99.4 | 8 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative phage integrase;<br>**PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c |
| 24 | c2kkvA_ | Alignment | not modelled | 99.4 | 13 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**integrase;<br>**PDBTitle:** solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h |
| 25 | c2khvA_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**phage integrase;<br>**PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b. |
| 26 | c2kj5A_ | Alignment | not modelled | 99.2 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**phage integrase;<br>**PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c |
| 27 | d1a0pa1 | Alignment | not modelled | 98.5 | 16 | **Fold:**SAM domain-like<br>**Superfamily:**lambda integrase-like, N-terminal domain |

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| | | | | | | **Family:**lambda integrase-like, N-terminal domain |
| 28 | d1f44a1 | Alignment | not modelled | 98.0 | 11 | **Fold:**SAM domain-like<br>**Superfamily:**lambda integrase-like, N-terminal domain<br>**Family:**lambda integrase-like, N-terminal domain |
| 29 | c2v6eB_ | Alignment | not modelled | 97.2 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protelemorase;<br>**PDBTitle:** protelomerase telk complexed with substrate dna |
| 30 | d1trra_ | Alignment | not modelled | 37.9 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 31 | d2d6ya1 | Alignment | not modelled | 28.9 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 32 | c2f4qA_ | Alignment | not modelled | 28.5 | 10 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**type i topoisomerase, putative;<br>**PDBTitle:** crystal structure of deinococcus radiodurans topoisomerase ib |
| 33 | c2h7fX_ | Alignment | not modelled | 27.8 | 15 | **PDB header:**isomerase/dna<br>**Chain:** X: **PDB Molecule:**dna topoisomerase 1;<br>**PDBTitle:** structure of variola topoisomerase covalently bound to dna |
| 34 | d1jhga_ | Alignment | not modelled | 26.1 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 35 | d1l8qa1 | Alignment | not modelled | 25.8 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV |
| 36 | c3fwcO_ | Alignment | not modelled | 21.6 | 11 | **PDB header:**cell cycle, transcription<br>**Chain:** O: **PDB Molecule:**protein sus1;<br>**PDBTitle:** sac3:sus1:cdc31 complex |
| 37 | d2auwa1 | Alignment | not modelled | 21.1 | 17 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**NE0471 C-terminal domain-like |
| 38 | c3sohB_ | Alignment | not modelled | 19.0 | 14 | **PDB header:**motor protein<br>**Chain:** B: **PDB Molecule:**flagellar motor switch protein flig;<br>**PDBTitle:** architecture of the flagellar rotor |
| 39 | c3lsgD_ | Alignment | not modelled | 18.7 | 13 | **PDB header:**transcription regulator<br>**Chain:** D: **PDB Molecule:**two-component response regulator yesn;<br>**PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586 |
| 40 | c1u78A_ | Alignment | not modelled | 18.6 | 8 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**transposable element tc3 transposase;<br>**PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna |
| 41 | c3ic7A_ | Alignment | not modelled | 17.1 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron |
| 42 | c3eetA_ | Alignment | not modelled | 17.0 | 14 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator |
| 43 | d1ijwc_ | Alignment | not modelled | 12.4 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 44 | d1hcra_ | Alignment | not modelled | 12.4 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Recombinase DNA-binding domain |
| 45 | d2aq0a1 | Alignment | not modelled | 11.0 | 16 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Hef domain-like |
| 46 | c3tqnC_ | Alignment | not modelled | 10.5 | 28 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family;<br>**PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii. |
| 47 | c3frwF_ | Alignment | not modelled | 9.9 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**putative trp repressor protein;<br>**PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum |
| 48 | d1fsea_ | Alignment | not modelled | 9.4 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 49 | d1a04a1 | Alignment | not modelled | 9.1 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 50 | c3bwgA_ | Alignment | not modelled | 9.0 | 10 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk;<br>**PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168 |
| 51 | c1x3uA_ | Alignment | not modelled | 8.9 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj;<br>**PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot |
| 52 | c2wv0H_ | Alignment | not modelled | 8.9 | 21 | **PDB header:**transcription<br>**Chain:** H: **PDB Molecule:**hth-type transcriptional repressor yvoa;<br>**PDBTitle:** crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis |
| 53 | d1s7oa | Alignment | not modelled | 8.9 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase |

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| | | | | | | sigma factors<br>**Family:**YlxM/p13-like |
| 54 | c2auwB_ | Alignment | not modelled | 8.1 | 17 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein ne0471;<br>**PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718 |
| 55 | c2b9sA_ | Alignment | not modelled | 7.9 | 12 | **PDB header:**isomerase/dna<br>**Chain:** A: **PDB Molecule:**topoisomerase i-like protein;<br>**PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex |
| 56 | c3neuA_ | Alignment | not modelled | 6.8 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lin1836 protein;<br>**PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262 |
| 57 | d1k78a1 | Alignment | not modelled | 6.7 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 58 | c2krfB_ | Alignment | not modelled | 6.5 | 13 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma;<br>**PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a |
| 59 | c2x48B_ | Alignment | not modelled | 6.4 | 26 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**cag38821;<br>**PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1 |
| 60 | c3fhkF_ | Alignment | not modelled | 6.3 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**upf0403 protein yphp;<br>**PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase |
| 61 | d1yioa1 | Alignment | not modelled | 6.3 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 62 | c2eqrA_ | Alignment | not modelled | 6.2 | 12 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1;<br>**PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1 |
| 63 | d1xc5a1 | Alignment | not modelled | 6.1 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 64 | d1bl0a2 | Alignment | not modelled | 6.0 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 65 | d1v4ra1 | Alignment | not modelled | 6.0 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**GntR-like transcriptional regulators |
| 66 | c2yqkA_ | Alignment | not modelled | 5.9 | 15 | **PDB header:**transcription/apoptosis<br>**Chain:** A: **PDB Molecule:**arginine-glutamic acid dipeptide repeats protein;<br>**PDBTitle:** solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats |
| 67 | c2rnjA_ | Alignment | not modelled | 5.7 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**response regulator protein vrar;<br>**PDBTitle:** nmr structure of the s. aureus vrar dna binding domain |
| 68 | d1lcda_ | Alignment | not modelled | 5.7 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 69 | d1rkta1 | Alignment | not modelled | 5.7 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 70 | d2g7la1 | Alignment | not modelled | 5.6 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 71 | c3by6C_ | Alignment | not modelled | 5.5 | 23 | **PDB header:**transcription regulator<br>**Chain:** C: **PDB Molecule:**predicted transcriptional regulator;<br>**PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni |
| 72 | c3korD_ | Alignment | not modelled | 5.5 | 18 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**possible trp repressor;<br>**PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 73 | d1m9ia2 | Alignment | not modelled | 5.5 | 16 | **Fold:**Annexin<br>**Superfamily:**Annexin<br>**Family:**Annexin |
| 74 | d1i4aa_ | Alignment | not modelled | 5.4 | 14 | **Fold:**Annexin<br>**Superfamily:**Annexin<br>**Family:**Annexin |
| 75 | d2csba1 | Alignment | not modelled | 5.4 | 23 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Topoisomerase V repeat domain |
| 76 | d1j09a1 | Alignment | not modelled | 5.4 | 12 | **Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases<br>**Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases<br>**Family:**C-terminal domain of glutamyl-tRNA synthetase (GluRS) |
| 77 | d1hm6a_ | Alignment | not modelled | 5.3 | 16 | **Fold:**Annexin<br>**Superfamily:**Annexin<br>**Family:**Annexin |
| 78 | d2gf5a1 | Alignment | not modelled | 5.3 | 8 | **Fold:**DEATH domain<br>**Superfamily:**DEATH domain<br>**Family:**DEATH domain, DD |
| 79 | d1d5ya2 | Alignment | not modelled | 5.2 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |

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| 80 | c2jpcA_ | Alignment | not modelled | 5.2 | 15 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**ssrb;<br>**PDBTitle:** ssrb dna binding protein |
| 81 | d2iw5b1 | Alignment | not modelled | 5.2 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 82 | d2ozga1 | Alignment | not modelled | 5.1 | 9 | **Fold:**SCP-like<br>**Superfamily:**SCP-like<br>**Family:**EF1021 C-terminal domain-like |
| 83 | d1efaa1 | Alignment | not modelled | 5.1 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**GalR/LacI-like bacterial regulator |
| 84 | c4a69C_ | Alignment | not modelled | 5.0 | 13 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**nuclear receptor corepressor 2;<br>**PDBTitle:** structure of hdac3 bound to corepressor and inositol tetraphosphate |
| 85 | c3f8mA_ | Alignment | not modelled | 5.0 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator;<br>**PDBTitle:** crystal structure of phnf from mycobacterium smegmatis |
| 86 | d2crga1 | Alignment | not modelled | 5.0 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |