



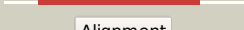

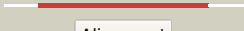









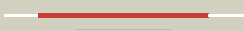





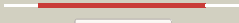

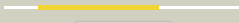






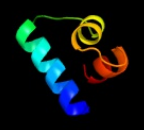









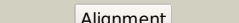



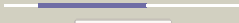



Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3204 (-) _3581311_3581616 |
| Date | Thu Aug 8 16:20:40 BST 2019 |
| Unique Job ID | 926d313673c5a14d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3gx4X |  Alignment |  | 100.0 | 40 | PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna |
| 2 | c2kimA |  Alignment |  | 100.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247. |
| 3 | c1sfeA |  Alignment |  | 100.0 | 25 | PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli |
| 4 | c4bhcA |  Alignment |  | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r37l variant |
| 5 | d1sfea1 |  Alignment |  | 100.0 | 26 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain |
| 6 | c1t39A |  Alignment |  | 100.0 | 30 | PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna |
| 7 | d1qnta1 |  Alignment |  | 100.0 | 29 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain |
| 8 | c4zyeA |  Alignment |  | 100.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase |
| 9 | c2g7hA |  Alignment |  | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529) |
| 10 | c1mgtA |  Alignment |  | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: protein (o6-methylguanine-dna methyltransferase); PDBTitle: crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1 |
| 11 | d1mgtal |  Alignment |  | 99.9 | 32 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain |

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|----|-------------------------|---|---|------|----|--|
| 12 | c1wrjA |  Alignment |  | 99.9 | 29 | PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfobolbus tokodaii |
| 13 | d1qgpa |  Alignment |  | 78.0 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain |
| 14 | d2cyya1 |  Alignment |  | 43.6 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 15 | d1xmka1 |  Alignment |  | 42.4 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain |
| 16 | d1qbjc |  Alignment |  | 28.5 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain |
| 17 | d2qxba1 |  Alignment |  | 27.3 | 12 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain |
| 18 | c1zgwA |  Alignment |  | 21.2 | 11 | PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna |
| 19 | c3i4pA |  Alignment |  | 20.9 | 15 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens |
| 20 | c4czdA |  Alignment |  | 20.4 | 14 | PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 21 | c2cfxD |  Alignment | not modelled | 19.7 | 18 | PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc |
| 22 | c4czdD |  Alignment | not modelled | 19.0 | 19 | PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway. |
| 23 | c1ilgA |  Alignment | not modelled | 18.7 | 21 | PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus |
| 24 | c2e1cA |  Alignment | not modelled | 18.4 | 18 | PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex |
| 25 | c2dbbA |  Alignment | not modelled | 18.4 | 13 | PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061 |
| 26 | c2y9xC |  Alignment | not modelled | 18.1 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: polyphenol oxidase; PDBTitle: crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone |
| 27 | c6j5bC |  Alignment | not modelled | 17.1 | 14 | PDB header: transcription/dna Chain: C: PDB Molecule: protein phosphate starvation response 1; PDBTitle: structural basis for the target dna recognition and binding by the myb2 domain of phosphate starvation response regulator 1 PDB header: ribosome |

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|----|-------------------------|-----------|--------------|------|----|---|
| 28 | c2xzm8 | Alignment | not modelled | 16.6 | 17 | Chain: 8: PDB Molecule: rps25e,; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 29 | c3b6aC | Alignment | not modelled | 15.5 | 24 | PDB header: transcription Chain: C: PDB Molecule: actr protein; PDBTitle: crystal structure of the streptomyces coelicolor tetr family protein2 actr in complex with actinorhodin |
| 30 | d2cg4a1 | Alignment | not modelled | 15.3 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 31 | d2cfxa1 | Alignment | not modelled | 14.8 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 32 | c5zreA | Alignment | not modelled | 14.6 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: tyrosinase; PDBTitle: tyrosinase from burkholderia thailandensis (bttyr) at high ph2 condition |
| 33 | c2dfwA | Alignment | not modelled | 13.8 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3 |
| 34 | d1s6la1 | Alignment | not modelled | 13.8 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like |
| 35 | c4pcqC | Alignment | not modelled | 13.5 | 23 | PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c) |
| 36 | c2l4aA | Alignment | not modelled | 12.9 | 14 | PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp |
| 37 | c3w6qC | Alignment | not modelled | 12.8 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: tyrosinase; PDBTitle: crystal structure of melb apo-protyrosinase from asperugillus oryzae |
| 38 | c2it0A | Alignment | not modelled | 12.5 | 16 | PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii |
| 39 | d1cf7b | Alignment | not modelled | 12.5 | 17 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp |
| 40 | c2l02B | Alignment | not modelled | 12.3 | 23 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375 |
| 41 | c2ia0A | Alignment | not modelled | 12.2 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864) |
| 42 | d1s99a | Alignment | not modelled | 11.3 | 31 | Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: Putative thiamin/HMP-binding protein YkoF |
| 43 | c2gqqB | Alignment | not modelled | 10.8 | 13 | PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp) |
| 44 | c3chmA | Alignment | not modelled | 10.8 | 13 | PDB header: plant protein Chain: A: PDB Molecule: cop9 signalosome complex subunit 7; PDBTitle: crystal structure of pci domain from a. thaliana cop9 signalosome2 subunit 7 (csn7) |
| 45 | c2vzbA | Alignment | not modelled | 10.5 | 28 | PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan |
| 46 | c4ouaB | Alignment | not modelled | 10.4 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: latent form of ppo4 tyrosinase; PDBTitle: coexistent single-crystal structure of latent and active mushroom2 tyrosinase (abppo4) mediated by a hexatungstotellurate(vi) |
| 47 | c1jfiA | Alignment | not modelled | 9.6 | 10 | PDB header: transcription/dna Chain: A: PDB Molecule: transcription regulator nc2 alpha chain; PDBTitle: crystal structure of the nc2-tbp-dna ternary complex |
| 48 | d1jfia | Alignment | not modelled | 9.6 | 10 | Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs |
| 49 | c5c17A | Alignment | not modelled | 9.3 | 21 | PDB header: lyase Chain: A: PDB Molecule: merb2; PDBTitle: crystal structure of the mercury-bound form of merb2 |
| 50 | c2e7xA | Alignment | not modelled | 9.2 | 10 | PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand |
| 51 | c2p6tH | Alignment | not modelled | 9.0 | 15 | PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis |
| 52 | c5xxuZ | Alignment | not modelled | 8.9 | 20 | PDB header: ribosome Chain: Z: PDB Molecule: ribosomal protein es25; PDBTitle: small subunit of toxoplasma gondii ribosome |
| 53 | c3ih9A | Alianment | not modelled | 8.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; |

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|----|--------------------------|-----------|--------------|-----|----|--|
| | | | | | | PDBTitle: crystal structure analysis of mglu in its tris form |
| 54 | c2cg4B | Alignment | not modelled | 8.8 | 18 | PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc |
| 55 | c3qthA | Alignment | not modelled | 8.5 | 21 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution |
| 56 | d2cqra1 | Alignment | not modelled | 8.4 | 21 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain |
| 57 | dluxca | Alignment | not modelled | 8.4 | 20 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 58 | c3u34D | Alignment | not modelled | 8.2 | 14 | PDB header: protein binding Chain: D: PDB Molecule: general stress protein; PDBTitle: crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri |
| 59 | dlg47a1 | Alignment | not modelled | 8.0 | 17 | Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain |
| 60 | dlilga1 | Alignment | not modelled | 7.4 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain |
| 61 | dlmkma1 | Alignment | not modelled | 7.3 | 10 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator IclR, N-terminal domain |
| 62 | c3db0B | Alignment | not modelled | 7.3 | 10 | PDB header: oxidoreductase Chain: B: PDB Molecule: lin2891 protein; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution |
| 63 | dl1mla1 | Alignment | not modelled | 7.2 | 21 | Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor |
| 64 | c5xyiZ | Alignment | not modelled | 7.2 | 20 | PDB header: ribosome Chain: Z: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 65 | d2ev0a1 | Alignment | not modelled | 7.0 | 19 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |
| 66 | c6btcA | Alignment | not modelled | 7.0 | 22 | PDB header: dna binding protein Chain: A: PDB Molecule: lp1413 - sccmec type iv-encoded dna binding protein; PDBTitle: sccmec type iv lp1413 - nucleic acids binding protein |
| 67 | d2isya1 | Alignment | not modelled | 6.9 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |
| 68 | c3t9aA | Alignment | not modelled | 6.7 | 21 | PDB header: transferase Chain: A: PDB Molecule: inositol pyrophosphate kinase; PDBTitle: crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0 |
| 69 | dl1u60a | Alignment | not modelled | 6.7 | 14 | Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase |
| 70 | c3frwF | Alignment | not modelled | 6.5 | 27 | PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trp protein from ruminococcus obeum |
| 71 | dl1biaa1 | Alignment | not modelled | 6.5 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like |
| 72 | c2ev5B | Alignment | not modelled | 6.5 | 19 | PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium |
| 73 | dl1bw6a | Alignment | not modelled | 6.2 | 14 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding |
| 74 | c3go5A | Alignment | not modelled | 6.2 | 18 | PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution |
| 75 | dl1rp3a1 | Alignment | not modelled | 6.1 | 38 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain |
| 76 | dl1g3wa1 | Alignment | not modelled | 6.1 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein |
| 77 | d2j85a1 | Alignment | not modelled | 6.1 | 19 | Fold: STIV B116-like Superfamily: STIV B116-like Family: STIV B116-like |
| 78 | dl1dwka1 | Alignment | not modelled | 6.1 | 10 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain |
| 79 | c3uo9B | Alignment | not modelled | 6.0 | 14 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; |

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|----|-------------------------|-----------|--------------|-----|----|---|
| | | | | | | PDBTitle: crystal structure of human gac in complex with glutamate and bptes |
| 80 | c3ss4C_ | Alignment | not modelled | 6.0 | 14 | PDB header: hydrolase Chain: C; PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form |
| 81 | c2iv1J_ | Alignment | not modelled | 5.9 | 10 | PDB header: lyase Chain: J; PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase |
| 82 | c6o6dA_ | Alignment | not modelled | 5.8 | 22 | PDB header: ligase Chain: A; PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori |
| 83 | c5w7sA_ | Alignment | not modelled | 5.6 | 35 | PDB header: transferase Chain: A; PDB Molecule: oxac; PDBTitle: crystal structure of oxac in complex with sinefungin and meleagrins |
| 84 | c4d18G_ | Alignment | not modelled | 5.5 | 16 | PDB header: signaling protein Chain: G; PDB Molecule: cop9 signalosome complex subunit 7a; PDBTitle: crystal structure of the cop9 signalosome |
| 85 | d1lcda_ | Alignment | not modelled | 5.5 | 28 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LacI-like bacterial regulator |
| 86 | d2ns0a1 | Alignment | not modelled | 5.4 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like |
| 87 | d1dpua_ | Alignment | not modelled | 5.4 | 18 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32 |
| 88 | c1dpuA_ | Alignment | not modelled | 5.4 | 18 | PDB header: dna binding protein Chain: A; PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88) |
| 89 | c1ponB_ | Alignment | not modelled | 5.4 | 24 | PDB header: calcium-binding protein Chain: B; PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr |
| 90 | c1f5tA_ | Alignment | not modelled | 5.3 | 16 | PDB header: transcription/dna Chain: A; PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence |
| 91 | c1dmIG_ | Alignment | not modelled | 5.2 | 21 | PDB header: dna binding protein/transferase Chain: G; PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol |