GDPRAN-NTF2 COMPLEX

1A2K

Display Files
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Sequence Display

The sequence display provides a graphical representation of the UniProtKB, PDB - ATOM and PDB - SEQRES sequences. Different 3rd party annotations can be graphically mapped on the sequence and displayed in the Jmol viewer.

The structure **1A2K** has in total **5** chains. These are represented by **2** sequence-unique entities.

Currently viewing **unique chains** only. **show all chains**

Sequence & Structure Relationships

Display Jmol

Enable Jmol to view annotations in 3

Chain A : NUCLEAR TRANSPORT FACTOR 2

FASTA | **Sequence & DSSP** | **Image**

Polymer 1
Length: 127 residues
Chain Type: polypeptide(L)
Reference: **UniProtKB** P61972

Display Parameters

Identical chains: **B** | show all chains

Currently displayed: **SEQRES sequen**

Display external (UniProtKB) seque

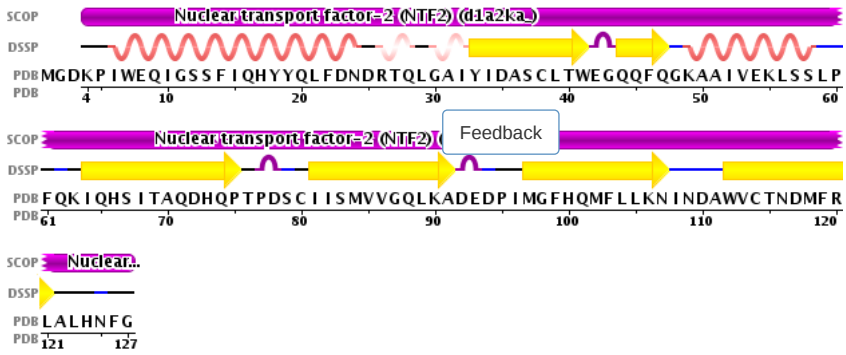
Mouse over an annotation to see more

Click annotation to enable Jmol.

Annotations *Add Annotations* Select

Domain Assignment:**SCOP** d1a2ka_ Nuclear transport factor-2 (NTF2): 124 residues
[hide] [reference]

Secondary Structure:**DSSP** 27% helical (4 helices; 35 residues)
[hide] [reference] 44% beta sheet (6 strands; 57 residues)



DSSP Legend

T: turn
E: beta strand
empty: no secondary structure assigned
G: 3/10-helix
S: bend
H: alpha helix

Chain D : RAN

FASTA | **Sequence & DSSP** | **Image**

Polymer 2
Length: 216 residues

Display Parameters

Identical chains: **C E** | show all chains

Chain Type: polypeptide(L)
Reference: **UniProtKB** P62825

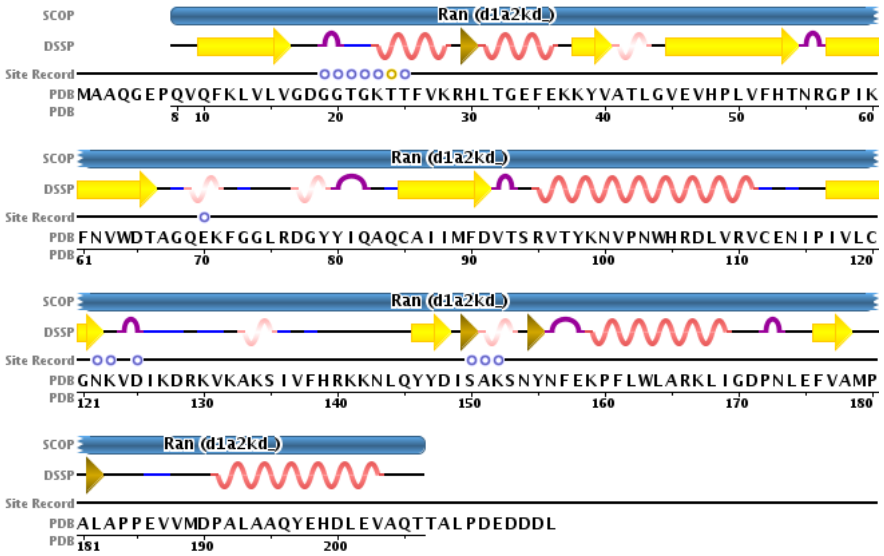
Currently displayed: **SEQRES sequen**
Display external (UniProtKB) seque
Mouse over an annotation to see more
Click annotation to enable Jmol.

Annotations

Domain Assignment:**SCOP** d1a2kd_ Ran: 199 residues
[hide] [reference]

Secondary Structure:**DSSP** 31% helical (10 helices; 68 residues)
[hide] [reference] 24% beta sheet (12 strands; 53 residues)

Structural Feature:**Site Record** 1A2K_D_AC6_19 BINDING SITE FOR RESIDUE GDP D 220 (SOFTWARE)
[hide] [reference] 1A2K_D_AC2_6 BINDING SITE FOR RESIDUE MG D 221 (SOFTWARE)



Site Record Legend
BINDING SITE FOR RESIDUE MG D 221 (SOFTWARE)
BINDING SITE FOR RESIDUE GDP D 220 (SOFTWARE)

DSSP Legend
T: turn
E: beta strand
empty: no secondary structure assigned
G: 3/10-helix
B: beta bridge
S: bend
H: alpha helix

Preferences

Jmol parameters

Show Jmol: No
Jmol width: 300 Jmol height: 300

Page parameters

Sequence to view: PDB SEQRES sequence Label residue ids by: ATOM record only
Sort chains by: Sort by polymer type then chain id
Font size: 12 Residues per row: 60
Chains to view: Unique chains (2 chains)
Chains per page: all (2)

Submit

References

The PDB to UniProt mapping is based on the data provided by the **EBI SIFTS** project. See also **Velankar et al., Nucleic Acids Research 33, D262-265 (2005)**.

SCOP Domain Assignment

SCOP: a structural classification of proteins database for the investigation of sequences and structures.
Murzin A.G., Brenner S.E., Hubbard T., Chothia C.
J Mol Biol 1995 Apr;247(4);536-40.
PMID: 7723011 PubMed

DSSP Secondary Structure

Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features.
Kabsch W., Sander C.
Biopolymers 1983 Dec;22(12);2577-637.
PMID: 6667333 PubMed

Site Record Structural Feature

MSDsite: a database search and retrieval system for the analysis and viewing of bound ligands and active sites.
Golovin A., Dimitropoulos D., Oldfield T., Rachedi A., Henrick K.
Proteins 2005 Jan;58(1);190-9.
PMID: 15468317 PubMed

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