



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 24, 2018 – 12:30 AM EST

PDB ID : 1QBK
Title : STRUCTURE OF THE KARYOPHERIN BETA2-RAN GPPNHP NUCLEAR TRANSPORT COMPLEX
Authors : Chook, Y.M.; Blobel, G.
Deposited on : 1999-04-23
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030736

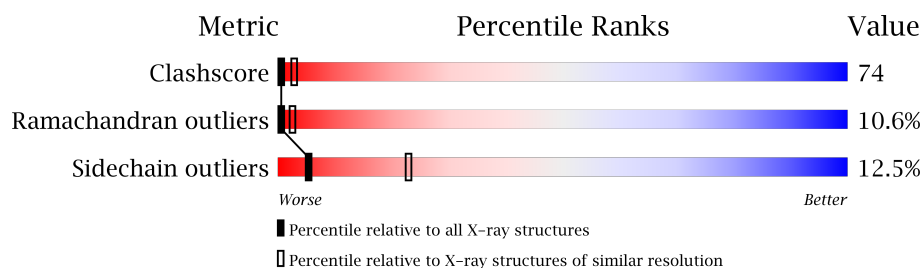
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

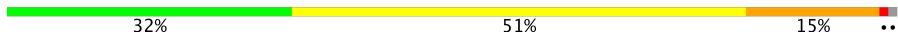

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	B	890	 32% 51% 15% ..
2	C	216	 24% 43% 19% • 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8572 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called KARYOPHERIN BETA2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	880	Total	C	N	O	S	Se	0	0	0
			7011	4471	1170	1320	26	24			

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	217	THR	ILE	CONFLICT	UNP Q92973
B	175	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	210	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	237	ARG	MET	MODIFIED RESIDUE	UNP Q92973
B	247	MET	MET	MODIFIED RESIDUE	UNP Q92973
B	254	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	261	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	308	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	429	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	432	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	482	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	564	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	566	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	575	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	624	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	641	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	672	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	680	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	710	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	739	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	743	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	749	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	789	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	820	MSE	MET	MODIFIED RESIDUE	UNP Q92973
B	852	MSE	MET	MODIFIED RESIDUE	UNP Q92973

- Molecule 2 is a protein called RAN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	190	Total	C	N	O	S	Se	0	0	0
			1528	993	265	264	3	3			

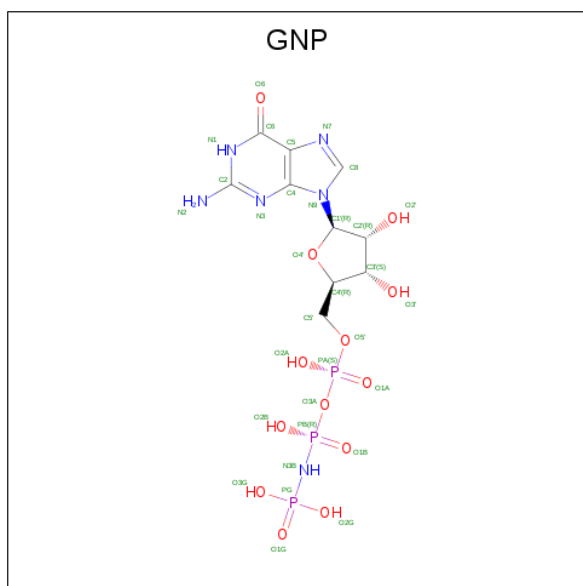
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	129	ARG	SER	CONFLICT	UNP P62826
C	89	MSE	MET	MODIFIED RESIDUE	UNP P62826
C	179	MSE	MET	MODIFIED RESIDUE	UNP P62826
C	189	MSE	MET	MODIFIED RESIDUE	UNP P62826

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



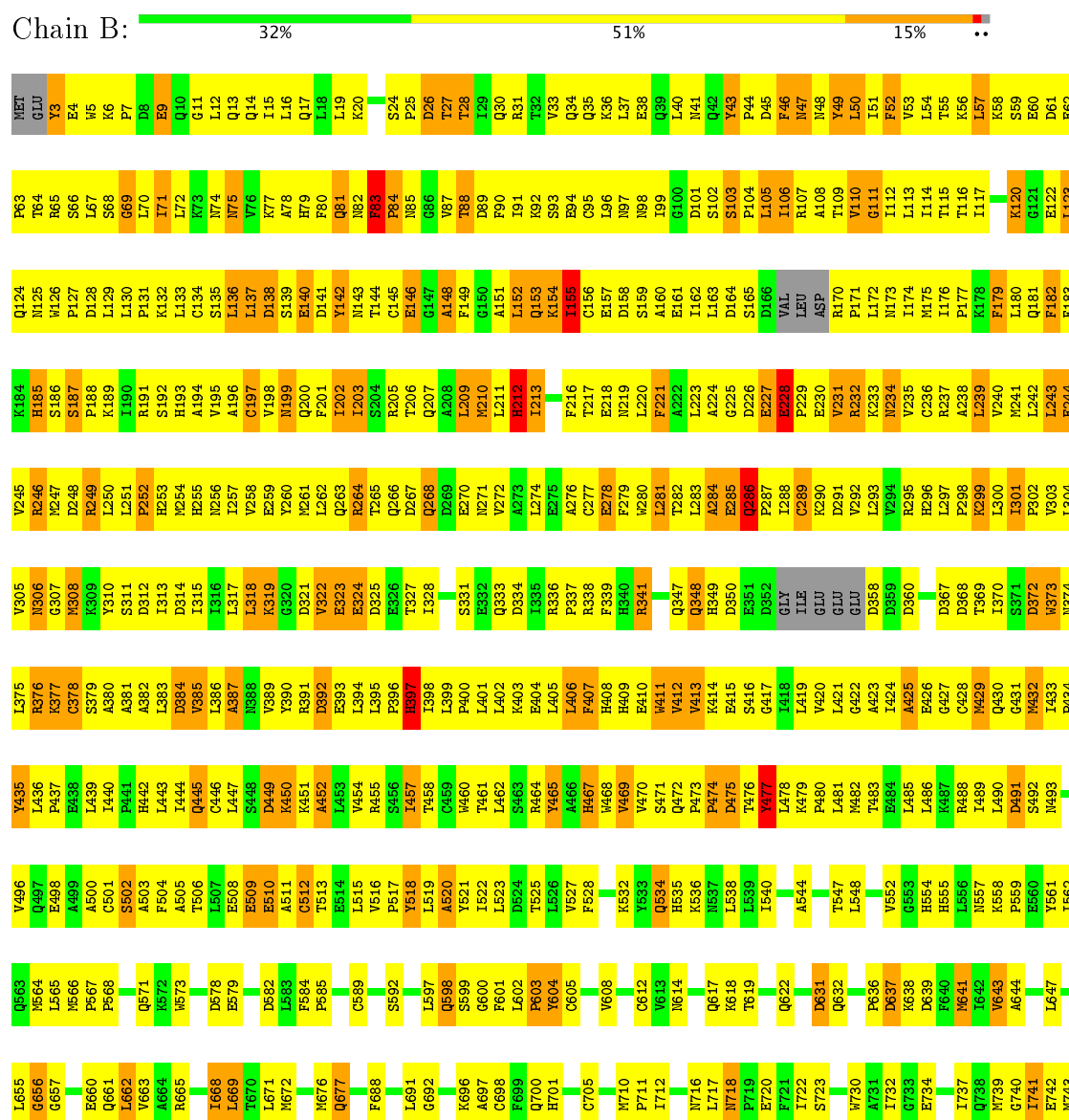
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

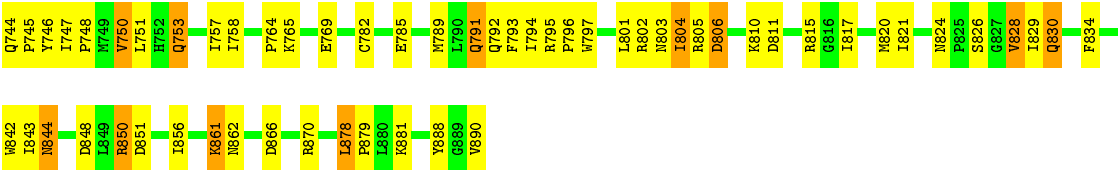
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

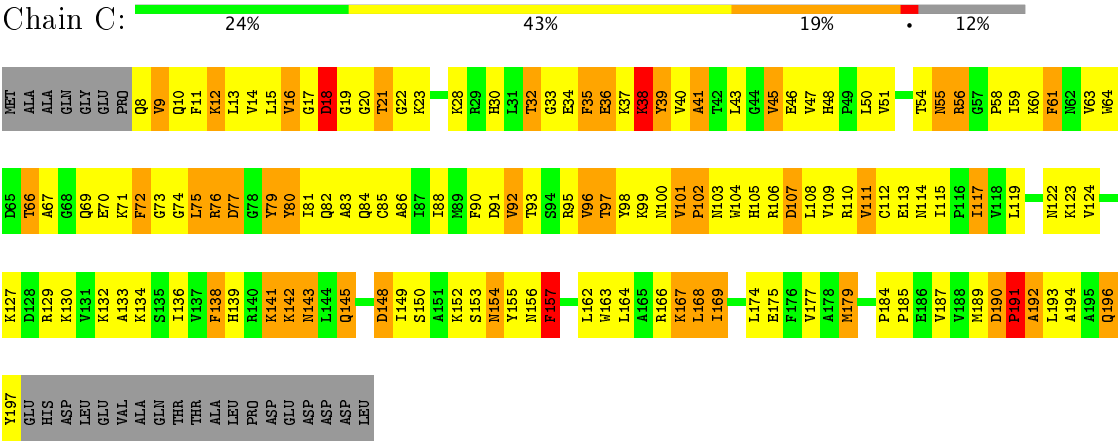
Note EDS was not executed.

• Molecule 1: KARYOPHERIN BETA2





• Molecule 2: RAN



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.11Å 133.11Å 138.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	500.00 – 3.00	Depositor
% Data completeness (in resolution range)	99.3 (500.00-3.00)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.267 , 0.315	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8572	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.56	2/7134 (0.0%)	0.71	0/9651
2	C	0.49	0/1564	0.69	0/2113
All	All	0.55	2/8698 (0.0%)	0.71	0/11764

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	605	CYS	CB-SG	-5.15	1.73	1.81
1	B	641	MSE	CG-SE	-5.03	1.78	1.95

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	7011	0	6991	1059	0
2	C	1528	0	1553	228	0
3	C	1	0	0	0	0
4	C	32	0	13	4	0
All	All	8572	0	8557	1265	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 74.

The worst 5 of 1265 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:83:ALA:HB3	2:C:112:CYS:SG	1.55	1.46
1:B:143:ASN:HA	1:B:148:ALA:O	1.42	1.17
1:B:196:ALA:HB2	1:B:233:LYS:HB3	1.31	1.12
2:C:12:LYS:HG2	2:C:83:ALA:HA	1.15	1.11
1:B:301:ILE:H	1:B:302:PRO:HD2	1.17	1.09

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	874/890 (98%)	604 (69%)	185 (21%)	85 (10%)	1	3
2	C	188/216 (87%)	130 (69%)	30 (16%)	28 (15%)	0	1
All	All	1062/1106 (96%)	734 (69%)	215 (20%)	113 (11%)	0	2

5 of 113 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	27	THR
1	B	50	LEU
1	B	81	GLN
1	B	83	PHE
1	B	103	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	790/778 (102%)	697 (88%)	93 (12%)	6	25
2	C	164/182 (90%)	138 (84%)	26 (16%)	3	14
All	All	954/960 (99%)	835 (88%)	119 (12%)	5	23

5 of 119 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	445	GLN
1	B	578	ASP
2	C	117	ILE
1	B	457	ILE
1	B	502	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	537	ASN
1	B	632	GLN
2	C	103	ASN
1	B	554	HIS
1	B	610	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	GNP	C	218	3	27,34,34	2.55	6 (22%)	26,54,54	1.29	3 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GNP	C	218	3	-	0/16/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	218	GNP	C4-N9	-6.84	1.38	1.47
4	C	218	GNP	C5-C6	-6.22	1.41	1.53
4	C	218	GNP	PG-O2G	-4.28	1.45	1.56
4	C	218	GNP	PB-O2B	-3.44	1.47	1.56
4	C	218	GNP	C8-N9	-2.98	1.37	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	218	GNP	O3G-PG-O2G	-2.53	100.60	107.69
4	C	218	GNP	O3G-PG-O1G	-2.21	107.80	113.41
4	C	218	GNP	O6-C6-C5	3.68	126.73	119.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	218	GNP	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.