



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1GCJ / pdb_00001gcj
Title : N-TERMINAL FRAGMENT OF IMPORTIN-BETA
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Deposited on : 2000-07-31
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

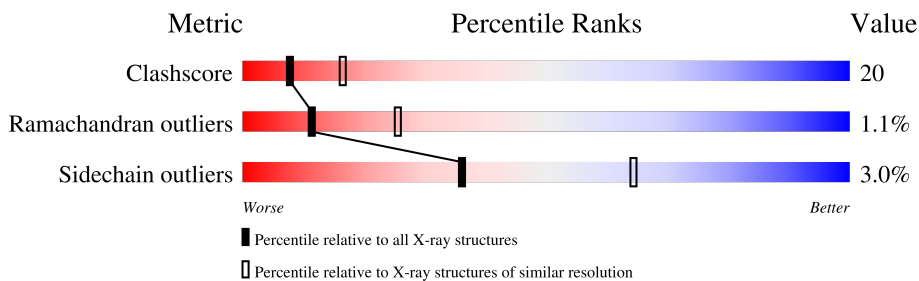
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	460	 63% 34% •
1	B	460	 65% 33% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7389 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 IMPORTIN BETA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	Se	0	0	0
			3589	2260	597	708	11	13			
1	B	460	Total	C	N	O	S	Se	0	0	0
			3589	2260	597	708	11	13			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P70168
A	146	MSE	MET	modified residue	UNP P70168
A	181	MSE	MET	modified residue	UNP P70168
A	219	MSE	MET	modified residue	UNP P70168
A	245	MSE	MET	modified residue	UNP P70168
A	252	MSE	MET	modified residue	UNP P70168
A	256	MSE	MET	modified residue	UNP P70168
A	268	MSE	MET	modified residue	UNP P70168
A	291	MSE	MET	modified residue	UNP P70168
A	353	MSE	MET	modified residue	UNP P70168
A	388	MSE	MET	modified residue	UNP P70168
A	410	MSE	MET	modified residue	UNP P70168
A	417	MSE	MET	modified residue	UNP P70168
A	450	VAL	-	cloning artifact	UNP P70168
A	451	PRO	-	cloning artifact	UNP P70168
A	452	ASN	-	cloning artifact	UNP P70168
A	453	SER	-	cloning artifact	UNP P70168
A	454	SER	-	cloning artifact	UNP P70168
A	500	PRO	-	cloning artifact	UNP P70168
A	501	ASP	-	cloning artifact	UNP P70168
A	502	TYR	-	cloning artifact	UNP P70168
A	503	ALA	-	cloning artifact	UNP P70168
A	504	SER	-	cloning artifact	UNP P70168
A	505	GLY	-	cloning artifact	UNP P70168
B	1	MSE	MET	modified residue	UNP P70168

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Chain	Residue	Modelled	Actual	Comment	Reference
B	146	MSE	MET	modified residue	UNP P70168
B	181	MSE	MET	modified residue	UNP P70168
B	219	MSE	MET	modified residue	UNP P70168
B	245	MSE	MET	modified residue	UNP P70168
B	252	MSE	MET	modified residue	UNP P70168
B	256	MSE	MET	modified residue	UNP P70168
B	268	MSE	MET	modified residue	UNP P70168
B	291	MSE	MET	modified residue	UNP P70168
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B	451	PRO	-	cloning artifact	UNP P70168
B	452	ASN	-	cloning artifact	UNP P70168
B	453	SER	-	cloning artifact	UNP P70168
B	454	SER	-	cloning artifact	UNP P70168
B	500	PRO	-	cloning artifact	UNP P70168
B	501	ASP	-	cloning artifact	UNP P70168
B	502	TYR	-	cloning artifact	UNP P70168
B	503	ALA	-	cloning artifact	UNP P70168
B	504	SER	-	cloning artifact	UNP P70168
B	505	GLY	-	cloning artifact	UNP P70168

- Molecule 2 is water.

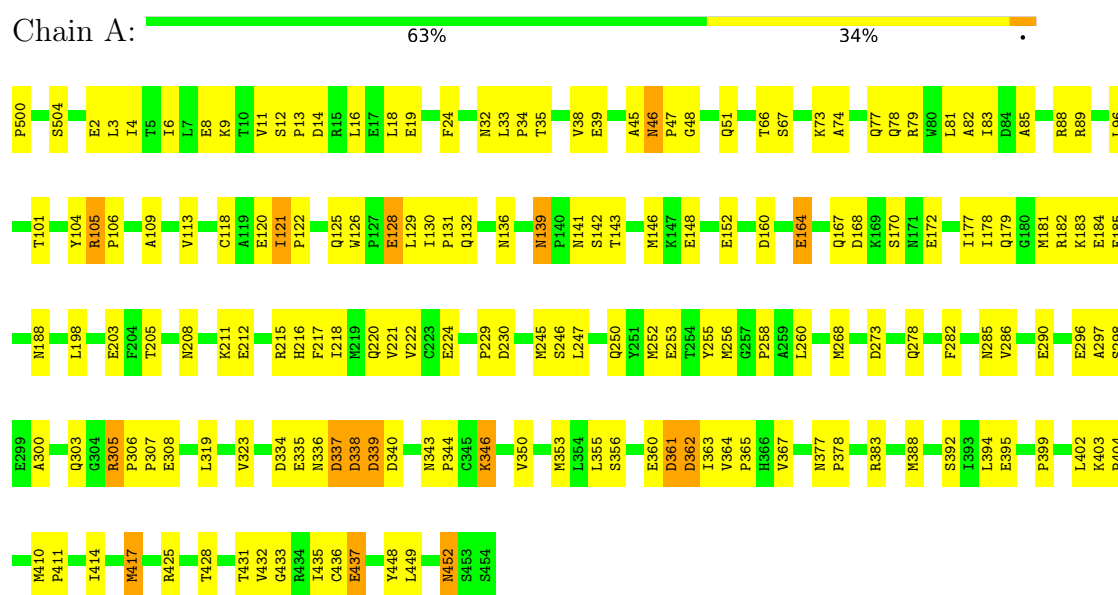
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	115	Total O 115 115	0	0
2	B	96	Total O 96 96	0	0

3 Residue-property plots

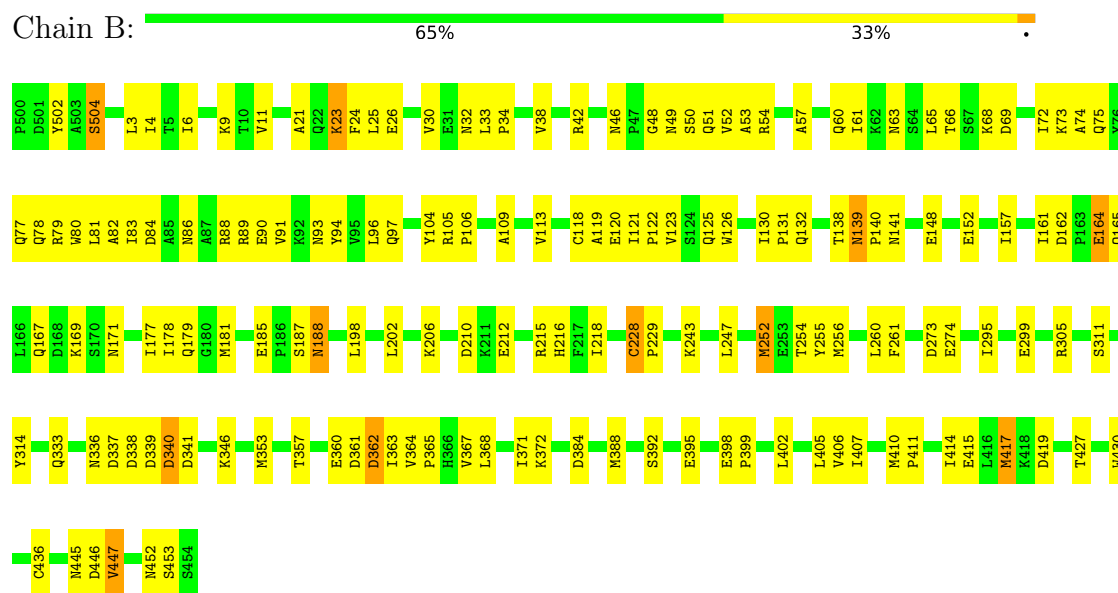
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: IMPORTIN BETA



• Molecule 1: IMPORTIN BETA



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.83Å 103.78Å 126.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.18 – 2.60	Depositor
% Data completeness (in resolution range)	97.9 (39.18-2.60)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.215 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7389	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A	0.41	0/3643	0.91	11/4938 (0.2%)
1	B	0.43	0/3643	0.89	12/4938 (0.2%)
All	All	0.42	0/7286	0.90	23/9876 (0.2%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	ASP	N-CA-C	-6.88	103.85	113.20
1	B	273	ASP	N-CA-C	6.28	118.12	111.28
1	B	252	MSE	N-CA-C	5.72	119.52	112.54
1	A	46	ASN	CA-C-N	5.70	125.38	119.56
1	A	46	ASN	C-N-CA	5.70	125.38	119.56

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A	3589	0	3563	144	0
1	B	3589	0	3563	147	0
2	A	115	0	0	15	0
2	B	96	0	0	7	0
All	All	7389	0	7126	285	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 20.

The worst 5 of 285 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)
1:A:105:ARG:HB3	1:A:106:PRO:HD3	1.44	0.99
1:B:105:ARG:HB3	1:B:106:PRO:HD3	1.45	0.98
1:B:188:ASN:HD22	1:B:188:ASN:H	1.12	0.95
1:A:170:SER:HB2	1:A:208:ASN:HD21	1.30	0.94
1:A:177:ILE:HG22	1:A:181:MSE:HE2	1.56	0.88

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	A	458/460 (100%)	436 (95%)	16 (4%)	6 (1%)	9	21
1	B	458/460 (100%)	439 (96%)	15 (3%)	4 (1%)	14	30
All	All	916/920 (100%)	875 (96%)	31 (3%)	10 (1%)	11	25

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	ASP
1	B	447	VAL
1	A	339	ASP
1	A	361	ASP
1	A	212	GLU

5.3.2 Protein sidechains [i](#)

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	A	399/386 (103%)	385 (96%)	14 (4%)	32	59
1	B	399/386 (103%)	389 (98%)	10 (2%)	42	69
All	All	798/772 (103%)	774 (97%)	24 (3%)	36	64

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	3	LEU
1	B	164	GLU
1	B	139	ASN
1	B	185	GLU
1	A	247	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	171	ASN
1	B	452	ASN
1	B	179	GLN
1	B	220	GLN
1	A	200	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.