

wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2023 – 10:23 PM EDT

PDB ID : 2OT8

Title : Karyopherin Beta2/Transportin-hnRNPM NLS Complex

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Deposited on : 2007-02-07

Resolution : 3.10 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 (i) 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 (1)) were used in the production of this report:

 $\begin{array}{ccc} \text{MolProbity} & : & 4.02\text{b-}467 \\ \text{Xtriage (Phenix)} & : & 1.13 \end{array}$

EDS: 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

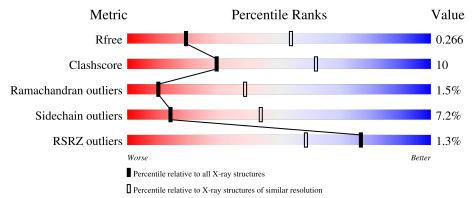
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 3.10 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\bf Similar \ resolution} \\ (\#{\bf Entries, \ resolution \ range(\AA)}) \end{array}$		
R_{free}	130704	1094 (3.10-3.10)		
Clashscore	141614	1184 (3.10-3.10)		
Ramachandran outliers	138981	1141 (3.10-3.10)		
Sidechain outliers	138945	1141 (3.10-3.10)		
RSRZ outliers	127900	1067 (3.10-3.10)		

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 <=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.

Mol	Chain	Length	Quality of chain				
1	A	852		74%	20%		
1	В	852	71	22%	• 5%		
2	С	30	43%	13%	43%		
2	D	30	53%	10% •	33%		



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 12802 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 Transportin-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	824	Total 6310	C 4040	N 1052	O 1167	S 51	0	0	0
1	В	813	Total 6196		N 1038	O 1145	S 50	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	GLY	-	linker	UNP Q92973
A	325	GLY	-	linker	UNP Q92973
A	326	SER	-	linker	UNP Q92973
A	327	GLY	-	linker	UNP Q92973
A	328	GLY	-	linker	UNP Q92973
В	324	GLY	-	linker	UNP Q92973
В	325	GLY	-	linker	UNP Q92973
В	326	SER	-	linker	UNP Q92973
В	327	GLY	-	linker	UNP Q92973
В	328	GLY	-	linker	UNP Q92973

• Molecule 2 is a protein called Heterogeneous nuclear ribonucleoprotein M.

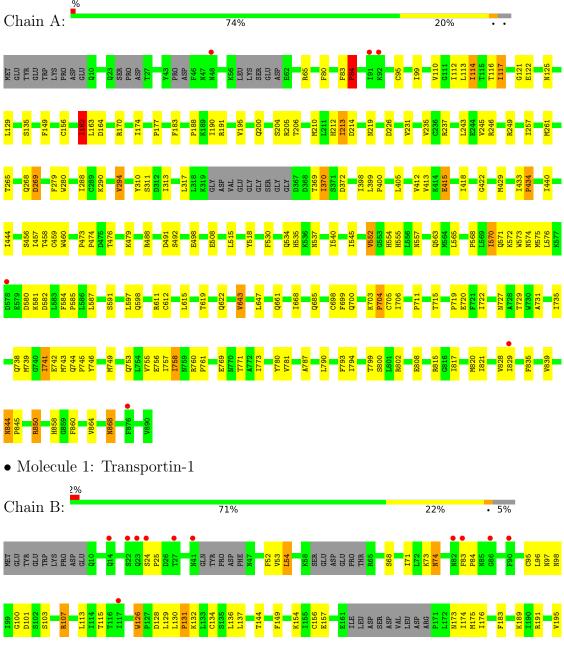
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
2	С	17	Total 135				0	0	0
2	D	20	Total 161		N 32	O 29	0	0	0



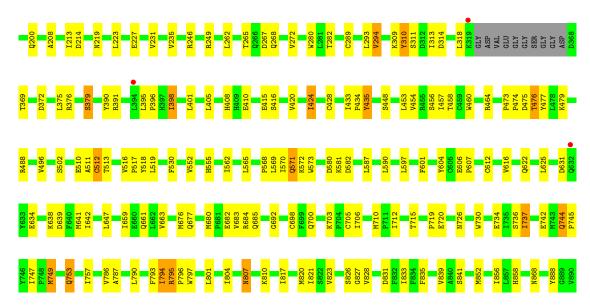
3 Residue-property plots (i)

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 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.

• Molecule 1: Transportin-1







• Molecule 2: Heterogeneous nuclear ribonucleoprotein M





• Molecule 2: Heterogeneous nuclear ribonucleoprotein M

Chain D: 53% 10% · 33%





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	153.20Å 155.00Å 141.53Å	D	
a, b, c, α , β , γ	90.00° 92.57° 90.00°	Depositor	
Resolution (Å)	50.00 - 3.10	Depositor	
Resolution (A)	48.46 - 3.00	EDS	
% Data completeness	98.8 (50.00-3.10)	Depositor	
(in resolution range)	96.1 (48.46-3.00)	EDS	
R_{merge}	0.07	Depositor	
R_{sum}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.69 (at 3.01Å)	Xtriage	
Refinement program	CNS 1.1	Depositor	
D.D.	0.255 , 0.290	Depositor	
R, R_{free}	0.228 , 0.266	DCC	
R_{free} test set	3234 reflections (5.08%)	wwPDB-VP	
Wilson B-factor (Å ²)	97.4	Xtriage	
Anisotropy	0.383	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32, 57.7	EDS	
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage	
	0.000 for k,h,-l		
Estimated twinning fraction	0.000 for -k,-h,-l	Xtriage	
	0.008 for -h,-k,l		
F_o, F_c correlation	0.95	EDS	
Total number of atoms	12802	wwPDB-VP	
Average B, all atoms (Å ²)	93.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 20.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.2968e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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		Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.42	0/6441	0.58	0/8775	
1	В	0.42	$2/6326 \ (0.0\%)$	0.56	1/8624 (0.0%)	
2	С	0.50	0/137	0.57	0/182	
2	D	0.50	0/164	0.62	0/218	
All	All	0.42	2/13068 (0.0%)	0.57	1/17799 (0.0%)	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
1	В	227	GLU	C-N	-5.57	1.21	1.34
1	В	570	ILE	C-N	5.27	1.46	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	В	25	PRO	N-CA-CB	5.74	110.19	103.30

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	6310	0	6131	115	0
1	В	6196	0	5960	124	0
2	С	135	0	119	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	161	0	157	3	0
All	All	12802	0	12367	240	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 10.

The worst 5 of 240 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:642:ILE:HD11	1:B:680:MET:HE3	1.38	1.04
1:A:746:TYR:HA	1:A:749:MET:HE3	1.61	0.83
1:B:821:ILE:HG12	1:B:828:VAL:HG21	1.63	0.80
1:A:112:ILE:O	1:A:116:THR:HG23	1.82	0.80
1:B:833:ILE:HD12	1:B:833:ILE:H	1.46	0.78

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	814/852 (96%)	743 (91%)	62 (8%)	9 (1%)	14 46
1	В	803/852 (94%)	721 (90%)	69 (9%)	13 (2%)	9 37
2	C	13/30 (43%)	10 (77%)	2 (15%)	1 (8%)	1 5
2	D	18/30 (60%)	11 (61%)	5 (28%)	2 (11%)	0 2
All	All	1648/1764 (93%)	1485 (90%)	138 (8%)	25 (2%)	10 39

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	PRO

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Mol	Chain	Res	Type
1	A	162	ILE
1	В	24	SER
1	В	512	CYS
2	D	55	LYS

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	Perce	entiles
1	A	673/762 (88%)	624 (93%)	49 (7%)	14	43
1	В	652/762~(86%)	606 (93%)	46 (7%)	14	44
2	С	13/26 (50%)	10 (77%)	3 (23%)	1	3
2	D	16/26 (62%)	16 (100%)	0	100	100
All	All	1354/1576 (86%)	1256 (93%)	98 (7%)	14	44

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	246	ARG
1	В	475	ASP
1	В	262	LEU
1	В	372	ASP
1	В	530	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	173	ASN
1	В	430	GLN
2	С	53	ASN
1	В	306	ASN
1	В	626	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 monosaccharides 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)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<rsrz></rsrz>	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	824/852 (96%)	-0.07	6 (0%) 87 75	49, 86, 136, 177	0
1	В	813/852 (95%)	0.04	14 (1%) 70 49	47, 87, 168, 200	0
2	С	17/30 (56%)	0.22	1 (5%) 22 10	66, 113, 147, 153	0
2	D	20/30 (66%)	0.17	0 100 100	67, 124, 165, 169	0
All	All	1674/1764 (94%)	-0.01	21 (1%) 77 59	47, 87, 156, 200	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	41	ASN	5.0
1	В	24	SER	4.3
1	В	27	THR	4.2
1	В	83	PHE	3.8
1	В	82	ASN	3.6

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.



6.5 Other polymers (i)

There are no such residues in this entry.

