



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2017 – 01:19 AM EDT

PDB ID : 4UAF
Title : Importin alpha 1 delta IBB in complex with Influenza PB2 nuclear localization domain
Authors : Pumroy, R.A.; Cingolani, G.
Deposited on : unknown
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

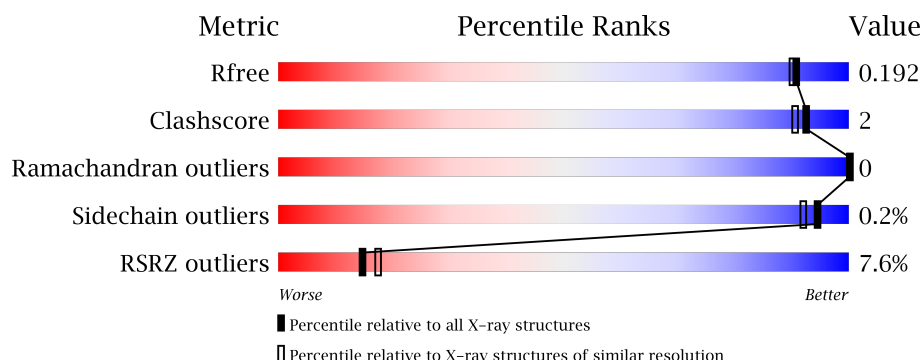
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
R_{free}	100719	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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.

Mol	Chain	Length	Quality of chain
1	B	466	<div> <div>4%</div> <div>87%</div> <div>9%</div> </div>
2	E	87	<div> <div>24%</div> <div>76%</div> <div>7%</div> <div>17%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4288 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 subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	425	Total	C	N	O	S	0	3	0
			3247	2069	549	619	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	64	MET	-	initiating methionine	UNP P52293
B	65	ALA	-	expression tag	UNP P52293
B	66	ASP	-	expression tag	UNP P52293
B	67	ILE	-	expression tag	UNP P52293
B	68	GLY	-	expression tag	UNP P52293
B	69	SER	ASN	engineered mutation	UNP P52293

- Molecule 2 is a protein called Polymerase basic protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	72	Total	C	N	O	S	0	1	0
			561	349	107	103	2			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	673	GLY	-	expression tag	UNP P31345
E	674	PRO	-	expression tag	UNP P31345
E	675	LEU	-	expression tag	UNP P31345
E	676	GLY	-	expression tag	UNP P31345
E	677	SER	-	expression tag	UNP P31345

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

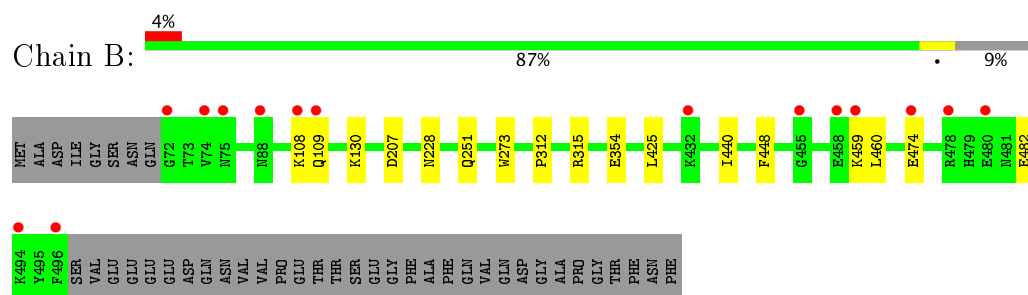
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	402	Total	O	0	0
			402	402		
4	E	68	Total	O	0	0
			68	68		

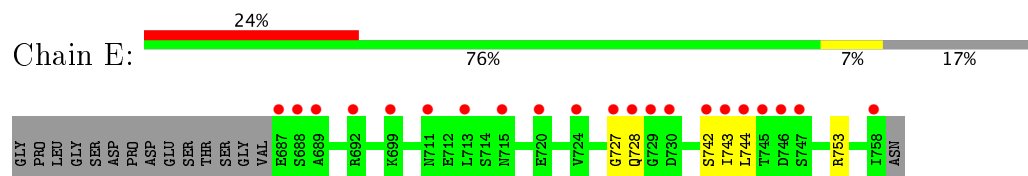
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: Importin subunit alpha-1



• Molecule 2: Polymerase basic protein 2



GLOBAL-STATISTICS INFOmissingINFO

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.34	0/3314	0.50	0/4516
2	E	0.25	0/566	0.47	0/755
All	All	0.33	0/3880	0.49	0/5271

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	3247	0	3330	13	0
2	E	561	0	607	4	0
3	B	10	0	0	0	0
4	B	402	0	0	1	0
4	E	68	0	0	0	0
All	All	4288	0	3937	14	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 2.

All (14) 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:B:315:ARG:HH12	2:E:743:ILE:HA	1.58	0.69
1:B:315:ARG:HH22	2:E:744:LEU:H	1.40	0.66
1:B:228:ASN:OD1	2:E:753[A]:ARG:NH2	2.25	0.61
1:B:207:ASP:OD1	1:B:251:GLN:NE2	2.32	0.60
1:B:482:GLU:HA	1:B:485:TYR:CE2	2.42	0.55
1:B:130:LYS:NZ	4:B:875:HOH:O	2.38	0.55
1:B:273:TRP:CD2	1:B:312:PRO:HB3	2.45	0.51
2:E:727:GLY:HA2	2:E:728:GLN:HA	1.55	0.48
1:B:425:LEU:HG	1:B:440:ILE:HG23	1.94	0.48
1:B:315:ARG:NH2	1:B:354:GLU:OE2	2.45	0.45
1:B:459:LYS:HB2	1:B:459:LYS:HE2	1.78	0.44
1:B:108:LYS:HA	1:B:109:GLN:HA	1.63	0.43
1:B:448:PHE:CD1	1:B:460:LEU:HD23	2.53	0.42
1:B:474:GLU:HA	1:B:492:ILE:HD11	2.01	0.41

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 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	426/466 (91%)	422 (99%)	4 (1%)	0	100	100
2	E	71/87 (82%)	69 (97%)	2 (3%)	0	100	100
All	All	497/553 (90%)	491 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

4.3.2 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	B	359/390 (92%)	359 (100%)	0	100	100
2	E	61/72 (85%)	60 (98%)	1 (2%)	68	53
All	All	420/462 (91%)	419 (100%)	1 (0%)	94	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	742	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

4.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

4.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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	$\# Z > 2$
3	PO4	B	601	-	4,4,4	0.71	0	6,6,6	0.44	0
3	PO4	B	602	-	4,4,4	0.73	0	6,6,6	0.40	0

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
3	PO4	B	601	-	-	0/0/0/0	0/0/0/0
3	PO4	B	602	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 Protein, DNA and RNA chains ⓘ

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, 95th 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>2	OWAB(Å ²)	Q<0.9
1	B	425/466 (91%)	-0.22	17 (4%) 39 44	17, 27, 61, 105	0
2	E	72/87 (82%)	1.29	21 (29%) 1 0	25, 47, 103, 119	0
All	All	497/553 (89%)	-0.00	38 (7%) 15 17	17, 28, 66, 119	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	743	ILE	10.3
1	B	108	LYS	7.6
2	E	758	ILE	7.5
2	E	745	THR	7.3
2	E	742	SER	6.7
2	E	727	GLY	6.4
2	E	728	GLN	6.4
1	B	109	GLN	5.9
2	E	746	ASP	5.8
2	E	713	LEU	4.7
1	B	74	VAL	4.3
2	E	688	SER	4.2
1	B	480	GLU	3.6
1	B	432	LYS	3.5
1	B	496	PHE	3.4
1	B	88	ASN	3.4
1	B	72	GLY	3.3
1	B	493	GLU	2.8
2	E	729	GLY	2.8
2	E	689	ALA	2.8
1	B	459	LYS	2.7
2	E	692	ARG	2.7
2	E	744	LEU	2.7
1	B	458	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
2	E	747	SER	2.5
2	E	720	GLU	2.4
2	E	711	ASN	2.3
1	B	75	ASN	2.3
1	B	485	TYR	2.3
2	E	730	ASP	2.3
2	E	715	ASN	2.2
1	B	478	ARG	2.2
1	B	455	GLY	2.1
1	B	494	LYS	2.1
2	E	687	GLU	2.1
2	E	699	LYS	2.0
2	E	724	VAL	2.0
1	B	474	GLU	2.0

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

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

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	PO4	B	602	5/5	0.98	0.09	0.01	62,62,62,63	0
3	PO4	B	601	5/5	0.97	0.18	-	48,48,49,49	0

5.5 Other polymers [i](#)

There are no such residues in this entry.