



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 7LF4 / pdb_000071f4
Title : Structure of importin a3 bound to the p50- and p65-NLSs
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Deposited on : 2021-01-15
Resolution : 2.85 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
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

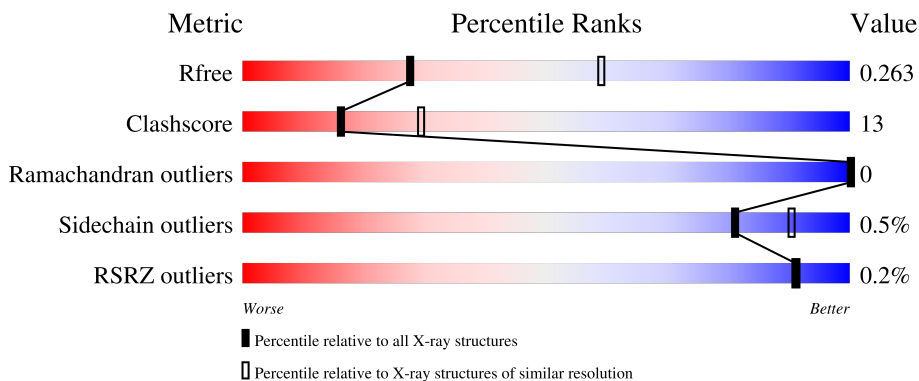
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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 $\leq 5\%$. 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	521	 59% 21% 20%
1	C	521	 56% 24% 20%
2	B	14	 29% 43% 7% 21%
2	F	14	 50% 21% 7% 21%
3	D	22	 59% 5% 36%

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Mol	Chain	Length	Quality of chain
3	E	22	 23% 32% 5% 41%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6859 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-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	416	3215	2041	544	616	14	3	1	0
1	C	416	3215	2041	544	616	14	0	1	0

- Molecule 2 is a protein called Nuclear factor NF-kappa-B p105 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	11	97	60	21	15	1	0	0	0
2	F	11	97	60	21	15	1	0	0	0

- Molecule 3 is a protein called Transcription factor p65.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	14	116	73	23	20	0	0	0
3	E	13	119	74	22	23	0	0	0

GLY
THR
PHE
GLY
PHE
ASN
SER
SER
ALA
ASN
VAL
PRO
THR
GLU
GLY
GLN
PHE

- Molecule 2: Nuclear factor NF-kappa-B p105 subunit

Chain B:  29% 43% 7% 21%

ASP
LYS
GLU
E433
V434
Q435
R436
K437
R438
Q439
K440
L441
M442
P443

- Molecule 2: Nuclear factor NF-kappa-B p105 subunit

Chain F:  50% 21% 7% 21%


ASP
LYS
GLU
E433
R436
Y437
R438
L441
M442
P443

- Molecule 3: Transcription factor p65

Chain D:  59% 5% 36%

ASP
ARG
HIS
ARG
I290
R296
S303
ILE
MET
LYS
LYS

- Molecule 3: Transcription factor p65

Chain E:  23% 32% 5% 41%

ASP
ARG
HIS
ARG
ILE
E291
R294
K295
R296
T297
Y298
E299
T300
F301
K302
S303
ILE
MET
LYS
LYS

4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.13Å 117.13Å 210.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	14.98 – 2.85 14.98 – 2.85	Depositor EDS
% Data completeness (in resolution range)	65.7 (14.98-2.85) 85.8 (14.98-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 2.86Å)	Xtrriage
Refinement program	PHENIX 1.18.2-3874	Depositor
R, R_{free}	0.197 , 0.238 0.230 , 0.263	Depositor DCC
R_{free} test set	1688 reflections (4.25%)	wwPDB-VP
Wilson B-factor (Å ²)	64.2	Xtrriage
Anisotropy	0.074	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6859	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

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	0.28	0/3278	0.64	2/4479 (0.0%)
1	C	0.25	0/3278	0.60	0/4479
2	B	0.27	0/97	0.75	0/126
2	F	0.22	0/97	0.62	0/126
3	D	0.19	0/117	0.64	0/153
3	E	0.28	0/120	0.74	0/156
All	All	0.27	0/6987	0.62	2/9519 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	LEU	CA-C-N	-5.26	113.84	122.79
1	A	73	LEU	C-N-CA	-5.26	113.84	122.79

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	3215	0	3239	82	0
1	C	3215	0	3239	93	0
2	B	97	0	109	11	0
2	F	97	0	109	9	0
3	D	116	0	113	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	119	0	119	6	0
All	All	6859	0	6928	180	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 13.

The worst 5 of 180 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:C:302:THR:HG22	1:C:342:ILE:HD11	1.59	0.83
1:C:466:GLN:HE22	1:C:481:ILE:HD13	1.42	0.83
1:A:96:ARG:HH11	2:B:442:MET:HE2	1.44	0.80
1:C:476:LEU:O	1:C:480:ILE:HD12	1.89	0.73
1:A:121:HIS:O	1:A:124:GLU:HG2	1.89	0.72

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	415/521 (80%)	401 (97%)	14 (3%)	0	100	100
1	C	415/521 (80%)	400 (96%)	15 (4%)	0	100	100
2	B	9/14 (64%)	9 (100%)	0	0	100	100
2	F	9/14 (64%)	9 (100%)	0	0	100	100
3	D	12/22 (54%)	11 (92%)	1 (8%)	0	100	100
3	E	11/22 (50%)	7 (64%)	4 (36%)	0	100	100
All	All	871/1114 (78%)	837 (96%)	34 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	365/460 (79%)	364 (100%)	1 (0%)	86	93
1	C	365/460 (79%)	365 (100%)	0	100	100
2	B	11/14 (79%)	10 (91%)	1 (9%)	9	19
2	F	11/14 (79%)	10 (91%)	1 (9%)	9	19
3	D	11/22 (50%)	11 (100%)	0	100	100
3	E	13/22 (59%)	12 (92%)	1 (8%)	12	25
All	All	776/992 (78%)	772 (100%)	4 (0%)	81	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	LEU
2	B	441	LEU
2	F	441	LEU
3	E	296	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	171	GLN
1	C	358	GLN
1	C	466	GLN
1	A	464	GLN
2	B	435	GLN

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](#)

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	A	416/521 (79%)	-0.65	1 (0%) 91 91	40, 66, 146, 230	1 (0%)
1	C	416/521 (79%)	-0.45	1 (0%) 91 91	36, 93, 188, 239	1 (0%)
2	B	11/14 (78%)	-0.11	0 100 100	72, 89, 107, 116	0
2	F	11/14 (78%)	0.29	0 100 100	104, 122, 170, 174	0
3	D	14/22 (63%)	0.10	0 100 100	63, 124, 154, 166	0
3	E	13/22 (59%)	-0.32	0 100 100	72, 97, 154, 176	0
All	All	881/1114 (79%)	-0.52	2 (0%) 91 91	36, 79, 174, 239	2 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	473	ILE	2.1
1	C	81	SER	2.0

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 oligosaccharides 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.