



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:29 PM UTC

PDB ID : 7RG1 / pdb_00007rg1
Title : Importin alpha2 in complex with MERS ORF4B H26A mutant
Authors : Munasinghe, T.S.; Tsimbalyuk, S.; Roby, J.A.; Aragao, D.; Forwood, J.K.
Deposited on : 2021-07-14
Resolution : 1.85 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

<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
Xtriage (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

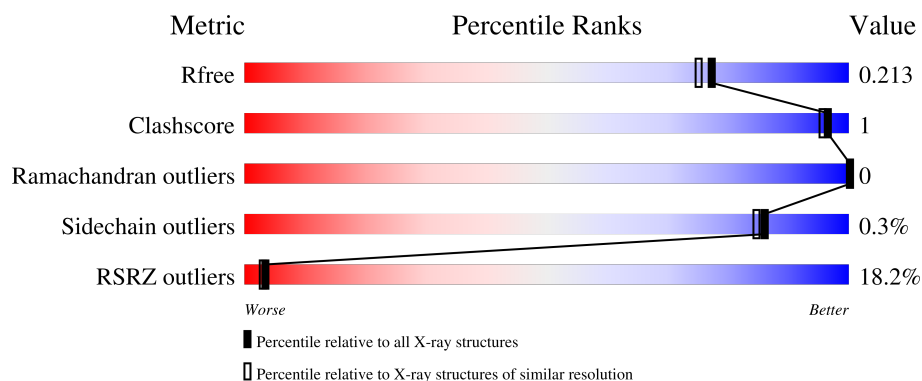
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	510	14% 80% 17%
2	B	21	57% 90% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7197 atoms, of which 3500 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
			Total	C	H	N	O	S			
1	A	425	6553	2063	3315	549	616	10	0	0	0

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	expression tag	UNP P52293
A	21	HIS	-	expression tag	UNP P52293
A	22	HIS	-	expression tag	UNP P52293
A	23	HIS	-	expression tag	UNP P52293
A	24	HIS	-	expression tag	UNP P52293
A	25	HIS	-	expression tag	UNP P52293
A	26	HIS	-	expression tag	UNP P52293
A	27	SER	-	expression tag	UNP P52293
A	28	SER	-	expression tag	UNP P52293
A	29	GLY	-	expression tag	UNP P52293
A	30	LEU	-	expression tag	UNP P52293
A	31	VAL	-	expression tag	UNP P52293
A	32	PRO	-	expression tag	UNP P52293
A	33	ARG	-	expression tag	UNP P52293
A	34	GLY	-	expression tag	UNP P52293
A	35	SER	-	expression tag	UNP P52293
A	36	GLY	-	expression tag	UNP P52293
A	37	MET	-	expression tag	UNP P52293
A	38	LEU	-	expression tag	UNP P52293
A	39	GLU	-	expression tag	UNP P52293
A	40	THR	-	expression tag	UNP P52293
A	41	ALA	-	expression tag	UNP P52293
A	42	ALA	-	expression tag	UNP P52293
A	43	ALA	-	expression tag	UNP P52293
A	44	LEU	-	expression tag	UNP P52293
A	45	PHE	-	expression tag	UNP P52293
A	46	GLU	-	expression tag	UNP P52293

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Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ARG	-	expression tag	UNP P52293
A	48	ASN	-	expression tag	UNP P52293
A	49	HIS	-	expression tag	UNP P52293
A	50	MET	-	expression tag	UNP P52293
A	51	ASP	-	expression tag	UNP P52293
A	52	SER	-	expression tag	UNP P52293
A	53	PRO	-	expression tag	UNP P52293
A	54	ASP	-	expression tag	UNP P52293
A	55	LEU	-	expression tag	UNP P52293
A	56	GLY	-	expression tag	UNP P52293
A	57	THR	-	expression tag	UNP P52293
A	58	ASP	-	expression tag	UNP P52293
A	59	ASP	-	expression tag	UNP P52293
A	60	ASP	-	expression tag	UNP P52293
A	61	ASP	-	expression tag	UNP P52293
A	62	LEU	-	expression tag	UNP P52293
A	63	ALA	-	expression tag	UNP P52293
A	64	MET	-	expression tag	UNP P52293
A	65	ALA	-	expression tag	UNP P52293
A	66	ASP	-	expression tag	UNP P52293
A	67	ILE	-	expression tag	UNP P52293
A	68	GLY	-	expression tag	UNP P52293
A	69	SER	-	expression tag	UNP P52293

- Molecule 2 is a protein called ORF4b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	19	Total	C	H	N	O	0	0	0
			350	104	185	38	23			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	26	ALA	HIS	engineered mutation	UNP T2BB21

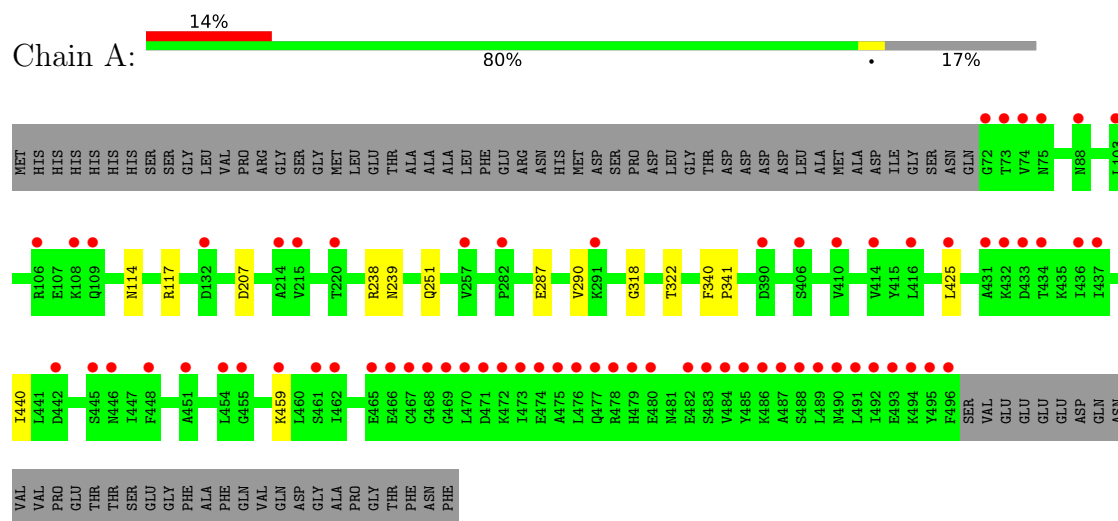
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	286	Total	O	0	0
			286	286		
3	B	8	Total	O	0	0
			8	8		

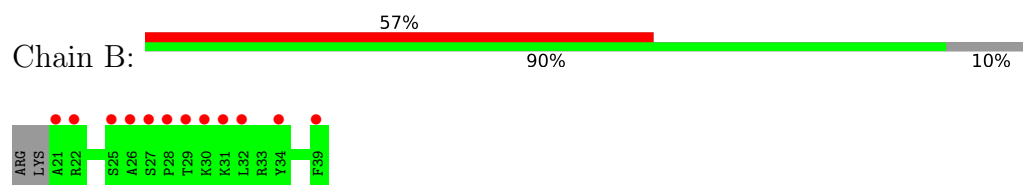
3 Residue-property plots [i](#)

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: Importin subunit alpha-1



• Molecule 2: ORF4b



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.95Å 89.65Å 100.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.63 – 1.85 29.63 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.63-1.85) 99.7 (29.63-1.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 1.85Å)	Xtriage
Refinement program	PHENIX 1.19rc4_4035	Depositor
R, R_{free}	0.200 , 0.211 0.201 , 0.213	Depositor DCC
R_{free} test set	3171 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7197	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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	0.12	0/3296	0.29	0/4492
2	B	0.10	0/167	0.29	0/218
All	All	0.12	0/3463	0.29	0/4710

There are no bond length outliers.

There are no bond angle outliers.

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	3238	3315	3315	7	0
2	B	165	185	188	0	0
3	A	286	0	0	0	0
3	B	8	0	0	0	0
All	All	3697	3500	3503	7	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 1.

All (7) 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:318:GLY:O	1:A:322:THR:HG23	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:LEU:HG	1:A:440:ILE:HG23	1.87	0.55
1:A:287:GLU:HA	1:A:290:VAL:HG22	1.91	0.52
1:A:207:ASP:OD1	1:A:251:GLN:NE2	2.46	0.48
1:A:340:PHE:N	1:A:341:PRO:CD	2.78	0.46
1:A:238:ARG:O	1:A:239:ASN:HB2	2.16	0.45
1:A:114:ASN:OD1	1:A:117:ARG:NH2	2.52	0.41

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	423/510 (83%)	418 (99%)	5 (1%)	0	100	100
2	B	17/21 (81%)	17 (100%)	0	0	100	100
All	All	440/531 (83%)	435 (99%)	5 (1%)	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	356/426 (84%)	355 (100%)	1 (0%)	86	85
2	B	17/19 (90%)	17 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	373/445 (84%)	372 (100%)	1 (0%)	86	85

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

Mol	Chain	Res	Type
1	A	459	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	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

6.1 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	A	425/510 (83%)	0.61	69 (16%) 4 4	22, 34, 84, 103	0
2	B	19/21 (90%)	2.68	12 (63%) 0 0	37, 54, 97, 103	0
All	All	444/531 (83%)	0.70	81 (18%) 3 3	22, 35, 87, 103	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	32	LEU	6.2
1	A	485	TYR	6.0
1	A	72	GLY	5.6
1	A	492	ILE	5.2
1	A	496	PHE	5.0
1	A	434	THR	5.0
1	A	489	LEU	4.8
1	A	487	ALA	4.8
1	A	467	CYS	4.8
2	B	28	PRO	4.7
1	A	484	VAL	4.6
1	A	470	LEU	4.5
2	B	29	THR	4.3
1	A	491	LEU	4.3
1	A	74	VAL	4.2
2	B	21	ALA	4.0
2	B	26	ALA	4.0
1	A	73	THR	3.8
2	B	39	PHE	3.6
1	A	477	GLN	3.6
1	A	495	TYR	3.4
1	A	475	ALA	3.4
1	A	88	ASN	3.4
2	B	30	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	31	LYS	3.3
2	B	34	TYR	3.3
1	A	473	ILE	3.3
1	A	486	LYS	3.2
1	A	432	LYS	3.2
1	A	462	ILE	3.0
1	A	448	PHE	3.0
1	A	483	SER	2.9
1	A	488	SER	2.9
1	A	468	GLY	2.9
1	A	480	GLU	2.8
1	A	257	VAL	2.8
1	A	414	VAL	2.7
1	A	482	GLU	2.7
1	A	215	VAL	2.7
1	A	410	VAL	2.7
2	B	22	ARG	2.6
1	A	494	LYS	2.6
1	A	451	ALA	2.6
1	A	436	ILE	2.6
1	A	469	GLY	2.6
1	A	479	HIS	2.5
1	A	478	ARG	2.5
2	B	27	SER	2.5
1	A	474	GLU	2.5
1	A	461	SER	2.4
1	A	431	ALA	2.4
1	A	455	GLY	2.4
1	A	476	LEU	2.3
1	A	291	LYS	2.3
1	A	416	LEU	2.3
1	A	446	ASN	2.3
1	A	490	ASN	2.3
1	A	108	LYS	2.3
1	A	75	ASN	2.3
1	A	103	LEU	2.3
1	A	425	LEU	2.2
1	A	437	ILE	2.2
1	A	472	LYS	2.2
1	A	109	GLN	2.2
1	A	465	GLU	2.2
1	A	493	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	433	ASP	2.2
1	A	445	SER	2.2
1	A	132	ASP	2.1
1	A	406	SER	2.1
1	A	214	ALA	2.1
1	A	454	LEU	2.1
1	A	442	ASP	2.1
1	A	282	PRO	2.1
1	A	390	ASP	2.1
1	A	471	ASP	2.1
1	A	466	GLU	2.0
1	A	220	THR	2.0
1	A	459	LYS	2.0
2	B	25	SER	2.0
1	A	106	ARG	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.