



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 21, 2021 – 04:02 PM EDT

PDB ID : 7RFY
Title : Importin alpha3 in complex with MERS ORF4B
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Deposited on : 2021-07-14
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.22
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

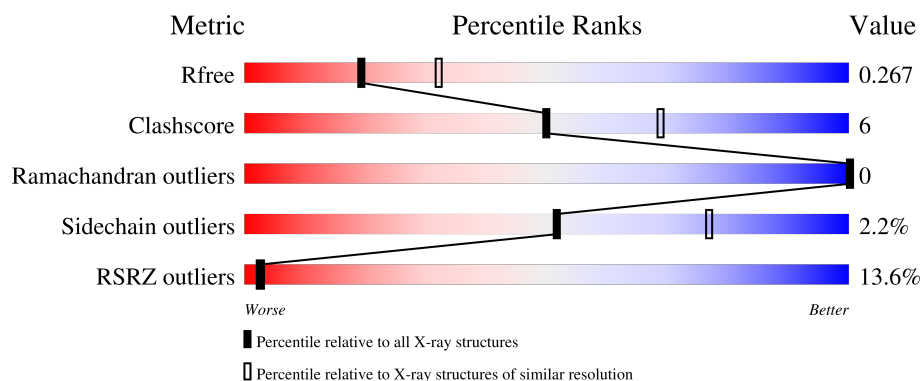
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	459	
2	B	21	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6190 atoms, of which 3047 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
1	A	389	Total	C	H	N	O	S	0	0	0
			5904	1915	2900	510	567	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	SER	-	expression tag	UNP O00629

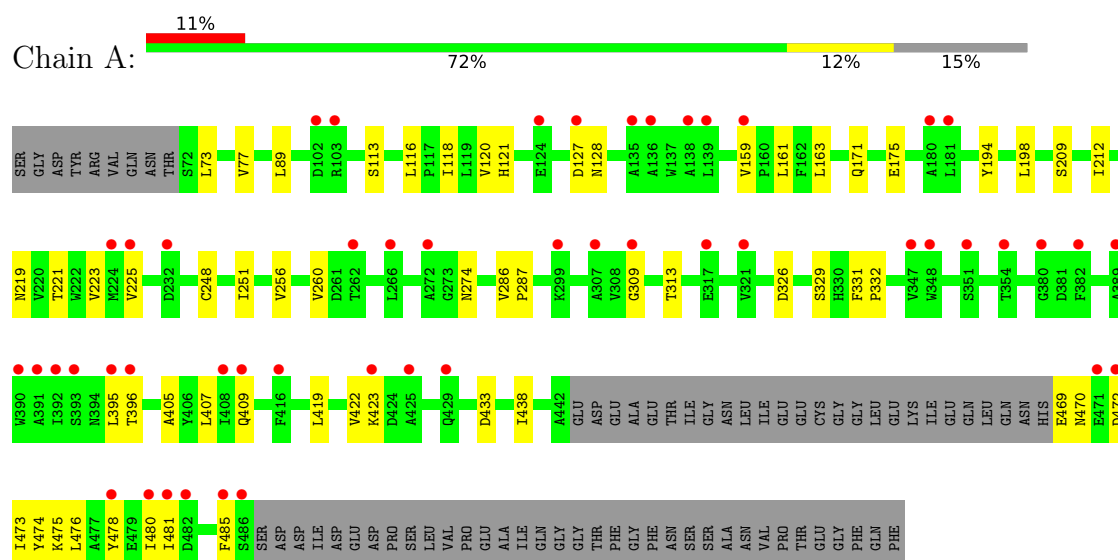
- Molecule 2 is a protein called ORF4b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	15	Total	C	H	N	O	0	0	0
			286	86	147	34	19			

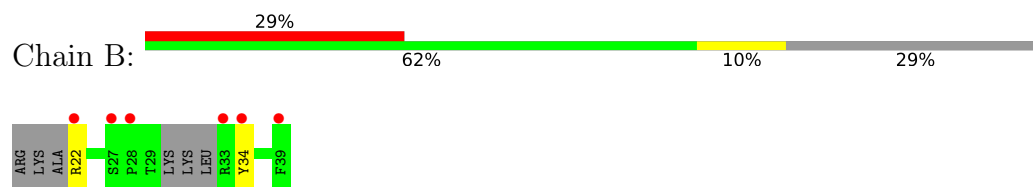
3 Residue-property plots [i](#)

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-3



• Molecule 2: ORF4b



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.22Å 59.71Å 82.64Å 90.00° 98.89° 90.00°	Depositor
Resolution (Å)	25.99 – 2.50 25.99 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.6 (25.99-2.50) 97.6 (25.99-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.50Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.249 , 0.267 0.249 , 0.267	Depositor DCC
R_{free} test set	785 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6190	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% 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

5.1 Standard geometry

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	0.26	0/3062	0.40	0/4187
2	B	0.23	0/141	0.44	0/183
All	All	0.26	0/3203	0.40	0/4370

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

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	3004	2900	3042	37	0
2	B	139	147	147	0	0
All	All	3143	3047	3189	37	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 6.

All (37) 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:481:ILE:O	1:A:485:PHE:HB3	1.96	0.65
1:A:396:THR:HG21	1:A:438:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:LEU:O	1:A:77:VAL:HG23	2.01	0.60
1:A:221:THR:O	1:A:225:VAL:HG23	2.03	0.58
1:A:309:GLY:O	1:A:313:THR:HG23	2.06	0.56
1:A:395:LEU:HD23	1:A:395:LEU:O	2.07	0.54
1:A:478:TYR:HA	1:A:481:ILE:HG12	1.90	0.52
1:A:171:GLN:NE2	1:A:175:GLU:OE1	2.43	0.52
1:A:209:SER:O	1:A:212:ILE:HG22	2.10	0.52
1:A:478:TYR:HA	1:A:481:ILE:CD1	2.40	0.52
1:A:120:VAL:HG13	1:A:161:LEU:HD12	1.92	0.51
1:A:469:GLU:HG2	1:A:474:TYR:CE2	2.47	0.50
1:A:476:LEU:O	1:A:480:ILE:HG13	2.12	0.50
1:A:219:ASN:O	1:A:223:VAL:HG23	2.11	0.49
1:A:478:TYR:HA	1:A:481:ILE:HD11	1.94	0.49
1:A:395:LEU:HD22	1:A:407:LEU:HD11	1.94	0.49
1:A:470:ASN:OD1	1:A:472:ASP:HB2	2.14	0.48
1:A:326:ASP:OD1	1:A:329:SER:OG	2.31	0.47
1:A:331:PHE:N	1:A:332:PRO:CD	2.78	0.47
1:A:478:TYR:O	1:A:481:ILE:HG12	2.15	0.47
1:A:419:LEU:O	1:A:422:VAL:HG22	2.15	0.47
1:A:116:LEU:O	1:A:120:VAL:HG23	2.15	0.46
1:A:77:VAL:HG13	1:A:118:ILE:HD12	1.97	0.46
1:A:395:LEU:HD22	1:A:407:LEU:CD1	2.46	0.45
1:A:478:TYR:HA	1:A:481:ILE:CG1	2.47	0.44
1:A:256:VAL:O	1:A:260:VAL:HG23	2.18	0.44
1:A:194:TYR:CZ	1:A:198:LEU:HD11	2.53	0.43
1:A:77:VAL:HG21	1:A:113:SER:HB2	2.01	0.43
1:A:433:ASP:HA	1:A:476:LEU:HD21	2.01	0.43
1:A:286:VAL:N	1:A:287:PRO:CD	2.82	0.42
1:A:127:ASP:OD1	1:A:127:ASP:N	2.52	0.42
1:A:473:ILE:HG22	1:A:474:TYR:N	2.35	0.42
1:A:159:VAL:O	1:A:163:LEU:HD23	2.20	0.41
1:A:470:ASN:HB3	1:A:473:ILE:HD13	2.02	0.41
1:A:248:CYS:O	1:A:251:ILE:HG22	2.21	0.41
1:A:476:LEU:HG	1:A:480:ILE:HD11	2.02	0.41
1:A:405:ALA:O	1:A:409:GLN:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	385/459 (84%)	374 (97%)	11 (3%)	0	100	100
2	B	11/21 (52%)	11 (100%)	0	0	100	100
All	All	396/480 (82%)	385 (97%)	11 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	341/400 (85%)	335 (98%)	6 (2%)	59	81
2	B	15/20 (75%)	13 (87%)	2 (13%)	4	7
All	All	356/420 (85%)	348 (98%)	8 (2%)	52	77

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	LEU
1	A	121	HIS
1	A	128	ASN
1	A	274	ASN
1	A	423	LYS
1	A	475	LYS
2	B	22	ARG
2	B	34	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	ASN
1	A	132	GLN
1	A	176	GLN
1	A	226	ASN
1	A	274	ASN
1	A	352	ASN
1	A	385	GLN
1	A	403	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 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

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	389/459 (84%)	0.78	49 (12%) 3 3	51, 78, 121, 143	0
2	B	15/21 (71%)	1.43	6 (40%) 0 0	69, 87, 121, 124	0
All	All	404/480 (84%)	0.80	55 (13%) 3 2	51, 79, 121, 143	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	485	PHE	7.0
1	A	478	TYR	6.7
1	A	391	ALA	5.5
1	A	425	ALA	5.4
1	A	389	ALA	5.2
1	A	471	GLU	5.1
1	A	382	PHE	4.7
2	B	39	PHE	4.0
1	A	486	SER	3.8
2	B	28	PRO	3.7
1	A	103	ARG	3.7
1	A	396	THR	3.6
1	A	423	LYS	3.6
1	A	136	ALA	3.5
1	A	392	ILE	3.2
1	A	480	ILE	3.2
1	A	429	GLN	3.2
1	A	393	SER	3.2
1	A	351	SER	3.2
1	A	409	GLN	3.2
1	A	139	LEU	3.1
1	A	135	ALA	3.1
2	B	34	TYR	3.1
1	A	472	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	266	LEU	2.9
1	A	272	ALA	2.9
1	A	390	TRP	2.8
2	B	27	SER	2.8
1	A	181	LEU	2.7
1	A	180	ALA	2.7
1	A	481	ILE	2.6
1	A	317	GLU	2.6
2	B	22	ARG	2.5
1	A	416	PHE	2.5
1	A	159	VAL	2.5
1	A	138	ALA	2.5
1	A	127	ASP	2.5
1	A	225	VAL	2.4
1	A	321	VAL	2.4
1	A	348	TRP	2.4
1	A	262	THR	2.4
1	A	395	LEU	2.4
1	A	482	ASP	2.3
1	A	299	LYS	2.2
1	A	309	GLY	2.2
1	A	347	VAL	2.2
1	A	224	MET	2.2
1	A	232	ASP	2.2
1	A	380	GLY	2.2
1	A	354	THR	2.1
1	A	408	ILE	2.1
1	A	307	ALA	2.1
2	B	33	ARG	2.1
1	A	124	GLU	2.1
1	A	102	ASP	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 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.