



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 24, 2022 – 12:10 pm GMT

PDB ID : 7QJJ  
Title : X-Ray Structure of a Mn<sup>2+</sup> soak of EleNRMT in complex with two Nanobodies at 4.6Å  
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Deposited on : 2021-12-16  
Resolution : 4.60 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](mailto: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.

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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	:	2.24
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

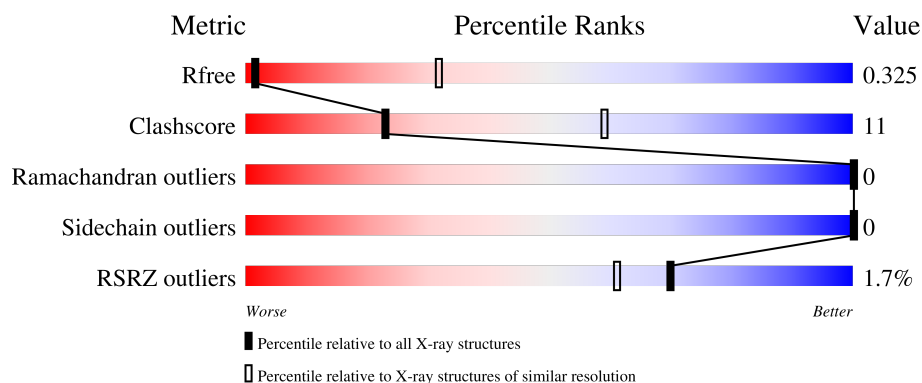
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.60 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	1062 (5.40-3.80)
Clashscore	141614	1130 (5.40-3.80)
Ramachandran outliers	138981	1074 (5.40-3.80)
Sidechain outliers	138945	1055 (5.40-3.80)
RSRZ outliers	127900	1113 (5.50-3.70)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	438	<div> <div>2%</div> <div>65%</div> <div>26%</div> <div>9%</div> </div>
1	E	438	<div> <div>2%</div> <div>64%</div> <div>27%</div> <div>9%</div> </div>
2	C	117	<div> <div>85%</div> <div>14%</div> <div>.</div> </div>
2	F	117	<div> <div>85%</div> <div>14%</div> <div>.</div> </div>
3	B	121	<div> <div>%</div> <div>71%</div> <div>29%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	121	<div><div>%</div><div><div></div><div>71%</div><div>29%</div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9634 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 Divalent metal cation transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	0	0
			2967	1974	468	505	20			
1	E	398	Total	C	N	O	S	0	0	0
			2967	1974	468	505	20			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	GLN	GLU	engineered mutation	UNP A0A369N1S1
A	151	SER	ALA	engineered mutation	UNP A0A369N1S1
A	193	GLN	GLU	engineered mutation	UNP A0A369N1S1
A	207	HIS	ARG	engineered mutation	UNP A0A369N1S1
A	244	THR	SER	engineered mutation	UNP A0A369N1S1
A	256	VAL	ILE	engineered mutation	UNP A0A369N1S1
A	275	ALA	SER	engineered mutation	UNP A0A369N1S1
A	366	ILE	VAL	engineered mutation	UNP A0A369N1S1
A	385	ILE	VAL	engineered mutation	UNP A0A369N1S1
A	418	LEU	VAL	engineered mutation	UNP A0A369N1S1
A	429	ALA	VAL	engineered mutation	UNP A0A369N1S1
E	88	GLN	GLU	engineered mutation	UNP A0A369N1S1
E	151	SER	ALA	engineered mutation	UNP A0A369N1S1
E	193	GLN	GLU	engineered mutation	UNP A0A369N1S1
E	207	HIS	ARG	engineered mutation	UNP A0A369N1S1
E	244	THR	SER	engineered mutation	UNP A0A369N1S1
E	256	VAL	ILE	engineered mutation	UNP A0A369N1S1
E	275	ALA	SER	engineered mutation	UNP A0A369N1S1
E	366	ILE	VAL	engineered mutation	UNP A0A369N1S1
E	385	ILE	VAL	engineered mutation	UNP A0A369N1S1
E	418	LEU	VAL	engineered mutation	UNP A0A369N1S1
E	429	ALA	VAL	engineered mutation	UNP A0A369N1S1

- Molecule 2 is a protein called Elen-Nb1-Nb2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	117	Total	C	N	O	S	0	0	0
			908	565	167	171	5			
2	F	117	Total	C	N	O	S	0	0	0
			908	565	167	171	5			

- Molecule 3 is a protein called Elen-Nb1-Nb2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	121	Total	C	N	O	S	0	0	0
			941	591	171	176	3			
3	G	121	Total	C	N	O	S	0	0	0
			941	591	171	176	3			

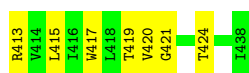
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		
4	E	1	Total	Mn	0	0
			1	1		

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.

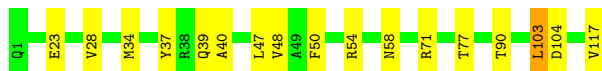
- [illegible]

- Chain E:
- 
- 64% 27% 9%
- Met  
Met  
Met  
Lys  
Lys  
Asn  
Glu  
Lys  
Leu  
Glu  
Leu  
Leu  
Asp  
Val  
Val  
Asp  
Ala  
Ala  
Glu  
Ser  
Thr  
Glu  
Leu  
Val  
Glu  
Val  
Glu  
Pro  
Glu  
Lys  
Lys  
Gln  
Pro  
Lys  
Lys  
Ile  
Trp  
Leu  
Leu  
Leu  
A41  
A42  
L43  
I47  
M51  
A52  
G53  
N54  
D55  
A56  
G57  
T61  
Y62  
S63  
G66
- F71  
A72  
L74  
W75  
V76  
M80  
L83  
L84  
I85  
V86  
V87  
M94  
T98  
G99  
K100  
A103  
R109  
L114  
A121  
L122  
M126  
V127  
A128  
T129  
T130  
F131  
S132  
E133  
A138  
E142  
M143  
Y149  
W160  
L161  
L162  
V163  
V164  
V171  
L176  
Y181  
F182  
Y183  
T184
- Y185  
A189  
P194  
N195  
W196  
E197  
E198  
T201  
S202  
P206  
F214  
M221  
T224  
A227  
P228  
W229  
M230  
M231  
F232  
F233  
N234  
Q235  
F249  
A262  
V265  
A266  
W267  
V271  
T272  
T273  
G274  
A275  
V276  
L277  
Q280  
I284  
E285  
R292  
A293  
L294  
A298  
G299  
H300  
Y301
- F306  
A307  
S314  
F315  
L316  
A317  
A318  
L321  
P322  
T325  
A326  
F327  
V328  
I329  
C330  
E331  
A332  
A337  
S340  
F341  
K342  
W343  
K344  
K350  
F353  
I357  
I366  
P367  
N368  
I369  
N382  
G383  
L384  
I385  
L386  
P387  
V388  
L389  
L390  
V391  
I395  
D399  
K400  
R407  
S408



• Molecule 2: Elen-Nb1-Nb2

Chain C: 85% 14%



• Molecule 2: Elen-Nb1-Nb2

Chain F: 85% 14%



• Molecule 3: Elen-Nb1-Nb2

Chain B: 71% 29%



• Molecule 3: Elen-Nb1-Nb2

Chain G: 71% 29%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.90Å 115.93Å 148.66Å 90.00° 107.59° 90.00°	Depositor
Resolution (Å)	12.00 – 4.60 12.00 – 4.60	Depositor EDS
% Data completeness (in resolution range)	99.0 (12.00-4.60) 96.8 (12.00-4.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.54 (at 4.52Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, $R_{free}$	0.284 , 0.327 0.285 , 0.325	Depositor DCC
$R_{free}$ test set	795 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	177.0	Xtriage
Anisotropy	0.856	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.177 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	9634	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	270.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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

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	0/3030	0.46	0/4135
1	E	0.26	0/3030	0.46	0/4135
2	C	0.26	0/925	0.58	1/1248 (0.1%)
2	F	0.26	0/925	0.58	1/1248 (0.1%)
3	B	0.26	0/963	0.58	0/1305
3	G	0.27	0/963	0.58	0/1305
All	All	0.26	0/9836	0.51	2/13376 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	103	LEU	CA-CB-CG	5.62	128.23	115.30
2	C	103	LEU	CA-CB-CG	5.59	128.16	115.30

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	2967	0	3125	72	8
1	E	2967	0	3125	72	8
2	C	908	0	896	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	908	0	896	13	0
3	B	941	0	906	28	0
3	G	941	0	906	28	0
4	A	1	0	0	0	0
4	E	1	0	0	0	0
All	All	9634	0	9854	222	8

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 11.

The worst 5 of 222 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)
3:G:34:LEU:HB2	3:G:79:VAL:HG21	1.72	0.71
3:B:34:LEU:HB2	3:B:79:VAL:HG21	1.72	0.71
1:E:273:THR:HG23	1:E:277:LEU:HD12	1.75	0.68
1:A:273:THR:HG23	1:A:277:LEU:HD12	1.75	0.66
1:E:340:SER:HB2	1:E:344:LYS:HB2	1.77	0.66

The worst 5 of 8 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:LYS:CE	1:E:344:LYS:CE[2_444]	1.11	1.09
1:A:342:LYS:CB	1:E:342:LYS:O[2_444]	1.17	1.03
1:A:342:LYS:O	1:E:342:LYS:CB[2_444]	1.20	1.00
1:A:342:LYS:O	1:E:342:LYS:CG[2_444]	1.73	0.47
1:A:342:LYS:CG	1:E:342:LYS:O[2_444]	1.87	0.33

## 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	396/438 (90%)	375 (95%)	21 (5%)	0	100	100
1	E	396/438 (90%)	375 (95%)	21 (5%)	0	100	100
2	C	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
2	F	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
3	B	119/121 (98%)	100 (84%)	19 (16%)	0	100	100
3	G	119/121 (98%)	100 (84%)	19 (16%)	0	100	100
All	All	1260/1352 (93%)	1160 (92%)	100 (8%)	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	308/345 (89%)	308 (100%)	0	100	100
1	E	308/345 (89%)	308 (100%)	0	100	100
2	C	96/96 (100%)	96 (100%)	0	100	100
2	F	96/96 (100%)	96 (100%)	0	100	100
3	B	95/95 (100%)	95 (100%)	0	100	100
3	G	95/95 (100%)	95 (100%)	0	100	100
All	All	998/1072 (93%)	998 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

### 5.3.3 RNA ⓘ

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	398/438 (90%)	0.11	10 (2%) 57 48	169, 257, 398, 745	0
1	E	398/438 (90%)	0.08	9 (2%) 60 51	189, 267, 392, 694	0
2	C	117/117 (100%)	-0.06	0 100 100	198, 265, 313, 368	0
2	F	117/117 (100%)	-0.01	0 100 100	185, 249, 301, 340	0
3	B	121/121 (100%)	-0.03	1 (0%) 86 79	201, 256, 322, 377	0
3	G	121/121 (100%)	-0.04	1 (0%) 86 79	201, 268, 328, 393	0
All	All	1272/1352 (94%)	0.04	21 (1%) 70 61	169, 260, 369, 745	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	52	ALA	7.3
1	A	41	ALA	6.2
1	A	48	VAL	5.1
1	A	42	ALA	4.5
1	E	43	LEU	4.5

### 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](#)

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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
4	MN	E	501	1/1	0.95	0.25	200,200,200,200	0
4	MN	A	501	1/1	0.98	0.25	182,182,182,182	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.