



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 18, 2024 – 02:19 PM EST

PDB ID : 4DYN  
Title : Crystal Structure of WSN/A Influenza Nucleoprotein with BMS-885838 Ligand Bound  
Authors : Lewis, H.A.; Baldwin, E.T.; Steinbacher, S.; Maskos, K.; Mortl, M.; Kiefer-sauer, R.; Edavettal, S.; McDonnell, P.A.; Pearce, B.C.; Langley, D.R.  
Deposited on : 2012-02-29  
Resolution : 2.40 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
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) : 2.36

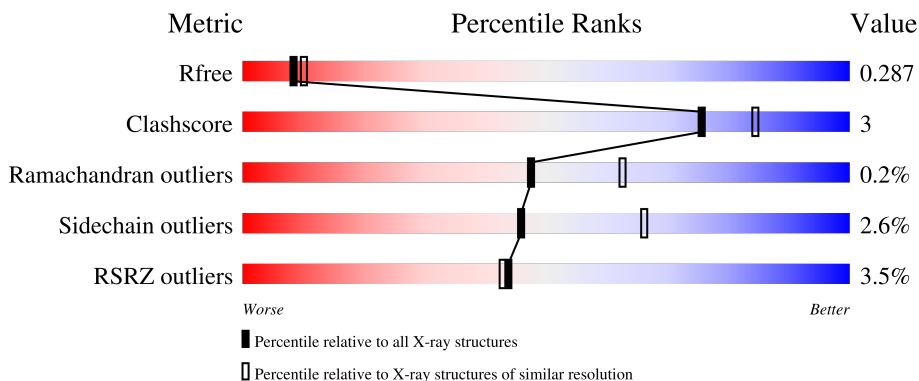
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	499	
1	B	499	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6623 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.

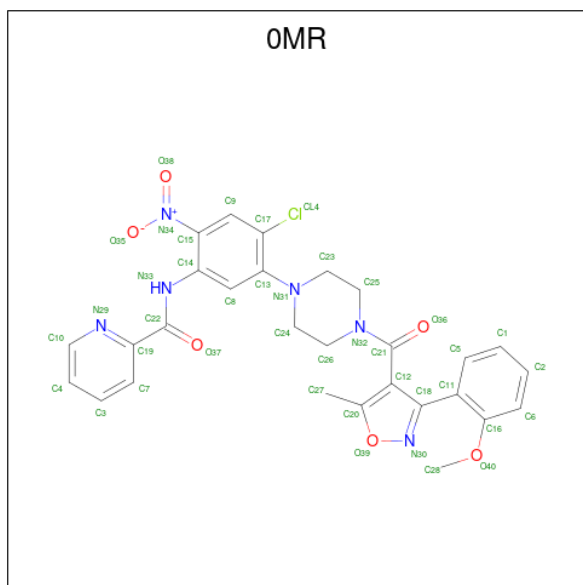
- Molecule 1 is a protein called Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	437	3284	2060	576	623	25	0	1	0
1	B	437	3162	1990	555	592	25	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	499	LEU	-	expression tag	UNP B4URF1
A	500	GLU	-	expression tag	UNP B4URF1
A	501	HIS	-	expression tag	UNP B4URF1
A	502	HIS	-	expression tag	UNP B4URF1
A	503	HIS	-	expression tag	UNP B4URF1
A	504	HIS	-	expression tag	UNP B4URF1
A	505	HIS	-	expression tag	UNP B4URF1
A	506	HIS	-	expression tag	UNP B4URF1
B	499	LEU	-	expression tag	UNP B4URF1
B	500	GLU	-	expression tag	UNP B4URF1
B	501	HIS	-	expression tag	UNP B4URF1
B	502	HIS	-	expression tag	UNP B4URF1
B	503	HIS	-	expression tag	UNP B4URF1
B	504	HIS	-	expression tag	UNP B4URF1
B	505	HIS	-	expression tag	UNP B4URF1
B	506	HIS	-	expression tag	UNP B4URF1

- Molecule 2 is N-[4-chloranyl-5-[4-[[3-(2-methoxyphenyl)-5-methyl-1,2-oxazol-4-yl]carbonyl]piperazin-1-yl]-2-nitro-phenyl]pyridine-2-carboxamide (three-letter code: OMR) (formula: C<sub>28</sub>H<sub>25</sub>ClN<sub>6</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Cl	N			O
2	A	1	41	28	1	6	6	0	0
2	B	1	41	28	1	6	6	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	64	64	64	0	0
3	B	31	31	31	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.61Å 145.61Å 145.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.90 – 2.40 48.54 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.90-2.40) 99.9 (48.54-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.49 (at 2.39Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.242 , 0.291 0.239 , 0.287	Depositor DCC
$R_{free}$ test set	982 reflections (2.43%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.6	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.029 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6623	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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: OMR

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	0.32	0/3340	0.46	0/4513
1	B	0.31	0/3217	0.45	0/4359
All	All	0.31	0/6557	0.45	0/8872

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	3284	0	3117	19	0
1	B	3162	0	2892	18	0
2	A	41	0	25	5	0
2	B	41	0	25	5	0
3	A	64	0	0	0	0
3	B	31	0	0	1	0
All	All	6623	0	6059	39	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 3.

All (39) 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:311:GLN:HE22	1:B:309:ASN:HA	1.29	0.96
1:A:311:GLN:NE2	1:B:309:ASN:HA	2.01	0.75
1:A:184:LYS:HD3	1:A:189:MET:HE1	1.69	0.74
1:A:189:MET:HA	1:A:189:MET:HE2	1.83	0.60
1:A:184:LYS:HD3	1:A:189:MET:CE	2.34	0.57
1:B:309:ASN:OD1	2:B:601:OMR:H16	2.06	0.54
2:B:601:OMR:H8	2:B:601:OMR:O37	2.09	0.52
2:B:601:OMR:H18	2:B:601:OMR:C18	2.39	0.52
2:A:601:OMR:H18	2:A:601:OMR:C18	2.41	0.50
1:B:422:ARG:N	1:B:423:PRO:HD2	2.27	0.50
1:A:154:LEU:HD13	1:A:161:PRO:HA	1.92	0.49
1:A:408:ILE:HG12	1:A:419:PRO:HD2	1.95	0.48
1:A:309:ASN:ND2	2:A:601:OMR:H16	2.28	0.48
1:A:273:LYS:HD3	1:A:298:LEU:HD23	1.96	0.47
1:B:324:HIS:HB3	1:B:358:LEU:HG	1.96	0.47
1:B:39:PHE:CZ	1:B:67:VAL:HB	2.49	0.46
1:A:302:ASP:HB2	1:A:303:PRO:HD3	1.95	0.46
1:A:221:ARG:O	1:A:225:ILE:HG12	2.16	0.46
1:A:141:SER:OG	1:A:169:GLY:HA2	2.15	0.46
1:B:36:ILE:HD13	1:B:120:TRP:HH2	1.81	0.45
2:A:601:OMR:H18	2:A:601:OMR:C11	2.47	0.44
2:B:601:OMR:H18	2:B:601:OMR:C11	2.48	0.44
2:A:601:OMR:H21	1:B:313:TYR:CG	2.53	0.44
1:B:334:HIS:HE1	3:B:708:HOH:O	2.01	0.44
1:A:51:ASP:HB3	1:B:287:SER:HA	1.99	0.44
1:A:313:TYR:CG	2:B:601:OMR:H21	2.53	0.43
1:A:424:THR:OG1	1:A:452:ARG:HD2	2.18	0.43
1:B:133:LEU:O	1:B:137:MET:HG3	2.19	0.43
1:A:287:SER:O	1:B:50[A]:SER:OG	2.37	0.42
2:A:601:OMR:O37	2:A:601:OMR:H8	2.19	0.42
1:B:160:ASP:HB3	1:B:163:MET:HG3	2.01	0.42
1:B:302:ASP:HB2	1:B:303:PRO:HD3	2.01	0.42
1:A:164:CYS:HA	1:A:167:MET:HG2	2.02	0.42
1:B:321:ASN:HD22	1:B:324:HIS:CE1	2.39	0.41
1:A:308:GLN:HA	1:A:382:ARG:HG2	2.02	0.41
1:B:190:VAL:HG13	1:B:256:LEU:HB3	2.03	0.41
1:B:321:ASN:HA	1:B:322:PRO:HD2	1.96	0.41
1:A:89:PRO:HB2	1:A:90:LYS:H	1.62	0.41
1:B:470:LYS:O	1:B:472:THR:N	2.55	0.40

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	428/499 (86%)	419 (98%)	9 (2%)	0	100	100
1	B	426/499 (85%)	417 (98%)	7 (2%)	2 (0%)	29	41
All	All	854/998 (86%)	836 (98%)	16 (2%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	471	ALA
1	B	17	GLY

### 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	326/425 (77%)	316 (97%)	10 (3%)	40	60
1	B	292/425 (69%)	286 (98%)	6 (2%)	53	72
All	All	618/850 (73%)	602 (97%)	16 (3%)	46	66

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ASP
1	A	151	THR
1	A	157	THR
1	A	176	SER

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Mol	Chain	Res	Type
1	A	302	ASP
1	A	339	GLU
1	A	389	ARG
1	A	395	ASN
1	A	416	ARG
1	A	472	THR
1	B	105	ARG
1	B	111	TYR
1	B	348	ARG
1	B	389	ARG
1	B	416	ARG
1	B	454	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	250	ASN
1	A	309	ASN
1	A	311	GLN
1	A	399	GLN
1	A	409	GLN
1	B	168	GLN
1	B	272	HIS
1	B	334	HIS
1	B	459	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

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
2	OMR	B	601	-	41,45,45	1.13	4 (9%)	49,64,64	1.21	5 (10%)
2	OMR	A	601	-	41,45,45	1.17	3 (7%)	49,64,64	1.28	7 (14%)

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
2	OMR	B	601	-	-	0/22/40/40	0/5/5/5
2	OMR	A	601	-	-	0/22/40/40	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	OMR	C11-C18	-4.97	1.44	1.49
2	B	601	OMR	C11-C18	-4.57	1.44	1.49
2	A	601	OMR	C21-N32	2.52	1.40	1.34
2	A	601	OMR	C12-C21	-2.50	1.47	1.51
2	B	601	OMR	C21-N32	2.49	1.40	1.34
2	B	601	OMR	C12-C21	-2.39	1.48	1.51
2	B	601	OMR	C22-N33	2.06	1.41	1.35

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	OMR	O40-C16-C11	3.44	121.39	116.26
2	B	601	OMR	O40-C16-C6	-3.30	118.72	124.37
2	A	601	OMR	O40-C16-C11	3.24	121.09	116.26
2	A	601	OMR	O40-C16-C6	-3.14	118.98	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	OMR	C13-C17-CL4	2.92	123.27	120.22
2	A	601	OMR	C8-C13-N31	-2.87	118.28	122.52
2	A	601	OMR	C8-C14-C15	2.74	120.07	116.68
2	B	601	OMR	C8-C14-C15	2.56	119.84	116.68
2	B	601	OMR	C8-C13-N31	-2.49	118.84	122.52
2	B	601	OMR	C13-C17-CL4	2.26	122.58	120.22
2	A	601	OMR	C12-C21-N32	2.09	120.25	117.87
2	A	601	OMR	C18-C12-C21	2.08	131.14	127.08

There are no chirality outliers.

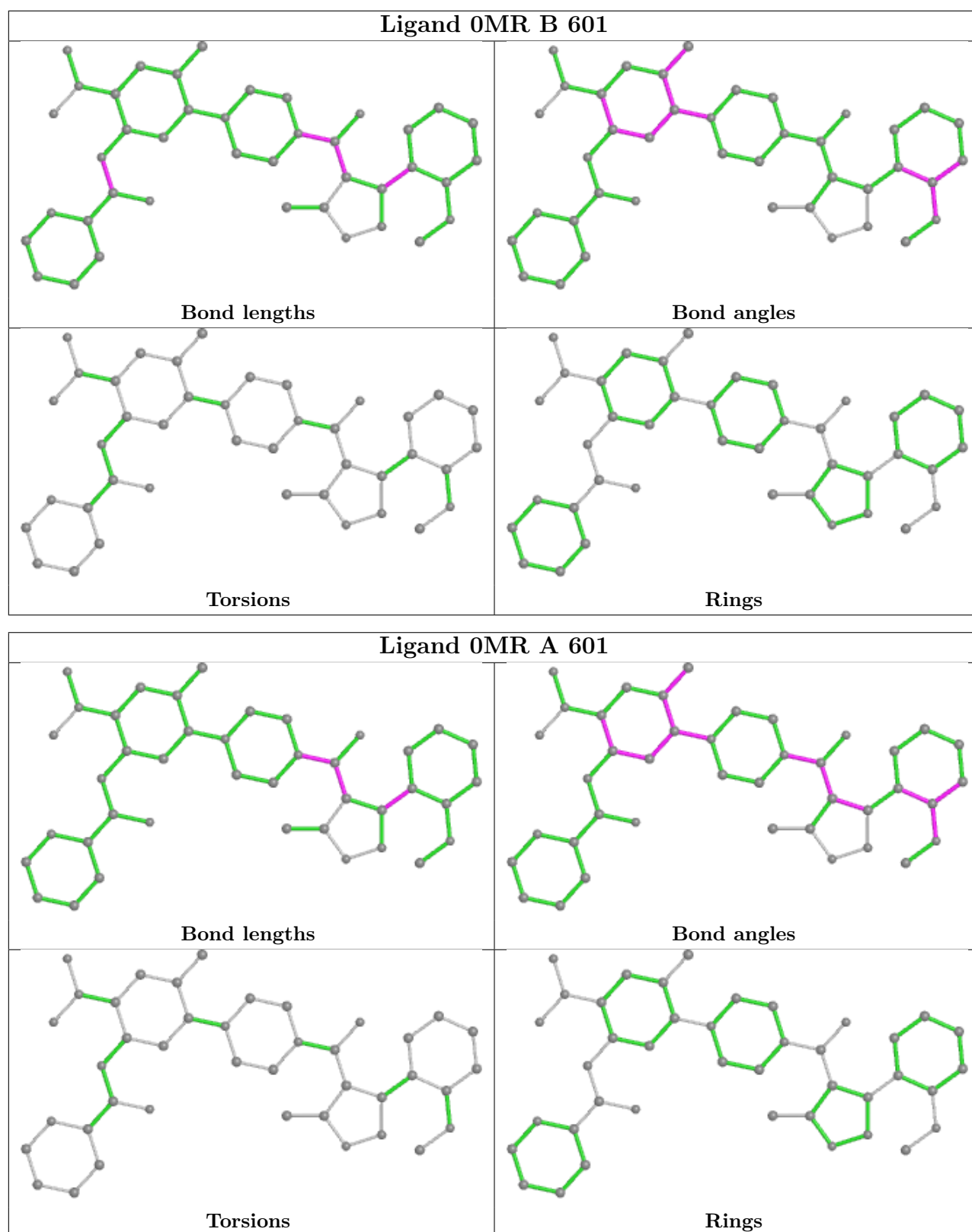
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	OMR	5	0
2	A	601	OMR	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	437/499 (87%)	0.08	7 (1%) 72 70	26, 36, 50, 59	0
1	B	437/499 (87%)	0.32	24 (5%) 25 24	29, 47, 71, 76	0
All	All	874/998 (87%)	0.20	31 (3%) 44 43	26, 41, 68, 76	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	ASN	3.5
1	B	239	VAL	3.3
1	B	261	ARG	3.1
1	B	83	PRO	3.0
1	B	356	GLY	3.0
1	B	15	THR	3.0
1	B	222	MET	2.9
1	A	126	GLY	2.8
1	B	223	CYS	2.8
1	B	214	ARG	2.8
1	B	248	PRO	2.7
1	B	403	SER	2.7
1	B	406	ILE	2.5
1	B	262	SER	2.5
1	B	216	ARG	2.4
1	A	72	ASP	2.4
1	B	10	TYR	2.4
1	B	247	ASN	2.4
1	A	429	PHE	2.4
1	B	242	VAL	2.3
1	B	249	GLY	2.3
1	B	238	MET	2.3
1	B	424	THR	2.3
1	A	127	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	487	TYR	2.2
1	B	353	VAL	2.2
1	B	244	GLU	2.2
1	A	365	ILE	2.1
1	B	453	PRO	2.1
1	B	258	PHE	2.1
1	A	318	PRO	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.

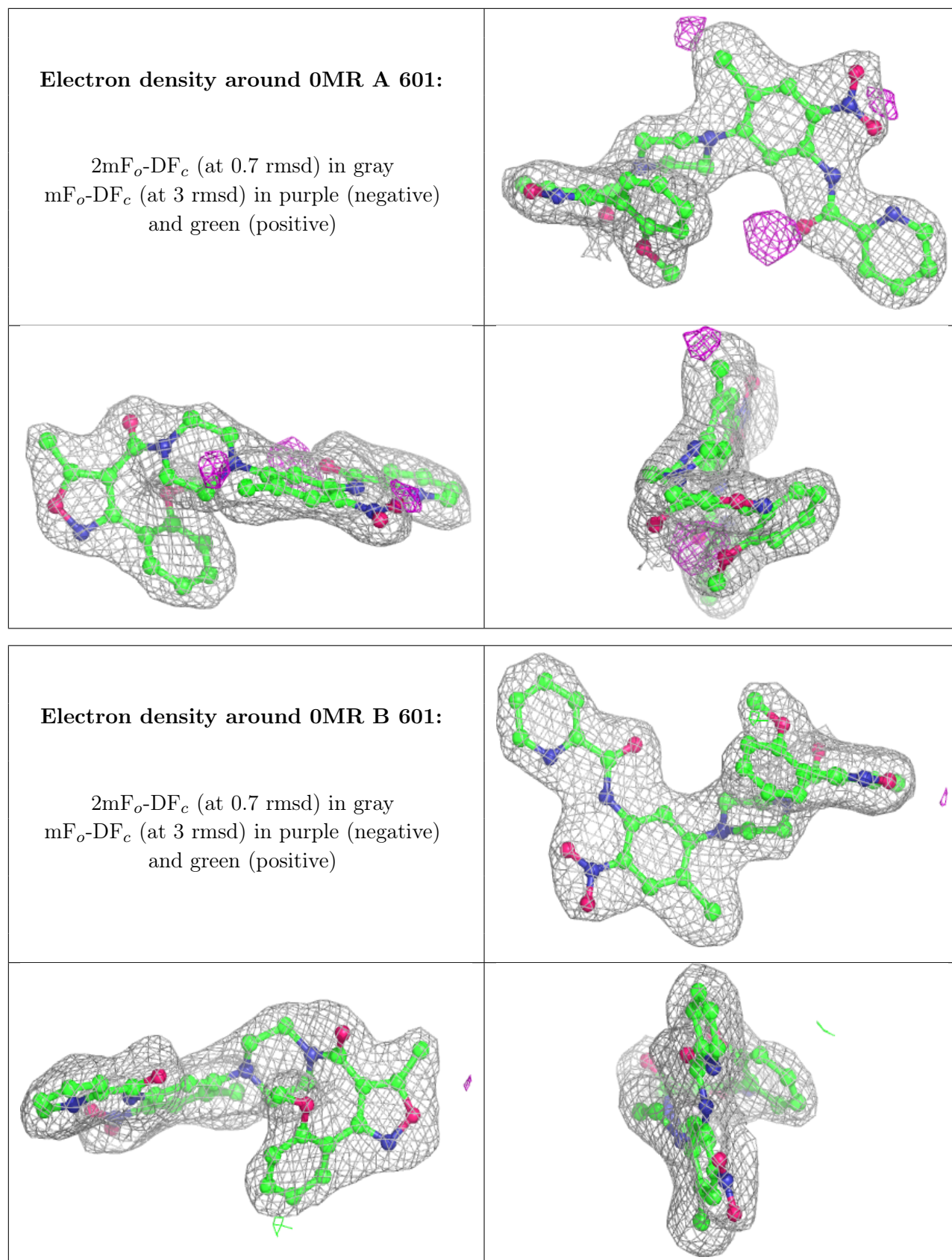
## 6.4 Ligands [i](#)

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
2	OMR	A	601	41/41	0.93	0.17	28,30,31,32	0
2	OMR	B	601	41/41	0.94	0.14	31,34,35,36	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.