

# wwPDB X-ray Structure Validation Summary Report (i)

#### Apr 3, 2024 – 07:14 pm BST

PDB ID : 8OXG

Title: Crystal structure of human methionine aminopeptidase-2 complexed with (3

R,4S,5S,6R)-5-methoxy-4-[(2R,3R)-2-methyl-3-(3-methyl-2-buten-1-yl)-2-oxir

anyl]-1-oxaspiro[2.5]oct-6-yl N-(trans-4-aminocyclohexyl)carbamate

Authors: Moss, S.; Cornelius, P.

Deposited on : 2023-05-02

Resolution : 1.73 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 (i) 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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (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)

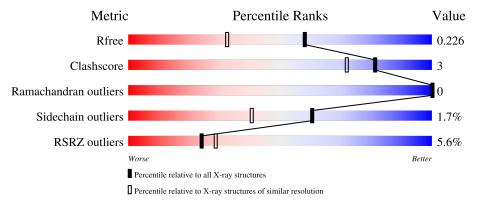
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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 <=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	384	6% 88%	8%	-
1	В	384	5% 87%	8%	 -



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12226 atoms, of which 5793 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 Methionine aminopeptidase 2.

Mol	Chain	Residues			Atom	S			ZeroOcc	AltConf	Trace
1	A	368	Total 5763	C 1824	H 2859	N 498	O 556	S 26	178	3	0
1	В	369	Total 5751	C 1820	11	N 498	O 555	S 24	177	1	0

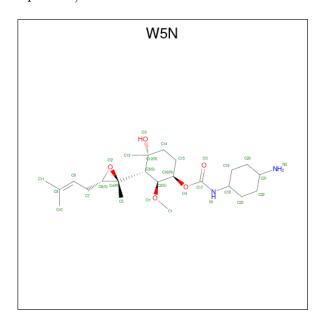
There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	MET	-	initiating methionine	UNP P50579
A	96	HIS	-	expression tag	UNP P50579
A	97	HIS	-	expression tag	UNP P50579
A	98	HIS	-	expression tag	UNP P50579
A	99	HIS	-	expression tag	UNP P50579
A	100	HIS	-	expression tag	UNP P50579
A	101	HIS	-	expression tag	UNP P50579
A	102	GLU	-	expression tag	UNP P50579
A	103	ASN	-	expression tag	UNP P50579
A	104	LEU	-	expression tag	UNP P50579
A	105	TYR	-	expression tag	UNP P50579
A	106	PHE	-	expression tag	UNP P50579
A	107	GLN	-	expression tag	UNP P50579
В	95	MET	-	initiating methionine	UNP P50579
В	96	HIS	-	expression tag	UNP P50579
В	97	HIS	-	expression tag	UNP P50579
В	98	HIS	-	expression tag	UNP P50579
В	99	HIS	-	expression tag	UNP P50579
В	100	HIS	-	expression tag	UNP P50579
В	101	HIS	-	expression tag	UNP P50579
В	102	GLU	-	expression tag	UNP P50579
В	103	ASN	-	expression tag	UNP P50579
В	104	LEU	-	expression tag	UNP P50579
В	105	TYR	-	expression tag	UNP P50579
В	106	PHE		expression tag	UNP P50579



Chain	Residue	Modelled	Actual	Comment	Reference
В	107	GLN	-	expression tag	UNP P50579

• Molecule 2 is [(1 {R},2 {S},3 {S},4 {R})-2-methoxy-4-methyl-3-[(2 {R},3 {S})-2-methyl-3-(3-methylbut-2-enyl)oxiran-2-yl]-4-oxidanyl-cyclohexyl] {N}-(4-azanylcyclohexyl)carba mate (three-letter code: W5N) (formula:  $C_{23}H_{40}N_2O_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	
9	A	1	Total	С	Н	N	О	1	0	
	А	1	70	23	40	2	5	1		
9	D	1	Total	С	Н	N	О	1	0	
	Ъ	1	70	23	40	2	5	1		

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Mn 2 2	0	0
3	В	2	Total Mn 2 2	0	0

• Molecule 4 is water.

$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	298	Total O 298 298	0	0



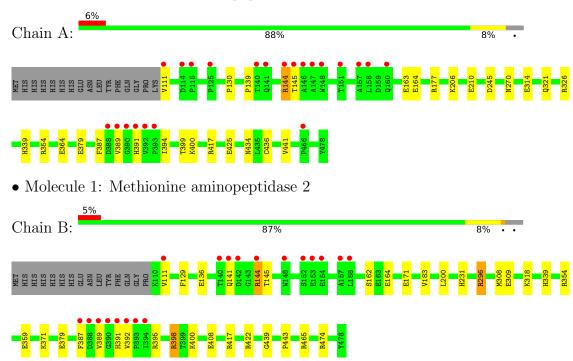
Mol	Chain	Residues	Ato	ms	ZeroOcc	AltConf
4	В	270	Total 270	O 270	0	0



# 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: Methionine aminopeptidase 2





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	119.05Å 101.13Å 83.74Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 98.75° 90.00°	Depositor
Resolution (Å)	44.84 - 1.73	Depositor
Resolution (A)	44.84 - 1.73	EDS
% Data completeness	99.8 (44.84-1.73)	Depositor
(in resolution range)	99.8 (44.84-1.73)	EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.68 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0352, REFMAC 5.8.0352	Depositor
D D	0.181 , 0.215	Depositor
$R, R_{free}$	0.193 , 0.226	DCC
$R_{free}$ test set	5131 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.7	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.40 , 44.3	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	12226	wwPDB-VP
Average B, all atoms $(Å^2)$	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: W5N, 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		nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.79	$4/2969 \ (0.1\%)$	1.07	4/4020 (0.1%)	
1	В	0.80	5/2962~(0.2%)	1.03	5/4011 (0.1%)	
All	All	0.80	$9/5931 \ (0.2\%)$	1.05	9/8031 (0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	В	0	5
All	All	0	7

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
1	A	379	GLU	CD-OE2	9.08	1.35	1.25
1	В	379	GLU	CD-OE2	7.39	1.33	1.25
1	A	364	GLU	CD-OE2	-7.01	1.18	1.25
1	A	425	GLU	CD-OE1	6.90	1.33	1.25
1	В	408	GLU	CD-OE2	6.26	1.32	1.25

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	326	ARG	NE-CZ-NH2	-16.51	112.05	120.30
1	A	326	ARG	NE-CZ-NH1	11.00	125.80	120.30
1	В	417	ARG	NE-CZ-NH2	-7.56	116.52	120.30
1	A	177	ARG	NE-CZ-NH1	5.75	123.18	120.30



Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	417	ARG	NE-CZ-NH2	5.65	123.13	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	144	ARG	Sidechain
1	A	354	ARG	Sidechain
1	В	144	ARG	Sidechain
1	В	296	ARG	Sidechain
1	В	354	ARG	Sidechain

#### 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	2904	2859	2846	14	0
1	В	2897	2854	2843	15	0
2	A	30	40	0	0	0
2	В	30	40	0	2	0
3	A	2	0	0	0	0
3	В	2	0	0	0	0
4	A	298	0	0	7	0
4	В	270	0	0	3	0
All	All	6433	5793	5689	28	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.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:206:LYS:NZ	4:A:601:HOH:O	2.07	0.84
1:B:231:HIS:CE1	2:B:501:W5N:C13	2.73	0.70
1:A:144:ARG:NH2	4:A:606:HOH:O	2.28	0.65



Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:210:GLU:OE1	4:A:602:HOH:O	2.16	0.61
1:B:391:HIS:O	1:B:391:HIS:ND1	2.33	0.55

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	Perce	ntiles	
1	A	369/384 (96%)	360 (98%)	9 (2%)	0	100	100
1	В	368/384 (96%)	354 (96%)	14 (4%)	0	100	100
All	All	737/768 (96%)	714 (97%)	23 (3%)	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	319/331 (96%)	314 (98%)	5 (2%)	62 44		
1	В	318/331 (96%)	312 (98%)	6 (2%)	57 36		
All	All	637/662 (96%)	626 (98%)	11 (2%)	60 41		

5 of 11 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	В	318	LYS
1	В	339	HIS
1	В	443	PRO
1	В	387	PHE
1	A	391	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	ASN
1	A	434	ASN
1	В	141	GLN
1	В	211	ASN
1	В	214	ASN

#### 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)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	Chain Res		Bo	ond leng	$ ag{ths}$	В	ond ang	gles
MOI	туре	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	W5N	A	501	1	31,32,32	0.90	1 (3%)	38,48,48	3.63	15 (39%)
2	W5N	В	501	1	31,32,32	0.74	0	38,48,48	2.67	6 (15%)

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	W5N	A	501	1	-	4/18/59/59	0/3/3/3
2	W5N	В	501	1	-	2/18/59/59	0/3/3/3

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
2	A	501	W5N	O2-C4	2.05	1.48	1.45

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	501	W5N	C5-C4-C6	-14.06	89.06	121.56
2	A	501	W5N	C5-C4-C6	-13.68	89.93	121.56
2	A	501	W5N	C18-N1-C17	8.53	135.45	122.30
2	A	501	W5N	O4-C17-N1	-7.32	100.83	110.32
2	A	501	W5N	C22-C21-C20	6.56	117.07	110.28

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	W5N	C4-C6-C7-C8
2	В	501	W5N	C4-C6-C7-C8
2	В	501	W5N	O2-C6-C7-C8
2	A	501	W5N	C16-C2-O1-C1
2	A	501	W5N	C7-C8-C9-C11

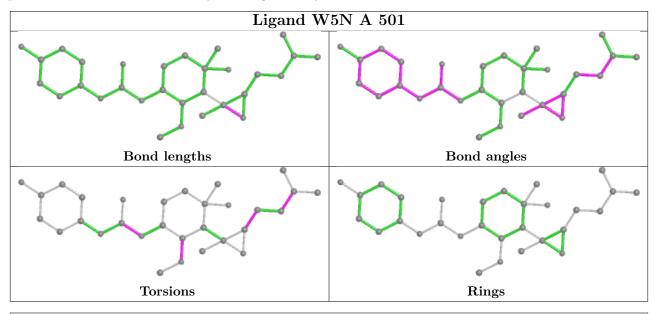
There are no ring outliers.

1 monomer is involved in 2 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	501	W5N	2	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 then 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 (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,  $95^{th}$  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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	368/384~(95%)	0.29	22 (5%) 21 26	18, 27, 53, 107	7 (1%)
1	В	369/384~(96%)	0.34	19 (5%) 28 33	17, 29, 52, 107	7 (1%)
All	All	$737/768 \ (95\%)$	0.31	41 (5%) 24 29	17, 28, 52, 107	14 (1%)

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	RSRZ
1	В	389	VAL	9.2
1	В	391	HIS	7.7
1	В	392	VAL	6.9
1	A	391	HIS	6.6
1	В	390	GLY	6.5

## 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.

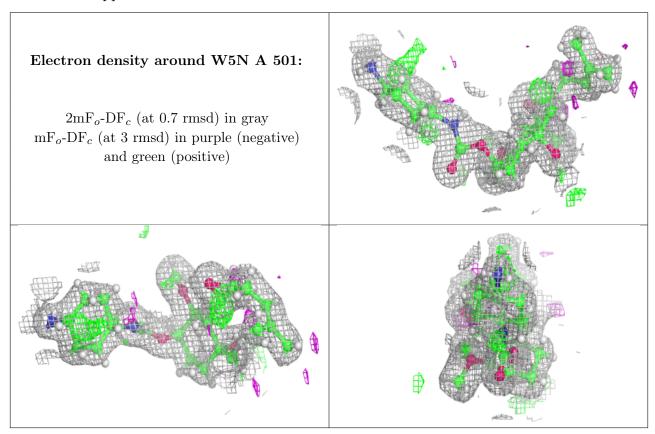
#### 6.4 Ligands (i)

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,  $95^{th}$  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.

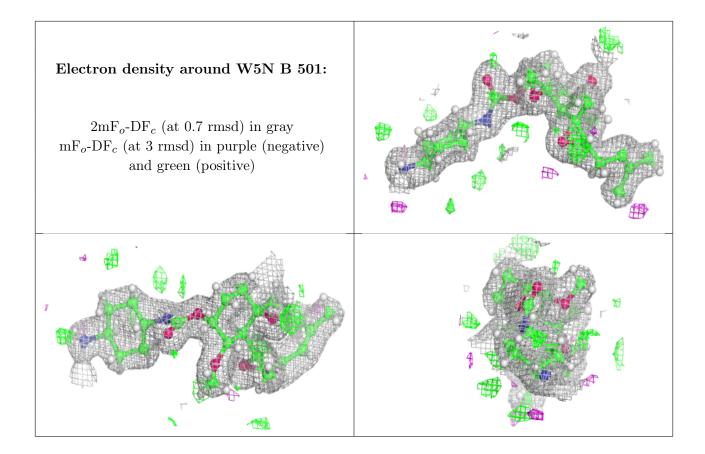


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	W5N	A	501	30/30	0.94	0.13	16,21,30,31	1
2	W5N	В	501	30/30	0.95	0.09	18,27,35,41	1
3	MN	В	503	1/1	0.99	0.13	21,21,21,21	0
3	MN	A	503	1/1	1.00	0.15	19,19,19,19	0
3	MN	В	502	1/1	1.00	0.13	19,19,19,19	0
3	MN	A	502	1/1	1.00	0.11	18,18,18,18	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.

