



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 6, 2023 – 01:10 pm BST

PDB ID : 6Z4G  
Title : A4V mutant of human SOD1 bound with ebselen in P21 space group  
Authors : Amporndanai, K.; Hasnain, S.S.  
Deposited on : 2020-05-25  
Resolution : 1.45 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.

The types of validation reports are described at

<https://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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.32.2  
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) : 2.32.2

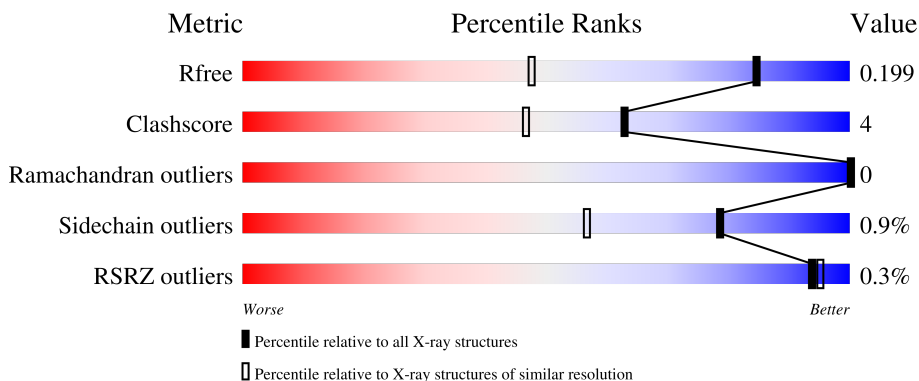
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.45 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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	AAA	153	91% 9%
1	BBB	153	94% 6%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 2498 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 Superoxide dismutase [Cu-Zn].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	153	1131	690	205	232	4	0	4	0
1	BBB	153	1106	678	201	223	4	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	4	VAL	ALA	engineered mutation	UNP P00441
BBB	4	VAL	ALA	engineered mutation	UNP P00441

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

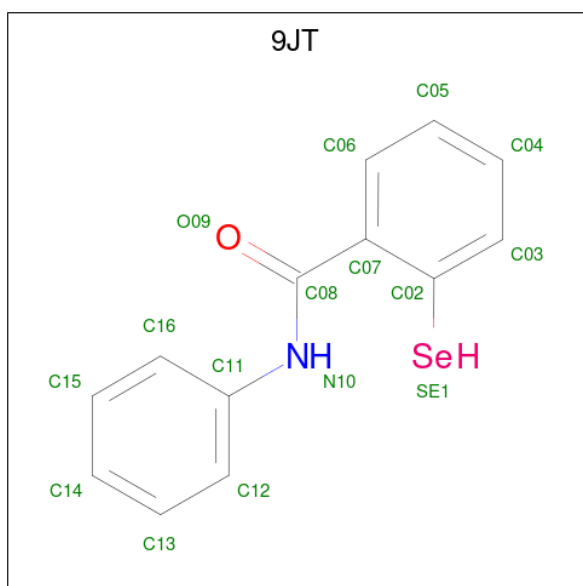
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	2	Total	Zn	0	0
			2	2		
2	BBB	2	Total	Zn	0	0
			2	2		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	C	O	0	0
			4	2	2		
3	AAA	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is N-phenyl-2-selanylbenzamide (three-letter code: 9JT) (formula: C<sub>13</sub>H<sub>11</sub>NOSe) (labeled as "Ligand of Interest" by depositor).



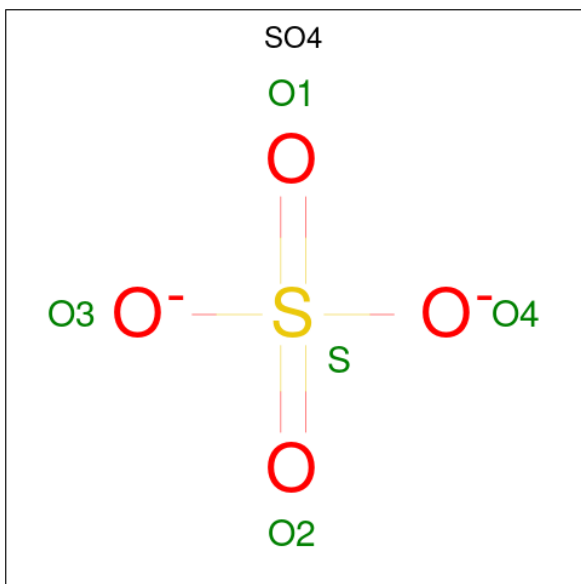
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	AAA	1	Total	C	N	O	Se	0	0
			16	13	1	1	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	Se		
4	BBB	1	16	13	1	1	1	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
5	AAA	1	5	4	1	0	0
5	BBB	1	5	4	1	0	0
5	BBB	1	5	4	1	0	0
5	BBB	1	5	4	1	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
6	AAA	1	1	1	0	0
6	BBB	1	1	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	AAA	97	Total O 97 97	0	0
7	BBB	98	Total O 98 98	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: Superoxide dismutase [Cu-Zn]



- Molecule 1: Superoxide dismutase [Cu-Zn]



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.95Å 67.72Å 50.65Å 90.00° 106.40° 90.00°	Depositor
Resolution (Å)	39.51 – 1.45 39.48 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.2 (39.51-1.45) 99.2 (39.48-1.45)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 1.45Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.156 , 0.193 0.166 , 0.199	Depositor DCC
$R_{free}$ test set	2259 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.0	Xtrriage
Anisotropy	0.416	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 40.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2498	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.44% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, ZN, SO4, CL, 9JT

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	AAA	0.89	0/1149	0.92	0/1549
1	BBB	0.81	0/1127	0.90	0/1521
All	All	0.85	0/2276	0.91	0/3070

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	AAA	1131	0	1083	12	0
1	BBB	1106	0	1065	7	0
2	AAA	2	0	0	0	0
2	BBB	2	0	0	0	0
3	AAA	8	0	6	0	0
4	AAA	16	0	0	1	0
4	BBB	16	0	0	1	0
5	AAA	5	0	0	0	0
5	BBB	15	0	0	0	0
6	AAA	1	0	0	1	0
6	BBB	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AAA	97	0	0	2	1
7	BBB	98	0	0	1	1
All	All	2498	0	2154	19	1

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 4.

The worst 5 of 19 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:AAA:1:ALA:HB2	7:AAA:338:HOH:O	1.74	0.87
6:BBB:207:CL:CL	7:BBB:306:HOH:O	2.36	0.80
1:AAA:15:GLN:HE21	1:AAA:36:LYS:CE	1.98	0.76
6:AAA:207:CL:CL	7:AAA:370:HOH:O	2.48	0.67
1:AAA:15:GLN:HE21	1:AAA:36:LYS:HE2	1.60	0.65

All (1) 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)
7:AAA:310:HOH:O	7:BBB:371:HOH:O[2_555]	1.97	0.23

## 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	AAA	155/153 (101%)	154 (99%)	1 (1%)	0	100	100
1	BBB	152/153 (99%)	152 (100%)	0	0	100	100
All	All	307/306 (100%)	306 (100%)	1 (0%)	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	AAA	122/119 (102%)	121 (99%)	1 (1%)	81	62
1	BBB	117/119 (98%)	115 (98%)	2 (2%)	60	28
All	All	239/238 (100%)	236 (99%)	3 (1%)	78	40

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	133	GLU
1	BBB	59[A]	SER
1	BBB	59[B]	SER

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

### 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 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	9JT	AAA	204	1	17,17,17	6.77	4 (23%)	21,22,22	1.41	3 (14%)
5	SO4	BBB	206	-	4,4,4	0.36	0	6,6,6	0.27	0
5	SO4	BBB	204	-	4,4,4	0.34	0	6,6,6	0.08	0
5	SO4	AAA	206	-	4,4,4	0.28	0	6,6,6	0.17	0
5	SO4	BBB	205	-	4,4,4	0.41	0	6,6,6	0.30	0
3	ACT	AAA	203	-	3,3,3	0.77	0	3,3,3	0.65	0
4	9JT	BBB	202	1	17,17,17	7.21	3 (17%)	21,22,22	2.10	5 (23%)
3	ACT	AAA	202	-	3,3,3	1.29	0	3,3,3	0.52	0

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
4	9JT	AAA	204	1	-	0/8/8/8	0/2/2/2
4	9JT	BBB	202	1	-	0/8/8/8	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	BBB	202	9JT	SE1-C02	-27.28	1.59	1.89
4	AAA	204	9JT	SE1-C02	-26.11	1.61	1.89
4	BBB	202	9JT	C02-C07	9.88	1.52	1.40
4	AAA	204	9JT	C02-C07	8.07	1.50	1.40
4	BBB	202	9JT	C11-N10	-4.10	1.33	1.41

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	BBB	202	9JT	C03-C02-C07	-6.74	111.01	120.62
4	AAA	204	9JT	C03-C02-C07	-3.75	115.28	120.62
4	BBB	202	9JT	C06-C07-C02	3.05	121.81	117.50
4	BBB	202	9JT	SE1-C02-C03	2.86	122.36	119.47
4	BBB	202	9JT	C11-N10-C08	-2.57	119.90	126.58

There are no chirality outliers.

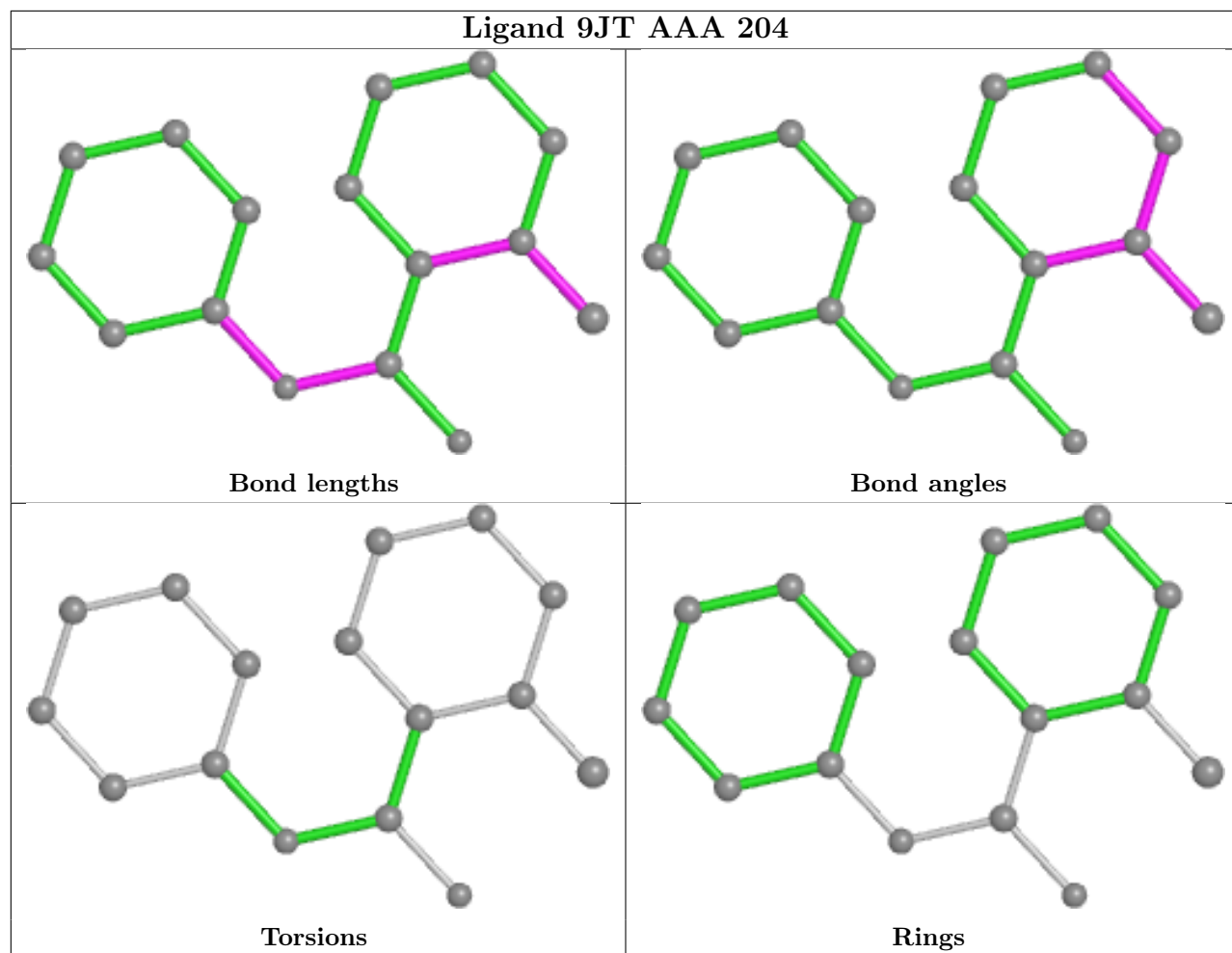
There are no torsion outliers.

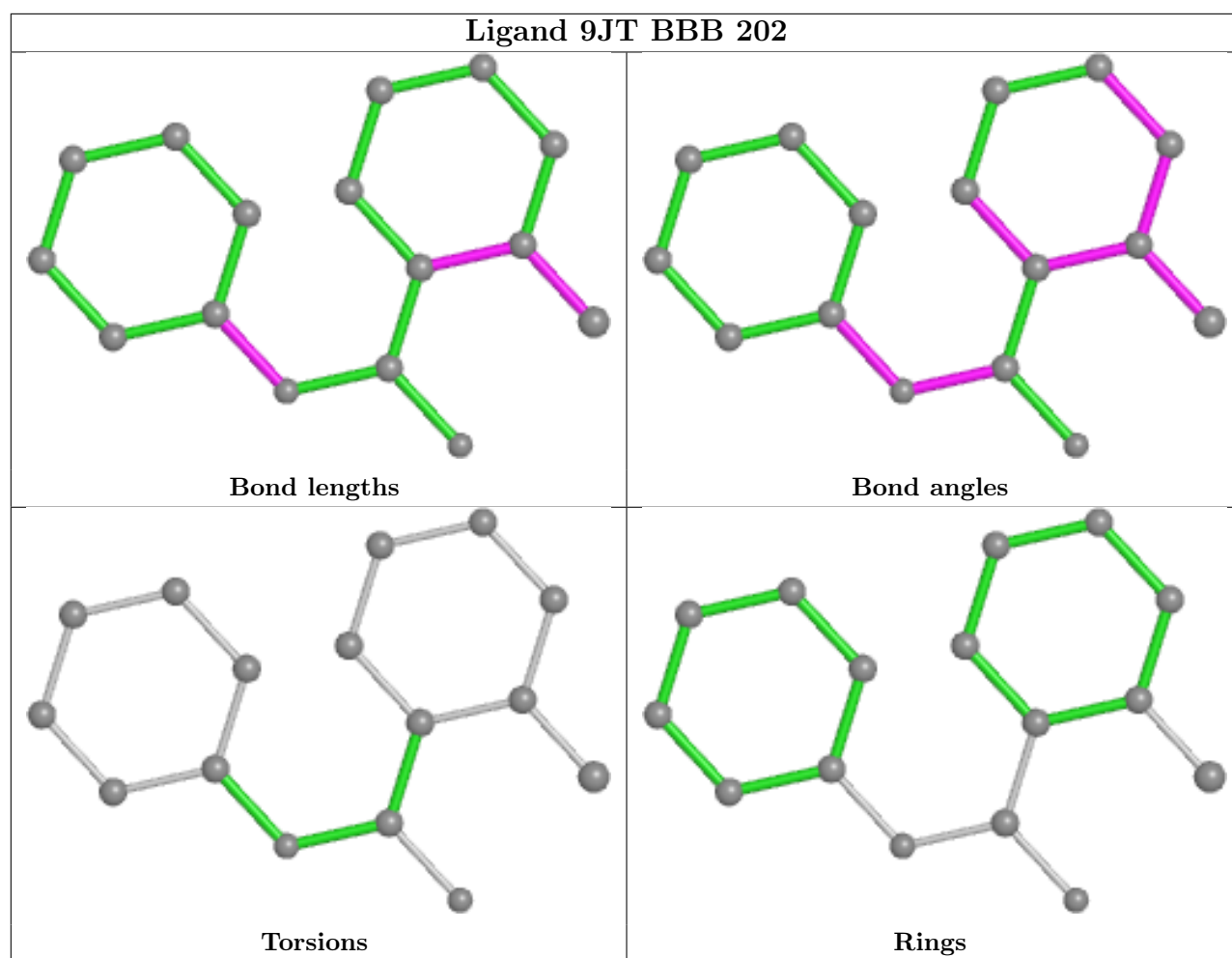
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	204	9JT	1	0
4	BBB	202	9JT	1	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 [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	AAA	153/153 (100%)	-0.39	1 (0%) 87   89	13, 20, 34, 45	0
1	BBB	153/153 (100%)	-0.29	0 100   100	13, 21, 36, 45	0
All	All	306/306 (100%)	-0.34	1 (0%) 94   95	13, 20, 35, 45	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	130	GLY	2.2

### 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
5	SO4	BBB	206	5/5	0.76	0.35	31,50,63,68	5
5	SO4	AAA	206	5/5	0.79	0.23	62,74,98,101	0
5	SO4	BBB	205	5/5	0.91	0.18	29,33,40,40	5
4	9JT	BBB	202	16/16	0.94	0.29	23,26,28,29	0

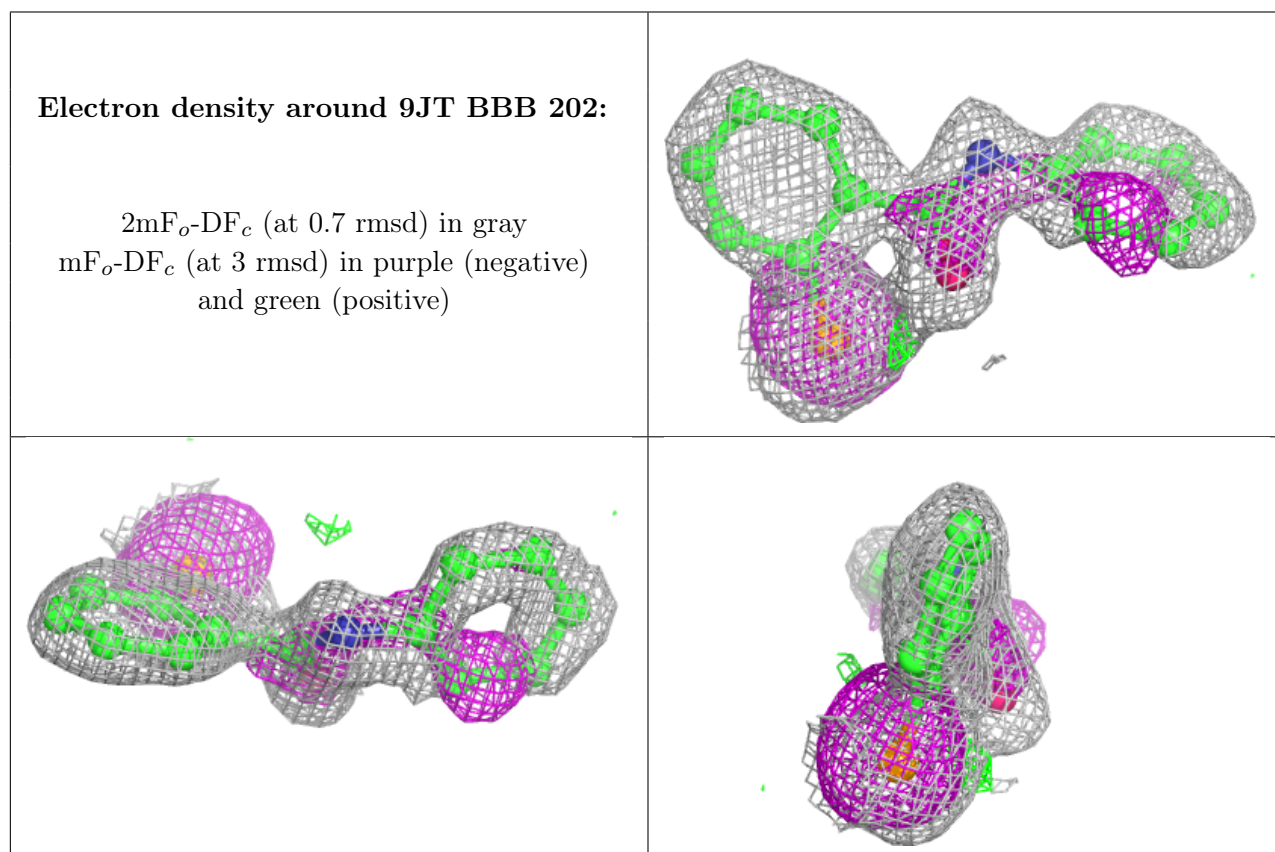
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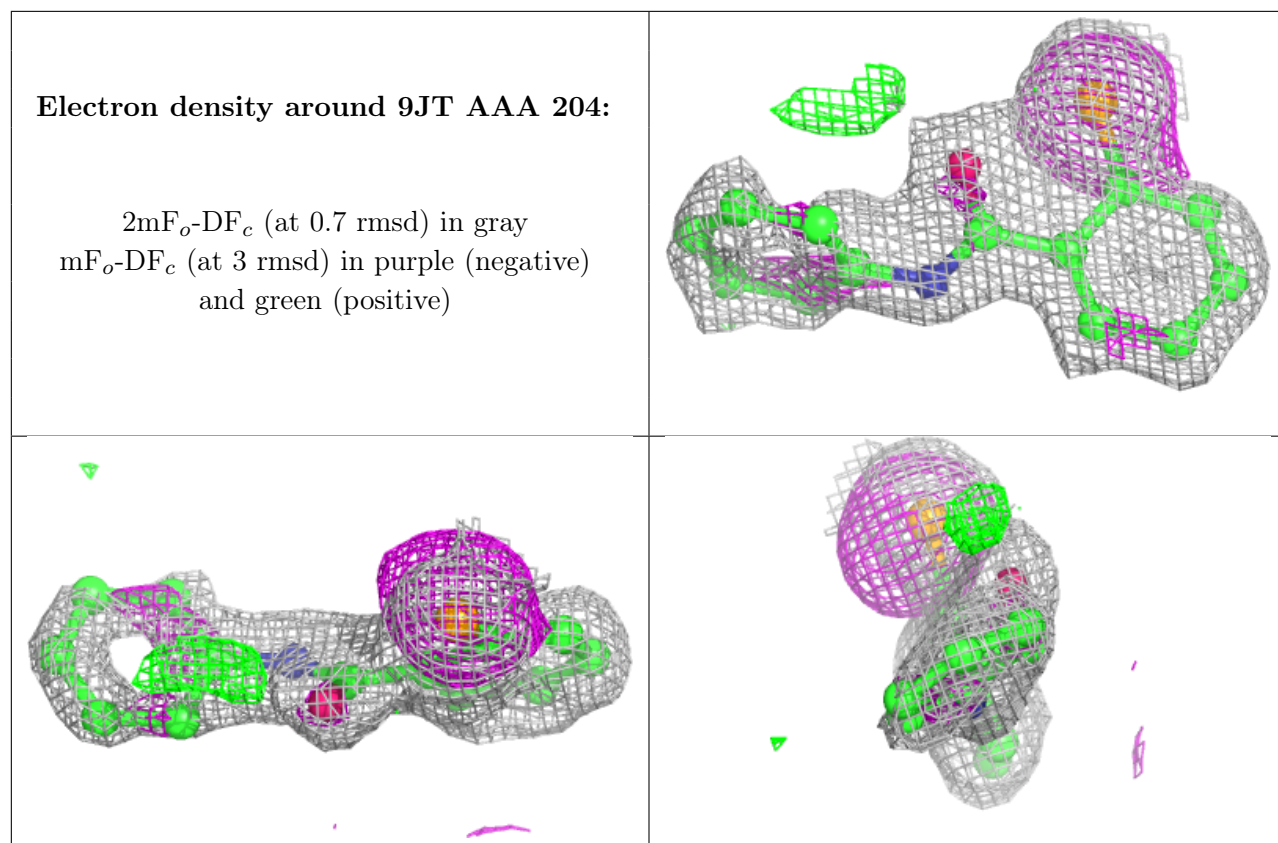


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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ACT	AAA	203	4/4	0.94	0.14	30,48,49,62	0
4	9JT	AAA	204	16/16	0.95	0.23	23,27,29,30	0
3	ACT	AAA	202	4/4	0.97	0.06	30,31,34,46	0
5	SO4	BBB	204	5/5	0.97	0.12	65,69,78,83	0
6	CL	BBB	207	1/1	0.97	0.06	36,36,36,36	0
6	CL	AAA	207	1/1	0.98	0.06	37,37,37,37	0
2	ZN	AAA	205	1/1	0.99	0.04	17,17,17,17	1
2	ZN	BBB	203	1/1	0.99	0.04	19,19,19,19	1
2	ZN	BBB	201	1/1	1.00	0.06	14,14,14,14	0
2	ZN	AAA	201	1/1	1.00	0.05	16,16,16,16	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.