Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2025 – 01:38 am GMT

PDB ID	:	8RTJ
Title	:	X-ray structure of lysozyme obtained upon reaction with [VIVO(8-HQ)2] in ethylene glycol
Authors	:	Paolillo, M.; Ferraro, G.; Merlino, A.
Deposited on	:	2024-01-26
Resolution	:	1.27 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

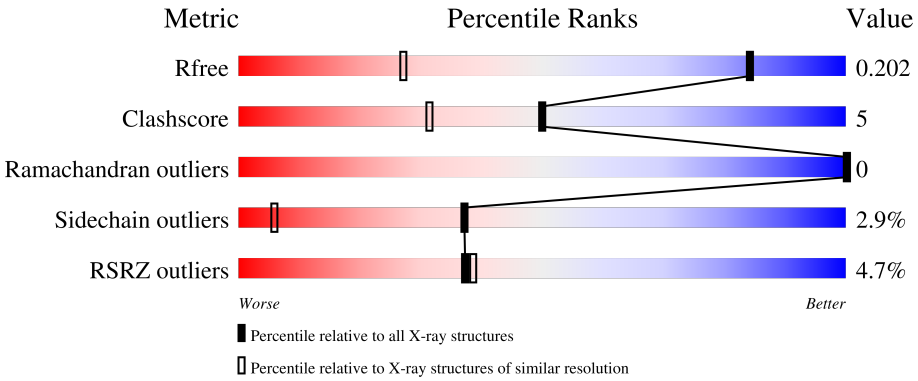
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 1.27 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}	164625	2484 (1.30-1.26)
Clashscore	180529	2694 (1.30-1.26)
Ramachandran outliers	177936	2628 (1.30-1.26)
Sidechain outliers	177891	2627 (1.30-1.26)
RSRZ outliers	164620	2481 (1.30-1.26)

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	AAA	129	5% 91% 8% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NO3	AAA	207	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 1248 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.

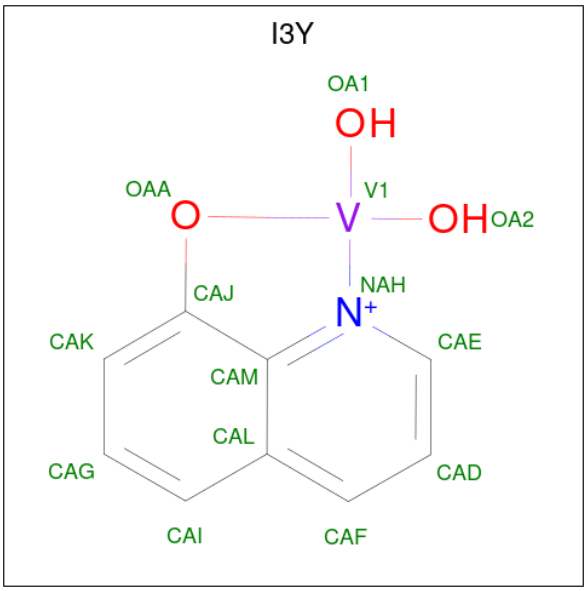
- Molecule 1 is a protein called Lysozyme C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	129	Total	C	N	O	S	0	7	0
			1045	639	203	193	10			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	1	Total	Na	0	0
			1	1		

- Molecule 3 is 2,2-bis($l^{1}-oxidanyl)-3-oxa-1$l^{4}-aza-2$l^{4}-vanadatricyclo[6.3.1.0^{4,12}]dodeca-1(12),4,6,8,10-pentaene (three-letter code: I3Y) (formula: $C_9H_8NO_3V$) (labeled as "Ligand of Interest" by depositor).

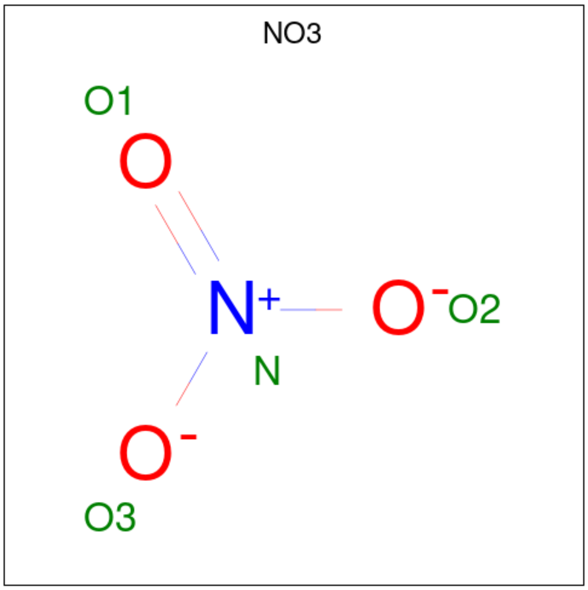


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	V	0	0
			14	9	1	3	1		

- Molecule 4 is VANADIUM ION (three-letter code: V) (formula: V).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total V 1 1	0	0

- Molecule 5 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0
5	AAA	1	Total N O 4 1 3	0	0

- Molecule 6 is water.

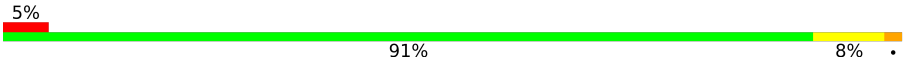
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	AAA	147	Total O 151 151	0	5

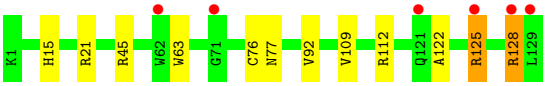
3 Residue-property plots (i)

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: Lysozyme C

Chain AAA:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	78.14Å 78.14Å 37.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.24 – 1.27 55.24 – 1.27	Depositor EDS
% Data completeness (in resolution range)	99.3 (55.24-1.27) 99.3 (55.24-1.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 1.27Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.174 , 0.197 0.180 , 0.202	Depositor DCC
R_{free} test set	1551 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	19.3	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	1248	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.73% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NO3, I3Y, V, NA

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	0.84	0/1079	0.96	2/1455 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AAA	112	ARG	NE-CZ-NH1	7.91	124.25	120.30
1	AAA	112	ARG	NE-CZ-NH2	-5.08	117.76	120.30

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	1045	0	999	10	0
2	AAA	1	0	0	0	0
3	AAA	14	0	0	0	0
4	AAA	1	0	0	0	0
5	AAA	36	0	0	4	0
6	AAA	151	0	0	4	0
All	All	1248	0	999	11	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 5.

All (11) 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:109[A]:VAL:HG23	6:AAA:348[A]:HOH:O	1.95	0.65
1:AAA:15:HIS:HE1	5:AAA:207:NO3:O3	1.87	0.57
1:AAA:21:ARG:NH2	5:AAA:210:NO3:O3	2.26	0.55
1:AAA:45:ARG:HD3	6:AAA:302:HOH:O	2.09	0.51
1:AAA:122:ALA:O	1:AAA:125:ARG:HG2	2.11	0.51
1:AAA:15:HIS:CE1	5:AAA:207:NO3:O3	2.66	0.48
1:AAA:125:ARG:HG3	1:AAA:125:ARG:O	2.15	0.47
1:AAA:15:HIS:HB3	1:AAA:92:VAL:HG11	1.98	0.46
5:AAA:212:NO3:O1	6:AAA:301[B]:HOH:O	2.21	0.43
1:AAA:128:ARG:HD2	6:AAA:434:HOH:O	2.20	0.41
1:AAA:63:TRP:O	1:AAA:76:CYS:HB2	2.21	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	AAA	133/129 (103%)	131 (98%)	2 (2%)	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	112/105 (107%)	109 (97%)	3 (3%)	40 7

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

Mol	Chain	Res	Type
1	AAA	77	ASN
1	AAA	125	ARG
1	AAA	128	ARG

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
5	NO3	AAA	212	-	1,3,3	1.11	0	0,3,3	-	-
3	I3Y	AAA	202	1	11,16,16	0.64	0	15,25,25	2.55	6 (40%)
5	NO3	AAA	210	-	1,3,3	0.54	0	0,3,3	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	NO3	AAA	208	-	1,3,3	0.25	0	0,3,3	-	-
5	NO3	AAA	206	2	1,3,3	0.09	0	0,3,3	-	-
5	NO3	AAA	207	-	1,3,3	0.27	0	0,3,3	-	-
5	NO3	AAA	209	-	1,3,3	0.22	0	0,3,3	-	-
5	NO3	AAA	204	-	1,3,3	0.01	0	0,3,3	-	-
5	NO3	AAA	205	-	1,3,3	1.54	0	0,3,3	-	-
5	NO3	AAA	211	-	1,3,3	0.45	0	0,3,3	-	-

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
3	I3Y	AAA	202	1	-	-	0/3/3/3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	AAA	202	I3Y	CAJ-CAM-NAH	5.31	118.95	115.17
3	AAA	202	I3Y	CAD-CAF-CAL	4.19	127.00	120.44
3	AAA	202	I3Y	CAF-CAL-CAM	-3.85	111.56	117.86
3	AAA	202	I3Y	CAD-CAE-NAH	-3.14	120.19	122.67
3	AAA	202	I3Y	CAE-NAH-CAM	2.82	120.85	117.65
3	AAA	202	I3Y	CAJ-CAM-CAL	-2.14	118.24	121.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

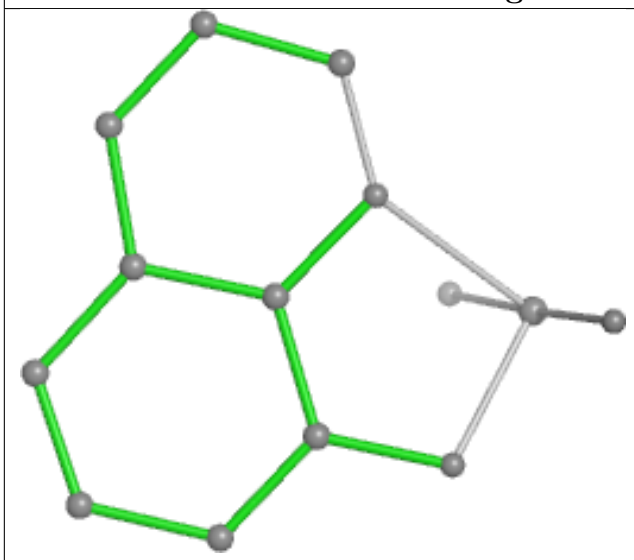
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AAA	212	NO3	1	0
5	AAA	210	NO3	1	0
5	AAA	207	NO3	2	0

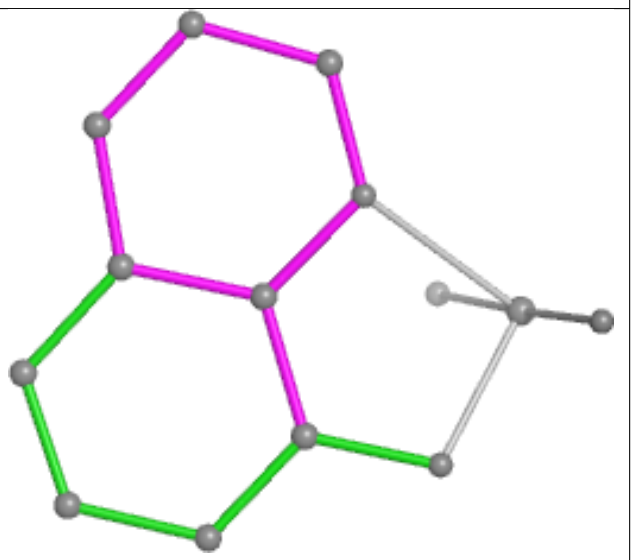
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

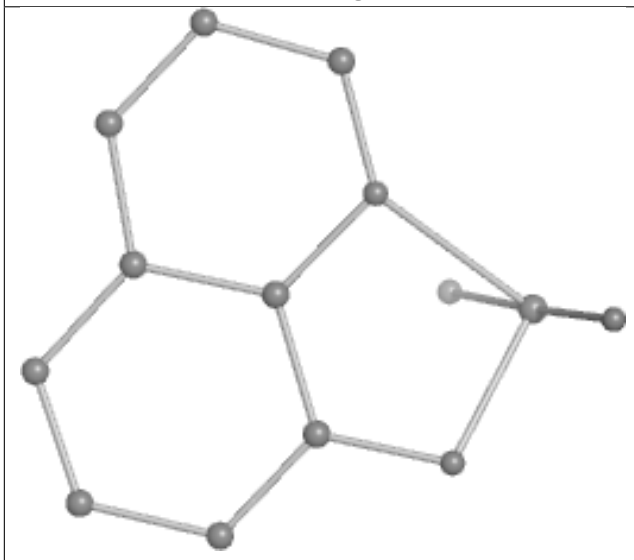
Ligand I3Y AAA 202



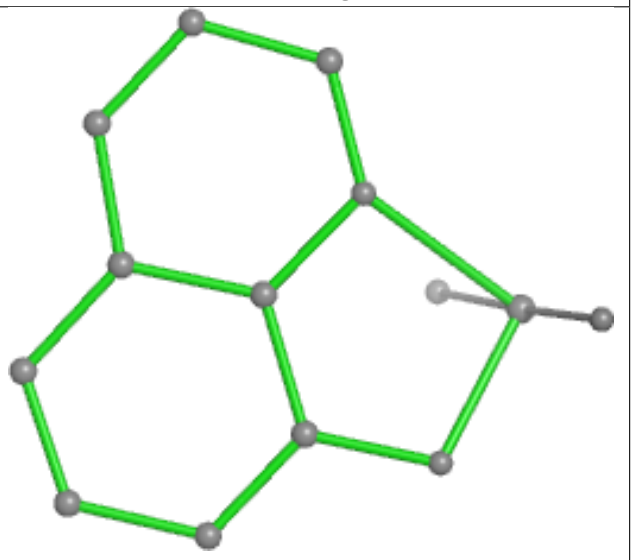
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

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, 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>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AAA	129/129 (100%)	0.56	6 (4%) 37 38	8, 21, 35, 50	7 (5%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	129	LEU	4.1
1	AAA	125	ARG	2.5
1	AAA	71	GLY	2.4
1	AAA	62	TRP	2.2
1	AAA	121	GLN	2.2
1	AAA	128	ARG	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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	B-factors(Å^2)	Q<0.9
3	I3Y	AAA	202	14/14	0.70	0.25	43,51,54,55	14

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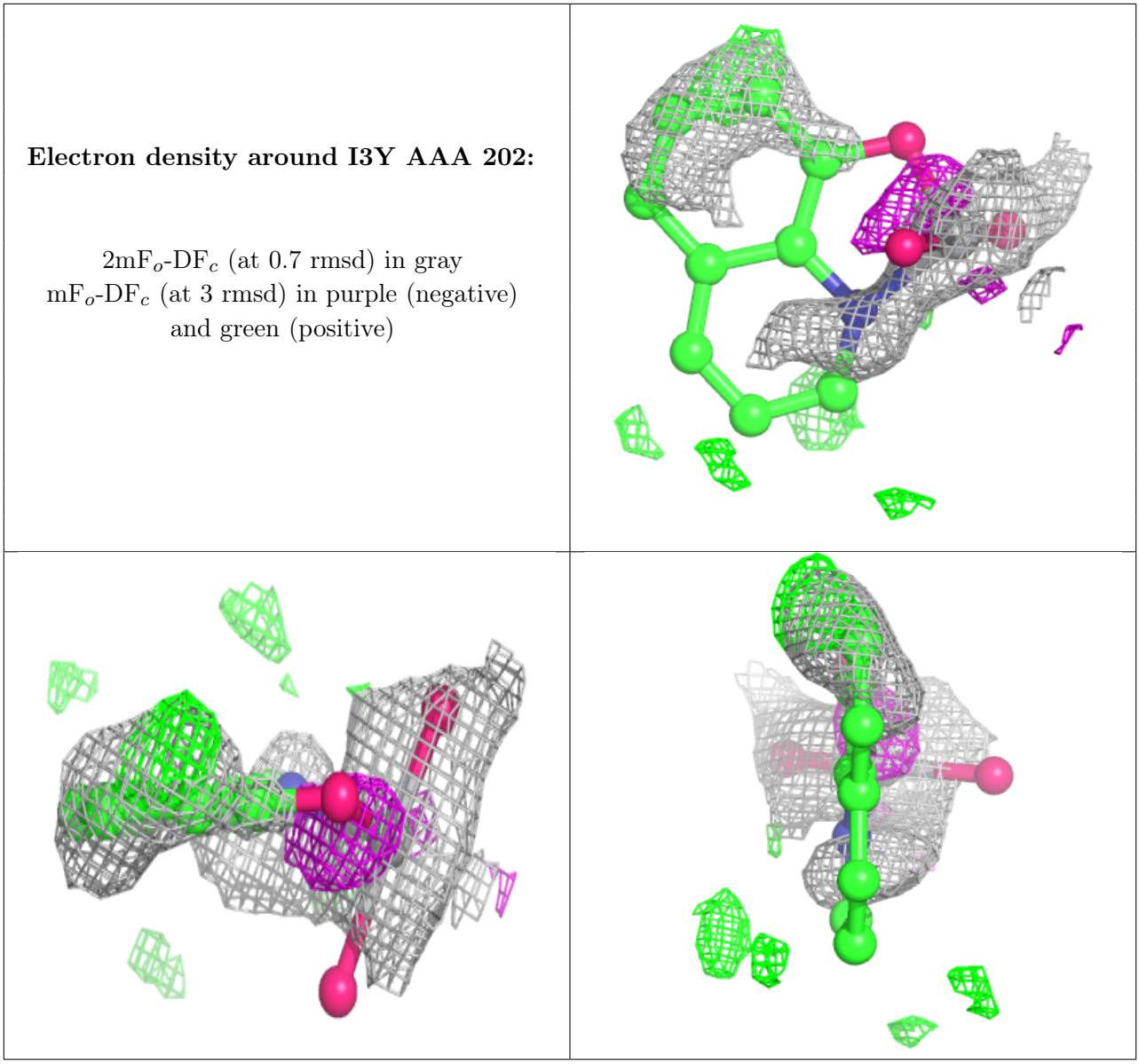
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NO3	AAA	208	4/4	0.79	0.12	29,41,43,45	0
5	NO3	AAA	209	4/4	0.79	0.12	44,49,50,55	0
5	NO3	AAA	207	4/4	0.81	0.11	37,45,46,53	0
5	NO3	AAA	205	4/4	0.82	0.16	18,26,34,35	4
5	NO3	AAA	211	4/4	0.87	0.14	27,44,45,50	0
5	NO3	AAA	204	4/4	0.88	0.09	35,36,43,48	0
5	NO3	AAA	210	4/4	0.89	0.09	32,36,39,40	0
4	V	AAA	203	1/1	0.89	0.13	55,55,55,55	1
5	NO3	AAA	212	4/4	0.90	0.10	27,32,34,34	4
5	NO3	AAA	206	4/4	0.91	0.09	23,28,31,33	0
2	NA	AAA	201	1/1	0.95	0.07	20,20,20,20	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.

Electron density around I3Y AAA 202:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.