

Full wwPDB X-ray Structure Validation Report (i)

Sep 5, 2023 – 12:49 PM EDT

PDB ID : 7RYK

Title: Hen egg-white lysozyme with ionic liquid ethanolammonium nitrate 1 mol%

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Deposited on : 2021-08-25

Resolution : 1.76 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 (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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.35

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)

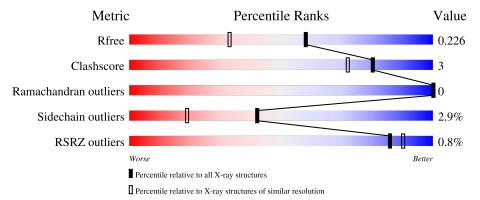
Validation Pipeline (wwPDB-VP) : 2.35

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 1.76 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	90%	10%		
1	BBB	129	89%	11%		



2 Entry composition (i)

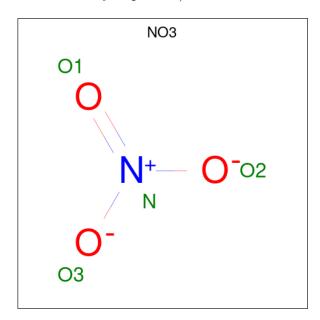
There are 3 unique types of molecules in this entry. The entry contains 4286 atoms, of which 2005 are hydrogens and 0 are deuteriums.

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 2026	C 632	H 997	N 199	O 188	S 10	0	4	0
1	BBB	129	Total 2049	C 638	H 1008	N 202	O 191	S 10	0	6	0

• Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO₃) (labeled as "Ligand of Interest" by depositor).



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

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

• Molecule 3 is water.

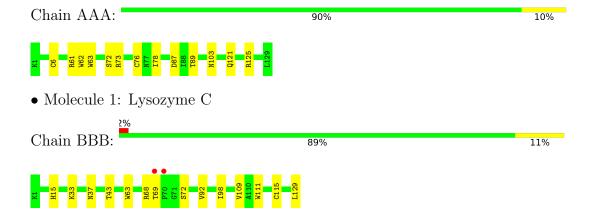
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	92	Total O 92 92	0	0
3	BBB	71	Total O 71 71	0	0



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: Lysozyme C





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	27.46Å 62.35Å 59.47Å	Donositon
a, b, c, α , β , γ	90.00° 90.57° 90.00°	Depositor
Resolution (Å)	29.75 - 1.76	Depositor
rtesolution (A)	31.18 - 1.76	EDS
% Data completeness	99.8 (29.75-1.76)	Depositor
(in resolution range)	99.8 (31.18-1.76)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.82 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.133 , 0.224	Depositor
it, it free	0.144 , 0.226	DCC
R_{free} test set	960 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.45, 39.4	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
	0.024 for -h,-l,-k	
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
	0.045 for h,-k,-l	
F_o, F_c correlation	0.97	EDS
Total number of atoms	4286	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 37.33 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3582e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



¹Intensities 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: NO3

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	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	AAA	0.76	0/1055	0.89	0/1425
1	BBB	0.79	0/1070	0.88	1/1446 (0.1%)
All	All	0.77	0/2125	0.89	1/2871 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	BBB	43	THR	CA-CB-OG1	-7.03	94.23	109.00

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	AAA	1029	997	998	6	1
1	BBB	1041	1008	1007	5	0
2	AAA	28	0	0	1	0
2	BBB	20	0	0	0	0
3	AAA	92	0	0	0	0
3	BBB	71	0	0	0	0
All	All	2281	2005	2005	11	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 3.

All (11) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:AAA:61:ARG:HG2	1:AAA:62:TRP:CD1	2.35	0.62
1:AAA:87[B]:ASP:OD1	1:AAA:89:THR:OG1	2.20	0.54
1:BBB:15:HIS:HB3	1:BBB:92:VAL:HG11	1.92	0.52
1:AAA:61:ARG:O	1:AAA:72:SER:HA	2.11	0.50
1:AAA:63:TRP:O	1:AAA:76:CYS:HB2	2.14	0.48
1:AAA:121:GLN:HG2	2:AAA:305:NO3:O3	2.15	0.46
1:BBB:111:TRP:CD1	1:BBB:115:CYS:HB2	2.54	0.42
1:BBB:63:TRP:CE2	1:BBB:98:ILE:HG12	2.55	0.41
1:BBB:69:THR:O	1:BBB:69:THR:HG23	2.20	0.41
1:AAA:62:TRP:CZ3	1:AAA:73:ARG:HG3	2.56	0.40
1:BBB:33:LYS:O	1:BBB:37:ASN:HA	2.21	0.40

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:AAA:6:CYS:H	1:AAA:103:ASN:HD21[2_546]	1.12	0.48

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	AAA	130/129 (101%)	128 (98%)	2 (2%)	0	100	100
1	BBB	133/129 (103%)	129 (97%)	4 (3%)	0	100	100
All	All	263/258 (102%)	257 (98%)	6 (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	109/105 (104%)	107 (98%)	2 (2%)	59 40		
1	BBB	111/105 (106%)	105 (95%)	6 (5%)	22 5		
All	All	220/210 (105%)	212 (96%)	8 (4%)	42 13		

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	78	ILE
1	AAA	125	ARG
1	BBB	68[A]	ARG
1	BBB	68[B]	ARG
1	BBB	72	SER
1	BBB	109[A]	VAL
1	BBB	109[B]	VAL
1	BBB	129	LEU

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)

12 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).

Mal	Mol Type		Res	Link	В	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	NO3	AAA	307	-	1,3,3	0.14	0	0,3,3	-	-
2	NO3	AAA	305	-	1,3,3	0.39	0	0,3,3	-	-
2	NO3	BBB	303	-	1,3,3	0.05	0	0,3,3	_	-
2	NO3	BBB	304	-	1,3,3	0.28	0	0,3,3	-	-
2	NO3	BBB	305	-	1,3,3	0.03	0	0,3,3	-	-
2	NO3	AAA	304	-	1,3,3	0.08	0	0,3,3	_	-
2	NO3	AAA	306	-	1,3,3	0.29	0	0,3,3	-	-
2	NO3	BBB	301	-	1,3,3	0.22	0	0,3,3	_	-
2	NO3	AAA	303	-	1,3,3	0.15	0	0,3,3	-	-
2	NO3	BBB	302	-	1,3,3	0.26	0	0,3,3	-	-
2	NO3	AAA	302	-	1,3,3	0.15	0	0,3,3	-	-
2	NO3	AAA	301	_	1,3,3	0.15	0	0,3,3	_	_

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.

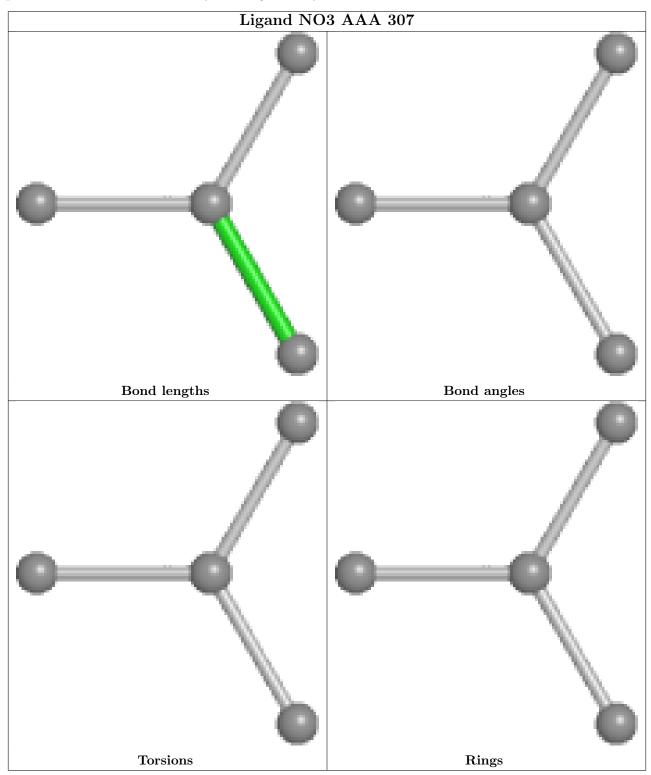
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	305	NO3	1	0

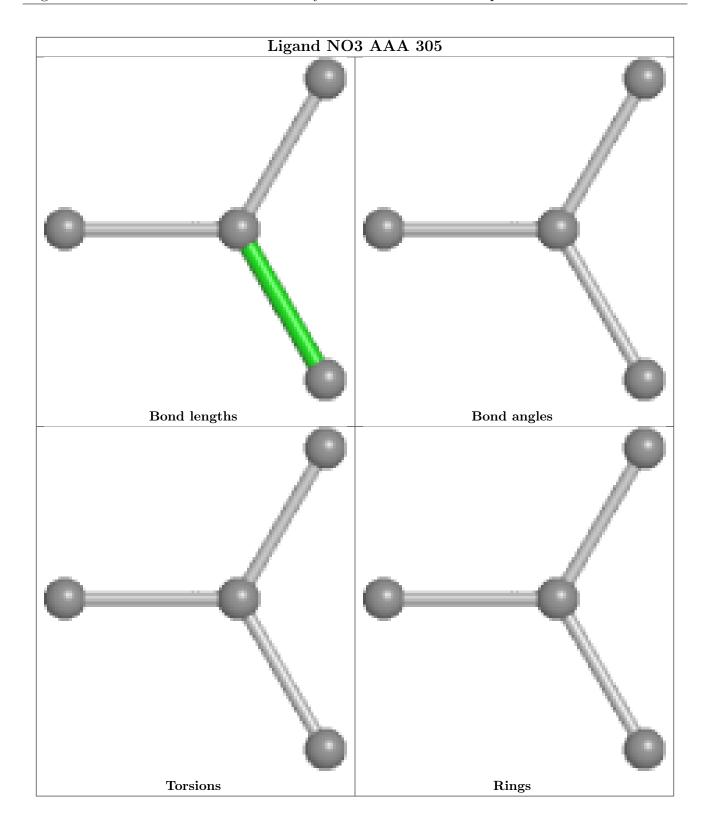
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



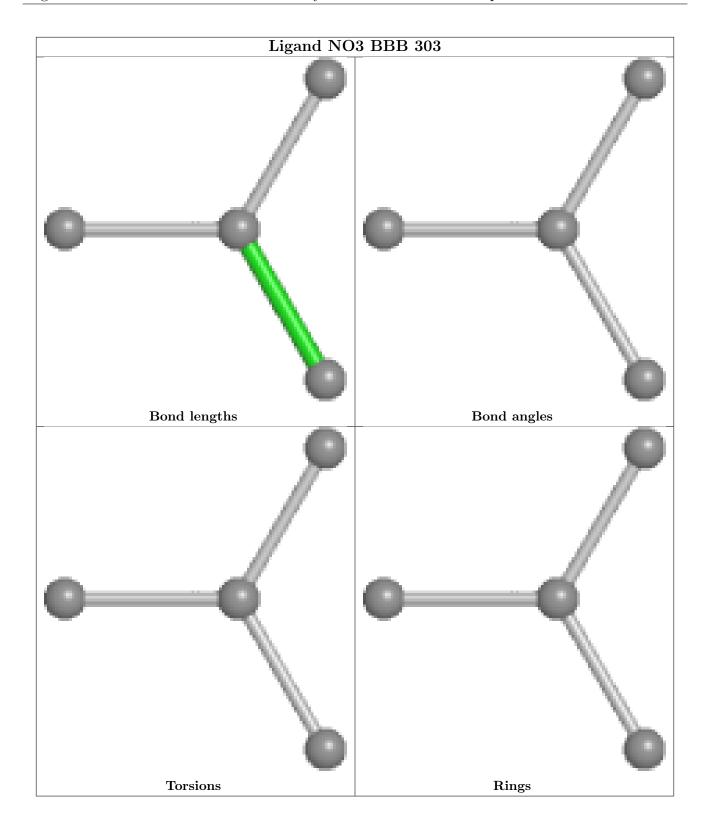
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.



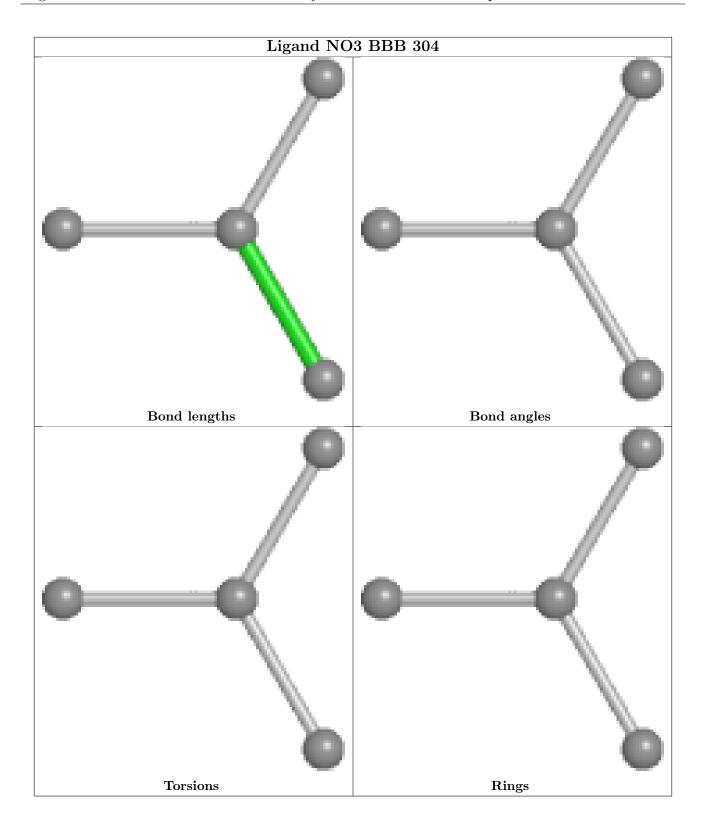




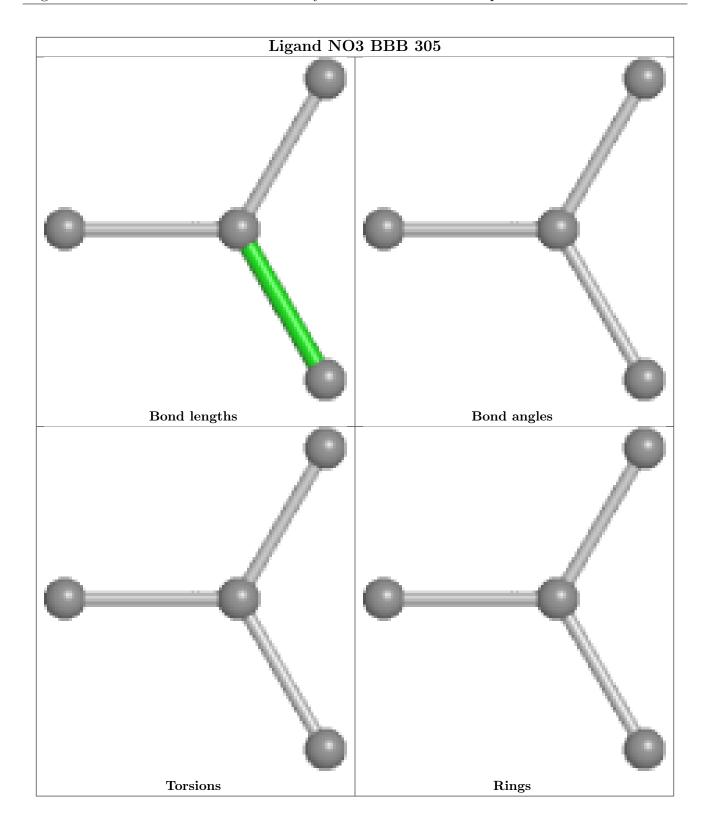




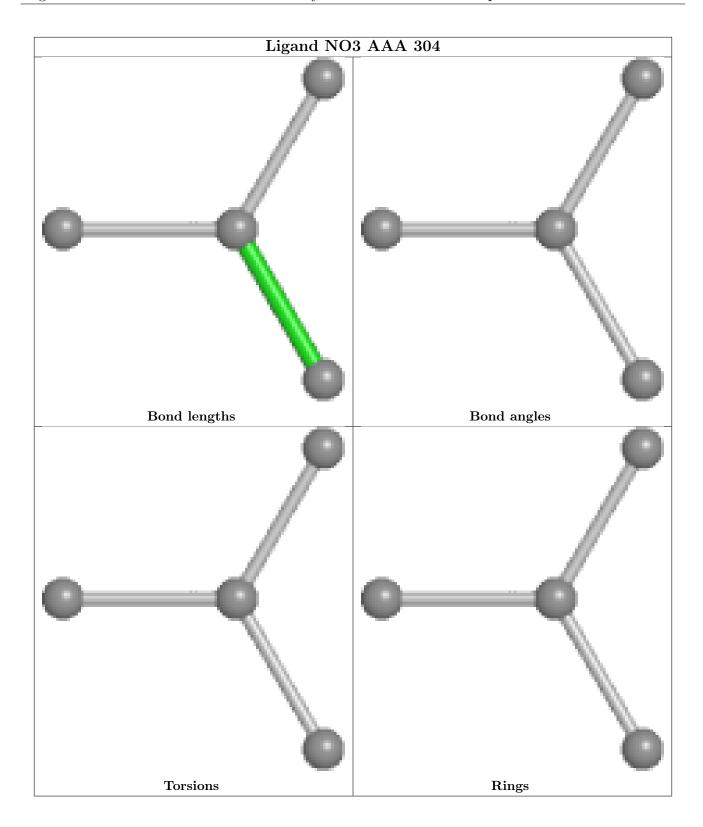




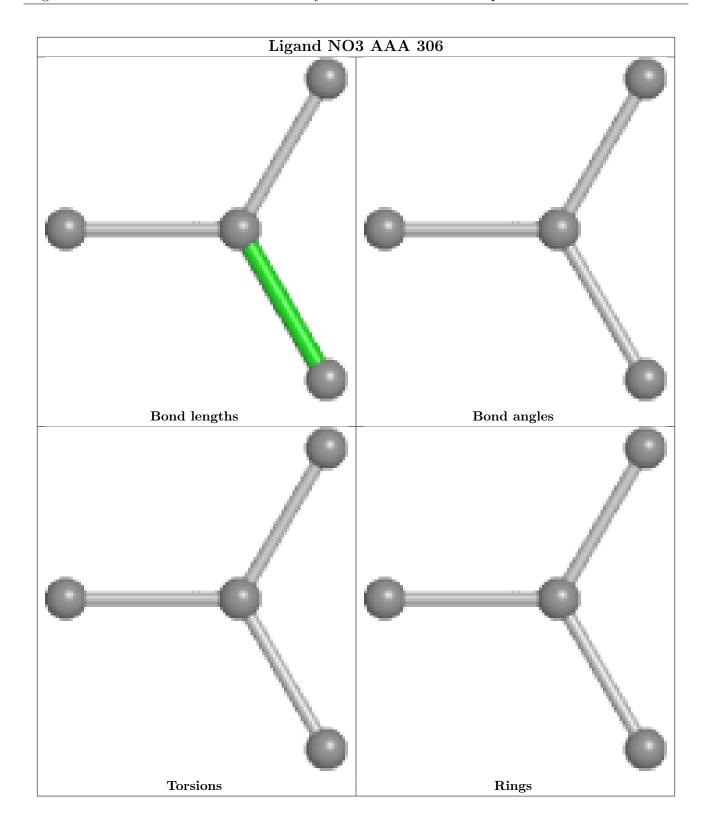




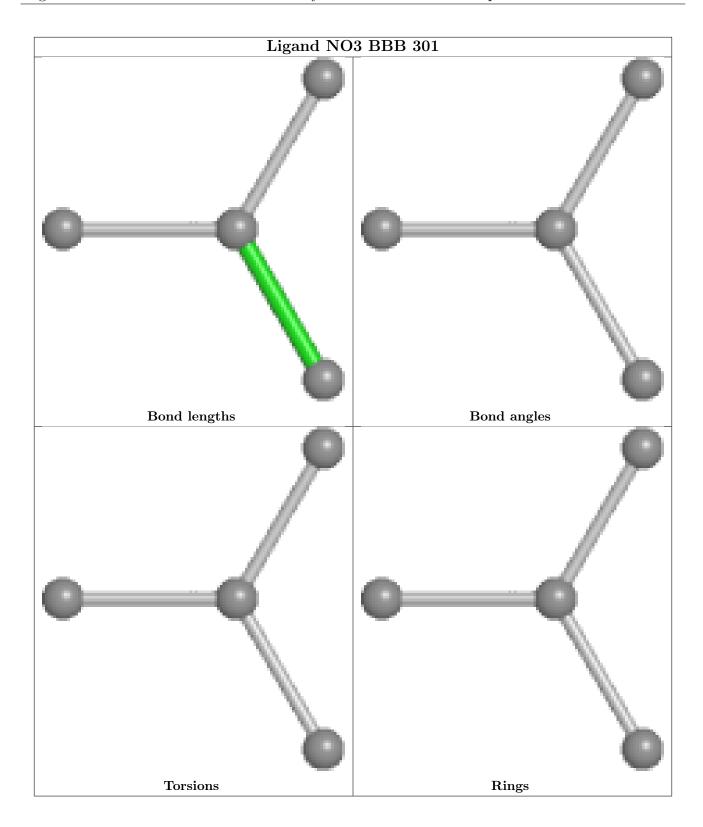




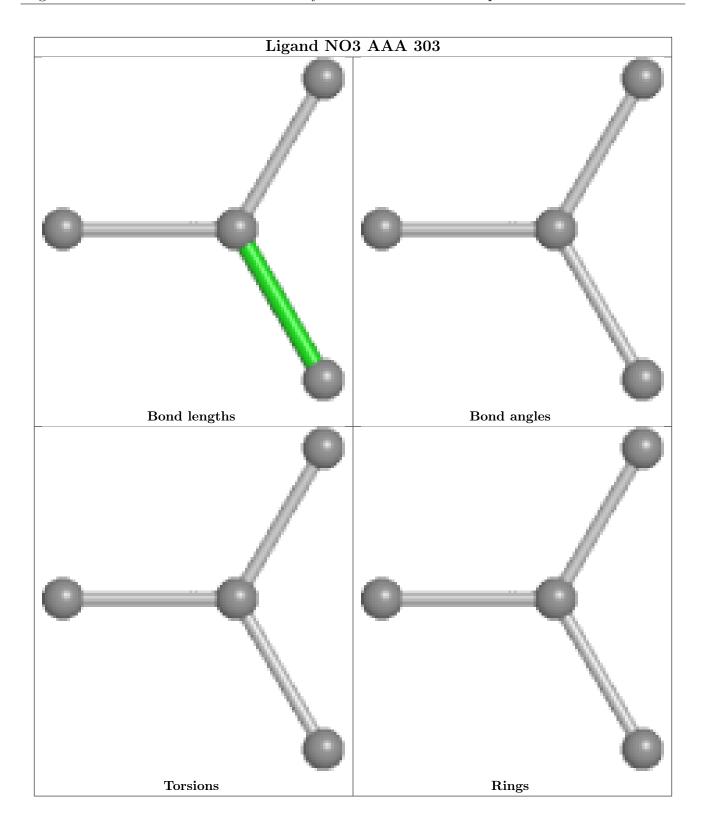




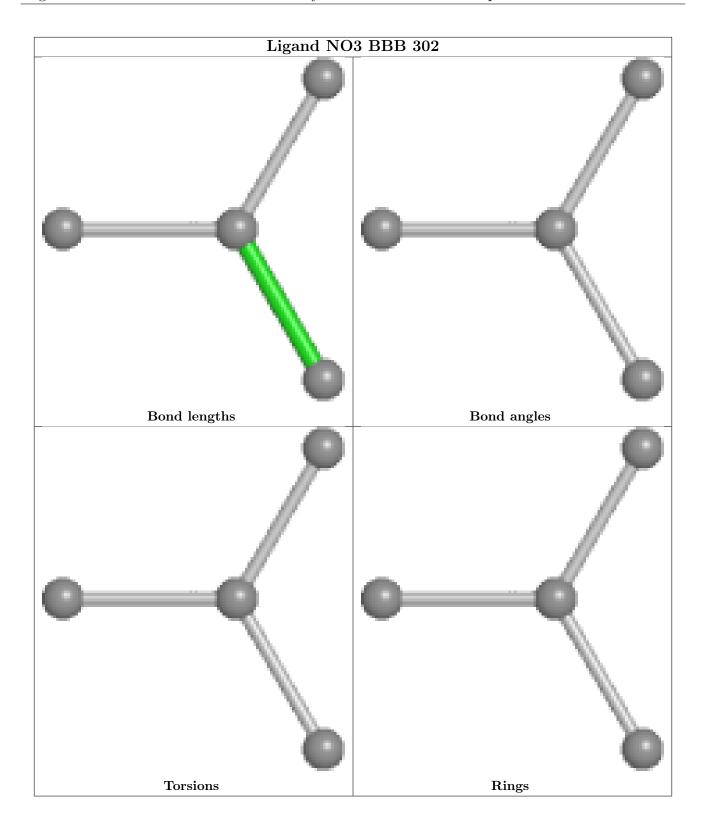




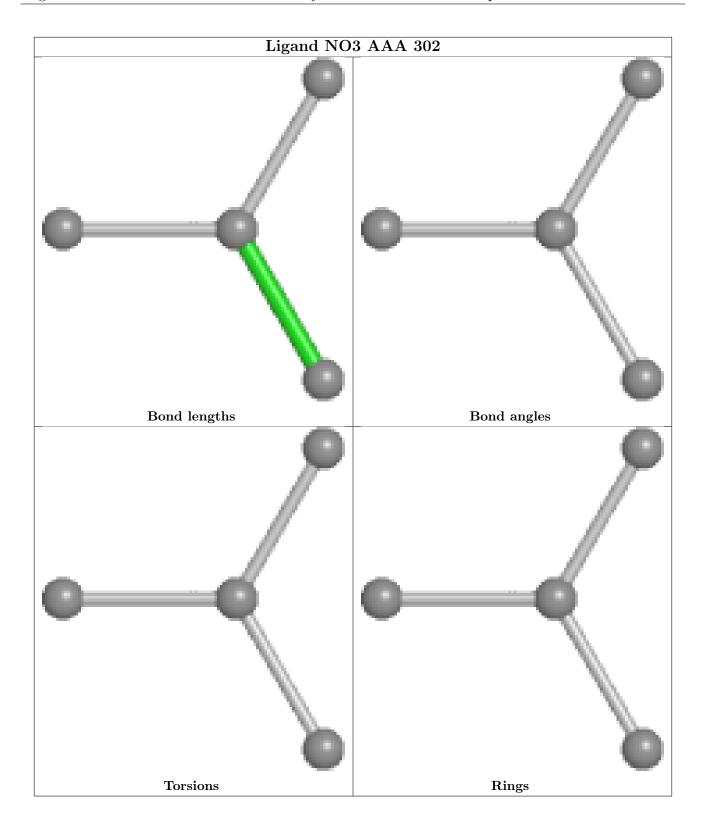




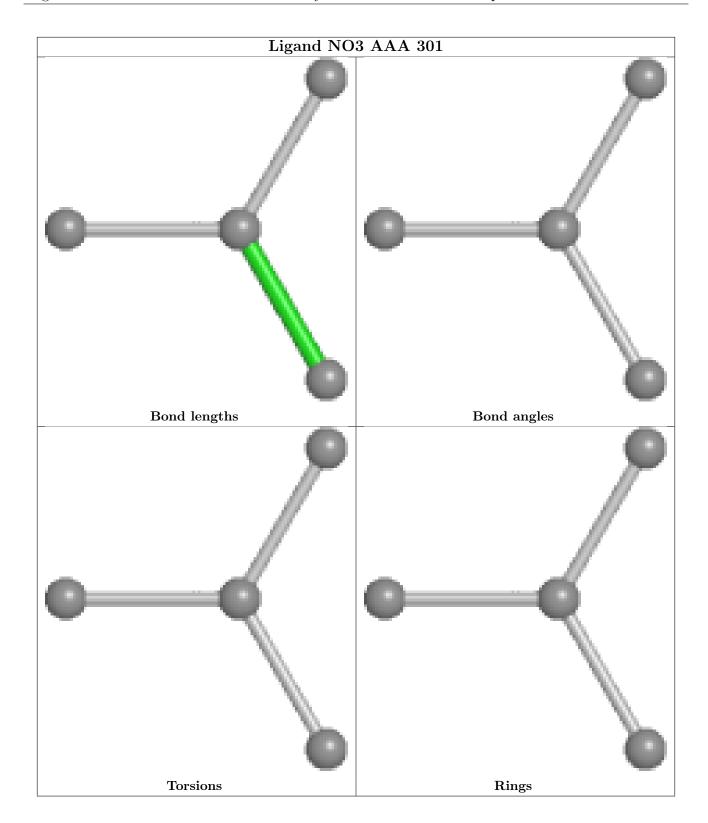












5.7 Other polymers (i)

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 $>$	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	AAA	129/129 (100%)	-0.39	0 100 100	11, 19, 39, 52	0
1	BBB	129/129 (100%)	-0.45	2 (1%) 72 79	12, 20, 38, 65	0
All	All	258/258 (100%)	-0.42	2 (0%) 86 90	11, 19, 39, 65	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	70	PRO	3.1
1	BBB	69	THR	2.3

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{ ilde{A}}^2)$	Q<0.9
2	NO3	AAA	306	4/4	0.87	0.13	38,39,50,53	0
2	NO3	BBB	304	4/4	0.90	0.12	38,42,46,46	0
2	NO3	BBB	303	4/4	0.92	0.12	38,41,42,44	0

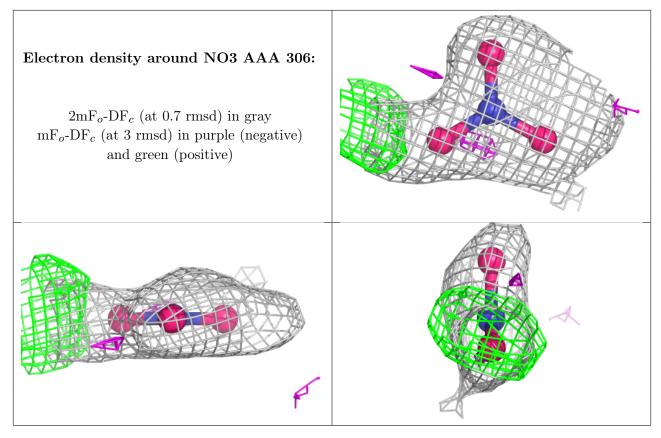
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	NO3	BBB	302	4/4	0.94	0.09	33,36,40,49	0
2	NO3	BBB	305	4/4	0.94	0.11	36,46,53,62	0
2	NO3	AAA	303	4/4	0.95	0.08	29,29,31,33	0
2	NO3	AAA	302	4/4	0.95	0.09	31,32,33,34	0
2	NO3	BBB	301	4/4	0.96	0.07	36,42,44,47	0
2	NO3	AAA	305	4/4	0.98	0.08	32,42,49,50	0
2	NO3	AAA	307	4/4	0.99	0.06	25,32,34,34	0
2	NO3	AAA	301	4/4	0.99	0.06	21,22,24,28	0
2	NO3	AAA	304	4/4	0.99	0.05	24,25,26,32	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.



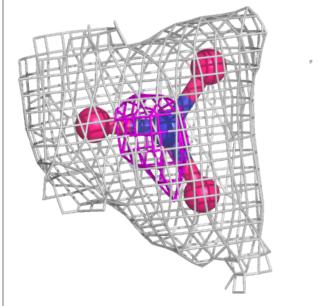


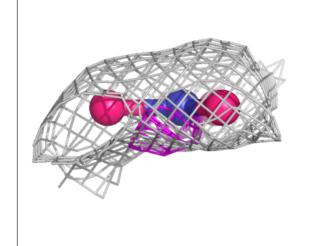
Electron density around NO3 BBB 304: 2mF_o-DF_c (at 0.7 rmsd) in gray mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

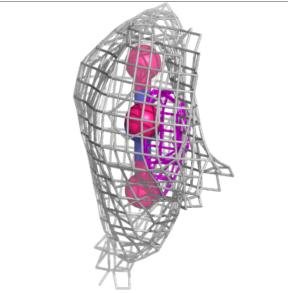


Electron density around NO3 BBB 303:

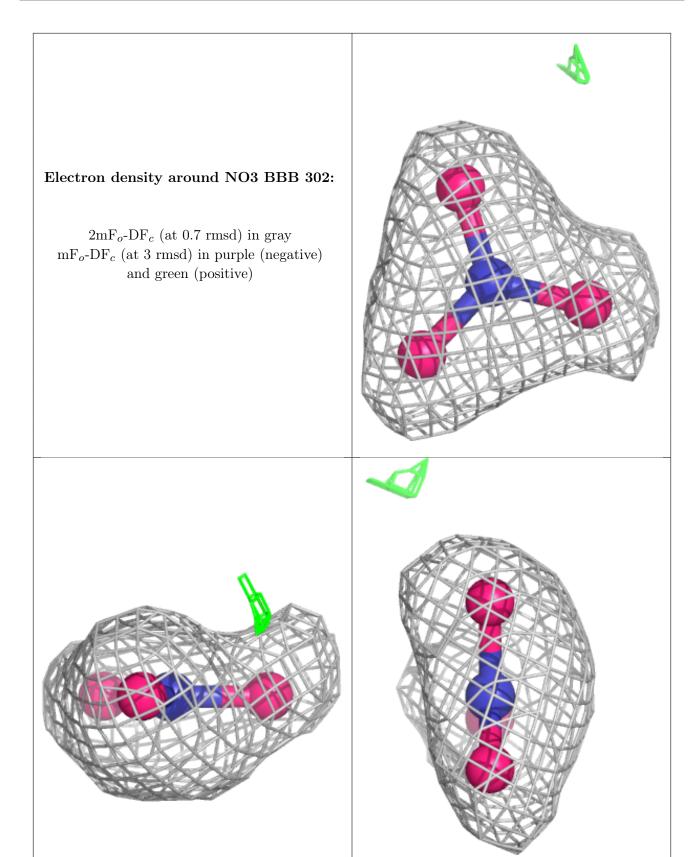
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)







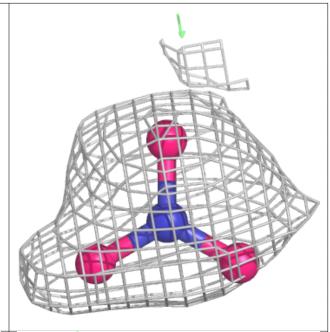


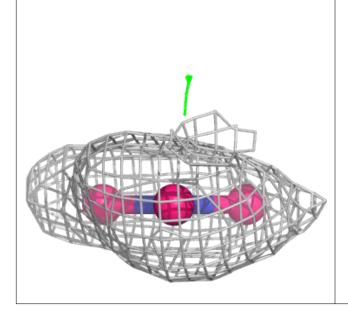


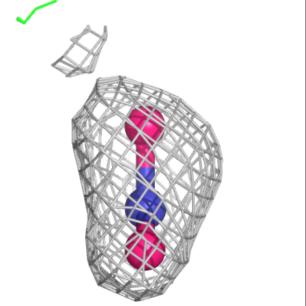


Electron density around NO3 BBB 305:

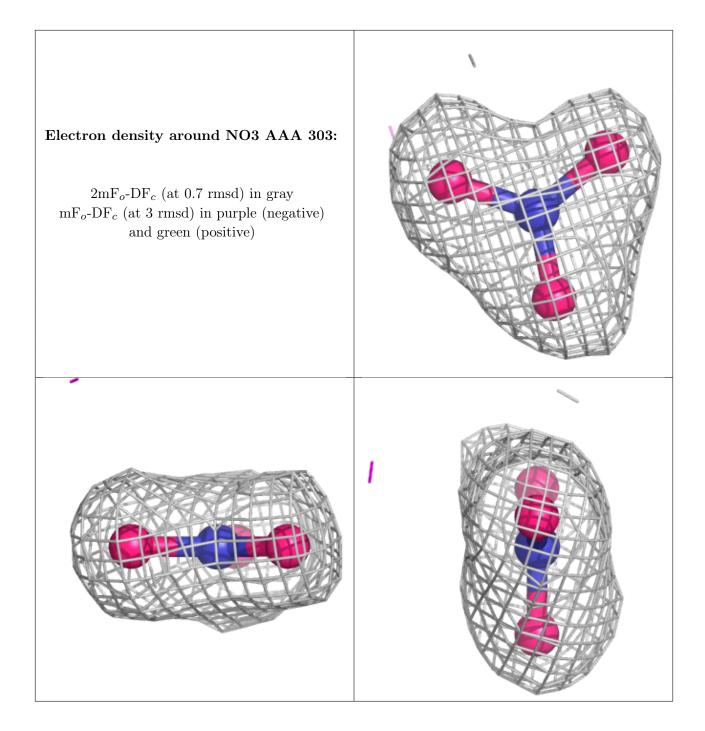
 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



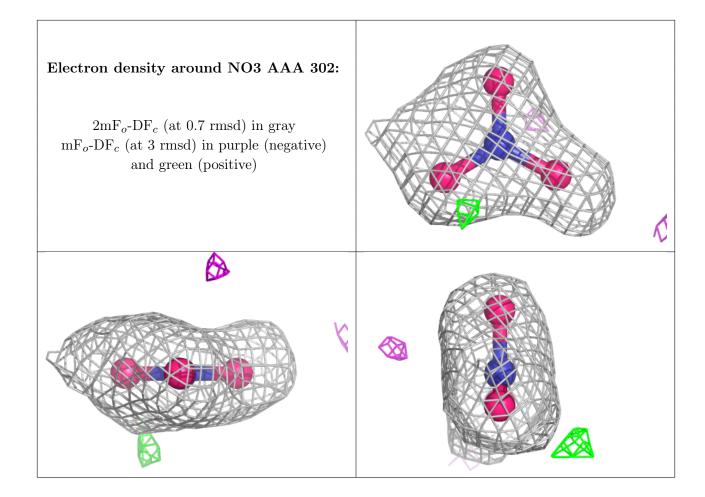








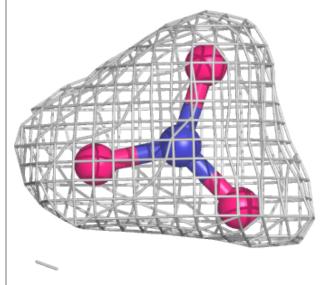


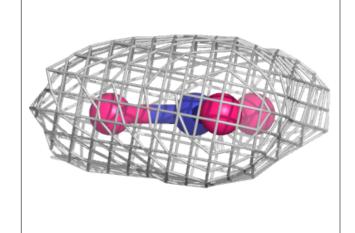


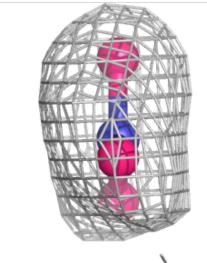


Electron density around NO3 BBB 301:

 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









Electron density around NO3 AAA 305: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray ${ m mF}_o{ m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

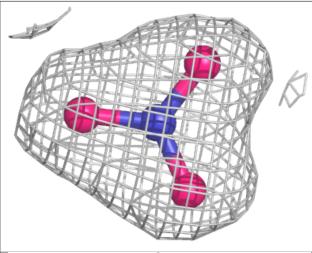


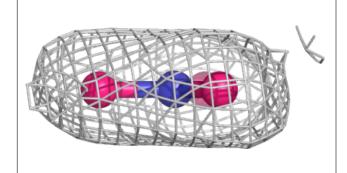
Electron density around NO3 AAA 307: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray ${ m mF}_o{ m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

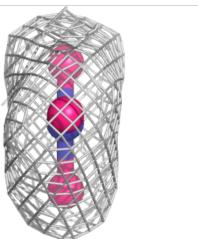


Electron density around NO3 AAA 301:

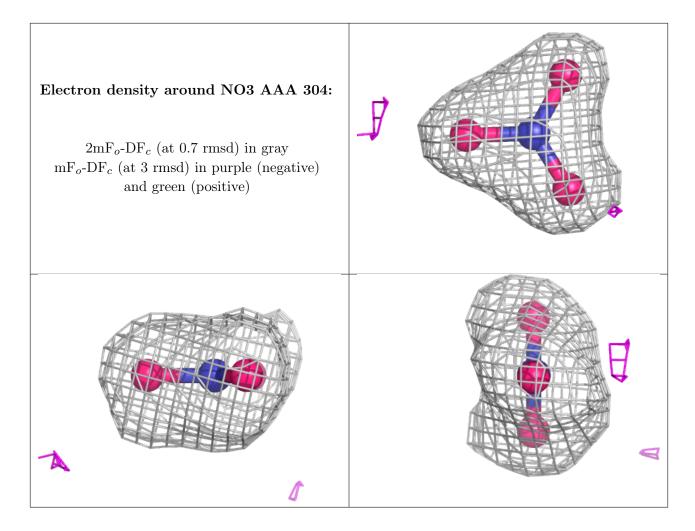
 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

