



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 10:01 AM EDT

PDB ID : 7Y78 / pdb_00007y78
Title : Crystal structure of Cry78Aa
Authors : Cao, B.B.; Nie, Y.F.; Wang, N.C.; Guan, Z.Y.; Zhang, D.L.; Zhang, J.
Deposited on : 2022-06-21
Resolution : 2.90 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

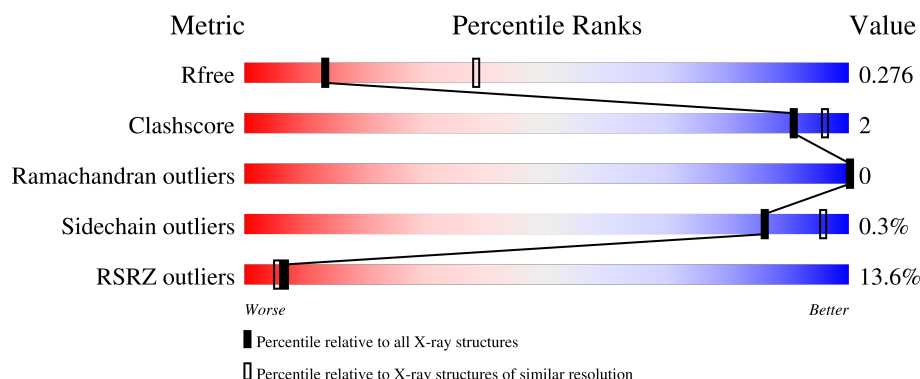
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 $\leq 5\%$. 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	350	11% 92% • • •
1	B	350	12% 94% • •
1	C	350	15% 94% • •
1	D	350	15% 93% • •

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
2	NH4	A	401	-	-	-	X
2	NH4	D	402	-	-	-	X
3	EDO	D	401	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10909 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.

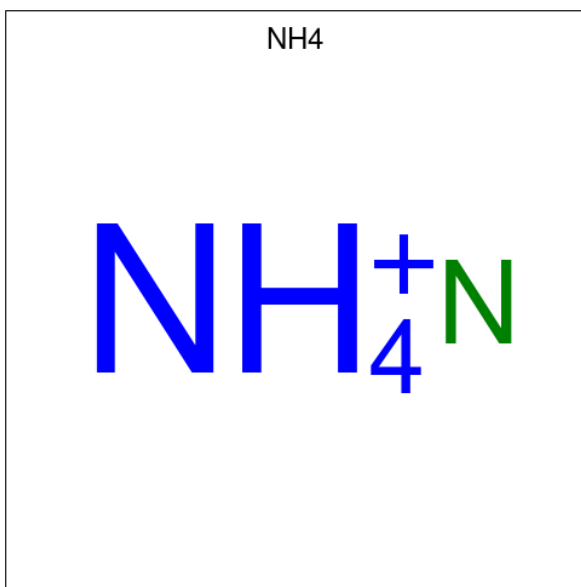
- Molecule 1 is a protein called Toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2724	1734	451	528	11			
1	B	341	Total	C	N	O	S	0	0	0
			2731	1739	452	529	11			
1	C	340	Total	C	N	O	S	0	0	0
			2721	1729	451	530	11			
1	D	339	Total	C	N	O	S	0	0	0
			2713	1725	450	527	11			

There are 12 discrepancies between the modelled and reference sequences:

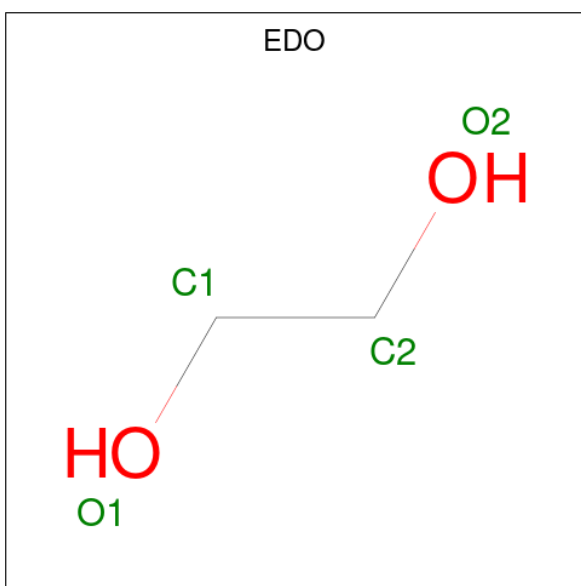
Chain	Residue	Modelled	Actual	Comment	Reference
A	10	ALA	-	expression tag	UNP A0A3S6Q0Y2
A	11	HIS	-	expression tag	UNP A0A3S6Q0Y2
A	12	MET	-	expression tag	UNP A0A3S6Q0Y2
B	10	ALA	-	expression tag	UNP A0A3S6Q0Y2
B	11	HIS	-	expression tag	UNP A0A3S6Q0Y2
B	12	MET	-	expression tag	UNP A0A3S6Q0Y2
C	10	ALA	-	expression tag	UNP A0A3S6Q0Y2
C	11	HIS	-	expression tag	UNP A0A3S6Q0Y2
C	12	MET	-	expression tag	UNP A0A3S6Q0Y2
D	10	ALA	-	expression tag	UNP A0A3S6Q0Y2
D	11	HIS	-	expression tag	UNP A0A3S6Q0Y2
D	12	MET	-	expression tag	UNP A0A3S6Q0Y2

- Molecule 2 is AMMONIUM ION (CCD ID: NH4) (formula: H₄N) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total N 1 1	0	0
2	B	1	Total N 1 1	0	0
2	C	1	Total N 1 1	0	0
2	D	1	Total N 1 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂) (labeled as "Ligand of Interest" by depositor).

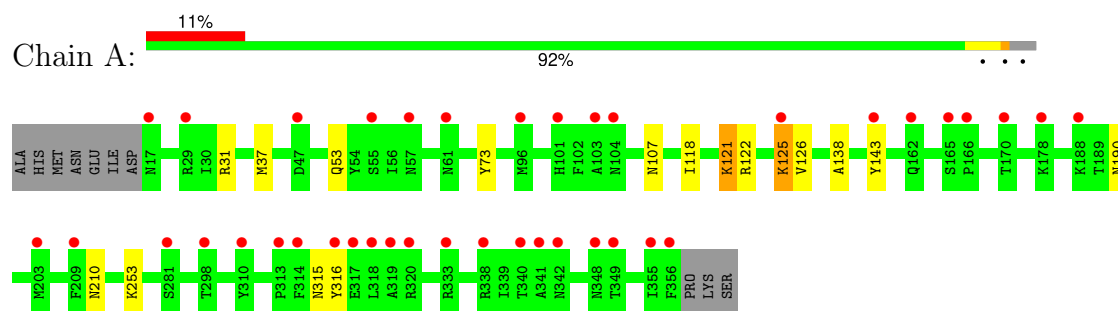


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0

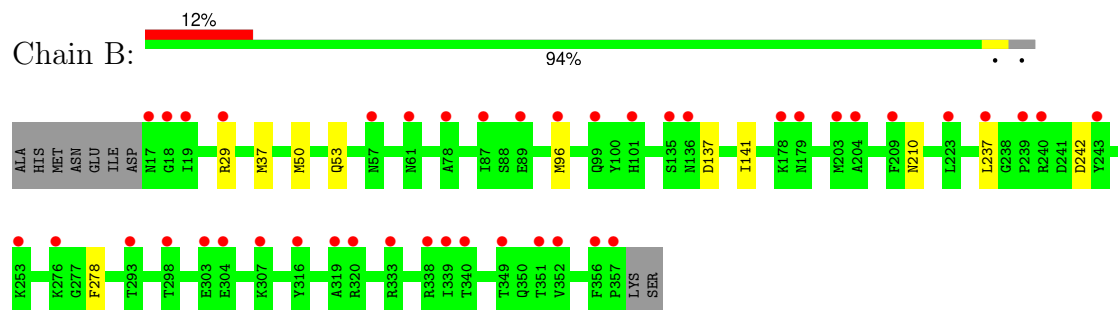
3 Residue-property plots [i](#)

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.

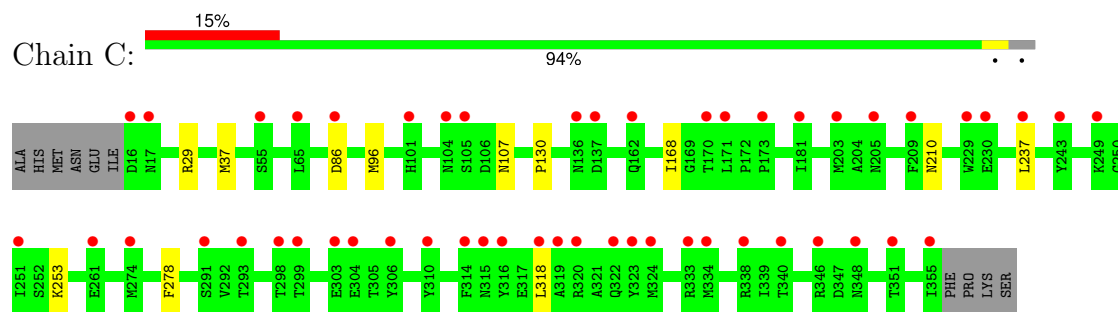
• Molecule 1: Toxin



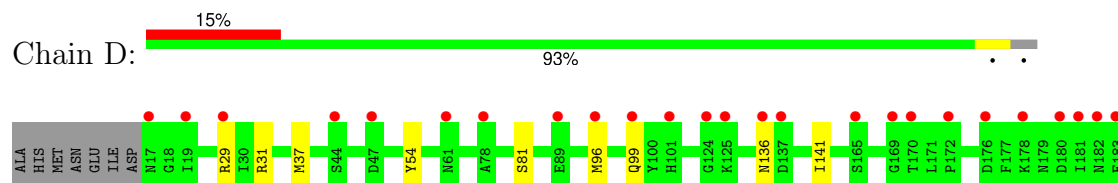
• Molecule 1: Toxin

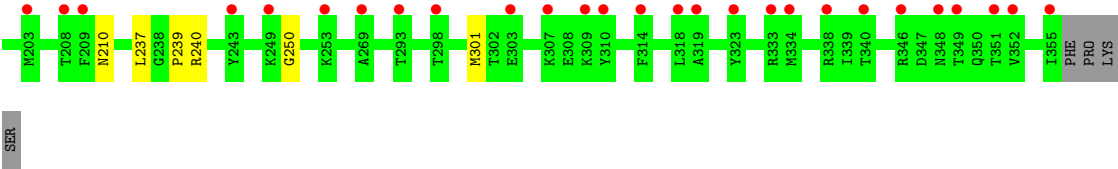


• Molecule 1: Toxin



• Molecule 1: Toxin





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	66.94Å 132.74Å 314.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 – 2.90 48.78 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.78-2.90) 99.5 (48.78-2.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.279 , 0.282 0.272 , 0.276	Depositor DCC
R_{free} test set	3163 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	67.2	Xtriage
Anisotropy	0.815	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10909	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NH4, EDO

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	0.46	0/2787	0.55	4/3779 (0.1%)
1	B	0.45	0/2795	0.48	0/3791
1	C	0.44	0/2783	0.48	1/3774 (0.0%)
1	D	0.45	0/2775	0.46	0/3763
All	All	0.45	0/11140	0.49	5/15107 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	316	TYR	N-CA-C	6.37	119.22	110.24
1	A	190	ASN	N-CA-C	-5.88	100.86	109.50
1	C	168	ILE	N-CA-C	5.44	115.78	108.17
1	A	315	ASN	CA-C-N	-5.36	113.34	120.90
1	A	315	ASN	C-N-CA	-5.36	113.34	120.90

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	2724	0	2648	9	0
1	B	2731	0	2655	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2721	0	2643	9	0
1	D	2713	0	2639	10	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	6	0	0
3	B	4	0	6	0	0
3	C	4	0	6	0	0
3	D	4	0	6	0	0
All	All	10909	0	10609	36	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 2.

All (36) 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:107:ASN:HB3	1:A:122:ARG:NH1	2.18	0.58
1:C:318:LEU:C	1:C:318:LEU:HD12	2.31	0.55
1:D:81:SER:OG	1:D:99:GLN:NE2	2.39	0.55
1:A:73:TYR:CZ	1:A:121:LYS:HG3	2.44	0.53
1:A:73:TYR:CE1	1:A:121:LYS:HG3	2.46	0.51
1:B:237:LEU:N	1:B:237:LEU:HD23	2.25	0.51
1:D:237:LEU:HD23	1:D:237:LEU:N	2.26	0.49
1:C:278:PHE:N	1:C:278:PHE:CD1	2.80	0.48
1:D:31:ARG:HA	1:D:37:MET:SD	2.54	0.48
1:B:237:LEU:HD23	1:B:237:LEU:H	1.79	0.47
1:A:118:ILE:O	1:A:126:VAL:HB	2.15	0.46
1:B:53:GLN:O	1:B:53:GLN:HG3	2.15	0.46
1:C:237:LEU:HD23	1:C:237:LEU:N	2.31	0.46
1:B:29:ARG:HG2	1:B:37:MET:SD	2.57	0.45
1:C:86:ASP:OD1	1:C:107:ASN:ND2	2.49	0.45
1:D:29:ARG:HG2	1:D:37:MET:SD	2.57	0.45
1:D:54:TYR:CD2	1:D:136:ASN:O	2.70	0.45
1:D:237:LEU:HD23	1:D:237:LEU:H	1.81	0.44
1:A:53:GLN:HB3	1:A:138:ALA:HB3	1.99	0.44
1:B:137:ASP:HB2	1:C:130:PRO:HB3	1.99	0.44
1:C:29:ARG:HG2	1:C:37:MET:SD	2.58	0.43
1:B:96:MET:SD	1:B:141:ILE:HG12	2.58	0.43
1:A:73:TYR:CE2	1:A:121:LYS:HG3	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:PHE:CD1	1:B:278:PHE:N	2.85	0.42
1:B:210:ASN:OD1	1:B:210:ASN:C	2.63	0.42
1:D:210:ASN:OD1	1:D:210:ASN:C	2.64	0.41
1:D:96:MET:SD	1:D:141:ILE:HG12	2.60	0.41
1:A:31:ARG:HA	1:A:37:MET:SD	2.60	0.41
1:B:242:ASP:OD1	1:B:242:ASP:C	2.63	0.41
1:A:125:LYS:HB3	1:A:143:TYR:C	2.45	0.40
1:D:250:GLY:HA2	1:D:301:MET:SD	2.61	0.40
1:B:50:MET:SD	1:C:96:MET:SD	3.19	0.40
1:C:237:LEU:HD23	1:C:237:LEU:H	1.87	0.40
1:A:210:ASN:OD1	1:A:210:ASN:C	2.65	0.40
1:C:210:ASN:OD1	1:C:210:ASN:C	2.63	0.40
1:D:239:PRO:O	1:D:240:ARG:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	338/350 (97%)	333 (98%)	5 (2%)	0	100	100
1	B	339/350 (97%)	335 (99%)	4 (1%)	0	100	100
1	C	338/350 (97%)	333 (98%)	5 (2%)	0	100	100
1	D	337/350 (96%)	335 (99%)	2 (1%)	0	100	100
All	All	1352/1400 (97%)	1336 (99%)	16 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	304/313 (97%)	301 (99%)	3 (1%)	68	89
1	B	305/313 (97%)	305 (100%)	0	100	100
1	C	304/313 (97%)	303 (100%)	1 (0%)	86	96
1	D	303/313 (97%)	303 (100%)	0	100	100
All	All	1216/1252 (97%)	1212 (100%)	4 (0%)	86	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	LYS
1	A	125	LYS
1	A	253	LYS
1	C	253	LYS

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

Mol	Chain	Res	Type
1	B	227	GLN
1	B	342	ASN
1	C	227	GLN
1	D	99	GLN
1	D	348	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are modelled with single atom - leaving 4 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	$\# Z > 2$
3	EDO	D	401	-	3,3,3	0.42	0	2,2,2	0.47	0
3	EDO	C	402	-	3,3,3	0.43	0	2,2,2	0.46	0
3	EDO	B	402	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	A	402	-	3,3,3	0.42	0	2,2,2	0.40	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
3	EDO	D	401	-	-	1/1/1/1	-
3	EDO	C	402	-	-	1/1/1/1	-
3	EDO	B	402	-	-	1/1/1/1	-
3	EDO	A	402	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	402	EDO	O1-C1-C2-O2
3	D	401	EDO	O1-C1-C2-O2

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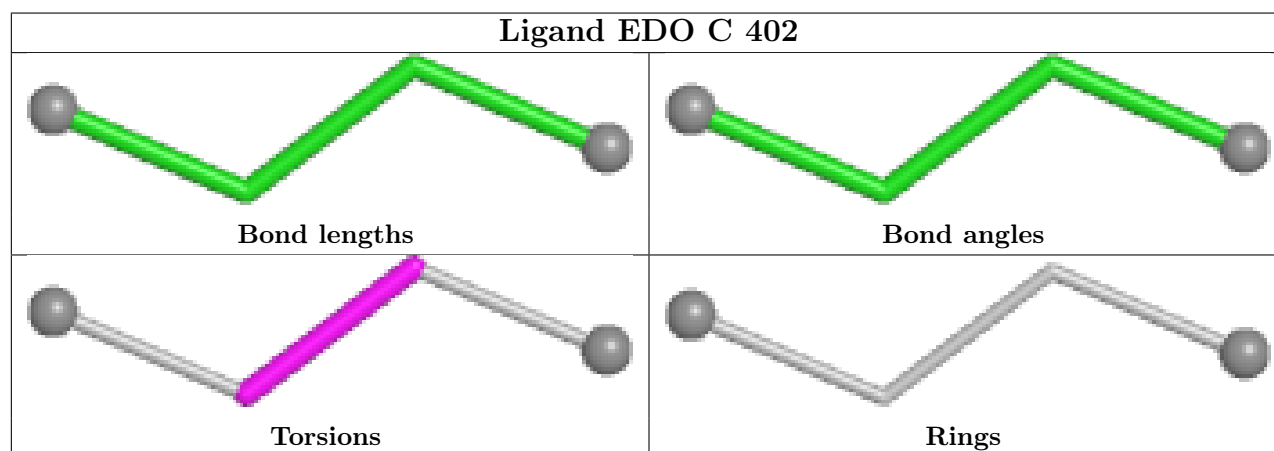
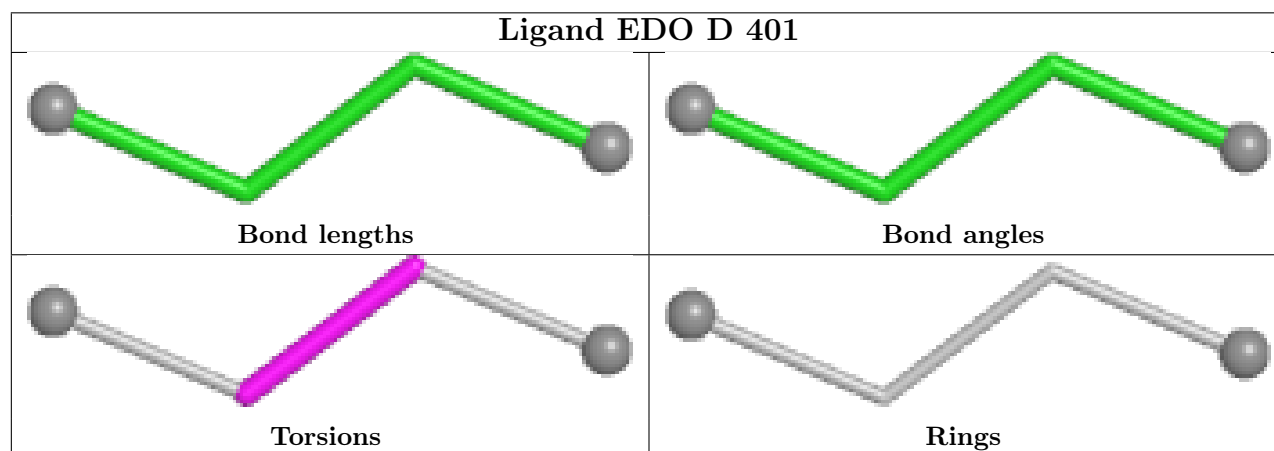
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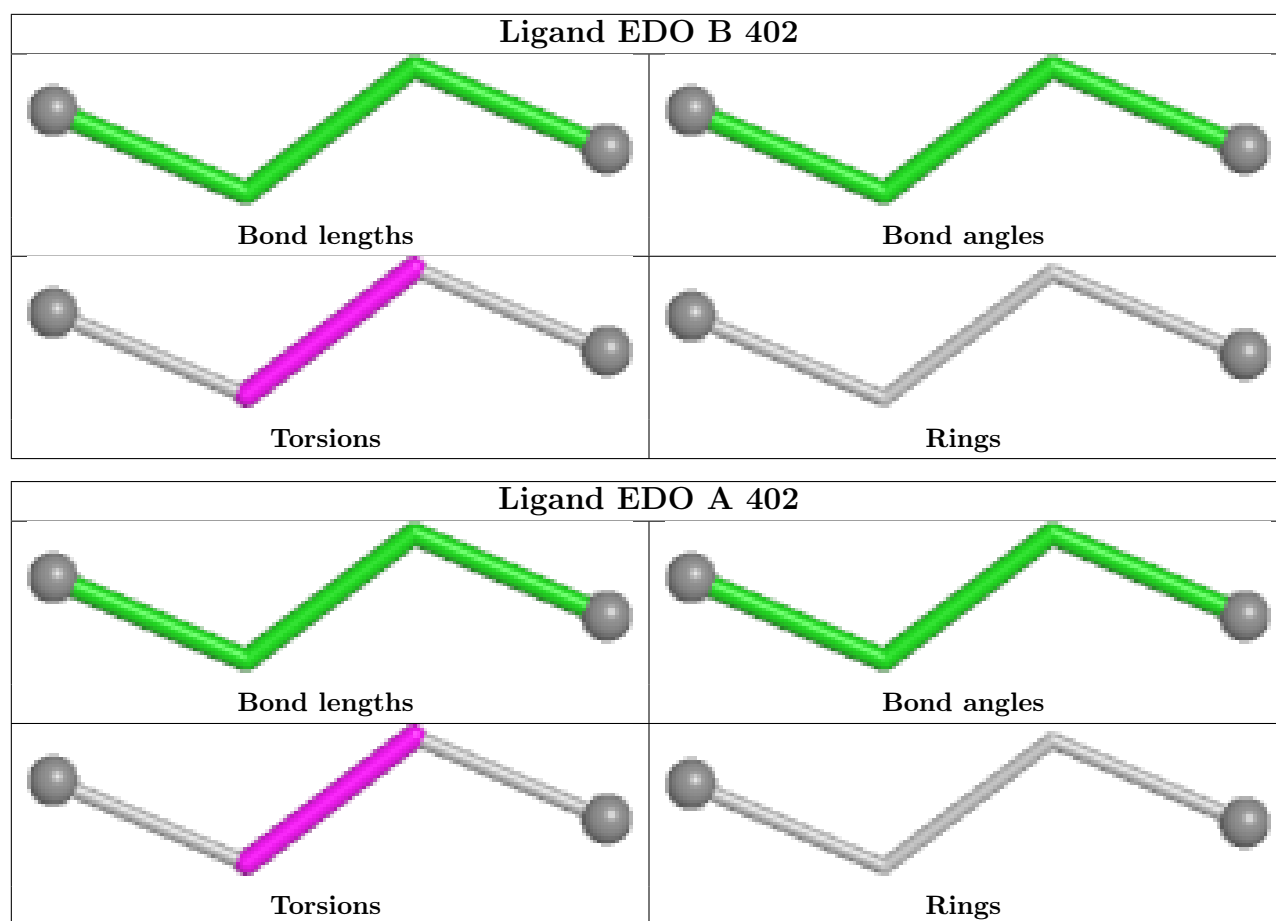
Mol	Chain	Res	Type	Atoms
3	A	402	EDO	O1-C1-C2-O2
3	B	402	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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

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, 95th 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	A	340/350 (97%)	0.93	39 (11%) 9 8	49, 70, 137, 201	0
1	B	341/350 (97%)	0.96	43 (12%) 8 6	47, 74, 128, 223	0
1	C	340/350 (97%)	1.15	51 (15%) 5 4	53, 71, 154, 215	0
1	D	339/350 (96%)	1.04	52 (15%) 5 4	51, 75, 139, 195	0
All	All	1360/1400 (97%)	1.02	185 (13%) 7 5	47, 72, 139, 223	0

All (185) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	318	LEU	7.7
1	B	357	PRO	6.0
1	B	356	PHE	6.0
1	C	101	HIS	5.6
1	A	356	PHE	5.5
1	C	136	ASN	5.4
1	B	338	ARG	5.1
1	C	346	ARG	5.0
1	B	57	ASN	4.9
1	A	104	ASN	4.8
1	C	333	ARG	4.8
1	A	316	TYR	4.8
1	D	355	ILE	4.5
1	A	333	ARG	4.5
1	C	355	ILE	4.5
1	C	303	GLU	4.4
1	A	57	ASN	4.3
1	C	104	ASN	4.1
1	B	135	SER	4.0
1	D	333	ARG	4.0
1	A	340	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	29	ARG	3.9
1	A	355	ILE	3.9
1	C	340	THR	3.8
1	D	136	ASN	3.8
1	B	136	ASN	3.7
1	D	351	THR	3.7
1	D	180	ASP	3.7
1	B	203	MET	3.7
1	D	125	LYS	3.7
1	C	170	THR	3.7
1	B	276	LYS	3.7
1	B	340	THR	3.6
1	C	318	LEU	3.6
1	A	314	PHE	3.6
1	B	99	GLN	3.6
1	D	29	ARG	3.6
1	D	338	ARG	3.6
1	C	105	SER	3.6
1	C	291	SER	3.6
1	A	17	ASN	3.5
1	B	253	LYS	3.5
1	C	55	SER	3.5
1	A	319	ALA	3.5
1	D	17	ASN	3.4
1	B	29	ARG	3.4
1	D	170	THR	3.4
1	C	243	TYR	3.4
1	B	240	ARG	3.3
1	D	293	THR	3.3
1	D	314	PHE	3.3
1	C	298	THR	3.3
1	C	351	THR	3.3
1	D	243	TYR	3.2
1	A	101	HIS	3.2
1	B	243	TYR	3.2
1	C	162	GLN	3.2
1	D	182	ASN	3.2
1	D	203	MET	3.2
1	D	340	THR	3.2
1	D	209	PHE	3.1
1	C	86	ASP	3.1
1	C	323	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	333	ARG	3.1
1	C	237	LEU	3.1
1	C	209	PHE	3.0
1	A	349	THR	3.0
1	D	178	LYS	3.0
1	B	298	THR	3.0
1	B	316	TYR	3.0
1	D	19	ILE	3.0
1	A	338	ARG	2.9
1	A	342	ASN	2.9
1	D	319	ALA	2.9
1	C	322	GLN	2.9
1	C	310	TYR	2.9
1	A	61	ASN	2.8
1	B	19	ILE	2.8
1	C	65	LEU	2.8
1	D	137	ASP	2.8
1	D	89	GLU	2.8
1	B	179	ASN	2.8
1	D	44	SER	2.7
1	D	78	ALA	2.7
1	A	310	TYR	2.7
1	B	101	HIS	2.7
1	D	124	GLY	2.7
1	D	253	LYS	2.7
1	A	178	LYS	2.7
1	C	181	ILE	2.6
1	D	176	ASP	2.6
1	B	307	LYS	2.6
1	C	319	ALA	2.6
1	D	249	LYS	2.6
1	D	96	MET	2.6
1	A	165	SER	2.6
1	A	320	ARG	2.6
1	A	203	MET	2.6
1	D	298	THR	2.6
1	B	209	PHE	2.6
1	B	237	LEU	2.5
1	C	338	ARG	2.5
1	B	96	MET	2.5
1	C	173	PRO	2.5
1	A	209	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	99	GLN	2.5
1	C	320	ARG	2.5
1	C	205	ASN	2.5
1	D	61	ASN	2.5
1	C	334	MET	2.5
1	A	55	SER	2.5
1	B	89	GLU	2.5
1	A	341	ALA	2.5
1	B	320	ARG	2.4
1	C	229	TRP	2.4
1	D	183	GLU	2.4
1	B	339	ILE	2.4
1	B	18	GLY	2.4
1	B	303	GLU	2.4
1	C	314	PHE	2.4
1	B	204	ALA	2.4
1	B	239	PRO	2.4
1	A	170	THR	2.4
1	A	298	THR	2.4
1	B	351	THR	2.4
1	D	334	MET	2.4
1	D	172	PRO	2.4
1	C	293	THR	2.4
1	A	188	LYS	2.3
1	A	348	ASN	2.3
1	A	281	SER	2.3
1	D	349	THR	2.3
1	D	307	LYS	2.3
1	B	304	GLU	2.3
1	C	137	ASP	2.3
1	C	316	TYR	2.3
1	B	352	VAL	2.3
1	D	348	ASN	2.3
1	B	78	ALA	2.3
1	C	324	MET	2.3
1	C	230	GLU	2.2
1	C	315	ASN	2.2
1	D	269	ALA	2.2
1	D	303	GLU	2.2
1	D	323	TYR	2.2
1	A	125	LYS	2.2
1	A	47	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	349	THR	2.2
1	D	208	THR	2.2
1	D	352	VAL	2.2
1	C	306	TYR	2.2
1	C	348	ASN	2.2
1	C	251	ILE	2.2
1	D	181	ILE	2.2
1	C	16	ASP	2.2
1	D	309	LYS	2.2
1	B	223	LEU	2.2
1	A	317	GLU	2.2
1	B	61	ASN	2.2
1	D	169	GLY	2.2
1	B	319	ALA	2.2
1	D	346	ARG	2.1
1	D	101	HIS	2.1
1	A	313	PRO	2.1
1	C	261	GLU	2.1
1	A	162	GLN	2.1
1	B	17	ASN	2.1
1	A	166	PRO	2.1
1	B	178	LYS	2.1
1	C	203	MET	2.1
1	C	299	THR	2.1
1	D	310	TYR	2.1
1	C	274	MET	2.0
1	D	165	SER	2.0
1	C	17	ASN	2.0
1	B	87	ILE	2.0
1	C	304	GLU	2.0
1	C	249	LYS	2.0
1	A	96	MET	2.0
1	C	171	LEU	2.0
1	D	318	LEU	2.0
1	A	103	ALA	2.0
1	B	293	THR	2.0
1	D	47	ASP	2.0
1	A	143	TYR	2.0

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 [i](#)

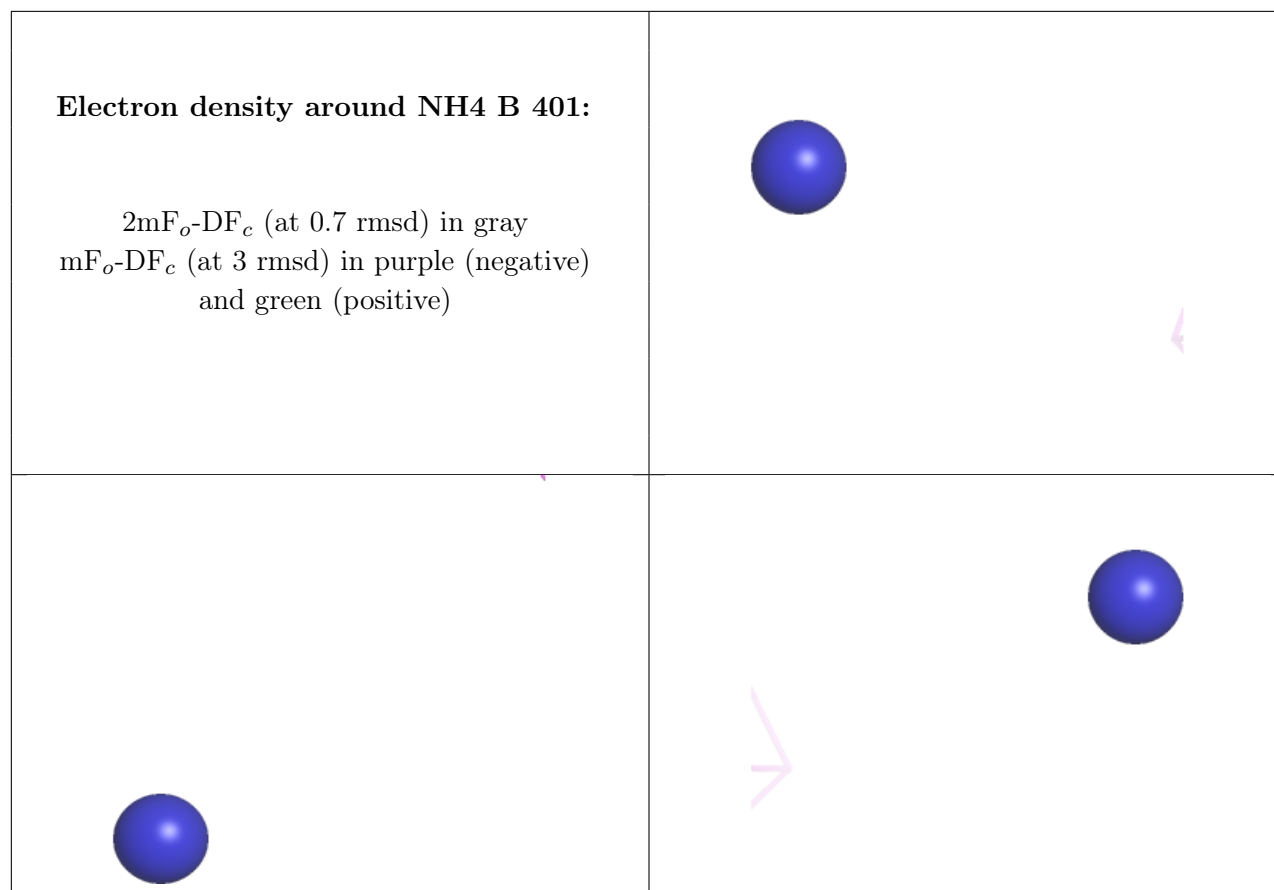
There are no oligosaccharides in this entry.

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, 95th 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.

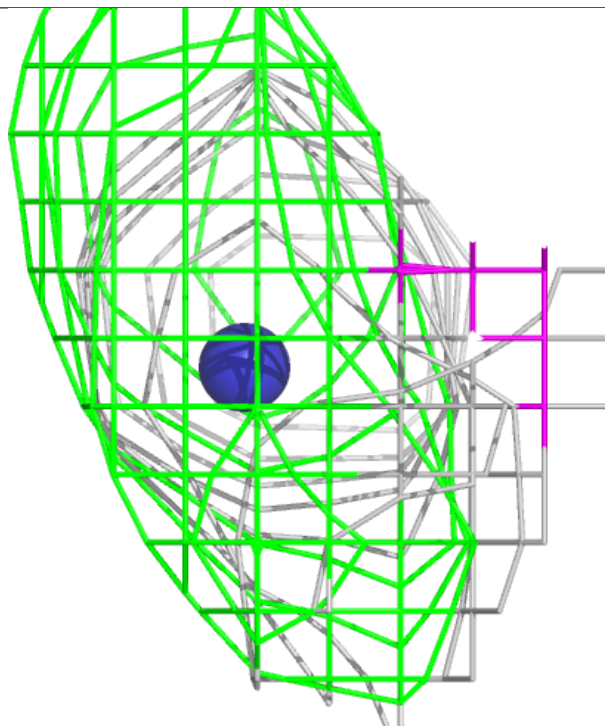
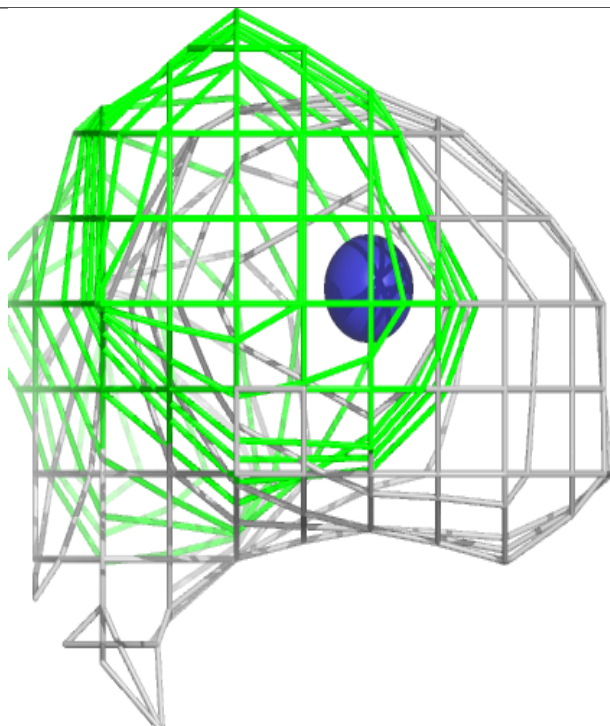
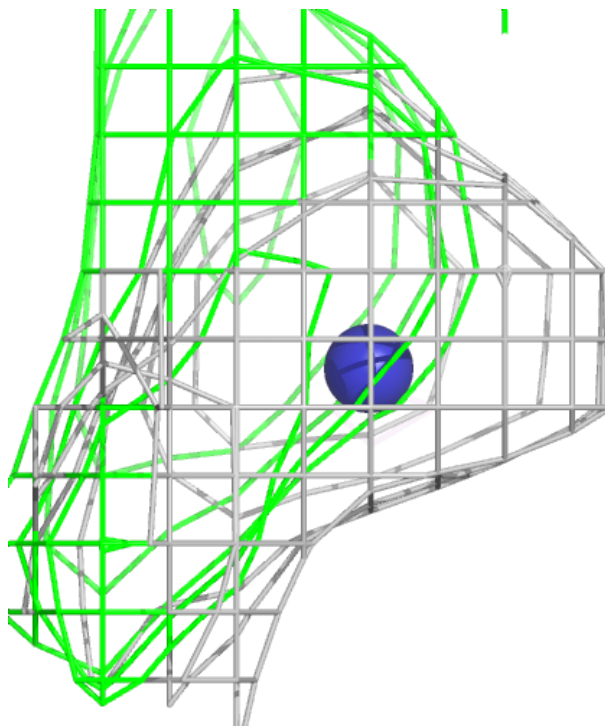
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NH4	B	401	1/1	0.08	0.33	77,77,77,77	0
2	NH4	A	401	1/1	0.24	0.57	60,60,60,60	0
2	NH4	C	401	1/1	0.31	0.29	86,86,86,86	0
3	EDO	D	401	4/4	0.58	0.41	79,80,82,85	0
3	EDO	C	402	4/4	0.67	0.31	78,79,82,82	0
3	EDO	A	402	4/4	0.70	0.23	57,65,67,68	0
2	NH4	D	402	1/1	0.77	0.47	63,63,63,63	0
3	EDO	B	402	4/4	0.87	0.13	55,57,58,58	0

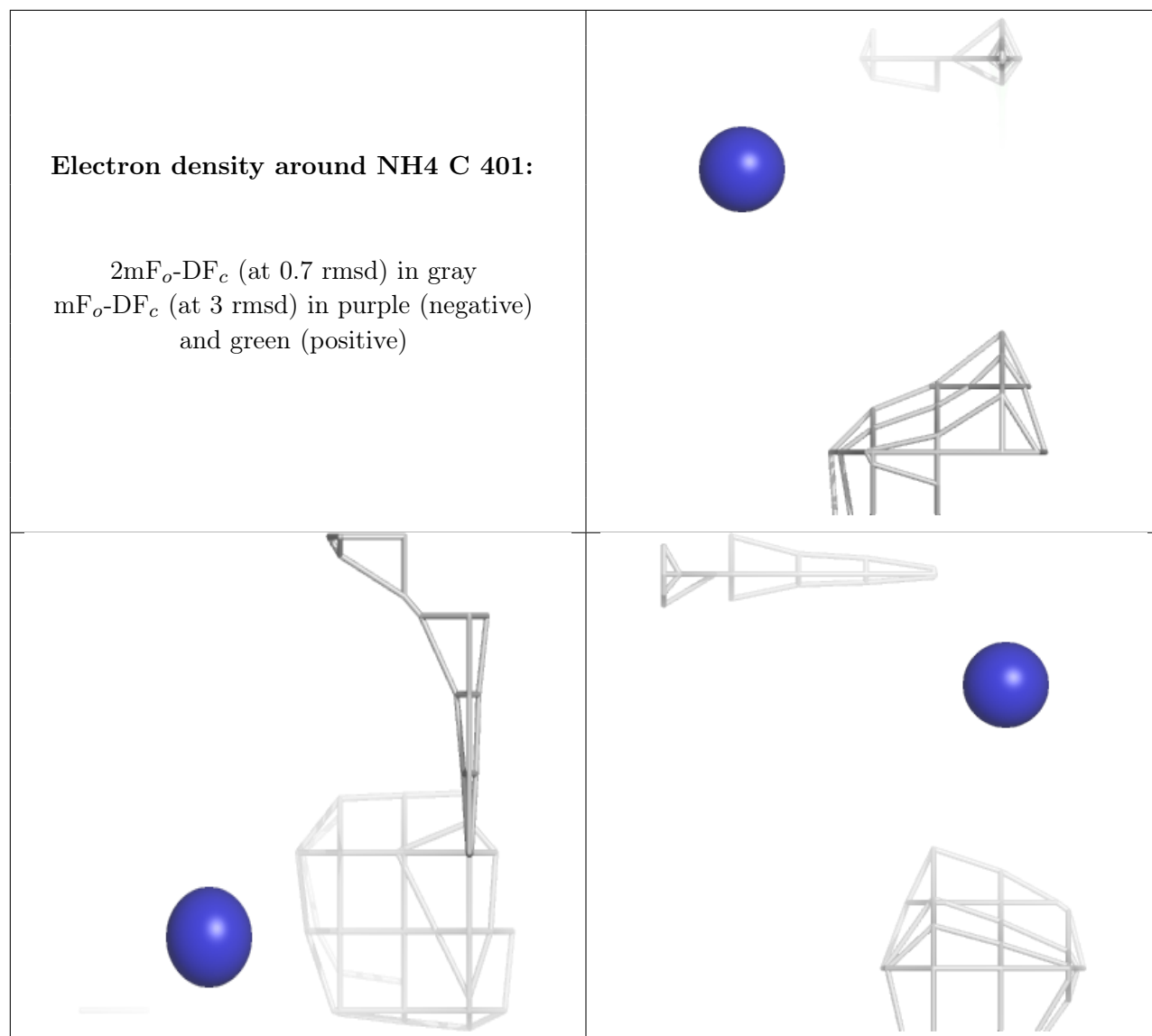
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around NH4 A 401:

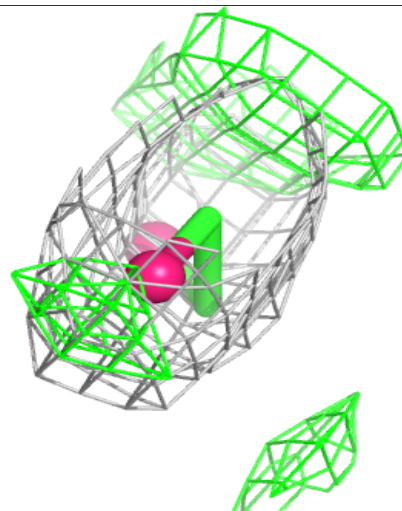
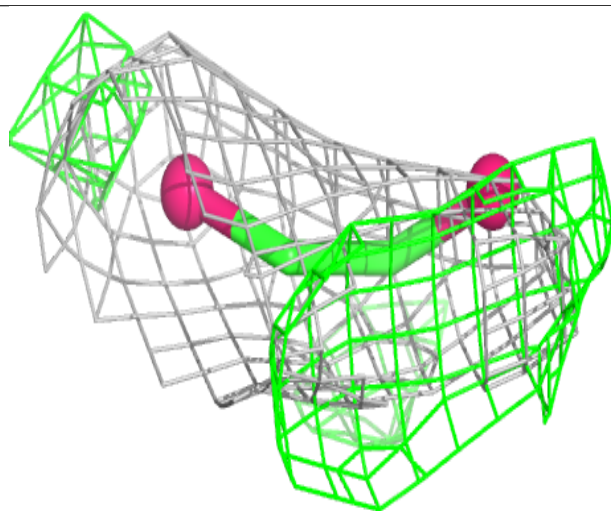
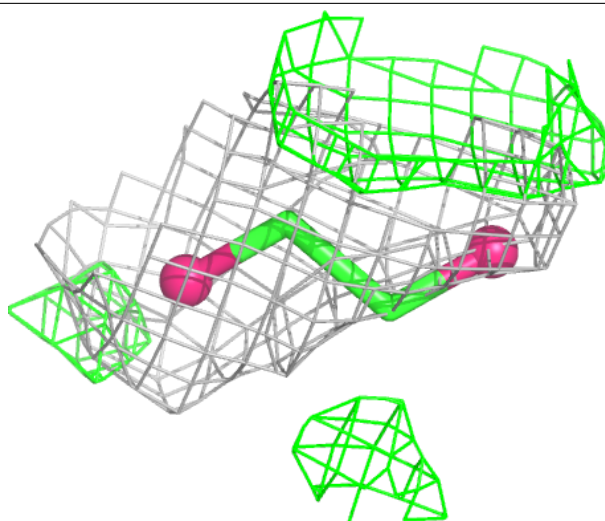
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





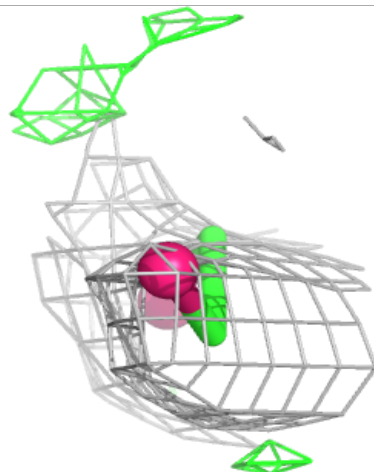
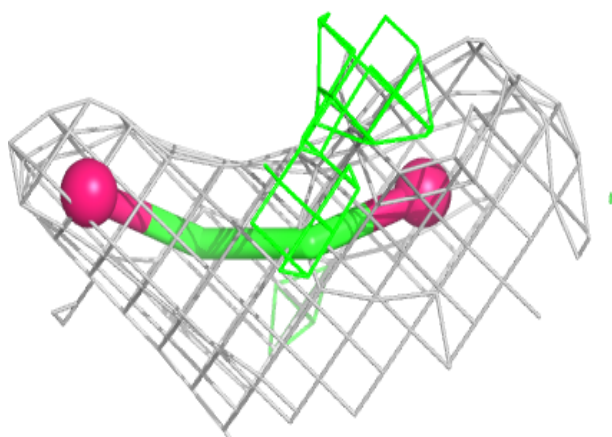
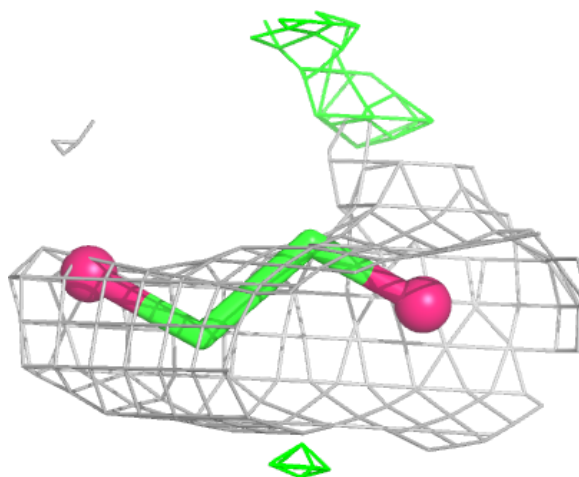
Electron density around EDO D 401:

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



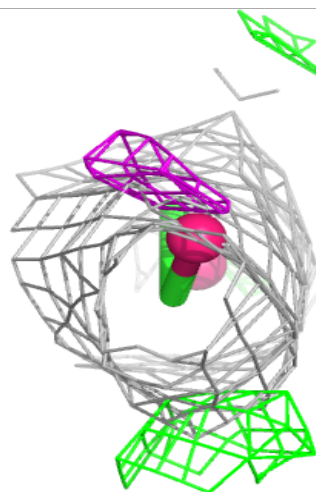
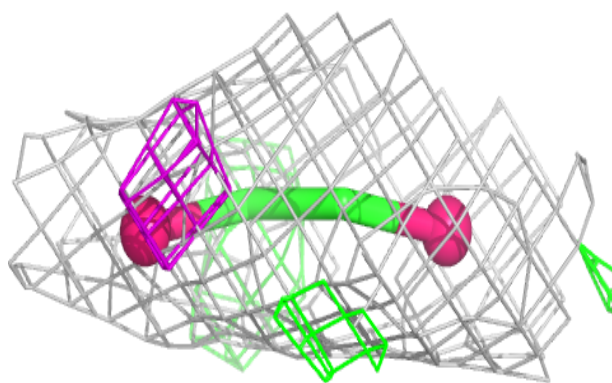
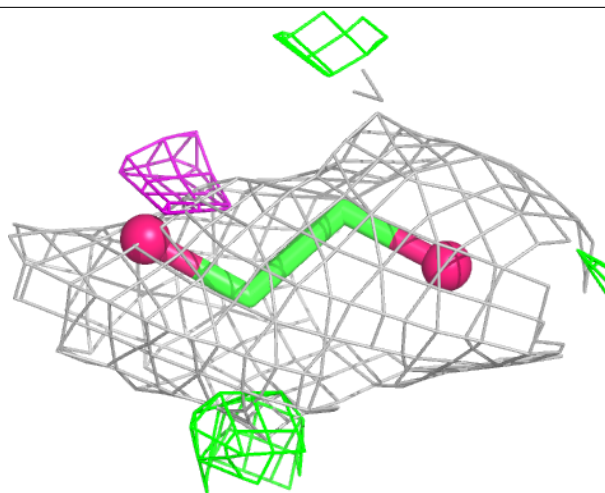
Electron density around EDO C 402:

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



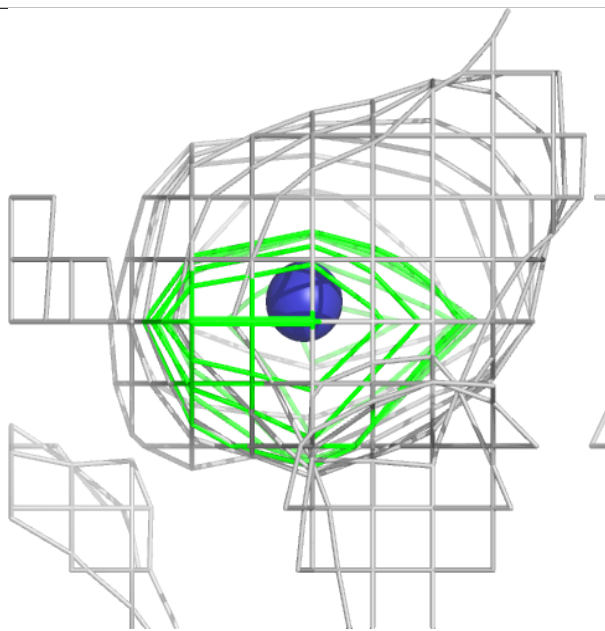
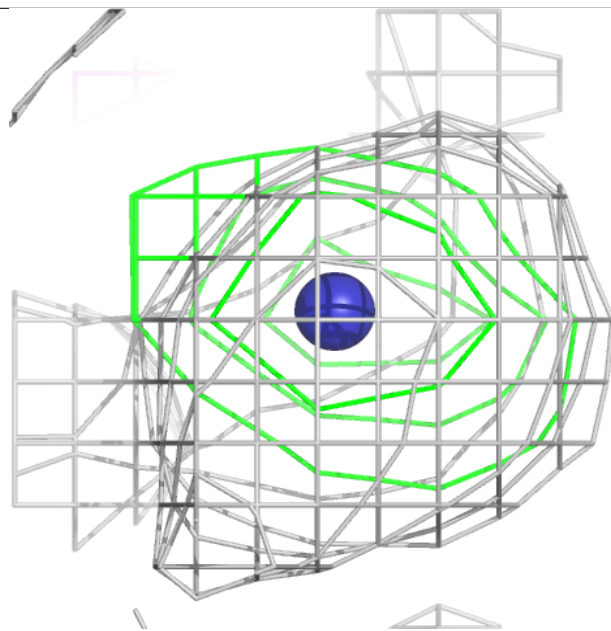
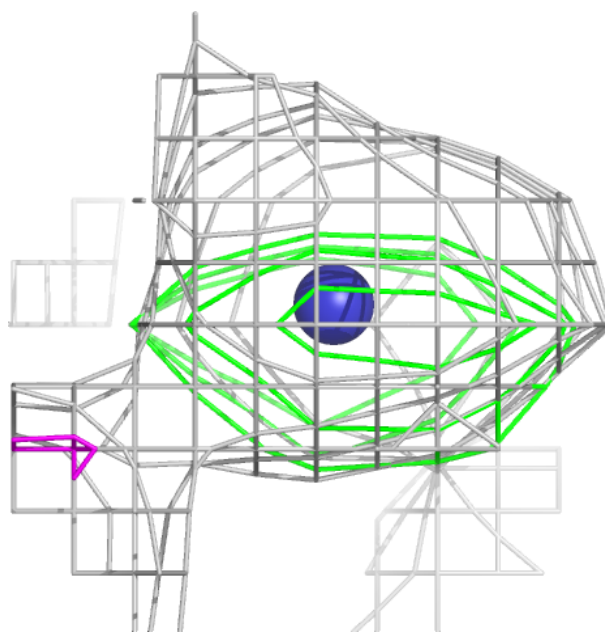
Electron density around EDO A 402:

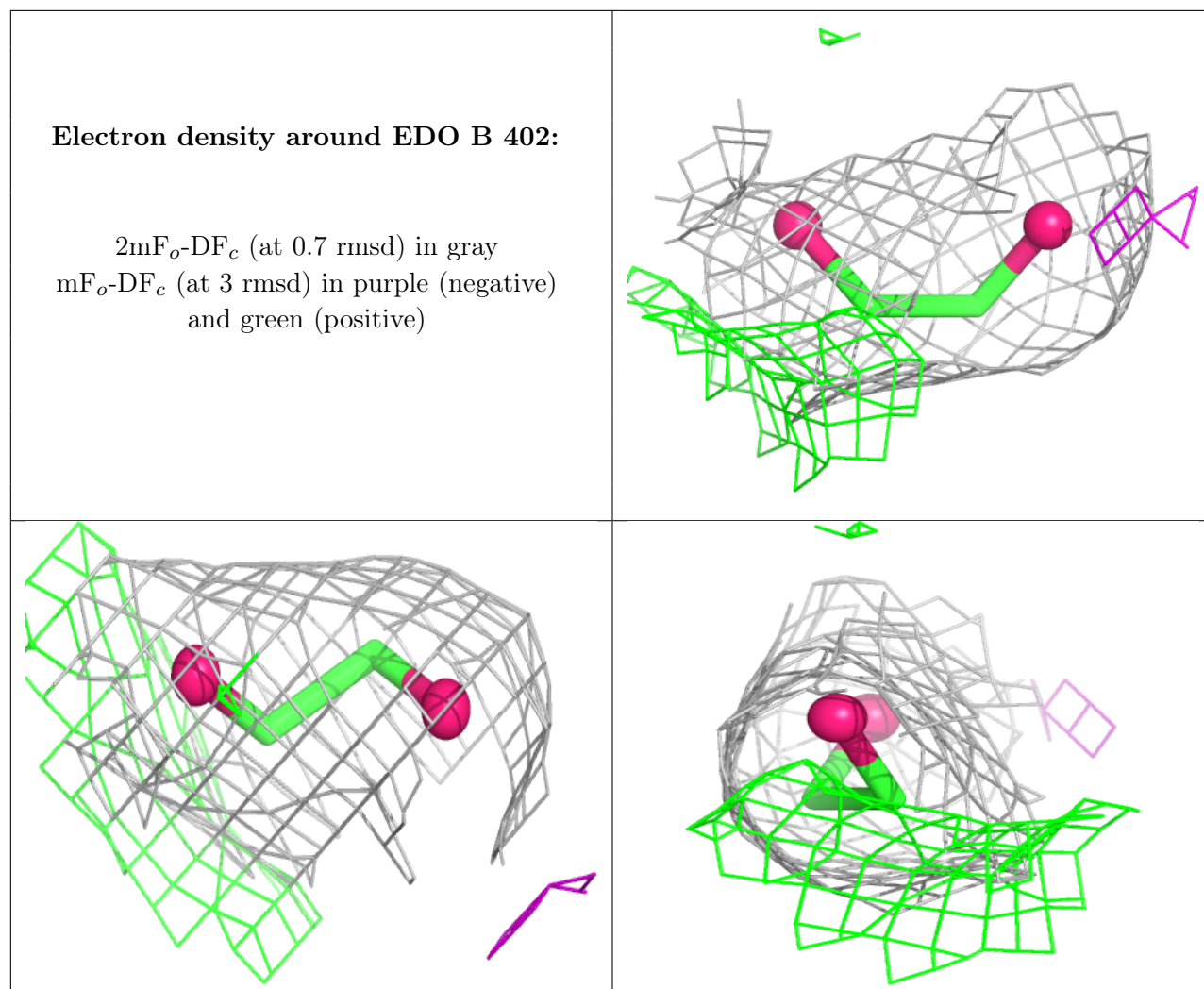
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around NH4 D 402:

$2mF_o-DF_c$ (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.