



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2022 – 10:03 AM EDT

PDB ID : 7UXX
Title : Crystal structure of SARS-CoV-2 nucleocapsid protein C-terminal domain
Authors : Bezerra, E.H.S.; Tonoli, C.C.C.; Soprano, A.S.; Franchini, K.G.; Trivella, D.B.B.; Benedetti, C.E.
Deposited on : 2022-05-06
Resolution : 1.85 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.28.1
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) : 2.28.1

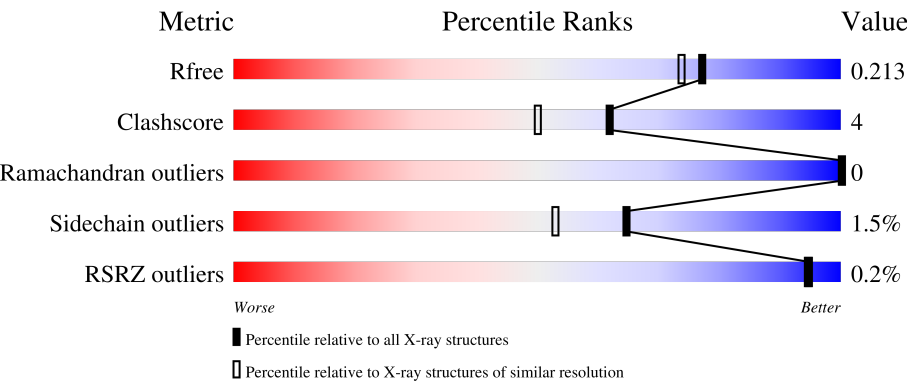
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	AAA	114	<div><div></div><div>89%</div><div>5%</div><div>••</div></div>
1	BBB	114	<div><div>%</div><div>82%</div><div>13%</div><div>•</div></div>
1	CCC	114	<div><div></div><div>90%</div><div>5%</div><div>•</div></div>
1	DDD	114	<div><div></div><div>83%</div><div>11%</div><div>••</div></div>
1	EEE	114	<div><div></div><div>89%</div><div>5%</div><div>••</div></div>

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Mol	Chain	Length	Quality of chain
1	FFF	114	<div><div></div><div>87%</div><div>9% . .</div></div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6301 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 Nucleoprotein.

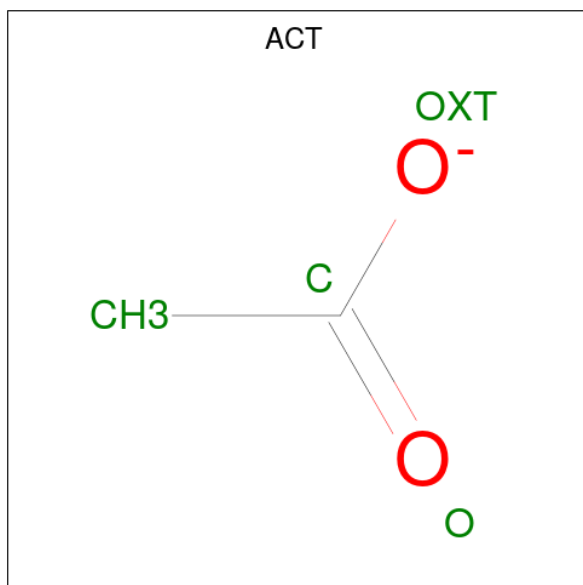
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	109	Total	C	N	O	S	0	3	0
			904	572	162	168	2			
1	BBB	109	Total	C	N	O	S	0	1	0
			886	562	160	162	2			
1	CCC	109	Total	C	N	O	S	0	0	0
			875	556	156	161	2			
1	DDD	109	Total	C	N	O	S	0	0	0
			875	556	156	161	2			
1	EEE	109	Total	C	N	O	S	0	1	0
			884	562	158	162	2			
1	FFF	110	Total	C	N	O	S	0	2	0
			896	568	159	166	3			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	C	O	0	0
			6	3	3		
2	BBB	1	Total	C	O	0	0
			6	3	3		
2	FFF	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	161	Total	O	0	0
			161	161		
4	BBB	146	Total	O	0	0
			146	146		
4	CCC	159	Total	O	0	0
			159	159		
4	DDD	157	Total	O	0	0
			157	157		
4	EEE	156	Total	O	0	0
			156	156		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	FFF	180	Total 180	O 180	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: Nucleoprotein

Chain AAA:  89% 5% . .



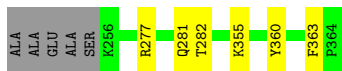
- Molecule 1: Nucleoprotein

Chain BBB:  % 82% 13% .




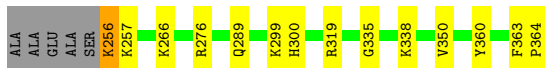
- Molecule 1: Nucleoprotein

Chain CCC:  90% 5% .



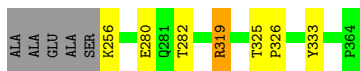
- Molecule 1: Nucleoprotein

Chain DDD:  83% 11% . .



- Molecule 1: Nucleoprotein

Chain EEE:  89% 5% . .



- Molecule 1: Nucleoprotein

Chain FFF:  87% 9% . .

ALA	ALA	ALA	ALA	S255	K256	K257	R276	T325	P326	K338	K342	K347	I357	Y360	F363	P364
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	43.62Å 119.75Å 128.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.81 – 1.85 43.81 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.81-1.85) 100.0 (43.81-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.163 , 0.207 0.173 , 0.213	Depositor DCC
R_{free} test set	2915 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	16.7	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6301	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.82% 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: GOL, ACT

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	0.71	0/927	0.82	0/1249
1	BBB	0.70	0/909	0.81	0/1225
1	CCC	0.70	0/898	0.81	0/1211
1	DDD	0.74	0/898	0.85	1/1211 (0.1%)
1	EEE	0.75	0/907	0.86	2/1222 (0.2%)
1	FFF	0.73	0/919	0.87	0/1239
All	All	0.72	0/5458	0.84	3/7357 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DDD	319	ARG	NE-CZ-NH2	-5.77	117.42	120.30
1	EEE	319	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	EEE	319	ARG	NE-CZ-NH2	-5.03	117.78	120.30

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	904	0	881	3	0
1	BBB	886	0	871	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CCC	875	0	859	5	0
1	DDD	875	0	859	12	0
1	EEE	884	0	871	6	0
1	FFF	896	0	878	10	0
2	AAA	6	0	8	0	0
2	BBB	6	0	8	0	0
2	FFF	6	0	8	0	0
3	DDD	4	0	3	0	0
4	AAA	161	0	0	1	0
4	BBB	146	0	0	6	0
4	CCC	159	0	0	3	0
4	DDD	157	0	0	3	0
4	EEE	156	0	0	2	0
4	FFF	180	0	0	3	0
All	All	6301	0	5246	47	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 4.

All (47) 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:BBB:322:MET:HE1	1:DDD:350:VAL:HG22	1.57	0.87
1:EEE:280:GLU:OE1	1:EEE:282:THR:HG22	1.83	0.79
1:AAA:289:GLN:O	1:AAA:293[A]:ARG:HG2	1.88	0.73
1:FFF:256:LYS:HD3	1:FFF:256:LYS:H	1.54	0.72
1:BBB:293[A]:ARG:NH1	4:BBB:1201:HOH:O	2.27	0.67
1:CCC:281:GLN:HG3	4:CCC:432:HOH:O	1.99	0.62
1:DDD:276:ARG:NH1	4:DDD:504:HOH:O	2.33	0.60
1:BBB:347:LYS:HE2	4:BBB:1206:HOH:O	2.02	0.58
1:EEE:280:GLU:OE1	1:EEE:282:THR:CG2	2.54	0.55
1:FFF:338:LYS:HE2	4:FFF:554:HOH:O	2.07	0.54
1:BBB:322:MET:HE1	1:DDD:350:VAL:CG2	2.36	0.53
1:BBB:303:GLN:NE2	4:BBB:1204:HOH:O	2.42	0.52
1:FFF:256:LYS:H	1:FFF:256:LYS:CD	2.18	0.52
1:BBB:277:ARG:HG3	1:BBB:292:ILE:HD11	1.90	0.52
1:FFF:342:LYS:HA	1:FFF:342:LYS:HE2	1.92	0.51
1:FFF:360:TYR:HA	1:FFF:363:PHE:CZ	2.45	0.50
1:BBB:322:MET:HE3	1:BBB:329:THR:CG2	2.41	0.50
1:DDD:266:LYS:CE	4:DDD:519:HOH:O	2.60	0.49
1:BBB:289:GLN:HG3	1:BBB:363:PHE:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FFF:325:THR:HB	1:FFF:326:PRO:HD2	1.96	0.47
4:AAA:536:HOH:O	1:CCC:282:THR:HB	2.15	0.47
1:BBB:347:LYS:CE	4:BBB:1206:HOH:O	2.62	0.47
1:DDD:289:GLN:HG3	1:DDD:363:PHE:CE2	2.50	0.46
1:FFF:347:LYS:H	1:FFF:347:LYS:CE	2.29	0.46
1:FFF:347:LYS:H	1:FFF:347:LYS:HE2	1.81	0.46
1:CCC:281:GLN:O	4:CCC:401:HOH:O	2.21	0.45
1:DDD:360:TYR:HA	1:DDD:363:PHE:CZ	2.51	0.45
1:AAA:256:LYS:HE2	1:AAA:268:TYR:CE2	2.52	0.45
1:BBB:293[A]:ARG:NH2	4:BBB:1209:HOH:O	2.50	0.45
1:DDD:276:ARG:NH2	1:DDD:364:PRO:O	2.50	0.45
1:BBB:330:TRP:CZ3	1:DDD:338:LYS:HB2	2.53	0.44
1:FFF:338:LYS:CE	4:FFF:554:HOH:O	2.65	0.44
1:CCC:355:LYS:HE3	4:CCC:430:HOH:O	2.17	0.44
1:DDD:299:LYS:HG3	1:DDD:300:HIS:ND1	2.34	0.43
1:BBB:290:GLU:HG3	1:BBB:293[A]:ARG:NH2	2.34	0.43
1:FFF:357:ILE:O	4:FFF:501:HOH:O	2.22	0.42
1:EEE:325:THR:HB	1:EEE:326:PRO:HD2	2.01	0.42
1:CCC:360:TYR:HA	1:CCC:363:PHE:CZ	2.54	0.41
1:BBB:259:ARG:NE	4:BBB:1207:HOH:O	2.49	0.41
1:DDD:256:LYS:HD3	1:DDD:257:LYS:H	1.85	0.41
1:AAA:269:ASN:HB2	1:AAA:292:ILE:O	2.21	0.41
1:EEE:256:LYS:NZ	4:EEE:406:HOH:O	2.52	0.41
1:BBB:333:TYR:CZ	1:DDD:335:GLY:HA3	2.56	0.41
1:BBB:319:ARG:O	1:BBB:333:TYR:HA	2.20	0.41
1:DDD:276:ARG:NH2	4:DDD:515:HOH:O	2.52	0.41
1:EEE:319:ARG:O	1:EEE:333:TYR:HA	2.20	0.41
1:EEE:256:LYS:NZ	4:EEE:408:HOH:O	2.55	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	AAA	110/114 (96%)	108 (98%)	2 (2%)	0	100	100
1	BBB	108/114 (95%)	106 (98%)	2 (2%)	0	100	100
1	CCC	107/114 (94%)	106 (99%)	1 (1%)	0	100	100
1	DDD	107/114 (94%)	106 (99%)	1 (1%)	0	100	100
1	EEE	108/114 (95%)	107 (99%)	1 (1%)	0	100	100
1	FFF	110/114 (96%)	109 (99%)	1 (1%)	0	100	100
All	All	650/684 (95%)	642 (99%)	8 (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	AAA	94/93 (101%)	92 (98%)	2 (2%)	53	38
1	BBB	92/93 (99%)	91 (99%)	1 (1%)	73	65
1	CCC	91/93 (98%)	90 (99%)	1 (1%)	73	65
1	DDD	91/93 (98%)	90 (99%)	1 (1%)	73	65
1	EEE	92/93 (99%)	92 (100%)	0	100	100
1	FFF	94/93 (101%)	91 (97%)	3 (3%)	39	22
All	All	554/558 (99%)	546 (99%)	8 (1%)	65	55

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

Mol	Chain	Res	Type
1	AAA	256	LYS
1	AAA	277	ARG
1	BBB	342	LYS
1	CCC	277	ARG
1	DDD	256	LYS
1	FFF	256	LYS
1	FFF	257	LYS

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Mol	Chain	Res	Type
1	FFF	276	ARG

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](#)

4 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	BBB	1101	-	5,5,5	0.21	0	5,5,5	0.56	0
2	GOL	AAA	401	-	5,5,5	0.17	0	5,5,5	0.62	0
3	ACT	DDD	401	-	1,3,3	5.12	1 (100%)	0,3,3	-	-
2	GOL	FFF	401	-	5,5,5	0.13	0	5,5,5	0.43	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
2	GOL	BBB	1101	-	-	2/4/4/4	-
2	GOL	AAA	401	-	-	2/4/4/4	-
2	GOL	FFF	401	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	DDD	401	ACT	CH3-C	5.12	1.55	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

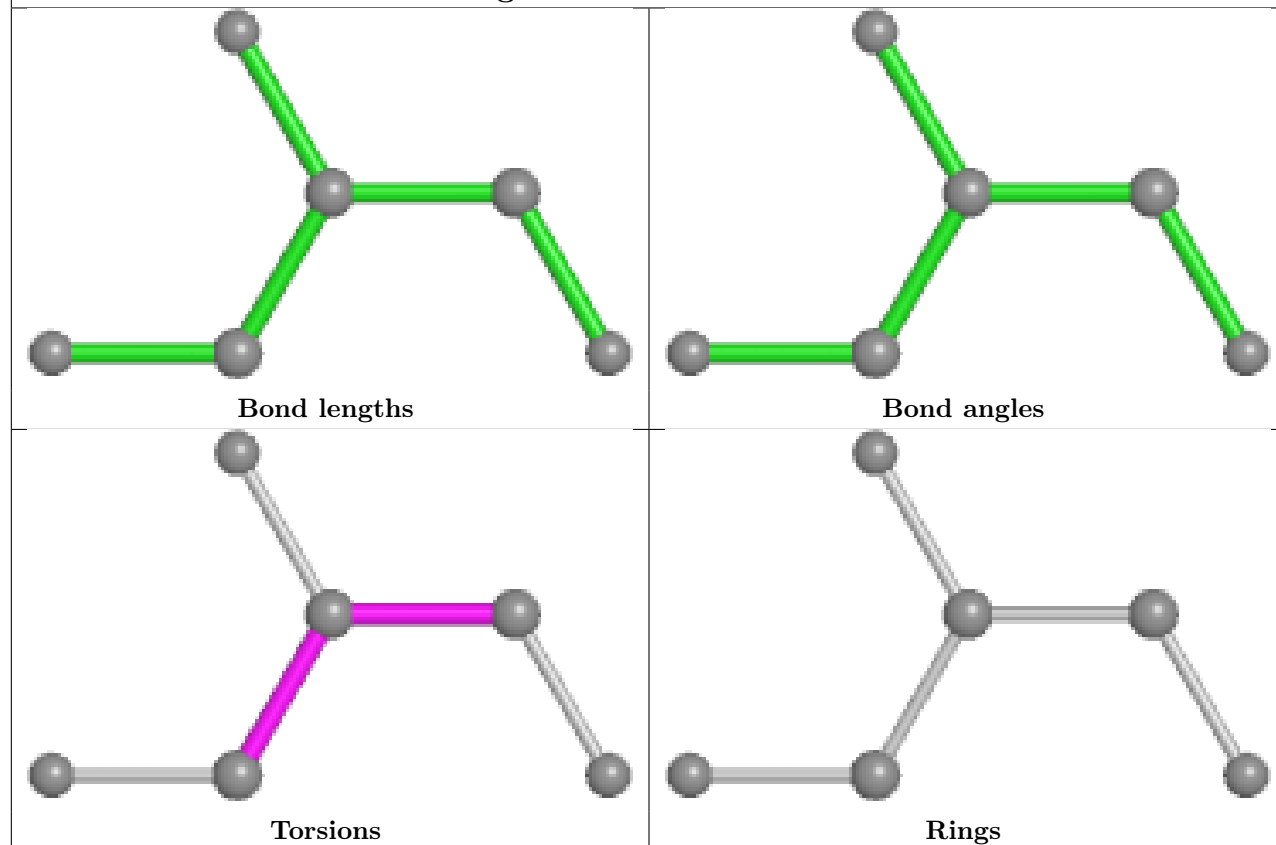
Mol	Chain	Res	Type	Atoms
2	AAA	401	GOL	C1-C2-C3-O3
2	BBB	1101	GOL	C1-C2-C3-O3
2	AAA	401	GOL	O2-C2-C3-O3
2	BBB	1101	GOL	O1-C1-C2-O2
2	FFF	401	GOL	C1-C2-C3-O3
2	FFF	401	GOL	O2-C2-C3-O3

There are no ring outliers.

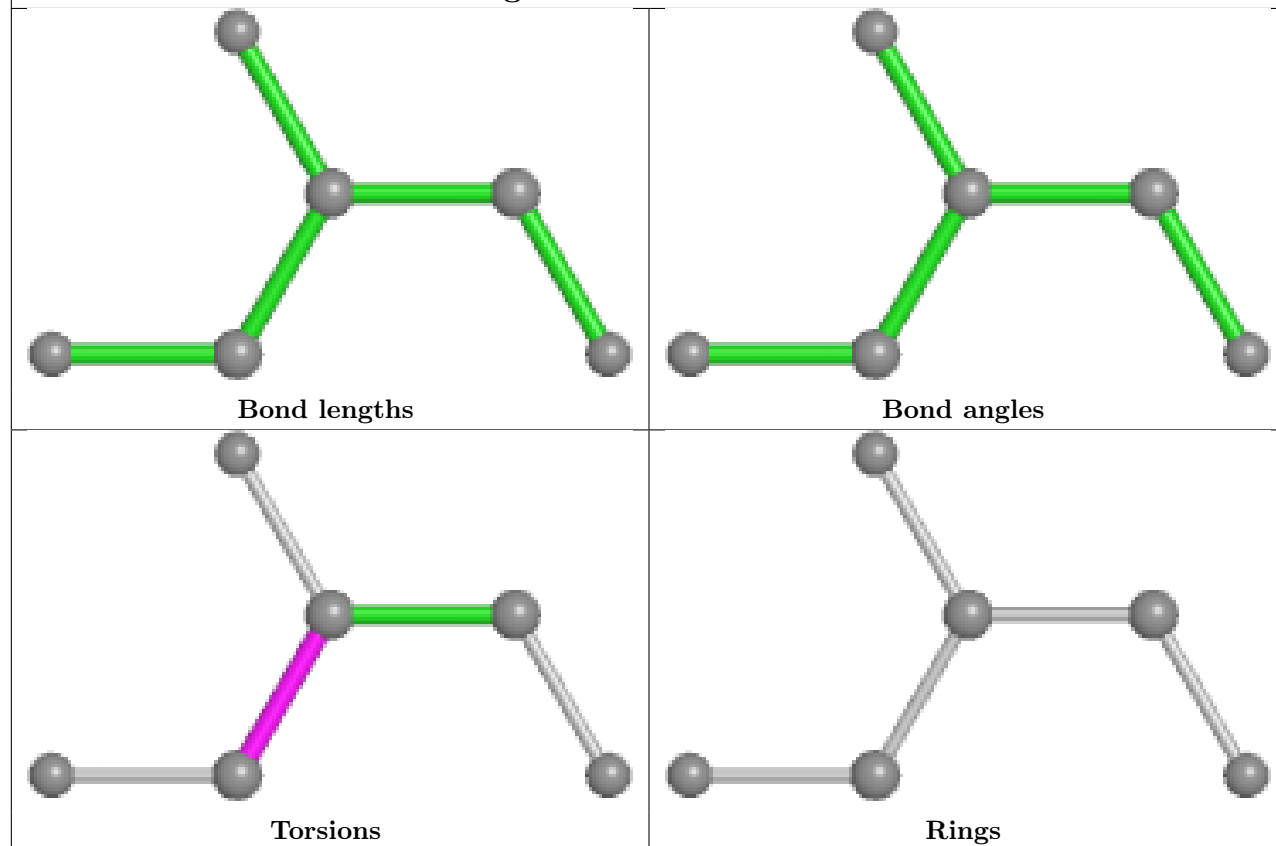
No monomer is involved in short contacts.

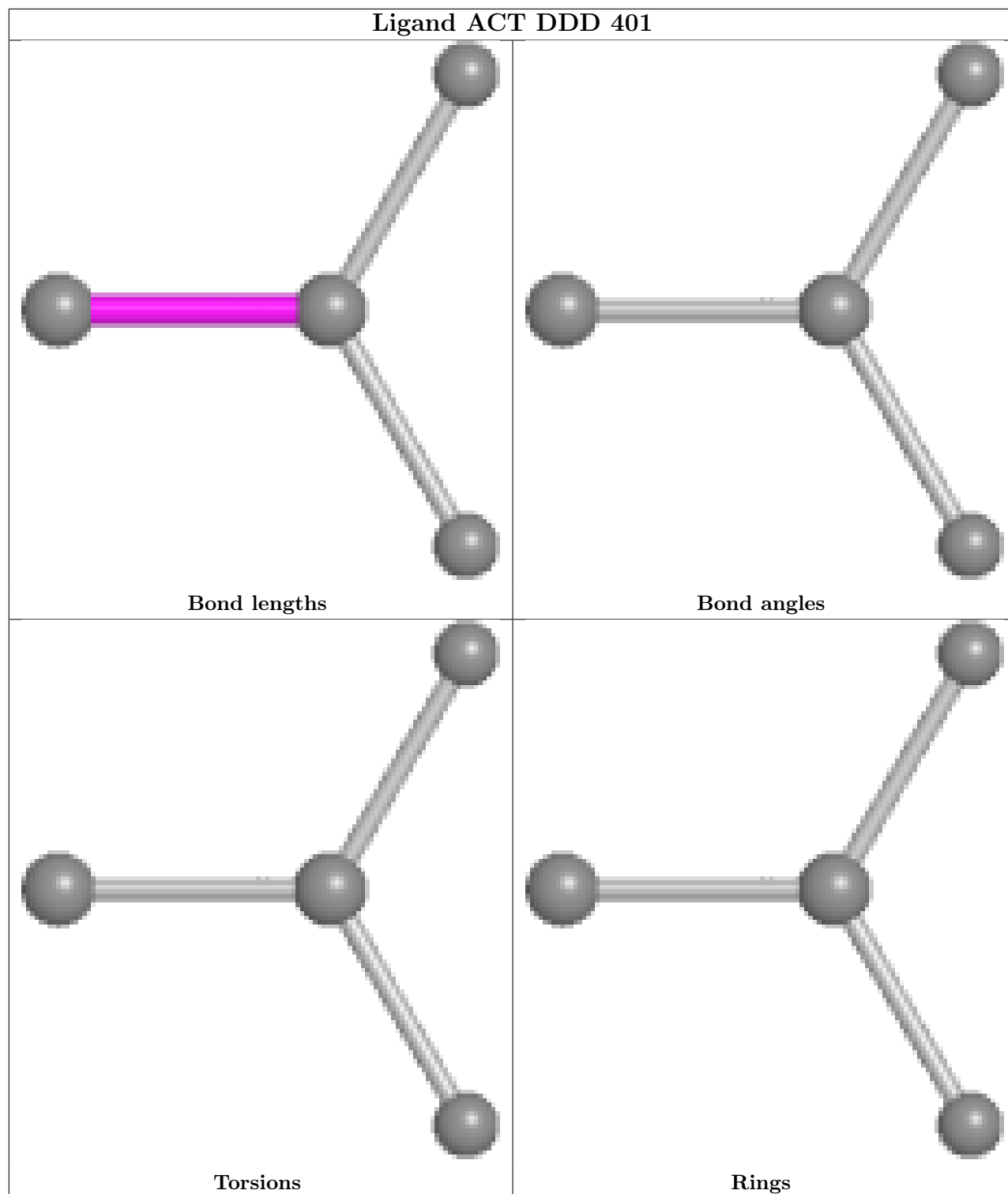
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

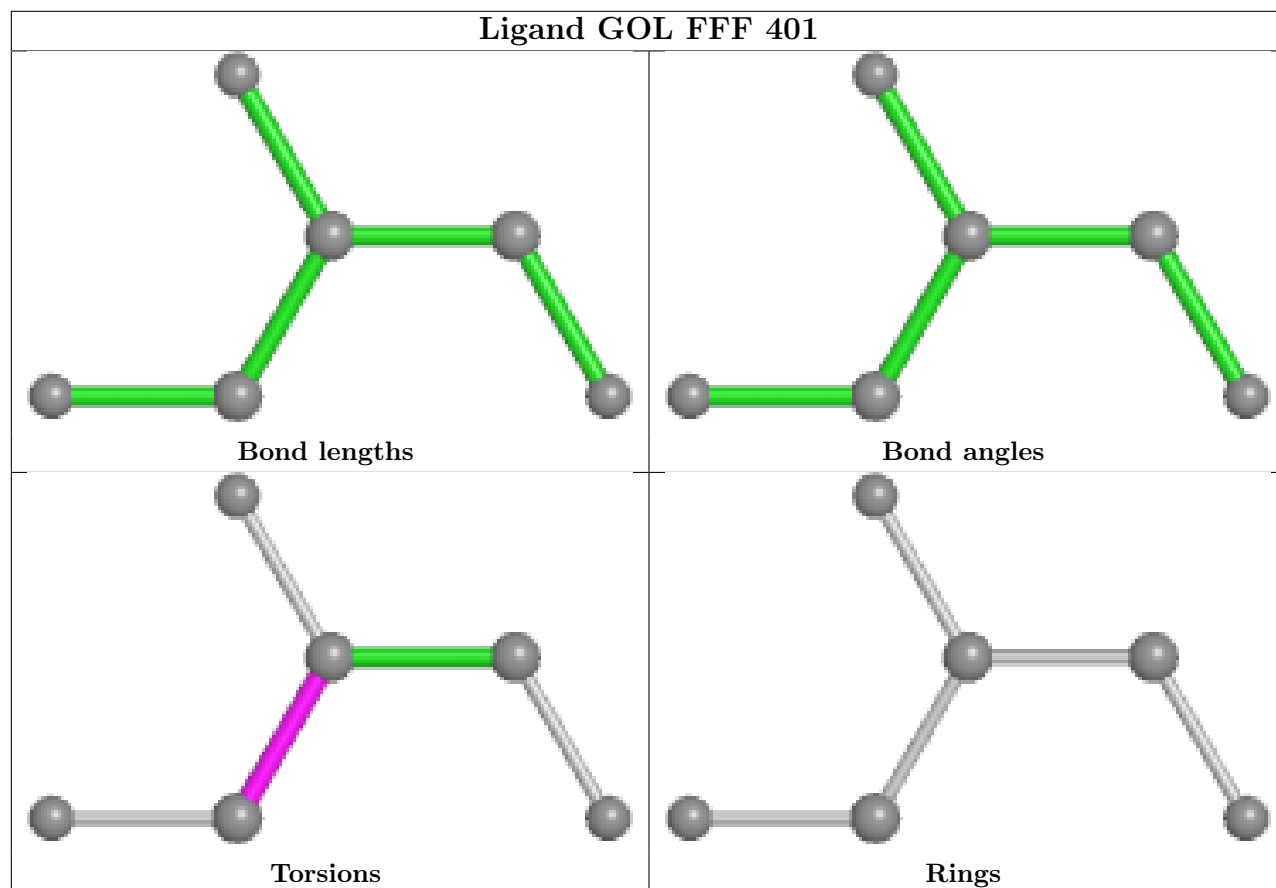
Ligand GOL BBB 1101



Ligand GOL AAA 401







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, 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	AAA	109/114 (95%)	-0.51	0 100 100	10, 15, 31, 55	0
1	BBB	109/114 (95%)	-0.40	1 (0%) 84 84	12, 19, 38, 59	0
1	CCC	109/114 (95%)	-0.54	0 100 100	9, 17, 30, 50	0
1	DDD	109/114 (95%)	-0.45	0 100 100	10, 19, 35, 51	0
1	EEE	109/114 (95%)	-0.45	0 100 100	9, 15, 35, 49	0
1	FFF	110/114 (96%)	-0.50	0 100 100	9, 14, 30, 48	0
All	All	655/684 (95%)	-0.47	1 (0%) 95 94	9, 16, 35, 59	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	364	PRO	4.0

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](#)

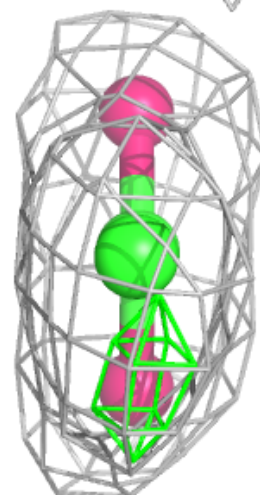
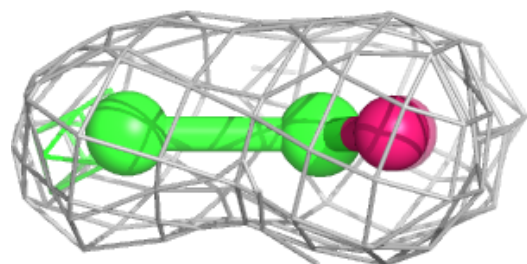
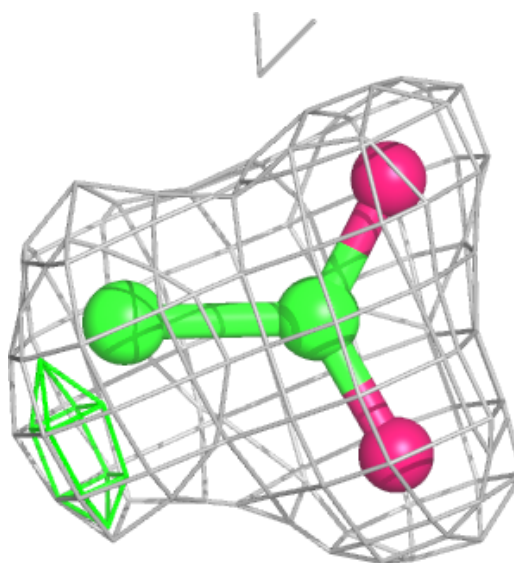
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ACT	DDD	401	4/4	0.87	0.16	29,30,31,34	0
2	GOL	BBB	1101	6/6	0.88	0.16	34,39,41,45	0
2	GOL	FFF	401	6/6	0.92	0.09	20,23,23,25	0
2	GOL	AAA	401	6/6	0.94	0.13	25,29,33,33	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.

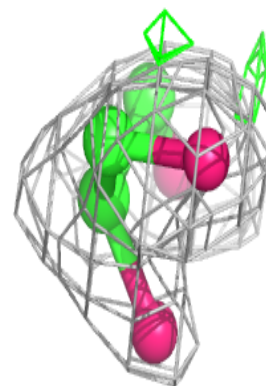
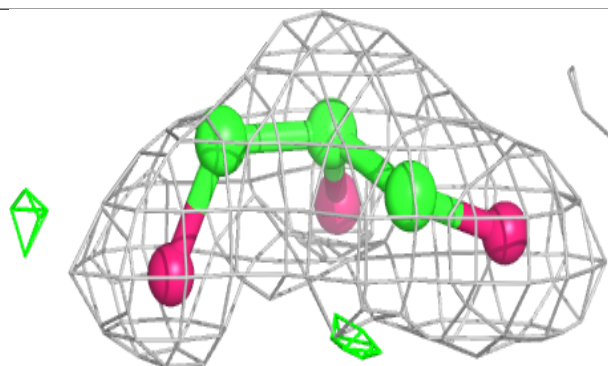
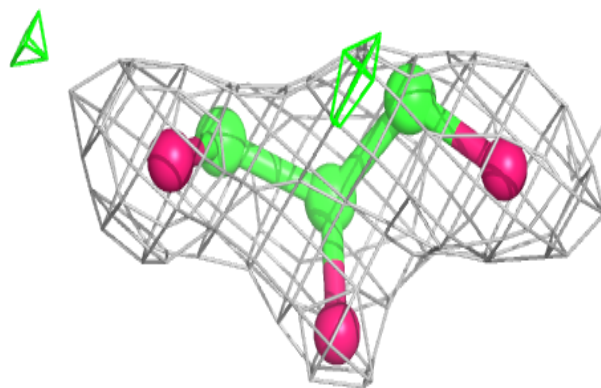
Electron density around ACT DDD 401:

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



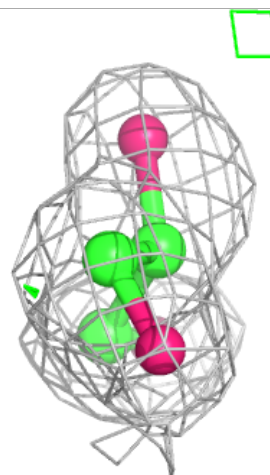
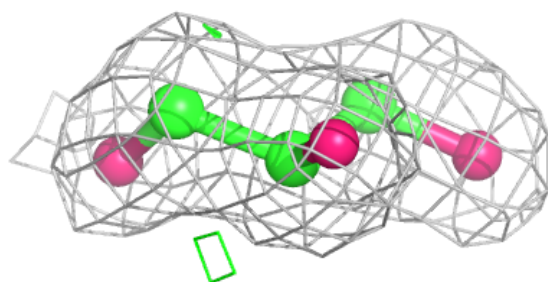
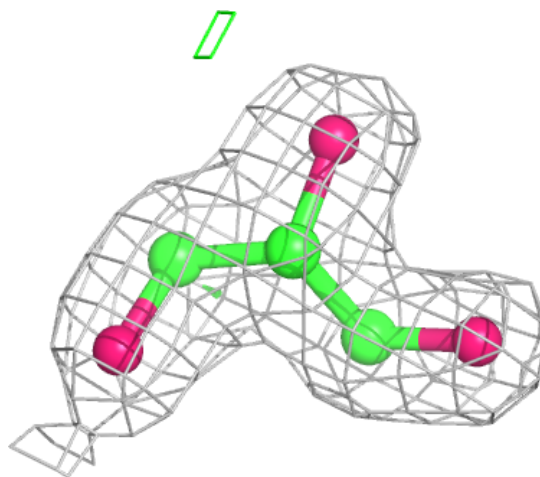
Electron density around GOL BBB 1101:

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



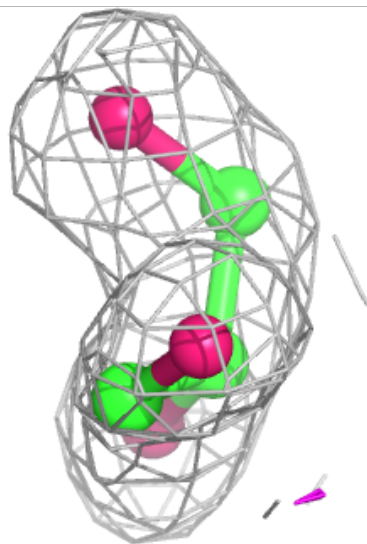
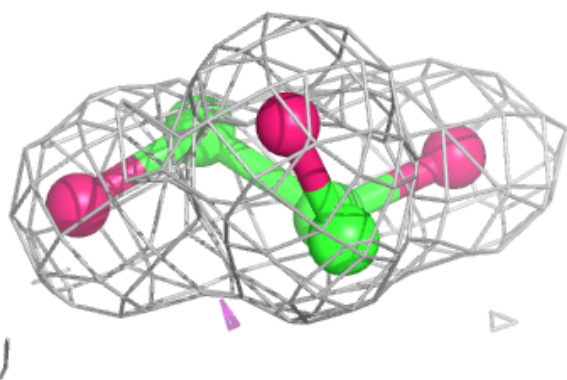
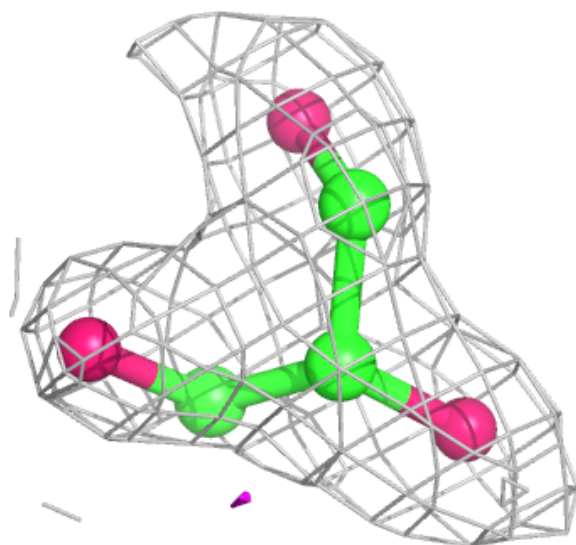
Electron density around GOL FFF 401:

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



Electron density around GOL AAA 401:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.