



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 18, 2020 – 11:20 AM BST

PDB ID : 4Q4Y
Title : Crystal structure of Coxsackievirus A24v soaked with Disialyllacto-N-tetraose (DSLNT)
Authors : Zocher, G.; Stehle, T.
Deposited on : 2014-04-15
Resolution : 1.88 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 : **FAILED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

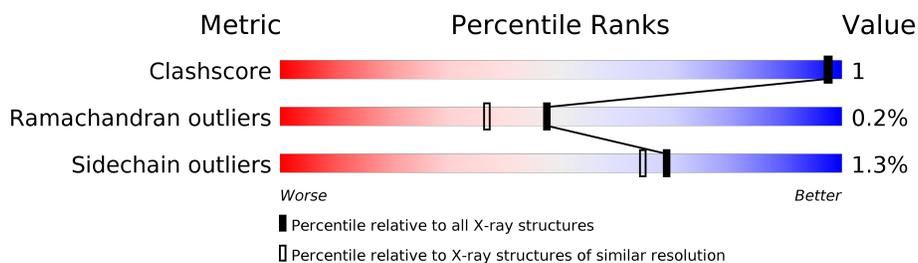
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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))
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7431 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 Coxsackievirus capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	281	2255	1433	382	432	8	0	3	0

- Molecule 2 is a protein called Coxsackievirus capsid protein VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	264	2067	1320	342	391	14	0	4	0

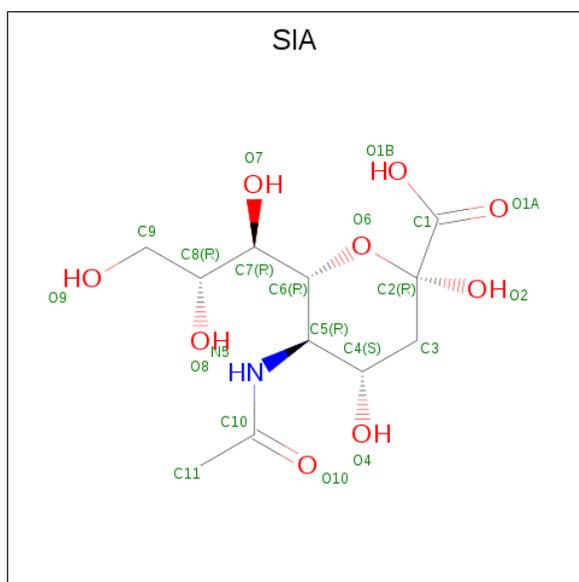
- Molecule 3 is a protein called Coxsackievirus capsid protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	234	1830	1174	290	345	21	0	6	0

- Molecule 4 is a protein called Coxsackievirus capsid protein VP4.

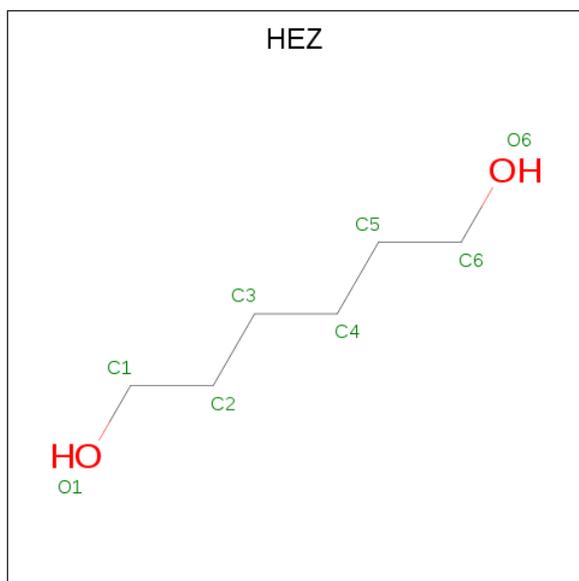
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	57	430	268	71	90	1	0	1	0

- Molecule 5 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula: C₁₁H₁₉NO₉).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
5	1	1	21	11	1	9	0	0

- Molecule 6 is HEXANE-1,6-DIOL (three-letter code: HEZ) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	1	1	8	6	2	0	0
6	1	1	8	6	2	0	0

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	2	1	Total Ca 1 1	0	0
7	1	3	Total Ca 3 3	0	0
7	3	1	Total Ca 1 1	0	0

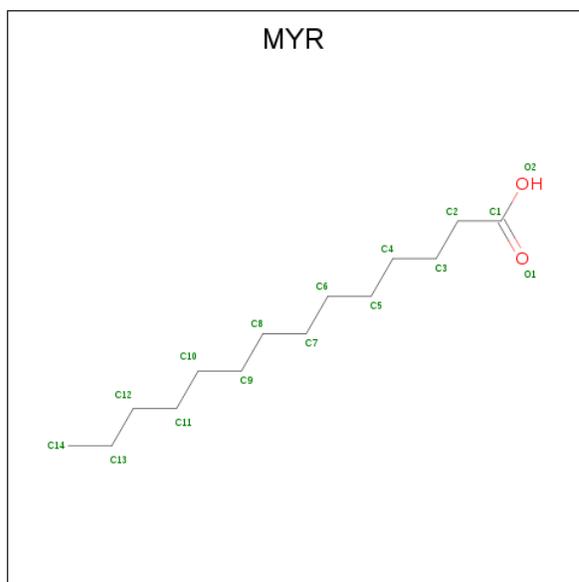
- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	2	1	Total Cl 1 1	0	0
8	1	4	Total Cl 4 4	0	0
8	3	2	Total Cl 2 2	0	0

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	2	1	Total Mg 1 1	0	0

- Molecule 10 is MYRISTIC ACID (three-letter code: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	4	1	Total	C	O	0	0
			6	5	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	1	280	Total	O	0	0
			280	280		
11	2	229	Total	O	0	0
			229	229		
11	3	223	Total	O	0	0
			223	223		
11	4	61	Total	O	0	0
			61	61		

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics i

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	304.48 Å 365.30 Å 366.49 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.78 – 1.88	Depositor
% Data completeness (in resolution range)	95.4 (49.78-1.88)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 1.88 Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.157 , (Not available)	Depositor
Wilson B-factor (Å ²)	12.6	Xtrriage
Anisotropy	0.288	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.006 for -h,-l,-k	Xtrriage
Total number of atoms	7431	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CL, CA, MYR, HEZ, SIA

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	1	0.36	0/2327	0.59	0/3178
2	2	0.30	0/2135	0.59	0/2916
3	3	0.31	0/1898	0.57	0/2585
4	4	0.36	0/440	0.51	0/594
All	All	0.33	0/6800	0.58	0/9273

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	2	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	82	LEU	Mainchain,Peptide

4.2 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	1	2255	0	2178	4	0
2	2	2067	0	1996	2	0
3	3	1830	0	1821	5	0
4	4	430	0	407	2	0
5	1	21	0	18	0	0
6	1	16	0	28	0	0
7	1	3	0	0	0	0
7	2	1	0	0	0	0
7	3	1	0	0	0	0
8	1	4	0	0	0	0
8	2	1	0	0	0	0
8	3	2	0	0	0	0
9	2	1	0	0	0	0
10	4	6	0	6	0	0
11	1	280	0	0	1	0
11	2	229	0	0	0	0
11	3	223	0	0	1	0
11	4	61	0	0	0	0
All	All	7431	0	6454	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 1.

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)
1:1:91:GLU:O	1:1:108[B]:THR:HG21	1.77	0.84
3:3:20:GLN:HE22	4:4:32:TYR:H	1.33	0.77
1:1:72:ARG:HH11	4:4:48:GLN:HE22	1.46	0.63
3:3:101:GLU:OE1	3:3:229:HIS:HD2	1.84	0.61
1:1:108[B]:THR:HG22	11:1:6105:HOH:O	2.06	0.55
1:1:91:GLU:O	1:1:108[B]:THR:CG2	2.52	0.52
2:2:48:ASN:HB3	2:2:49:PRO:CD	2.45	0.45
3:3:155:TRP:CD1	3:3:163:CYS:HB2	2.53	0.43
3:3:132[A]:SER:OG	3:3:190[A]:THR:OG1	2.38	0.41
3:3:139:LYS:NZ	11:3:819:HOH:O	2.53	0.41
2:2:179:LEU:HA	2:2:184:VAL:O	2.21	0.40

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 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	1	282/305 (92%)	273 (97%)	9 (3%)	0	100	100
2	2	266/271 (98%)	253 (95%)	11 (4%)	2 (1%)	19	9
3	3	238/240 (99%)	227 (95%)	11 (5%)	0	100	100
4	4	54/69 (78%)	52 (96%)	2 (4%)	0	100	100
All	All	840/885 (95%)	805 (96%)	33 (4%)	2 (0%)	47	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	48	ASN
2	2	83	PRO

4.3.2 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	1	249/268 (93%)	246 (99%)	3 (1%)	71	67
2	2	222/225 (99%)	220 (99%)	2 (1%)	78	76
3	3	213/212 (100%)	210 (99%)	3 (1%)	67	62
4	4	46/57 (81%)	45 (98%)	1 (2%)	52	43
All	All	730/762 (96%)	721 (99%)	9 (1%)	69	67

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	143	ARG
1	1	196	MET
1	1	284	GLU
2	2	72	LYS
2	2	263	ARG
3	3	75	LYS
3	3	148	MET
3	3	223	LEU
4	4	4	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	65	HIS
2	2	61	ASN
2	2	94	GLN
2	2	225	ASN
3	3	20	GLN
3	3	27	ASN
3	3	229	HIS
4	4	48	GLN

4.3.3 RNA [i](#)

There are no RNA molecules in this entry.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 13 are monoatomic - 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
5	SIA	1	5001	-	18,21,21	0.84	1 (5%)	21,31,31	0.71	0
6	HEZ	1	5002	-	7,7,7	0.23	0	6,6,6	0.55	0
10	MYR	4	101	4	5,5,15	0.64	0	4,4,15	0.84	0
6	HEZ	1	5003	-	7,7,7	0.33	0	6,6,6	0.37	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
5	SIA	1	5001	-	-	4/14/38/38	0/1/1/1
6	HEZ	1	5002	-	-	1/5/5/5	-
10	MYR	4	101	4	-	1/2/3/13	-
6	HEZ	1	5003	-	-	4/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1	5001	SIA	O2-C2	2.67	1.43	1.39

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	1	5001	SIA	O7-C7-C8-C9
5	1	5001	SIA	C6-C7-C8-O8
6	1	5002	HEZ	O1-C1-C2-C3
6	1	5003	HEZ	O1-C1-C2-C3
6	1	5003	HEZ	C4-C5-C6-O6
6	1	5003	HEZ	C3-C4-C5-C6
5	1	5001	SIA	C6-C7-C8-C9
5	1	5001	SIA	O7-C7-C8-O8
10	4	101	MYR	C1-C2-C3-C4

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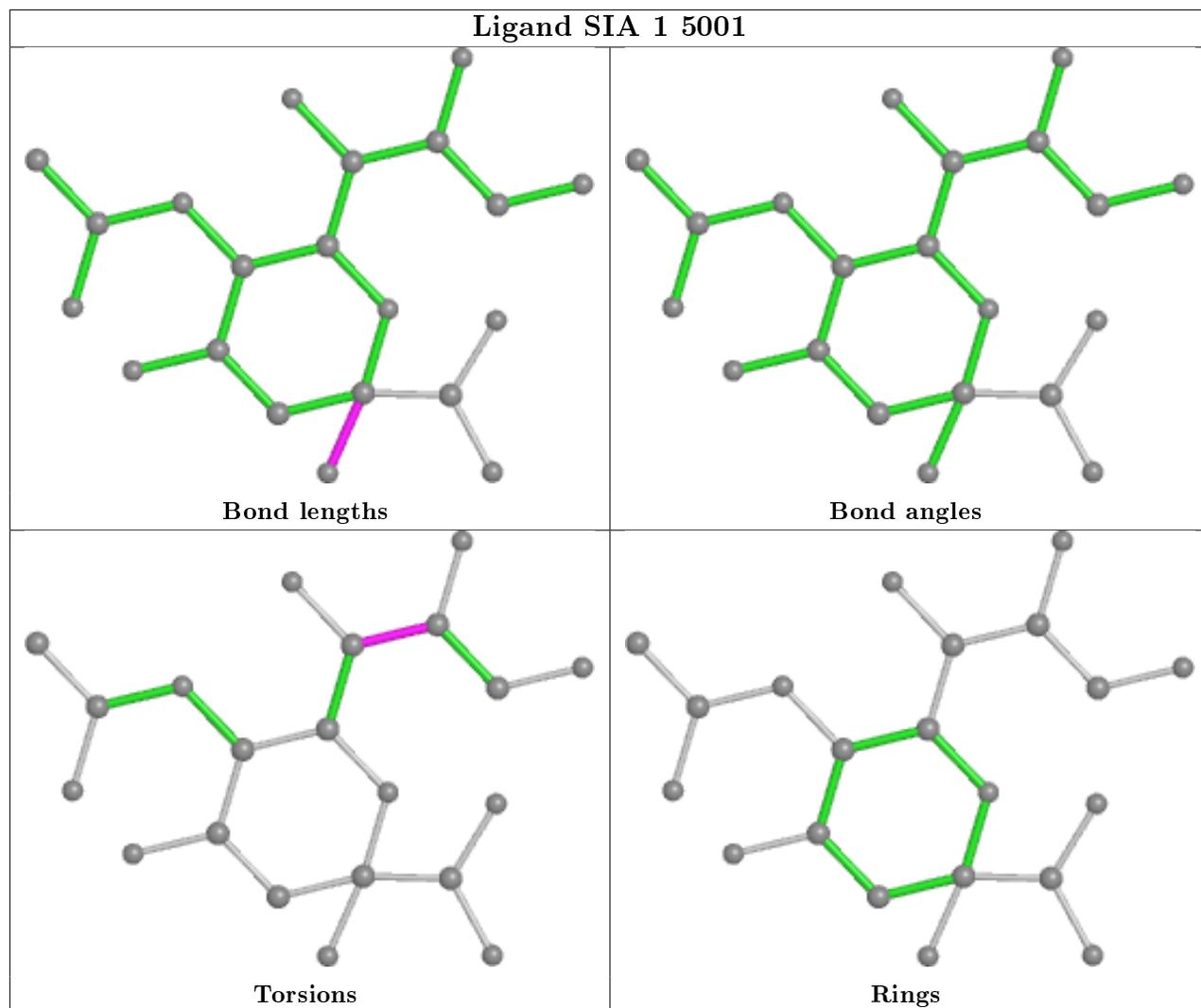
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Mol	Chain	Res	Type	Atoms
6	1	5003	HEZ	C1-C2-C3-C4

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.



4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

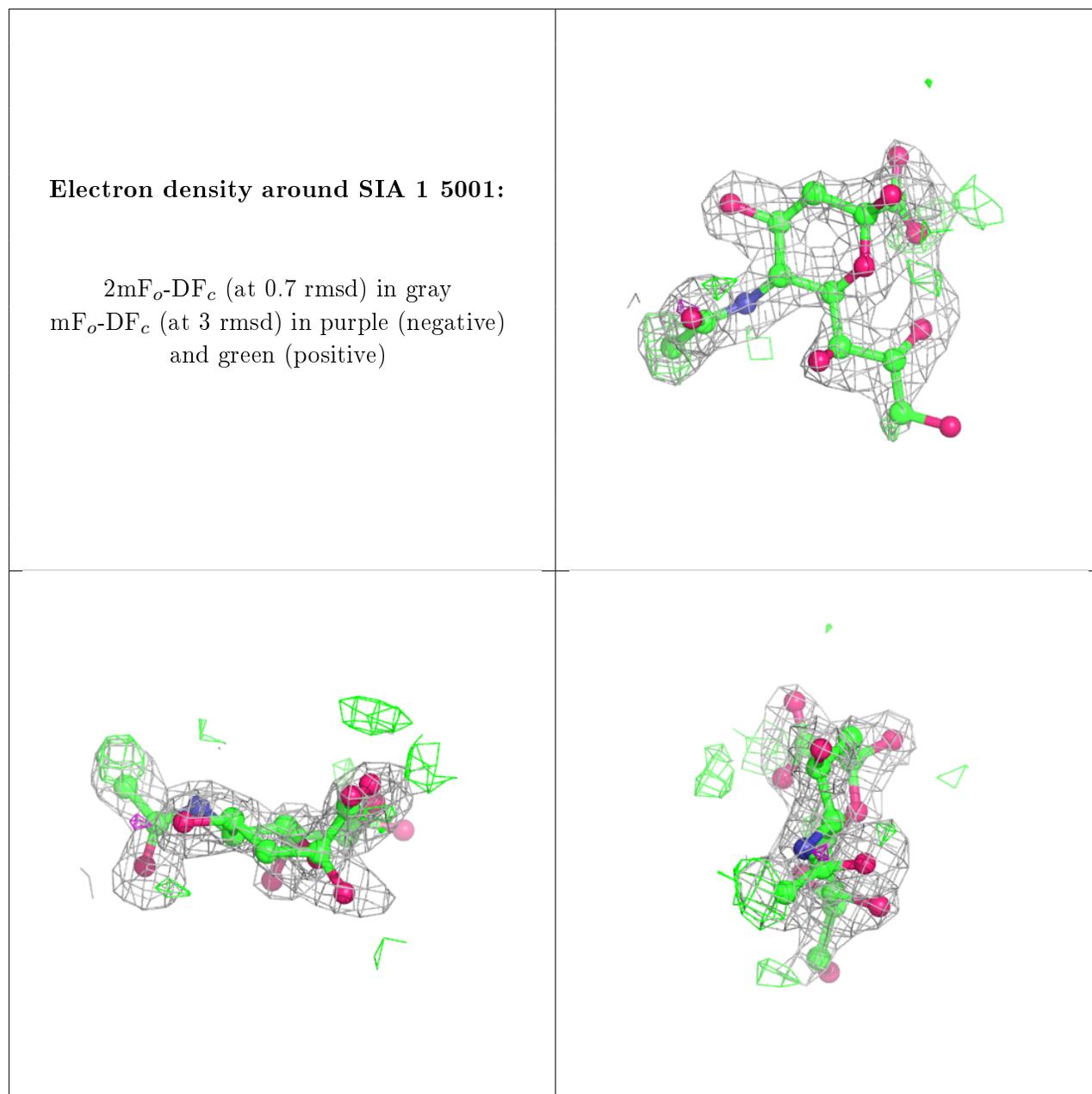
5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

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.



5.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.