



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 20, 2022 – 01:15 pm BST

PDB ID : 7OZ9
Title : Sulfated host glycan recognition by carbohydrate sulfatases of the human gut microbiota (BT3057-S1_16)
Authors : Cartmell, A.
Deposited on : 2021-06-27
Resolution : 1.91 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.8.4, 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 : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.28.1

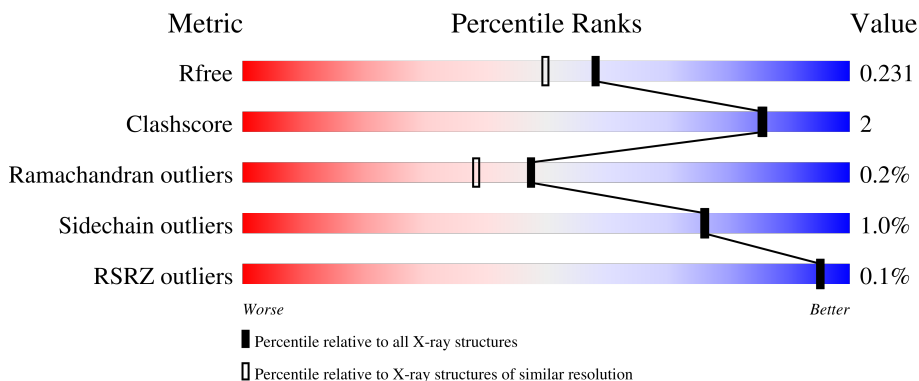
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	AAA	507	
1	BBB	507	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8067 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 N-acetylgalactosamine-6-sulfatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	482	3825	2425	664	714	22	0	4	0
1	BBB	483	3759	2387	651	700	21	0	1	0

There are 46 discrepancies between the modelled and reference sequences:

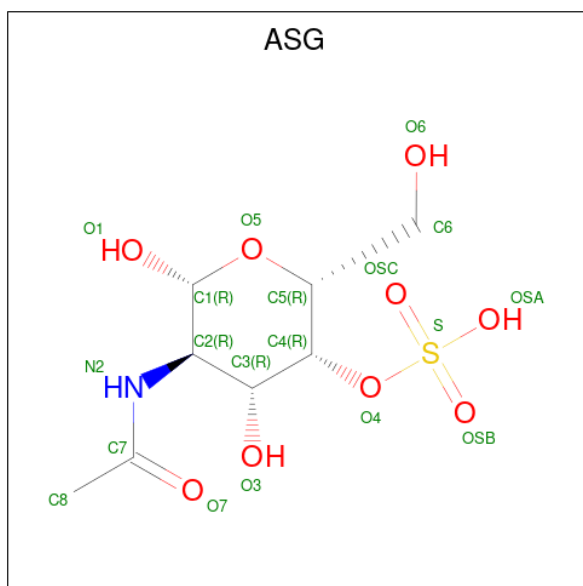
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	2	MET	-	initiating methionine	UNP Q8A397
AAA	3	GLY	-	expression tag	UNP Q8A397
AAA	4	SER	-	expression tag	UNP Q8A397
AAA	5	SER	-	expression tag	UNP Q8A397
AAA	6	HIS	-	expression tag	UNP Q8A397
AAA	7	HIS	-	expression tag	UNP Q8A397
AAA	8	HIS	-	expression tag	UNP Q8A397
AAA	9	HIS	-	expression tag	UNP Q8A397
AAA	10	HIS	-	expression tag	UNP Q8A397
AAA	11	HIS	-	expression tag	UNP Q8A397
AAA	12	SER	-	expression tag	UNP Q8A397
AAA	13	SER	-	expression tag	UNP Q8A397
AAA	14	GLY	-	expression tag	UNP Q8A397
AAA	15	LEU	-	expression tag	UNP Q8A397
AAA	16	VAL	-	expression tag	UNP Q8A397
AAA	17	PRO	-	expression tag	UNP Q8A397
AAA	18	ARG	-	expression tag	UNP Q8A397
AAA	19	GLY	-	expression tag	UNP Q8A397
AAA	20	SER	-	expression tag	UNP Q8A397
AAA	21	HIS	-	expression tag	UNP Q8A397
AAA	22	MET	-	expression tag	UNP Q8A397
AAA	23	ALA	-	expression tag	UNP Q8A397
AAA	24	SER	-	expression tag	UNP Q8A397
BBB	2	MET	-	initiating methionine	UNP Q8A397
BBB	3	GLY	-	expression tag	UNP Q8A397

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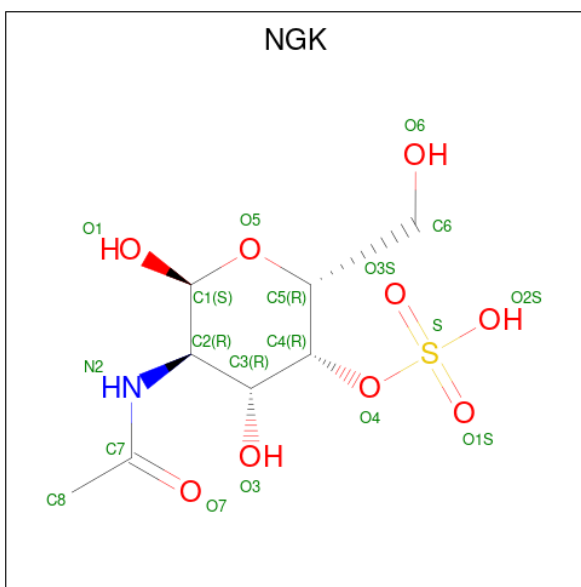
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	4	SER	-	expression tag	UNP Q8A397
BBB	5	SER	-	expression tag	UNP Q8A397
BBB	6	HIS	-	expression tag	UNP Q8A397
BBB	7	HIS	-	expression tag	UNP Q8A397
BBB	8	HIS	-	expression tag	UNP Q8A397
BBB	9	HIS	-	expression tag	UNP Q8A397
BBB	10	HIS	-	expression tag	UNP Q8A397
BBB	11	HIS	-	expression tag	UNP Q8A397
BBB	12	SER	-	expression tag	UNP Q8A397
BBB	13	SER	-	expression tag	UNP Q8A397
BBB	14	GLY	-	expression tag	UNP Q8A397
BBB	15	LEU	-	expression tag	UNP Q8A397
BBB	16	VAL	-	expression tag	UNP Q8A397
BBB	17	PRO	-	expression tag	UNP Q8A397
BBB	18	ARG	-	expression tag	UNP Q8A397
BBB	19	GLY	-	expression tag	UNP Q8A397
BBB	20	SER	-	expression tag	UNP Q8A397
BBB	21	HIS	-	expression tag	UNP Q8A397
BBB	22	MET	-	expression tag	UNP Q8A397
BBB	23	ALA	-	expression tag	UNP Q8A397
BBB	24	SER	-	expression tag	UNP Q8A397

- Molecule 2 is 2-acetamido-2-deoxy-4-O-sulfo-beta-D-galactopyranose (three-letter code: ASG) (formula: C₈H₁₅NO₉S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	S	0	1
			19	8	1	9	1		
2	BBB	1	Total	C	N	O	S	0	1
			19	8	1	9	1		

- Molecule 3 is 2-acetamido-2-deoxy-4-O-sulfo-alpha-D-galactopyranose (three-letter code: NGK) (formula: C₈H₁₅NO₉S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	S	0	1
			19	8	1	9	1		
3	BBB	1	Total	C	N	O	S	0	1
			19	8	1	9	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	1	Total	Ca	0	0
			1	1		
4	BBB	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	230	Total	O	0	0
			230	230		

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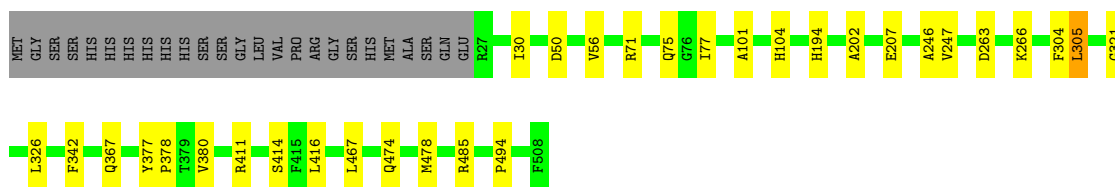
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	BBB	175	Total 175	O 175	0	0

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.

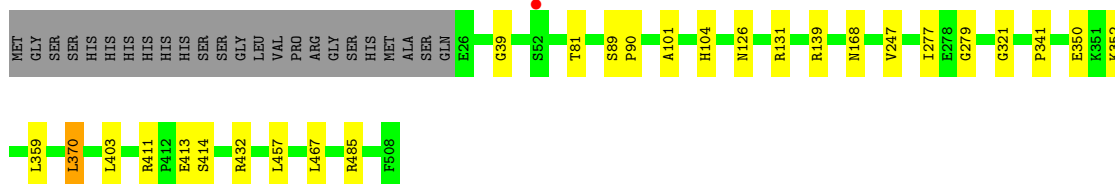
- Molecule 1: N-acetylgalactosamine-6-sulfatase

Chain AAA:  89% 6% 5%



- Molecule 1: N-acetylgalactosamine-6-sulfatase

Chain BBB:  90% 5% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.17Å 90.75Å 94.17Å 90.00° 98.55° 90.00°	Depositor
Resolution (Å)	65.52 – 1.91 65.43 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.6 (65.52-1.91) 99.6 (65.43-1.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 1.91Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.185 , 0.223 0.195 , 0.231	Depositor DCC
R_{free} test set	4097 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtrriage
Anisotropy	0.239	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8067	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 5.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ASG, NGK, CA

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	0/3927	0.81	0/5318
1	BBB	0.70	0/3860	0.79	0/5235
All	All	0.71	0/7787	0.80	0/10553

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	3825	0	3672	16	0
1	BBB	3759	0	3586	17	0
2	AAA	19	0	9	0	0
2	BBB	19	0	9	0	0
3	AAA	19	0	9	0	0
3	BBB	19	0	9	0	0
4	AAA	1	0	0	0	0
4	BBB	1	0	0	0	0
5	AAA	230	0	0	1	0
5	BBB	175	0	0	1	0
All	All	8067	0	7294	33	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.

The worst 5 of 33 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:370:LEU:HD21	1:BBB:413:GLU:HA	1.70	0.74
1:BBB:126:ASN:OD1	1:BBB:131:ARG:NH2	2.24	0.70
1:BBB:101:ALA:HA	1:BBB:104:HIS:CE1	2.28	0.69
1:BBB:359:LEU:HD11	1:BBB:403:LEU:HD12	1.75	0.68
1:AAA:416[A]:LEU:HD22	1:AAA:485[A]:ARG:HG2	1.83	0.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	484/507 (96%)	468 (97%)	15 (3%)	1 (0%)	47	38
1	BBB	482/507 (95%)	463 (96%)	18 (4%)	1 (0%)	47	38
All	All	966/1014 (95%)	931 (96%)	33 (3%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	321	GLY
1	BBB	321	GLY

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	399/427 (93%)	394 (99%)	5 (1%)	69	68
1	BBB	386/427 (90%)	383 (99%)	3 (1%)	81	82
All	All	785/854 (92%)	777 (99%)	8 (1%)	76	76

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	467	LEU
1	BBB	411	ARG
1	AAA	494	PRO
1	AAA	467	LEU
1	BBB	370	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](#)

Of 6 ligands modelled in this entry, 2 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	$\# Z > 2$
2	ASG	AAA	601[A]	4	19,19,19	0.45	0	23,28,28	0.69	1 (4%)
2	ASG	BBB	601[A]	4	19,19,19	0.44	0	23,28,28	0.69	0
3	NGK	BBB	602[B]	4	19,19,19	0.48	0	23,28,28	0.64	0
3	NGK	AAA	602[B]	4	19,19,19	0.44	0	23,28,28	0.81	1 (4%)

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	ASG	AAA	601[A]	4	-	0/11/31/31	0/1/1/1
2	ASG	BBB	601[A]	4	-	0/11/31/31	0/1/1/1
3	NGK	BBB	602[B]	4	-	0/11/31/31	0/1/1/1
3	NGK	AAA	602[B]	4	-	0/11/31/31	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AAA	602[B]	NGK	O5-C1-C2	3.17	112.70	109.52
2	AAA	601[A]	ASG	O5-C1-C2	2.36	111.89	109.52

There are no chirality outliers.

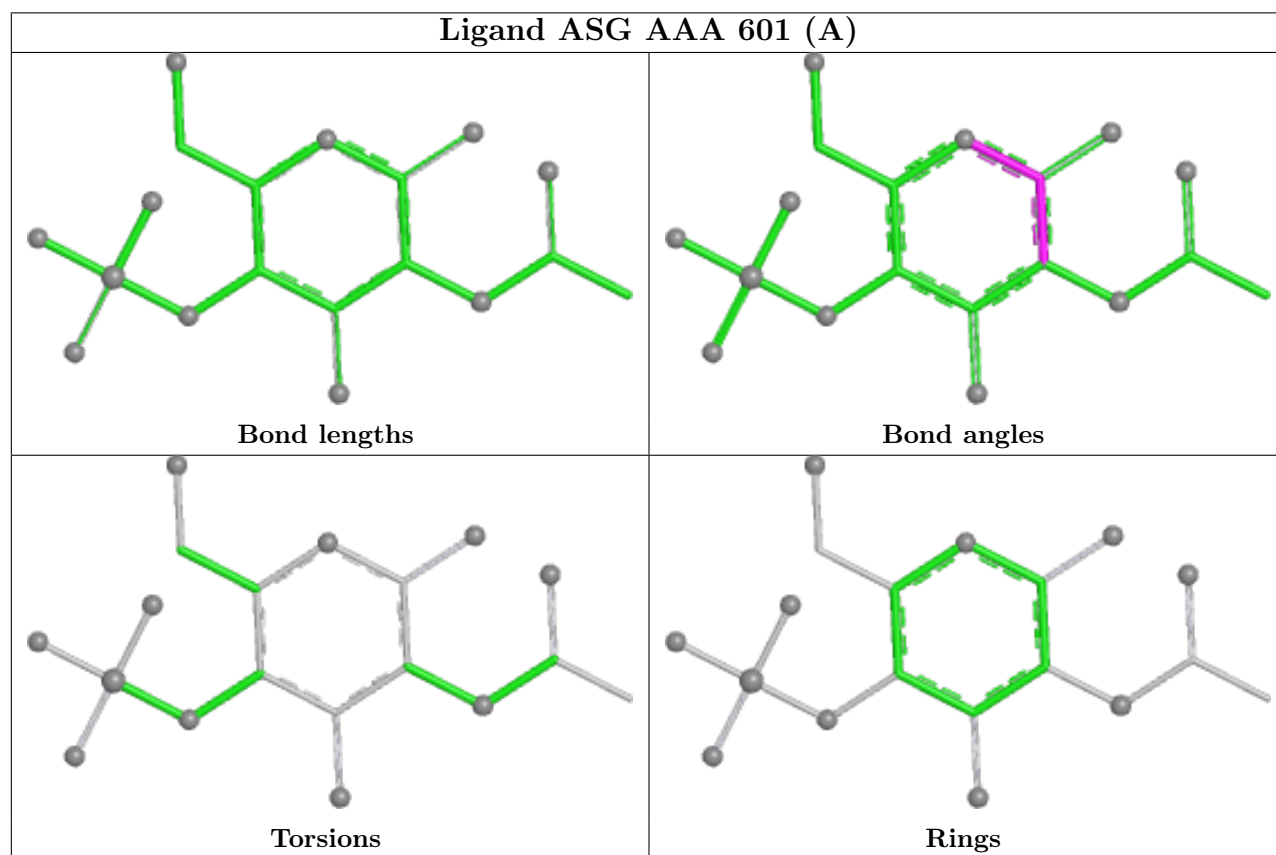
There are no torsion outliers.

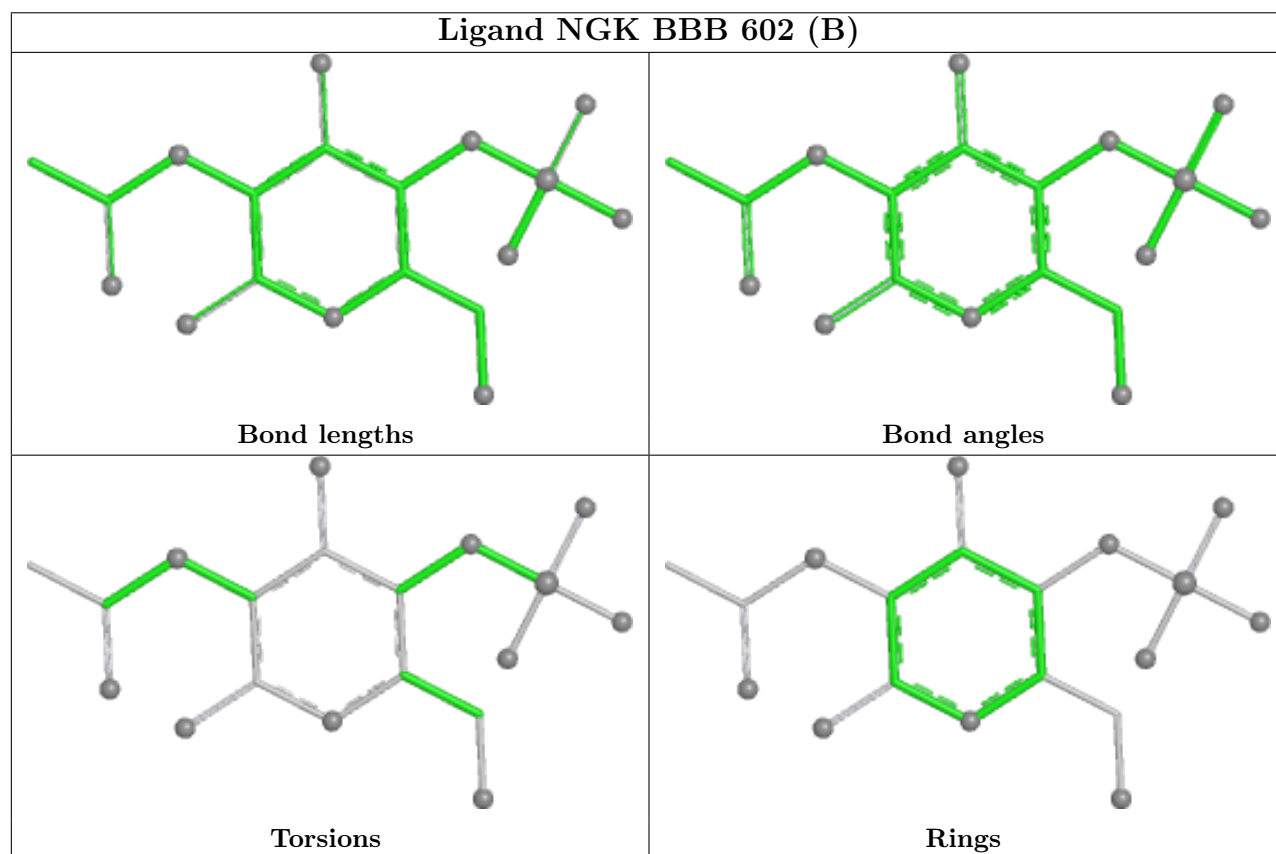
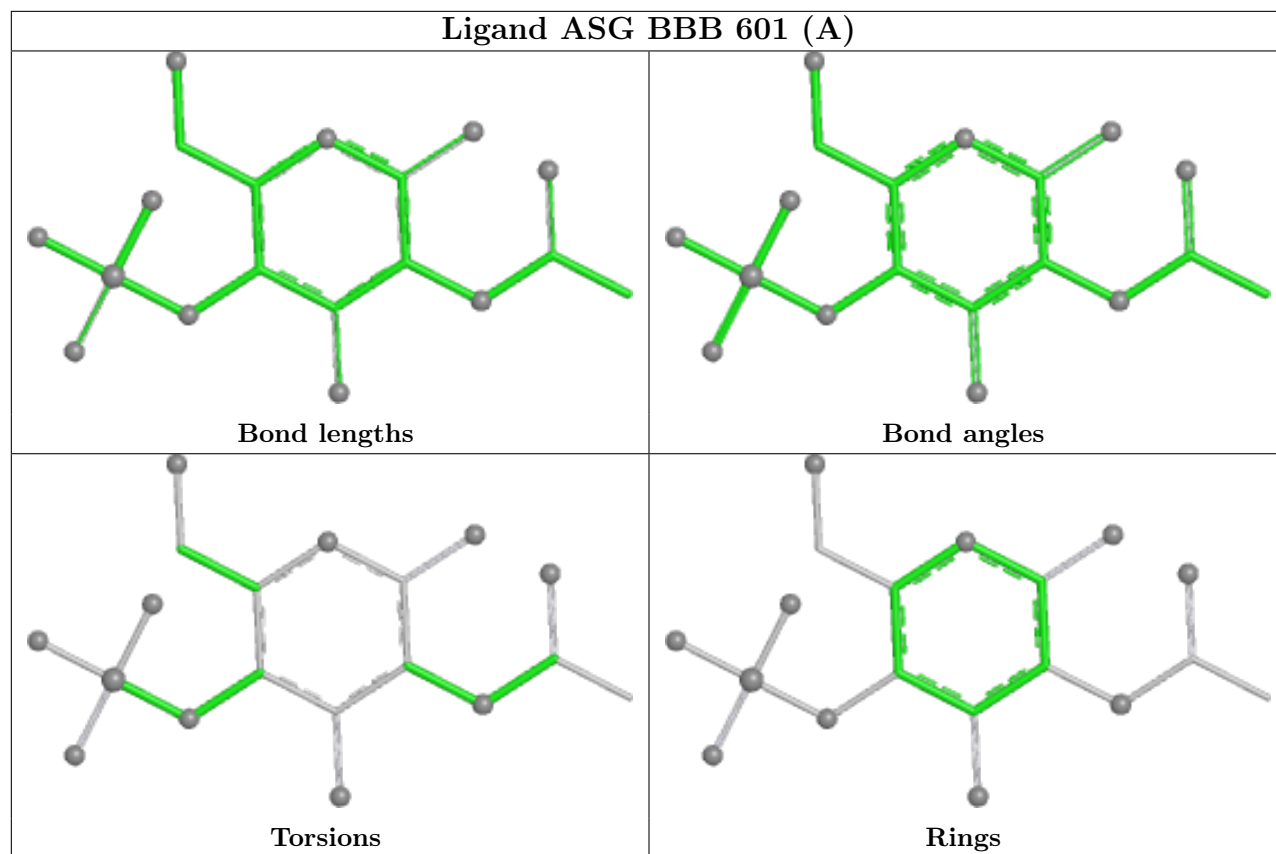
There are no ring outliers.

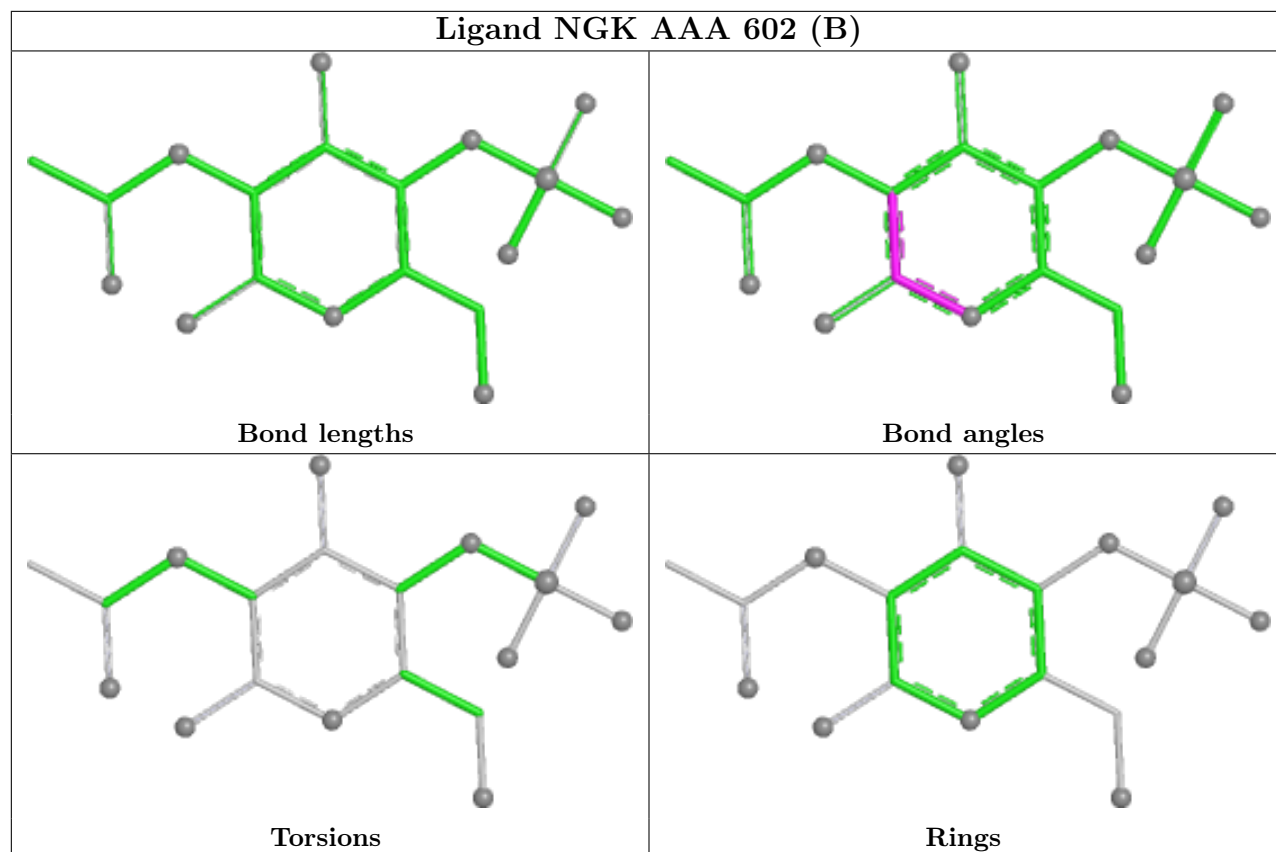
No monomer is involved in short contacts.

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 [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	482/507 (95%)	-0.50	0 100 100	12, 19, 33, 48	0
1	BBB	483/507 (95%)	-0.21	1 (0%) 95 95	15, 29, 49, 62	0
All	All	965/1014 (95%)	-0.36	1 (0%) 95 95	12, 23, 46, 62	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	52	SER	2.1

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.

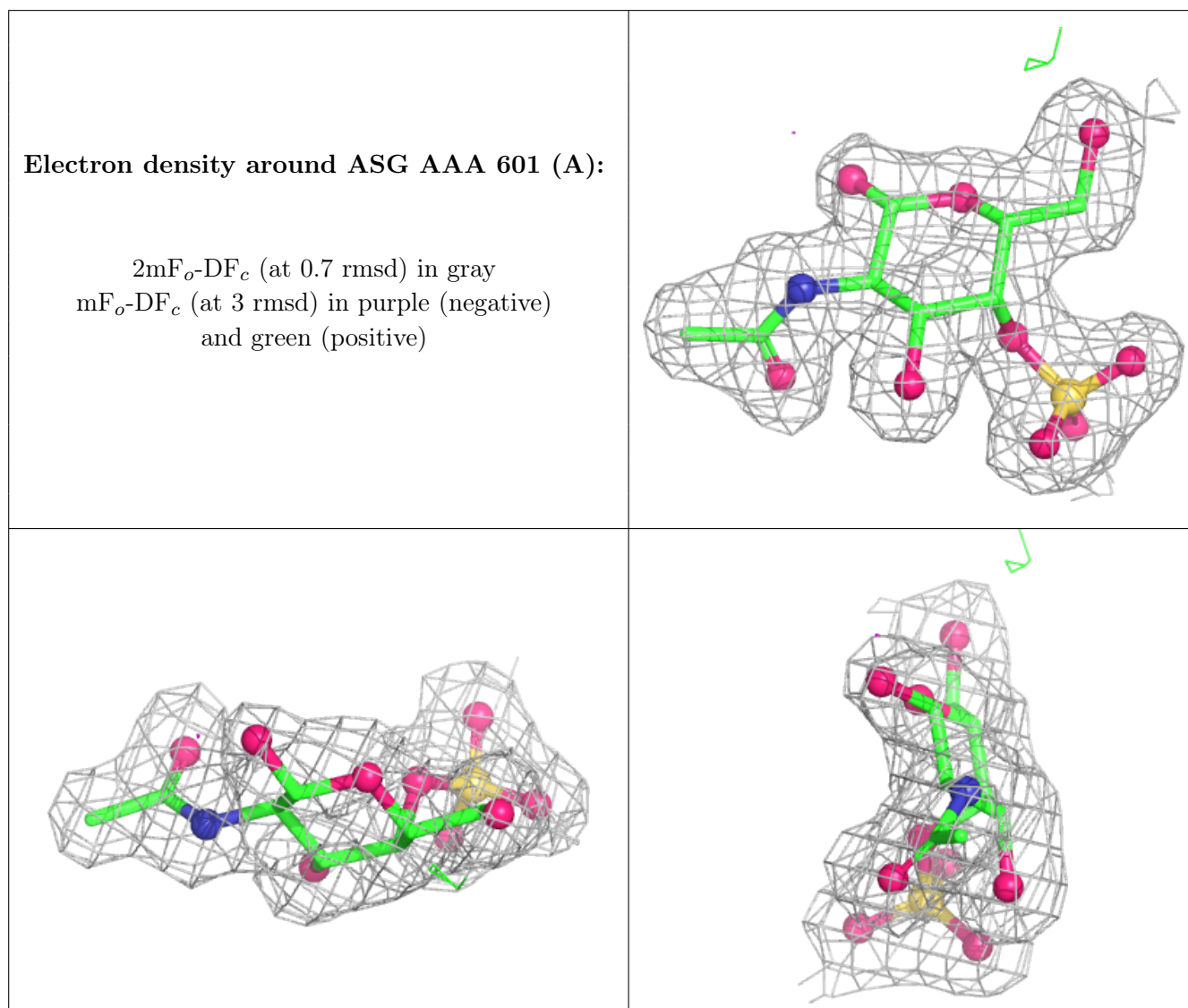
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ASG	AAA	601[A]	19/19	0.98	0.08	15,17,21,22	19
2	ASG	BBB	601[A]	19/19	0.98	0.09	20,21,25,25	19
3	NGK	AAA	602[B]	19/19	0.98	0.09	15,18,21,22	19
3	NGK	BBB	602[B]	19/19	0.98	0.09	20,22,26,26	19

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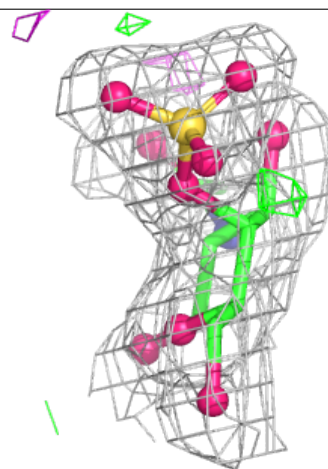
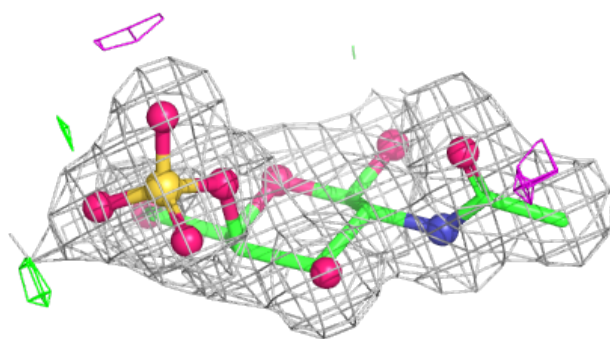
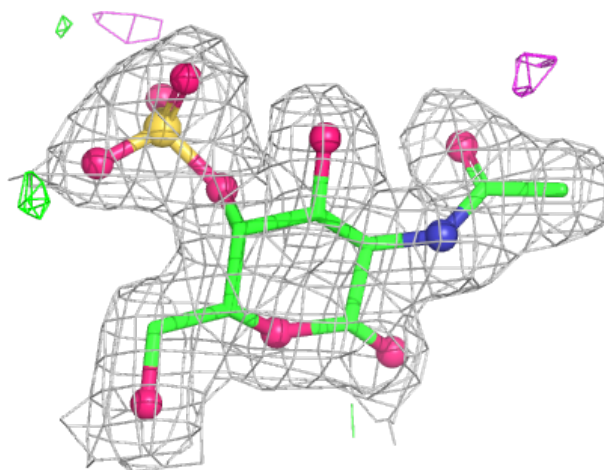
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CA	BBB	603	1/1	0.98	0.15	38,38,38,38	0
4	CA	AAA	603	1/1	1.00	0.09	31,31,31,31	0

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.



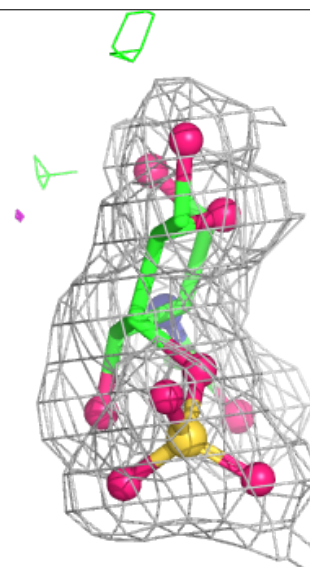
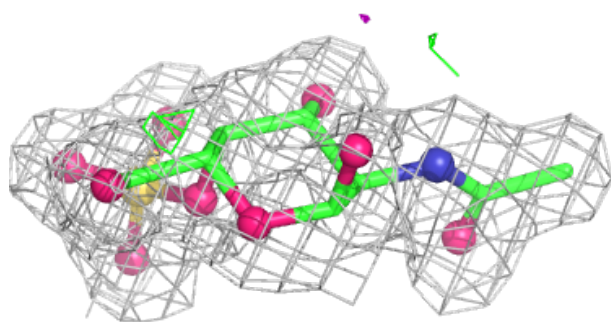
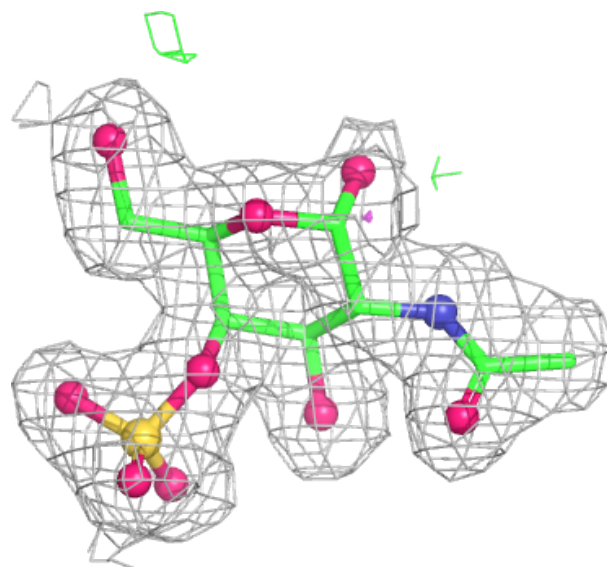
Electron density around ASG BBB 601 (A):

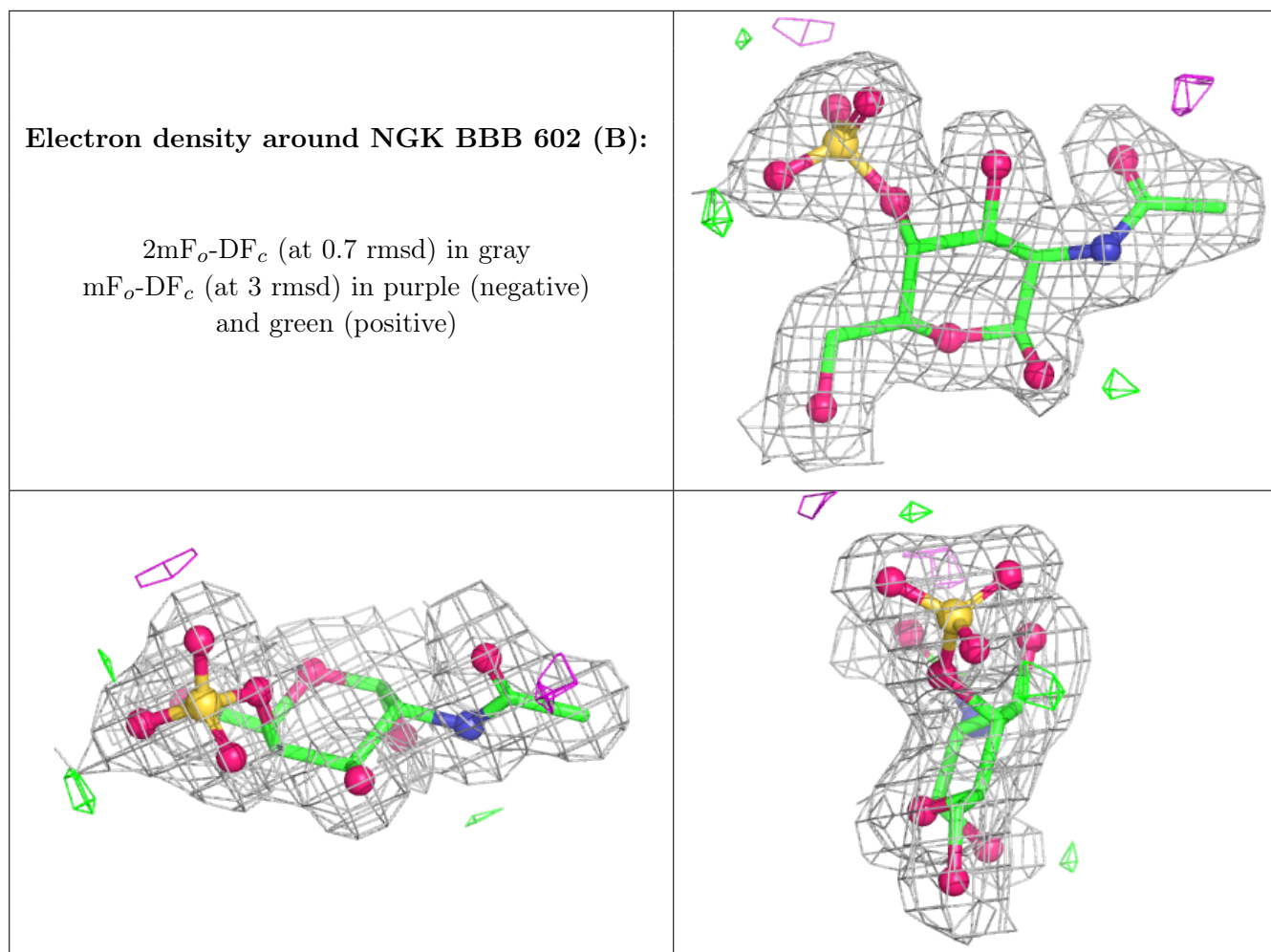
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around NGK AAA 602 (B):

$2mF_o - DF_c$ (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.