



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:40 PM UTC

PDB ID : 6Y66 / pdb_00006y66
Title : Structure of Goose Hemorrhagic Polyomavirus VP1 in complex with 2-O-Met
hyl-5-N-acetyl-alpha-D-neuraminic acid
Authors : Stroh, L.J.; Rustmeier, N.H.; Stehle, T.
Deposited on : 2020-02-26
Resolution : 1.95 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 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

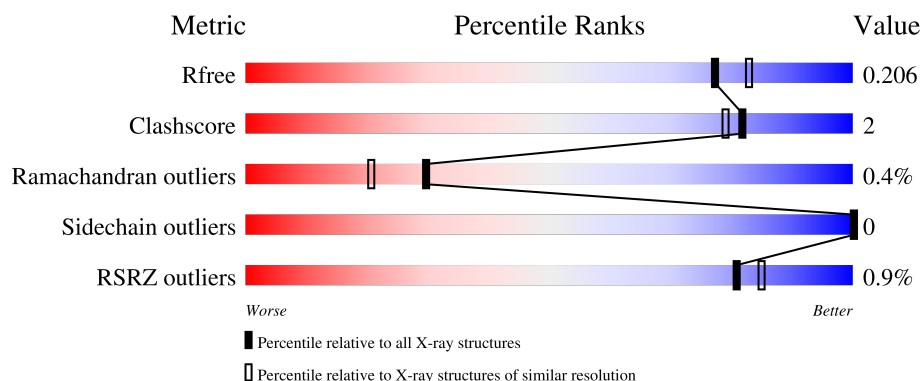
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	287	88% 5% 8%
1	BBB	287	87% 5% 8%
1	CCC	287	88% 5% 7%
1	DDD	287	85% 7% 8%
1	EEE	287	85% 7% 8%

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Mol	Chain	Length	Quality of chain
1	FFF	287	87% 5%8%
1	GGG	287	% 86% 8%7%
1	HHH	287	% 86% 6%8%
1	III	287	3% 87% 6%7%
1	JJJ	287	86% 8%7%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23150 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	265	Total	C	N	O	S	0	1	0
			2006	1262	341	386	17			
1	BBB	265	Total	C	N	O	S	0	1	0
			1999	1258	341	383	17			
1	CCC	267	Total	C	N	O	S	0	1	0
			2023	1271	346	388	18			
1	DDD	265	Total	C	N	O	S	0	2	0
			2008	1266	341	384	17			
1	EEE	265	Total	C	N	O	S	0	1	0
			2005	1262	342	384	17			
1	FFF	265	Total	C	N	O	S	0	1	0
			2002	1260	340	385	17			
1	GGG	268	Total	C	N	O	S	0	1	0
			2019	1270	344	387	18			
1	HHH	265	Total	C	N	O	S	0	2	0
			2010	1265	341	387	17			
1	III	267	Total	C	N	O	S	0	1	0
			2007	1263	343	383	18			
1	JJJ	268	Total	C	N	O	S	0	1	0
			2030	1275	348	389	18			

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	0	MET	-	initiating methionine	UNP Q80FI3
AAA	1	GLY	-	expression tag	UNP Q80FI3
AAA	2	SER	-	expression tag	UNP Q80FI3
AAA	3	SER	-	expression tag	UNP Q80FI3
AAA	4	HIS	-	expression tag	UNP Q80FI3
AAA	5	HIS	-	expression tag	UNP Q80FI3
AAA	6	HIS	-	expression tag	UNP Q80FI3
AAA	7	HIS	-	expression tag	UNP Q80FI3
AAA	8	HIS	-	expression tag	UNP Q80FI3

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Chain	Residue	Modelled	Actual	Comment	Reference
AAA	9	HIS	-	expression tag	UNP Q80FI3
AAA	10	SER	-	expression tag	UNP Q80FI3
AAA	11	SER	-	expression tag	UNP Q80FI3
AAA	12	GLY	-	expression tag	UNP Q80FI3
AAA	13	LEU	-	expression tag	UNP Q80FI3
AAA	14	VAL	-	expression tag	UNP Q80FI3
AAA	15	PRO	-	expression tag	UNP Q80FI3
AAA	16	ARG	-	expression tag	UNP Q80FI3
AAA	17	GLY	-	expression tag	UNP Q80FI3
AAA	18	SER	-	expression tag	UNP Q80FI3
AAA	19	HIS	-	expression tag	UNP Q80FI3
AAA	20	MET	-	expression tag	UNP Q80FI3
BBB	0	MET	-	initiating methionine	UNP Q80FI3
BBB	1	GLY	-	expression tag	UNP Q80FI3
BBB	2	SER	-	expression tag	UNP Q80FI3
BBB	3	SER	-	expression tag	UNP Q80FI3
BBB	4	HIS	-	expression tag	UNP Q80FI3
BBB	5	HIS	-	expression tag	UNP Q80FI3
BBB	6	HIS	-	expression tag	UNP Q80FI3
BBB	7	HIS	-	expression tag	UNP Q80FI3
BBB	8	HIS	-	expression tag	UNP Q80FI3
BBB	9	HIS	-	expression tag	UNP Q80FI3
BBB	10	SER	-	expression tag	UNP Q80FI3
BBB	11	SER	-	expression tag	UNP Q80FI3
BBB	12	GLY	-	expression tag	UNP Q80FI3
BBB	13	LEU	-	expression tag	UNP Q80FI3
BBB	14	VAL	-	expression tag	UNP Q80FI3
BBB	15	PRO	-	expression tag	UNP Q80FI3
BBB	16	ARG	-	expression tag	UNP Q80FI3
BBB	17	GLY	-	expression tag	UNP Q80FI3
BBB	18	SER	-	expression tag	UNP Q80FI3
BBB	19	HIS	-	expression tag	UNP Q80FI3
BBB	20	MET	-	expression tag	UNP Q80FI3
CCC	0	MET	-	initiating methionine	UNP Q80FI3
CCC	1	GLY	-	expression tag	UNP Q80FI3
CCC	2	SER	-	expression tag	UNP Q80FI3
CCC	3	SER	-	expression tag	UNP Q80FI3
CCC	4	HIS	-	expression tag	UNP Q80FI3
CCC	5	HIS	-	expression tag	UNP Q80FI3
CCC	6	HIS	-	expression tag	UNP Q80FI3
CCC	7	HIS	-	expression tag	UNP Q80FI3
CCC	8	HIS	-	expression tag	UNP Q80FI3

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Chain	Residue	Modelled	Actual	Comment	Reference
CCC	9	HIS	-	expression tag	UNP Q80FI3
CCC	10	SER	-	expression tag	UNP Q80FI3
CCC	11	SER	-	expression tag	UNP Q80FI3
CCC	12	GLY	-	expression tag	UNP Q80FI3
CCC	13	LEU	-	expression tag	UNP Q80FI3
CCC	14	VAL	-	expression tag	UNP Q80FI3
CCC	15	PRO	-	expression tag	UNP Q80FI3
CCC	16	ARG	-	expression tag	UNP Q80FI3
CCC	17	GLY	-	expression tag	UNP Q80FI3
CCC	18	SER	-	expression tag	UNP Q80FI3
CCC	19	HIS	-	expression tag	UNP Q80FI3
CCC	20	MET	-	expression tag	UNP Q80FI3
DDD	0	MET	-	initiating methionine	UNP Q80FI3
DDD	1	GLY	-	expression tag	UNP Q80FI3
DDD	2	SER	-	expression tag	UNP Q80FI3
DDD	3	SER	-	expression tag	UNP Q80FI3
DDD	4	HIS	-	expression tag	UNP Q80FI3
DDD	5	HIS	-	expression tag	UNP Q80FI3
DDD	6	HIS	-	expression tag	UNP Q80FI3
DDD	7	HIS	-	expression tag	UNP Q80FI3
DDD	8	HIS	-	expression tag	UNP Q80FI3
DDD	9	HIS	-	expression tag	UNP Q80FI3
DDD	10	SER	-	expression tag	UNP Q80FI3
DDD	11	SER	-	expression tag	UNP Q80FI3
DDD	12	GLY	-	expression tag	UNP Q80FI3
DDD	13	LEU	-	expression tag	UNP Q80FI3
DDD	14	VAL	-	expression tag	UNP Q80FI3
DDD	15	PRO	-	expression tag	UNP Q80FI3
DDD	16	ARG	-	expression tag	UNP Q80FI3
DDD	17	GLY	-	expression tag	UNP Q80FI3
DDD	18	SER	-	expression tag	UNP Q80FI3
DDD	19	HIS	-	expression tag	UNP Q80FI3
DDD	20	MET	-	expression tag	UNP Q80FI3
EEE	0	MET	-	initiating methionine	UNP Q80FI3
EEE	1	GLY	-	expression tag	UNP Q80FI3
EEE	2	SER	-	expression tag	UNP Q80FI3
EEE	3	SER	-	expression tag	UNP Q80FI3
EEE	4	HIS	-	expression tag	UNP Q80FI3
EEE	5	HIS	-	expression tag	UNP Q80FI3
EEE	6	HIS	-	expression tag	UNP Q80FI3
EEE	7	HIS	-	expression tag	UNP Q80FI3
EEE	8	HIS	-	expression tag	UNP Q80FI3

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Chain	Residue	Modelled	Actual	Comment	Reference
EEE	9	HIS	-	expression tag	UNP Q80FI3
EEE	10	SER	-	expression tag	UNP Q80FI3
EEE	11	SER	-	expression tag	UNP Q80FI3
EEE	12	GLY	-	expression tag	UNP Q80FI3
EEE	13	LEU	-	expression tag	UNP Q80FI3
EEE	14	VAL	-	expression tag	UNP Q80FI3
EEE	15	PRO	-	expression tag	UNP Q80FI3
EEE	16	ARG	-	expression tag	UNP Q80FI3
EEE	17	GLY	-	expression tag	UNP Q80FI3
EEE	18	SER	-	expression tag	UNP Q80FI3
EEE	19	HIS	-	expression tag	UNP Q80FI3
EEE	20	MET	-	expression tag	UNP Q80FI3
FFF	0	MET	-	initiating methionine	UNP Q80FI3
FFF	1	GLY	-	expression tag	UNP Q80FI3
FFF	2	SER	-	expression tag	UNP Q80FI3
FFF	3	SER	-	expression tag	UNP Q80FI3
FFF	4	HIS	-	expression tag	UNP Q80FI3
FFF	5	HIS	-	expression tag	UNP Q80FI3
FFF	6	HIS	-	expression tag	UNP Q80FI3
FFF	7	HIS	-	expression tag	UNP Q80FI3
FFF	8	HIS	-	expression tag	UNP Q80FI3
FFF	9	HIS	-	expression tag	UNP Q80FI3
FFF	10	SER	-	expression tag	UNP Q80FI3
FFF	11	SER	-	expression tag	UNP Q80FI3
FFF	12	GLY	-	expression tag	UNP Q80FI3
FFF	13	LEU	-	expression tag	UNP Q80FI3
FFF	14	VAL	-	expression tag	UNP Q80FI3
FFF	15	PRO	-	expression tag	UNP Q80FI3
FFF	16	ARG	-	expression tag	UNP Q80FI3
FFF	17	GLY	-	expression tag	UNP Q80FI3
FFF	18	SER	-	expression tag	UNP Q80FI3
FFF	19	HIS	-	expression tag	UNP Q80FI3
FFF	20	MET	-	expression tag	UNP Q80FI3
GGG	0	MET	-	initiating methionine	UNP Q80FI3
GGG	1	GLY	-	expression tag	UNP Q80FI3
GGG	2	SER	-	expression tag	UNP Q80FI3
GGG	3	SER	-	expression tag	UNP Q80FI3
GGG	4	HIS	-	expression tag	UNP Q80FI3
GGG	5	HIS	-	expression tag	UNP Q80FI3
GGG	6	HIS	-	expression tag	UNP Q80FI3
GGG	7	HIS	-	expression tag	UNP Q80FI3
GGG	8	HIS	-	expression tag	UNP Q80FI3

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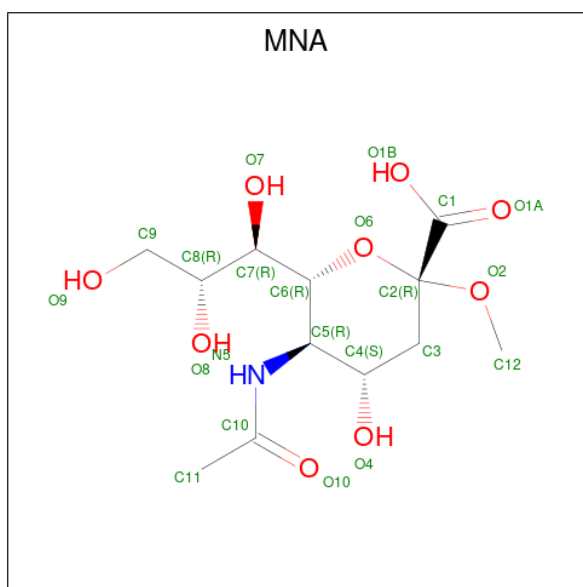
Chain	Residue	Modelled	Actual	Comment	Reference
GGG	9	HIS	-	expression tag	UNP Q80FI3
GGG	10	SER	-	expression tag	UNP Q80FI3
GGG	11	SER	-	expression tag	UNP Q80FI3
GGG	12	GLY	-	expression tag	UNP Q80FI3
GGG	13	LEU	-	expression tag	UNP Q80FI3
GGG	14	VAL	-	expression tag	UNP Q80FI3
GGG	15	PRO	-	expression tag	UNP Q80FI3
GGG	16	ARG	-	expression tag	UNP Q80FI3
GGG	17	GLY	-	expression tag	UNP Q80FI3
GGG	18	SER	-	expression tag	UNP Q80FI3
GGG	19	HIS	-	expression tag	UNP Q80FI3
GGG	20	MET	-	expression tag	UNP Q80FI3
HHH	0	MET	-	initiating methionine	UNP Q80FI3
HHH	1	GLY	-	expression tag	UNP Q80FI3
HHH	2	SER	-	expression tag	UNP Q80FI3
HHH	3	SER	-	expression tag	UNP Q80FI3
HHH	4	HIS	-	expression tag	UNP Q80FI3
HHH	5	HIS	-	expression tag	UNP Q80FI3
HHH	6	HIS	-	expression tag	UNP Q80FI3
HHH	7	HIS	-	expression tag	UNP Q80FI3
HHH	8	HIS	-	expression tag	UNP Q80FI3
HHH	9	HIS	-	expression tag	UNP Q80FI3
HHH	10	SER	-	expression tag	UNP Q80FI3
HHH	11	SER	-	expression tag	UNP Q80FI3
HHH	12	GLY	-	expression tag	UNP Q80FI3
HHH	13	LEU	-	expression tag	UNP Q80FI3
HHH	14	VAL	-	expression tag	UNP Q80FI3
HHH	15	PRO	-	expression tag	UNP Q80FI3
HHH	16	ARG	-	expression tag	UNP Q80FI3
HHH	17	GLY	-	expression tag	UNP Q80FI3
HHH	18	SER	-	expression tag	UNP Q80FI3
HHH	19	HIS	-	expression tag	UNP Q80FI3
HHH	20	MET	-	expression tag	UNP Q80FI3
III	0	MET	-	initiating methionine	UNP Q80FI3
III	1	GLY	-	expression tag	UNP Q80FI3
III	2	SER	-	expression tag	UNP Q80FI3
III	3	SER	-	expression tag	UNP Q80FI3
III	4	HIS	-	expression tag	UNP Q80FI3
III	5	HIS	-	expression tag	UNP Q80FI3
III	6	HIS	-	expression tag	UNP Q80FI3
III	7	HIS	-	expression tag	UNP Q80FI3
III	8	HIS	-	expression tag	UNP Q80FI3

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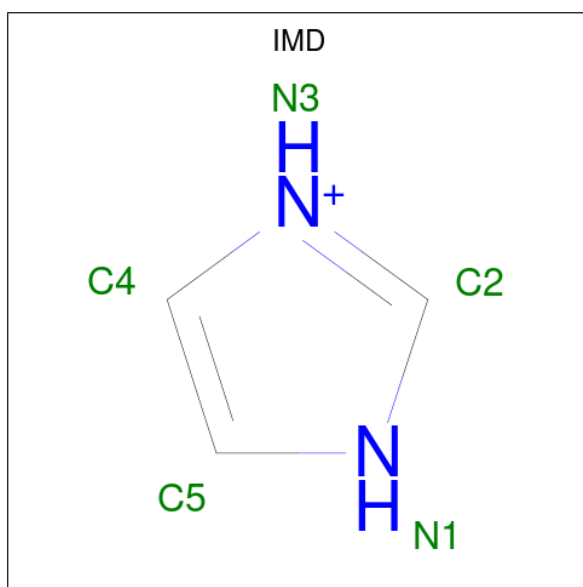
Chain	Residue	Modelled	Actual	Comment	Reference
III	9	HIS	-	expression tag	UNP Q80FI3
III	10	SER	-	expression tag	UNP Q80FI3
III	11	SER	-	expression tag	UNP Q80FI3
III	12	GLY	-	expression tag	UNP Q80FI3
III	13	LEU	-	expression tag	UNP Q80FI3
III	14	VAL	-	expression tag	UNP Q80FI3
III	15	PRO	-	expression tag	UNP Q80FI3
III	16	ARG	-	expression tag	UNP Q80FI3
III	17	GLY	-	expression tag	UNP Q80FI3
III	18	SER	-	expression tag	UNP Q80FI3
III	19	HIS	-	expression tag	UNP Q80FI3
III	20	MET	-	expression tag	UNP Q80FI3
JJJ	0	MET	-	initiating methionine	UNP Q80FI3
JJJ	1	GLY	-	expression tag	UNP Q80FI3
JJJ	2	SER	-	expression tag	UNP Q80FI3
JJJ	3	SER	-	expression tag	UNP Q80FI3
JJJ	4	HIS	-	expression tag	UNP Q80FI3
JJJ	5	HIS	-	expression tag	UNP Q80FI3
JJJ	6	HIS	-	expression tag	UNP Q80FI3
JJJ	7	HIS	-	expression tag	UNP Q80FI3
JJJ	8	HIS	-	expression tag	UNP Q80FI3
JJJ	9	HIS	-	expression tag	UNP Q80FI3
JJJ	10	SER	-	expression tag	UNP Q80FI3
JJJ	11	SER	-	expression tag	UNP Q80FI3
JJJ	12	GLY	-	expression tag	UNP Q80FI3
JJJ	13	LEU	-	expression tag	UNP Q80FI3
JJJ	14	VAL	-	expression tag	UNP Q80FI3
JJJ	15	PRO	-	expression tag	UNP Q80FI3
JJJ	16	ARG	-	expression tag	UNP Q80FI3
JJJ	17	GLY	-	expression tag	UNP Q80FI3
JJJ	18	SER	-	expression tag	UNP Q80FI3
JJJ	19	HIS	-	expression tag	UNP Q80FI3
JJJ	20	MET	-	expression tag	UNP Q80FI3

- Molecule 2 is 2-O-methyl-5-N-acetyl- α -D-neuraminic acid (CCD ID: MNA) (formula: $C_{12}H_{21}NO_9$) (labeled as "Ligand of Interest" by depositor).



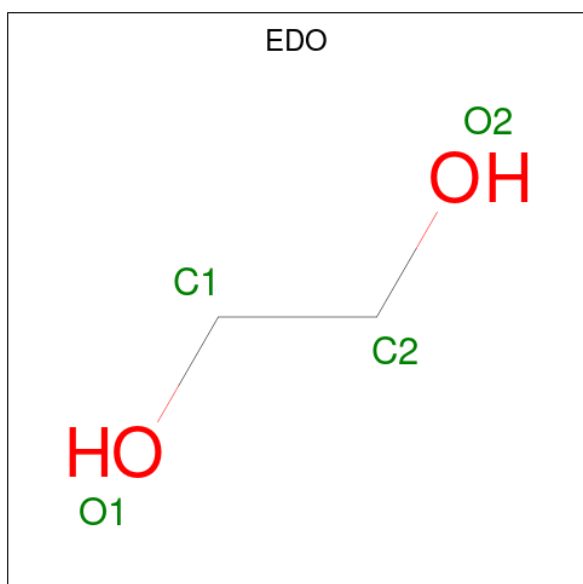
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	0	0
			22	12	1	9		
2	BBB	1	Total	C	N	O	0	0
			22	12	1	9		
2	CCC	1	Total	C	N	O	0	0
			22	12	1	9		
2	DDD	1	Total	C	N	O	0	0
			22	12	1	9		
2	EEE	1	Total	C	N	O	0	0
			22	12	1	9		
2	FFF	1	Total	C	N	O	0	0
			22	12	1	9		
2	GGG	1	Total	C	N	O	0	0
			22	12	1	9		
2	HHH	1	Total	C	N	O	0	0
			22	12	1	9		
2	III	1	Total	C	N	O	0	0
			22	12	1	9		
2	JJJ	1	Total	C	N	O	0	0
			22	12	1	9		

- Molecule 3 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	C	N	0	0
			5	3	2		
3	CCC	1	Total	C	N	0	0
			5	3	2		
3	DDD	1	Total	C	N	0	0
			5	3	2		
3	EEE	1	Total	C	N	0	0
			5	3	2		
3	GGG	1	Total	C	N	0	0
			5	3	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total C O 4 2 2	0	0
4	AAA	1	Total C O 4 2 2	0	0
4	AAA	1	Total C O 4 2 2	0	0
4	BBB	1	Total C O 4 2 2	0	0
4	CCC	1	Total C O 4 2 2	0	0
4	CCC	1	Total C O 4 2 2	0	0
4	DDD	1	Total C O 4 2 2	0	0
4	DDD	1	Total C O 4 2 2	0	0
4	EEE	1	Total C O 4 2 2	0	0
4	EEE	1	Total C O 4 2 2	0	0
4	EEE	1	Total C O 4 2 2	0	0
4	EEE	1	Total C O 4 2 2	0	0
4	EEE	1	Total C O 4 2 2	0	0
4	FFF	1	Total C O 4 2 2	0	0
4	FFF	1	Total C O 4 2 2	0	0
4	GGG	1	Total C O 4 2 2	0	0
4	GGG	1	Total C O 4 2 2	0	0
4	HHH	1	Total C O 4 2 2	0	0
4	HHH	1	Total C O 4 2 2	0	0
4	III	1	Total C O 4 2 2	0	0
4	JJJ	1	Total C O 4 2 2	0	0
4	JJJ	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

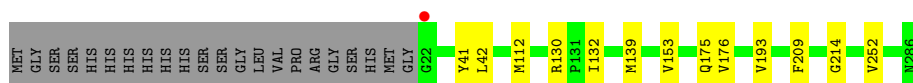
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	264	Total 264	O 264	0	0
5	BBB	256	Total 261	O 261	0	5
5	CCC	265	Total 271	O 271	0	6
5	DDD	279	Total 284	O 284	0	5
5	EEE	255	Total 260	O 260	0	5
5	FFF	281	Total 284	O 284	0	3
5	GGG	265	Total 272	O 272	0	7
5	HHH	256	Total 261	O 261	0	5
5	III	261	Total 264	O 264	0	3
5	JJJ	283	Total 287	O 287	0	4

3 Residue-property plots

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: Capsid protein VP1

Chain AAA: 



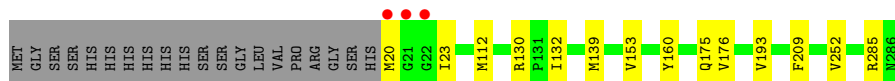
- Molecule 1: Capsid protein VP1

Chain BBB: 



- Molecule 1: Capsid protein VP1

Chain CCC: 



- Molecule 1: Capsid protein VP1

Chain DDD: 



- Molecule 1: Capsid protein VP1

Chain EEE: 



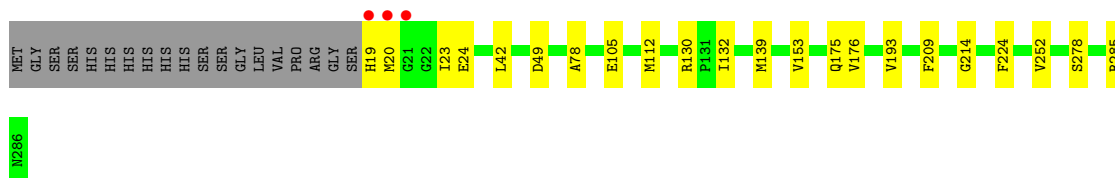
- Molecule 1: Capsid protein VP1

Chain FFF: 87% 5% 8%



- Molecule 1: Capsid protein VP1

Chain GGG: 86% 8% 7%



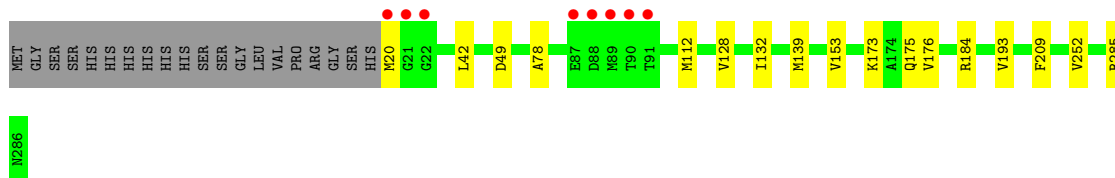
- Molecule 1: Capsid protein VP1

Chain HHH: 86% 6% 8%



- Molecule 1: Capsid protein VP1

Chain III: 87% 6% 7%



- Molecule 1: Capsid protein VP1

Chain JJJ: 86% 8% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	87.46Å 90.54Å 101.22Å 94.23° 98.09° 107.87°	Depositor
Resolution (Å)	49.58 – 1.95 49.58 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.7 (49.58-1.95) 97.7 (49.58-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.165 , 0.201 0.173 , 0.206	Depositor DCC
R_{free} test set	2069 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	23150	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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: IMD, MNA, 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	AAA	0.99	0/2054	1.13	1/2804 (0.0%)
1	BBB	0.96	0/2047	1.12	1/2797 (0.0%)
1	CCC	0.94	0/2071	1.12	2/2825 (0.1%)
1	DDD	0.97	0/2059	1.15	1/2811 (0.0%)
1	EEE	0.95	0/2053	1.12	3/2802 (0.1%)
1	FFF	0.96	0/2050	1.14	1/2800 (0.0%)
1	GGG	0.97	0/2067	1.12	1/2821 (0.0%)
1	HHH	0.96	0/2058	1.13	2/2811 (0.1%)
1	III	0.97	0/2055	1.13	1/2805 (0.0%)
1	JJJ	0.97	0/2079	1.13	2/2837 (0.1%)
All	All	0.96	0/20593	1.13	15/28113 (0.1%)

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FFF	130	ARG	CB-CA-C	-7.07	98.68	109.50
1	CCC	130	ARG	CB-CA-C	-7.05	98.71	109.50
1	BBB	130	ARG	CB-CA-C	-7.01	98.44	109.52
1	AAA	130	ARG	CB-CA-C	-6.97	98.14	109.56
1	DDD	130	ARG	CB-CA-C	-6.94	98.88	109.50

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	2006	0	1957	6	0
1	BBB	1999	0	1946	7	0
1	CCC	2023	0	1978	7	0
1	DDD	2008	0	1963	14	0
1	EEE	2005	0	1959	12	0
1	FFF	2002	0	1945	8	0
1	GGG	2019	0	1967	15	0
1	HHH	2010	0	1956	9	0
1	III	2007	0	1951	11	0
1	JJJ	2030	0	1976	14	0
2	AAA	22	0	20	0	0
2	BBB	22	0	20	0	0
2	CCC	22	0	20	0	0
2	DDD	22	0	20	0	0
2	EEE	22	0	20	0	0
2	FFF	22	0	20	0	0
2	GGG	22	0	20	0	0
2	HHH	22	0	20	0	0
2	III	22	0	20	0	0
2	JJJ	22	0	20	0	0
3	AAA	5	0	5	0	0
3	CCC	5	0	5	0	0
3	DDD	5	0	5	0	0
3	EEE	5	0	5	0	0
3	GGG	5	0	5	0	0
4	AAA	12	0	18	0	0
4	BBB	4	0	6	0	0
4	CCC	8	0	12	0	0
4	DDD	8	0	12	0	0
4	EEE	20	0	30	1	0
4	FFF	8	0	12	0	0
4	GGG	8	0	12	0	0
4	HHH	8	0	12	0	0
4	III	4	0	6	0	0
4	JJJ	8	0	12	0	0
5	AAA	264	0	0	0	0
5	BBB	261	0	0	1	0
5	CCC	271	0	0	1	0
5	DDD	284	0	0	3	0
5	EEE	260	0	0	4	0
5	FFF	284	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	GGG	272	0	0	4	0
5	HHH	261	0	0	1	0
5	III	264	0	0	5	0
5	JJJ	287	0	0	4	0
All	All	23150	0	19955	101	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 101 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:DDD:85[A]:LEU:HD11	1:DDD:281:LYS:HE2	1.44	0.99
1:DDD:85[A]:LEU:CD1	1:DDD:281:LYS:HE2	2.22	0.68
1:GGG:19:HIS:N	5:GGG:502:HOH:O	2.26	0.68
1:HHH:49:ASP:OD1	5:HHH:501:HOH:O	2.13	0.66
1:FFF:130:ARG:HG3	5:FFF:598:HOH:O	2.01	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	264/287 (92%)	256 (97%)	7 (3%)	1 (0%)	30	21
1	BBB	264/287 (92%)	255 (97%)	8 (3%)	1 (0%)	30	21
1	CCC	266/287 (93%)	257 (97%)	8 (3%)	1 (0%)	30	21
1	DDD	265/287 (92%)	255 (96%)	9 (3%)	1 (0%)	30	21
1	EEE	264/287 (92%)	254 (96%)	9 (3%)	1 (0%)	30	21
1	FFF	264/287 (92%)	255 (97%)	8 (3%)	1 (0%)	30	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GGG	267/287 (93%)	258 (97%)	8 (3%)	1 (0%)	30	21
1	HHH	265/287 (92%)	256 (97%)	8 (3%)	1 (0%)	30	21
1	III	266/287 (93%)	257 (97%)	8 (3%)	1 (0%)	30	21
1	JJJ	267/287 (93%)	257 (96%)	9 (3%)	1 (0%)	30	21
All	All	2652/2870 (92%)	2560 (96%)	82 (3%)	10 (0%)	30	21

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	FFF	176	VAL
1	AAA	176	VAL
1	BBB	176	VAL
1	CCC	176	VAL
1	DDD	176	VAL

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	222/243 (91%)	222 (100%)	0	100	100
1	BBB	220/243 (90%)	220 (100%)	0	100	100
1	CCC	224/243 (92%)	224 (100%)	0	100	100
1	DDD	221/243 (91%)	221 (100%)	0	100	100
1	EEE	221/243 (91%)	221 (100%)	0	100	100
1	FFF	220/243 (90%)	220 (100%)	0	100	100
1	GGG	222/243 (91%)	222 (100%)	0	100	100
1	HHH	222/243 (91%)	222 (100%)	0	100	100
1	III	219/243 (90%)	219 (100%)	0	100	100
1	JJJ	224/243 (92%)	224 (100%)	0	100	100
All	All	2215/2430 (91%)	2215 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

37 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	$\# Z > 2$
4	EDO	JJJ	402	-	3,3,3	0.26	0	2,2,2	0.14	0
4	EDO	EEE	403	-	3,3,3	0.35	0	2,2,2	0.33	0
2	MNA	AAA	401	-	22,22,22	0.80	1 (4%)	26,32,32	1.00	2 (7%)
4	EDO	EEE	406	-	3,3,3	0.21	0	2,2,2	0.27	0
4	EDO	EEE	407	-	3,3,3	0.24	0	2,2,2	0.22	0
4	EDO	AAA	404	-	3,3,3	0.21	0	2,2,2	0.29	0
2	MNA	III	401	-	22,22,22	0.78	1 (4%)	26,32,32	0.87	0
4	EDO	DDD	403	-	3,3,3	0.20	0	2,2,2	0.15	0
3	IMD	EEE	402	-	5,5,5	0.35	0	5,5,5	0.69	0
4	EDO	AAA	405	-	3,3,3	0.19	0	2,2,2	0.13	0
4	EDO	BBB	402	-	3,3,3	0.17	0	2,2,2	0.24	0
4	EDO	HHH	402	-	3,3,3	0.08	0	2,2,2	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	FFF	403	-	3,3,3	0.21	0	2,2,2	0.21	0
3	IMD	AAA	402	-	5,5,5	0.31	0	5,5,5	0.67	0
2	MNA	BBB	401	-	22,22,22	0.69	1 (4%)	26,32,32	0.88	0
4	EDO	EEE	405	-	3,3,3	0.08	0	2,2,2	0.06	0
2	MNA	DDD	401	-	22,22,22	0.90	2 (9%)	26,32,32	0.82	1 (3%)
4	EDO	FFF	402	-	3,3,3	0.21	0	2,2,2	0.14	0
2	MNA	HHH	401	-	22,22,22	0.81	1 (4%)	26,32,32	0.91	1 (3%)
4	EDO	JJJ	403	-	3,3,3	0.07	0	2,2,2	0.11	0
4	EDO	III	402	-	3,3,3	0.34	0	2,2,2	0.26	0
4	EDO	CCC	403	-	3,3,3	0.10	0	2,2,2	0.05	0
4	EDO	EEE	404	-	3,3,3	0.18	0	2,2,2	0.24	0
4	EDO	AAA	403	-	3,3,3	0.17	0	2,2,2	0.38	0
4	EDO	GGG	404	-	3,3,3	0.21	0	2,2,2	0.13	0
2	MNA	EEE	401	-	22,22,22	0.91	1 (4%)	26,32,32	1.00	1 (3%)
2	MNA	GGG	401	-	22,22,22	0.84	0	26,32,32	0.79	0
2	MNA	CCC	401	-	22,22,22	0.66	0	26,32,32	0.80	1 (3%)
4	EDO	GGG	403	-	3,3,3	0.15	0	2,2,2	0.31	0
3	IMD	CCC	402	-	5,5,5	0.36	0	5,5,5	0.70	0
2	MNA	JJJ	401	-	22,22,22	0.77	0	26,32,32	0.88	0
4	EDO	DDD	404	-	3,3,3	0.06	0	2,2,2	0.16	0
3	IMD	GGG	402	-	5,5,5	0.24	0	5,5,5	0.67	0
4	EDO	HHH	403	-	3,3,3	0.27	0	2,2,2	0.21	0
3	IMD	DDD	402	-	5,5,5	0.44	0	5,5,5	0.65	0
2	MNA	FFF	401	-	22,22,22	0.80	1 (4%)	26,32,32	0.92	0
4	EDO	CCC	404	-	3,3,3	0.18	0	2,2,2	0.27	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
4	EDO	JJJ	402	-	-	1/1/1/1	-
4	EDO	EEE	403	-	-	1/1/1/1	-
2	MNA	AAA	401	-	-	1/23/41/41	0/1/1/1
4	EDO	EEE	406	-	-	0/1/1/1	-
4	EDO	EEE	407	-	-	1/1/1/1	-
4	EDO	AAA	404	-	-	0/1/1/1	-
2	MNA	III	401	-	-	1/23/41/41	0/1/1/1
4	EDO	DDD	403	-	-	0/1/1/1	-
3	IMD	EEE	402	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	AAA	405	-	-	1/1/1/1	-
4	EDO	BBB	402	-	-	0/1/1/1	-
4	EDO	HHH	402	-	-	0/1/1/1	-
4	EDO	FFF	403	-	-	1/1/1/1	-
3	IMD	AAA	402	-	-	-	0/1/1/1
2	MNA	BBB	401	-	-	3/23/41/41	0/1/1/1
4	EDO	EEE	405	-	-	1/1/1/1	-
2	MNA	DDD	401	-	-	1/23/41/41	0/1/1/1
4	EDO	FFF	402	-	-	0/1/1/1	-
2	MNA	HHH	401	-	-	2/23/41/41	0/1/1/1
4	EDO	JJJ	403	-	-	1/1/1/1	-
4	EDO	III	402	-	-	1/1/1/1	-
4	EDO	CCC	403	-	-	0/1/1/1	-
4	EDO	EEE	404	-	-	1/1/1/1	-
4	EDO	AAA	403	-	-	1/1/1/1	-
4	EDO	GGG	404	-	-	1/1/1/1	-
2	MNA	EEE	401	-	-	4/23/41/41	0/1/1/1
2	MNA	GGG	401	-	-	2/23/41/41	0/1/1/1
2	MNA	CCC	401	-	-	2/23/41/41	0/1/1/1
4	EDO	GGG	403	-	-	1/1/1/1	-
3	IMD	CCC	402	-	-	-	0/1/1/1
4	EDO	DDD	404	-	-	0/1/1/1	-
2	MNA	JJJ	401	-	-	3/23/41/41	0/1/1/1
4	EDO	HHH	403	-	-	0/1/1/1	-
3	IMD	GGG	402	-	-	-	0/1/1/1
3	IMD	DDD	402	-	-	-	0/1/1/1
2	MNA	FFF	401	-	-	1/23/41/41	0/1/1/1
4	EDO	CCC	404	-	-	0/1/1/1	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	DDD	401	MNA	O1B-C1	-2.58	1.21	1.30
2	HHH	401	MNA	O1B-C1	-2.38	1.21	1.30
2	AAA	401	MNA	O6-C2	2.29	1.45	1.42
2	DDD	401	MNA	O6-C2	2.24	1.45	1.42
2	EEE	401	MNA	O1B-C1	-2.14	1.22	1.30

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	HHH	401	MNA	C3-C4-C5	2.29	113.26	109.72
2	DDD	401	MNA	C3-C4-C5	2.08	112.93	109.72
2	AAA	401	MNA	O1A-C1-C2	-2.06	117.57	123.79
2	AAA	401	MNA	C3-C4-C5	2.05	112.89	109.72
2	CCC	401	MNA	C3-C4-C5	2.05	112.89	109.72

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

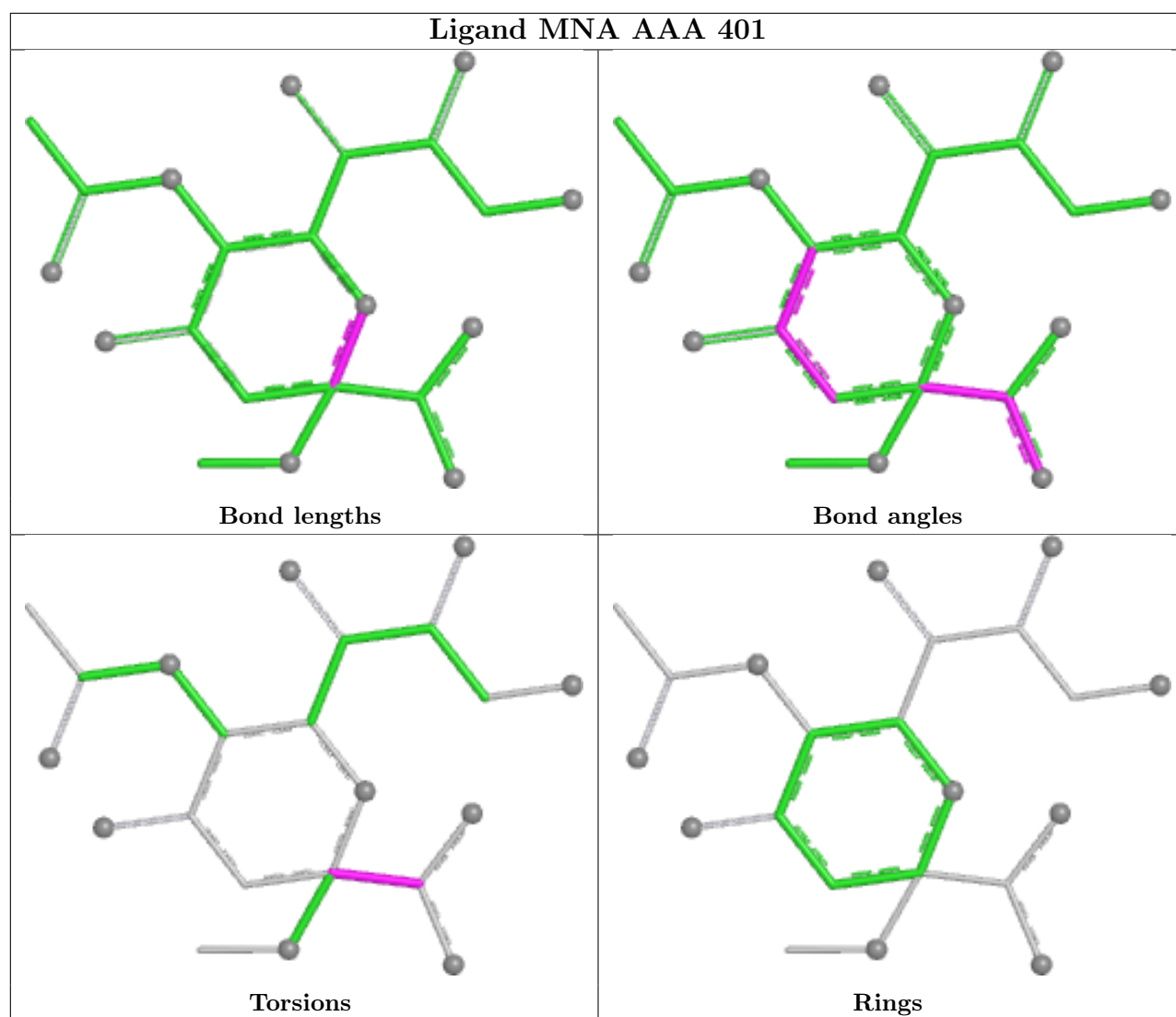
Mol	Chain	Res	Type	Atoms
2	AAA	401	MNA	O1B-C1-C2-O2
2	BBB	401	MNA	O1B-C1-C2-O2
2	CCC	401	MNA	O1B-C1-C2-O2
2	DDD	401	MNA	O1B-C1-C2-O2
2	EEE	401	MNA	O1A-C1-C2-C3

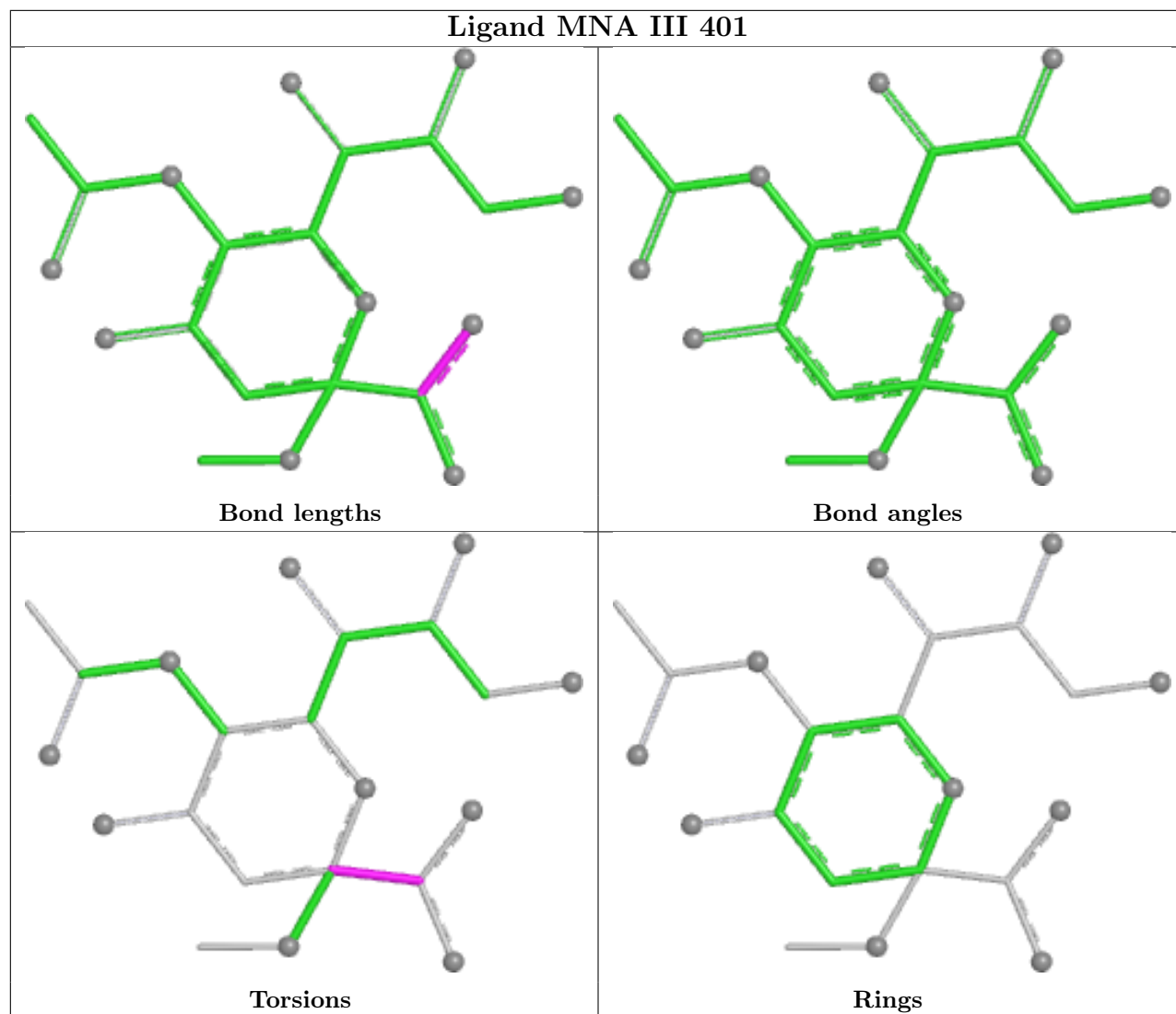
There are no ring outliers.

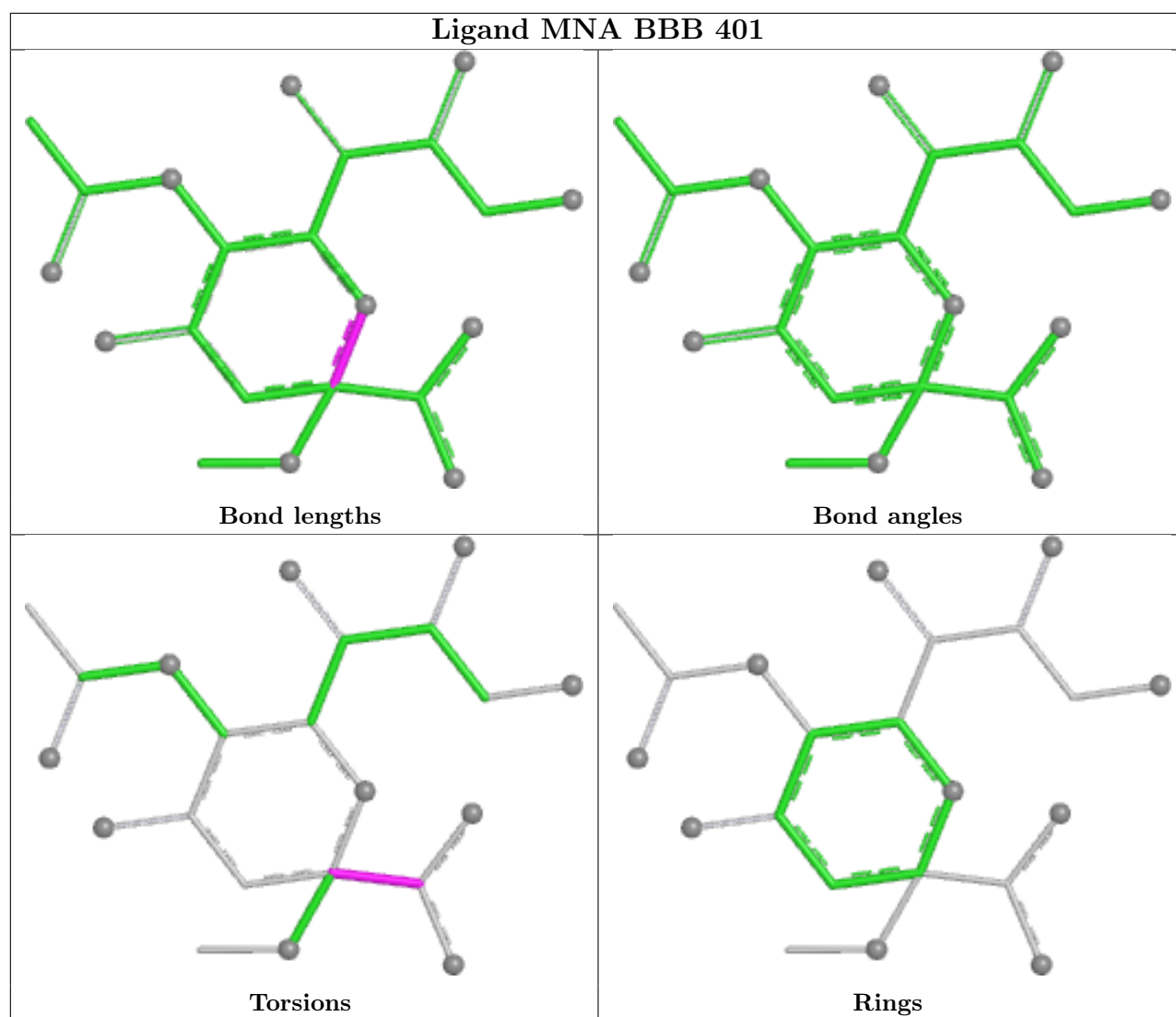
1 monomer is involved in 1 short contact:

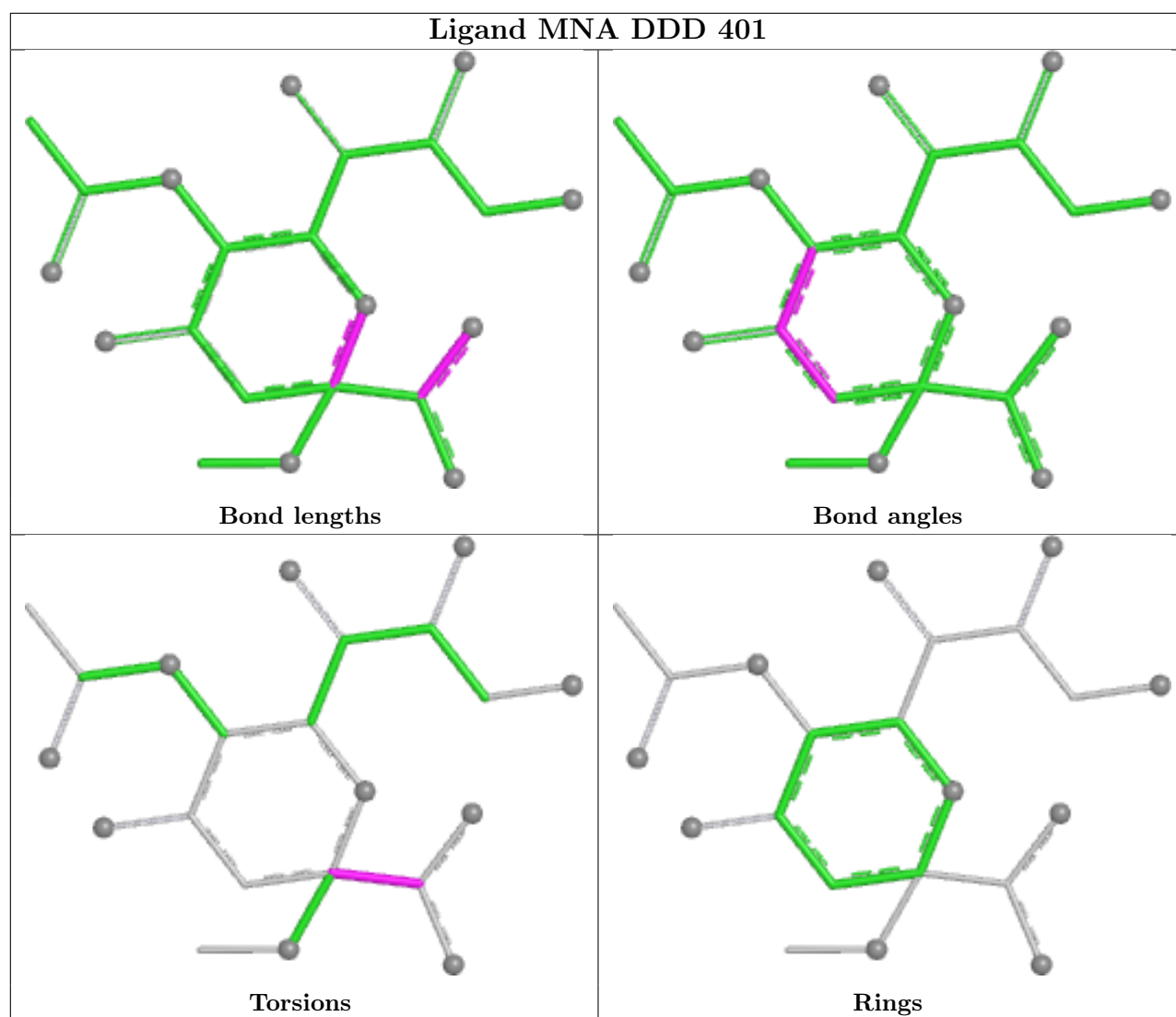
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	EEE	403	EDO	1	0

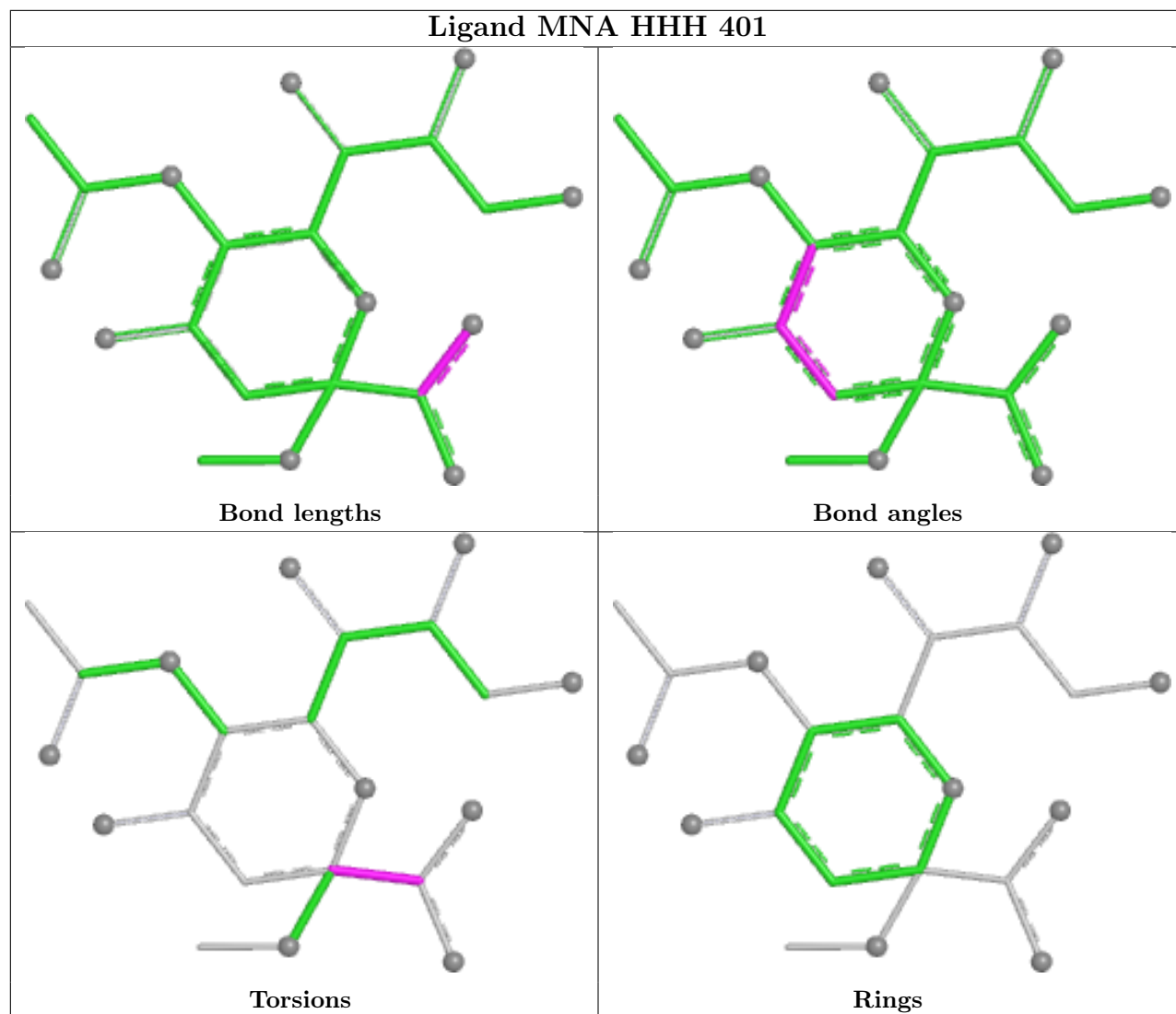
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

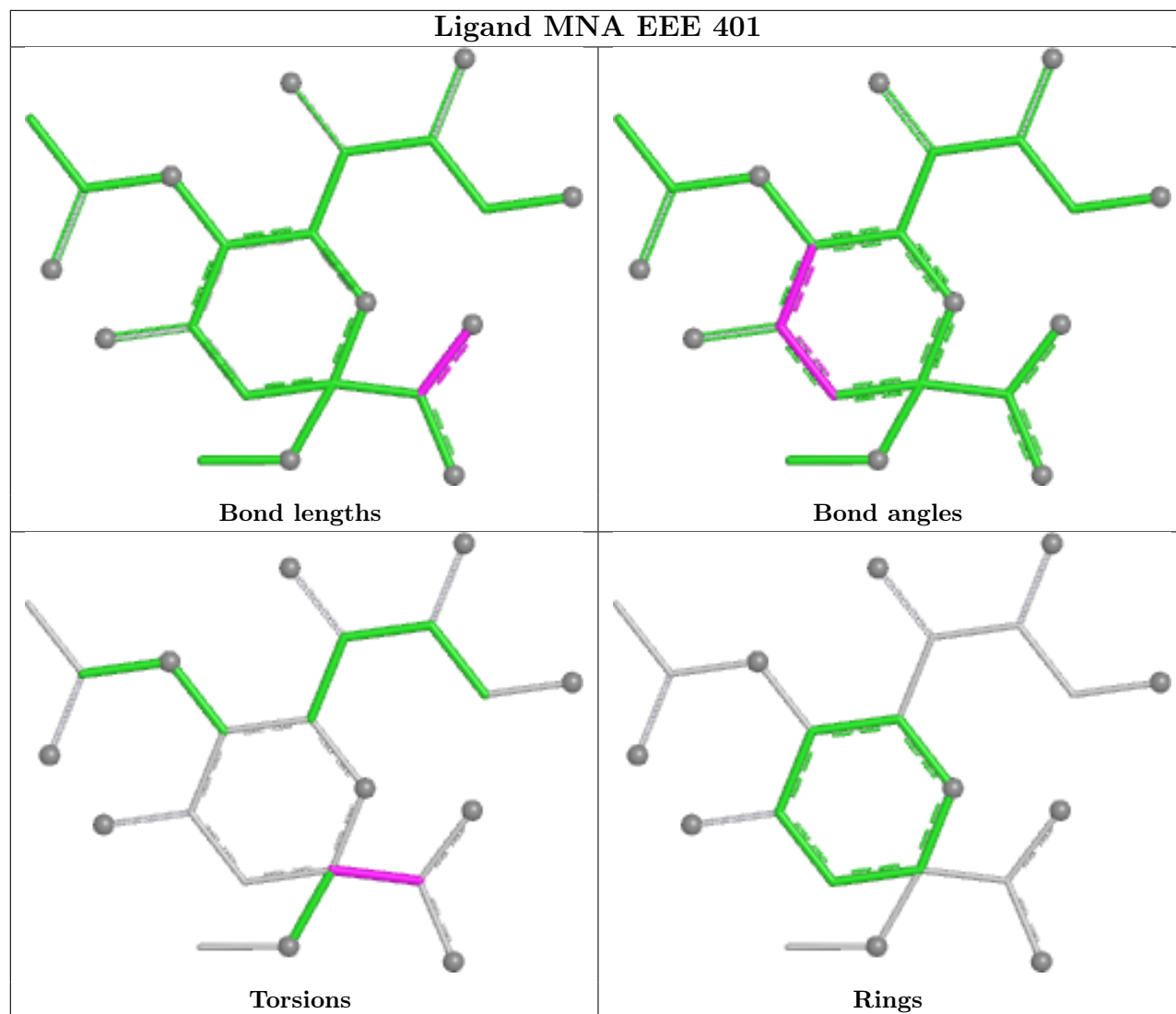


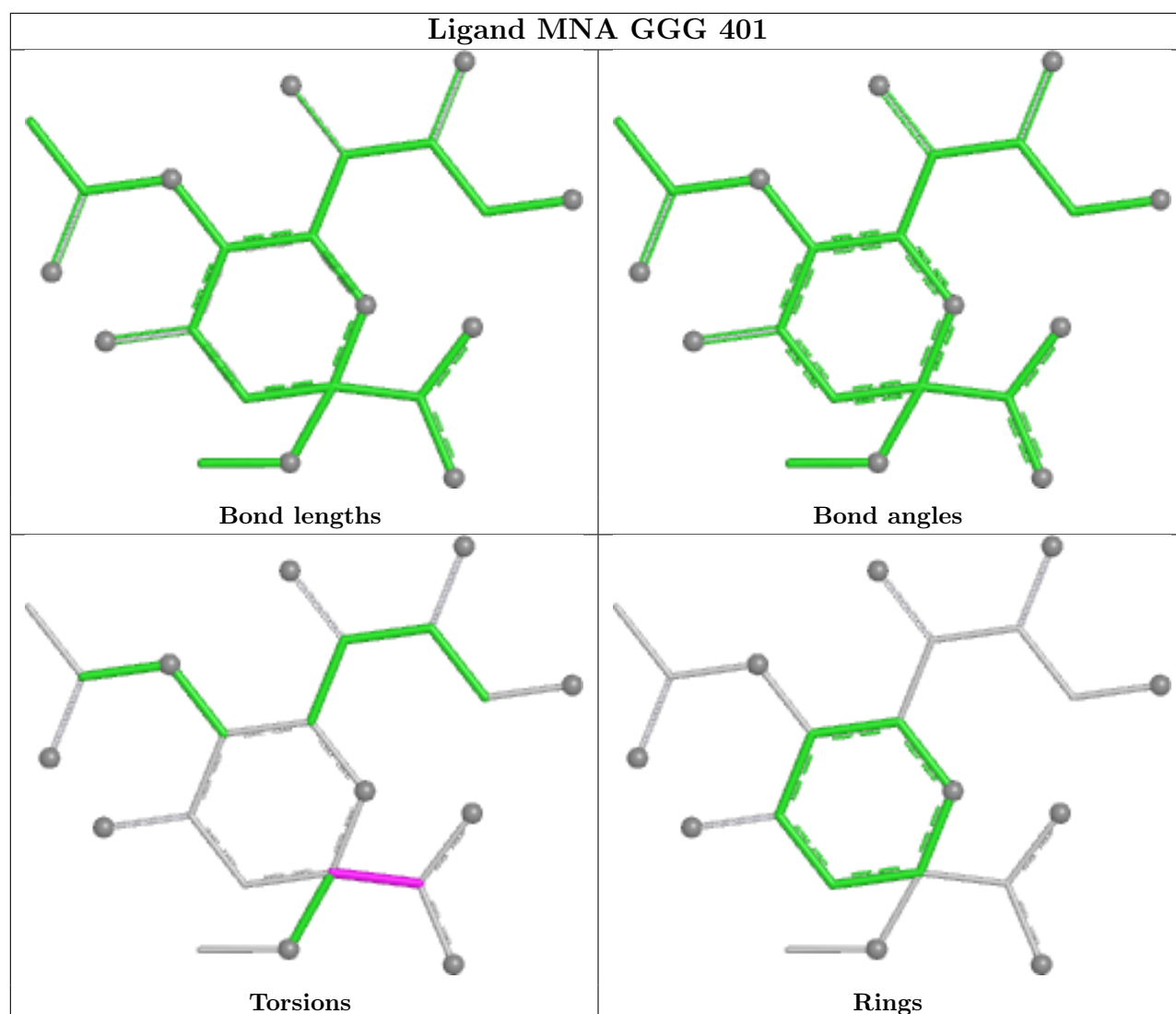


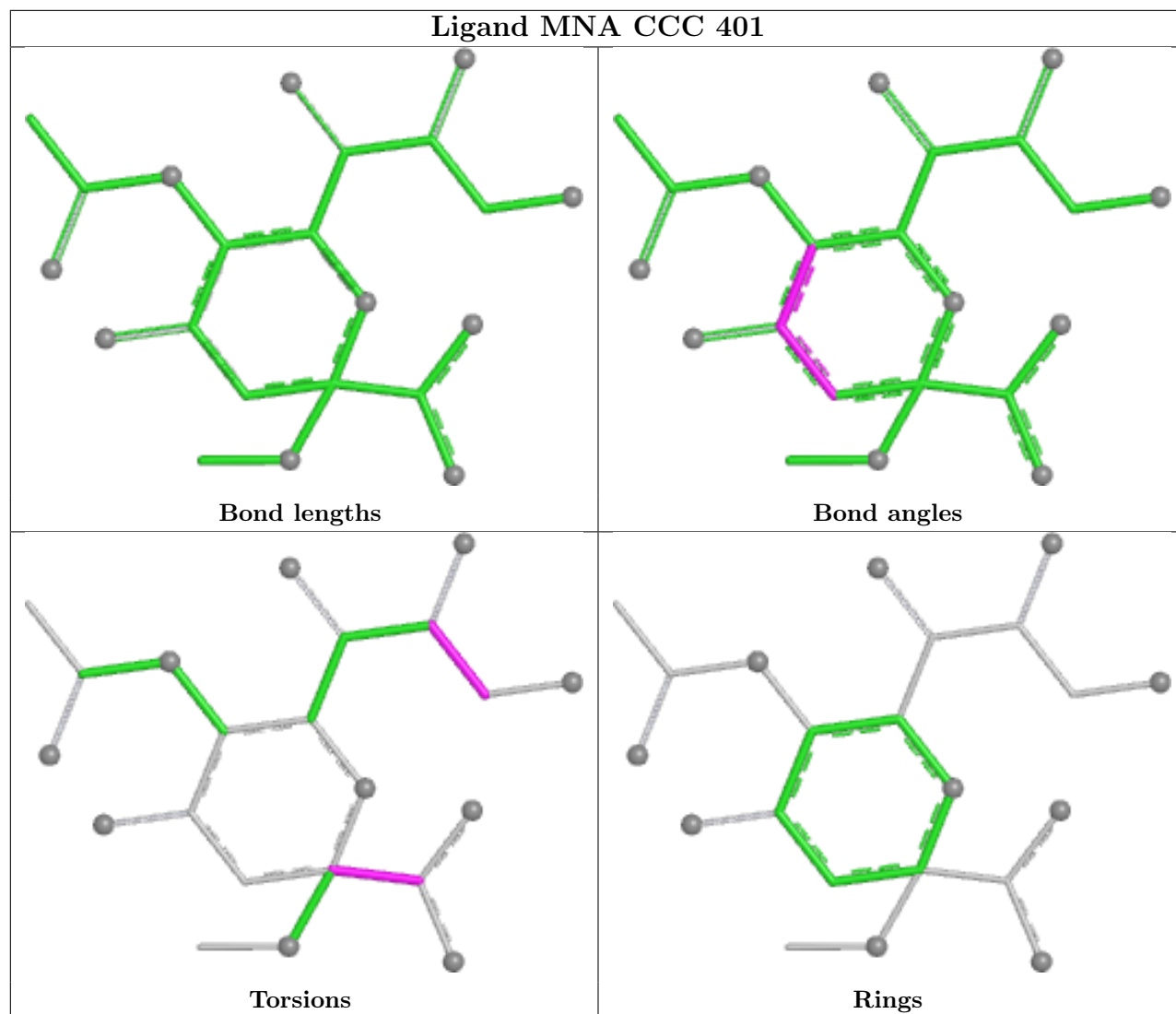




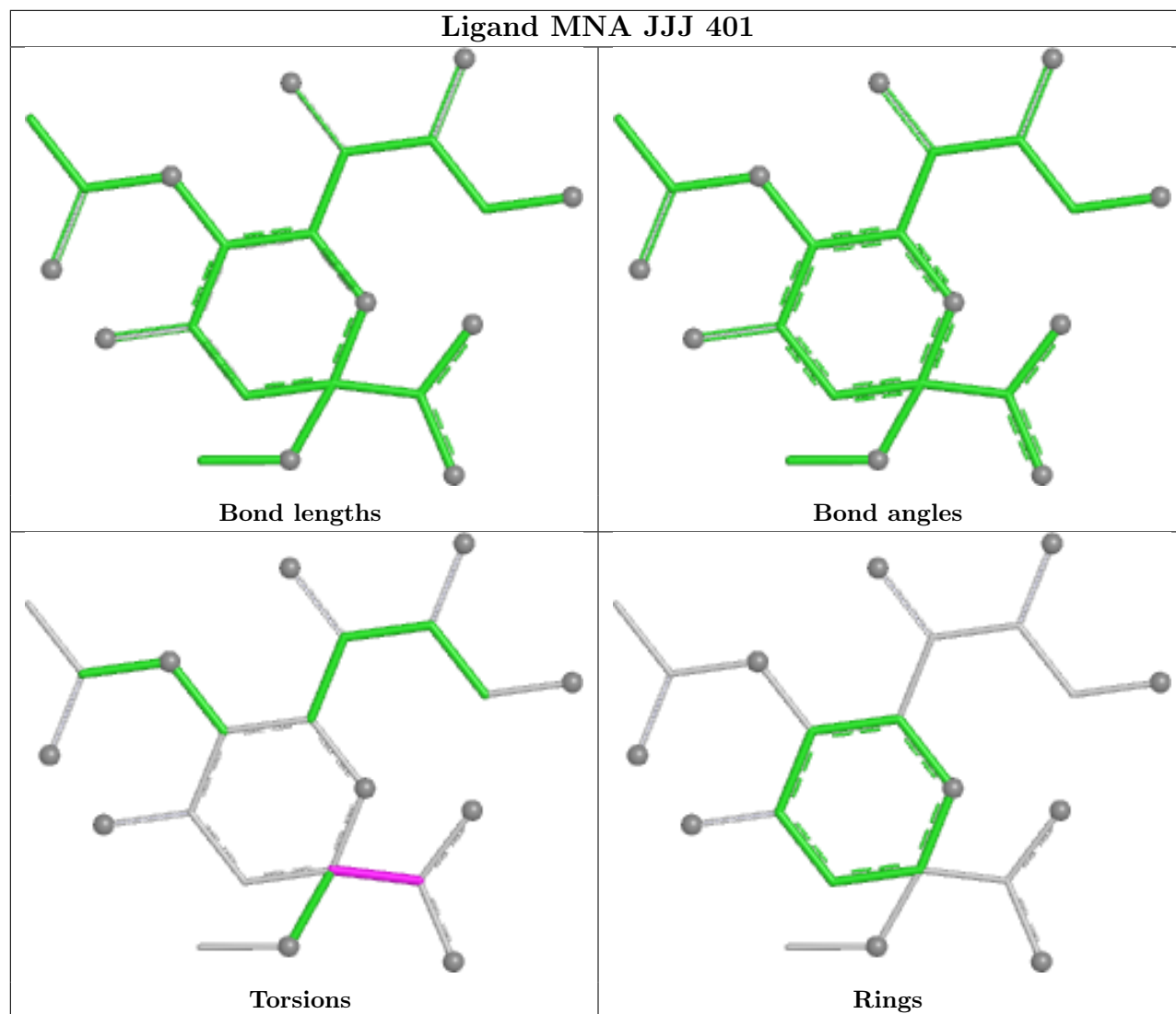


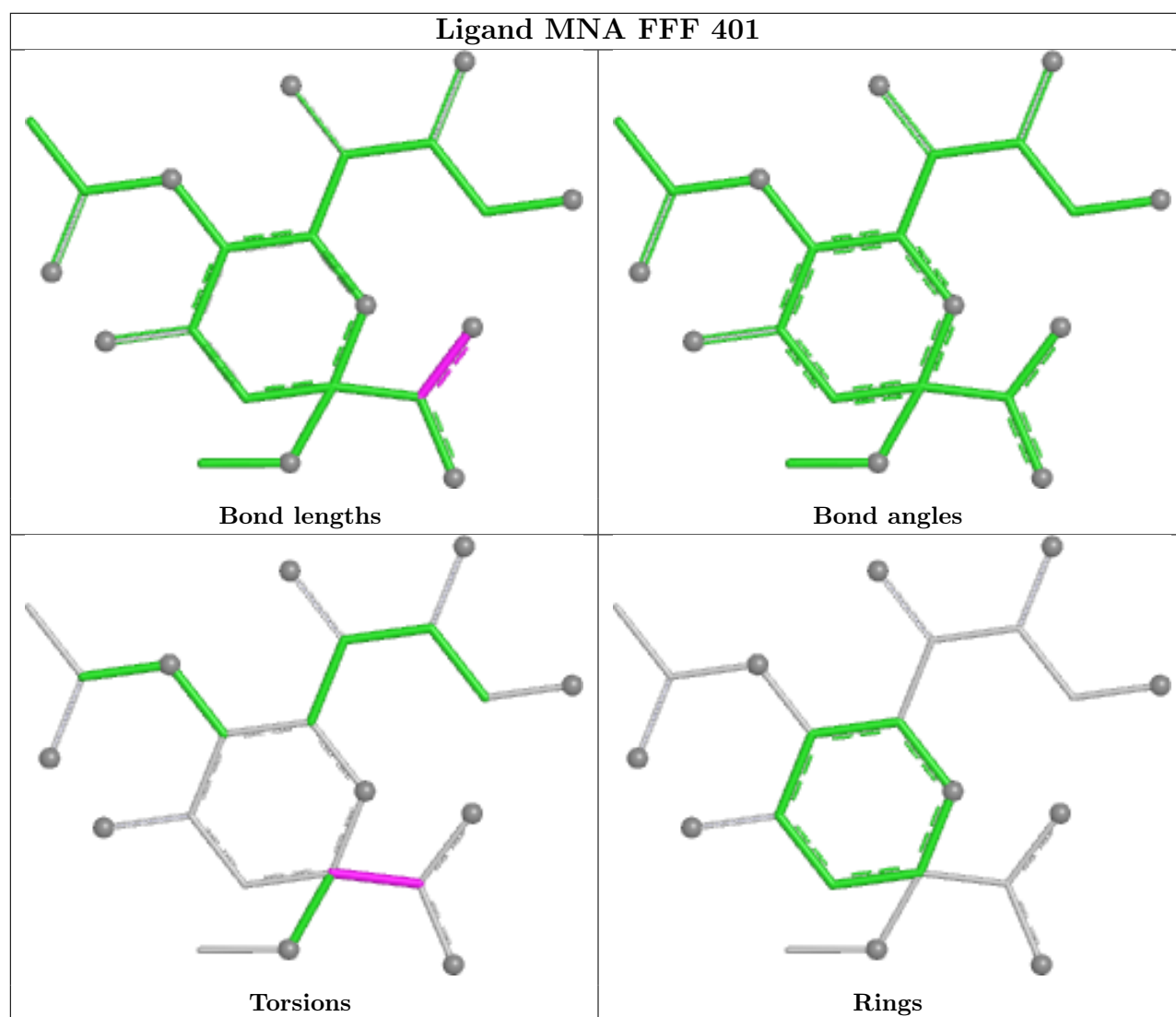






Ligand MNA JJJ 401





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	265/287 (92%)	-0.24	1 (0%) 88 91	8, 18, 26, 44	1 (0%)
1	BBB	265/287 (92%)	-0.24	1 (0%) 88 91	8, 18, 31, 45	1 (0%)
1	CCC	267/287 (93%)	-0.33	3 (1%) 78 83	7, 16, 29, 60	1 (0%)
1	DDD	265/287 (92%)	-0.33	2 (0%) 82 86	7, 15, 30, 49	2 (0%)
1	EEE	265/287 (92%)	-0.33	1 (0%) 88 91	7, 16, 28, 41	1 (0%)
1	FFF	265/287 (92%)	-0.28	1 (0%) 88 91	7, 17, 29, 40	1 (0%)
1	GGG	268/287 (93%)	-0.28	3 (1%) 78 83	6, 16, 33, 54	1 (0%)
1	HHH	265/287 (92%)	-0.28	3 (1%) 78 83	6, 15, 33, 53	2 (0%)
1	III	267/287 (93%)	-0.27	8 (2%) 52 59	7, 15, 35, 65	1 (0%)
1	JJJ	268/287 (93%)	-0.31	1 (0%) 88 91	7, 17, 26, 50	1 (0%)
All	All	2660/2870 (92%)	-0.29	24 (0%) 81 85	6, 16, 30, 65	12 (0%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CCC	21	GLY	4.0
1	HHH	90	THR	3.7
1	III	21	GLY	3.6
1	III	88	ASP	3.5
1	GGG	21	GLY	3.4

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
4	EDO	EEE	404	4/4	0.79	0.15	45,46,46,49	0
4	EDO	HHH	402	4/4	0.80	0.16	46,46,48,49	0
2	MNA	EEE	401	22/22	0.82	0.14	24,39,54,56	0
4	EDO	HHH	403	4/4	0.83	0.18	41,42,44,44	0
4	EDO	EEE	405	4/4	0.84	0.14	35,39,40,44	0
3	IMD	DDD	402	5/5	0.88	0.10	22,22,24,25	0
4	EDO	BBB	402	4/4	0.88	0.12	35,35,36,37	0
4	EDO	DDD	404	4/4	0.88	0.12	40,43,44,45	0
4	EDO	EEE	403	4/4	0.88	0.12	34,35,36,36	0
4	EDO	EEE	406	4/4	0.89	0.15	43,44,44,44	0
4	EDO	FFF	402	4/4	0.89	0.13	40,40,41,44	0
4	EDO	AAA	405	4/4	0.89	0.15	42,43,44,45	0
4	EDO	CCC	404	4/4	0.89	0.14	33,37,41,43	0
4	EDO	III	402	4/4	0.89	0.11	25,30,33,33	0
4	EDO	DDD	403	4/4	0.90	0.13	36,40,42,44	0
4	EDO	JJJ	402	4/4	0.90	0.12	35,36,37,40	0
2	MNA	III	401	22/22	0.91	0.09	21,26,32,34	0
4	EDO	GGG	404	4/4	0.91	0.14	43,44,45,46	0
3	IMD	AAA	402	5/5	0.91	0.07	20,21,22,23	0
4	EDO	AAA	404	4/4	0.92	0.09	33,34,35,35	0
2	MNA	BBB	401	22/22	0.92	0.08	21,24,31,32	0
4	EDO	FFF	403	4/4	0.92	0.12	38,39,39,42	0
3	IMD	EEE	402	5/5	0.92	0.07	24,24,25,26	0
4	EDO	JJJ	403	4/4	0.92	0.13	42,42,43,43	0
2	MNA	FFF	401	22/22	0.93	0.08	17,22,28,31	0
2	MNA	GGG	401	22/22	0.93	0.08	16,22,30,32	0
2	MNA	CCC	401	22/22	0.93	0.08	16,22,26,31	0
2	MNA	DDD	401	22/22	0.94	0.07	15,20,26,31	0
4	EDO	EEE	407	4/4	0.94	0.11	31,32,33,34	0
2	MNA	JJJ	401	22/22	0.94	0.07	16,23,32,36	0
3	IMD	GGG	402	5/5	0.94	0.06	20,20,21,21	0
2	MNA	AAA	401	22/22	0.94	0.07	18,23,30,35	0

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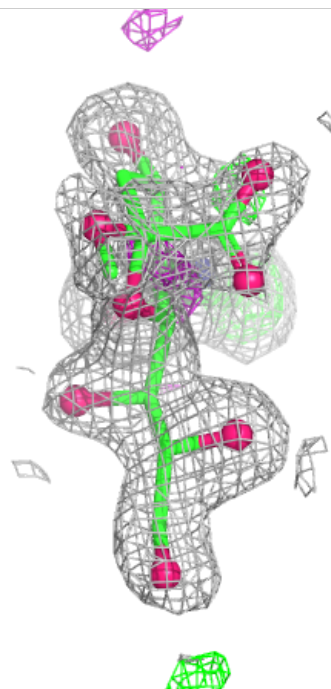
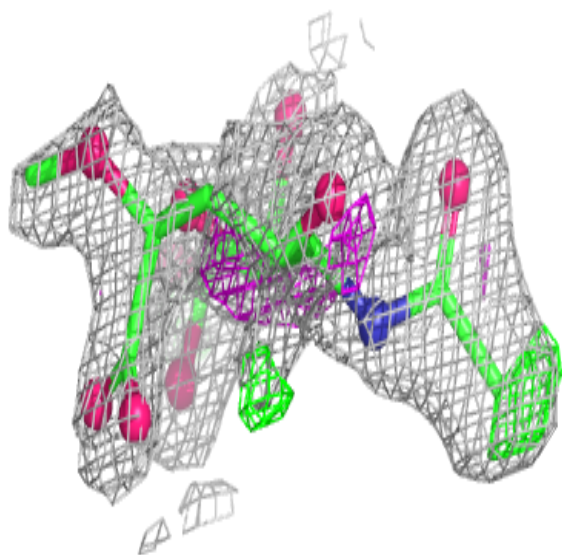
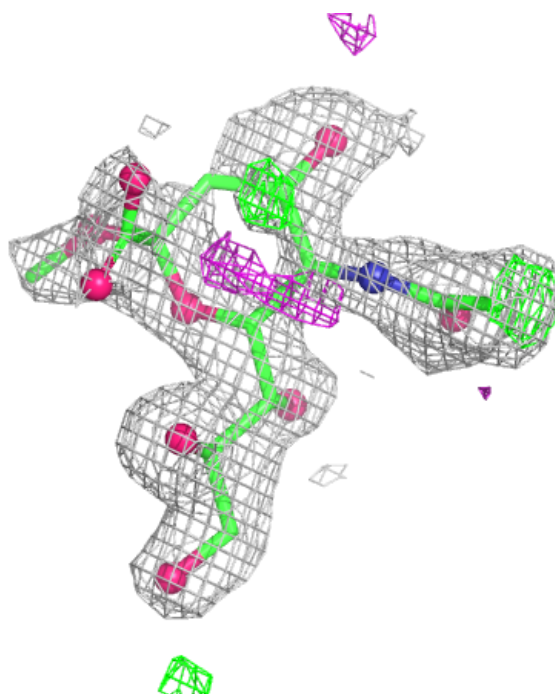
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	IMD	CCC	402	5/5	0.95	0.06	20,21,22,22	0
4	EDO	CCC	403	4/4	0.95	0.08	22,27,28,30	0
2	MNA	HHH	401	22/22	0.95	0.07	16,20,26,29	0
4	EDO	AAA	403	4/4	0.96	0.06	25,28,30,30	0
4	EDO	GGG	403	4/4	0.97	0.07	29,32,33,36	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.

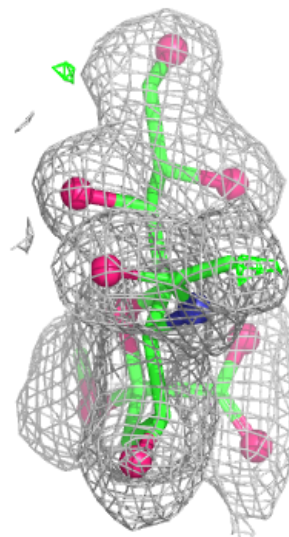
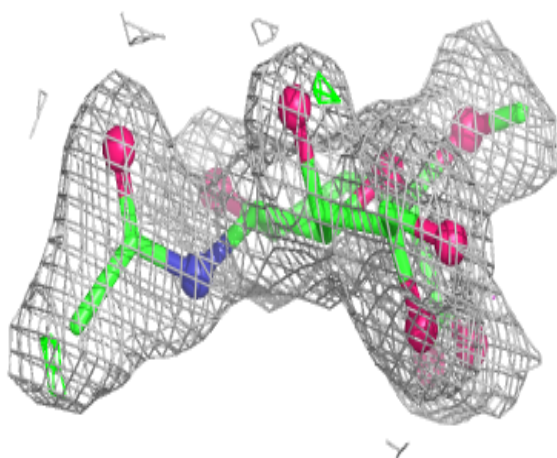
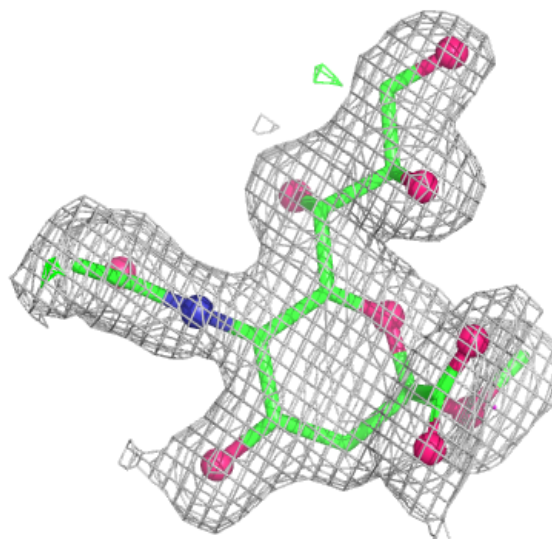
Electron density around MNA EEE 401:

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



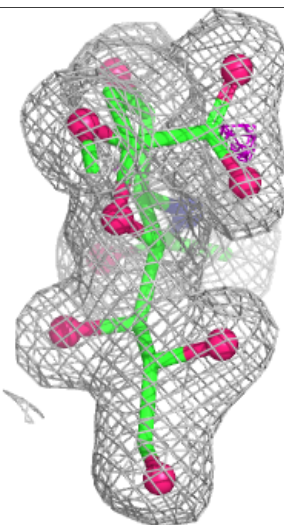
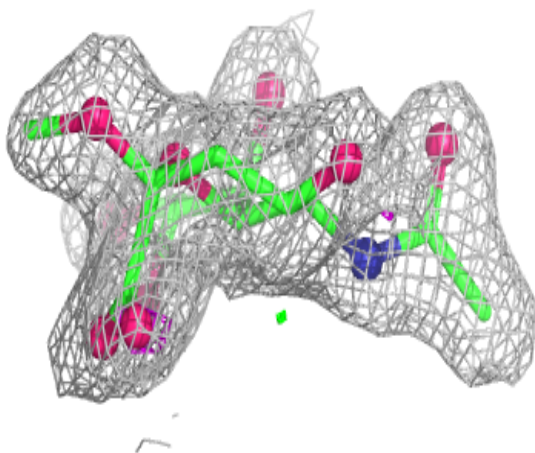
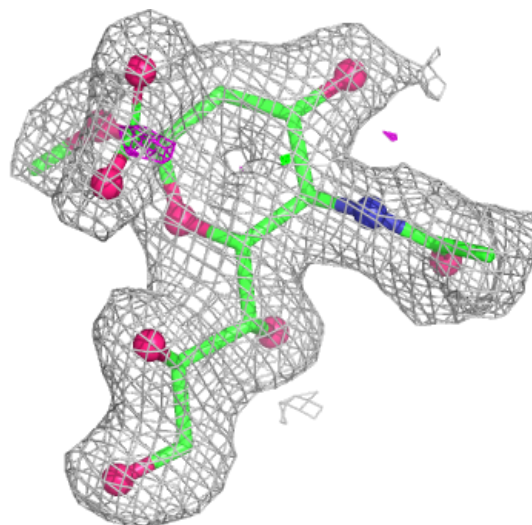
Electron density around MNA III 401:

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and green (positive)



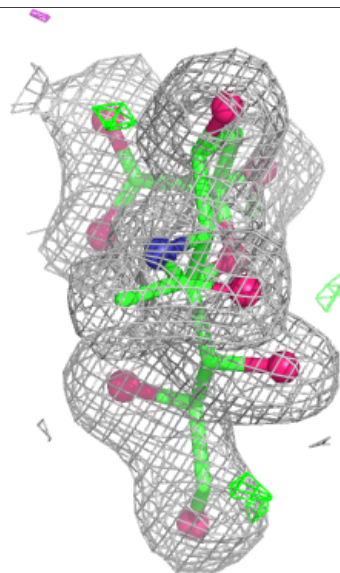
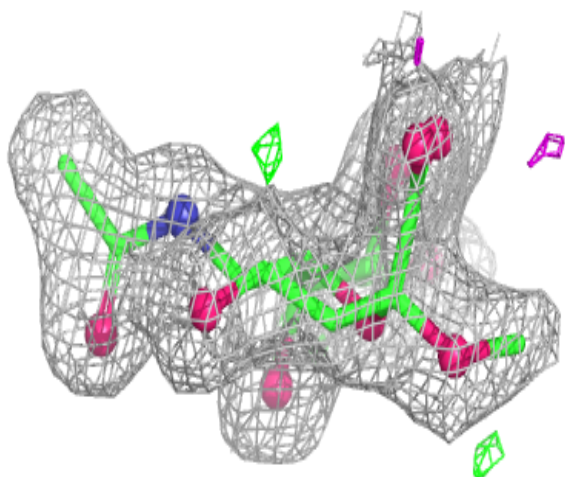
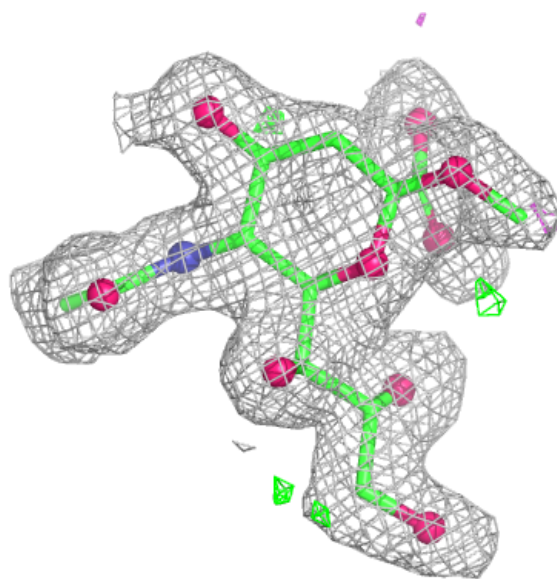
Electron density around MNA BBB 401:

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and green (positive)



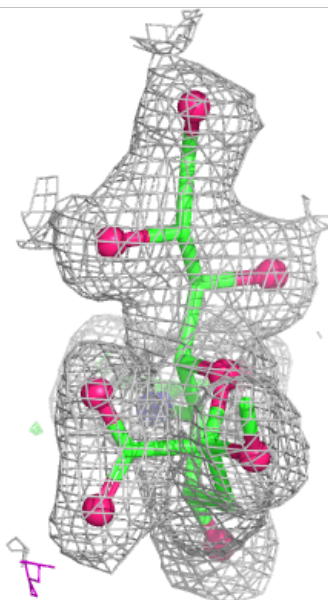
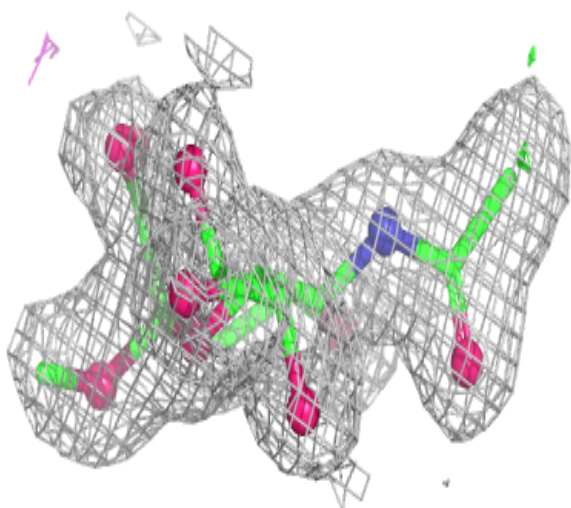
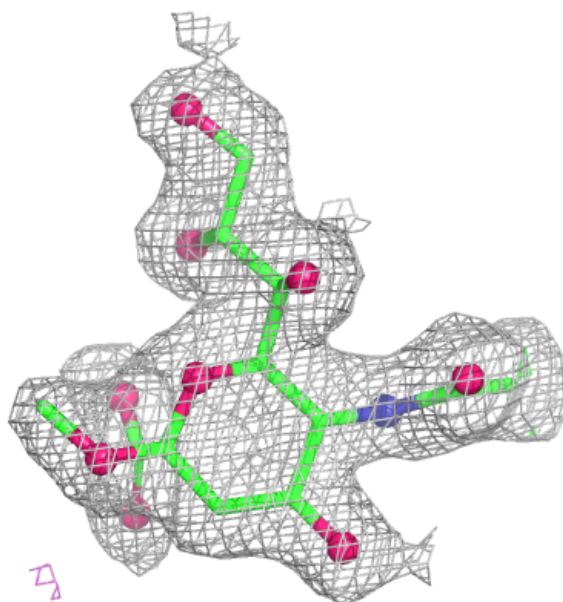
Electron density around MNA FFF 401:

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



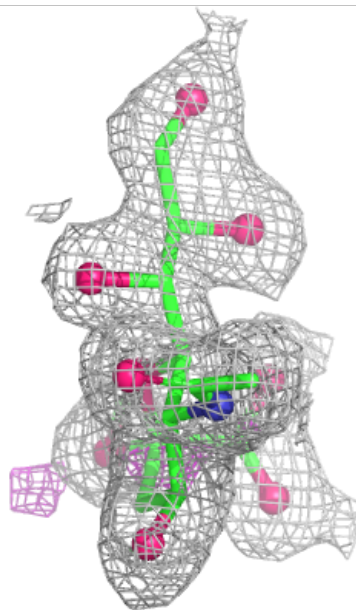
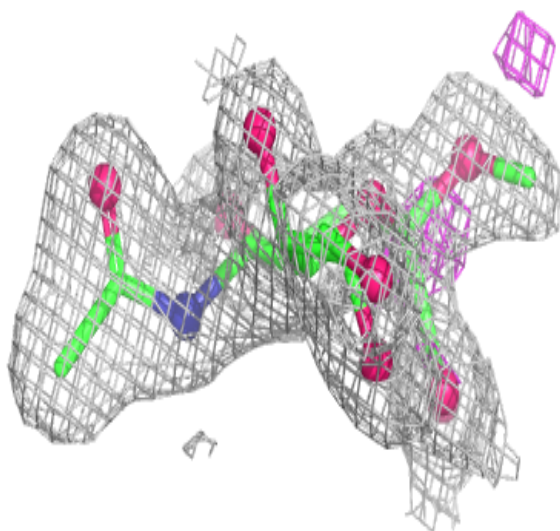
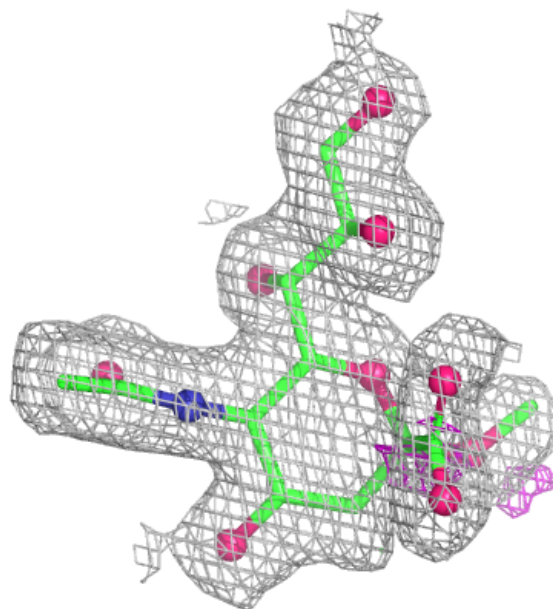
Electron density around MNA GGG 401:

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



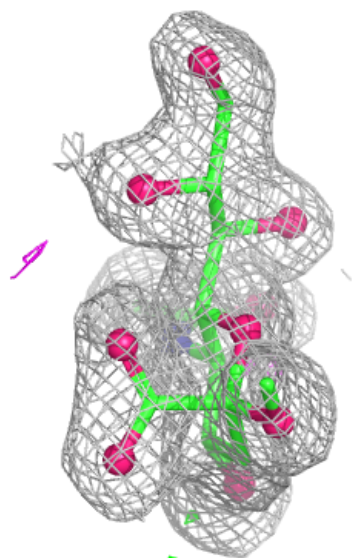
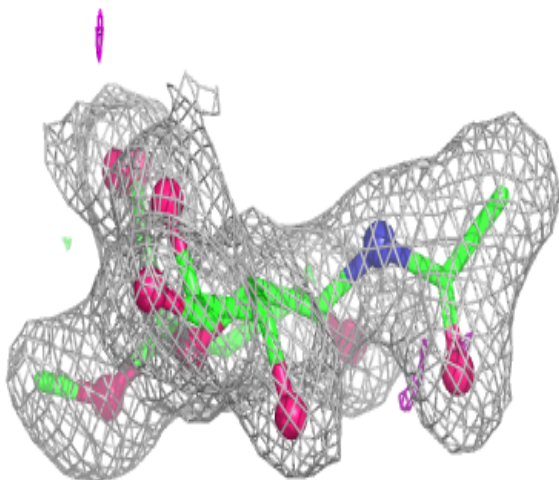
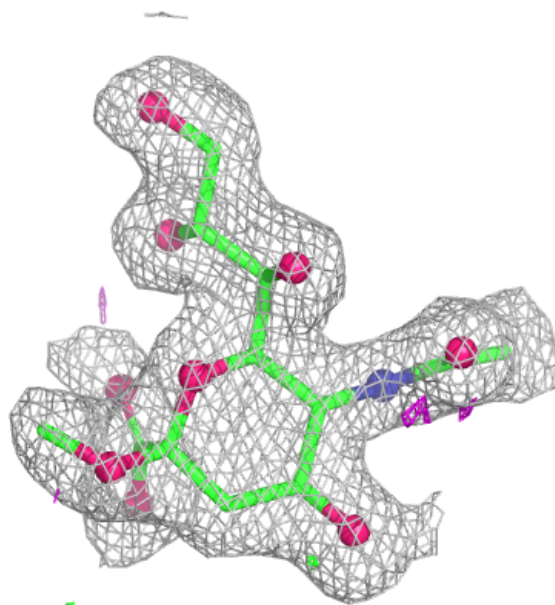
Electron density around MNA CCC 401:

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



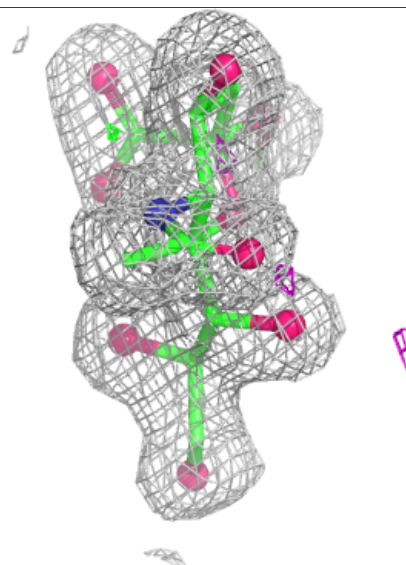
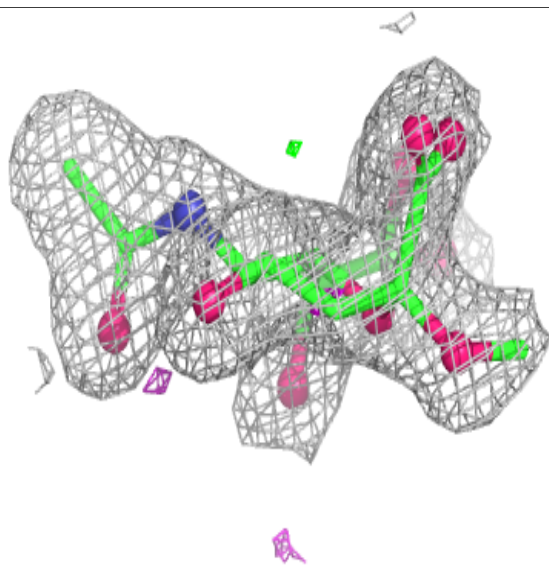
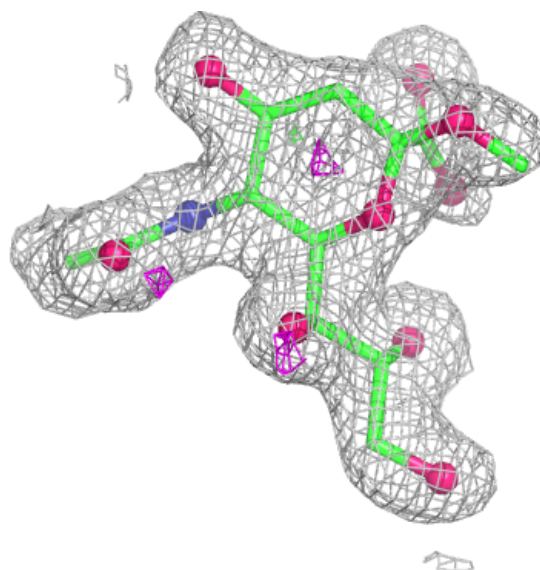
Electron density around MNA DDD 401:

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



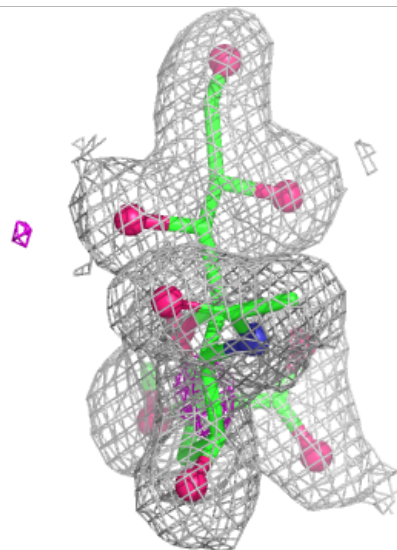
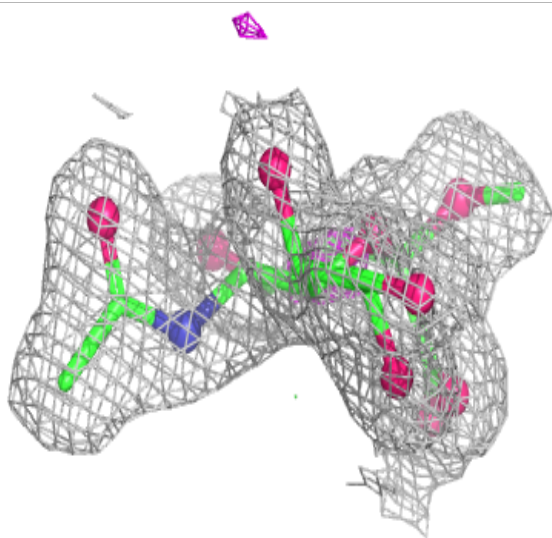
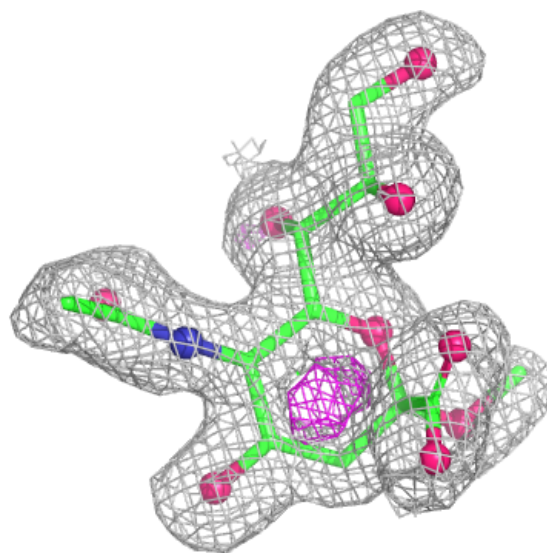
Electron density around MNA JJJ 401:

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and green (positive)



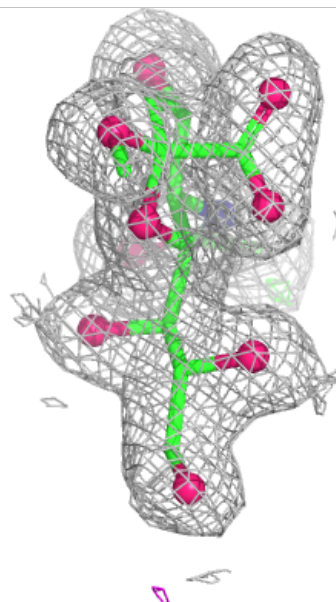
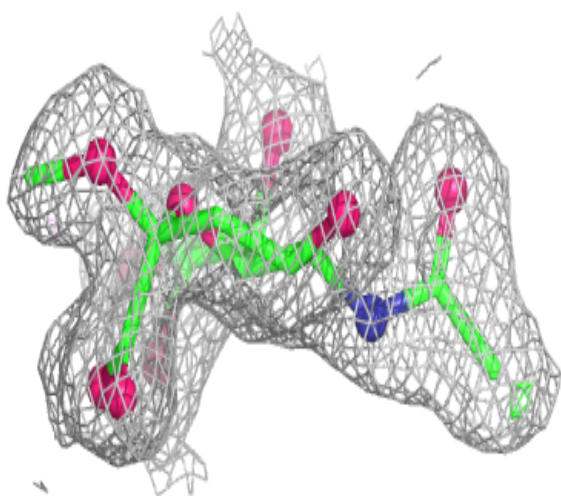
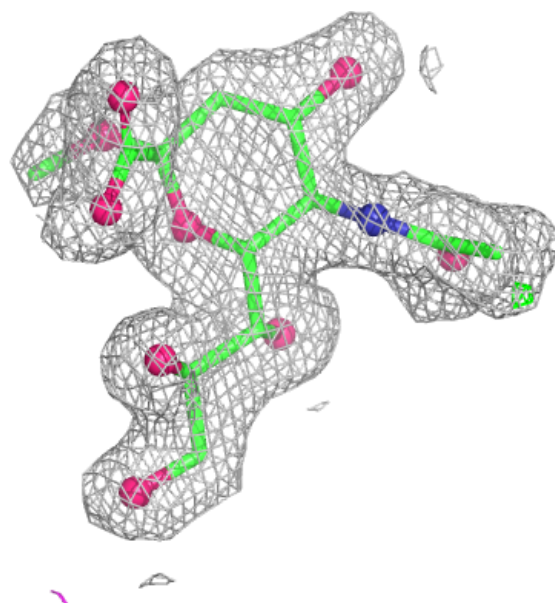
Electron density around MNA AAA 401:

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



Electron density around MNA HHH 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 ⓘ

There are no such residues in this entry.