



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:15 PM UTC

PDB ID : 3EBL / pdb_00003ebl
Title : Crystal Structure of Rice GID1 complexed with GA4
Authors : Shimada, A.; Nakatsu, T.; Ueguchi-Tanaka, M.; Kato, H.; Matsuoka, M.
Deposited on : 2008-08-28
Resolution : 1.90 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)
Xtrriage (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

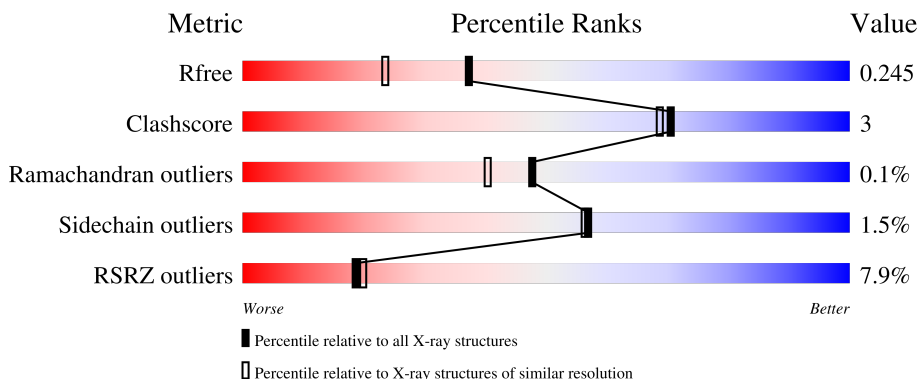
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



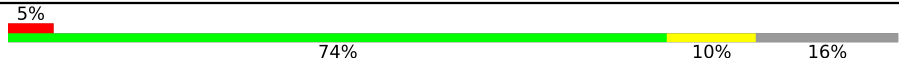
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	A	365	
1	B	365	
1	C	365	
1	D	365	
1	E	365	

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Mol	Chain	Length	Quality of chain
1	F	365	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '5%', a large green segment labeled '74%', a yellow segment labeled '10%', and a grey segment at the end labeled '16%'.</p>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16004 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 Gibberellin receptor GID1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	2538	1608	453	467	10	0	5	0
1	B	318	2483	1575	442	456	10	0	2	0
1	C	301	2360	1503	415	432	10	0	2	0
1	D	315	2450	1561	429	450	10	0	0	0
1	E	315	2392	1527	415	440	10	0	2	0
1	F	305	2374	1516	414	435	9	0	2	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	355	GLY	-	expression tag	UNP Q6L545
A	356	SER	-	expression tag	UNP Q6L545
A	357	HIS	-	expression tag	UNP Q6L545
A	358	HIS	-	expression tag	UNP Q6L545
A	359	HIS	-	expression tag	UNP Q6L545
A	360	HIS	-	expression tag	UNP Q6L545
A	361	HIS	-	expression tag	UNP Q6L545
A	362	HIS	-	expression tag	UNP Q6L545
A	363	HIS	-	expression tag	UNP Q6L545
A	364	HIS	-	expression tag	UNP Q6L545
A	365	HIS	-	expression tag	UNP Q6L545
A	366	HIS	-	expression tag	UNP Q6L545
B	355	GLY	-	expression tag	UNP Q6L545
B	356	SER	-	expression tag	UNP Q6L545
B	357	HIS	-	expression tag	UNP Q6L545
B	358	HIS	-	expression tag	UNP Q6L545
B	359	HIS	-	expression tag	UNP Q6L545

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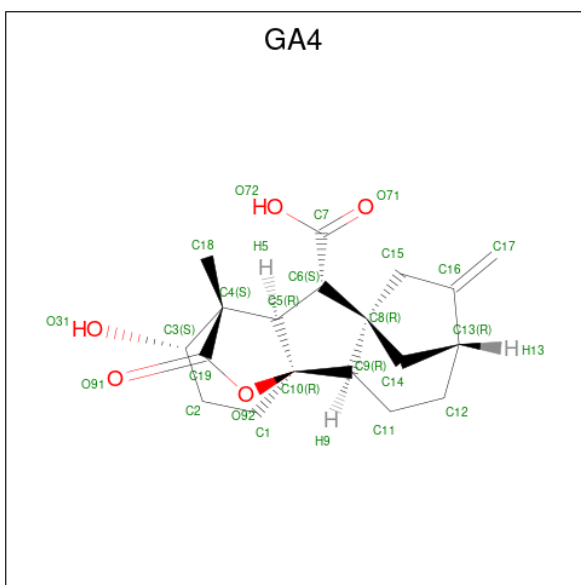
Chain	Residue	Modelled	Actual	Comment	Reference
B	360	HIS	-	expression tag	UNP Q6L545
B	361	HIS	-	expression tag	UNP Q6L545
B	362	HIS	-	expression tag	UNP Q6L545
B	363	HIS	-	expression tag	UNP Q6L545
B	364	HIS	-	expression tag	UNP Q6L545
B	365	HIS	-	expression tag	UNP Q6L545
B	366	HIS	-	expression tag	UNP Q6L545
C	355	GLY	-	expression tag	UNP Q6L545
C	356	SER	-	expression tag	UNP Q6L545
C	357	HIS	-	expression tag	UNP Q6L545
C	358	HIS	-	expression tag	UNP Q6L545
C	359	HIS	-	expression tag	UNP Q6L545
C	360	HIS	-	expression tag	UNP Q6L545
C	361	HIS	-	expression tag	UNP Q6L545
C	362	HIS	-	expression tag	UNP Q6L545
C	363	HIS	-	expression tag	UNP Q6L545
C	364	HIS	-	expression tag	UNP Q6L545
C	365	HIS	-	expression tag	UNP Q6L545
C	366	HIS	-	expression tag	UNP Q6L545
D	355	GLY	-	expression tag	UNP Q6L545
D	356	SER	-	expression tag	UNP Q6L545
D	357	HIS	-	expression tag	UNP Q6L545
D	358	HIS	-	expression tag	UNP Q6L545
D	359	HIS	-	expression tag	UNP Q6L545
D	360	HIS	-	expression tag	UNP Q6L545
D	361	HIS	-	expression tag	UNP Q6L545
D	362	HIS	-	expression tag	UNP Q6L545
D	363	HIS	-	expression tag	UNP Q6L545
D	364	HIS	-	expression tag	UNP Q6L545
D	365	HIS	-	expression tag	UNP Q6L545
D	366	HIS	-	expression tag	UNP Q6L545
E	355	GLY	-	expression tag	UNP Q6L545
E	356	SER	-	expression tag	UNP Q6L545
E	357	HIS	-	expression tag	UNP Q6L545
E	358	HIS	-	expression tag	UNP Q6L545
E	359	HIS	-	expression tag	UNP Q6L545
E	360	HIS	-	expression tag	UNP Q6L545
E	361	HIS	-	expression tag	UNP Q6L545
E	362	HIS	-	expression tag	UNP Q6L545
E	363	HIS	-	expression tag	UNP Q6L545
E	364	HIS	-	expression tag	UNP Q6L545
E	365	HIS	-	expression tag	UNP Q6L545

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Chain	Residue	Modelled	Actual	Comment	Reference
E	366	HIS	-	expression tag	UNP Q6L545
F	355	GLY	-	expression tag	UNP Q6L545
F	356	SER	-	expression tag	UNP Q6L545
F	357	HIS	-	expression tag	UNP Q6L545
F	358	HIS	-	expression tag	UNP Q6L545
F	359	HIS	-	expression tag	UNP Q6L545
F	360	HIS	-	expression tag	UNP Q6L545
F	361	HIS	-	expression tag	UNP Q6L545
F	362	HIS	-	expression tag	UNP Q6L545
F	363	HIS	-	expression tag	UNP Q6L545
F	364	HIS	-	expression tag	UNP Q6L545
F	365	HIS	-	expression tag	UNP Q6L545
F	366	HIS	-	expression tag	UNP Q6L545

- Molecule 2 is GIBBERELLIN A4 (CCD ID: GA4) (formula: C₁₉H₂₄O₅).



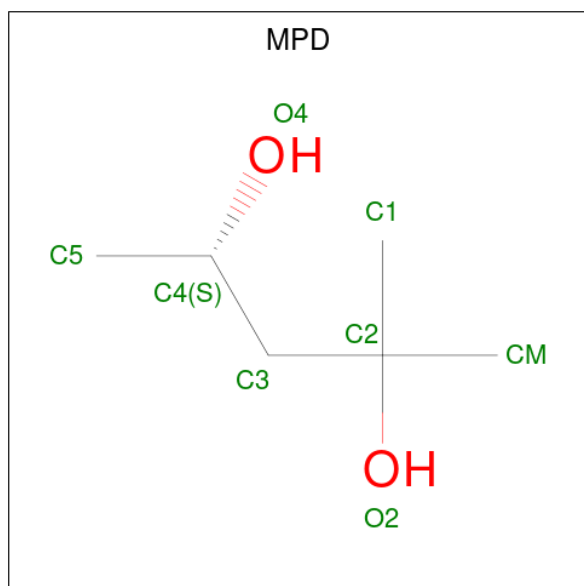
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			24	19	5		
2	B	1	Total	C	O	0	0
			24	19	5		
2	C	1	Total	C	O	0	0
			24	19	5		
2	D	1	Total	C	O	0	0
			24	19	5		
2	E	1	Total	C	O	0	0
			24	19	5		

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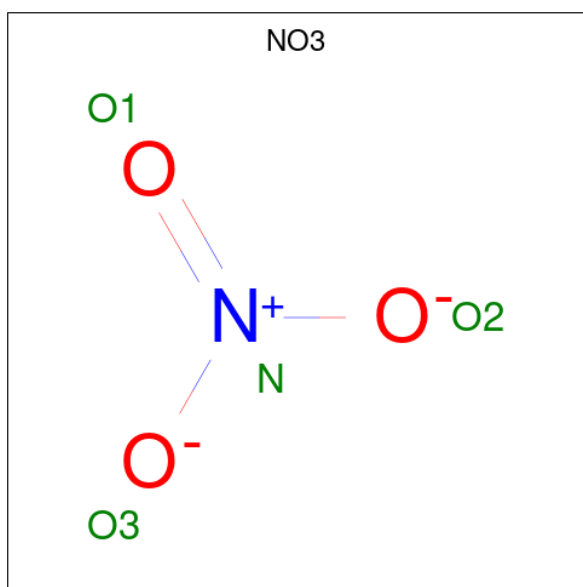
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	F	1	24	19	5	0	0

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	8	6	2	0	0
3	B	1	8	6	2	0	0
3	C	1	8	6	2	0	0
3	D	1	8	6	2	0	0
3	E	1	8	6	2	0	0
3	F	1	8	6	2	0	0

- Molecule 4 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



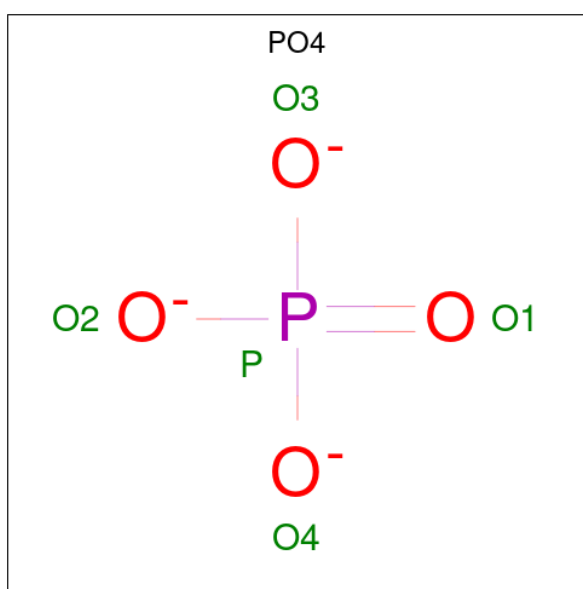
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		
4	C	1	Total	N	O	0	0
			4	1	3		
4	C	1	Total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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total N O 4 1 3	0	0
4	F	1	Total N O 4 1 3	0	0
4	F	1	Total N O 4 1 3	0	0
4	F	1	Total N O 4 1 3	0	0

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O P 5 4 1	0	0
5	E	1	Total O P 5 4 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	249	Total O 249 249	0	0
6	B	204	Total O 204 204	0	0
6	C	183	Total O 183 183	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	204	Total 204	O 204	0	0
6	E	124	Total 124	O 124	0	0
6	F	169	Total 169	O 169	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.76Å 133.90Å 118.89Å 90.00° 104.95° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 20.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.90) 98.6 (20.00-1.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.89Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.244 0.202 , 0.245	Depositor DCC
R_{free} test set	9765 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	26.8	Xtrriage
Anisotropy	0.345	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16004	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: PO4, GA4, MPD, NO3

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.88	1/2630 (0.0%)	0.92	0/3573
1	B	0.85	0/2554	0.90	0/3471
1	C	0.82	1/2430 (0.0%)	0.94	4/3301 (0.1%)
1	D	0.84	0/2514	0.91	2/3419 (0.1%)
1	E	0.73	0/2463	0.90	0/3359
1	F	0.78	0/2445	0.88	1/3324 (0.0%)
All	All	0.82	2/15036 (0.0%)	0.91	7/20447 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	153	ASN	CA-C	-5.28	1.47	1.53
1	A	24	ILE	CA-CB	5.22	1.61	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	192	VAL	N-CA-C	7.36	118.89	108.36
1	F	120	HIS	N-CA-C	5.70	118.10	110.35
1	D	144	LEU	CB-CA-C	-5.34	101.77	110.85
1	C	274	GLY	CA-C-N	5.33	126.50	119.84
1	C	274	GLY	C-N-CA	5.33	126.50	119.84

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	A	2538	0	2417	16	0
1	B	2483	0	2362	11	0
1	C	2360	0	2243	19	0
1	D	2450	0	2313	14	0
1	E	2392	0	2215	20	0
1	F	2374	0	2233	17	0
2	A	24	0	23	0	0
2	B	24	0	23	0	0
2	C	24	0	23	0	0
2	D	24	0	23	0	0
2	E	24	0	23	0	0
2	F	24	0	23	0	0
3	A	8	0	14	1	0
3	B	8	0	14	1	0
3	C	8	0	14	1	0
3	D	8	0	14	1	0
3	E	8	0	14	1	0
3	F	8	0	14	1	0
4	A	16	0	0	1	0
4	B	12	0	0	0	0
4	C	16	0	0	2	0
4	D	12	0	0	0	0
4	E	4	0	0	0	0
4	F	12	0	0	1	0
5	B	5	0	0	0	0
5	E	5	0	0	0	0
6	A	249	0	0	2	0
6	B	204	0	0	0	0
6	C	183	0	0	3	0
6	D	204	0	0	0	0
6	E	124	0	0	0	0
6	F	169	0	0	0	0
All	All	16004	0	14005	97	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 3.

The worst 5 of 97 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:E:144:LEU:CD1	1:E:345:SER:HB2	2.15	0.77
3:E:501:MPD:H13	3:F:501:MPD:H13	1.67	0.77
1:A:26:ASN:HD22	1:B:26:ASN:HD22	1.35	0.74
1:C:177:MET:HE2	1:C:216:VAL:CG1	2.21	0.70
1:A:231:THR:HG22	4:A:602:NO3:O3	1.92	0.70

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	A	324/365 (89%)	315 (97%)	9 (3%)	0	100	100
1	B	314/365 (86%)	300 (96%)	14 (4%)	0	100	100
1	C	297/365 (81%)	287 (97%)	9 (3%)	1 (0%)	36	29
1	D	311/365 (85%)	301 (97%)	10 (3%)	0	100	100
1	E	311/365 (85%)	297 (96%)	14 (4%)	0	100	100
1	F	301/365 (82%)	294 (98%)	6 (2%)	1 (0%)	36	29
All	All	1858/2190 (85%)	1794 (97%)	62 (3%)	2 (0%)	48	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	286	ALA
1	F	73	SER

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	A	265/302 (88%)	261 (98%)	4 (2%)	57	56
1	B	256/302 (85%)	253 (99%)	3 (1%)	63	63
1	C	245/302 (81%)	241 (98%)	4 (2%)	55	54
1	D	248/302 (82%)	244 (98%)	4 (2%)	55	54
1	E	237/302 (78%)	234 (99%)	3 (1%)	61	61
1	F	239/302 (79%)	234 (98%)	5 (2%)	47	44
All	All	1490/1812 (82%)	1467 (98%)	23 (2%)	57	56

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	276	ASN
1	E	290	ILE
1	E	261	GLU
1	F	69	ILE
1	B	262	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	221	ASN
1	F	179	GLN
1	E	206	HIS
1	F	72	GLN
1	D	221	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 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
3	MPD	A	501	-	7,7,7	0.38	0	9,10,10	0.38	0
4	NO3	B	601	-	1,3,3	3.63	1 (100%)	0,3,3	-	-
2	GA4	C	401	-	28,28,28	1.18	3 (10%)	46,49,49	1.97	10 (21%)
4	NO3	D	601	-	1,3,3	3.38	1 (100%)	0,3,3	-	-
2	GA4	F	401	-	28,28,28	1.36	3 (10%)	46,49,49	1.67	7 (15%)
3	MPD	C	501	-	7,7,7	0.32	0	9,10,10	0.52	0
4	NO3	C	601	-	1,3,3	3.50	1 (100%)	0,3,3	-	-
4	NO3	F	602	-	1,3,3	3.28	1 (100%)	0,3,3	-	-
4	NO3	F	603	-	1,3,3	3.32	1 (100%)	0,3,3	-	-
4	NO3	C	602	-	1,3,3	3.33	1 (100%)	0,3,3	-	-
3	MPD	B	501	-	7,7,7	0.36	0	9,10,10	0.40	0
3	MPD	D	501	-	7,7,7	0.44	0	9,10,10	0.25	0
4	NO3	A	604	-	1,3,3	3.40	1 (100%)	0,3,3	-	-
3	MPD	F	501	-	7,7,7	0.23	0	9,10,10	0.45	0
3	MPD	E	501	-	7,7,7	0.29	0	9,10,10	0.45	0
5	PO4	B	701	-	4,4,4	0.81	0	6,6,6	0.45	0
4	NO3	C	604	-	1,3,3	3.17	1 (100%)	0,3,3	-	-
4	NO3	A	601	-	1,3,3	3.11	1 (100%)	0,3,3	-	-
5	PO4	E	701	-	4,4,4	0.84	0	6,6,6	0.53	0
4	NO3	E	601	-	1,3,3	3.32	1 (100%)	0,3,3	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NO3	B	604	-	1,3,3	3.23	1 (100%)	0,3,3	-	-
4	NO3	D	602	-	1,3,3	3.37	1 (100%)	0,3,3	-	-
4	NO3	C	603	-	1,3,3	3.30	1 (100%)	0,3,3	-	-
2	GA4	B	401	-	28,28,28	1.46	4 (14%)	46,49,49	1.85	9 (19%)
4	NO3	D	603	-	1,3,3	3.33	1 (100%)	0,3,3	-	-
4	NO3	F	601	-	1,3,3	3.31	1 (100%)	0,3,3	-	-
4	NO3	B	602	-	1,3,3	3.23	1 (100%)	0,3,3	-	-
2	GA4	D	401	-	28,28,28	1.36	3 (10%)	46,49,49	1.87	10 (21%)
2	GA4	E	401	-	28,28,28	1.33	3 (10%)	46,49,49	2.18	13 (28%)
2	GA4	A	401	-	28,28,28	1.27	4 (14%)	46,49,49	2.07	13 (28%)
4	NO3	A	602	-	1,3,3	3.51	1 (100%)	0,3,3	-	-
4	NO3	A	603	-	1,3,3	3.45	1 (100%)	0,3,3	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MPD	A	501	-	-	0/5/5/5	-
3	MPD	D	501	-	-	0/5/5/5	-
3	MPD	F	501	-	-	0/5/5/5	-
2	GA4	B	401	-	-	0/4/80/80	-
2	GA4	C	401	-	-	0/4/80/80	-
2	GA4	A	401	-	-	0/4/80/80	-
3	MPD	E	501	-	-	0/5/5/5	-
2	GA4	D	401	-	-	0/4/80/80	-
2	GA4	F	401	-	-	0/4/80/80	-
3	MPD	C	501	-	-	0/5/5/5	-
2	GA4	E	401	-	-	0/4/80/80	-
3	MPD	B	501	-	-	0/5/5/5	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	GA4	O92-C10	-4.82	1.41	1.47
2	F	401	GA4	O92-C19	4.41	1.44	1.36
2	B	401	GA4	O92-C19	4.34	1.44	1.36
2	E	401	GA4	O92-C19	4.24	1.44	1.36
4	B	601	NO3	O1-N	3.63	1.42	1.24

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	GA4	C15-C16-C13	8.15	114.27	107.46
2	B	401	GA4	C15-C16-C13	7.94	114.10	107.46
2	E	401	GA4	C15-C16-C13	7.26	113.53	107.46
2	A	401	GA4	C15-C16-C13	7.13	113.42	107.46
2	D	401	GA4	C15-C16-C13	6.55	112.94	107.46

There are no chirality outliers.

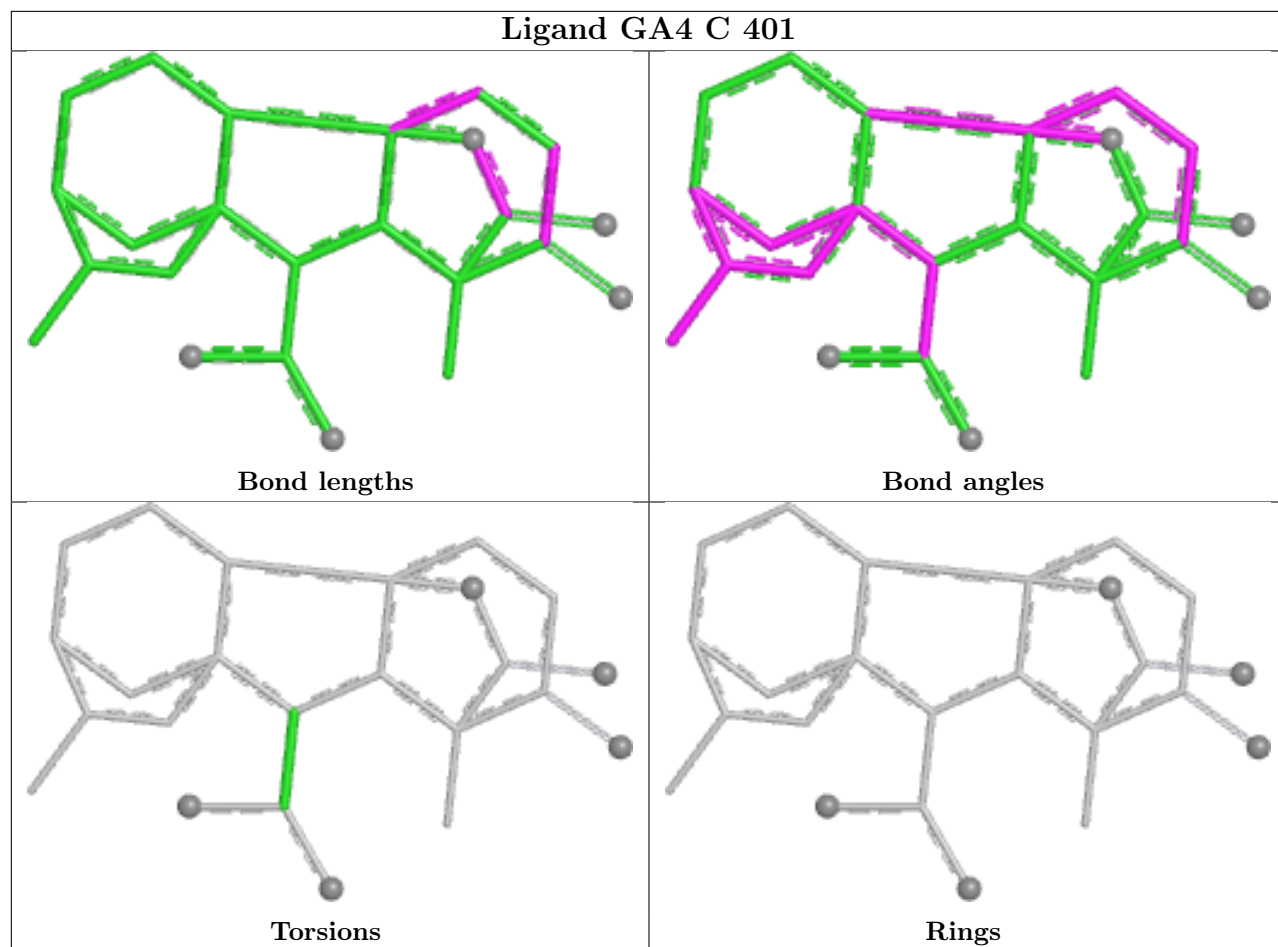
There are no torsion outliers.

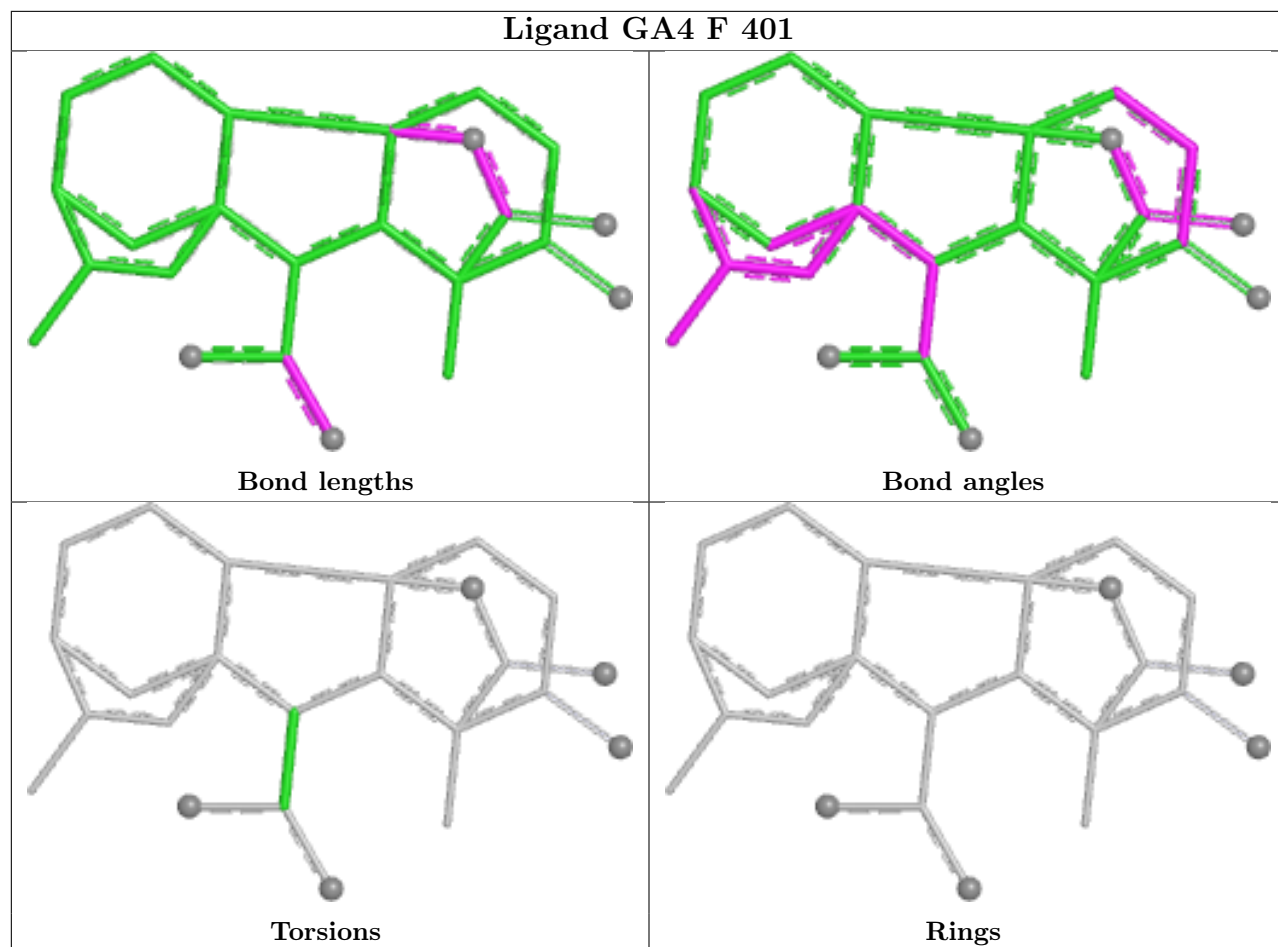
There are no ring outliers.

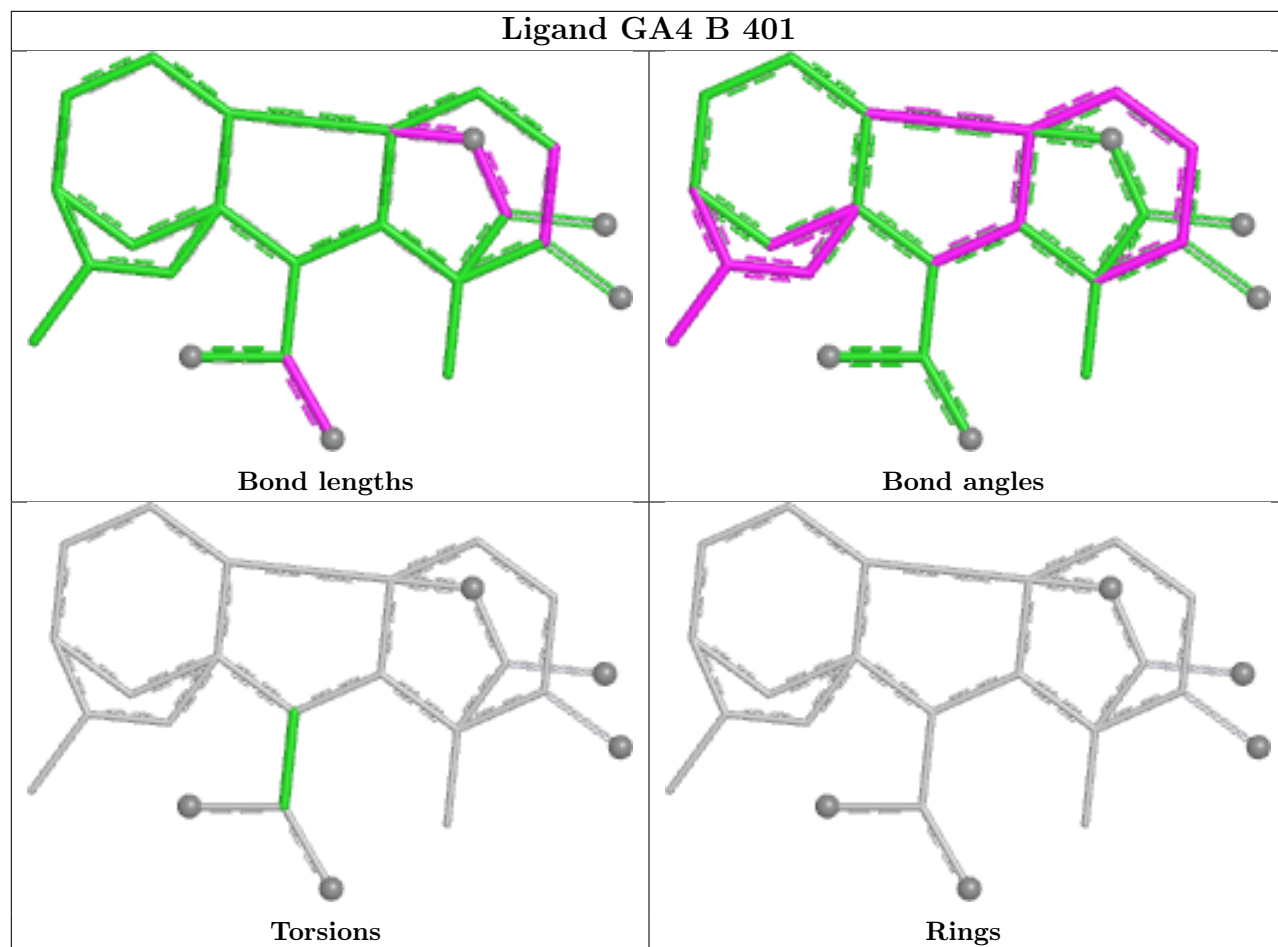
10 monomers are involved in 7 short contacts:

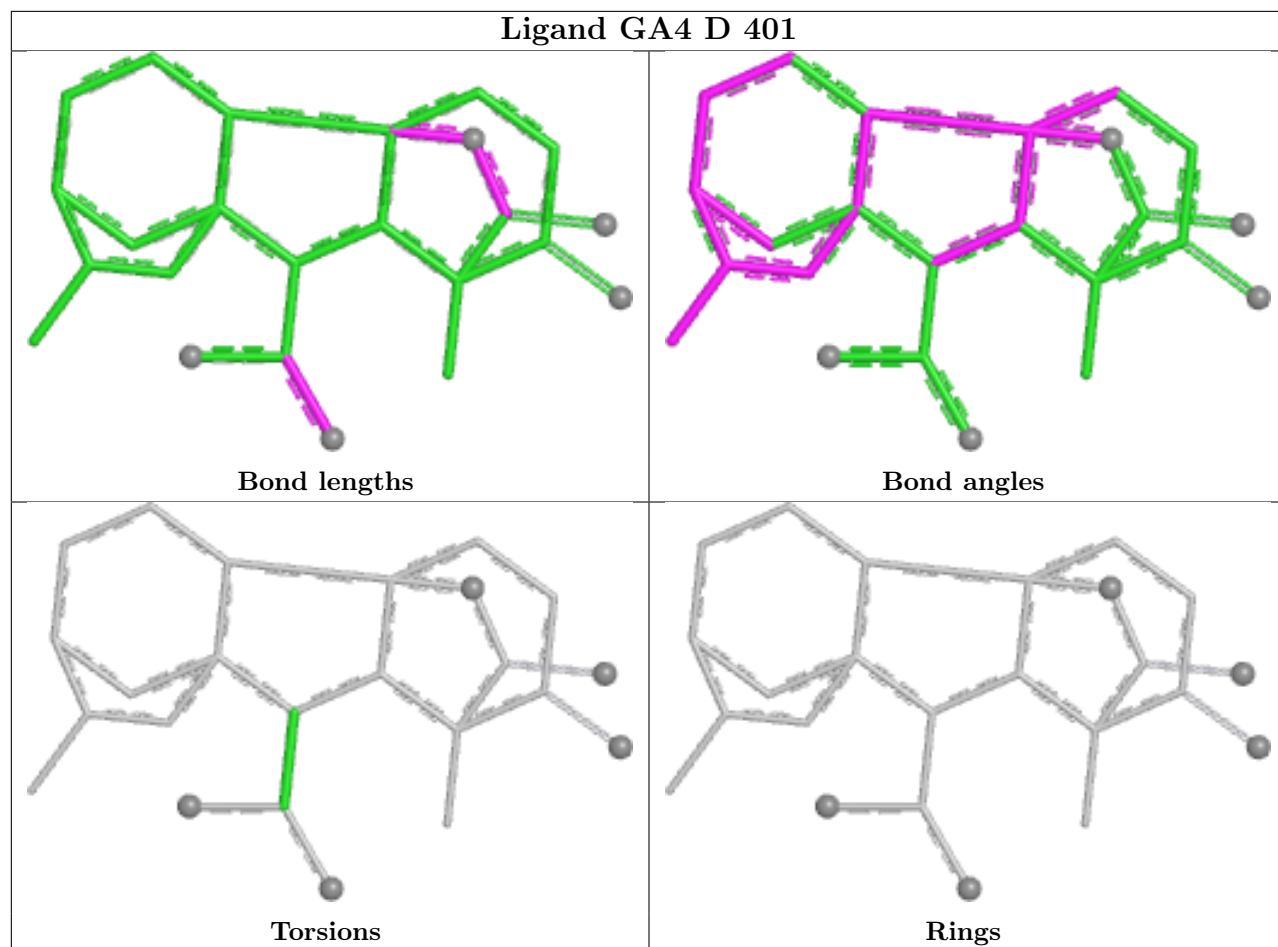
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	MPD	1	0
3	C	501	MPD	1	0
4	F	602	NO3	1	0
4	C	602	NO3	1	0
3	B	501	MPD	1	0
3	D	501	MPD	1	0
3	F	501	MPD	1	0
3	E	501	MPD	1	0
4	C	604	NO3	1	0
4	A	602	NO3	1	0

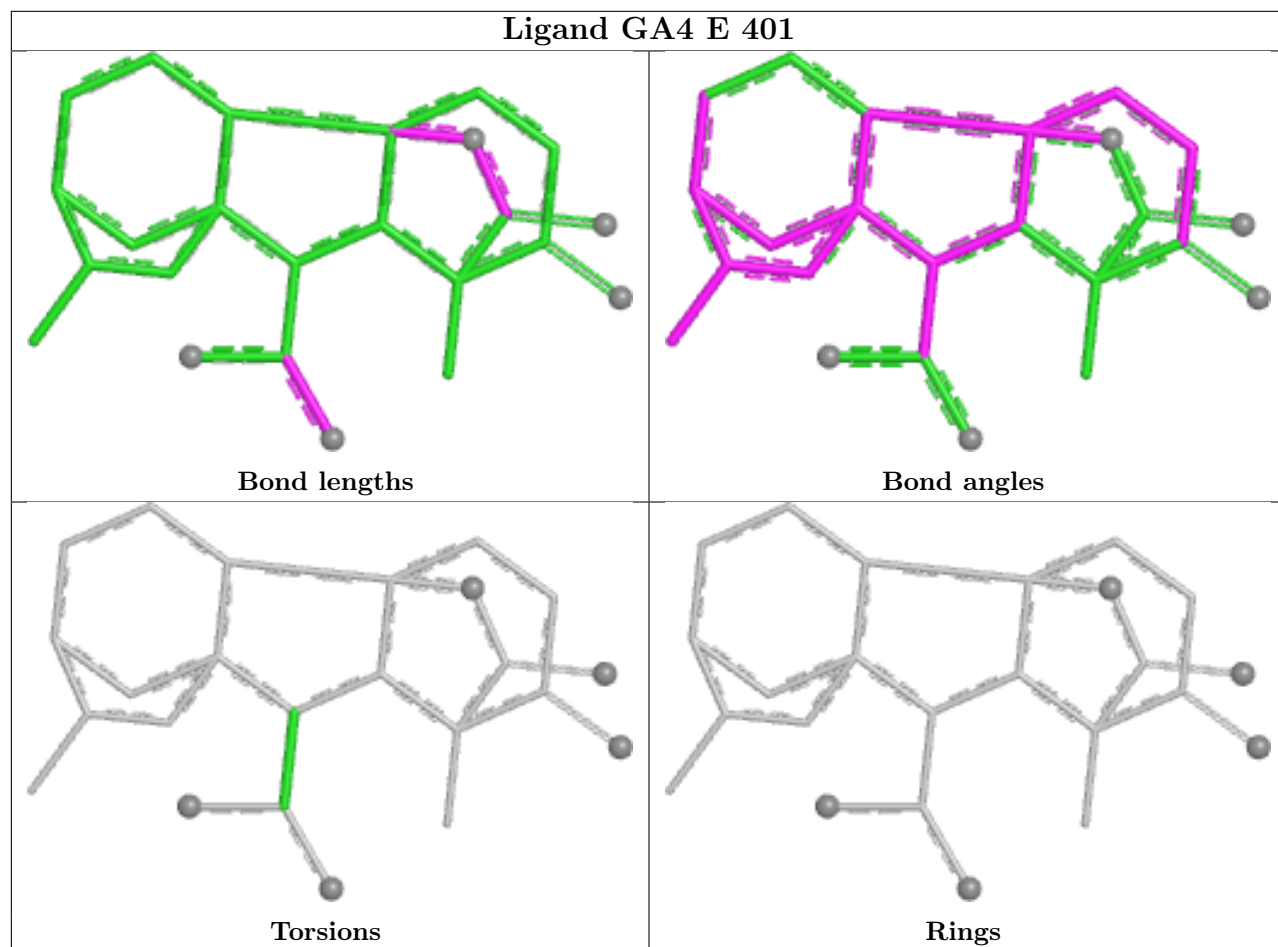
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

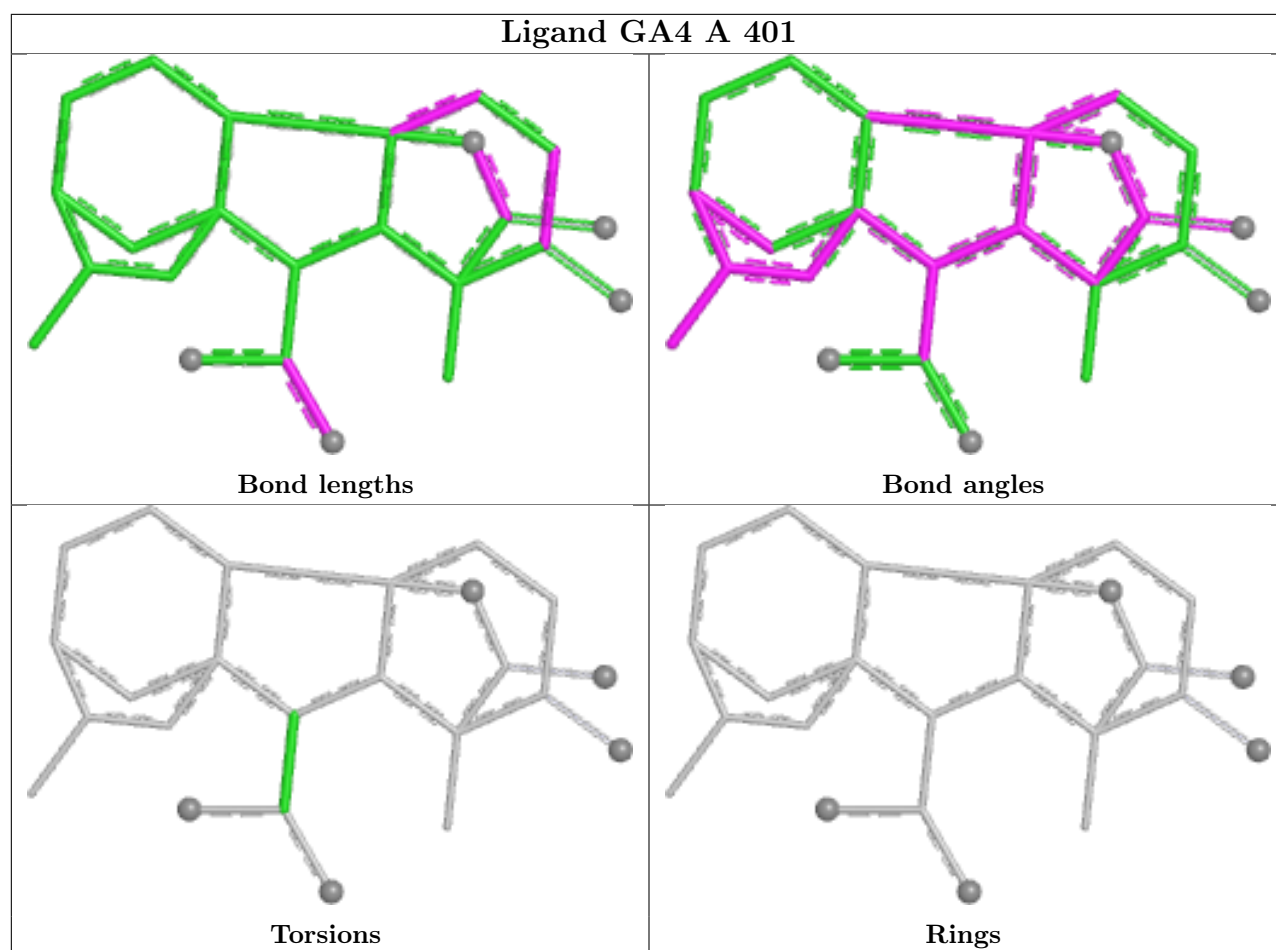












5.7 Other polymers [i](#)

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	A	323/365 (88%)	0.03	11 (3%) 48 51	17, 28, 48, 64	5 (1%)
1	B	318/365 (87%)	0.38	25 (7%) 18 20	18, 31, 55, 73	2 (0%)
1	C	301/365 (82%)	0.43	15 (4%) 34 36	17, 34, 52, 62	2 (0%)
1	D	315/365 (86%)	0.37	24 (7%) 20 21	18, 31, 52, 60	0
1	E	315/365 (86%)	1.14	55 (17%) 4 4	18, 42, 62, 84	2 (0%)
1	F	305/365 (83%)	0.42	19 (6%) 26 28	21, 35, 54, 65	2 (0%)
All	All	1877/2190 (85%)	0.46	149 (7%) 18 20	17, 33, 56, 84	13 (0%)

The worst 5 of 149 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	104	LEU	5.8
1	B	103	PHE	5.6
1	B	188	ALA	5.0
1	E	101	LEU	4.8
1	A	101	LEU	4.5

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 oligosaccharides in this entry.

6.4 Ligands

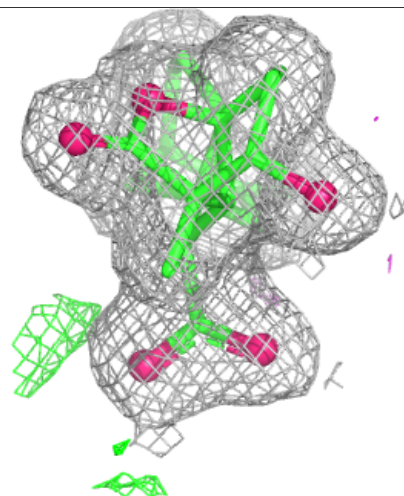
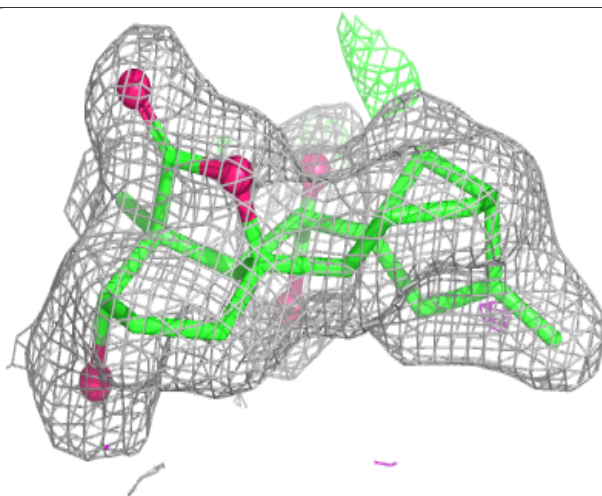
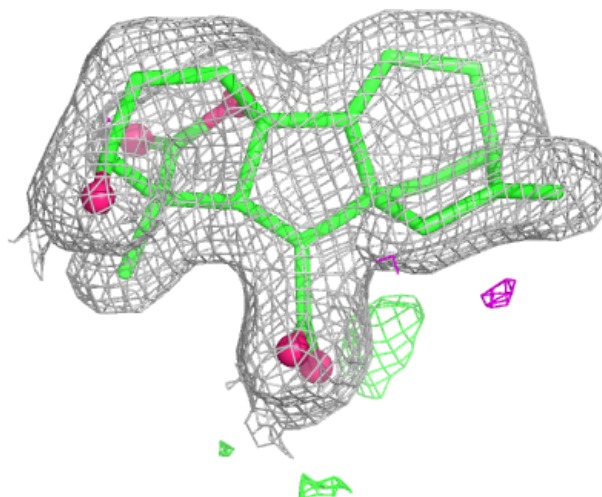
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NO3	D	602	4/4	0.78	0.23	58,58,58,58	0
5	PO4	B	701	5/5	0.79	0.15	79,80,81,82	0
4	NO3	E	601	4/4	0.81	0.15	80,80,80,80	0
4	NO3	A	604	4/4	0.82	0.19	58,58,59,59	0
4	NO3	B	601	4/4	0.83	0.15	54,55,55,55	0
4	NO3	A	602	4/4	0.83	0.19	42,44,45,46	0
4	NO3	C	601	4/4	0.84	0.16	55,56,56,57	0
4	NO3	D	601	4/4	0.84	0.13	62,62,62,63	0
3	MPD	B	501	8/8	0.84	0.14	37,40,41,41	0
3	MPD	D	501	8/8	0.84	0.14	39,42,44,44	0
4	NO3	A	601	4/4	0.84	0.13	48,49,50,50	0
4	NO3	C	602	4/4	0.85	0.21	48,49,50,50	0
4	NO3	B	602	4/4	0.87	0.20	48,48,48,49	0
4	NO3	F	601	4/4	0.87	0.13	63,63,63,63	0
4	NO3	F	602	4/4	0.87	0.17	56,56,57,57	0
4	NO3	F	603	4/4	0.87	0.16	54,54,55,55	0
4	NO3	C	603	4/4	0.87	0.17	63,63,63,63	0
5	PO4	E	701	5/5	0.87	0.11	81,82,82,83	0
4	NO3	B	604	4/4	0.88	0.14	54,55,55,55	0
4	NO3	A	603	4/4	0.88	0.12	56,56,56,56	0
4	NO3	C	604	4/4	0.89	0.13	51,53,53,54	0
3	MPD	A	501	8/8	0.90	0.11	31,37,39,40	0
4	NO3	D	603	4/4	0.90	0.11	54,54,54,54	0
3	MPD	C	501	8/8	0.91	0.10	34,37,38,39	0
3	MPD	F	501	8/8	0.91	0.10	35,37,38,41	0
3	MPD	E	501	8/8	0.93	0.09	41,44,47,47	0
2	GA4	E	401	24/24	0.95	0.07	26,29,31,33	0
2	GA4	B	401	24/24	0.96	0.05	17,19,21,22	0
2	GA4	F	401	24/24	0.96	0.06	18,22,27,29	0
2	GA4	C	401	24/24	0.97	0.05	17,21,23,26	0
2	GA4	D	401	24/24	0.97	0.05	17,21,23,26	0
2	GA4	A	401	24/24	0.98	0.05	15,18,21,24	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.

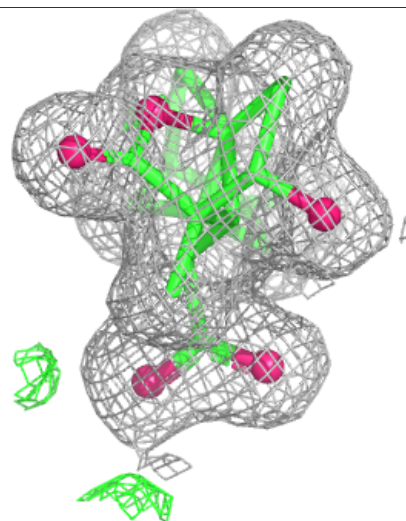
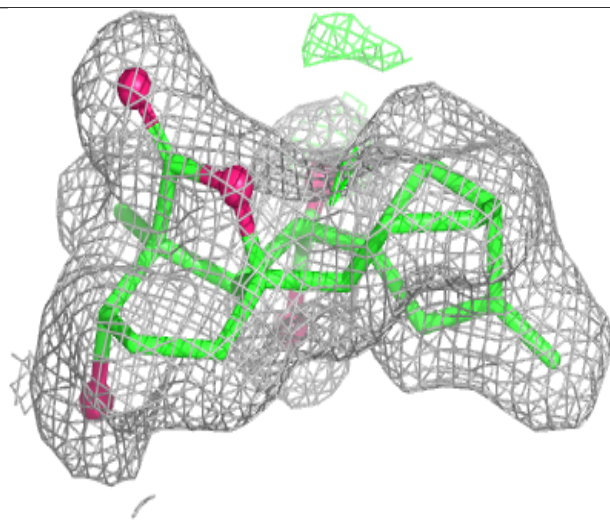
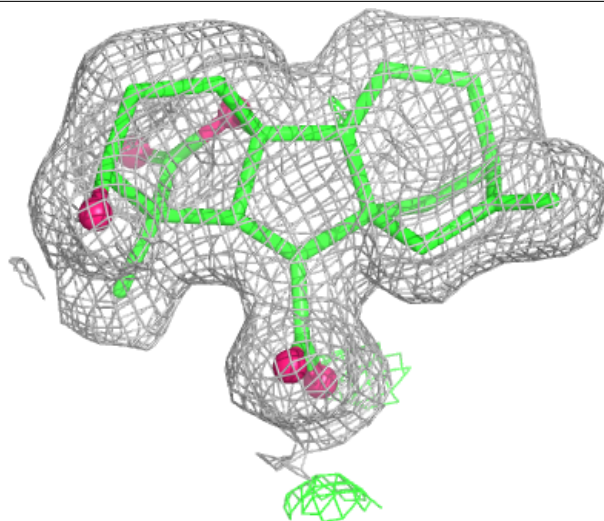
Electron density around GA4 E 401:

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



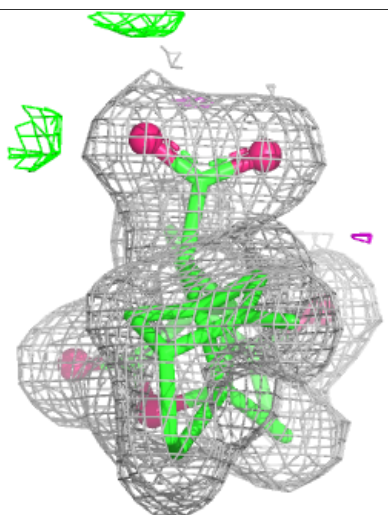
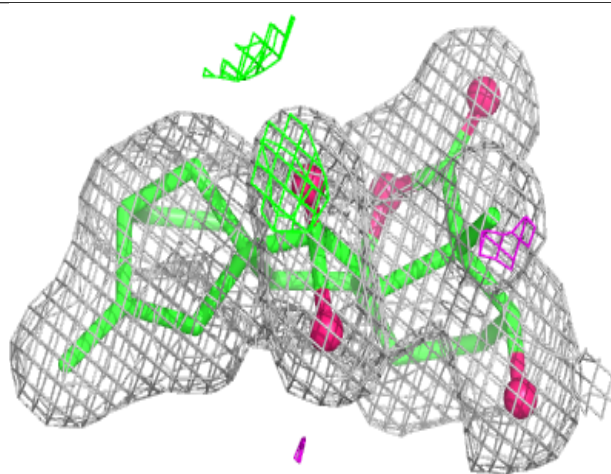
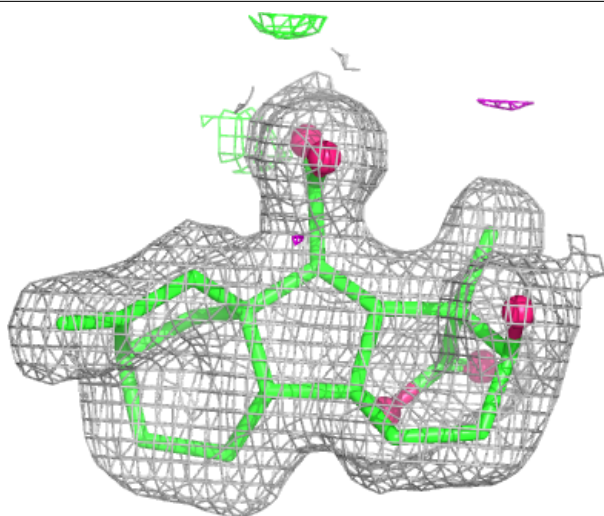
Electron density around GA4 B 401:

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



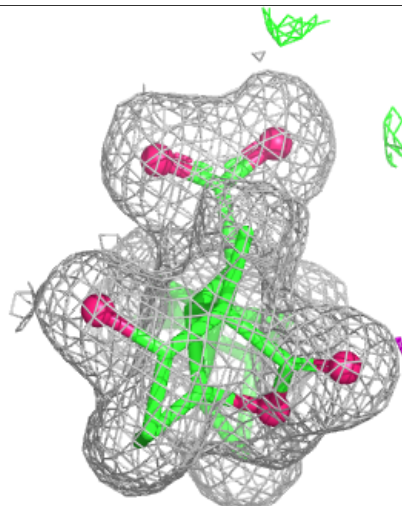
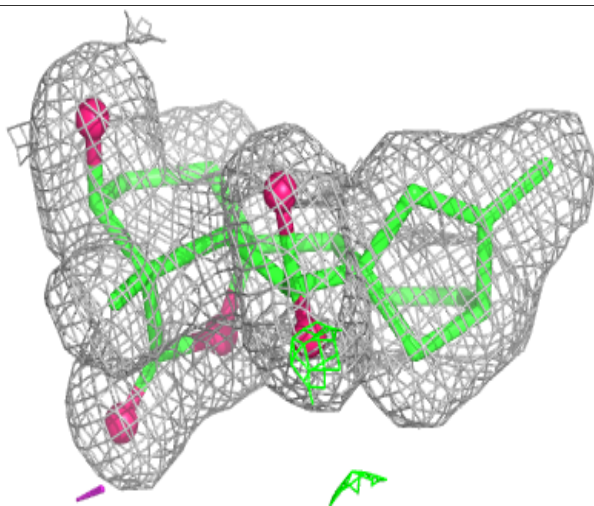
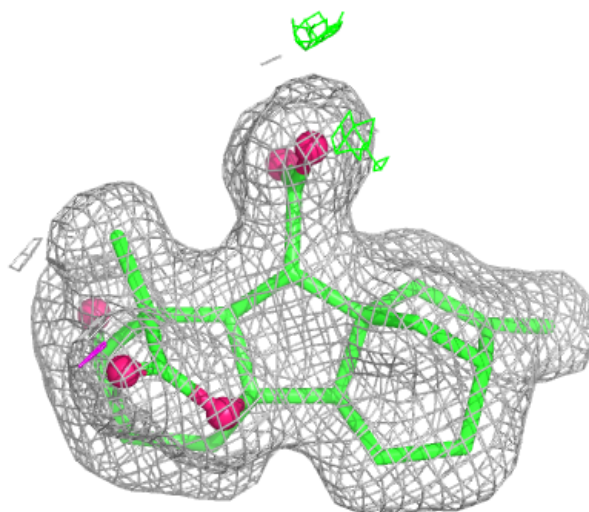
Electron density around GA4 F 401:

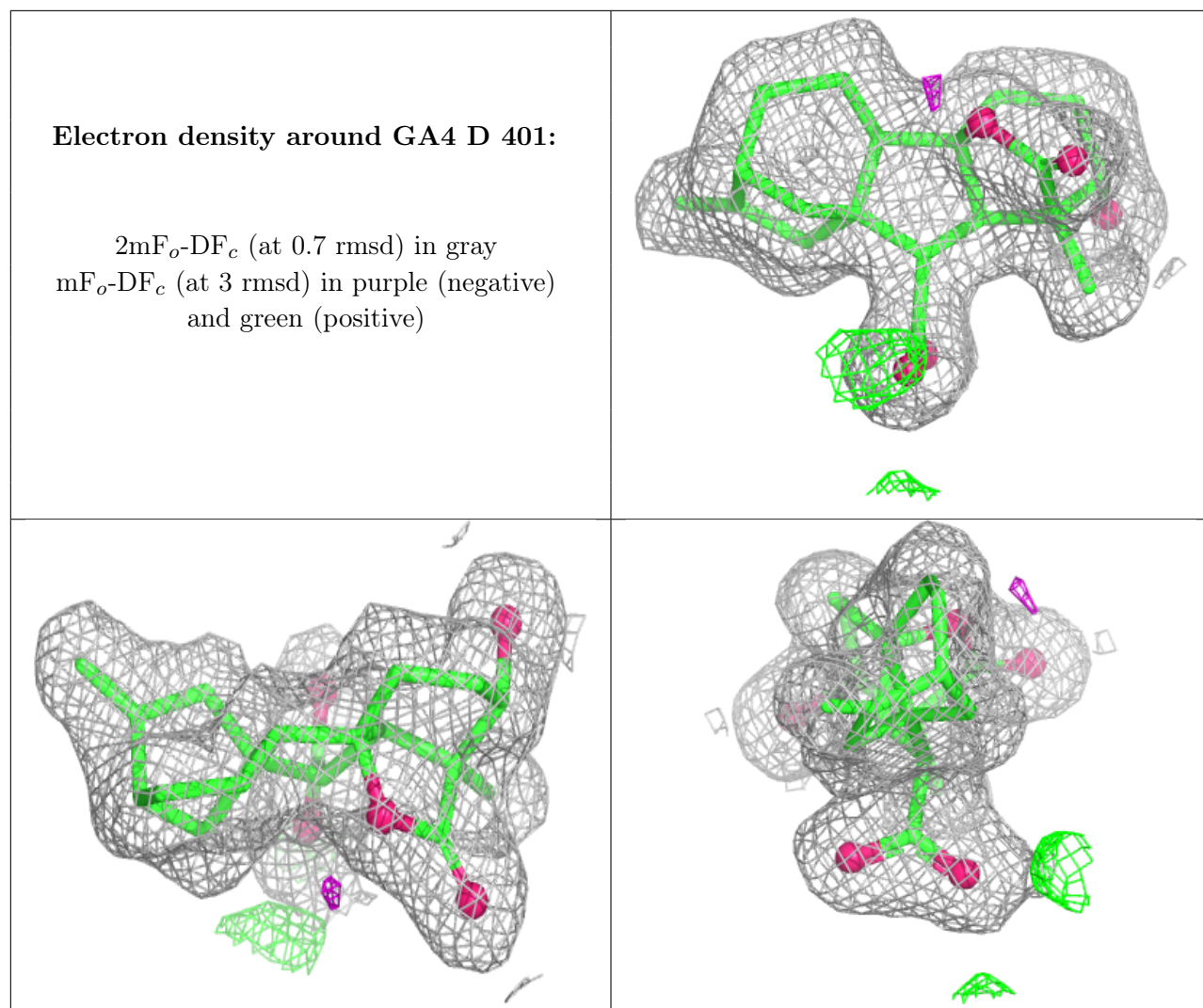
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

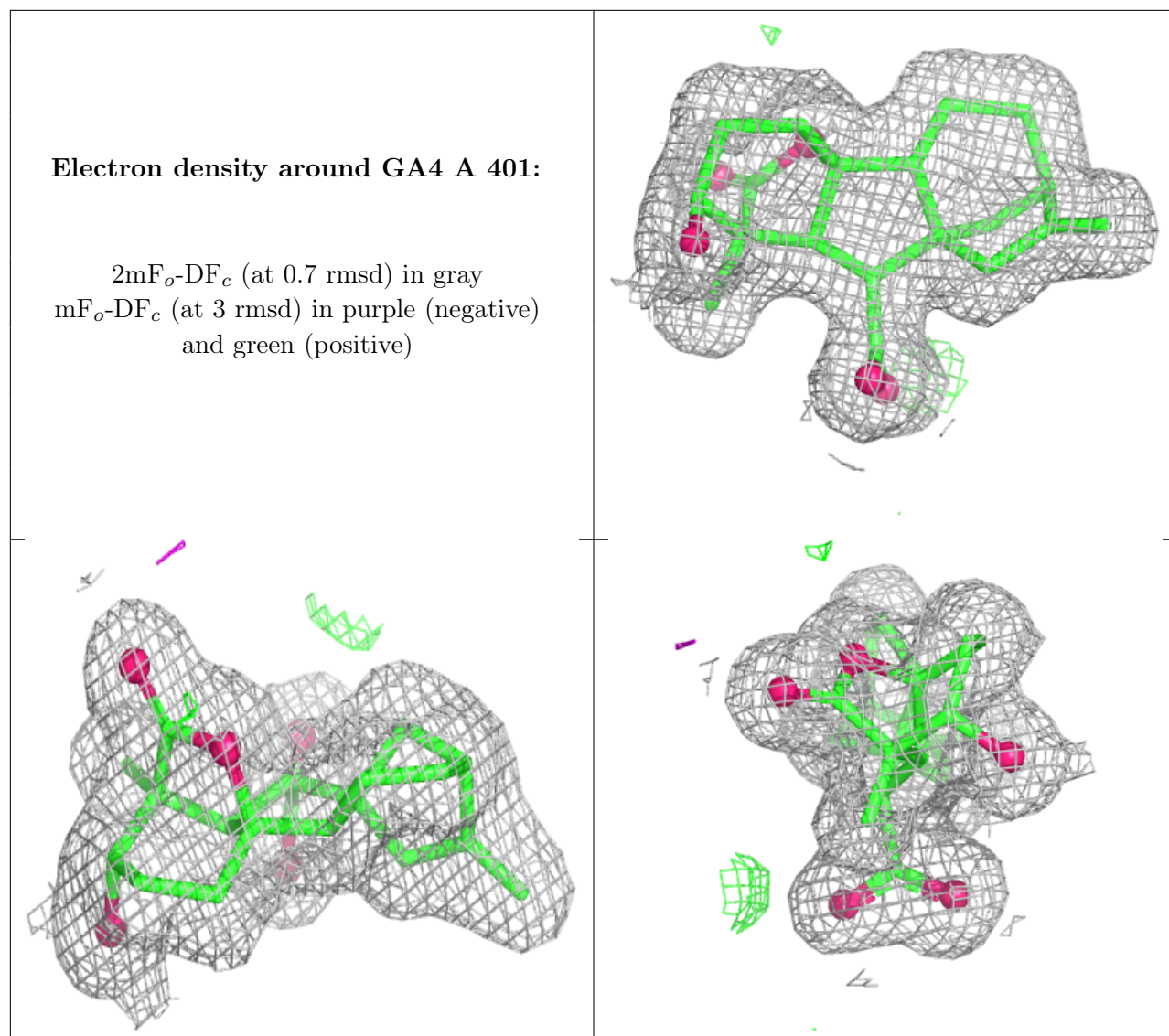


Electron density around GA4 C 401:

$2mF_o-DF_c$ (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.