



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:03 AM UTC

PDB ID : 1MX1 / pdb_00001mx1
Title : Crystal Structure of Human Liver Carboxylesterase in complex with tacrine
Authors : Bencharit, S.; Morton, C.L.; Hyatt, J.L.; Kuhn, P.; Danks, M.K.; Potter, P.M.;
Redinbo, M.R.
Deposited on : 2002-10-01
Resolution : 2.40 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

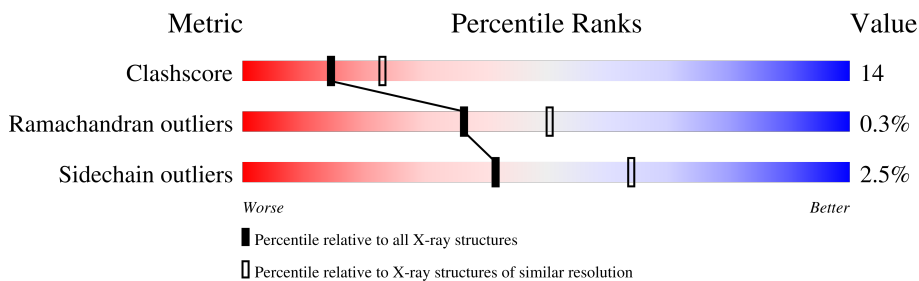
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	548	
1	B	548	
1	C	548	
1	D	548	
1	E	548	
1	F	548	
2	G	2	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SIA	A	1602	-	-	X	-
4	SIA	B	2602	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 27468 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 liver Carboxylesterase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	532	4130	2662	685	763	20	0	0	0
1	B	531	4124	2659	684	761	20	0	0	0
1	C	531	4124	2659	684	761	20	0	0	0
1	D	531	4124	2659	684	761	20	0	0	0
1	E	531	4124	2659	684	761	20	0	0	0
1	F	531	4124	2659	684	761	20	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

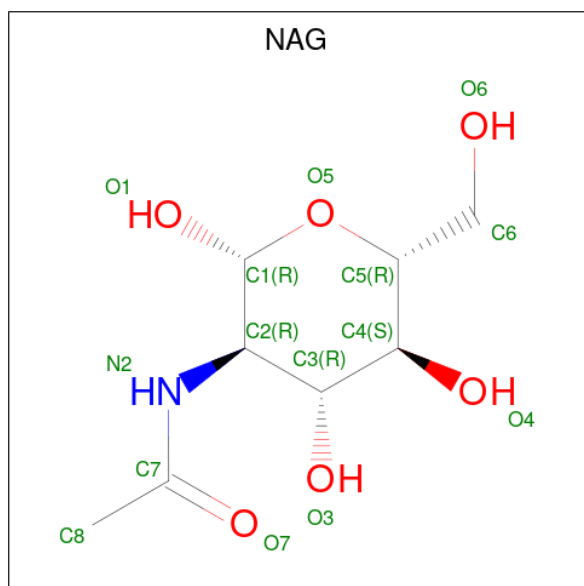
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P23141
B	?	-	GLN	deletion	UNP P23141
C	?	-	GLN	deletion	UNP P23141
D	?	-	GLN	deletion	UNP P23141
E	?	-	GLN	deletion	UNP P23141
F	?	-	GLN	deletion	UNP P23141

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



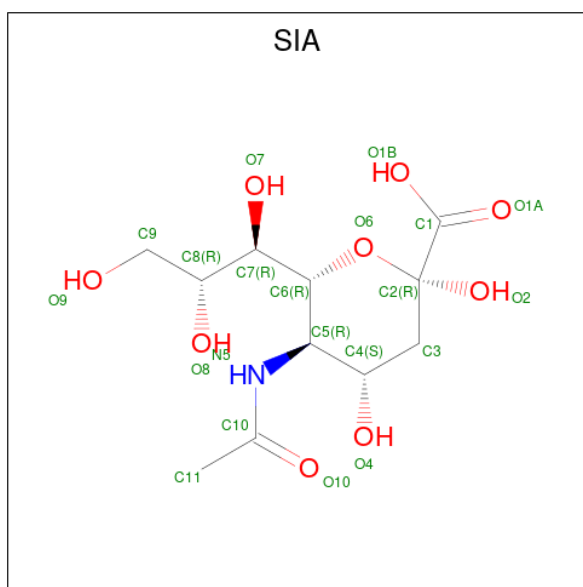
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	G	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



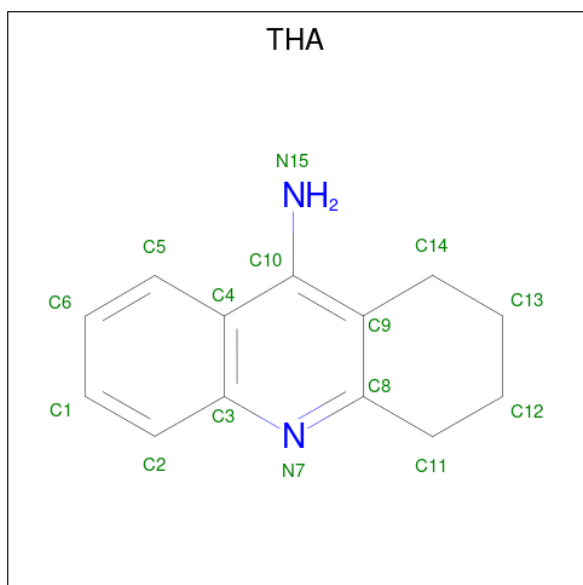
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0
3	B	1	14	8	1	5	0	0
3	D	1	14	8	1	5	0	0
3	E	1	14	8	1	5	0	0
3	F	1	14	8	1	5	0	0
3	F	1	14	8	1	5	0	0

- Molecule 4 is N-acetyl-alpha-neuraminic acid (CCD ID: SIA) (formula: $C_{11}H_{19}NO_9$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	21	11	1	9	0	0
4	B	1	21	11	1	9	0	0
4	D	1	21	11	1	9	1	0
4	E	1	21	11	1	9	1	0

- Molecule 5 is TACRINE (CCD ID: THA) (formula: $C_{13}H_{14}N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	1
			60	52	8		
5	B	1	Total	C	N	0	1
			60	52	8		
5	C	1	Total	C	N	0	1
			75	65	10		
5	D	1	Total	C	N	0	1
			75	65	10		
5	E	1	Total	C	N	0	1
			75	65	10		
5	F	1	Total	C	N	0	1
			60	52	8		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	374	Total	O	0	0
			374	374		
6	B	359	Total	O	0	0
			359	359		
6	C	362	Total	O	0	0
			362	362		
6	D	306	Total	O	0	0
			306	306		
6	E	357	Total	O	0	0
			357	357		
6	F	359	Total	O	0	0
			359	359		

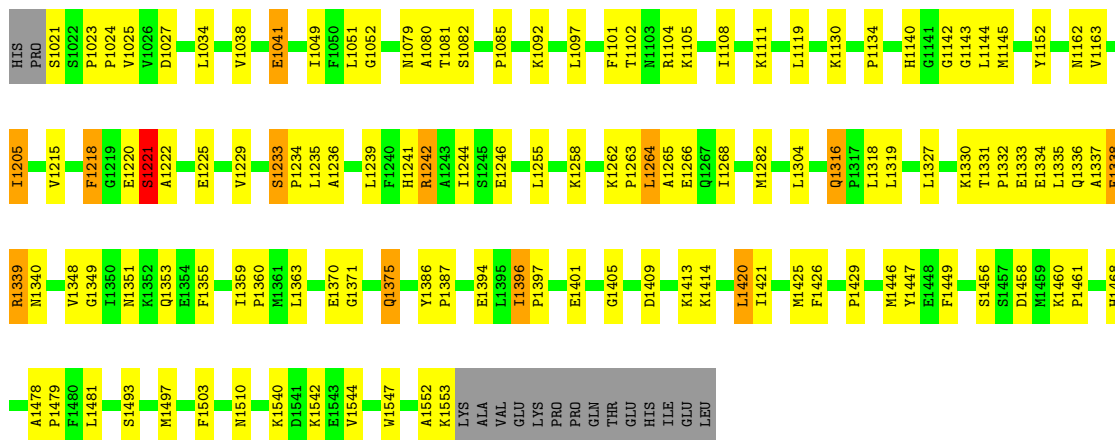
3 Residue-property plots [i](#)

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. 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. 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.


Note EDS was not executed.

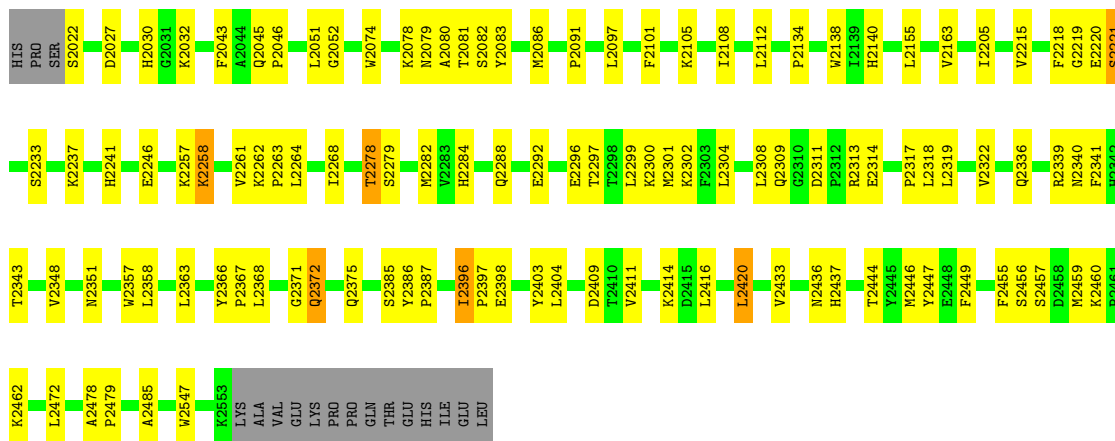
- Molecule 1: liver Carboxylesterase I

Chain A: 



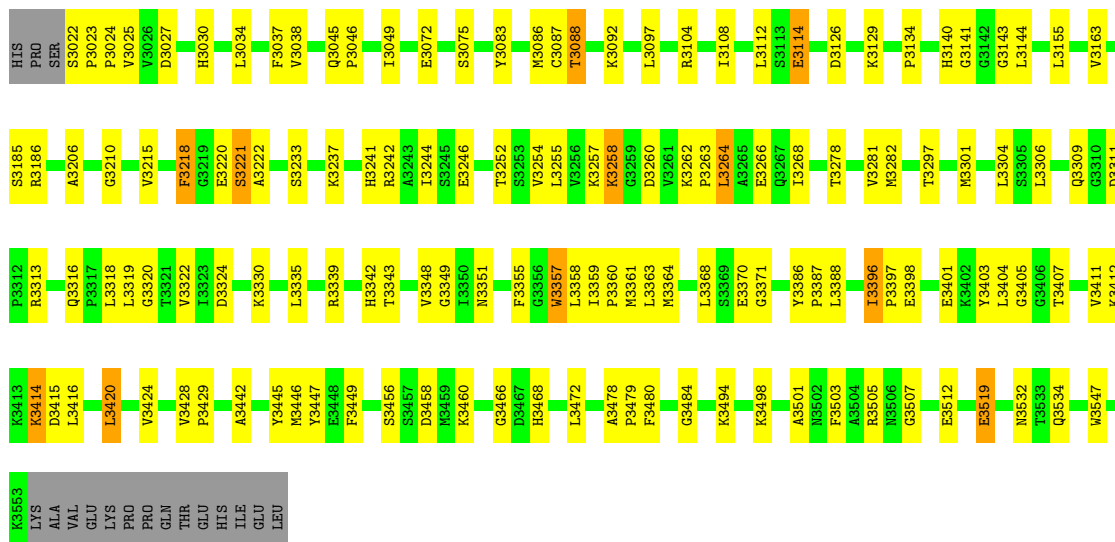
- Molecule 1: liver Carboxylesterase I

Chain B: 

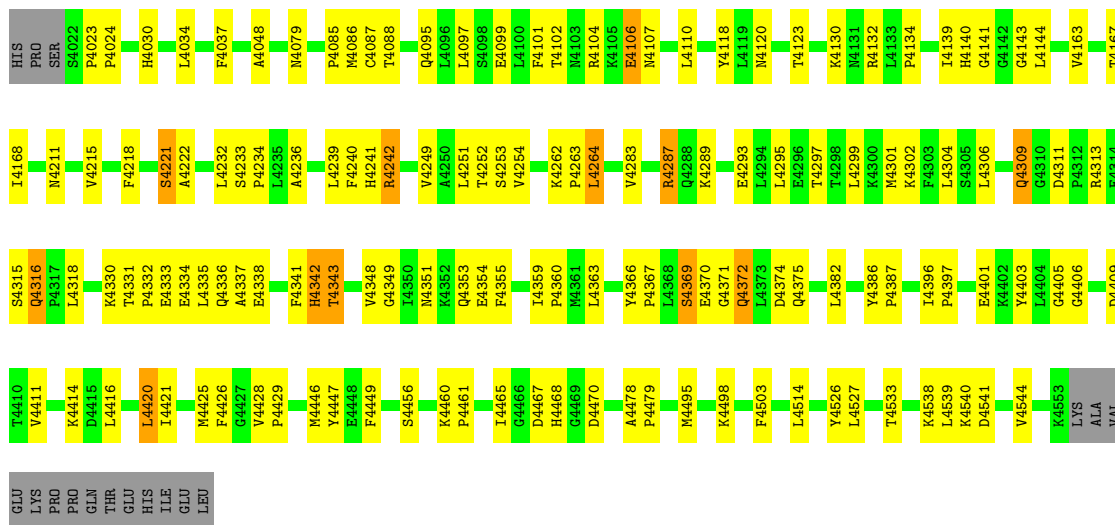


- Molecule 1: liver Carboxylesterase I

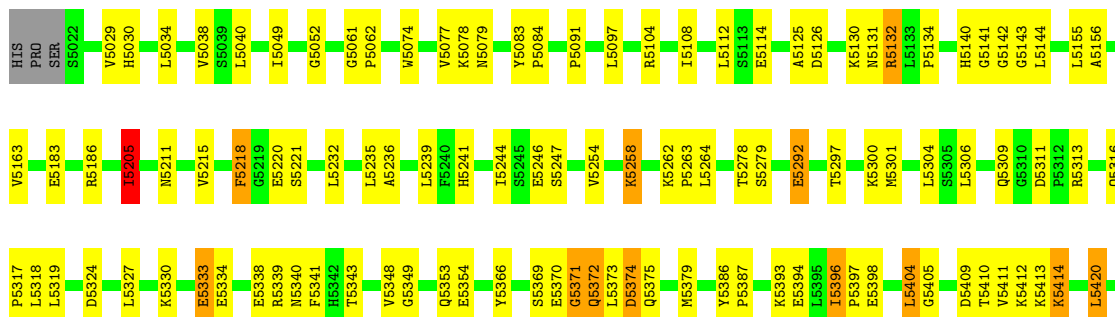
Chain C: 

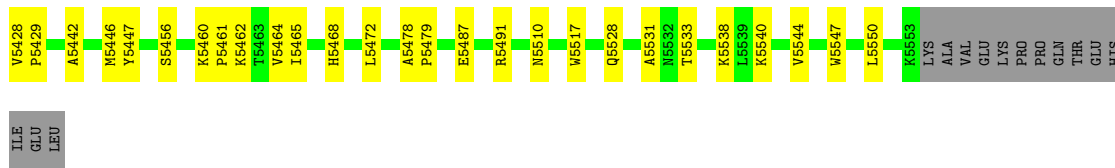


• Molecule 1: liver Carboxylesterase I



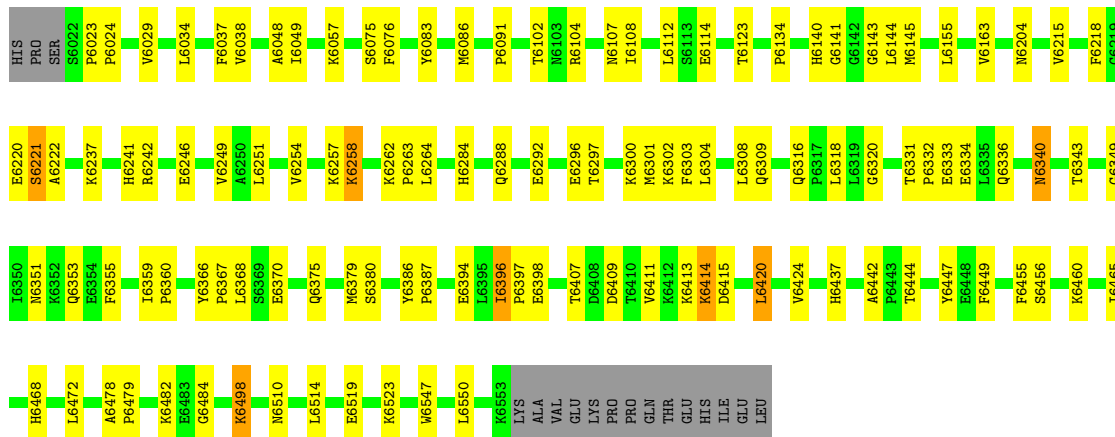
• Molecule 1: liver Carboxylesterase I





- Molecule 1: liver Carboxylesterase I

Chain F: 75% 20%



- Molecule 2: 2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 50% 50%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.02Å 117.03Å 176.01Å 90.00° 95.69° 90.00°	Depositor
Resolution (Å)	19.98 – 2.40	Depositor
% Data completeness (in resolution range)	99.4 (19.98-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.162 , 0.207	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	27468	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

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: SIA, NAG, NDG, THA

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	0.40	0/4236	0.90	8/5754 (0.1%)
1	B	0.39	0/4230	0.90	3/5746 (0.1%)
1	C	0.40	0/4230	0.89	4/5746 (0.1%)
1	D	0.38	0/4230	0.88	7/5746 (0.1%)
1	E	0.39	0/4230	0.89	9/5746 (0.2%)
1	F	0.40	0/4230	0.89	6/5746 (0.1%)
All	All	0.40	0/25386	0.89	37/34484 (0.1%)

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3075	SER	N-CA-C	8.83	122.55	111.69
1	F	6075	SER	N-CA-C	8.43	121.69	111.40
1	D	4342	HIS	N-CA-C	7.17	121.20	109.72
1	D	4337	ALA	N-CA-C	-6.72	103.88	111.07
1	D	4221	SER	CB-CA-C	-6.18	108.82	117.23

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	A	4130	0	4131	126	0
1	B	4124	0	4126	112	0
1	C	4124	0	4126	135	0
1	D	4124	0	4126	115	0
1	E	4124	0	4125	113	0
1	F	4124	0	4126	101	0
2	G	28	0	24	2	0
3	A	14	0	13	0	0
3	B	14	0	13	3	0
3	D	14	0	13	0	0
3	E	14	0	13	1	0
3	F	28	0	26	1	0
4	A	21	0	18	31	0
4	B	21	0	18	16	0
4	D	21	0	18	7	0
4	E	21	0	18	7	0
5	A	60	0	56	13	0
5	B	60	0	56	9	0
5	C	75	0	70	12	0
5	D	75	0	70	13	0
5	E	75	0	70	14	0
5	F	60	0	56	7	0
6	A	374	0	0	26	0
6	B	359	0	0	15	0
6	C	362	0	0	18	0
6	D	306	0	0	9	0
6	E	357	0	0	20	0
6	F	359	0	0	12	0
All	All	27468	0	25312	709	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 14.

The worst 5 of 709 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:A:1052:GLY:HA3	4:A:1602:SIA:H32	1.24	1.19
4:B:2602:SIA:H111	6:C:3881:HOH:O	1.42	1.18
4:B:2602:SIA:H113	1:C:3278:THR:HB	1.29	1.14
4:A:1602:SIA:H111	1:B:2278:THR:HB	1.31	1.12
1:C:3258:LYS:H	1:C:3258:LYS:HE2	1.09	1.12

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	530/548 (97%)	509 (96%)	20 (4%)	1 (0%)	43	58
1	B	529/548 (96%)	508 (96%)	20 (4%)	1 (0%)	43	58
1	C	529/548 (96%)	509 (96%)	17 (3%)	3 (1%)	21	32
1	D	529/548 (96%)	499 (94%)	28 (5%)	2 (0%)	30	43
1	E	529/548 (96%)	505 (96%)	24 (4%)	0	100	100
1	F	529/548 (96%)	505 (96%)	22 (4%)	2 (0%)	30	43
All	All	3175/3288 (97%)	3035 (96%)	131 (4%)	9 (0%)	36	50

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1339	ARG
1	D	4253	SER
1	C	3185	SER
1	F	6340	ASN
1	B	2357	TRP

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	448/463 (97%)	438 (98%)	10 (2%)	45	67

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	447/463 (96%)	436 (98%)	11 (2%)	42	64
1	C	447/463 (96%)	434 (97%)	13 (3%)	37	60
1	D	447/463 (96%)	435 (97%)	12 (3%)	39	62
1	E	447/463 (96%)	434 (97%)	13 (3%)	37	60
1	F	447/463 (96%)	438 (98%)	9 (2%)	48	70
All	All	2683/2778 (97%)	2615 (98%)	68 (2%)	42	64

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	5414	LYS
1	F	6155	LEU
1	F	6420	LEU
1	C	3155	LEU
1	C	3088	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	4375	GLN
1	E	5353	GLN
1	D	4450	GLN
1	E	5131	ASN
1	E	5537	GLN

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](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	G	1	1,2	14,14,15	0.76	0	17,19,21	0.68	0
2	NDG	G	2	2	14,14,15	1.13	1 (7%)	17,19,21	1.51	4 (23%)

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	NAG	G	1	1,2	-	2/6/23/26	0/1/1/1
2	NDG	G	2	2	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	NDG	O5-C5	3.02	1.49	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2	NDG	C6-C5-C4	-3.09	105.43	113.02
2	G	2	NDG	C3-C4-C5	2.70	115.12	110.23
2	G	2	NDG	O5-C1-C2	-2.26	107.80	111.29
2	G	2	NDG	C4-C3-C2	-2.03	108.04	111.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	2	NDG	C1-C2-N2-C7
2	G	2	NDG	C8-C7-N2-C2
2	G	2	NDG	O7-C7-N2-C2
2	G	1	NAG	C8-C7-N2-C2

Continued on next page...

Continued from previous page...

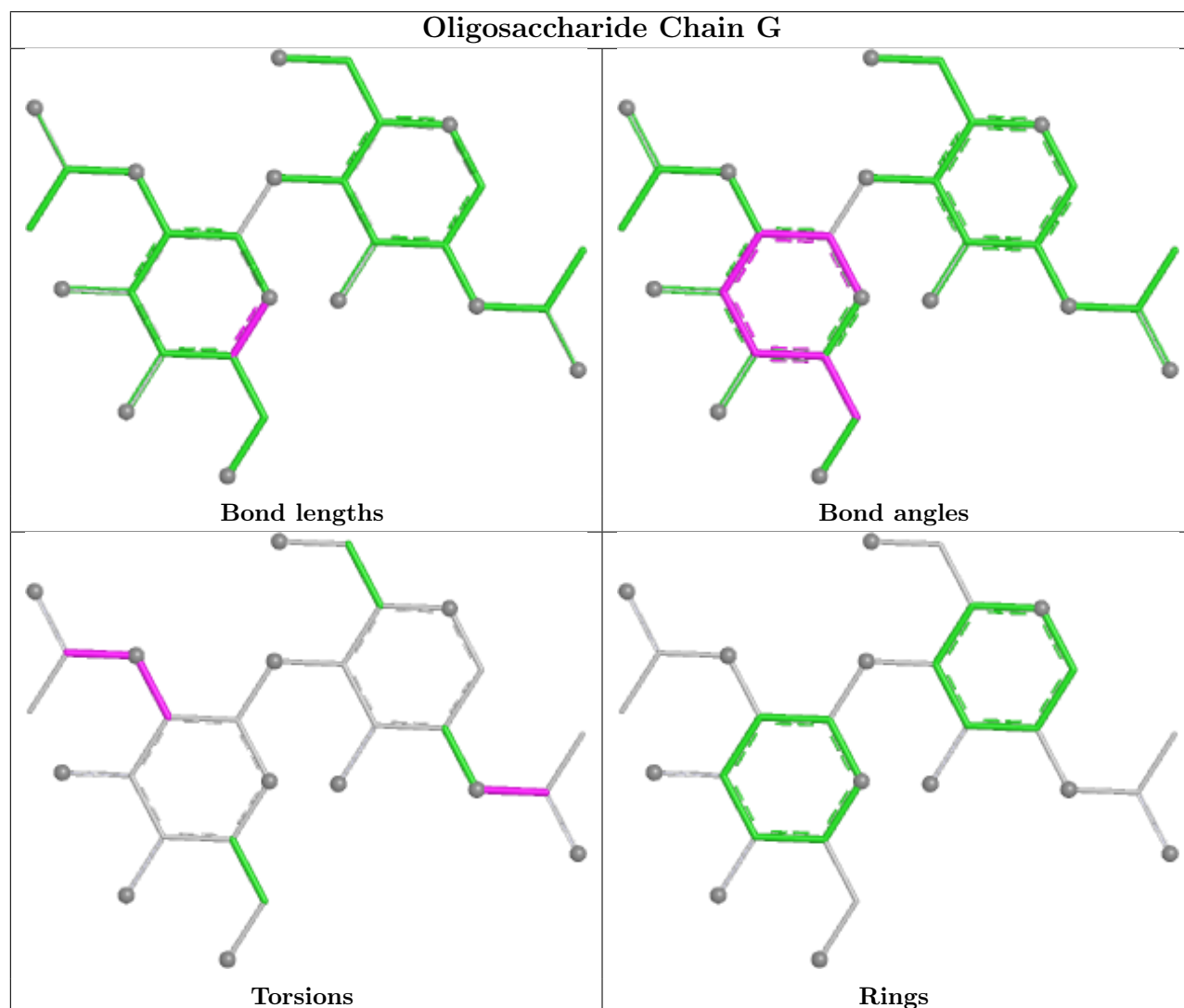
Mol	Chain	Res	Type	Atoms
2	G	1	NAG	O7-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	2	NDG	2	0
2	G	1	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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
5	THA	E	5603[B]	-	17,17,17	2.41	7 (41%)	22,24,24	1.63	3 (13%)
5	THA	F	6603[D]	-	17,17,17	2.39	7 (41%)	22,24,24	1.62	3 (13%)
5	THA	F	6603[A]	-	17,17,17	2.40	7 (41%)	22,24,24	1.69	3 (13%)
5	THA	C	3601[E]	-	17,17,17	2.46	7 (41%)	22,24,24	1.62	4 (18%)
4	SIA	D	4602	-	21,21,21	1.16	1 (4%)	24,31,31	1.16	3 (12%)
3	NAG	D	4601	1	14,14,15	0.51	0	17,19,21	0.68	1 (5%)
5	THA	E	5603[C]	-	17,17,17	2.43	7 (41%)	22,24,24	1.63	3 (13%)
5	THA	A	1603[D]	-	17,17,17	2.39	7 (41%)	22,24,24	1.59	3 (13%)
5	THA	A	1603[A]	-	17,17,17	2.41	7 (41%)	22,24,24	1.64	3 (13%)
5	THA	C	3601[D]	-	17,17,17	2.34	7 (41%)	22,24,24	1.66	3 (13%)
5	THA	B	2603[D]	-	17,17,17	2.41	7 (41%)	22,24,24	1.59	3 (13%)
4	SIA	A	1602	-	21,21,21	0.96	1 (4%)	24,31,31	1.34	4 (16%)
5	THA	C	3601[A]	-	17,17,17	2.43	7 (41%)	22,24,24	1.60	3 (13%)
5	THA	B	2603[A]	-	17,17,17	2.42	7 (41%)	22,24,24	1.70	3 (13%)
5	THA	F	6603[B]	-	17,17,17	2.38	7 (41%)	22,24,24	1.59	3 (13%)
5	THA	A	1603[B]	-	17,17,17	2.45	7 (41%)	22,24,24	1.64	3 (13%)
5	THA	F	6603[C]	-	17,17,17	2.36	7 (41%)	22,24,24	1.65	3 (13%)
5	THA	D	4603[E]	-	17,17,17	2.38	7 (41%)	22,24,24	1.59	3 (13%)
5	THA	C	3601[B]	-	17,17,17	2.46	7 (41%)	22,24,24	1.67	3 (13%)
5	THA	B	2603[B]	-	17,17,17	2.45	7 (41%)	22,24,24	1.63	3 (13%)
3	NAG	B	2601	1	14,14,15	0.56	0	17,19,21	0.86	1 (5%)
5	THA	D	4603[D]	-	17,17,17	2.44	7 (41%)	22,24,24	1.64	3 (13%)
3	NAG	A	1601	1	14,14,15	0.65	0	17,19,21	0.65	0
5	THA	D	4603[A]	-	17,17,17	2.43	7 (41%)	22,24,24	1.66	3 (13%)
3	NAG	E	5601	1	14,14,15	0.59	0	17,19,21	0.71	1 (5%)
5	THA	C	3601[C]	-	17,17,17	2.43	7 (41%)	22,24,24	1.59	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	THA	B	2603[C]	-	17,17,17	2.39	7 (41%)	22,24,24	1.63	3 (13%)
5	THA	A	1603[C]	-	17,17,17	2.37	7 (41%)	22,24,24	1.65	3 (13%)
3	NAG	F	6602	-	14,14,15	0.50	0	17,19,21	0.67	1 (5%)
3	NAG	F	6601	1	14,14,15	0.50	0	17,19,21	0.90	1 (5%)
5	THA	D	4603[B]	-	17,17,17	2.43	7 (41%)	22,24,24	1.60	3 (13%)
5	THA	E	5603[E]	-	17,17,17	2.41	7 (41%)	22,24,24	1.63	3 (13%)
5	THA	E	5603[D]	-	17,17,17	2.44	7 (41%)	22,24,24	1.62	4 (18%)
4	SIA	E	5602	-	21,21,21	1.04	1 (4%)	24,31,31	1.46	4 (16%)
5	THA	E	5603[A]	-	17,17,17	2.45	7 (41%)	22,24,24	1.61	3 (13%)
5	THA	D	4603[C]	-	17,17,17	2.42	7 (41%)	22,24,24	1.62	3 (13%)
4	SIA	B	2602	-	21,21,21	1.04	0	24,31,31	1.13	2 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	THA	E	5603[B]	-	-	-	0/3/3/3
5	THA	F	6603[D]	-	-	-	0/3/3/3
5	THA	F	6603[A]	-	-	-	0/3/3/3
5	THA	C	3601[E]	-	-	-	0/3/3/3
4	SIA	D	4602	-	-	2/20/38/38	0/1/1/1
3	NAG	D	4601	1	-	2/6/23/26	0/1/1/1
5	THA	E	5603[C]	-	-	-	0/3/3/3
5	THA	A	1603[D]	-	-	-	0/3/3/3
5	THA	A	1603[A]	-	-	-	0/3/3/3
5	THA	C	3601[D]	-	-	-	0/3/3/3
5	THA	B	2603[D]	-	-	-	0/3/3/3
4	SIA	A	1602	-	-	3/20/38/38	0/1/1/1
5	THA	C	3601[A]	-	-	-	0/3/3/3
5	THA	B	2603[A]	-	-	-	0/3/3/3
5	THA	F	6603[B]	-	-	-	0/3/3/3
5	THA	A	1603[B]	-	-	-	0/3/3/3
5	THA	F	6603[C]	-	-	-	0/3/3/3
5	THA	D	4603[E]	-	-	-	0/3/3/3
5	THA	C	3601[B]	-	-	-	0/3/3/3
5	THA	B	2603[B]	-	-	-	0/3/3/3
3	NAG	B	2601	1	-	4/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	THA	D	4603[D]	-	-	-	0/3/3/3
3	NAG	A	1601	1	-	3/6/23/26	0/1/1/1
5	THA	D	4603[A]	-	-	-	0/3/3/3
3	NAG	E	5601	1	-	4/6/23/26	0/1/1/1
5	THA	C	3601[C]	-	-	-	0/3/3/3
5	THA	B	2603[C]	-	-	-	0/3/3/3
5	THA	A	1603[C]	-	-	-	0/3/3/3
3	NAG	F	6602	-	-	2/6/23/26	0/1/1/1
3	NAG	F	6601	1	-	2/6/23/26	0/1/1/1
5	THA	D	4603[B]	-	-	-	0/3/3/3
5	THA	E	5603[E]	-	-	-	0/3/3/3
5	THA	E	5603[D]	-	-	-	0/3/3/3
4	SIA	E	5602	-	-	1/20/38/38	0/1/1/1
5	THA	E	5603[A]	-	-	-	0/3/3/3
5	THA	D	4603[C]	-	-	-	0/3/3/3
4	SIA	B	2602	-	-	1/20/38/38	0/1/1/1

The worst 5 of 192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	3601[E]	THA	C14-C9	5.27	1.59	1.51
5	B	2603[B]	THA	C14-C9	5.20	1.59	1.51
5	D	4603[B]	THA	C14-C9	5.11	1.59	1.51
5	E	5603[D]	THA	C14-C9	5.10	1.59	1.51
5	C	3601[A]	THA	C14-C9	5.10	1.59	1.51

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	6603[C]	THA	C8-N7-C3	4.78	123.33	117.67
5	D	4603[D]	THA	C8-N7-C3	4.77	123.32	117.67
5	B	2603[A]	THA	C8-N7-C3	4.77	123.31	117.67
5	B	2603[B]	THA	C8-N7-C3	4.75	123.29	117.67
5	E	5603[B]	THA	C8-N7-C3	4.74	123.29	117.67

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	2601	NAG	C8-C7-N2-C2
3	B	2601	NAG	O7-C7-N2-C2

Continued on next page...

Continued from previous page...

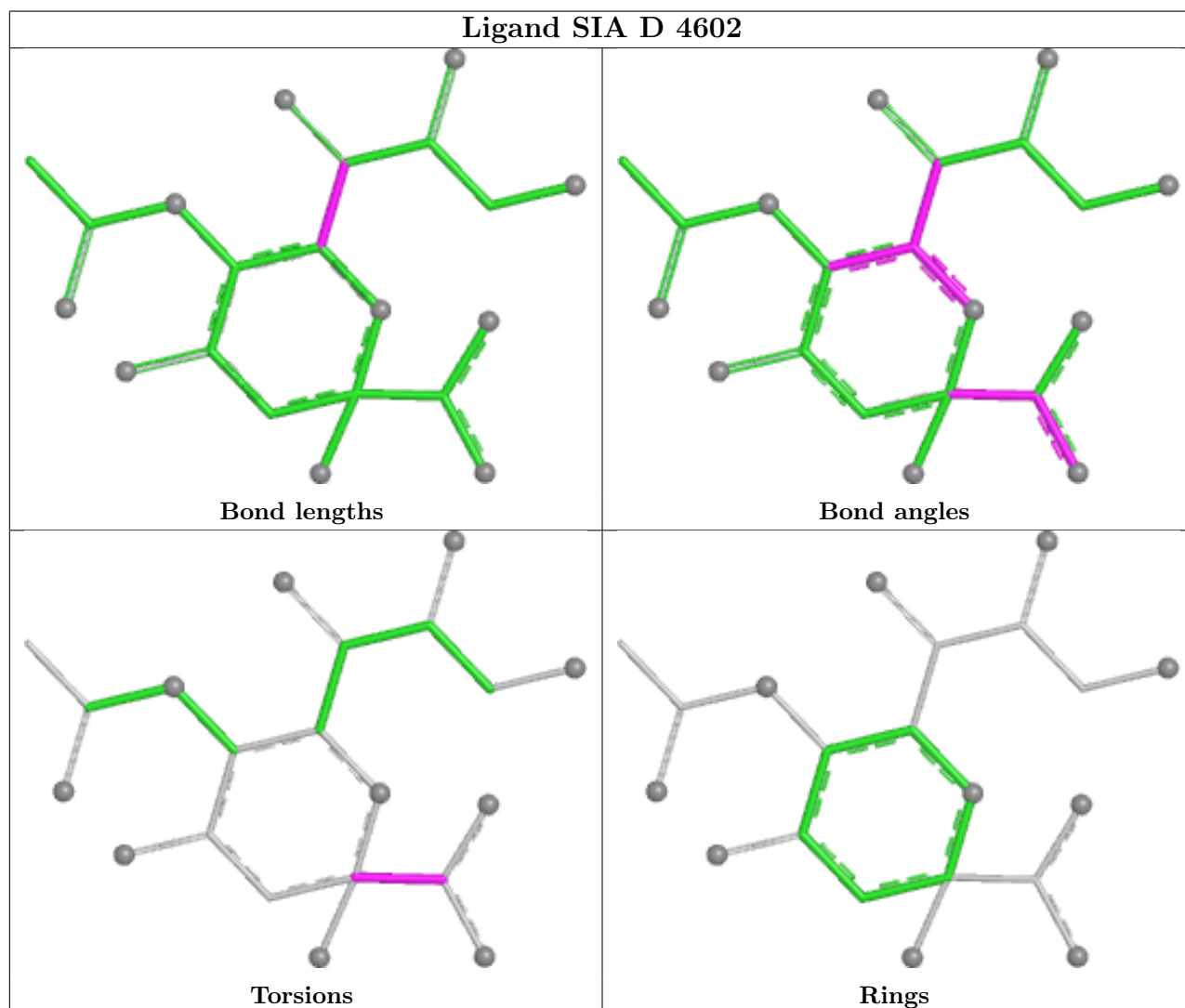
Mol	Chain	Res	Type	Atoms
3	E	5601	NAG	C8-C7-N2-C2
3	E	5601	NAG	O7-C7-N2-C2
3	B	2601	NAG	O5-C5-C6-O6

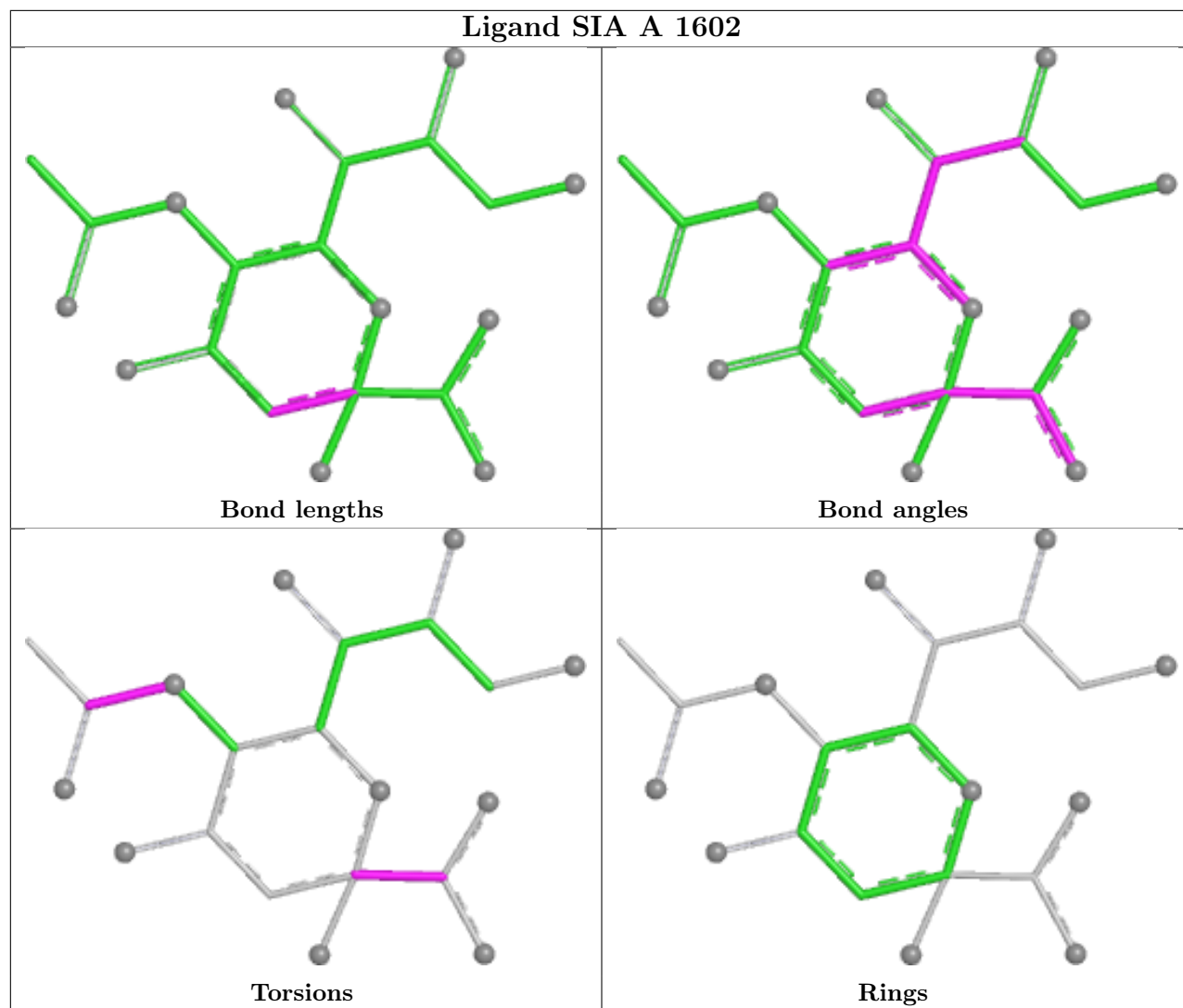
There are no ring outliers.

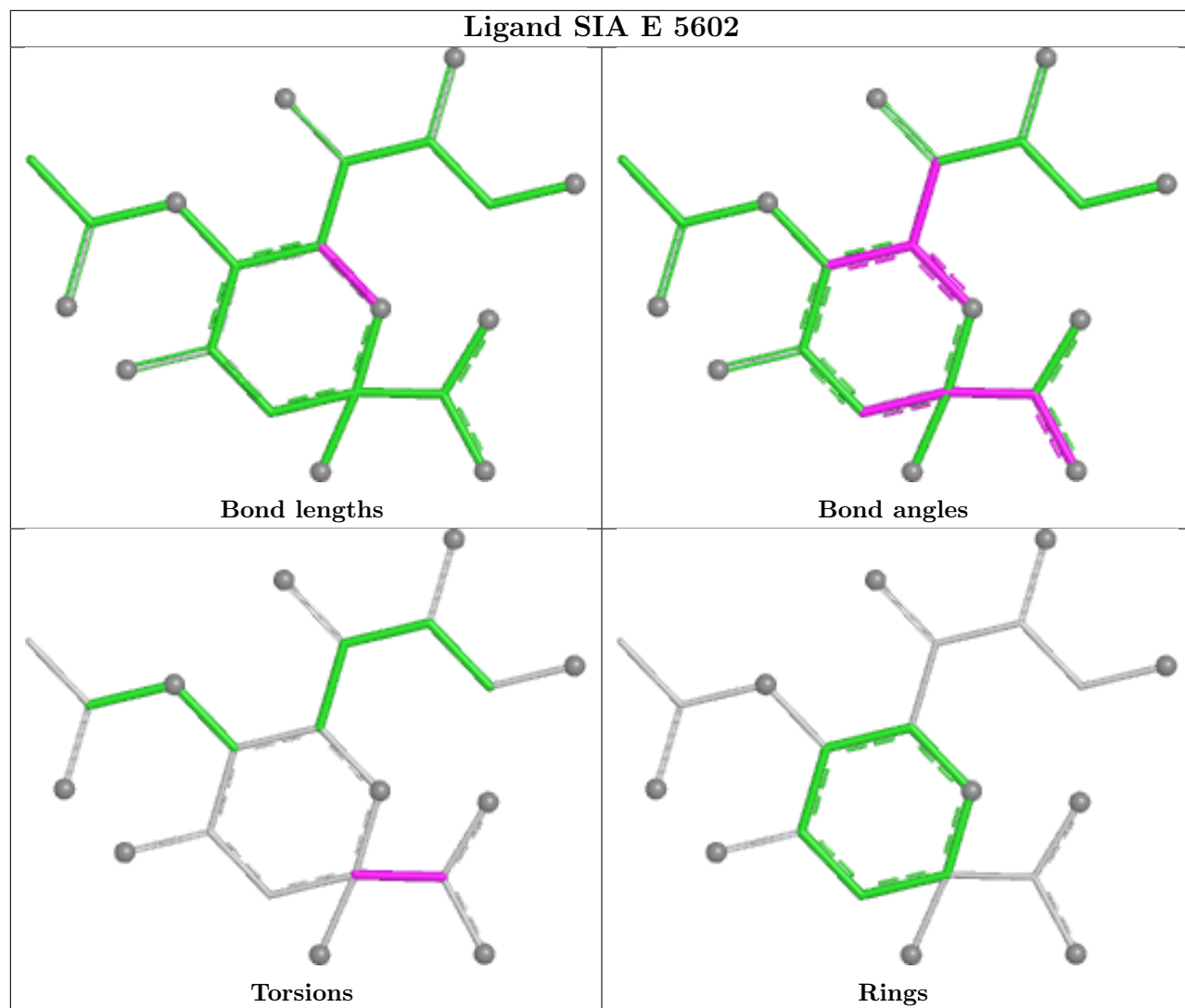
33 monomers are involved in 134 short contacts:

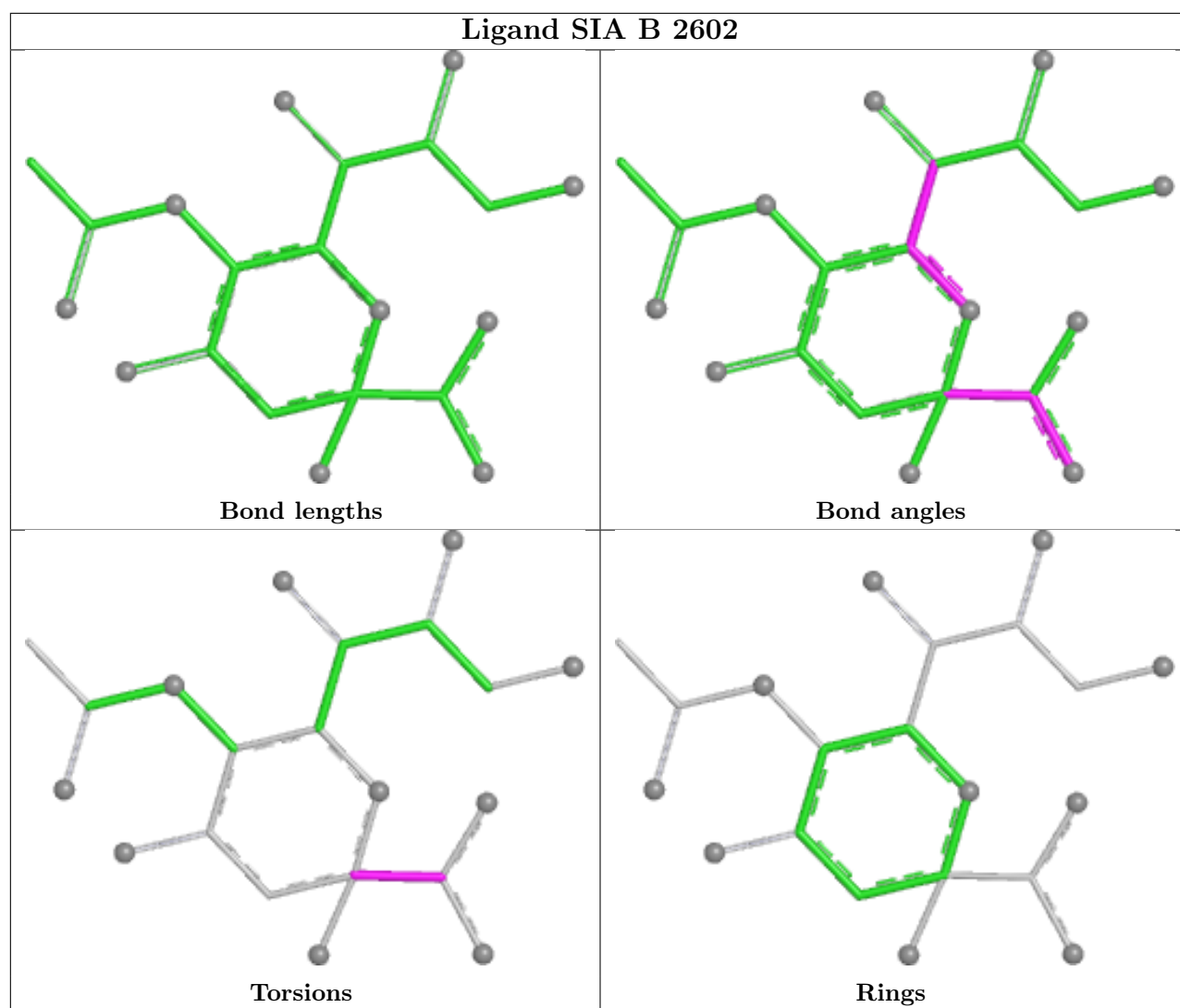
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	5603[B]	THA	2	0
5	F	6603[D]	THA	2	0
5	C	3601[E]	THA	3	0
4	D	4602	SIA	7	0
5	E	5603[C]	THA	3	0
5	A	1603[D]	THA	3	0
5	A	1603[A]	THA	3	0
5	C	3601[D]	THA	4	0
5	B	2603[D]	THA	1	0
4	A	1602	SIA	31	0
5	C	3601[A]	THA	3	0
5	B	2603[A]	THA	2	0
5	F	6603[B]	THA	2	0
5	A	1603[B]	THA	3	0
5	F	6603[C]	THA	3	0
5	D	4603[E]	THA	3	0
5	C	3601[B]	THA	1	0
5	B	2603[B]	THA	5	0
3	B	2601	NAG	3	0
5	D	4603[A]	THA	4	0
3	E	5601	NAG	1	0
5	C	3601[C]	THA	1	0
5	B	2603[C]	THA	1	0
5	A	1603[C]	THA	4	0
3	F	6602	NAG	1	0
3	F	6601	NAG	1	0
5	D	4603[B]	THA	4	0
5	E	5603[E]	THA	4	0
5	E	5603[D]	THA	3	0
4	E	5602	SIA	7	0
5	E	5603[A]	THA	2	0
5	D	4603[C]	THA	2	0
4	B	2602	SIA	16	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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.