



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 03:07 AM BST

PDB ID : 2HRQ
Title : Crystal structure of Human Liver Carboxylesterase 1 (hCE1) in covalent complex with the nerve agent Soman (GD)
Authors : Fleming, C.D.; Redinbo, M.R.
Deposited on : 2006-07-20
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

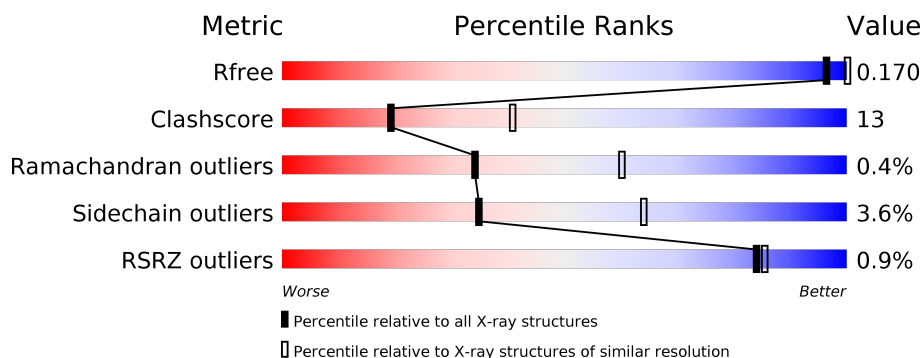
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



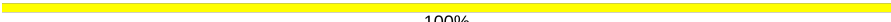
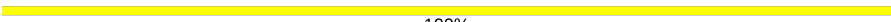
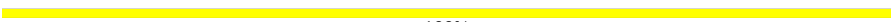
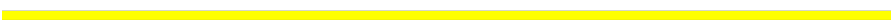


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	532	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div>.</div> </div> </div>
1	B	532	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>24%</div> <div>.</div> </div> </div>
1	C	532	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>27%</div> <div>.</div> </div> </div>
1	D	532	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>25%</div> <div>.</div> </div> </div>
1	E	532	<div> <div></div> <div> <div></div> <div>75%</div> <div>23%</div> <div>.</div> </div> </div>
1	F	532	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>24%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 100%
2	I	2	 100%
2	J	2	 100%
2	K	2	 100%
2	L	2	 100%

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
5	SIA	D	482	-	-	-	X
6	SO4	F	685	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 26340 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.

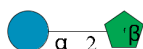
- Molecule 1 is a protein called Liver carboxylesterase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	B	531	Total	C	N	O	S	0	0	0
			4124	2659	684	761	20			
1	C	531	Total	C	N	O	S	0	0	0
			4124	2659	684	761	20			
1	D	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	E	531	Total	C	N	O	S	0	0	0
			4124	2659	684	761	20			
1	F	531	Total	C	N	O	S	0	0	0
			4125	2659	684	762	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP Q9UK77
B	?	-	GLN	deletion	UNP Q9UK77
C	?	-	GLN	deletion	UNP Q9UK77
D	?	-	GLN	deletion	UNP Q9UK77
E	?	-	GLN	deletion	UNP Q9UK77
F	?	-	GLN	deletion	UNP Q9UK77

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



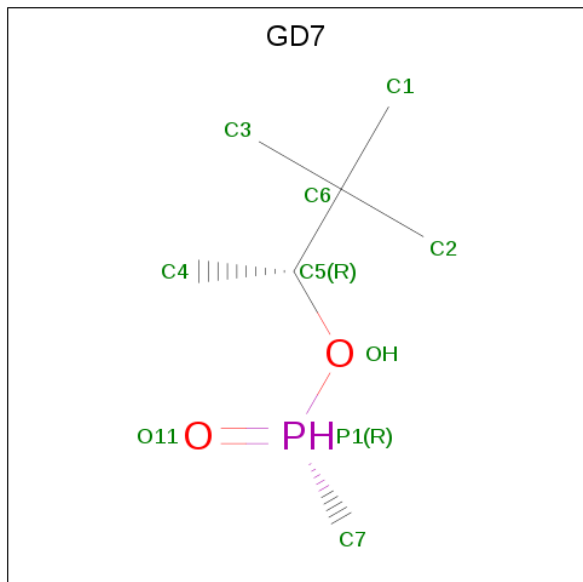
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	G	2	Total	C	O	0	0	0
			23	12	11			

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	H	2	Total	C	O	0	0	0
			23	12	11			
2	I	2	Total	C	O	0	0	0
			23	12	11			
2	J	2	Total	C	O	0	0	0
			23	12	11			
2	K	2	Total	C	O	0	0	0
			23	12	11			
2	L	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is (1R)-1,2,2-TRIMETHYLPROPYL (R)-METHYLPHOSPHINATE (three-letter code: GD7) (formula: C₇H₁₇O₂P).



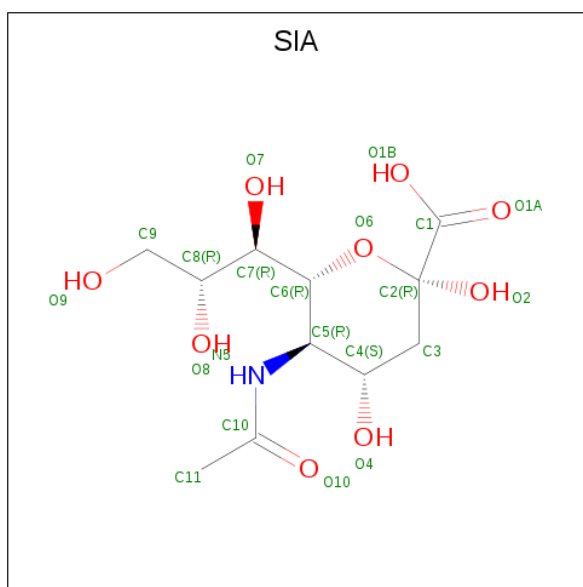
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			10	7	2	1		
3	B	1	Total	C	O	P	0	0
			10	7	2	1		
3	C	1	Total	C	O	P	0	0
			10	7	2	1		
3	D	1	Total	C	O	P	0	0
			10	7	2	1		
3	E	1	Total	C	O	P	0	0
			10	7	2	1		
3	F	1	Total	C	O	P	0	0
			10	7	2	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	C	1	Total	O	S	0	0
			5	4	1		
6	C	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		
6	F	1	Total	O	S	0	0
			5	4	1		
6	F	1	Total	O	S	0	0
			5	4	1		

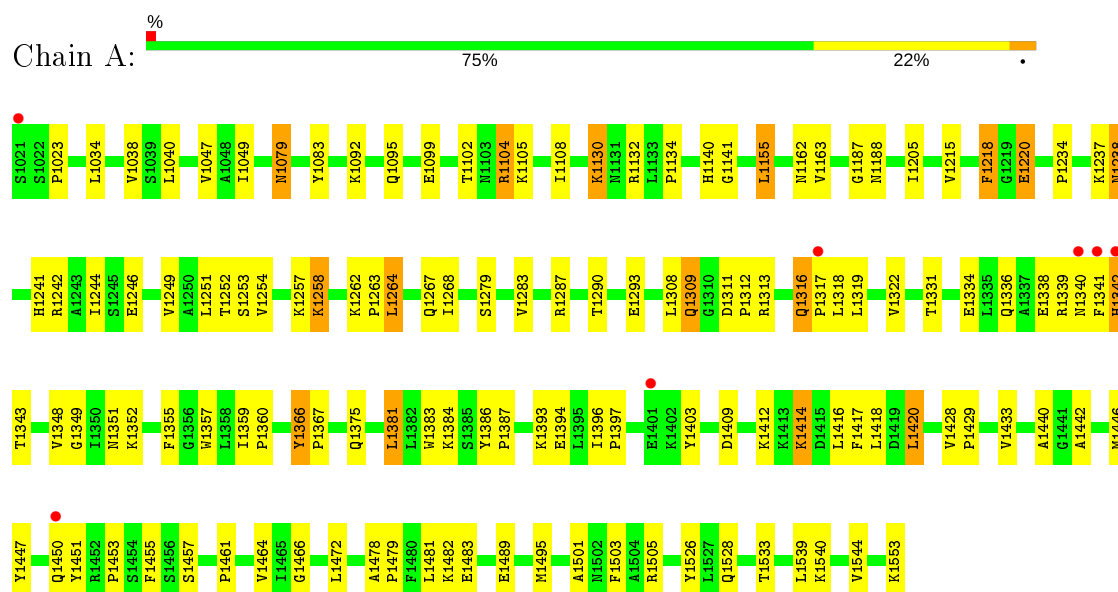
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	193	Total 193	O 193	0	0
7	B	166	Total 166	O 166	0	0
7	C	205	Total 205	O 205	0	0
7	D	186	Total 186	O 186	0	0
7	E	153	Total 153	O 153	0	0
7	F	212	Total 212	O 212	0	0

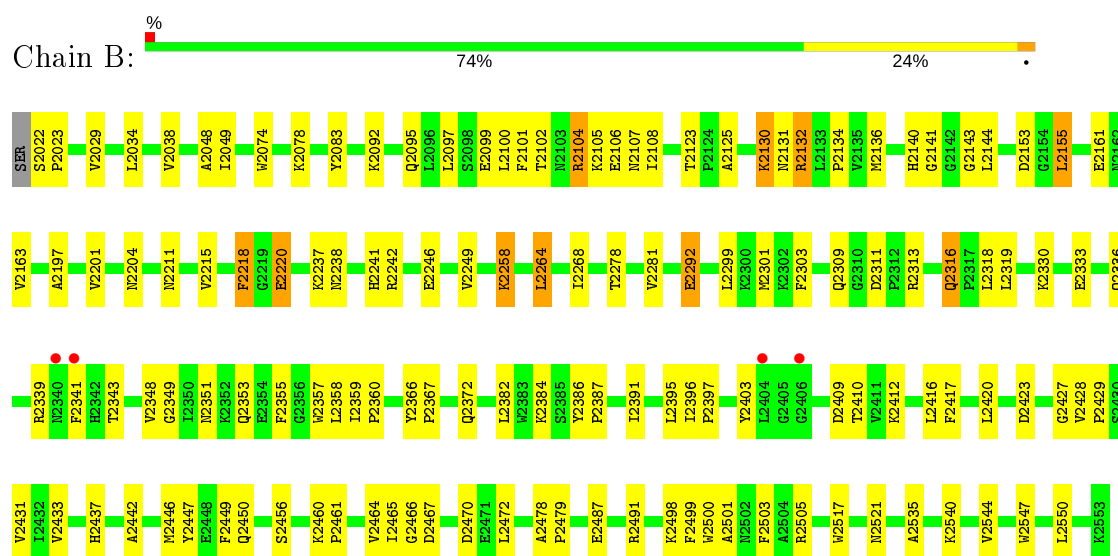
3 Residue-property plots

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.

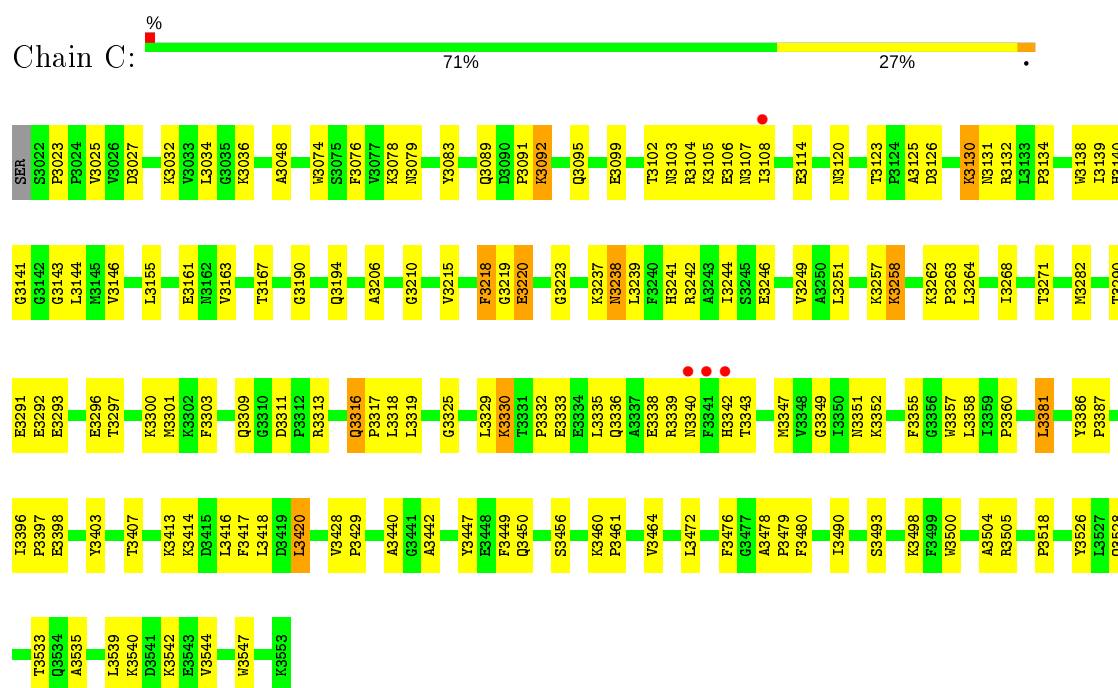
- Molecule 1: Liver carboxylesterase 1



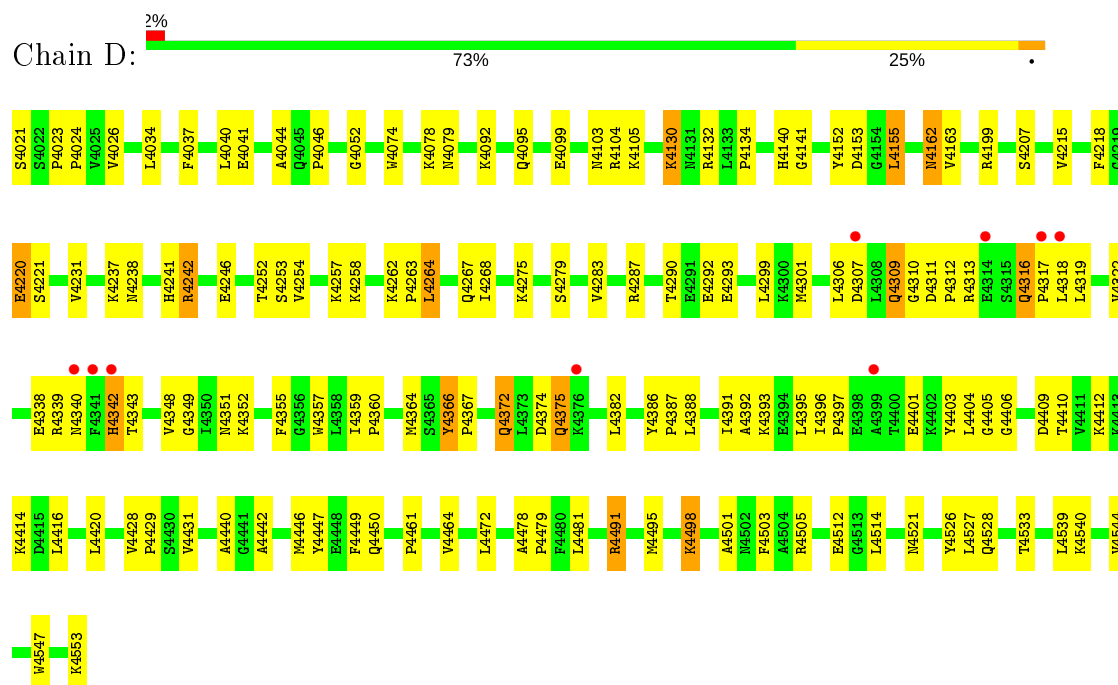
- Molecule 1: Liver carboxylesterase 1



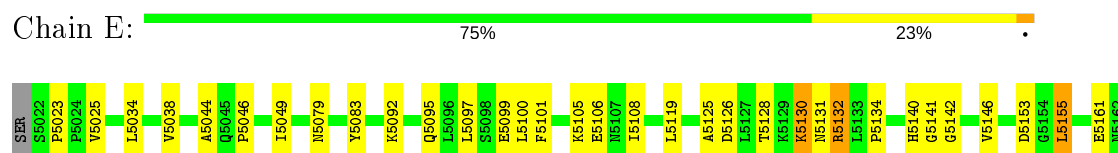
- Molecule 1: Liver carboxylesterase 1

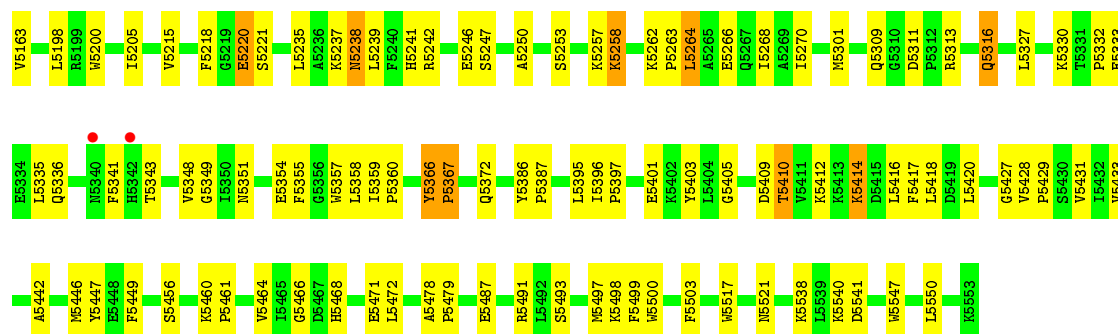


- Molecule 1: Liver carboxylesterase 1

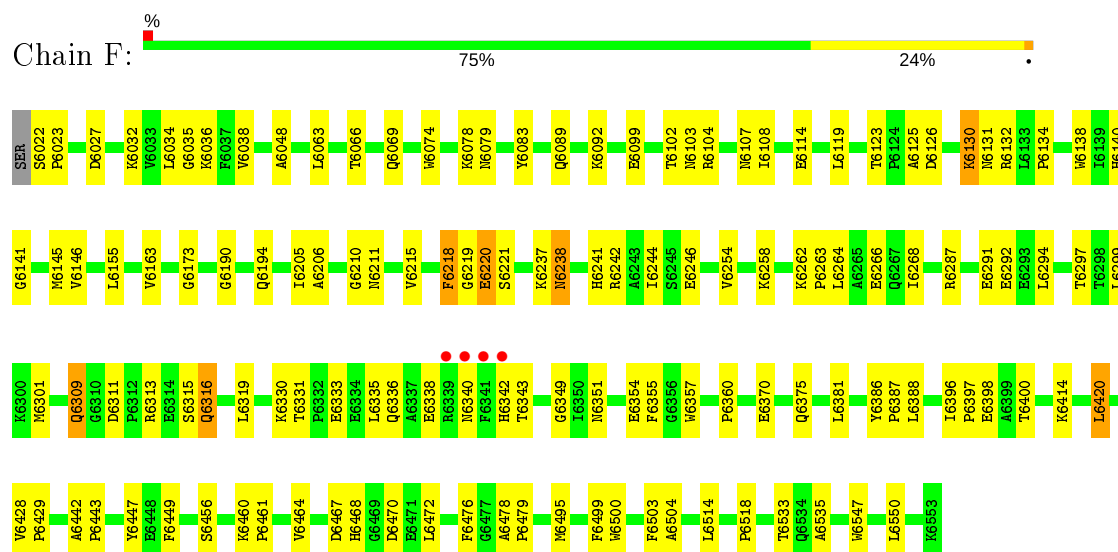


- Molecule 1: Liver carboxylesterase 1

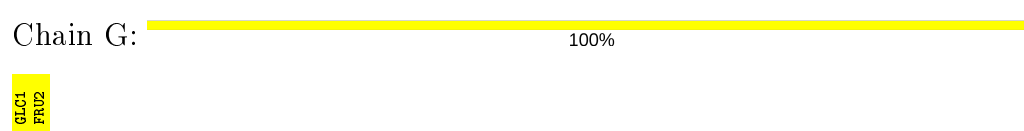




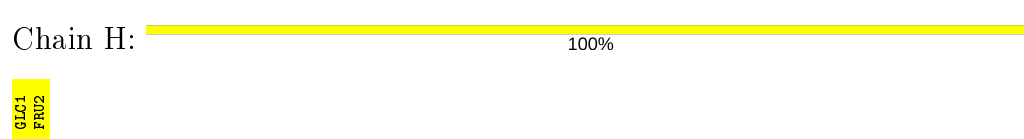
- Molecule 1: Liver carboxylesterase 1



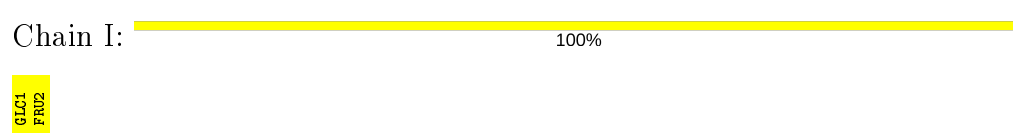
- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain J:  100%

GLC1
FRU2

- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain K:  100%

GLC1
FRU2

- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain L:  100%

GLC1
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.46 Å 181.19 Å 203.05 Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	42.91 – 2.70 42.90 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (42.91-2.70) 99.8 (42.90-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.79 (at 2.69 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.170 , 0.225 0.171 , 0.170	Depositor DCC
R_{free} test set	5468 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 23.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.457 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	26340	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, GD7, GLC, SIA, SO4, FRU

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	0.36	1/4236 (0.0%)	0.59	1/5754 (0.0%)
1	B	0.35	1/4230 (0.0%)	0.58	1/5746 (0.0%)
1	C	0.38	1/4230 (0.0%)	0.61	1/5746 (0.0%)
1	D	0.36	1/4236 (0.0%)	0.59	1/5754 (0.0%)
1	E	0.35	1/4230 (0.0%)	0.58	1/5746 (0.0%)
1	F	0.37	1/4231 (0.0%)	0.61	1/5746 (0.0%)
All	All	0.36	6/25393 (0.0%)	0.59	6/34492 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	3092	LYS	CE-NZ	-6.21	1.33	1.49
1	F	6092	LYS	CE-NZ	-6.18	1.33	1.49
1	B	2092	LYS	CE-NZ	-6.13	1.33	1.49
1	E	5092	LYS	CE-NZ	-6.09	1.33	1.49
1	A	1092	LYS	CE-NZ	-6.08	1.33	1.49

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1092	LYS	CD-CE-NZ	5.58	124.52	111.70
1	D	4092	LYS	CD-CE-NZ	5.56	124.48	111.70
1	C	3092	LYS	CD-CE-NZ	5.55	124.46	111.70
1	F	6092	LYS	CD-CE-NZ	5.51	124.38	111.70
1	E	5092	LYS	CD-CE-NZ	5.35	124.00	111.70

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	4130	0	4129	106	0
1	B	4124	0	4125	102	0
1	C	4124	0	4125	113	0
1	D	4130	0	4129	109	0
1	E	4124	0	4125	98	0
1	F	4125	0	4124	101	0
2	G	23	0	21	0	0
2	H	23	0	21	0	0
2	I	23	0	21	0	0
2	J	23	0	21	0	0
2	K	23	0	21	0	0
2	L	23	0	21	0	0
3	A	10	0	16	0	0
3	B	10	0	16	0	0
3	C	10	0	16	0	0
3	D	10	0	16	0	0
3	E	10	0	16	2	0
3	F	10	0	16	0	0
4	A	14	0	13	5	0
4	B	14	0	13	0	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
4	E	14	0	13	1	0
4	F	14	0	13	2	0
5	A	21	0	18	6	0
5	B	21	0	18	5	0
5	C	21	0	18	5	0
5	D	21	0	18	2	0
5	E	21	0	18	6	0
5	F	21	0	18	4	0
6	A	10	0	0	0	0
6	B	10	0	0	0	0
6	C	10	0	0	1	0
6	D	10	0	0	0	0
6	E	5	0	0	0	0
6	F	15	0	0	0	0
7	A	193	0	0	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	166	0	0	11	0
7	C	205	0	0	8	0
7	D	186	0	0	11	0
7	E	153	0	0	6	0
7	F	212	0	0	9	0
All	All	26340	0	25165	648	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 13.

The worst 5 of 648 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)
4:A:179:NAG:H82	7:A:8924:HOH:O	1.48	1.12
1:C:3343:THR:HB	1:C:3442:ALA:HB2	1.23	1.11
1:F:6343:THR:HB	1:F:6442:ALA:HB2	1.14	1.10
1:D:4491:ARG:HB2	1:D:4491:ARG:HH11	1.17	1.08
1:A:1079:ASN:H	5:A:182:SIA:H112	1.23	1.00

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	530/532 (100%)	497 (94%)	29 (6%)	4 (1%)	19	43
1	B	529/532 (99%)	495 (94%)	34 (6%)	0	100	100
1	C	529/532 (99%)	502 (95%)	25 (5%)	2 (0%)	34	60
1	D	530/532 (100%)	496 (94%)	32 (6%)	2 (0%)	34	60
1	E	529/532 (99%)	498 (94%)	27 (5%)	4 (1%)	19	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	529/532 (99%)	500 (94%)	28 (5%)	1 (0%)	47	73
All	All	3176/3192 (100%)	2988 (94%)	175 (6%)	13 (0%)	34	60

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	5238	ASN
1	F	6238	ASN
1	C	3076	PHE
1	C	3238	ASN
1	D	4253	SER

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	A	448/448 (100%)	430 (96%)	18 (4%)	31	60
1	B	447/448 (100%)	432 (97%)	15 (3%)	37	66
1	C	447/448 (100%)	432 (97%)	15 (3%)	37	66
1	D	448/448 (100%)	426 (95%)	22 (5%)	25	52
1	E	447/448 (100%)	433 (97%)	14 (3%)	40	69
1	F	447/448 (100%)	435 (97%)	12 (3%)	44	74
All	All	2684/2688 (100%)	2588 (96%)	96 (4%)	35	64

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3358	LEU
1	D	4162	ASN
1	F	6264	LEU
1	C	3381	LEU
1	D	4021	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	3241	HIS
1	D	4140	HIS
1	F	6340	ASN
1	C	3450	GLN
1	D	4241	HIS

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 ⓘ

12 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	GLC	G	1	2	11,11,12	1.65	2 (18%)	15,15,17	0.95	0
2	FRU	G	2	2	11,12,12	1.60	1 (9%)	10,18,18	1.07	1 (10%)
2	GLC	H	1	2	11,11,12	1.67	3 (27%)	15,15,17	1.02	1 (6%)
2	FRU	H	2	2	11,12,12	1.51	1 (9%)	10,18,18	0.89	0
2	GLC	I	1	2	11,11,12	1.53	2 (18%)	15,15,17	1.01	1 (6%)
2	FRU	I	2	2	11,12,12	1.49	1 (9%)	10,18,18	0.94	0
2	GLC	J	1	2	11,11,12	1.59	2 (18%)	15,15,17	0.99	1 (6%)
2	FRU	J	2	2	11,12,12	1.70	1 (9%)	10,18,18	0.75	0
2	GLC	K	1	2	11,11,12	1.65	2 (18%)	15,15,17	1.01	1 (6%)
2	FRU	K	2	2	11,12,12	1.52	1 (9%)	10,18,18	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	L	1	2	11,11,12	1.54	1 (9%)	15,15,17	1.07	1 (6%)
2	FRU	L	2	2	11,12,12	1.39	1 (9%)	10,18,18	1.05	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
2	GLC	G	1	2	-	2/2/19/22	0/1/1/1
2	FRU	G	2	2	-	5/5/24/24	0/1/1/1
2	GLC	H	1	2	-	2/2/19/22	0/1/1/1
2	FRU	H	2	2	-	1/5/24/24	0/1/1/1
2	GLC	I	1	2	-	0/2/19/22	0/1/1/1
2	FRU	I	2	2	-	0/5/24/24	0/1/1/1
2	GLC	J	1	2	-	0/2/19/22	0/1/1/1
2	FRU	J	2	2	-	2/5/24/24	0/1/1/1
2	GLC	K	1	2	-	2/2/19/22	0/1/1/1
2	FRU	K	2	2	-	2/5/24/24	0/1/1/1
2	GLC	L	1	2	-	0/2/19/22	0/1/1/1
2	FRU	L	2	2	-	0/5/24/24	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	2	FRU	O2-C2	5.37	1.49	1.40
2	G	2	FRU	O2-C2	5.11	1.49	1.40
2	K	2	FRU	O2-C2	4.74	1.48	1.40
2	H	2	FRU	O2-C2	4.67	1.48	1.40
2	I	2	FRU	O2-C2	4.58	1.48	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	1	GLC	C1-O5-C5	2.32	115.33	112.19
2	K	1	GLC	C1-O5-C5	2.20	115.18	112.19
2	G	2	FRU	O1-C1-C2	-2.18	107.24	111.86
2	H	1	GLC	C1-O5-C5	2.13	115.08	112.19
2	J	1	GLC	C1-O5-C5	2.10	115.04	112.19

There are no chirality outliers.

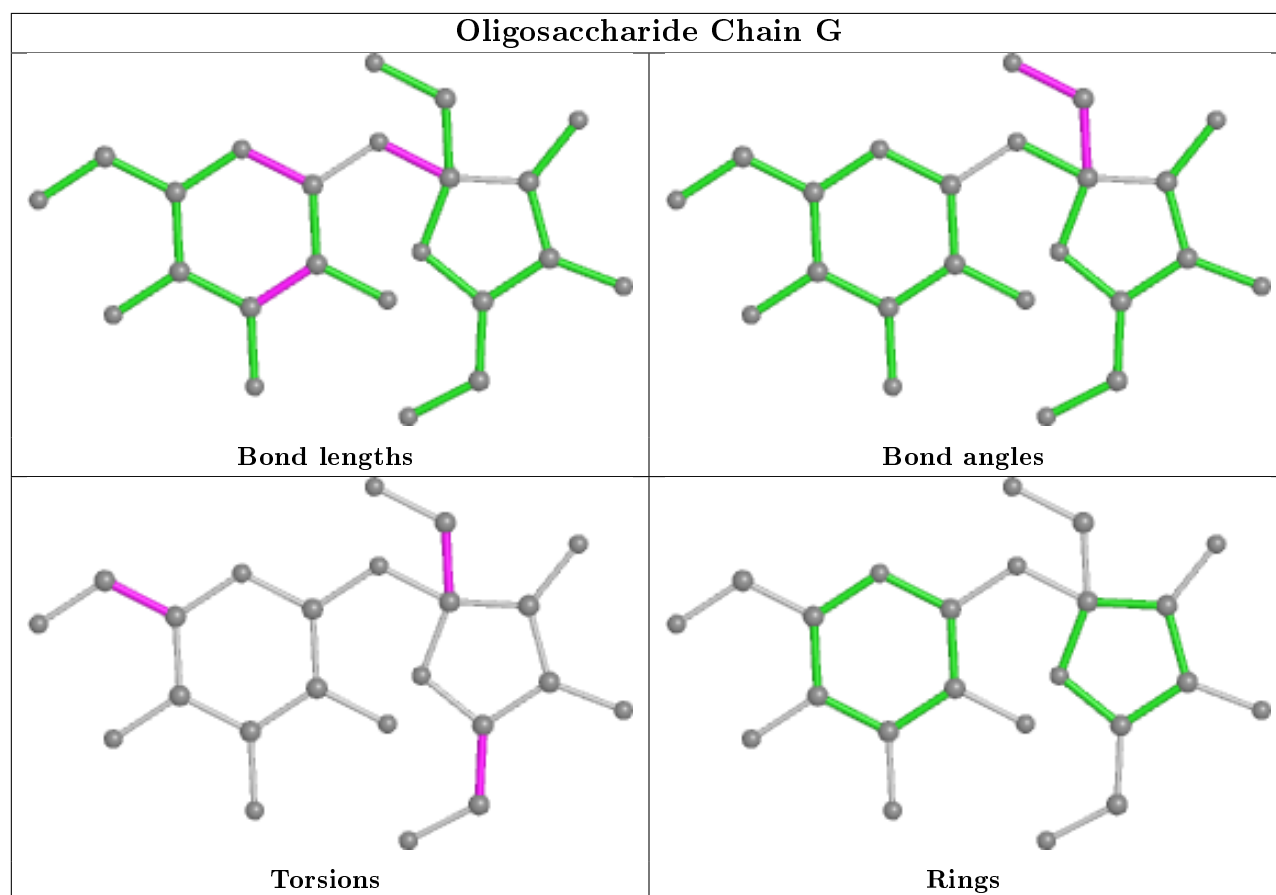
5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	2	FRU	O1-C1-C2-O2
2	J	2	FRU	O5-C5-C6-O6
2	G	2	FRU	O5-C5-C6-O6
2	J	2	FRU	C4-C5-C6-O6
2	G	2	FRU	C4-C5-C6-O6

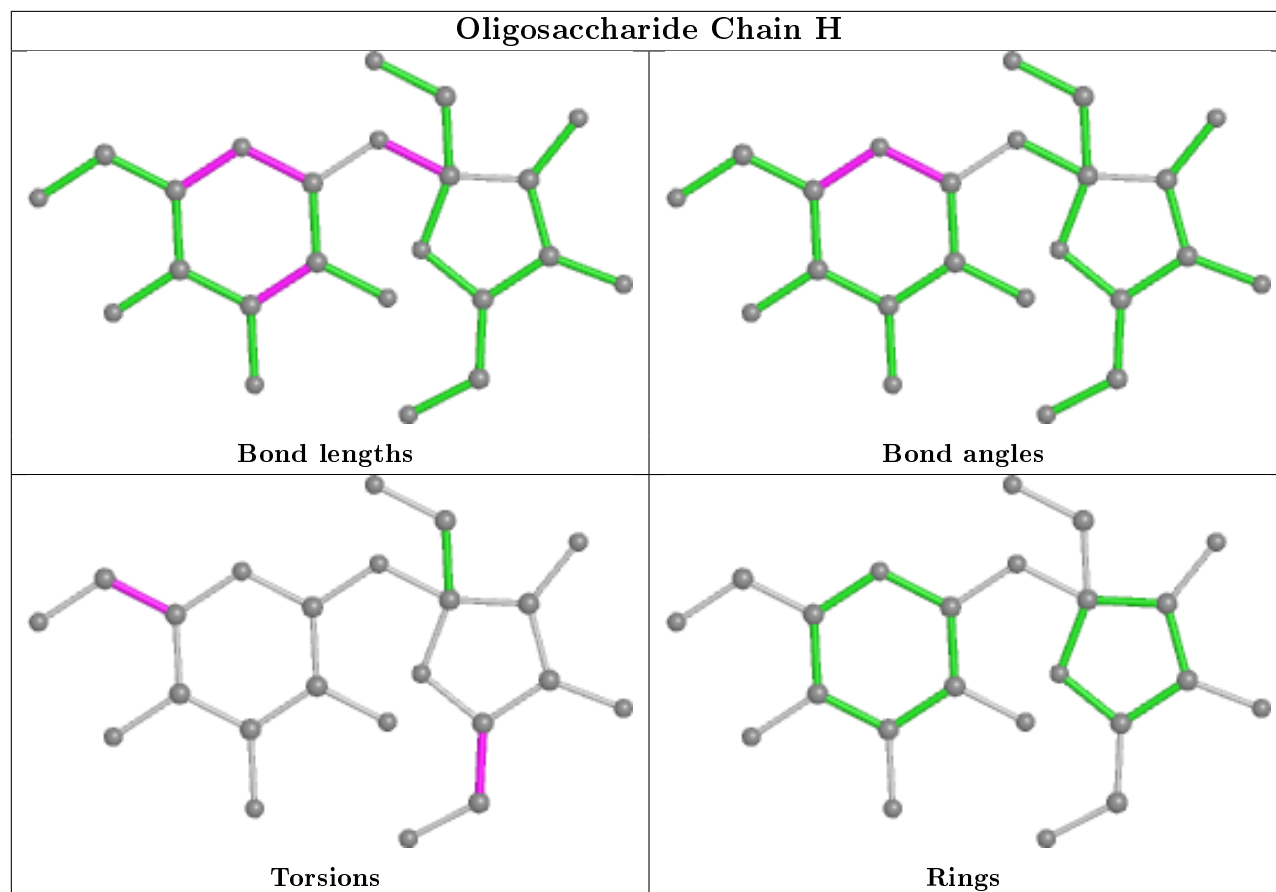
There are no ring outliers.

No monomer is involved in short contacts.

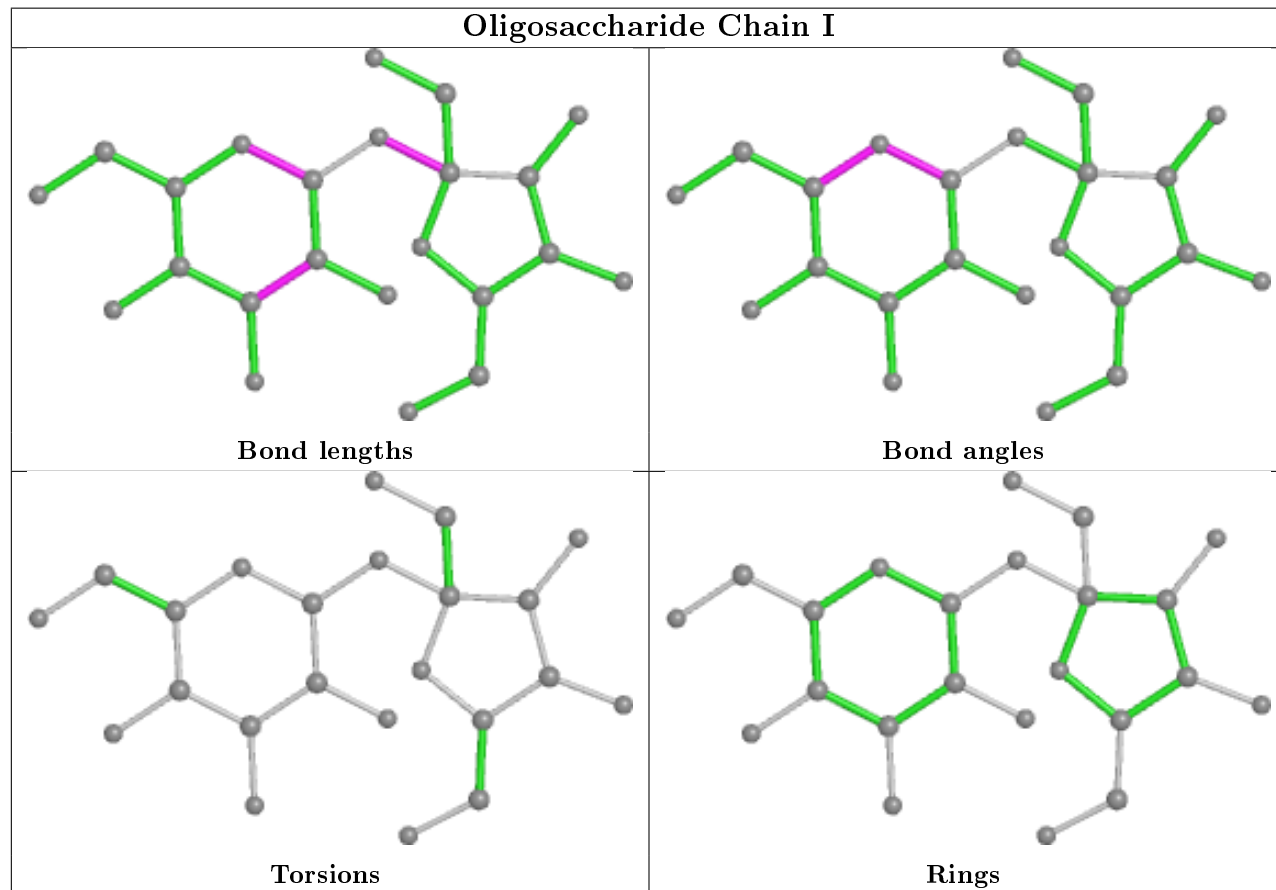
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



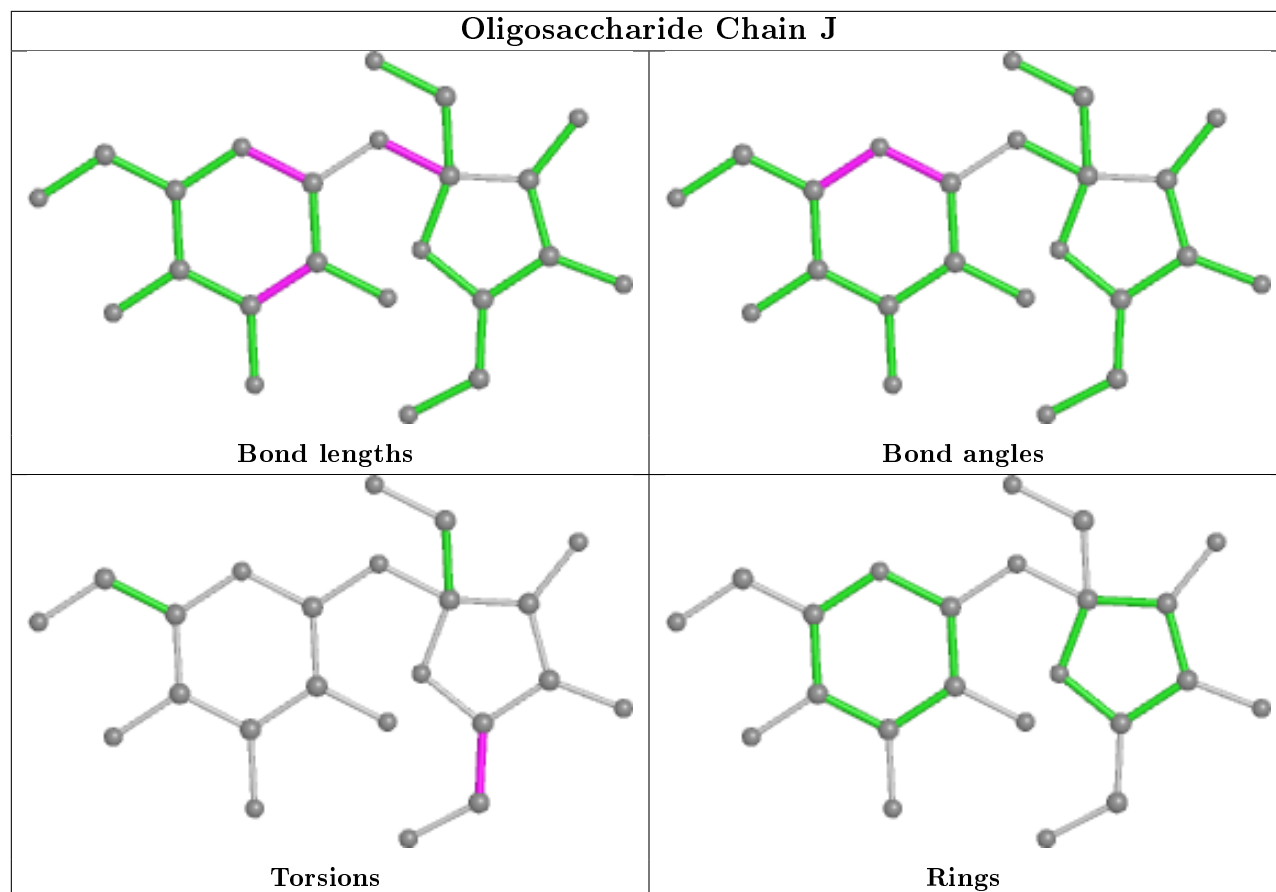
Oligosaccharide Chain H



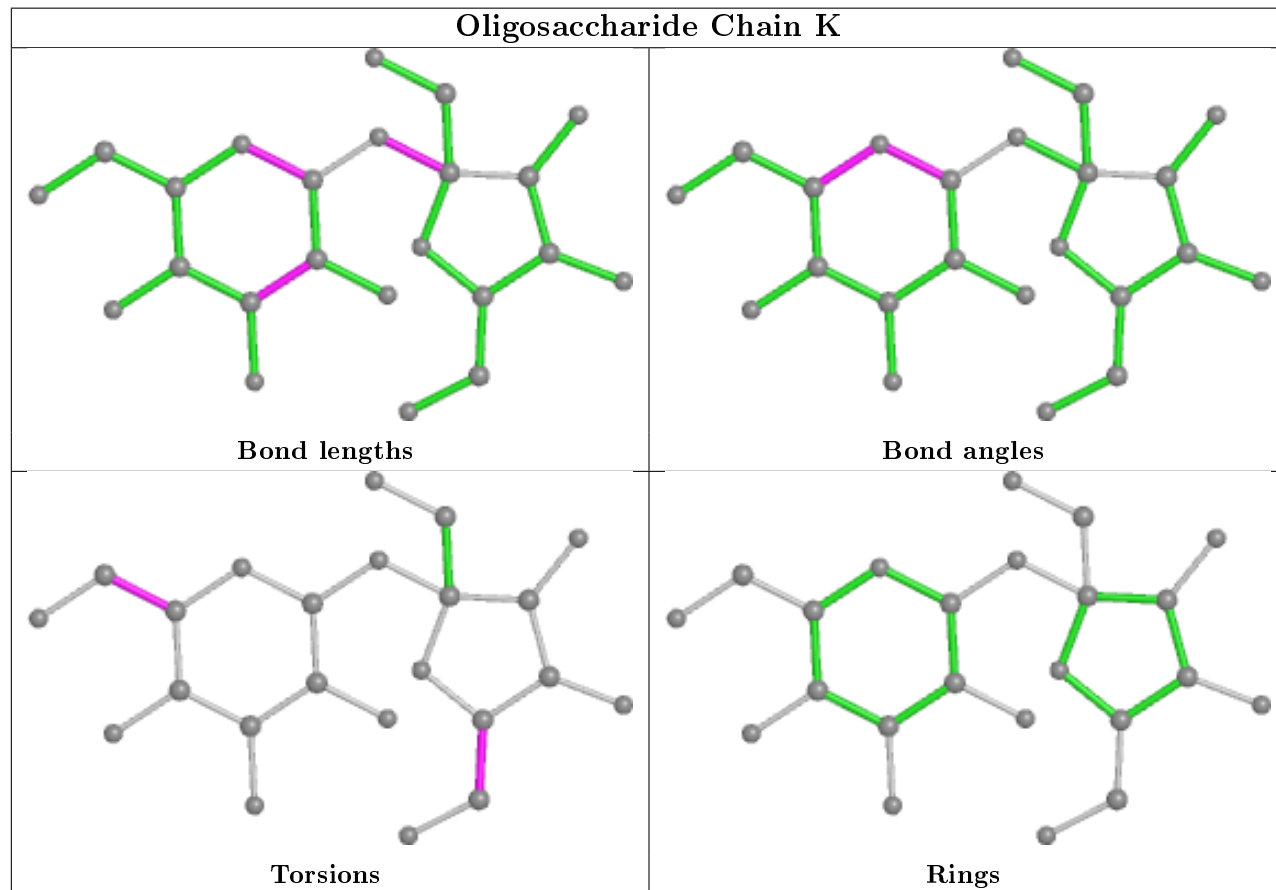
Oligosaccharide Chain I

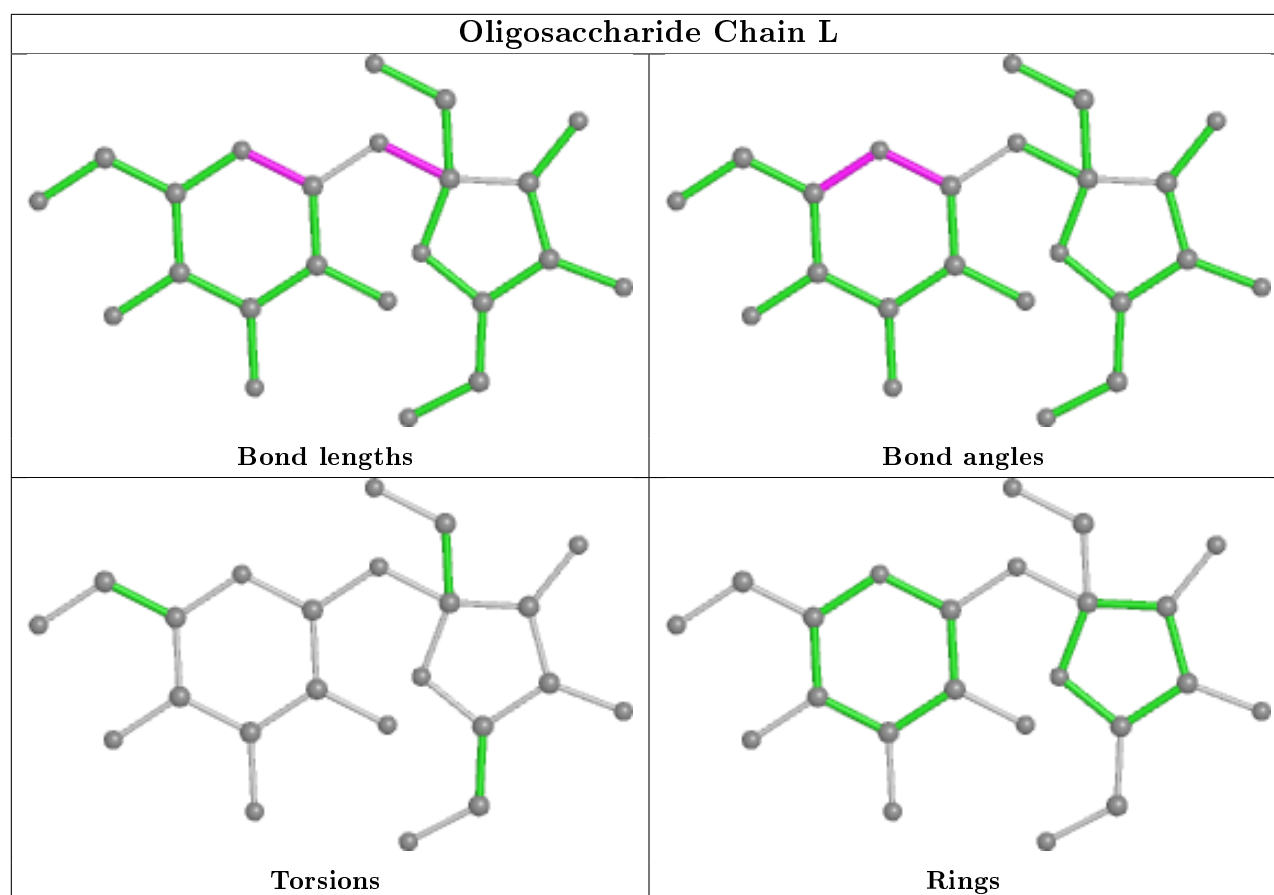


Oligosaccharide Chain J



Oligosaccharide Chain K





5.6 Ligand geometry [i](#)

30 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	GD7	B	1	1	6,9,9	0.86	0	7,13,13	0.29	0
3	GD7	C	1	1	6,9,9	0.83	0	7,13,13	0.24	0
6	SO4	F	685	-	4,4,4	0.28	0	6,6,6	0.06	0
4	NAG	B	279	1	14,14,15	0.74	0	17,19,21	0.73	0
6	SO4	F	485	-	4,4,4	0.27	0	6,6,6	0.06	0
4	NAG	E	579	1	14,14,15	0.57	0	17,19,21	0.67	0
6	SO4	B	385	-	4,4,4	0.26	0	6,6,6	0.07	0
5	SIA	F	682	-	18,21,21	0.95	0	21,31,31	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GD7	A	1	1	6,9,9	0.83	0	7,13,13	0.14	0
6	SO4	C	184	-	4,4,4	0.26	0	6,6,6	0.08	0
6	SO4	F	684	-	4,4,4	0.25	0	6,6,6	0.05	0
5	SIA	D	482	-	18,21,21	0.89	2 (11%)	21,31,31	0.74	0
6	SO4	D	585	-	4,4,4	0.27	0	6,6,6	0.05	0
4	NAG	F	679	1	14,14,15	0.64	0	17,19,21	0.76	0
5	SIA	E	582	-	18,21,21	1.01	0	21,31,31	0.98	1 (4%)
3	GD7	E	1	1	6,9,9	0.81	0	7,13,13	0.20	0
6	SO4	E	584	-	4,4,4	0.27	0	6,6,6	0.06	0
5	SIA	C	382	-	18,21,21	0.83	0	21,31,31	0.68	1 (4%)
3	GD7	F	1	1	6,9,9	0.83	0	7,13,13	0.26	0
6	SO4	A	284	-	4,4,4	0.26	0	6,6,6	0.05	0
6	SO4	A	185	-	4,4,4	0.27	0	6,6,6	0.06	0
5	SIA	A	182	-	18,21,21	0.95	2 (11%)	21,31,31	0.67	0
3	GD7	D	1	1	6,9,9	0.86	0	7,13,13	0.13	0
6	SO4	D	484	-	4,4,4	0.27	0	6,6,6	0.05	0
6	SO4	C	384	-	4,4,4	0.26	0	6,6,6	0.05	0
6	SO4	B	285	-	4,4,4	0.25	0	6,6,6	0.12	0
4	NAG	D	479	1	14,14,15	0.80	1 (7%)	17,19,21	0.65	0
4	NAG	C	379	1	14,14,15	0.66	0	17,19,21	0.77	0
4	NAG	A	179	1	14,14,15	0.78	1 (7%)	17,19,21	0.59	0
5	SIA	B	282	-	18,21,21	1.00	1 (5%)	21,31,31	0.93	1 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GD7	E	1	1	-	0/6/10/10	-
3	GD7	B	1	1	-	0/6/10/10	-
3	GD7	C	1	1	-	0/6/10/10	-
5	SIA	F	682	-	-	7/14/38/38	0/1/1/1
4	NAG	B	279	1	-	6/6/23/26	0/1/1/1
3	GD7	A	1	1	-	0/6/10/10	-
5	SIA	C	382	-	-	4/14/38/38	0/1/1/1
3	GD7	F	1	1	-	0/6/10/10	-
4	NAG	E	579	1	-	6/6/23/26	0/1/1/1
4	NAG	C	379	1	-	6/6/23/26	0/1/1/1
5	SIA	D	482	-	-	4/14/38/38	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	179	1	-	6/6/23/26	0/1/1/1
5	SIA	A	182	-	-	8/14/38/38	0/1/1/1
3	GD7	D	1	1	-	0/6/10/10	-
4	NAG	F	679	1	-	6/6/23/26	0/1/1/1
4	NAG	D	479	1	-	6/6/23/26	0/1/1/1
5	SIA	E	582	-	-	8/14/38/38	0/1/1/1
5	SIA	B	282	-	-	11/14/38/38	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	479	NAG	C1-C2	2.44	1.56	1.52
5	D	482	SIA	O6-C2	2.35	1.45	1.43
4	A	179	NAG	C1-C2	2.24	1.55	1.52
5	A	182	SIA	C3-C2	2.11	1.54	1.51
5	B	282	SIA	C7-C6	2.09	1.55	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	282	SIA	O6-C6-C7	2.78	111.58	107.29
5	E	582	SIA	O6-C6-C7	2.77	111.56	107.29
5	C	382	SIA	O6-C6-C7	2.00	110.38	107.29

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	279	NAG	C8-C7-N2-C2
4	B	279	NAG	O7-C7-N2-C2
4	E	579	NAG	C8-C7-N2-C2
4	E	579	NAG	O7-C7-N2-C2
5	F	682	SIA	C4-C5-N5-C10

There are no ring outliers.

11 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	579	NAG	1	0

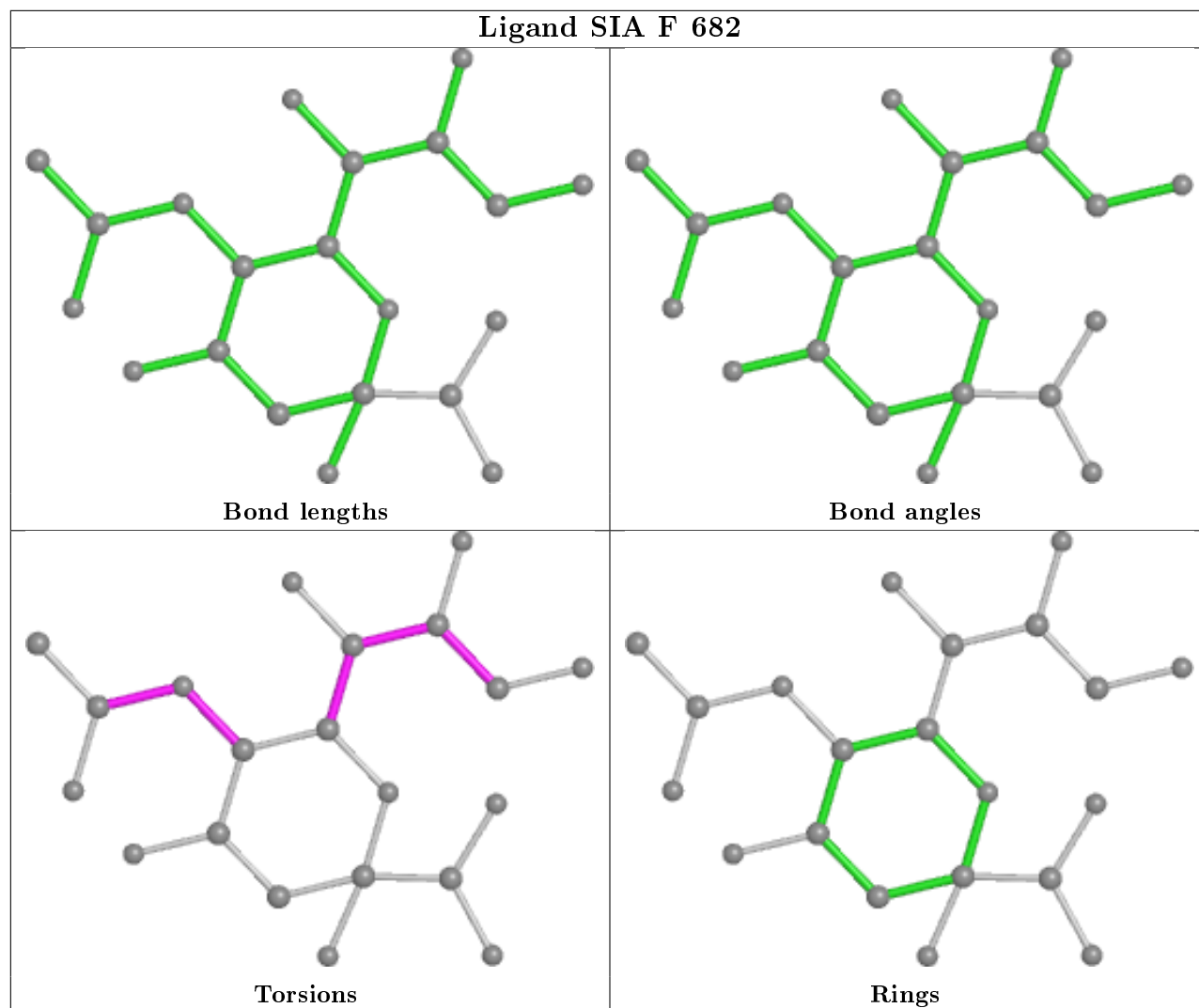
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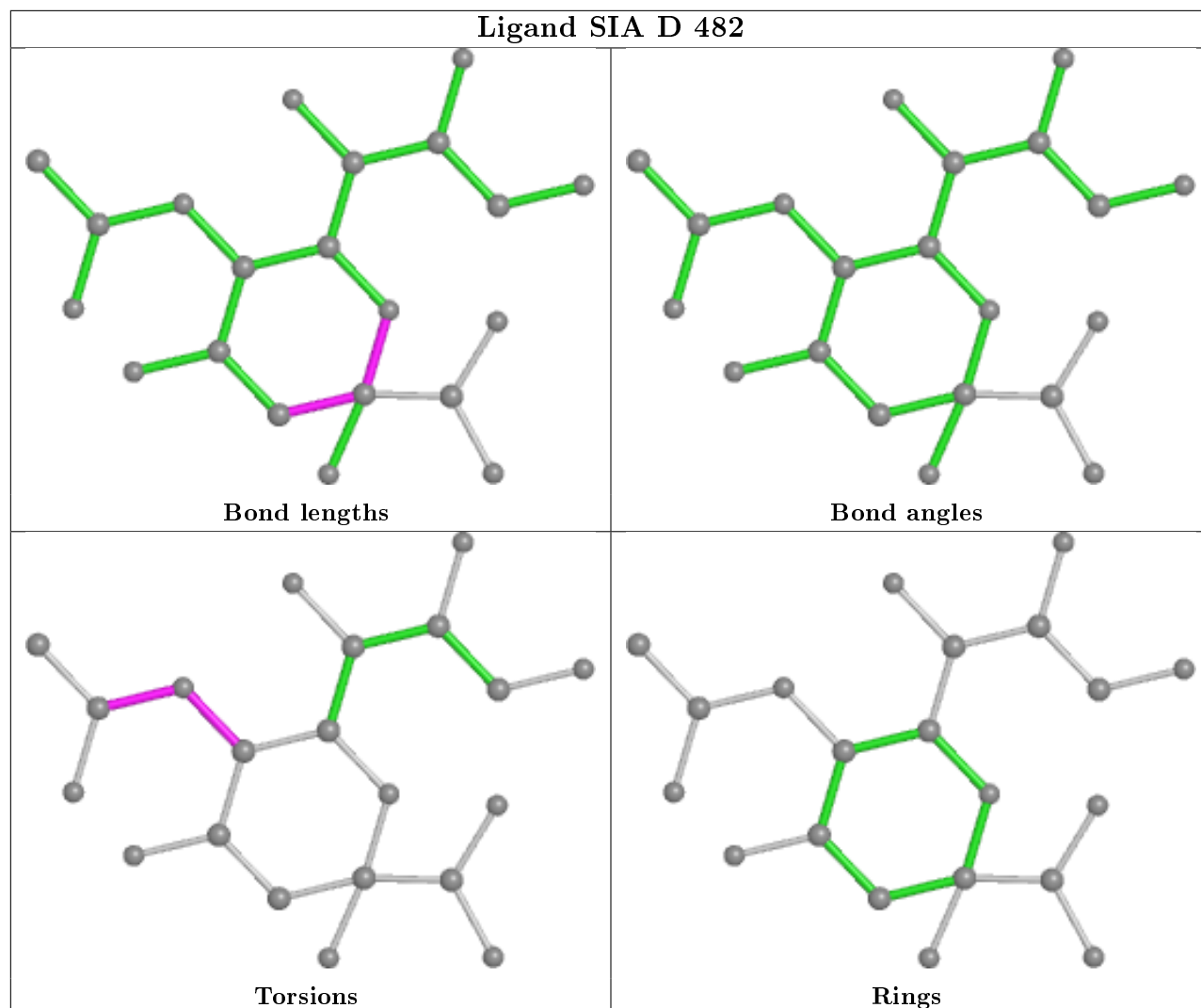
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	682	SIA	4	0
6	C	184	SO4	1	0
5	D	482	SIA	2	0
4	F	679	NAG	2	0
5	E	582	SIA	6	0
3	E	1	GD7	2	0
5	C	382	SIA	5	0
5	A	182	SIA	6	0
4	A	179	NAG	5	0
5	B	282	SIA	5	0

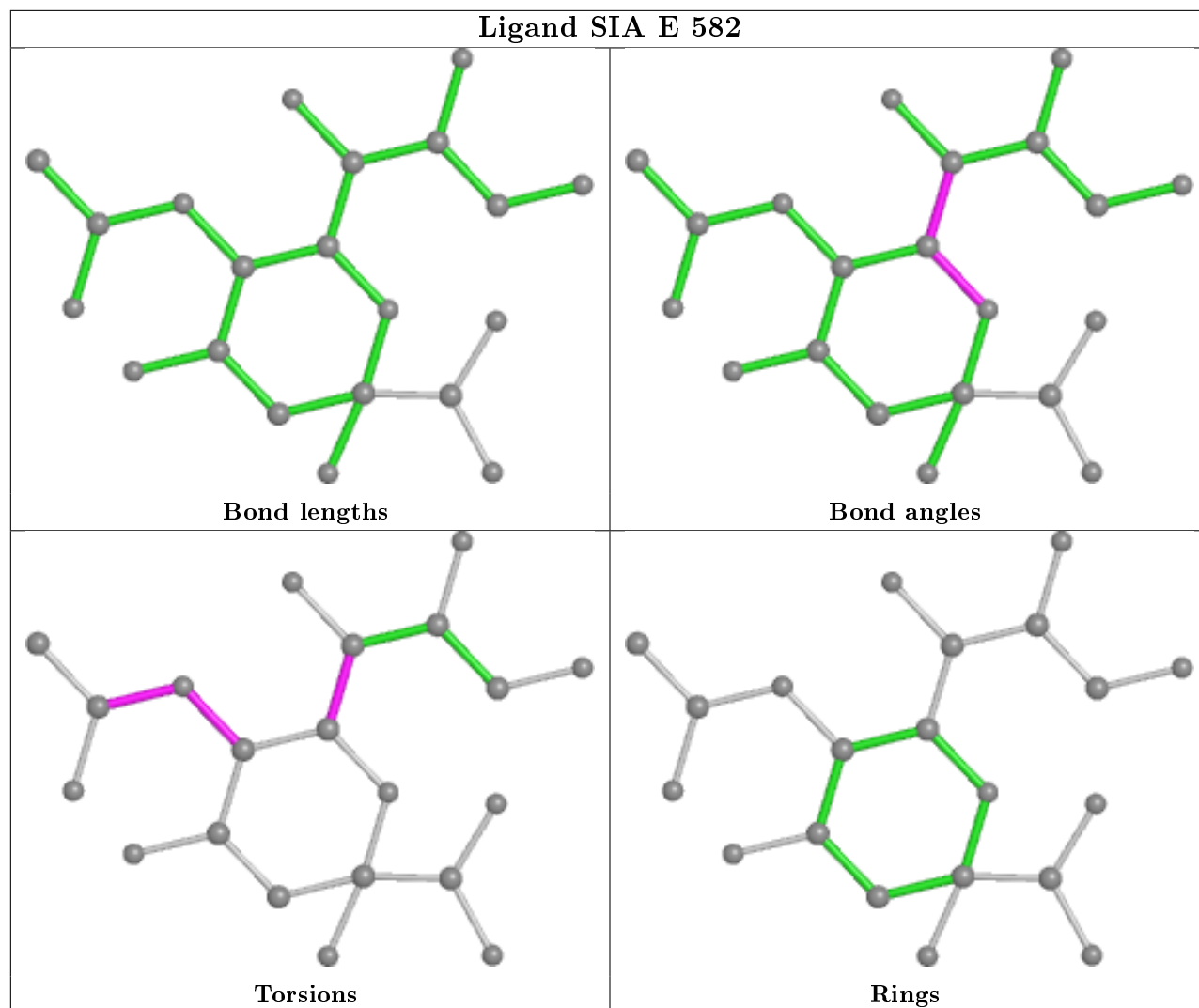
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 SIA F 682

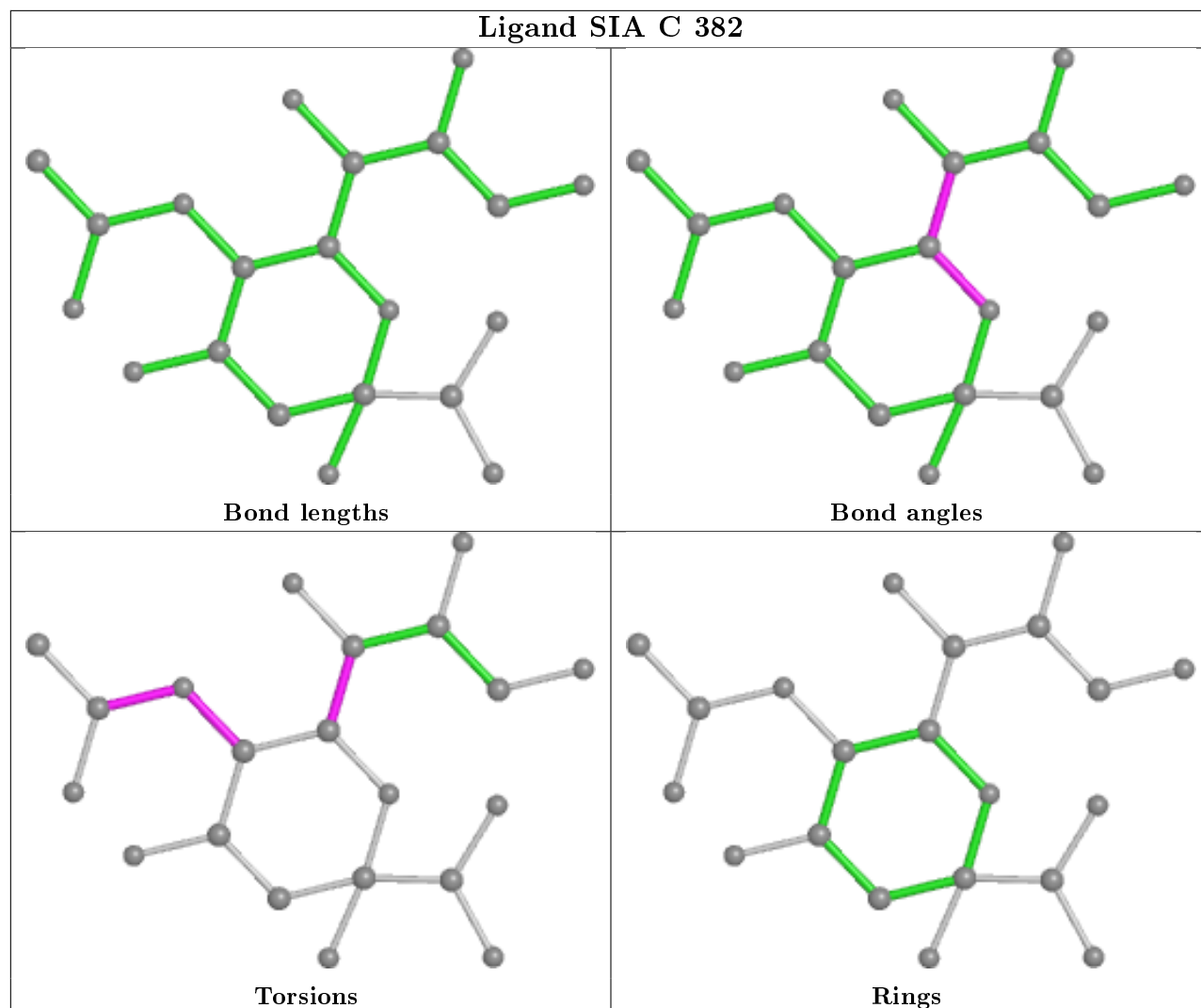


Ligand SIA D 482

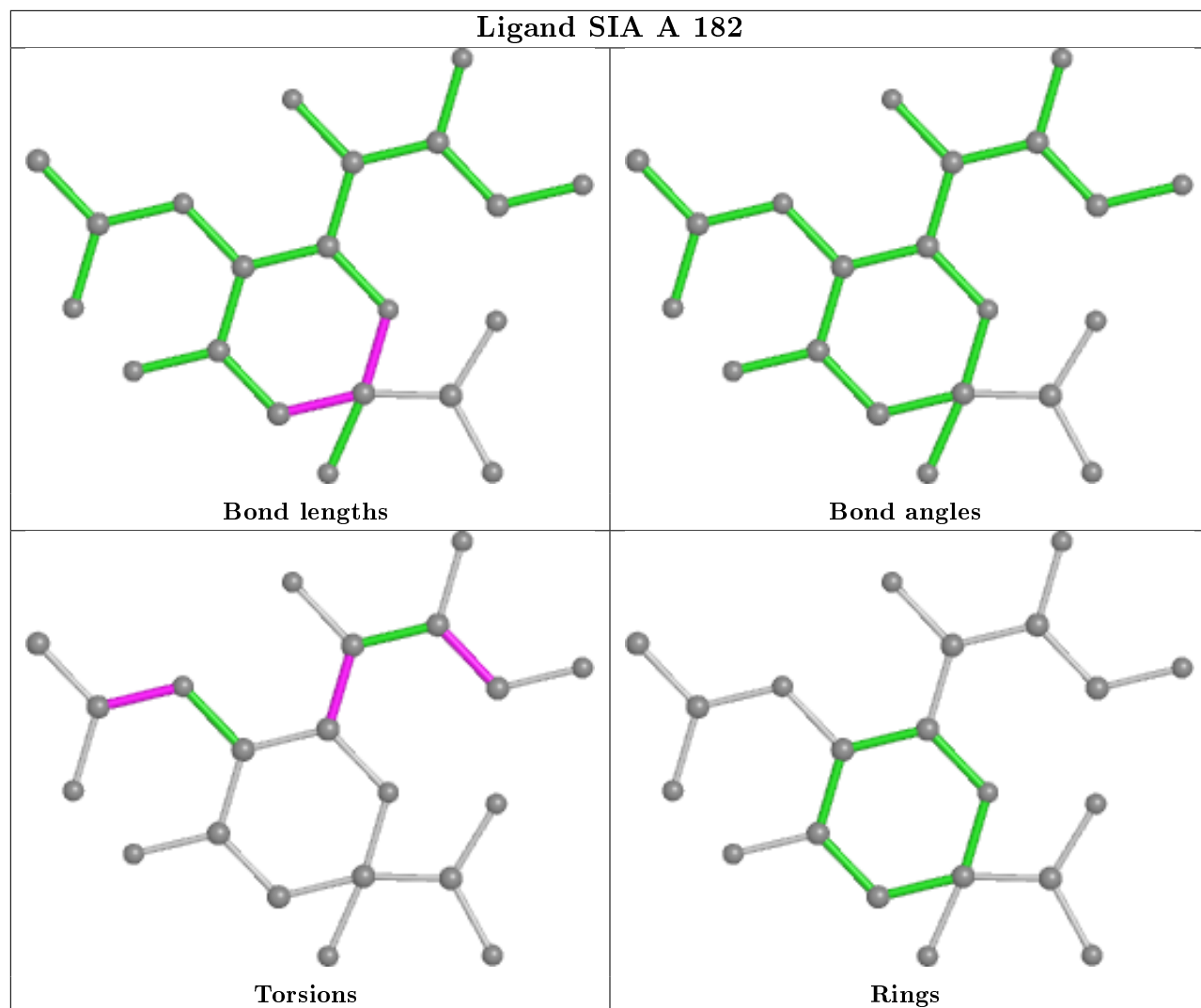


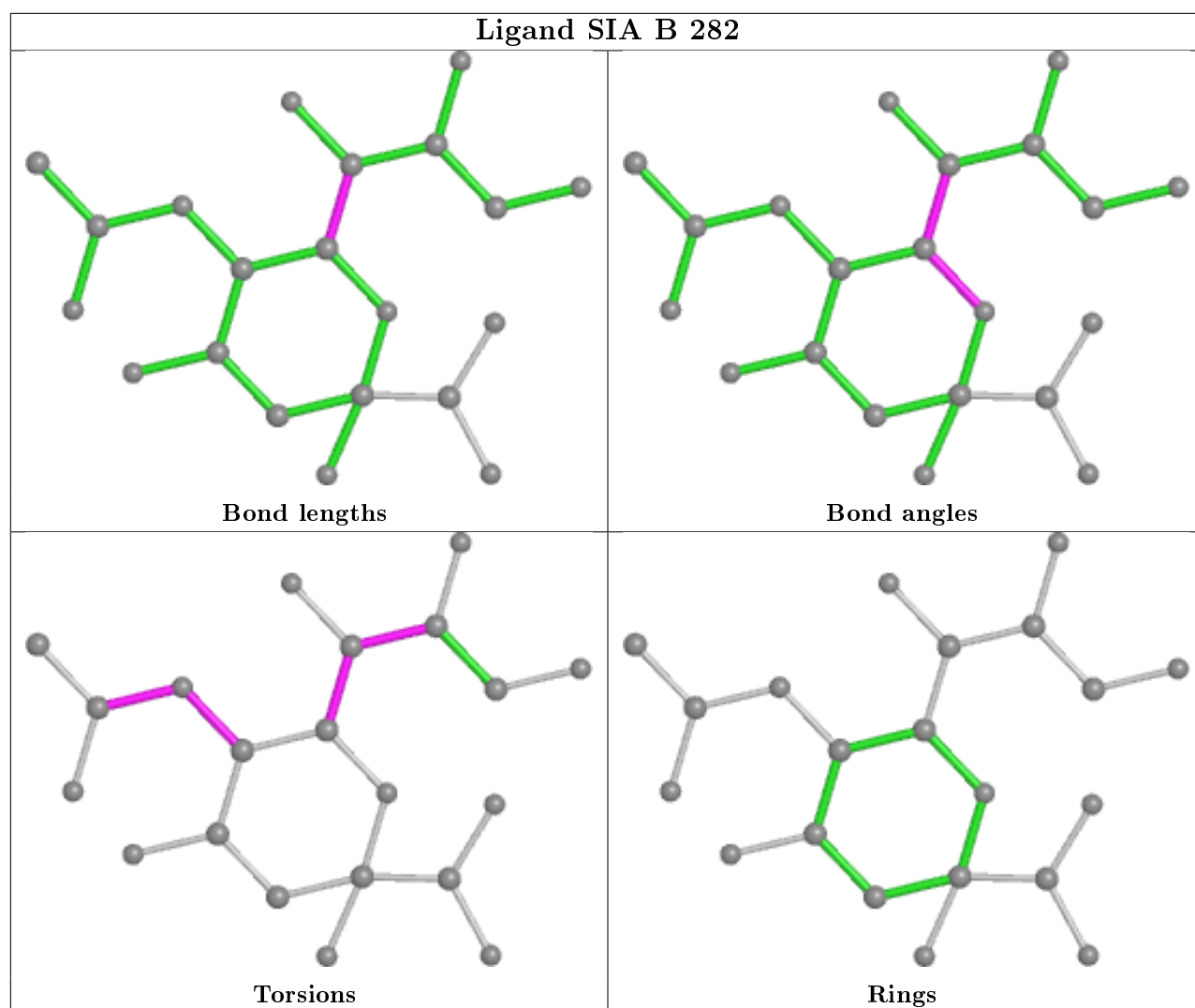


Ligand SIA C 382



Ligand SIA A 182





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	532/532 (100%)	-0.21	7 (1%) 77 78	10, 27, 69, 89	0
1	B	531/532 (99%)	-0.21	4 (0%) 86 87	12, 32, 68, 90	0
1	C	531/532 (99%)	-0.35	4 (0%) 86 87	6, 24, 46, 83	0
1	D	532/532 (100%)	-0.21	9 (1%) 70 72	9, 27, 69, 89	0
1	E	531/532 (99%)	-0.19	2 (0%) 92 93	11, 31, 69, 88	0
1	F	531/532 (99%)	-0.34	4 (0%) 86 87	8, 25, 46, 92	0
All	All	3188/3192 (99%)	-0.25	30 (0%) 84 85	6, 27, 64, 92	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1342	HIS	6.3
1	B	2340	ASN	5.2
1	D	4341	PHE	5.0
1	D	4340	ASN	4.6
1	A	1341	PHE	4.6

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

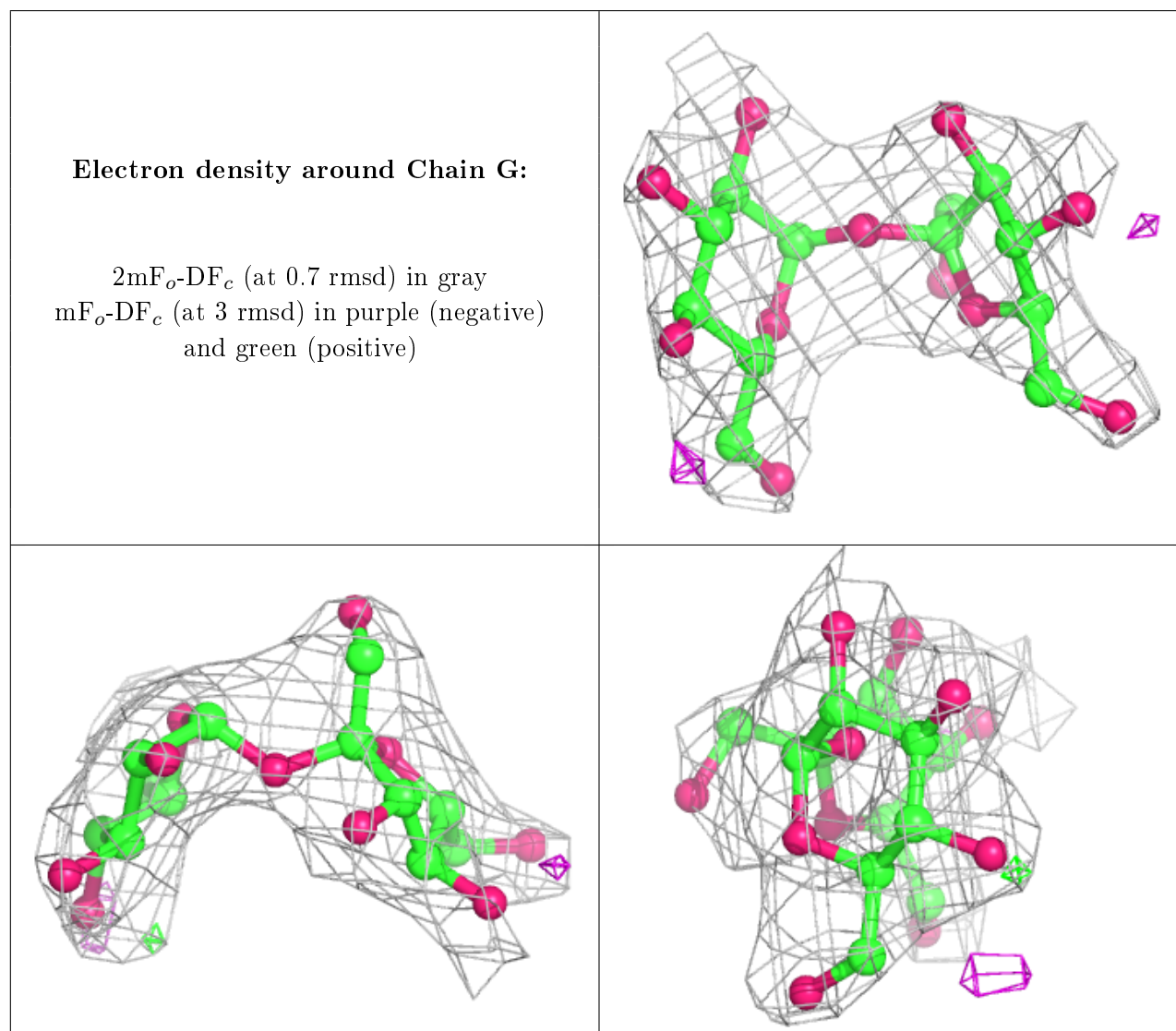
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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.

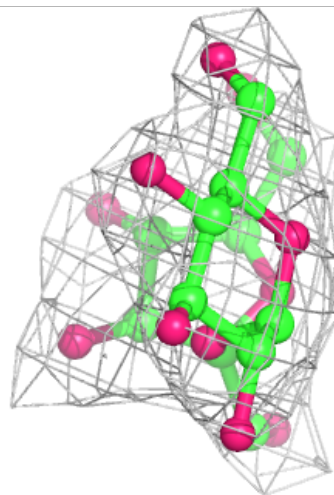
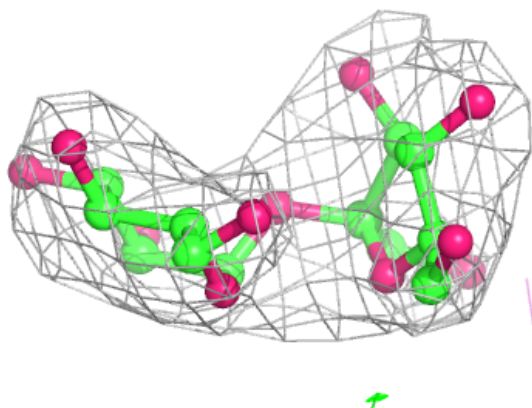
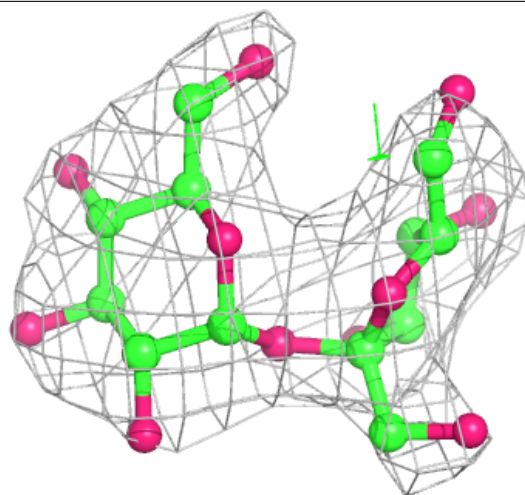
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FRU	J	2	12/12	0.83	0.25	69,70,73,77	0
2	FRU	K	2	12/12	0.90	0.18	67,70,72,73	0
2	GLC	K	1	11/12	0.90	0.16	66,68,68,69	0
2	FRU	G	2	12/12	0.91	0.19	66,70,71,71	0
2	GLC	G	1	11/12	0.92	0.18	57,60,61,62	0
2	FRU	H	2	12/12	0.92	0.16	63,65,66,67	0
2	GLC	J	1	11/12	0.92	0.17	61,62,63,65	0
2	FRU	L	2	12/12	0.92	0.16	31,34,36,39	0
2	GLC	H	1	11/12	0.92	0.17	63,65,65,66	0
2	GLC	L	1	11/12	0.96	0.14	27,30,31,33	0
2	GLC	I	1	11/12	0.96	0.16	27,28,29,31	0
2	FRU	I	2	12/12	0.97	0.13	28,33,34,38	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



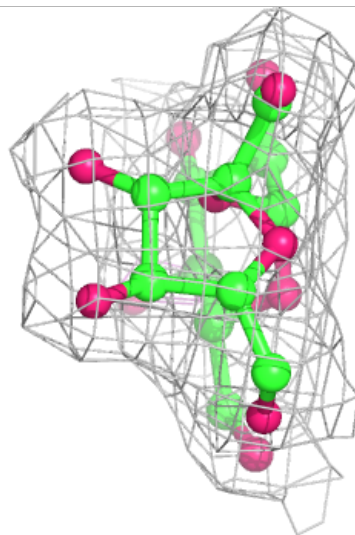
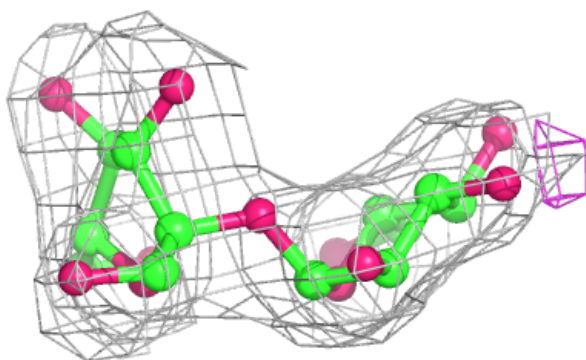
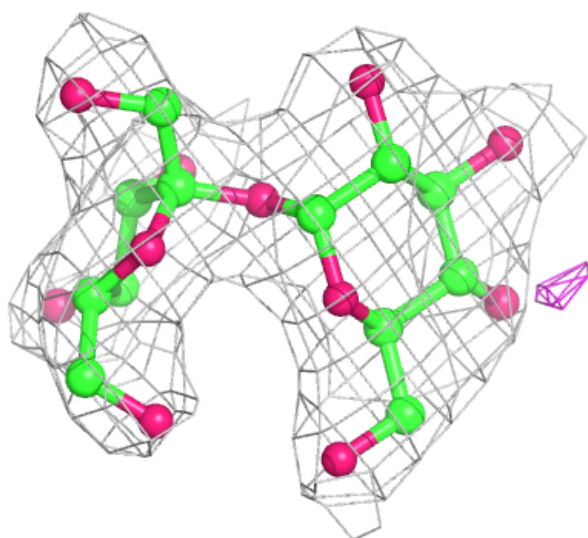
Electron density around Chain H:

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



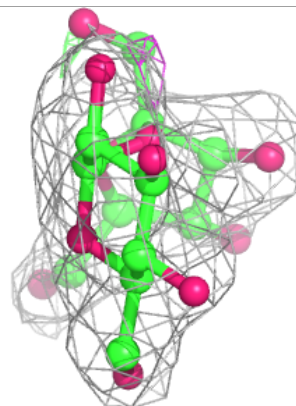
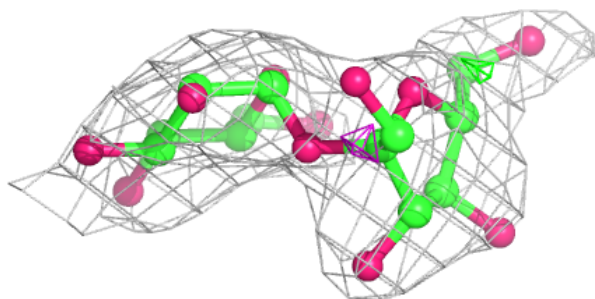
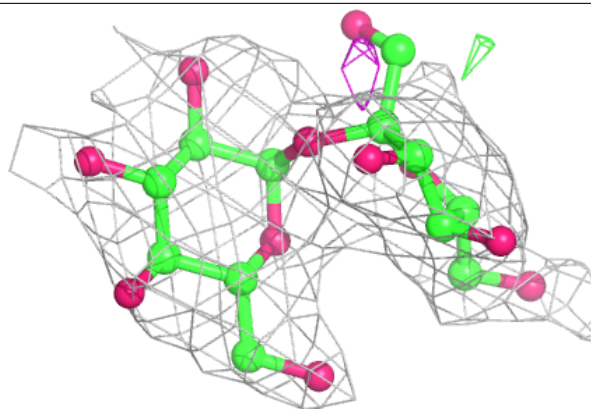
Electron density around Chain I:

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



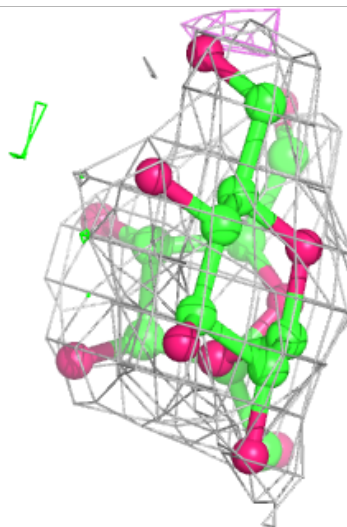
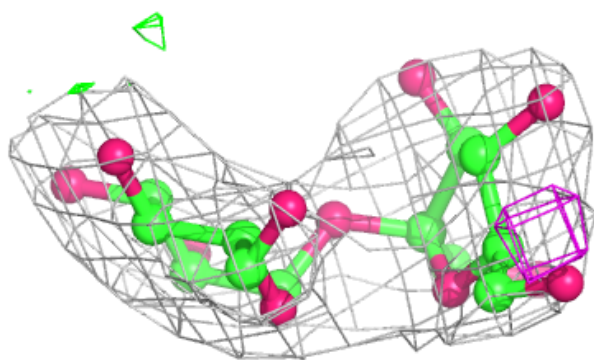
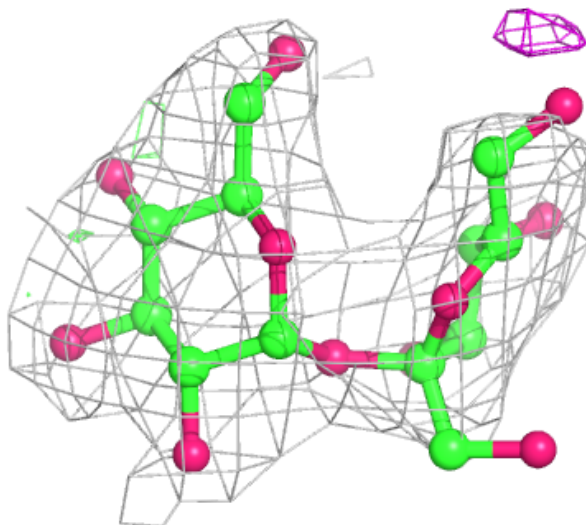
Electron density around Chain J:

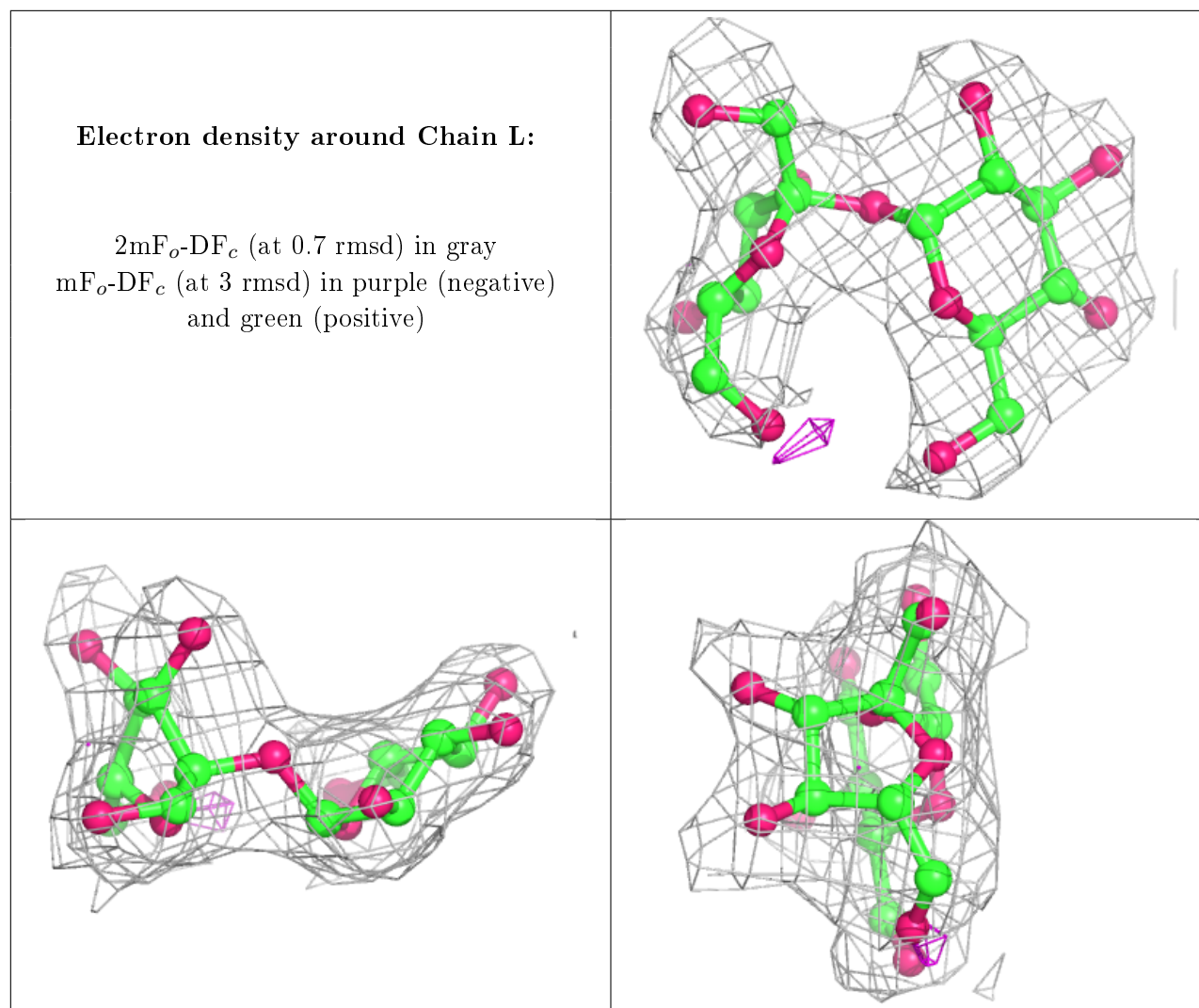
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

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





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
5	SIA	D	482	21/21	0.61	0.41	90,97,100,100	0
4	NAG	A	179	14/15	0.61	0.36	59,62,64,64	0
4	NAG	C	379	14/15	0.66	0.40	68,73,75,75	0
6	SO4	F	685	5/5	0.66	0.54	130,131,131,131	0
5	SIA	A	182	21/21	0.71	0.38	80,90,91,92	0
6	SO4	F	684	5/5	0.76	0.37	105,106,106,106	0
4	NAG	D	479	14/15	0.76	0.35	59,62,65,65	0
4	NAG	F	679	14/15	0.78	0.33	64,69,70,71	0

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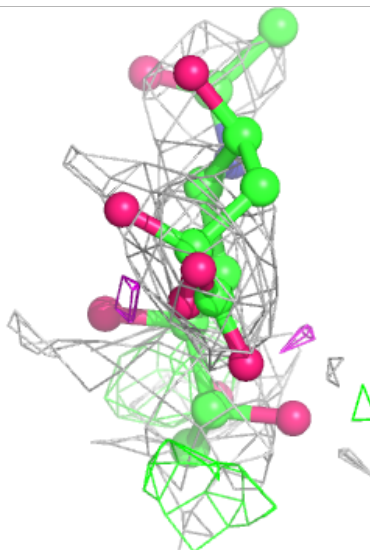
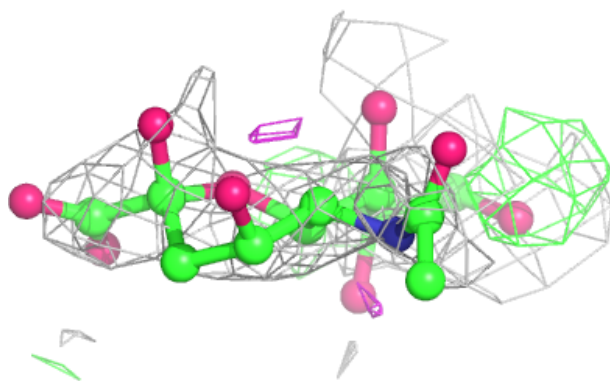
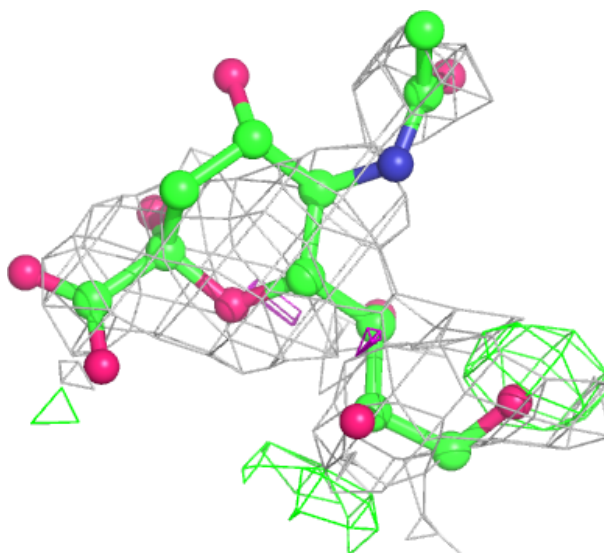
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	SIA	E	582	21/21	0.79	0.30	36,54,60,61	0
5	SIA	C	382	21/21	0.79	0.28	67,78,82,82	0
6	SO4	B	385	5/5	0.79	0.35	109,110,110,111	0
5	SIA	B	282	21/21	0.80	0.32	46,59,64,65	0
6	SO4	C	184	5/5	0.81	0.42	122,122,122,123	0
6	SO4	D	585	5/5	0.82	0.43	120,121,121,121	0
4	NAG	E	579	14/15	0.83	0.34	63,68,71,71	0
4	NAG	B	279	14/15	0.83	0.47	69,73,77,77	0
5	SIA	F	682	21/21	0.84	0.26	58,65,68,68	0
6	SO4	A	185	5/5	0.85	0.49	133,133,134,134	0
6	SO4	A	284	5/5	0.85	0.38	125,125,125,125	0
6	SO4	D	484	5/5	0.86	0.38	128,128,128,129	0
6	SO4	C	384	5/5	0.86	0.24	99,100,100,100	0
6	SO4	E	584	5/5	0.88	0.24	96,96,96,97	0
6	SO4	F	485	5/5	0.89	0.33	115,115,115,115	0
6	SO4	B	285	5/5	0.90	0.27	91,92,92,93	0
3	GD7	D	1	10/10	0.91	0.27	44,49,51,53	0
3	GD7	A	1	10/10	0.92	0.30	45,50,53,55	0
3	GD7	B	1	10/10	0.94	0.25	39,43,44,45	0
3	GD7	F	1	10/10	0.95	0.27	34,41,41,42	0
3	GD7	C	1	10/10	0.96	0.28	39,44,45,45	0
3	GD7	E	1	10/10	0.96	0.23	33,40,43,44	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.

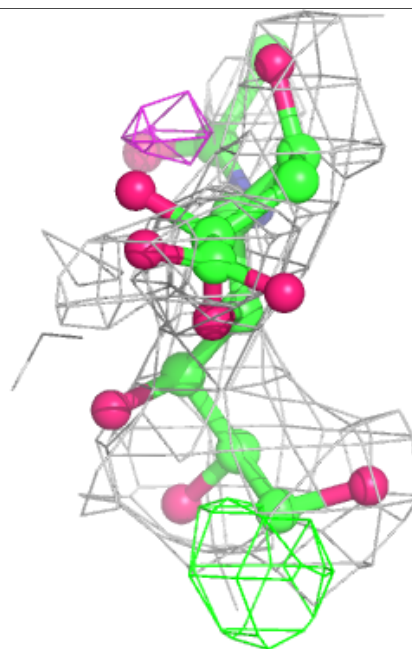
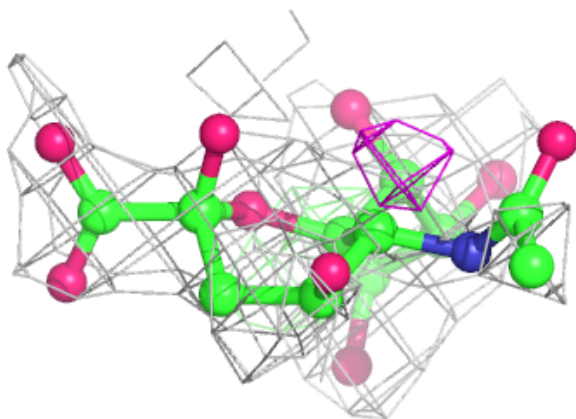
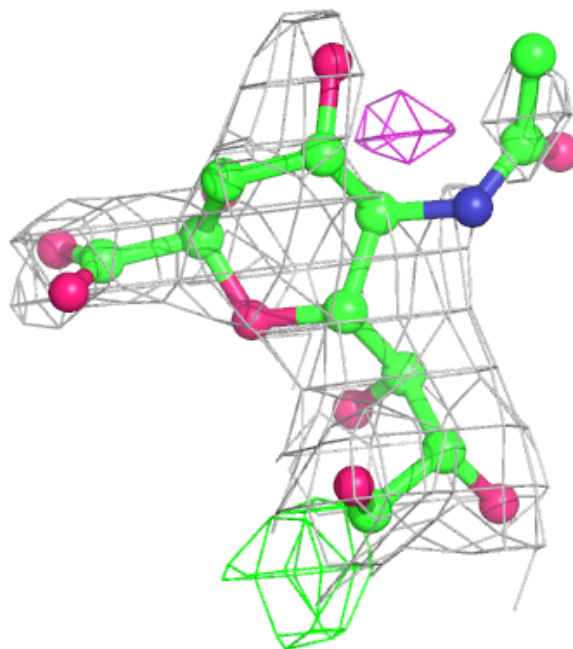
Electron density around SIA D 482:

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



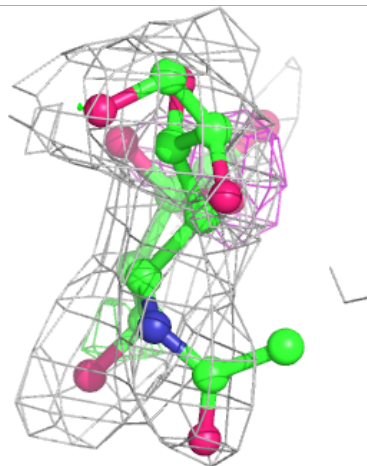
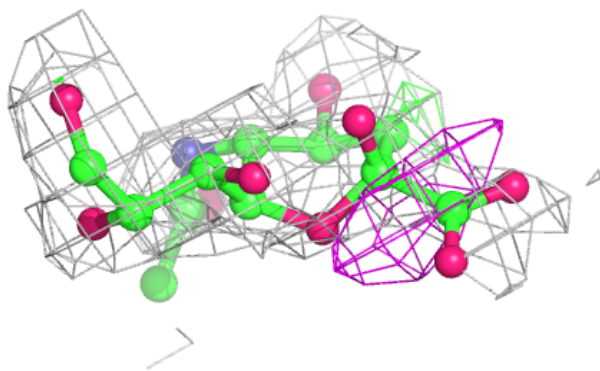
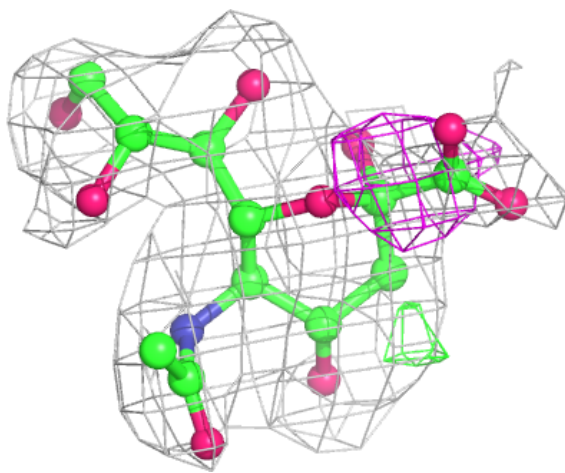
Electron density around SIA A 182:

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



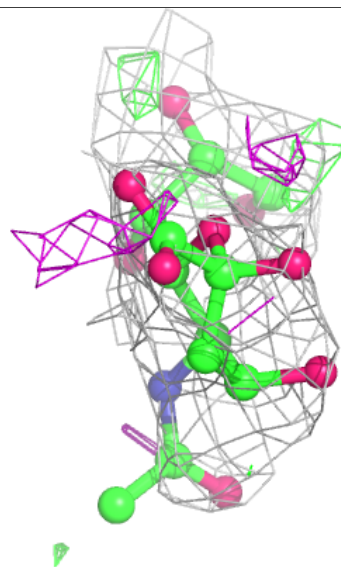
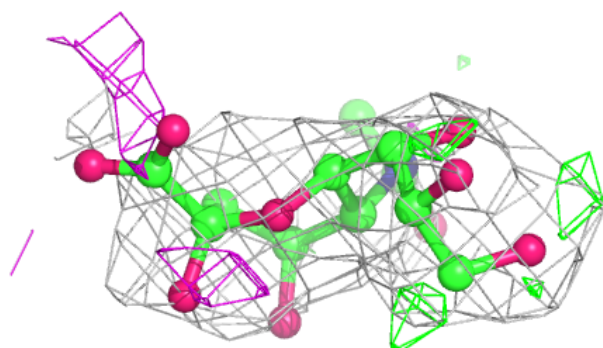
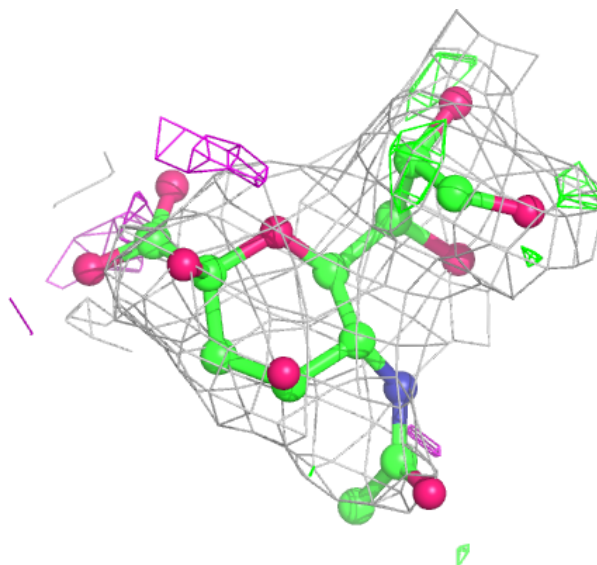
Electron density around SIA E 582:

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



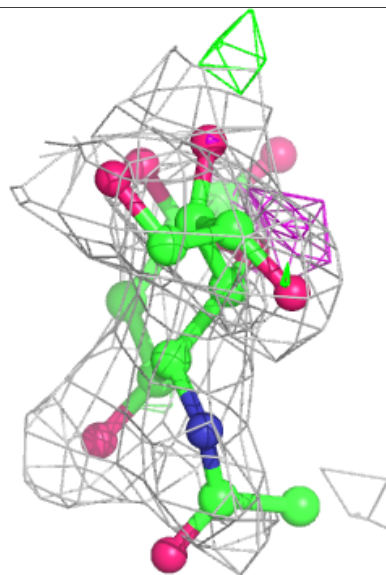
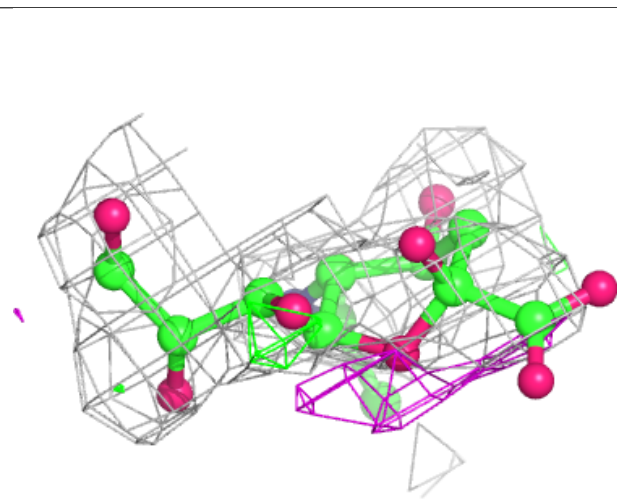
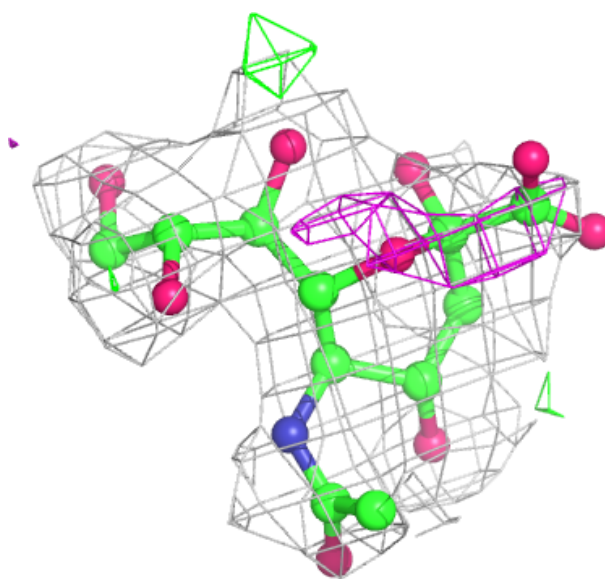
Electron density around SIA C 382:

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



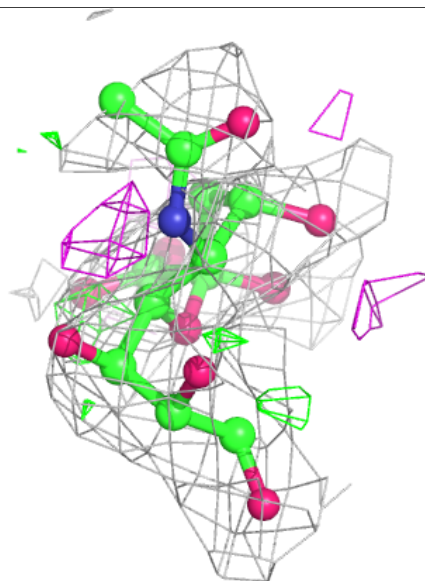
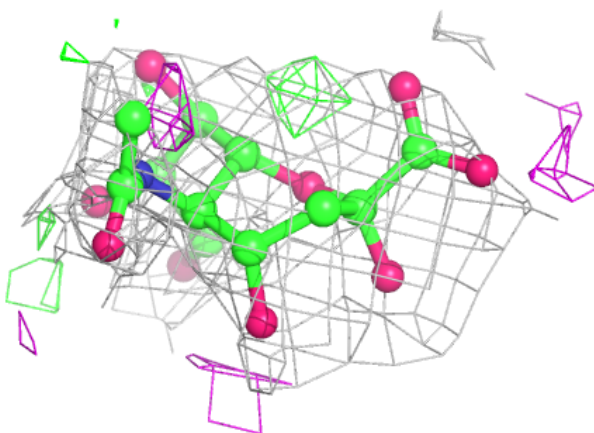
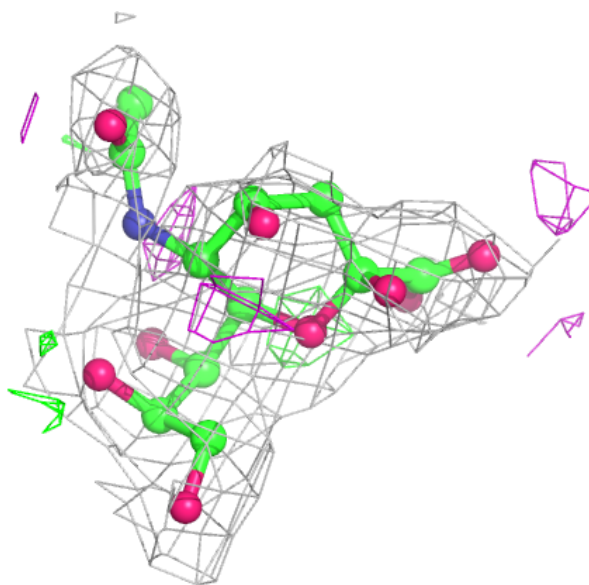
Electron density around SIA B 282:

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 SIA F 682:

$2mF_o-DF_c$ (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.