wwPDB X-ray Structure Validation Summary Report (i)

Oct 15, 2023 – 04:52 PM EDT

PDB ID	:	2H7C
Title	:	Crystal structure of human carboxylesterase in complex with Coenzyme A
Authors	:	Bencharit, S.; Edwards, C.C.; Morton, C.L.; Howard-Williams, E.L.; Potter, P.M.; Redinbo, M.R.
Deposited on	:	2006-06-02
Resolution	:	2.00 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 (i) 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 (1)) were used in the production of this report:

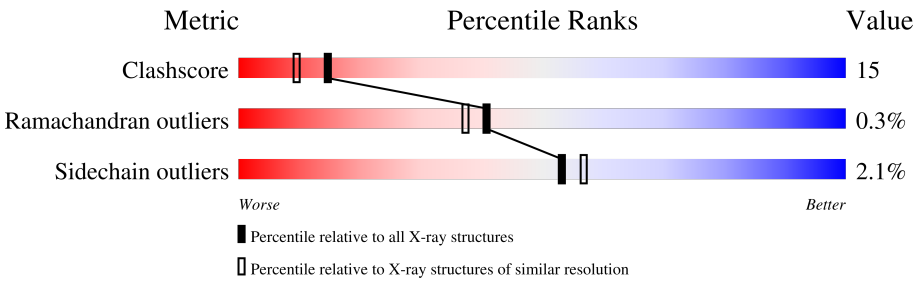
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	542	76% 21% • •
1	B	542	80% 18% •
1	C	542	73% 23% • •
1	D	542	77% 20% • •
1	E	542	75% 22% •
1	F	542	76% 21% • •
2	G	2	50% 50%
2	H	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
4	COA	A	1	X	-	X	-
4	COA	B	2	X	-	X	-
4	COA	C	3	X	-	X	-
4	COA	D	4	X	-	X	-
4	COA	E	5	X	-	X	-
4	COA	F	6	X	-	X	-
5	NAG	C	379	X	-	-	-
6	SIA	D	482	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 27978 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.

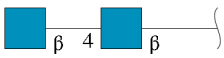
- Molecule 1 is a protein called Liver carboxylesterase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	532	4132	2663	686	762	21	0	1	0
1	B	531	4104	2646	681	756	21	0	1	0
1	C	531	4130	2662	685	762	21	0	1	0
1	D	532	4136	2665	686	764	21	0	1	0
1	E	531	4130	2662	685	762	21	0	1	0
1	F	531	4129	2662	685	761	21	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

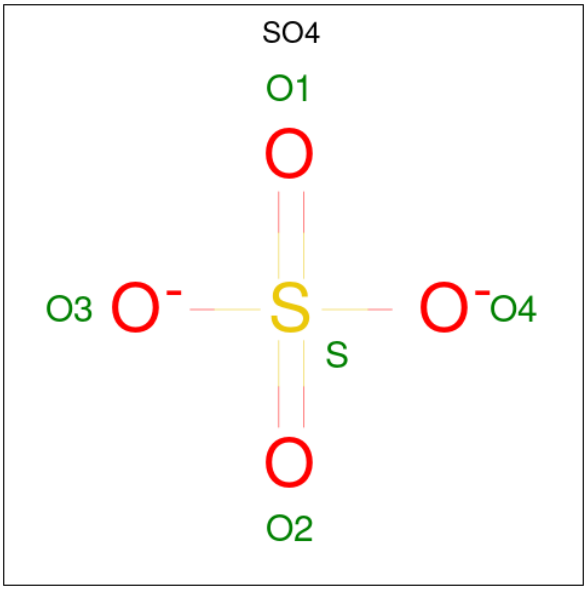
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P23141
B	?	-	GLN	deletion	UNP P23141
C	?	-	GLN	deletion	UNP P23141
D	?	-	GLN	deletion	UNP P23141
E	?	-	GLN	deletion	UNP P23141
F	?	-	GLN	deletion	UNP P23141

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-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
			Total	C	N	O			
2	H	2	28	16	2	10	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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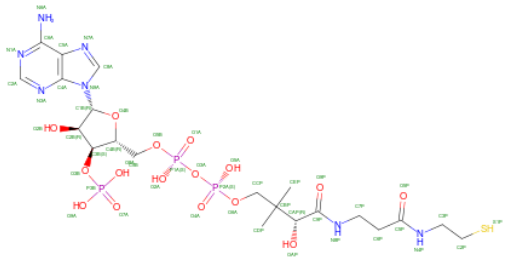
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	F	1	5	4	1	0	0
			Total	O	S		
3	F	1	5	4	1	0	0

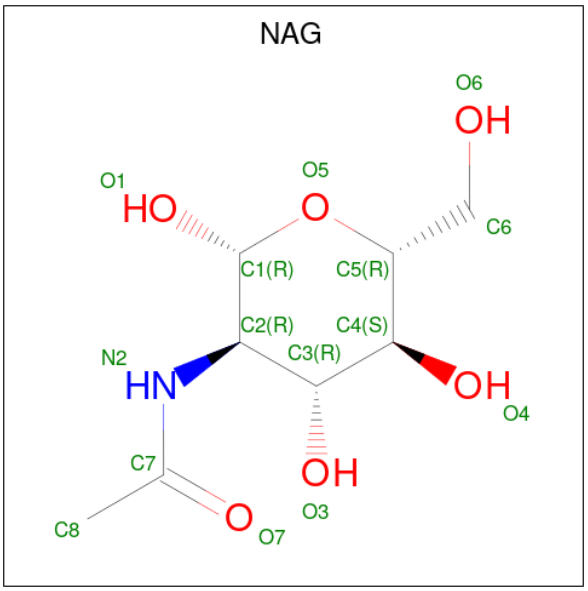
- Molecule 4 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).

COA



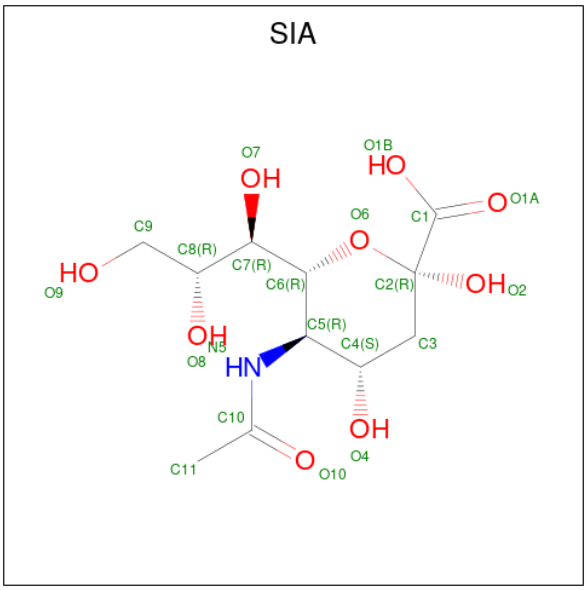
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
4	A	1	48	21	7	16	3	1	0	0
			Total	C	N	O	P	S		
4	B	1	48	21	7	16	3	1	0	0
			Total	C	N	O	P	S		
4	C	1	48	21	7	16	3	1	0	0
			Total	C	N	O	P	S		
4	D	1	48	21	7	16	3	1	0	0
			Total	C	N	O	P	S		
4	E	1	48	21	7	16	3	1	0	0
			Total	C	N	O	P	S		
4	F	1	48	21	7	16	3	1	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	474	474	474	0	0
7	B	500	500	500	0	0
7	C	404	404	404	0	0
7	D	480	480	480	0	0
7	E	448	448	448	0	0
7	F	409	409	409	0	0

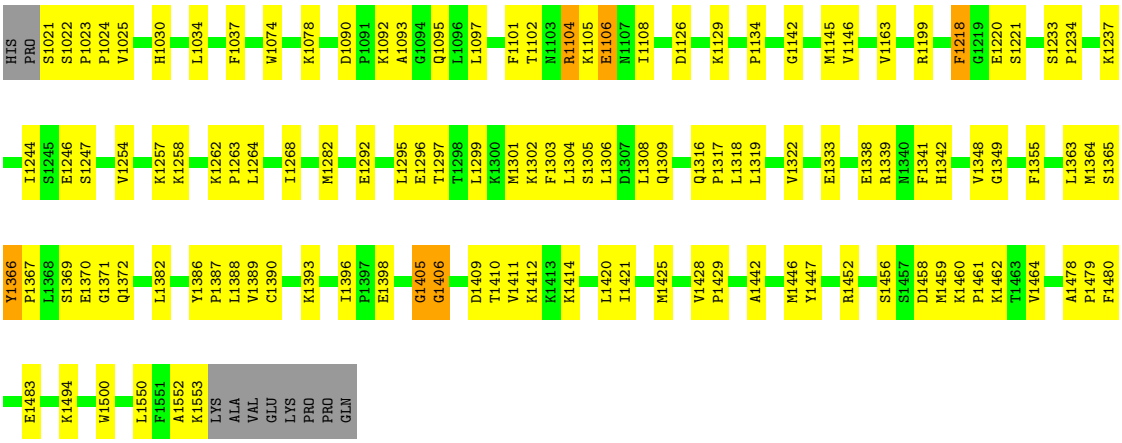
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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.

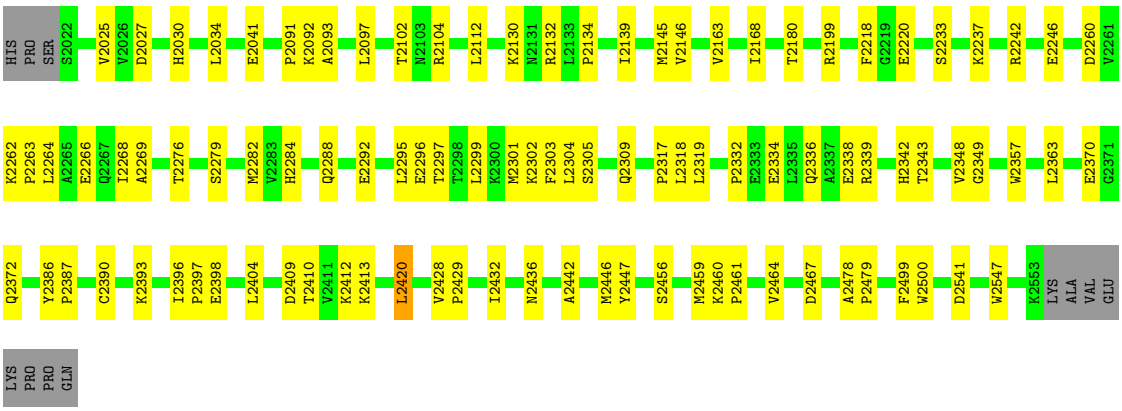
• Molecule 1: Liver carboxylesterase 1

Chain A: 76% 21% • •



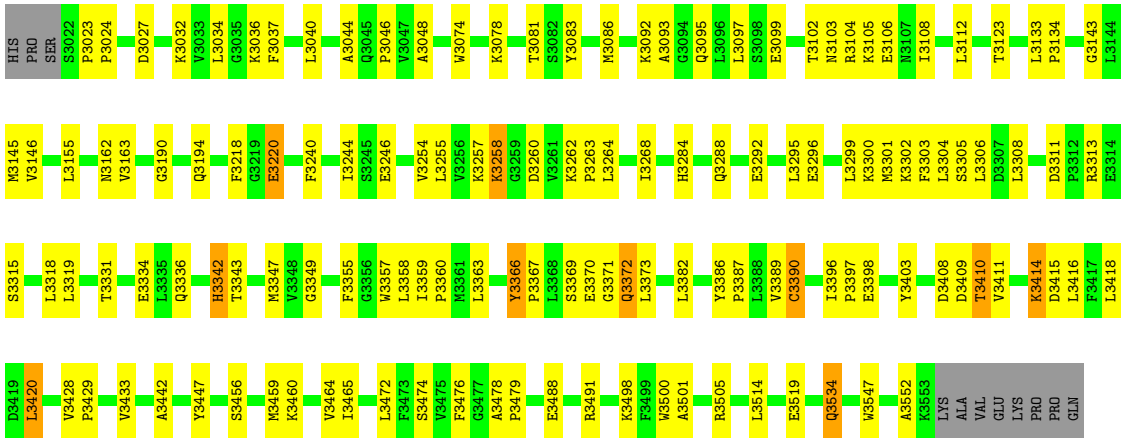
• Molecule 1: Liver carboxylesterase 1

Chain B: 80% 18% •



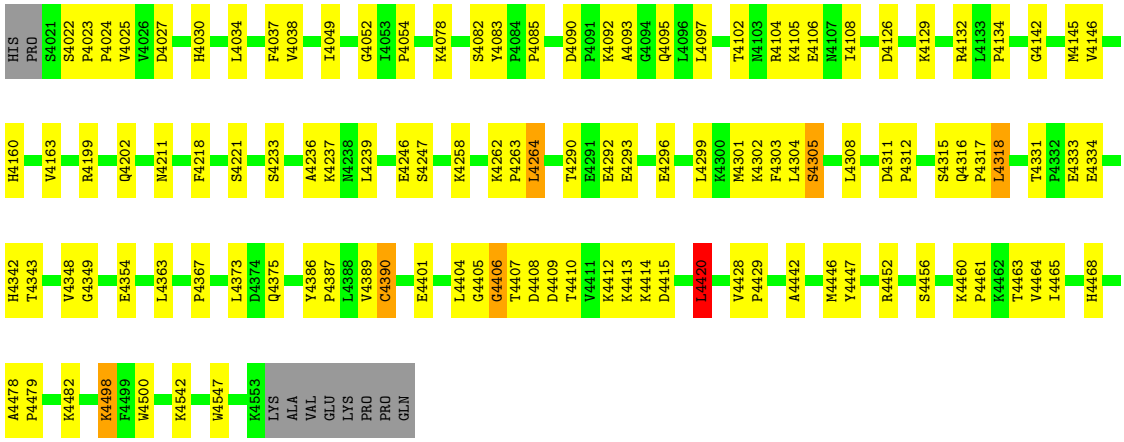
• Molecule 1: Liver carboxylesterase 1

Chain C: 73% 23% • •



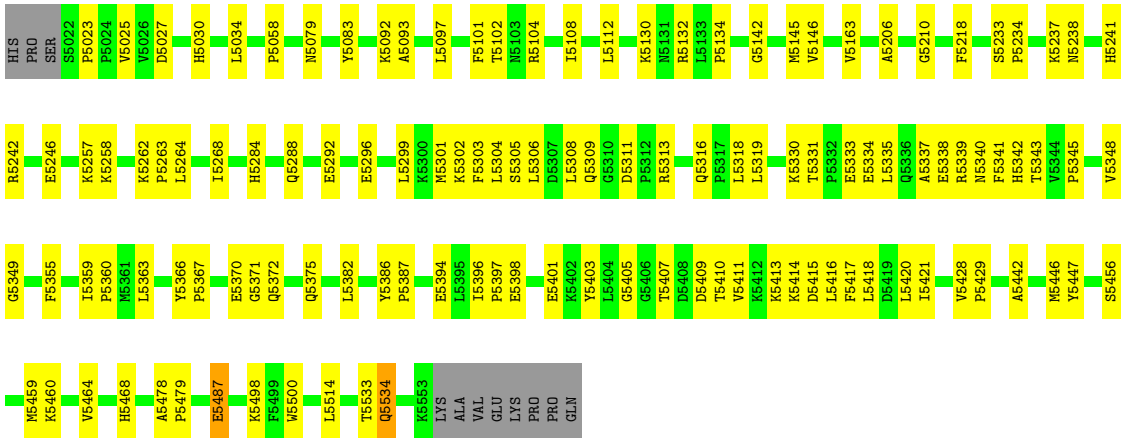
• Molecule 1: Liver carboxylesterase 1

Chain D:



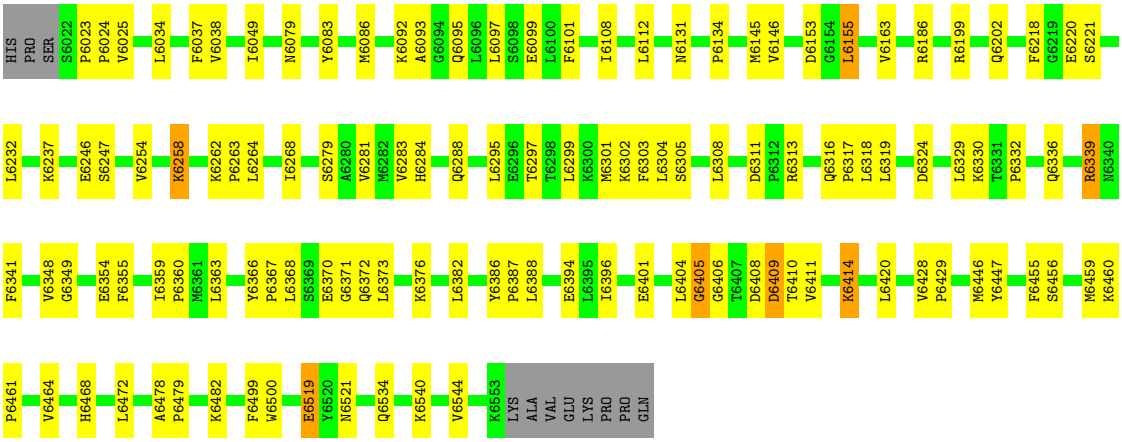
• Molecule 1: Liver carboxylesterase 1

Chain E:



• Molecule 1: Liver carboxylesterase 1

Chain F:

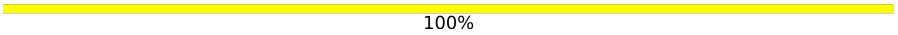


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:

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

Chain H:



4 Data and refinement statistics (i)

Xtriage (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	88.99Å 115.37Å 175.53Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	29.10 – 2.00	Depositor
% Data completeness (in resolution range)	97.1 (29.10-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.183 , 0.221	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	27978	wwPDB-VP
Average B, all atoms (Å^2)	28.0	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, SO4, COA

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	0.33	0/4238	0.58	0/5757
1	B	0.33	0/4210	0.58	0/5725
1	C	0.31	0/4236	0.57	0/5754
1	D	0.33	0/4242	0.60	1/5762 (0.0%)
1	E	0.32	0/4236	0.56	0/5754
1	F	0.32	0/4236	0.56	0/5754
All	All	0.32	0/25398	0.58	1/34506 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	4420	LEU	CA-CB-CG	5.64	128.28	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	3390[B]	CYS	Mainchain

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Mol	Chain	Res	Type	Group
1	D	4390[B]	CYS	Mainchain

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	4132	0	4131	140	0
1	B	4104	0	4075	121	0
1	C	4130	0	4129	141	0
1	D	4136	0	4135	133	0
1	E	4130	0	4130	135	0
1	F	4129	0	4130	144	0
2	G	28	0	25	1	0
2	H	28	0	25	4	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
3	C	10	0	0	0	0
3	D	15	0	0	0	0
3	E	5	0	0	0	0
3	F	10	0	0	0	0
4	A	48	0	32	28	0
4	B	48	0	32	30	0
4	C	48	0	32	21	0
4	D	48	0	32	25	0
4	E	48	0	32	24	0
4	F	48	0	32	28	0
5	B	14	0	13	1	0
5	C	14	0	13	1	0
5	D	14	0	13	0	0
5	E	14	0	13	1	0
6	D	21	0	18	9	0
6	E	21	0	18	5	0
7	A	474	0	0	14	0
7	B	500	0	0	21	0
7	C	404	0	0	20	0
7	D	480	0	0	19	0
7	E	448	0	0	20	0
7	F	409	0	0	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	27978	0	25060	770	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 15.

The worst 5 of 770 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:C:3258:LYS:H	1:C:3258:LYS:HD3	1.12	1.15
1:B:2093:ALA:HB1	4:B:2:COA:H121	1.35	1.08
2:H:1:NAG:H61	2:H:2:NAG:H83	1.33	1.08
1:A:1093:ALA:HB1	4:A:1:COA:H121	1.42	1.00
1:C:3414:LYS:HZ3	1:E:5370:GLU:HA	1.25	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	531/542 (98%)	505 (95%)	24 (4%)	2 (0%)	34	30
1	B	530/542 (98%)	512 (97%)	17 (3%)	1 (0%)	47	44
1	C	530/542 (98%)	506 (96%)	22 (4%)	2 (0%)	34	30
1	D	531/542 (98%)	509 (96%)	20 (4%)	2 (0%)	34	30
1	E	530/542 (98%)	509 (96%)	20 (4%)	1 (0%)	47	44
1	F	530/542 (98%)	511 (96%)	17 (3%)	2 (0%)	34	30
All	All	3182/3252 (98%)	3052 (96%)	120 (4%)	10 (0%)	41	37

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1406	GLY
1	C	3410	THR
1	D	4410	THR
1	E	5341	PHE
1	F	6405	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	448/457 (98%)	441 (98%)	7 (2%)	62	67
1	B	440/457 (96%)	433 (98%)	7 (2%)	62	67
1	C	448/457 (98%)	433 (97%)	15 (3%)	38	37
1	D	449/457 (98%)	438 (98%)	11 (2%)	49	51
1	E	448/457 (98%)	441 (98%)	7 (2%)	62	67
1	F	448/457 (98%)	439 (98%)	9 (2%)	55	58
All	All	2681/2742 (98%)	2625 (98%)	56 (2%)	53	57

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3534	GLN
1	F	6534	GLN
1	D	4414	LYS
1	F	6519	GLU
1	F	6258	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	4030	HIS
1	F	6375	GLN
1	D	4340	ASN
1	F	6532	ASN

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Mol	Chain	Res	Type
1	E	5534	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)

4 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	0.67	0	17,19,21	0.90	0
2	NAG	G	2	2	14,14,15	0.85	0	17,19,21	1.15	2 (11%)
2	NAG	H	1	1,2	14,14,15	0.56	0	17,19,21	0.66	0
2	NAG	H	2	2	14,14,15	0.56	0	17,19,21	0.60	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	NAG	G	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	G	2	2	-	6/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	2	NAG	C1-O5-C5	3.08	116.37	112.19
2	G	2	NAG	C2-N2-C7	-2.20	119.78	122.90

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

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

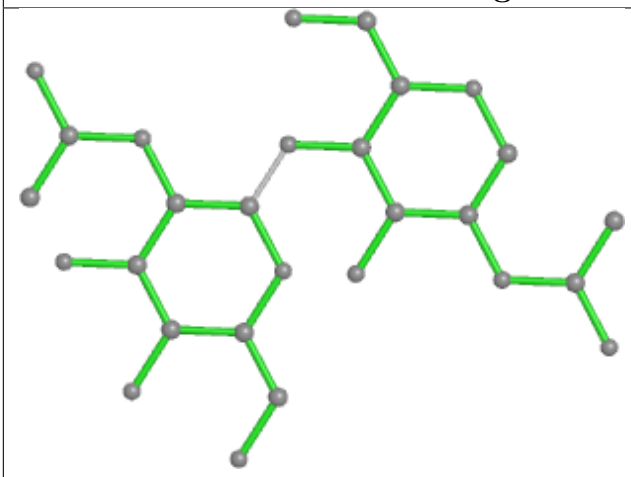
There are no ring outliers.

4 monomers are involved in 5 short contacts:

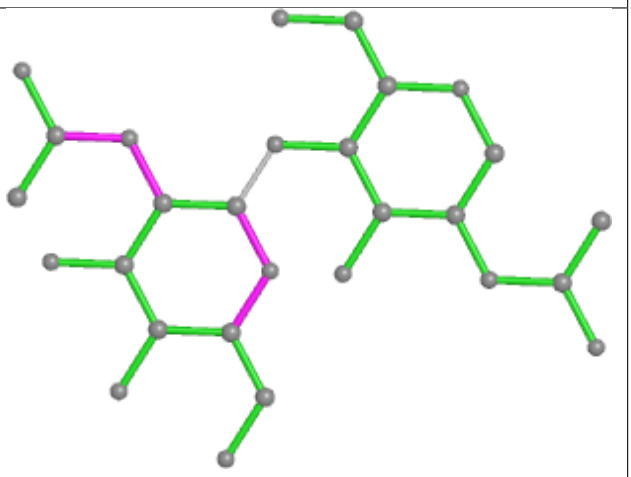
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	2	NAG	3	0
2	G	1	NAG	1	0
2	G	2	NAG	1	0
2	H	1	NAG	3	0

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

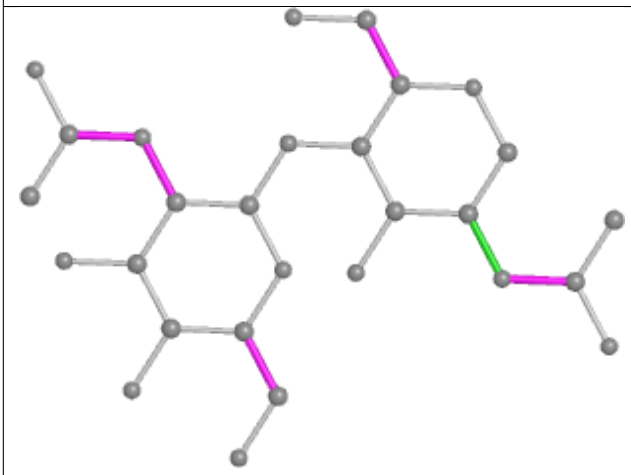
Oligosaccharide Chain G



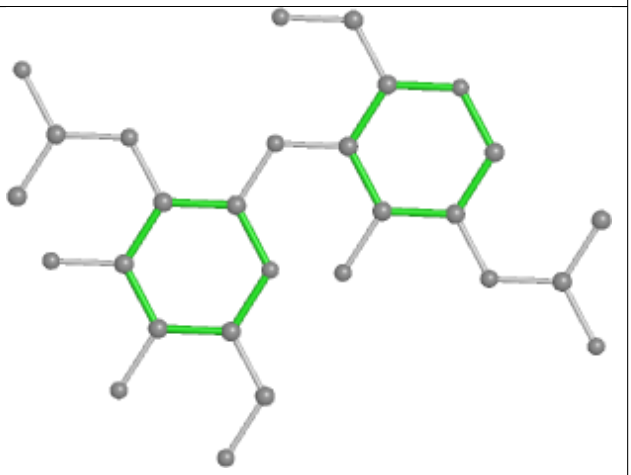
Bond lengths



Bond angles

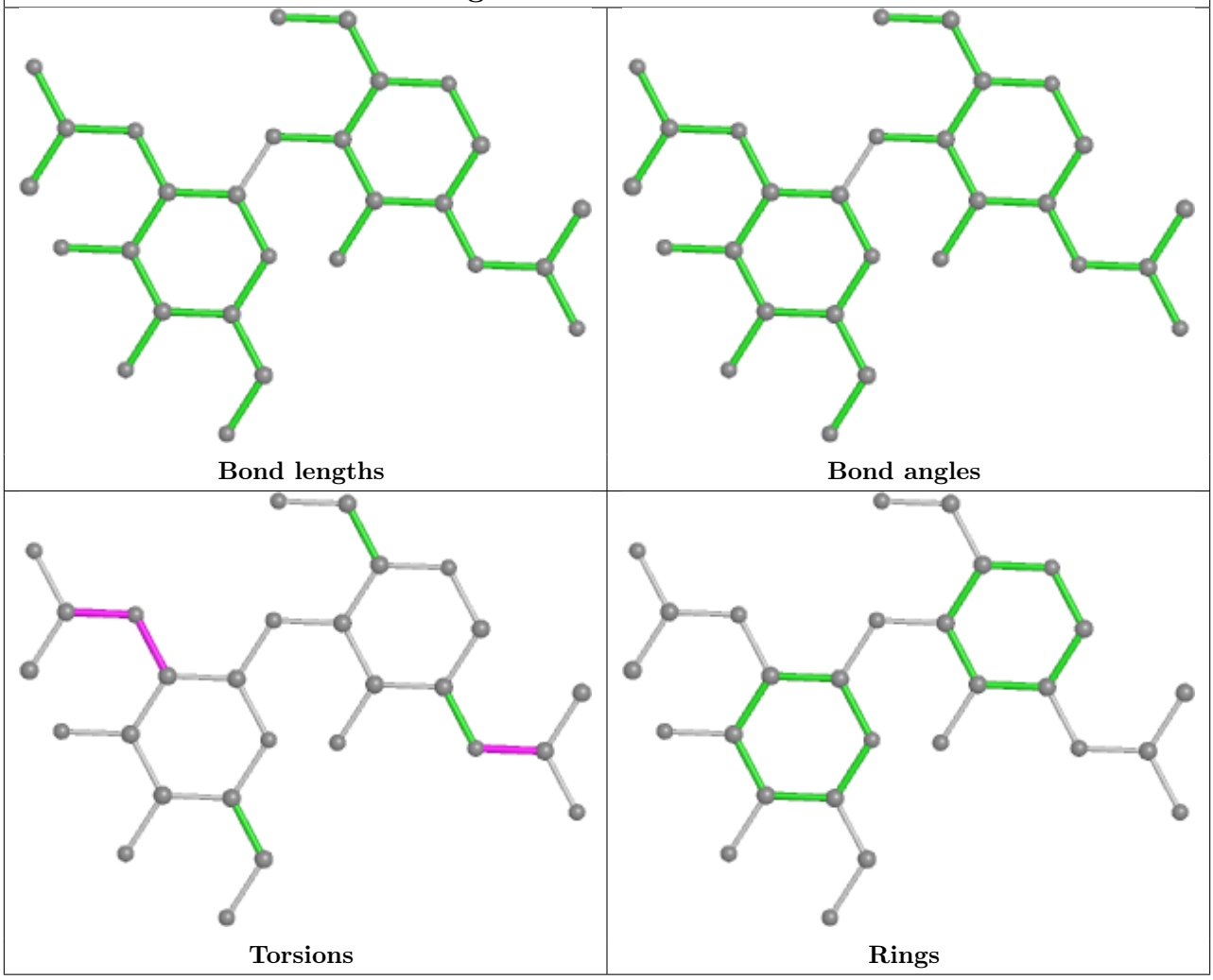


Torsions



Rings

Oligosaccharide Chain H



5.6 Ligand geometry (i)

24 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	SO4	A	285	-	4,4,4	0.25	0	6,6,6	0.06	0
4	COA	F	6	-	41,50,50	3.08	7 (17%)	52,75,75	2.75	15 (28%)
3	SO4	E	585	-	4,4,4	0.27	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	B	279	1	14,14,15	0.53	0	17,19,21	0.75	1 (5%)
3	SO4	A	185	-	4,4,4	0.27	0	6,6,6	0.05	0
3	SO4	C	184	-	4,4,4	0.23	0	6,6,6	0.07	0
5	NAG	E	579	1	14,14,15	0.57	0	17,19,21	0.66	0
3	SO4	D	684	-	4,4,4	0.24	0	6,6,6	0.09	0
4	COA	B	2	-	41,50,50	3.06	7 (17%)	52,75,75	2.74	15 (28%)
6	SIA	E	582	-	21,21,21	0.84	0	25,31,31	1.15	3 (12%)
3	SO4	D	484	-	4,4,4	0.26	0	6,6,6	0.06	0
5	NAG	D	479	1	14,14,15	0.48	0	17,19,21	0.70	1 (5%)
3	SO4	F	685	-	4,4,4	0.26	0	6,6,6	0.08	0
4	COA	C	3	-	41,50,50	3.12	7 (17%)	52,75,75	2.73	14 (26%)
5	NAG	C	379	1	14,14,15	0.56	0	17,19,21	0.67	0
4	COA	E	5	-	41,50,50	3.09	7 (17%)	52,75,75	2.76	15 (28%)
4	COA	A	1	-	41,50,50	3.11	7 (17%)	52,75,75	2.82	15 (28%)
4	COA	D	4	-	41,50,50	3.05	7 (17%)	52,75,75	2.71	15 (28%)
3	SO4	B	384	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	D	485	-	4,4,4	0.27	0	6,6,6	0.06	0
3	SO4	C	385	-	4,4,4	0.27	0	6,6,6	0.04	0
6	SIA	D	482	-	21,21,21	0.79	0	25,31,31	1.10	2 (8%)
3	SO4	B	284	-	4,4,4	0.25	0	6,6,6	0.06	0
3	SO4	F	584	-	4,4,4	0.26	0	6,6,6	0.07	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	COA	E	5	-	1/1/11/13	11/44/64/64	0/3/3/3
4	COA	A	1	-	1/1/11/13	13/44/64/64	0/3/3/3
5	NAG	B	279	1	-	2/6/23/26	0/1/1/1
5	NAG	E	579	1	-	4/6/23/26	0/1/1/1
4	COA	B	2	-	1/1/11/13	13/44/64/64	0/3/3/3
4	COA	F	6	-	1/1/11/13	12/44/64/64	0/3/3/3
4	COA	D	4	-	1/1/11/13	14/44/64/64	0/3/3/3
6	SIA	E	582	-	-	9/20/38/38	0/1/1/1
5	NAG	D	479	1	-	3/6/23/26	0/1/1/1
4	COA	C	3	-	1/1/11/13	12/44/64/64	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SIA	D	482	-	-	7/20/38/38	0/1/1/1
5	NAG	C	379	1	1/1/5/7	5/6/23/26	0/1/1/1

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	3	COA	C4A-N3A	9.86	1.49	1.35
4	D	4	COA	C4A-N3A	9.70	1.49	1.35
4	A	1	COA	C4A-N3A	9.70	1.49	1.35
4	F	6	COA	C4A-N3A	9.69	1.49	1.35
4	E	5	COA	C4A-N3A	9.56	1.48	1.35

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1	COA	O5P-C5P-N4P	-10.47	103.25	123.01
4	E	5	COA	O5P-C5P-N4P	-10.29	103.59	123.01
4	D	4	COA	O5P-C5P-N4P	-10.20	103.76	123.01
4	F	6	COA	O5P-C5P-N4P	-10.12	103.92	123.01
4	B	2	COA	O5P-C5P-N4P	-9.99	104.15	123.01

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1	COA	CAP
4	B	2	COA	CAP
4	C	3	COA	CAP
4	D	4	COA	CAP
4	E	5	COA	CAP

5 of 105 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	COA	C5B-O5B-P1A-O3A
4	A	1	COA	O9P-C9P-CAP-CBP
4	A	1	COA	CAP-C9P-N8P-C7P
4	A	1	COA	O9P-C9P-N8P-C7P
4	A	1	COA	O5P-C5P-N4P-C3P

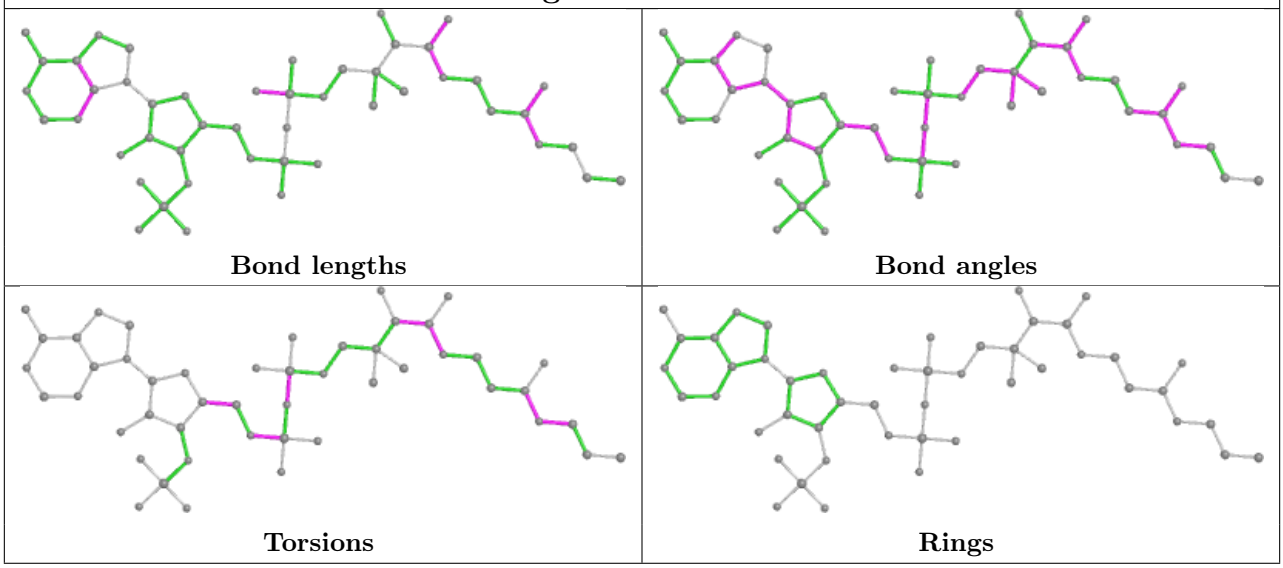
There are no ring outliers.

11 monomers are involved in 173 short contacts:

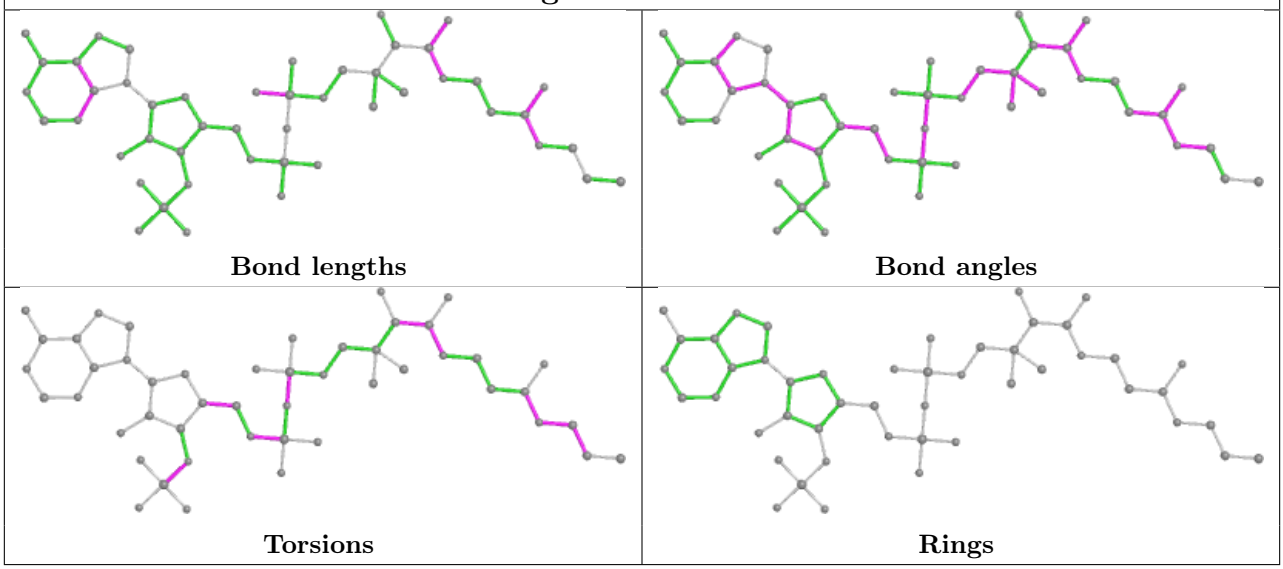
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	6	COA	28	0
5	B	279	NAG	1	0
5	E	579	NAG	1	0
4	B	2	COA	30	0
6	E	582	SIA	5	0
4	C	3	COA	21	0
5	C	379	NAG	1	0
4	E	5	COA	24	0
4	A	1	COA	28	0
4	D	4	COA	25	0
6	D	482	SIA	9	0

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 then 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.

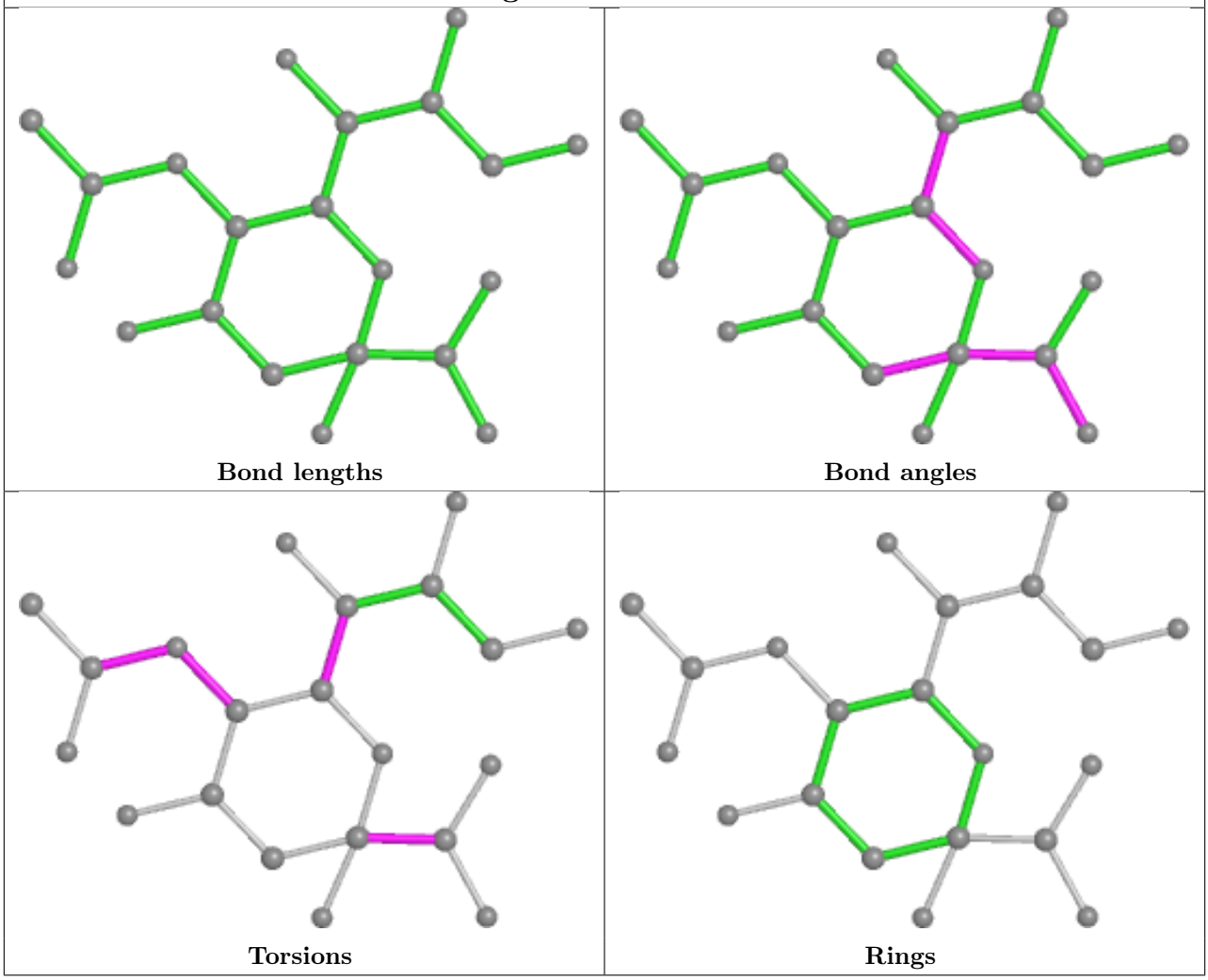
Ligand COA F 6



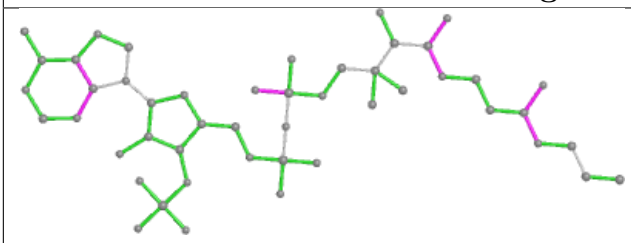
Ligand COA B 2



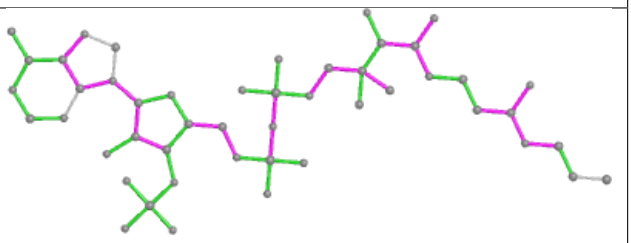
Ligand SIA E 582



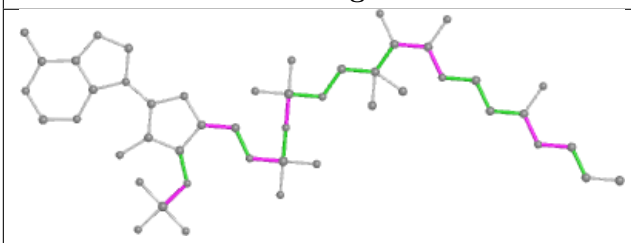
Ligand COA C 3



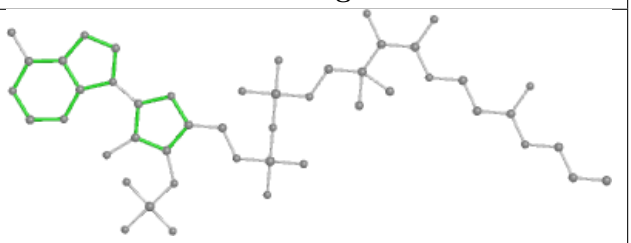
Bond lengths



Bond angles

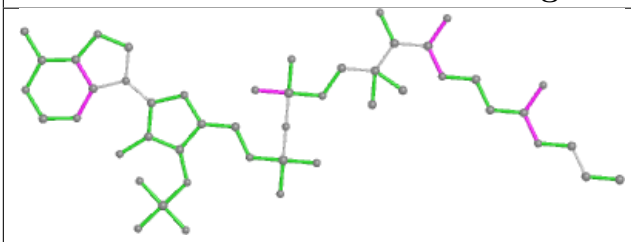


Torsions

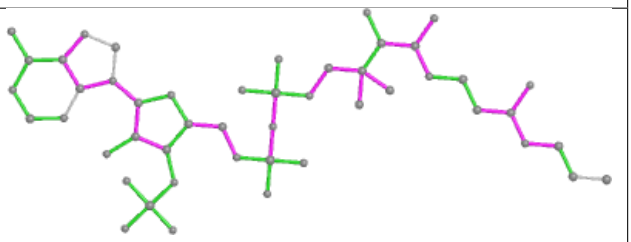


Rings

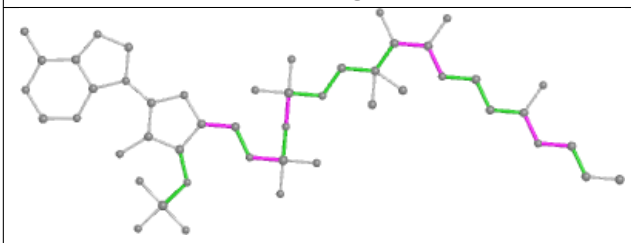
Ligand COA E 5



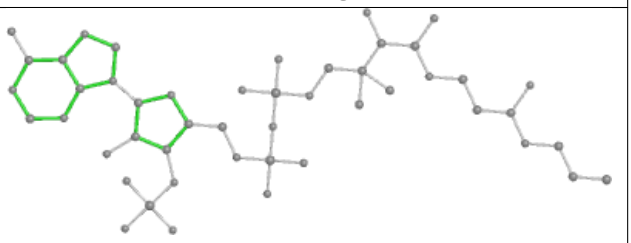
Bond lengths



Bond angles

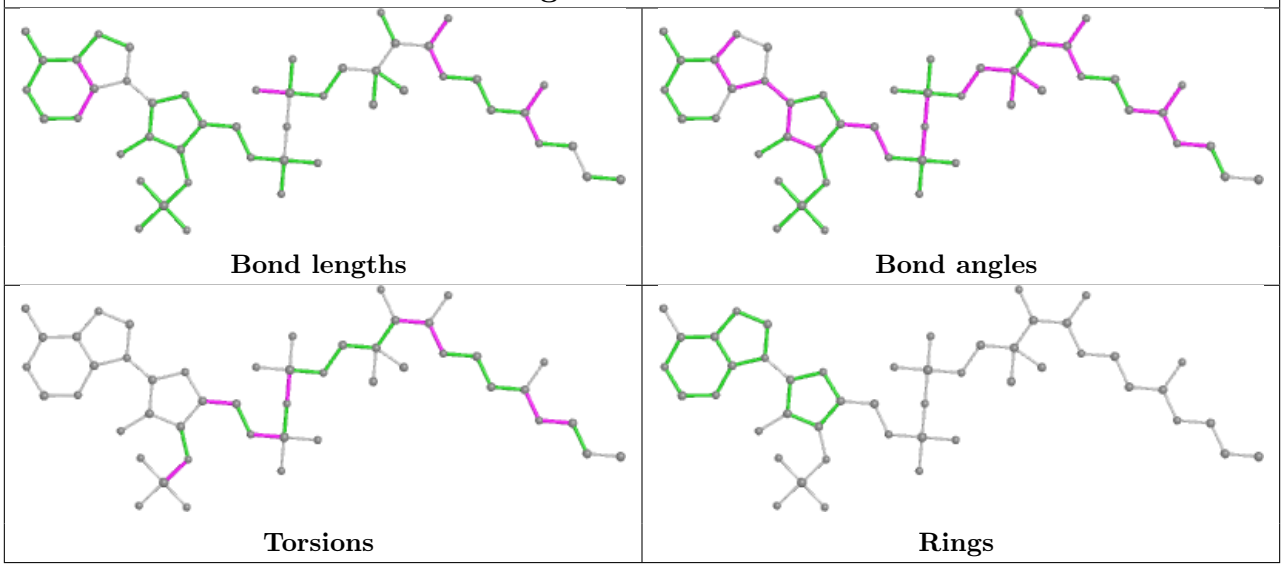


Torsions

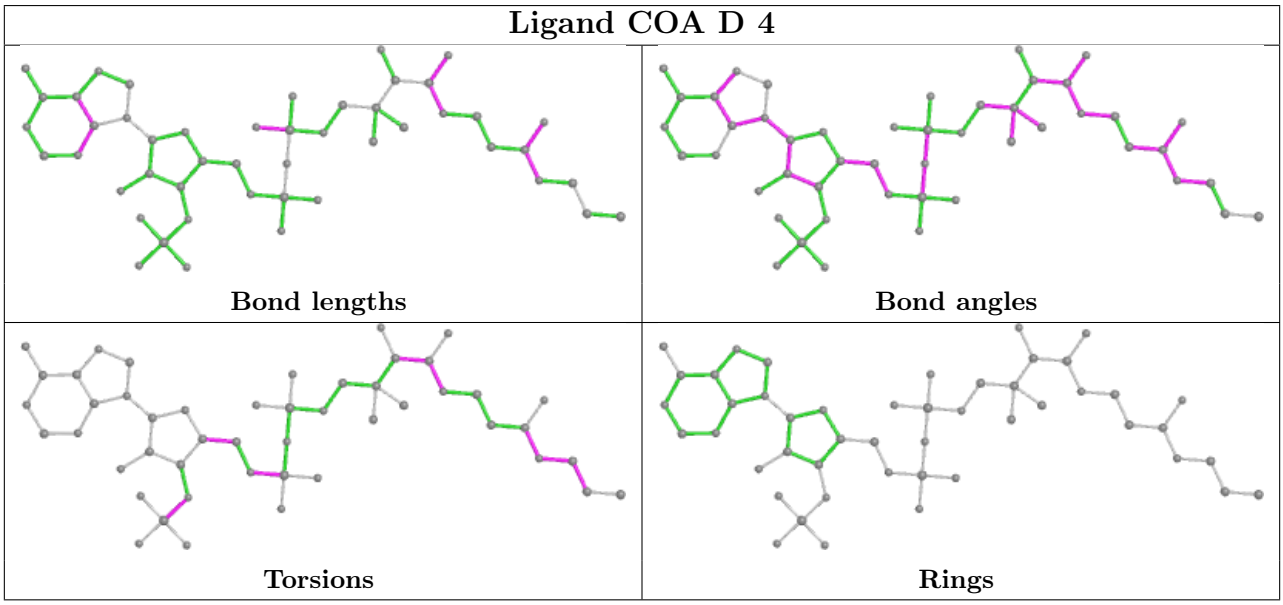


Rings

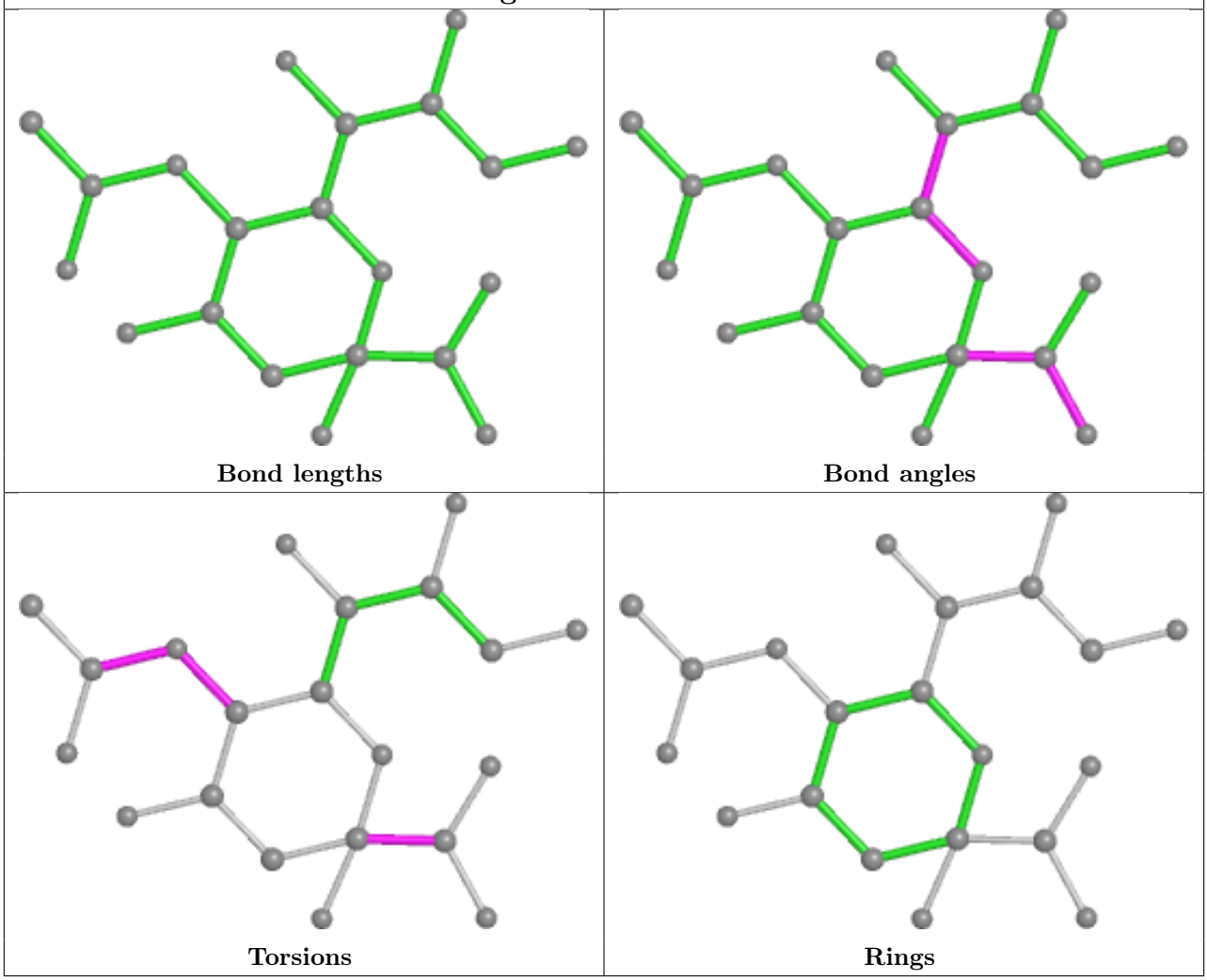
Ligand COA A 1



Ligand COA D 4



Ligand SIA D 482



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	4389:VAL	C	4390[B]:CYS	N	1.61

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1390[B]:CYS	C	1391:ILE	N	1.10

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.