



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:15 AM UTC

PDB ID : 2H7C / pdb_00002h7c
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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	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

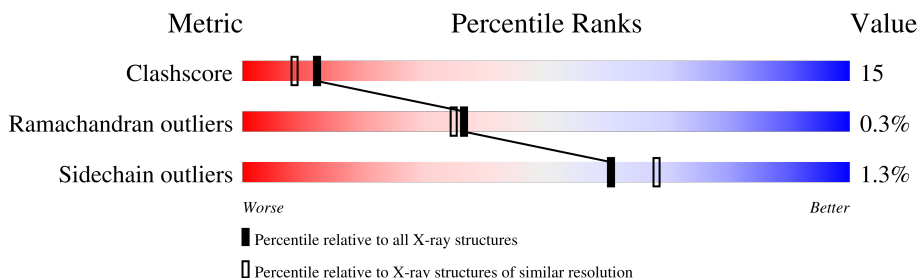
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	542	
1	B	542	
1	C	542	
1	D	542	
1	E	542	
1	F	542	
2	G	2	
2	H	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	COA	A	1	X	-	X	-
4	COA	B	2	X	-	X	-
4	COA	C	3	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
1	A	532	Total	C	N	O	S	0	1	0
			4132	2663	686	762	21			
1	B	531	Total	C	N	O	S	0	1	0
			4104	2646	681	756	21			
1	C	531	Total	C	N	O	S	0	1	0
			4130	2662	685	762	21			
1	D	532	Total	C	N	O	S	0	1	0
			4136	2665	686	764	21			
1	E	531	Total	C	N	O	S	0	1	0
			4130	2662	685	762	21			
1	F	531	Total	C	N	O	S	0	1	0
			4129	2662	685	761	21			

There are 6 discrepancies between the modelled and reference sequences:

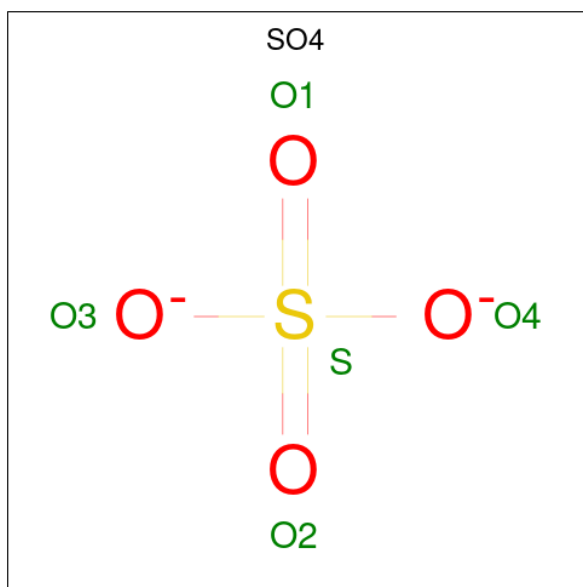
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P23141
B	?	-	GLN	deletion	UNP P23141
C	?	-	GLN	deletion	UNP P23141
D	?	-	GLN	deletion	UNP P23141
E	?	-	GLN	deletion	UNP P23141
F	?	-	GLN	deletion	UNP P23141

- 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
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



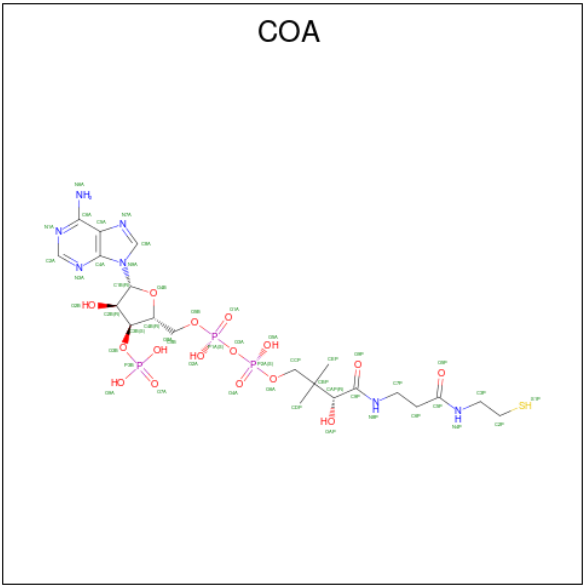
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total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

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

- Molecule 4 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



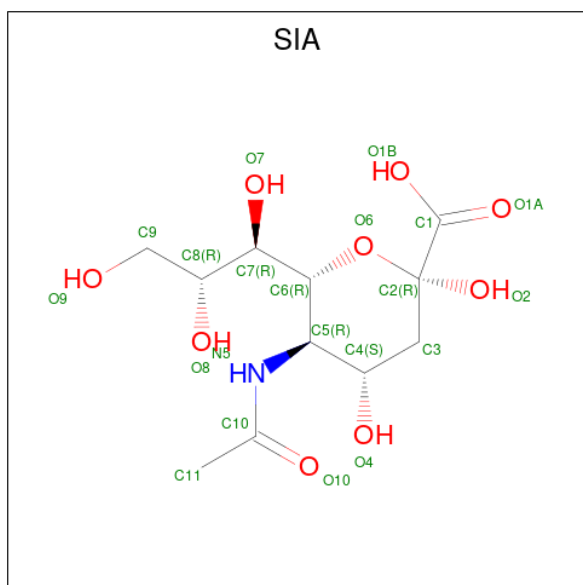
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
4	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
4	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
4	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
4	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
4	F	1	Total	C	N	O	P	S	0	0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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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



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

- Molecule 7 is water.

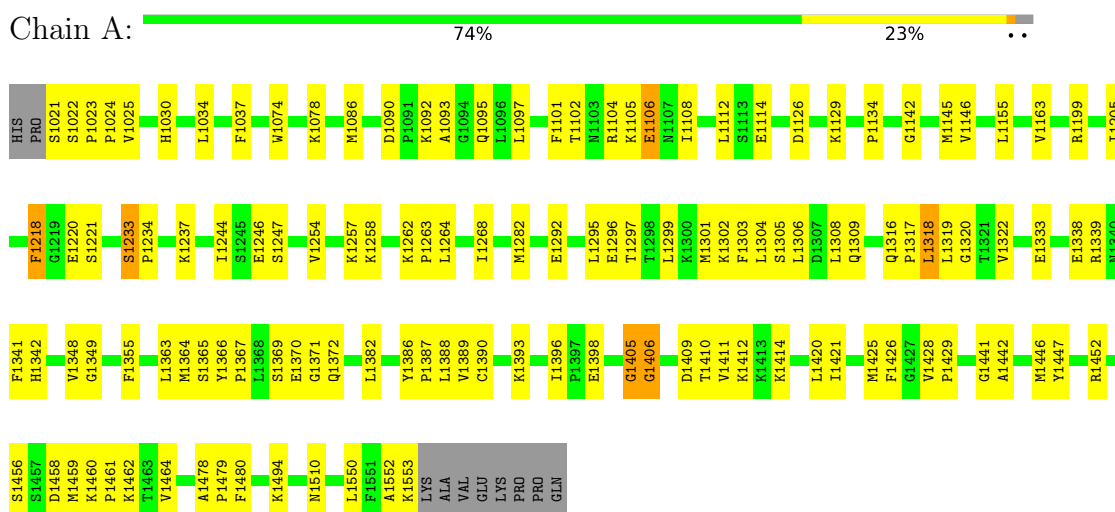
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	474	Total	O	0	0
			474	474		
7	B	500	Total	O	0	0
			500	500		
7	C	404	Total	O	0	0
			404	404		
7	D	480	Total	O	0	0
			480	480		
7	E	448	Total	O	0	0
			448	448		
7	F	409	Total	O	0	0
			409	409		

3 Residue-property plots

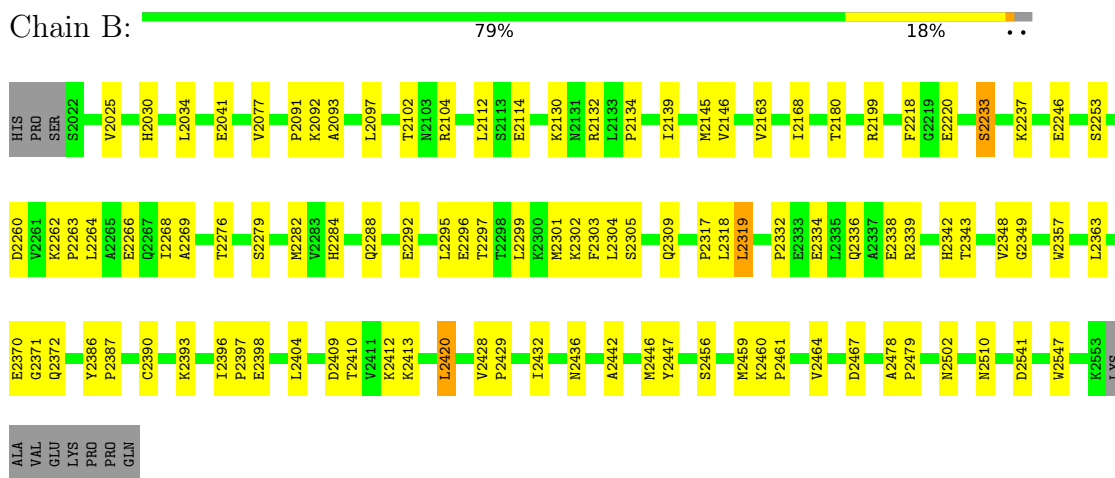
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



- Molecule 1: Liver carboxylesterase 1

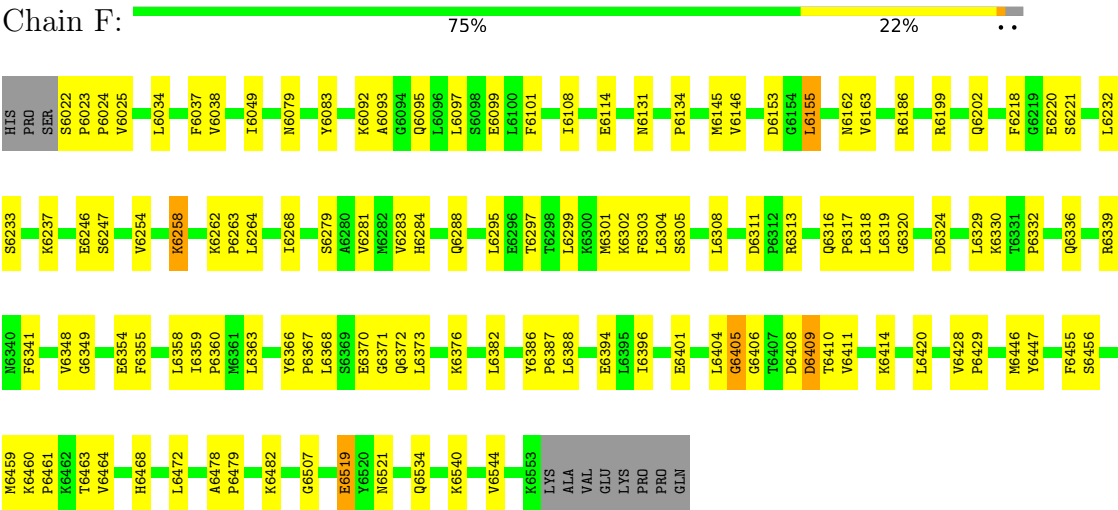


- Molecule 1: Liver carboxylesterase 1

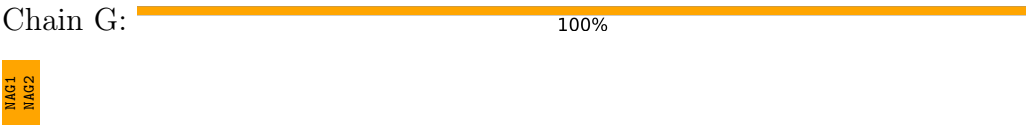




• Molecule 1: Liver carboxylesterase 1



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



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



4 Data and refinement statistics

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

5.1 Standard geometry

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

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	0.39	0/4238	0.89	7/5757 (0.1%)
1	B	0.39	0/4210	0.87	8/5725 (0.1%)
1	C	0.37	0/4236	0.88	4/5754 (0.1%)
1	D	0.39	0/4242	0.88	5/5762 (0.1%)
1	E	0.39	0/4236	0.87	6/5754 (0.1%)
1	F	0.39	0/4236	0.85	6/5754 (0.1%)
All	All	0.39	0/25398	0.87	36/34506 (0.1%)

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.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	5343	THR	N-CA-C	8.65	121.95	110.53
1	B	2253	SER	N-CA-C	7.32	120.18	111.33
1	D	4253	SER	N-CA-C	7.14	120.88	111.75
1	A	1320	GLY	N-CA-C	6.74	120.57	111.20
1	F	6320	GLY	N-CA-C	6.72	120.55	111.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	3390[B]	CYS	Mainchain
1	D	4390[B]	CYS	Mainchain

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	4132	0	4131	143	0
1	B	4104	0	4075	123	0
1	C	4130	0	4129	145	0
1	D	4136	0	4135	137	0
1	E	4130	0	4130	143	0
1	F	4129	0	4130	145	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	26	0
4	B	48	0	32	28	0
4	C	48	0	32	20	0
4	D	48	0	32	23	0
4	E	48	0	32	21	0
4	F	48	0	32	26	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	779	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 779 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:C:3414:LYS:HZ3	1:E:5370:GLU:HA	1.12	1.10
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

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%)	30	27
1	B	530/542 (98%)	512 (97%)	17 (3%)	1 (0%)	43	42
1	C	530/542 (98%)	506 (96%)	22 (4%)	2 (0%)	30	27
1	D	531/542 (98%)	509 (96%)	20 (4%)	2 (0%)	30	27
1	E	530/542 (98%)	509 (96%)	20 (4%)	1 (0%)	43	42
1	F	530/542 (98%)	511 (96%)	17 (3%)	2 (0%)	30	27
All	All	3182/3252 (98%)	3052 (96%)	120 (4%)	10 (0%)	36	35

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 ⓘ

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%)	444 (99%)	4 (1%)	70	78
1	B	440/457 (96%)	437 (99%)	3 (1%)	76	82
1	C	448/457 (98%)	437 (98%)	11 (2%)	42	45
1	D	449/457 (98%)	441 (98%)	8 (2%)	51	58
1	E	448/457 (98%)	444 (99%)	4 (1%)	70	78
1	F	448/457 (98%)	442 (99%)	6 (1%)	61	68
All	All	2681/2742 (98%)	2645 (99%)	36 (1%)	61	68

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	5394	GLU
1	F	6534	GLN
1	E	5534	GLN
1	F	6218	PHE
1	C	3264	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	5030	HIS
1	E	5537	GLN
1	E	5131	ASN
1	E	5522	GLN

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Mol	Chain	Res	Type
1	F	6107	ASN

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 ⓘ

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	2,1	14,14,15	0.66	0	17,19,21	0.92	1 (5%)
2	NAG	G	2	2	14,14,15	0.88	0	17,19,21	1.18	2 (11%)
2	NAG	H	1	2,1	14,14,15	0.56	0	17,19,21	0.69	1 (5%)
2	NAG	H	2	2	14,14,15	0.58	0	17,19,21	0.63	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	2,1	-	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	2,1	-	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 (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2	NAG	C1-O5-C5	3.12	116.37	112.19
2	G	2	NAG	C2-N2-C7	-2.33	119.78	122.90
2	H	1	NAG	C2-N2-C7	-2.05	120.16	122.90
2	G	1	NAG	C2-N2-C7	-2.04	120.17	122.90

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

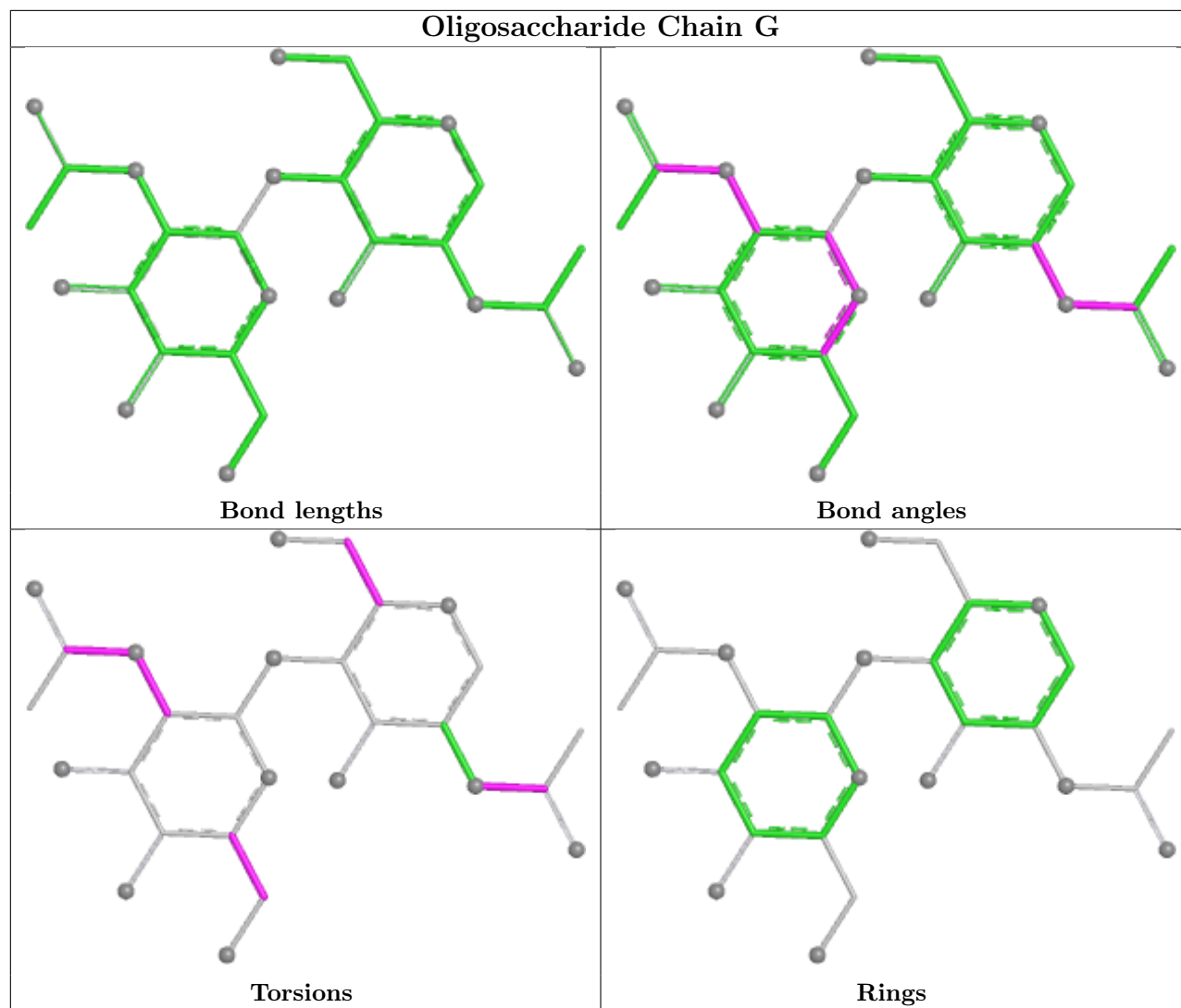
Mol	Chain	Res	Type	Atoms
2	G	2	NAG	C8-C7-N2-C2
2	G	2	NAG	O7-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2
2	H	1	NAG	O7-C7-N2-C2
2	H	2	NAG	C8-C7-N2-C2

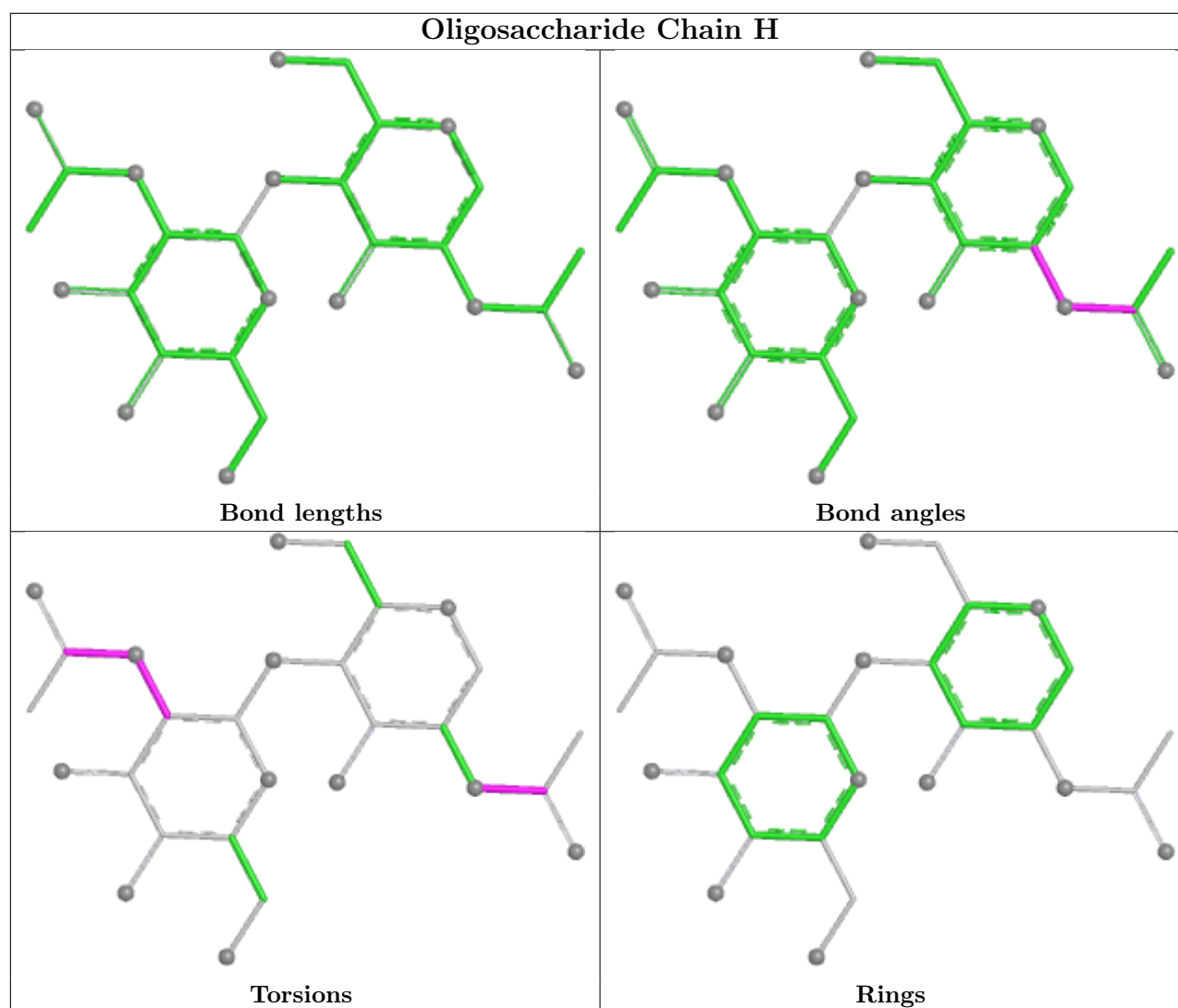
There are no ring outliers.

4 monomers are involved in 5 short contacts:

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

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





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	$\# Z > 2$
5	NAG	D	479	1	14,14,15	0.49	0	17,19,21	0.73	1 (5%)
3	SO4	C	385	-	4,4,4	0.38	0	6,6,6	0.06	0
5	NAG	C	379	1	14,14,15	0.58	0	17,19,21	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	185	-	4,4,4	0.38	0	6,6,6	0.08	0
4	COA	D	4	-	47,50,50	2.94	11 (23%)	69,75,75	2.74	18 (26%)
3	SO4	C	184	-	4,4,4	0.35	0	6,6,6	0.11	0
3	SO4	D	684	-	4,4,4	0.35	0	6,6,6	0.12	0
4	COA	B	2	-	47,50,50	2.94	11 (23%)	69,75,75	2.78	19 (27%)
3	SO4	A	285	-	4,4,4	0.36	0	6,6,6	0.10	0
6	SIA	D	482	-	21,21,21	0.80	0	24,31,31	1.13	2 (8%)
5	NAG	B	279	1	14,14,15	0.54	0	17,19,21	0.78	1 (5%)
4	COA	E	5	-	47,50,50	2.95	10 (21%)	69,75,75	2.79	19 (27%)
3	SO4	F	584	-	4,4,4	0.37	0	6,6,6	0.11	0
3	SO4	F	685	-	4,4,4	0.37	0	6,6,6	0.10	0
4	COA	C	3	-	47,50,50	2.99	12 (25%)	69,75,75	2.78	18 (26%)
3	SO4	D	485	-	4,4,4	0.38	0	6,6,6	0.09	0
3	SO4	D	484	-	4,4,4	0.36	0	6,6,6	0.08	0
4	COA	A	1	-	47,50,50	2.98	12 (25%)	69,75,75	2.85	18 (26%)
4	COA	F	6	-	47,50,50	2.96	13 (27%)	69,75,75	2.80	18 (26%)
3	SO4	B	284	-	4,4,4	0.36	0	6,6,6	0.08	0
5	NAG	E	579	1	14,14,15	0.59	0	17,19,21	0.69	0
3	SO4	E	585	-	4,4,4	0.38	0	6,6,6	0.09	0
3	SO4	B	384	-	4,4,4	0.35	0	6,6,6	0.11	0
6	SIA	E	582	-	21,21,21	0.85	0	24,31,31	1.19	3 (12%)

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	NAG	D	479	1	-	3/6/23/26	0/1/1/1
4	COA	A	1	-	1/1/11/13	12/48/64/64	0/3/3/3
5	NAG	C	379	1	1/1/5/7	4/6/23/26	0/1/1/1
5	NAG	B	279	1	-	2/6/23/26	0/1/1/1
4	COA	F	6	-	1/1/11/13	13/48/64/64	0/3/3/3
5	NAG	E	579	1	-	4/6/23/26	0/1/1/1
4	COA	D	4	-	1/1/11/13	13/48/64/64	0/3/3/3
4	COA	E	5	-	1/1/11/13	13/48/64/64	0/3/3/3
6	SIA	D	482	-	-	5/20/38/38	0/1/1/1
4	COA	B	2	-	1/1/11/13	13/48/64/64	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	COA	C	3	-	1/1/11/13	13/48/64/64	0/3/3/3
6	SIA	E	582	-	-	10/20/38/38	0/1/1/1

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	3	COA	O5P-C5P	9.52	1.42	1.23
4	B	2	COA	O5P-C5P	9.46	1.42	1.23
4	E	5	COA	O5P-C5P	9.46	1.42	1.23
4	A	1	COA	O5P-C5P	9.45	1.42	1.23
4	F	6	COA	O9P-C9P	9.44	1.41	1.23

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2	COA	O9P-C9P-N8P	-10.10	101.62	122.98
4	A	1	COA	O5P-C5P-N4P	-10.08	103.25	123.03
4	E	5	COA	O5P-C5P-N4P	-9.91	103.59	123.03
4	C	3	COA	O9P-C9P-N8P	-9.90	102.03	122.98
4	A	1	COA	O9P-C9P-N8P	-9.88	102.08	122.98

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:

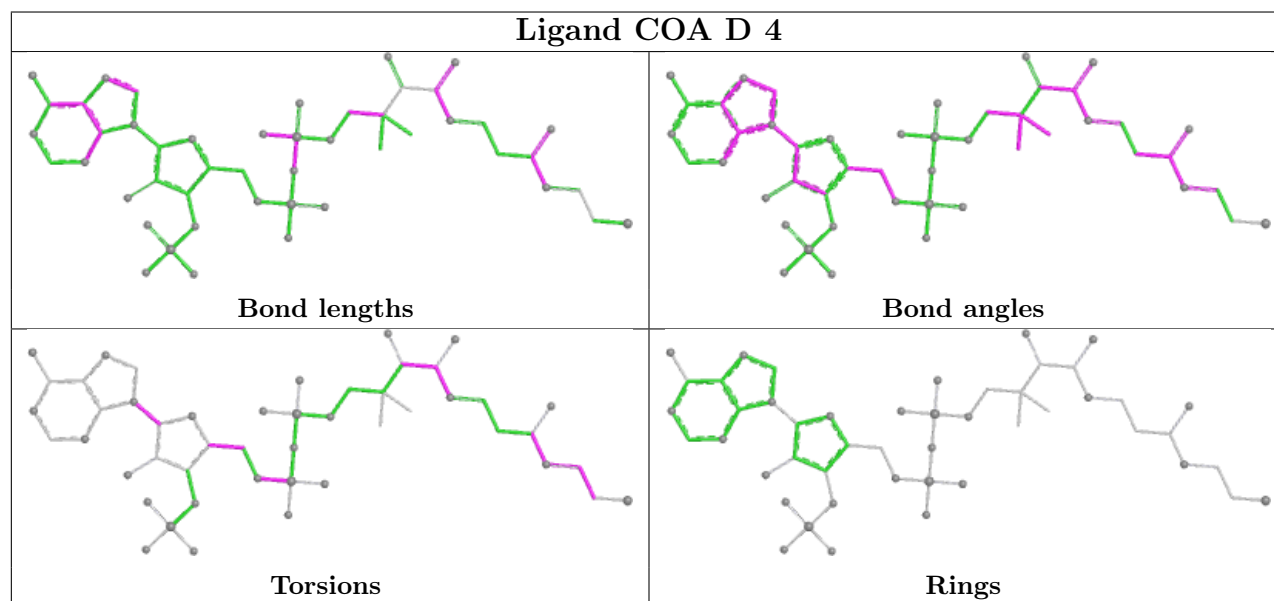
Mol	Chain	Res	Type	Atoms
4	A	1	COA	C5B-O5B-P1A-O2A
4	A	1	COA	C5B-O5B-P1A-O3A
4	A	1	COA	O9P-C9P-CAP-CBP
4	A	1	COA	CAP-C9P-N8P-C7P
4	A	1	COA	O9P-C9P-N8P-C7P

There are no ring outliers.

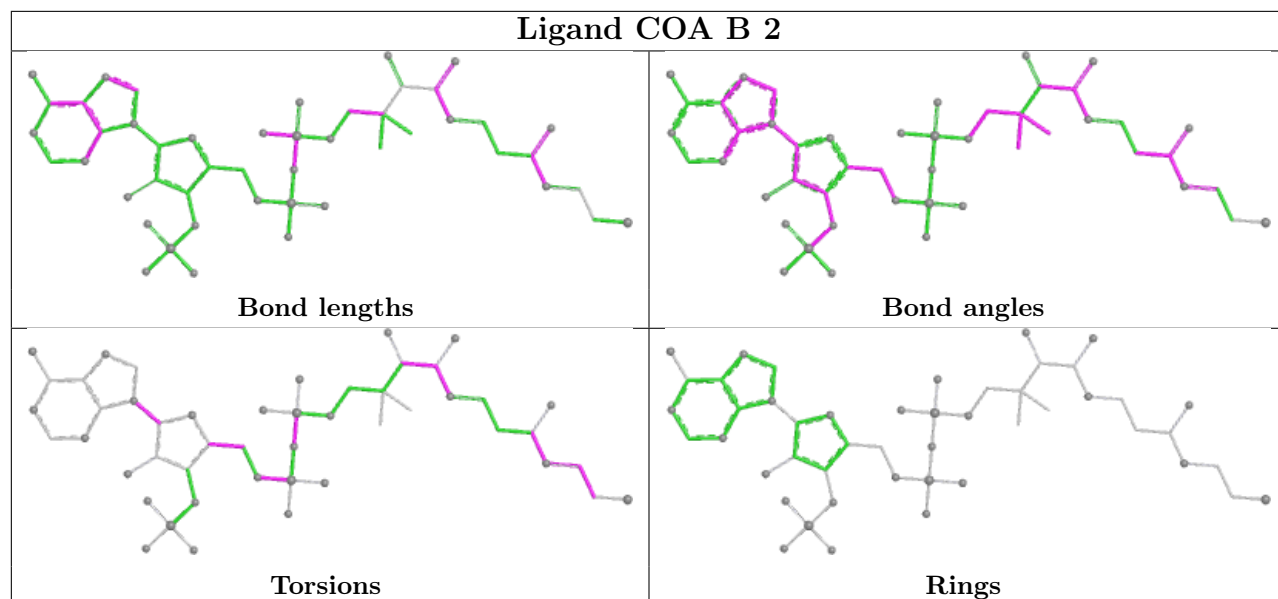
11 monomers are involved in 161 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	379	NAG	1	0
4	D	4	COA	23	0
4	B	2	COA	28	0
6	D	482	SIA	9	0
5	B	279	NAG	1	0
4	E	5	COA	21	0
4	C	3	COA	20	0
4	A	1	COA	26	0
4	F	6	COA	26	0
5	E	579	NAG	1	0
6	E	582	SIA	5	0

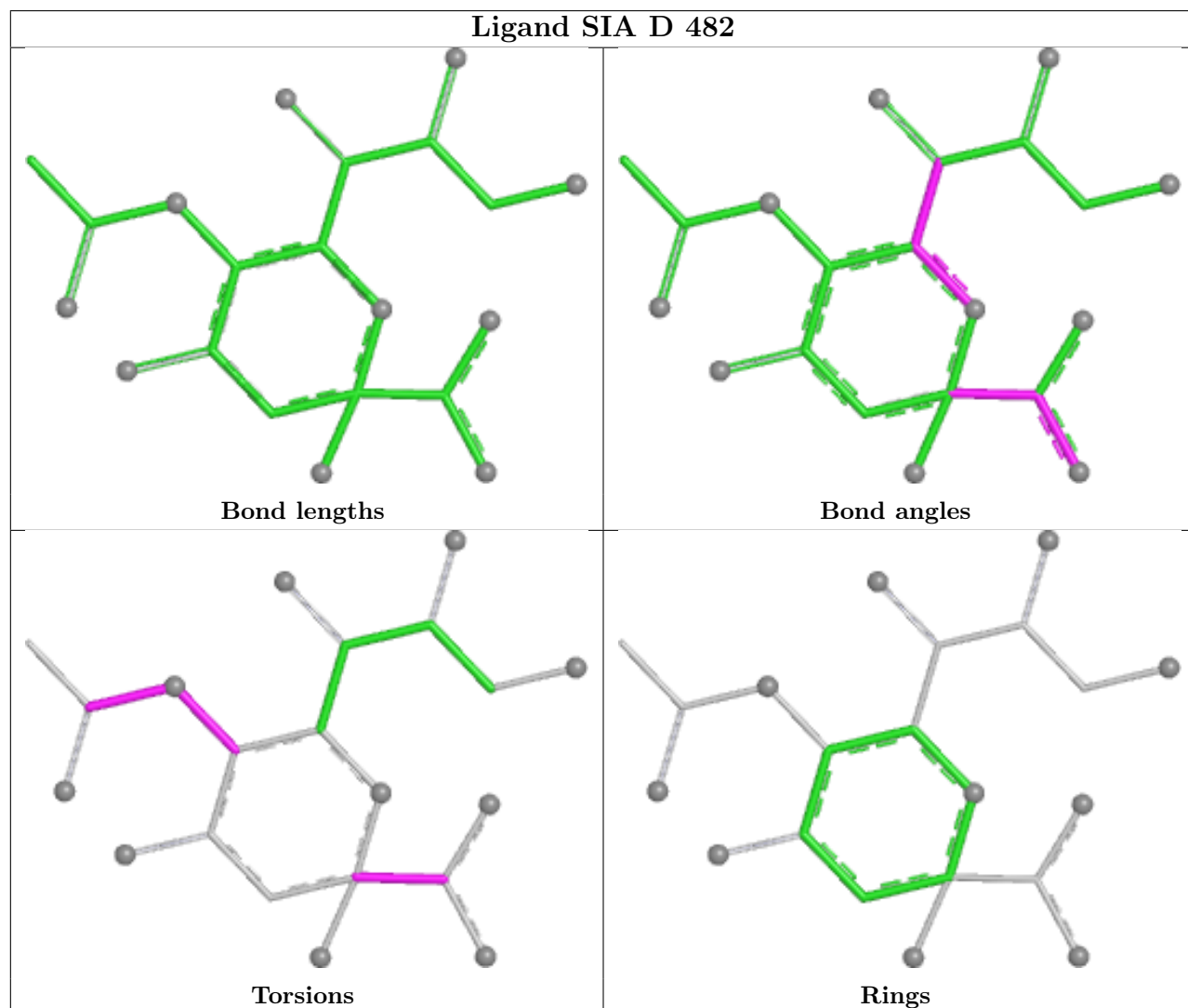
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



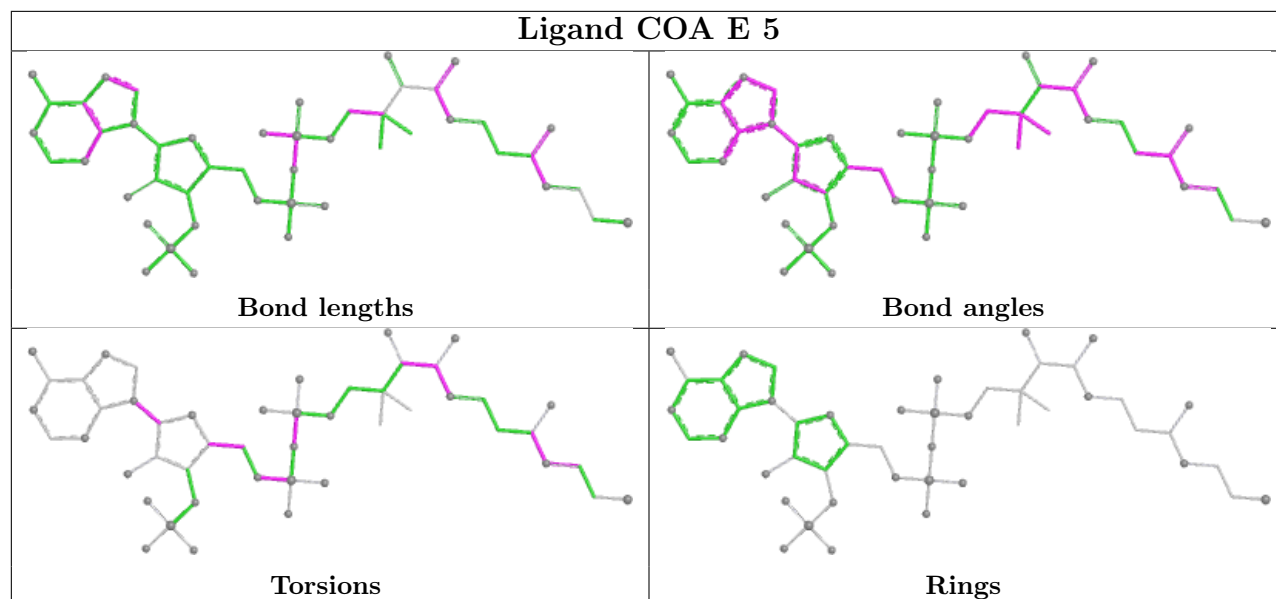
Ligand COA B 2



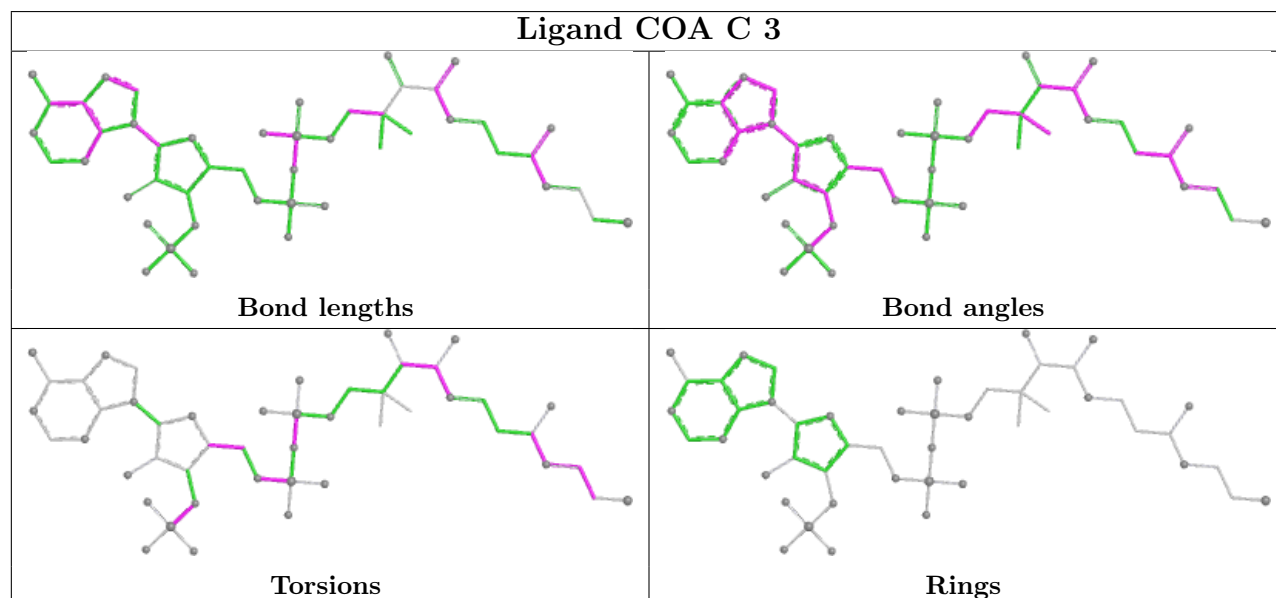
Ligand SIA D 482



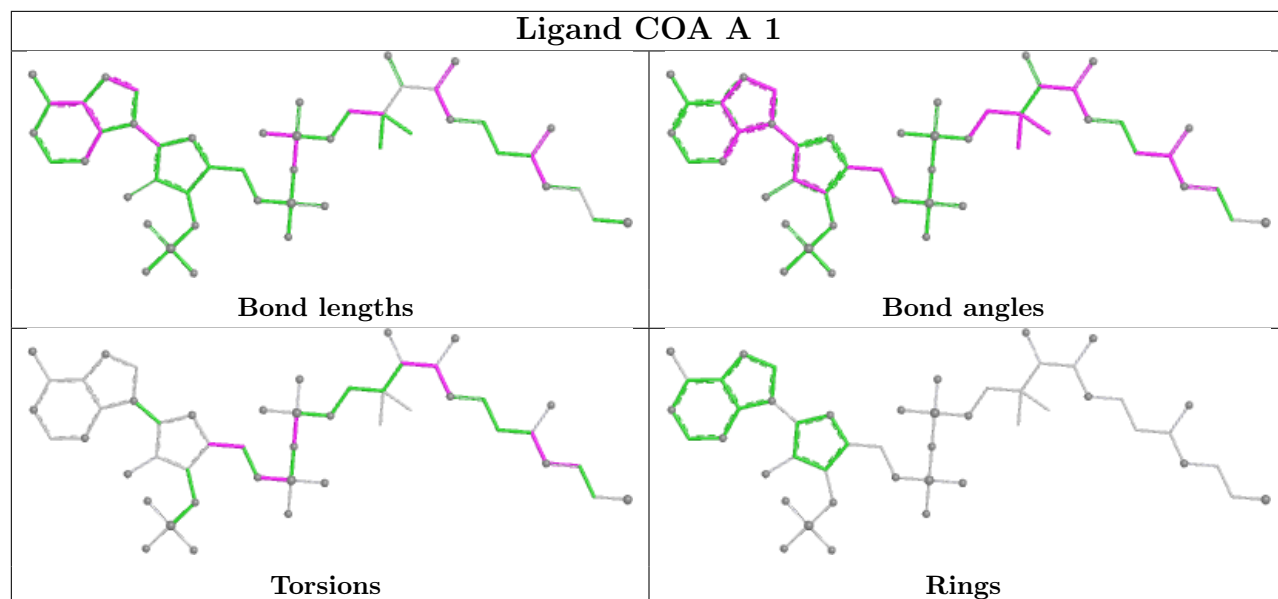
Ligand COA E 5



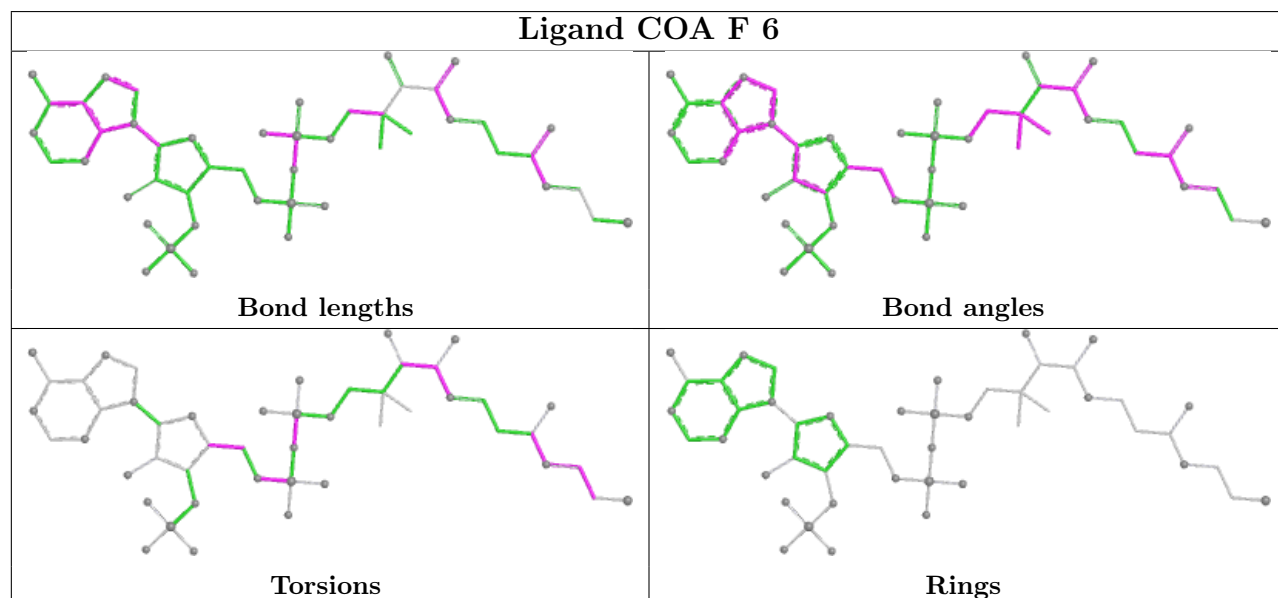
Ligand COA C 3

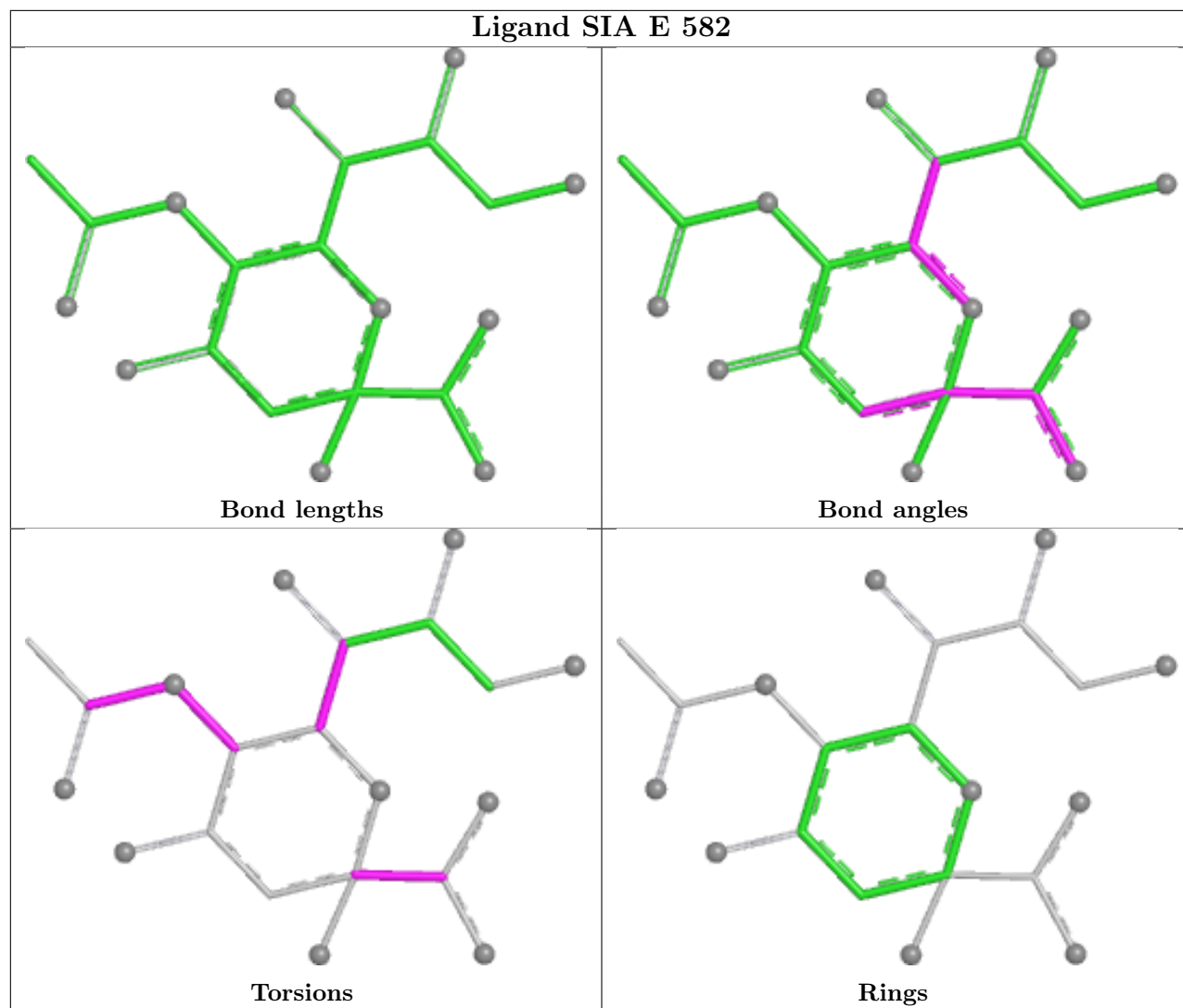


Ligand COA A 1



Ligand COA F 6





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
1	A	1390[B]:CYS	C	1391:ILE	N	1.10

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.