



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:00 PM GMT

PDB ID : 1MX1
Title : Crystal Structure of Human Liver Carboxylesterase in complex with tacrine
Authors : Bencharit, S.; Morton, C.L.; Hyatt, J.L.; Kuhn, P.; Danks, M.K.; Potter, P.M.;
Redinbo, M.R.
Deposited on : 2002-10-01
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

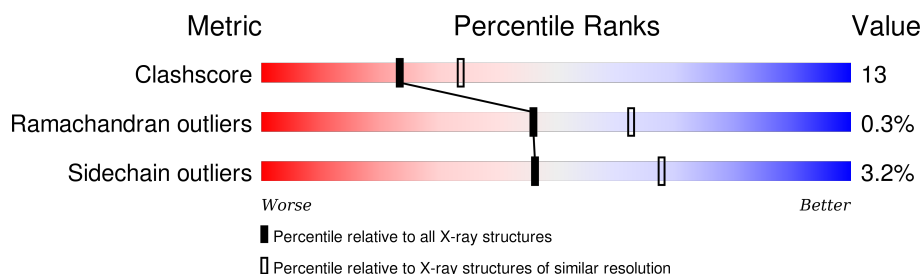
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

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

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
3	SIA	A	182	-	-	X	-
3	SIA	B	282	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27468 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called liver Carboxylesterase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	531	Total	C	N	O	S	0	0	0
			4124	2659	684	761	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
			4124	2659	684	761	20			

There are 6 discrepancies between the modelled and reference sequences:

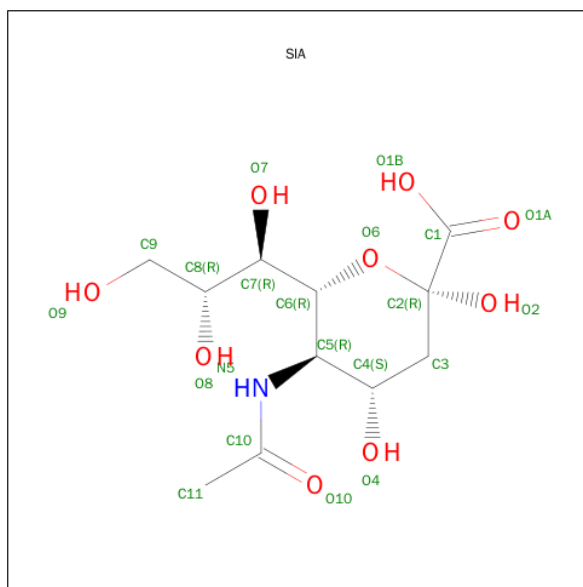
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	DELETION	UNP P23141
B	?	-	GLN	DELETION	UNP P23141
C	?	-	GLN	DELETION	UNP P23141
D	?	-	GLN	DELETION	UNP P23141
E	?	-	GLN	DELETION	UNP P23141
F	?	-	GLN	DELETION	UNP P23141

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is SUGAR (O-SIALIC ACID) (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).

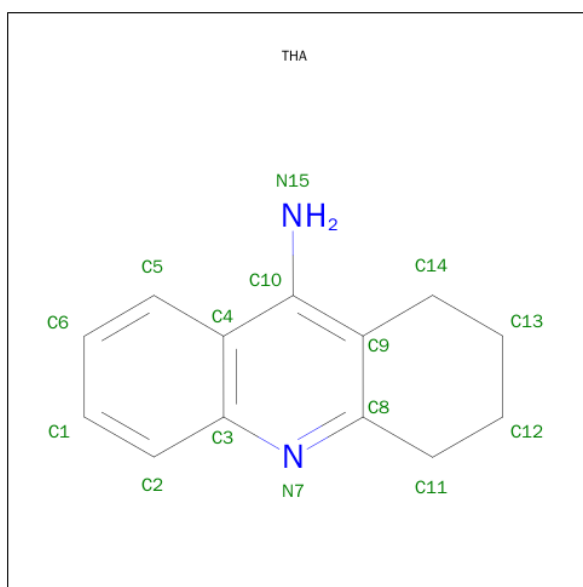


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	11	1	9		
3	B	1	Total	C	N	O	0	0
			21	11	1	9		
3	D	1	Total	C	N	O	1	0
			21	11	1	9		
3	E	1	Total	C	N	O	1	0
			21	11	1	9		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 5 is TACRINE (three-letter code: THA) (formula: C₁₃H₁₄N₂).



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

- Molecule 6 is water.

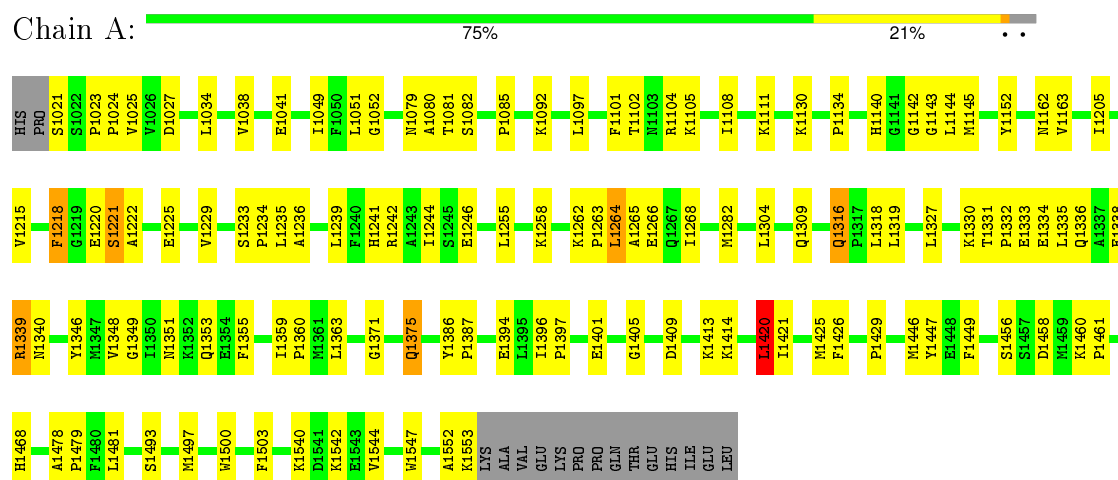
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	364	Total	O	0	0
			364	364		
6	B	360	Total	O	0	0
			360	360		
6	C	371	Total	O	0	0
			371	371		
6	D	306	Total	O	0	0
			306	306		
6	E	353	Total	O	0	0
			353	353		
6	F	363	Total	O	0	0
			363	363		

3 Residue-property plots

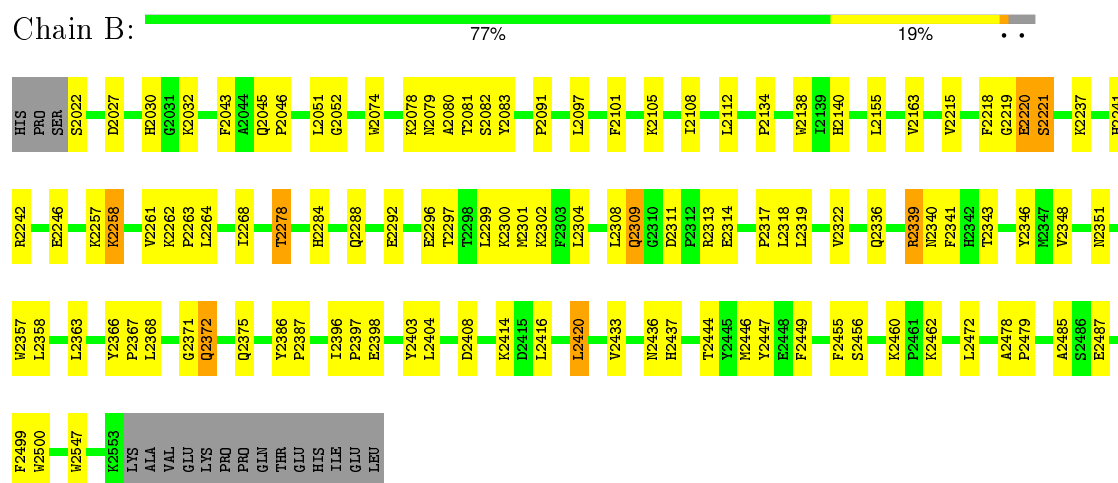
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

- Molecule 1: liver Carboxylesterase I

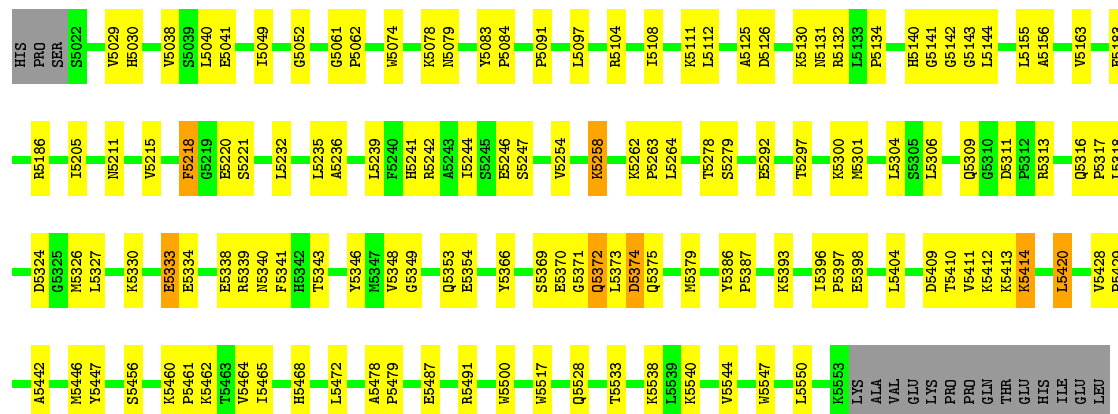


- Molecule 1: liver Carboxylesterase I

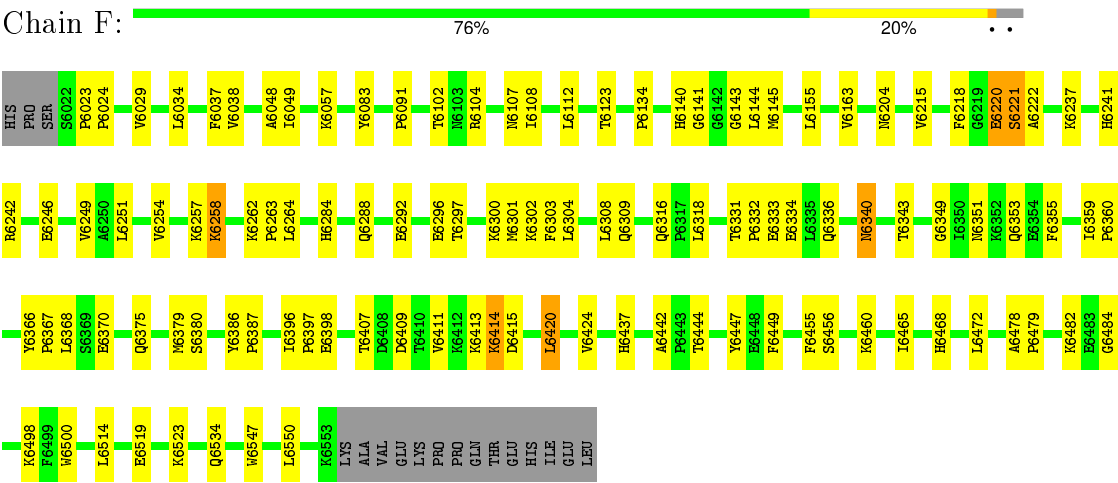


- Molecule 1: liver Carboxylesterase I





● Molecule 1: liver Carboxylesterase I



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0/4236	0.58	1/5754 (0.0%)
1	B	0.33	0/4230	0.58	0/5746
1	C	0.34	0/4230	0.59	0/5746
1	D	0.32	0/4230	0.56	0/5746
1	E	0.33	0/4230	0.58	0/5746
1	F	0.34	0/4230	0.57	0/5746
All	All	0.33	0/25386	0.58	1/34484 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1420	LEU	CA-CB-CG	5.36	127.63	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4130	0	4131	117	0
1	B	4124	0	4126	107	0
1	C	4124	0	4126	126	0
1	D	4124	0	4126	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	4124	0	4125	112	0
1	F	4124	0	4126	97	0
2	A	14	0	13	0	0
2	B	14	0	13	3	0
2	D	14	0	13	0	0
2	E	14	0	13	1	0
2	F	28	0	26	1	0
3	A	21	0	18	30	0
3	B	21	0	18	16	0
3	D	21	0	18	7	0
3	E	21	0	18	7	0
4	C	28	0	25	2	0
5	A	60	0	56	13	0
5	B	60	0	56	9	0
5	C	75	0	70	12	0
5	D	75	0	70	10	0
5	E	75	0	70	14	0
5	F	60	0	56	7	0
6	A	364	0	0	25	0
6	B	360	0	0	16	0
6	C	371	0	0	17	0
6	D	306	0	0	9	0
6	E	353	0	0	22	0
6	F	363	0	0	12	0
All	All	27468	0	25313	671	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 671 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:GLY:HA3	3:A:182:SIA:H32	1.24	1.19
3:B:282:SIA:H111	6:C:7197:HOH:O	1.42	1.18
3:B:282:SIA:H113	1:C:3278:THR:HB	1.29	1.14
3:A:182:SIA:H111	1:B:2278:THR:HB	1.31	1.12
1:C:3258:LYS:HE2	1:C:3258:LYS:H	1.09	1.12

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	530/548 (97%)	509 (96%)	20 (4%)	1 (0%)	52	69
1	B	529/548 (96%)	508 (96%)	20 (4%)	1 (0%)	52	69
1	C	529/548 (96%)	509 (96%)	17 (3%)	3 (1%)	30	43
1	D	529/548 (96%)	499 (94%)	28 (5%)	2 (0%)	39	56
1	E	529/548 (96%)	505 (96%)	24 (4%)	0	100	100
1	F	529/548 (96%)	505 (96%)	22 (4%)	2 (0%)	39	56
All	All	3175/3288 (97%)	3035 (96%)	131 (4%)	9 (0%)	46	63

5 of 9 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	448/463 (97%)	437 (98%)	11 (2%)	55	76
1	B	447/463 (96%)	428 (96%)	19 (4%)	35	55
1	C	447/463 (96%)	432 (97%)	15 (3%)	44	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	447/463 (96%)	432 (97%)	15 (3%)	44	65
1	E	447/463 (96%)	433 (97%)	14 (3%)	47	69
1	F	447/463 (96%)	436 (98%)	11 (2%)	55	76
All	All	2683/2778 (97%)	2598 (97%)	85 (3%)	46	68

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3264	LEU
1	D	4242	ARG
1	F	6258	LYS
1	C	3346	TYR
1	C	3519	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	3436	ASN
1	D	4316	GLN
1	F	6351	ASN
1	C	3534	GLN
1	D	4140	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 ⓘ

2 carbohydrates 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	$\# Z > 2$
4	NAG	C	379	1,4	14,14,15	0.76	0	15,19,21	0.71	0
4	NDG	C	380	4	14,14,15	1.04	1 (7%)	15,19,21	1.40	3 (20%)

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	NAG	C	379	1,4	-	0/6/23/26	0/1/1/1
4	NDG	C	380	4	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	380	NDG	O-C5	2.66	1.49	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	380	NDG	C6-C5-C4	-3.08	105.43	113.02
4	C	380	NDG	C4-C3-C2	-2.05	108.04	111.23
4	C	380	NDG	C3-C4-C5	2.82	115.12	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	379	NAG	2	0
4	C	380	NDG	2	0

5.6 Ligand geometry

37 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	THA	A	1[A]	-	17,17,17	2.47	7 (41%)	20,24,24	1.69	4 (20%)
5	THA	A	1[B]	-	17,17,17	2.54	8 (47%)	20,24,24	1.68	4 (20%)
5	THA	A	1[C]	-	17,17,17	2.47	8 (47%)	20,24,24	1.72	4 (20%)
5	THA	A	1[D]	-	17,17,17	2.49	7 (41%)	20,24,24	1.65	3 (15%)
2	NAG	A	179	1	14,14,15	0.61	0	15,19,21	0.70	1 (6%)
3	SIA	A	182	1	17,21,21	1.00	1 (5%)	19,31,31	1.11	2 (10%)
5	THA	B	2[A]	-	17,17,17	2.51	8 (47%)	20,24,24	1.76	3 (15%)
5	THA	B	2[B]	-	17,17,17	2.53	8 (47%)	20,24,24	1.67	4 (20%)
5	THA	B	2[C]	-	17,17,17	2.45	8 (47%)	20,24,24	1.67	4 (20%)
5	THA	B	2[D]	-	17,17,17	2.50	8 (47%)	20,24,24	1.64	4 (20%)
2	NAG	B	279	1	14,14,15	0.55	0	15,19,21	0.92	1 (6%)
3	SIA	B	282	-	17,21,21	0.89	0	19,31,31	1.02	1 (5%)
5	THA	C	3[A]	-	17,17,17	2.51	8 (47%)	20,24,24	1.66	4 (20%)
5	THA	C	3[B]	-	17,17,17	2.56	8 (47%)	20,24,24	1.73	4 (20%)
5	THA	C	3[C]	-	17,17,17	2.52	8 (47%)	20,24,24	1.64	4 (20%)
5	THA	C	3[D]	-	17,17,17	2.40	8 (47%)	20,24,24	1.70	4 (20%)
5	THA	C	3[E]	-	17,17,17	2.52	7 (41%)	20,24,24	1.63	5 (25%)
5	THA	D	4[A]	-	17,17,17	2.53	8 (47%)	20,24,24	1.71	3 (15%)
5	THA	D	4[B]	-	17,17,17	2.48	8 (47%)	20,24,24	1.64	4 (20%)
5	THA	D	4[C]	-	17,17,17	2.50	8 (47%)	20,24,24	1.66	3 (15%)
5	THA	D	4[D]	-	17,17,17	2.53	8 (47%)	20,24,24	1.69	4 (20%)
5	THA	D	4[E]	-	17,17,17	2.44	8 (47%)	20,24,24	1.63	4 (20%)
2	NAG	D	479	1	14,14,15	0.49	0	15,19,21	0.71	1 (6%)
3	SIA	D	482	-	17,21,21	1.16	1 (5%)	19,31,31	0.91	1 (5%)
5	THA	E	5[A]	-	17,17,17	2.54	8 (47%)	20,24,24	1.66	4 (20%)
5	THA	E	5[B]	-	17,17,17	2.48	8 (47%)	20,24,24	1.68	4 (20%)
5	THA	E	5[C]	-	17,17,17	2.50	8 (47%)	20,24,24	1.69	4 (20%)
5	THA	E	5[D]	-	17,17,17	2.49	7 (41%)	20,24,24	1.63	4 (20%)
5	THA	E	5[E]	-	17,17,17	2.47	8 (47%)	20,24,24	1.67	4 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	579	1	14,14,15	0.56	0	15,19,21	0.77	1 (6%)
3	SIA	E	582	-	17,21,21	1.02	1 (5%)	19,31,31	1.16	2 (10%)
5	THA	F	6[A]	-	17,17,17	2.51	8 (47%)	20,24,24	1.76	3 (15%)
5	THA	F	6[B]	-	17,17,17	2.45	8 (47%)	20,24,24	1.64	4 (20%)
5	THA	F	6[C]	-	17,17,17	2.45	8 (47%)	20,24,24	1.69	4 (20%)
5	THA	F	6[D]	-	17,17,17	2.46	8 (47%)	20,24,24	1.66	4 (20%)
2	NAG	F	679	1	14,14,15	0.48	0	15,19,21	0.92	1 (6%)
2	NAG	F	680	-	14,14,15	0.48	0	15,19,21	0.69	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	THA	A	1[A]	-	-	0/0/7/7	0/3/3/3
5	THA	A	1[B]	-	-	0/0/7/7	0/3/3/3
5	THA	A	1[C]	-	-	0/0/7/7	0/3/3/3
5	THA	A	1[D]	-	-	0/0/7/7	0/3/3/3
2	NAG	A	179	1	-	0/6/23/26	0/1/1/1
3	SIA	A	182	1	-	0/14/38/38	0/1/1/1
5	THA	B	2[A]	-	-	0/0/7/7	0/3/3/3
5	THA	B	2[B]	-	-	0/0/7/7	0/3/3/3
5	THA	B	2[C]	-	-	0/0/7/7	0/3/3/3
5	THA	B	2[D]	-	-	0/0/7/7	0/3/3/3
2	NAG	B	279	1	-	0/6/23/26	0/1/1/1
3	SIA	B	282	-	-	0/14/38/38	0/1/1/1
5	THA	C	3[A]	-	-	0/0/7/7	0/3/3/3
5	THA	C	3[B]	-	-	0/0/7/7	0/3/3/3
5	THA	C	3[C]	-	-	0/0/7/7	0/3/3/3
5	THA	C	3[D]	-	-	0/0/7/7	0/3/3/3
5	THA	C	3[E]	-	-	0/0/7/7	0/3/3/3
5	THA	D	4[A]	-	-	0/0/7/7	0/3/3/3
5	THA	D	4[B]	-	-	0/0/7/7	0/3/3/3
5	THA	D	4[C]	-	-	0/0/7/7	0/3/3/3
5	THA	D	4[D]	-	-	0/0/7/7	0/3/3/3
5	THA	D	4[E]	-	-	0/0/7/7	0/3/3/3
2	NAG	D	479	1	-	0/6/23/26	0/1/1/1
3	SIA	D	482	-	-	0/14/38/38	0/1/1/1
5	THA	E	5[A]	-	-	0/0/7/7	0/3/3/3
5	THA	E	5[B]	-	-	0/0/7/7	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	THA	E	5[C]	-	-	0/0/7/7	0/3/3/3
5	THA	E	5[D]	-	-	0/0/7/7	0/3/3/3
5	THA	E	5[E]	-	-	0/0/7/7	0/3/3/3
2	NAG	E	579	1	-	0/6/23/26	0/1/1/1
3	SIA	E	582	-	-	0/14/38/38	0/1/1/1
5	THA	F	6[A]	-	-	0/0/7/7	0/3/3/3
5	THA	F	6[B]	-	-	0/0/7/7	0/3/3/3
5	THA	F	6[C]	-	-	0/0/7/7	0/3/3/3
5	THA	F	6[D]	-	-	0/0/7/7	0/3/3/3
2	NAG	F	679	1	-	0/6/23/26	0/1/1/1
2	NAG	F	680	-	-	0/6/23/26	0/1/1/1

The worst 5 of 215 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	6[C]	THA	C3-N7	-2.30	1.33	1.37
5	E	5[B]	THA	C3-N7	-2.23	1.33	1.37
5	F	6[B]	THA	C3-N7	-2.20	1.33	1.37
5	E	5[C]	THA	C3-N7	-2.18	1.33	1.37
5	A	1[C]	THA	C3-N7	-2.18	1.33	1.37

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	6[A]	THA	C14-C9-C8	-4.11	117.94	121.05
5	B	2[A]	THA	C14-C9-C8	-4.06	117.97	121.05
5	A	1[C]	THA	C14-C9-C8	-3.95	118.05	121.05
5	C	3[B]	THA	C14-C9-C8	-3.93	118.07	121.05
5	D	4[A]	THA	C14-C9-C8	-3.81	118.16	121.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

33 monomers are involved in 130 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1[A]	THA	3	0
5	A	1[B]	THA	3	0
5	A	1[C]	THA	4	0
5	A	1[D]	THA	3	0
3	A	182	SIA	30	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	2[A]	THA	2	0
5	B	2[B]	THA	5	0
5	B	2[C]	THA	1	0
5	B	2[D]	THA	1	0
2	B	279	NAG	3	0
3	B	282	SIA	16	0
5	C	3[A]	THA	3	0
5	C	3[B]	THA	1	0
5	C	3[C]	THA	1	0
5	C	3[D]	THA	4	0
5	C	3[E]	THA	3	0
5	D	4[A]	THA	3	0
5	D	4[B]	THA	3	0
5	D	4[C]	THA	2	0
5	D	4[E]	THA	2	0
3	D	482	SIA	7	0
5	E	5[A]	THA	2	0
5	E	5[B]	THA	2	0
5	E	5[C]	THA	3	0
5	E	5[D]	THA	3	0
5	E	5[E]	THA	4	0
2	E	579	NAG	1	0
3	E	582	SIA	7	0
5	F	6[B]	THA	2	0
5	F	6[C]	THA	3	0
5	F	6[D]	THA	2	0
2	F	679	NAG	1	0
2	F	680	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.