



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 11:12 PM UTC

PDB ID : 3OAX / pdb_00003oax
Title : Crystal structure of bovine rhodopsin with beta-ionone
Authors : Makino, C.L.; Riley, C.K.; Looney, J.; Crouch, R.K.; Okada, T.
Deposited on : 2010-08-05
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

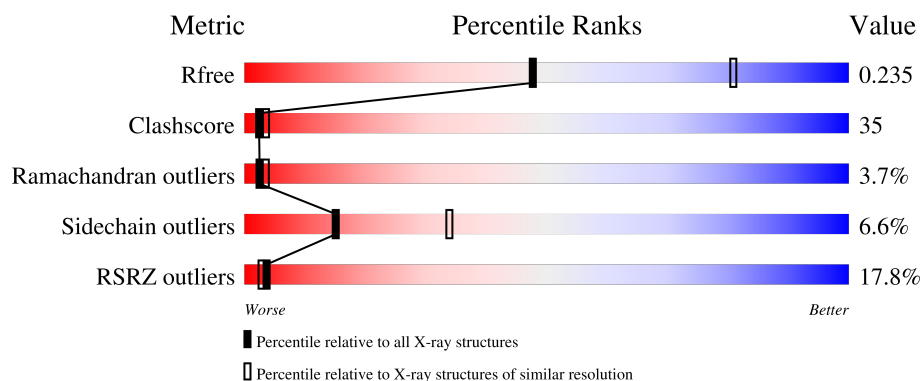
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 $\leq 5\%$. 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	349	16% 52% 40% 8%
1	B	349	19% 49% 45% 6%
2	C	3	33% 67%
3	D	2	50% 50%
3	F	2	50% 50%

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Mol	Chain	Length	Quality of chain
4	E	4	

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
11	ID3	B	6026	-	-	X	-

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 6015 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.

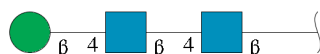
- Molecule 1 is a protein called Rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2749	1818	424	481	26			
1	B	349	Total	C	N	O	S	0	0	0
			2749	1818	424	481	26			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP P02699
B	0	ACE	-	acetylation	UNP P02699

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



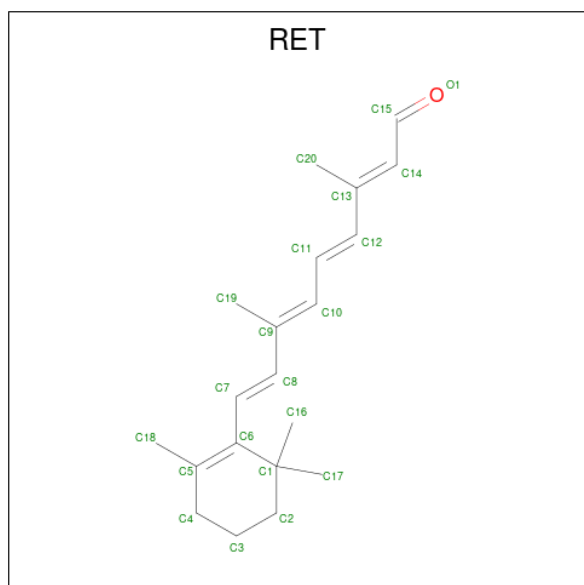
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranoside-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



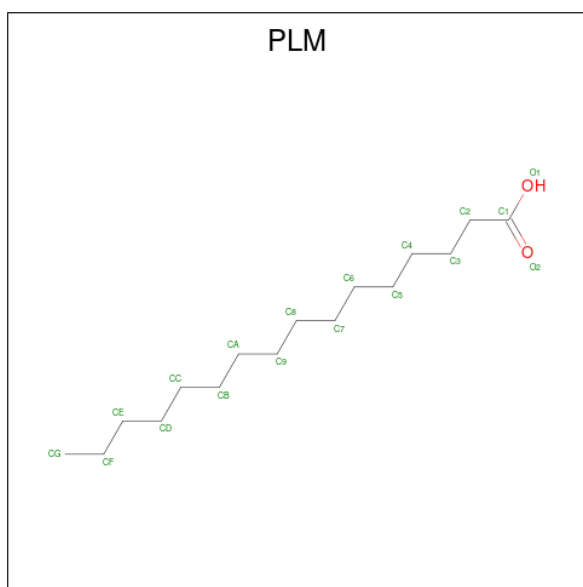
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is RETINAL (CCD ID: RET) (formula: C₂₀H₂₈O).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	C	0	0
			20	20		
5	B	1	Total	C	0	0
			20	20		

- Molecule 6 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			17	16	1		
6	A	1	Total	C	O	0	0
			17	16	1		
6	B	1	Total	C	O	0	0
			17	16	1		
6	B	1	Total	C	O	0	0
			17	16	1		

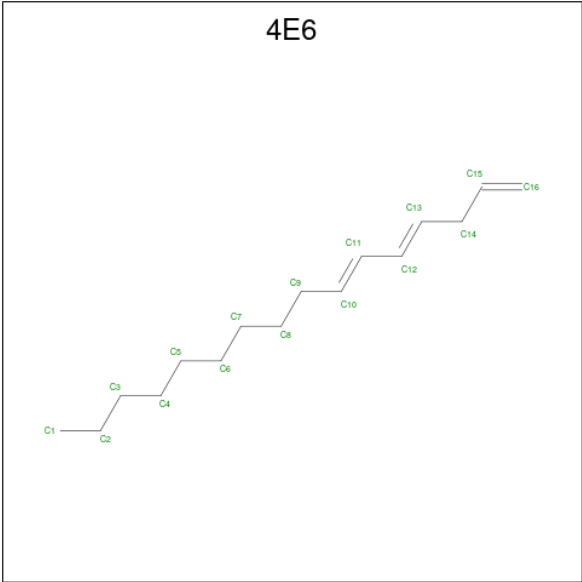
- Molecule 7 is MERCURY (II) ION (CCD ID: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	3	Total	Hg	0	0
			3	3		
7	B	3	Total	Hg	0	0
			3	3		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

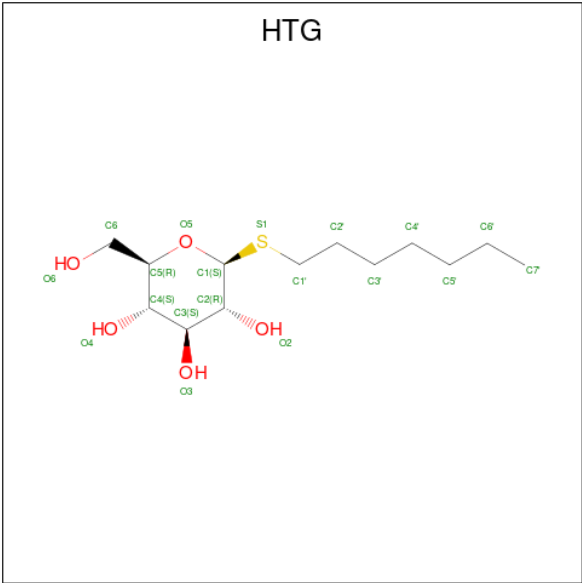
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	4	Total	Zn	0	0
			4	4		
8	B	3	Total	Zn	0	0
			3	3		

- Molecule 9 is (4E,6E)-hexadeca-1,4,6-triene (CCD ID: 4E6) (formula: C₁₆H₂₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C		0	0
			16	16			
9	B	1	Total	C		0	0
			16	16			

- Molecule 10 is heptyl 1-thio-beta-D-glucopyranoside (CCD ID: HTG) (formula: C₁₃H₂₆O₅S).



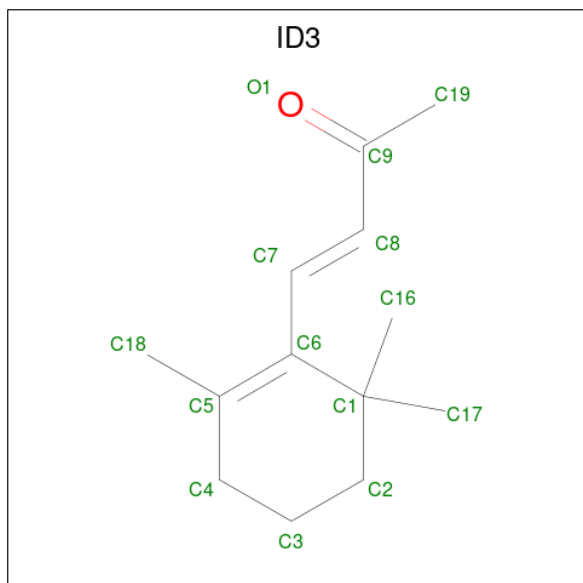
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	O	S	0	0
			19	13	5	1		
10	A	1	Total	C	O	S	0	0
			19	13	5	1		

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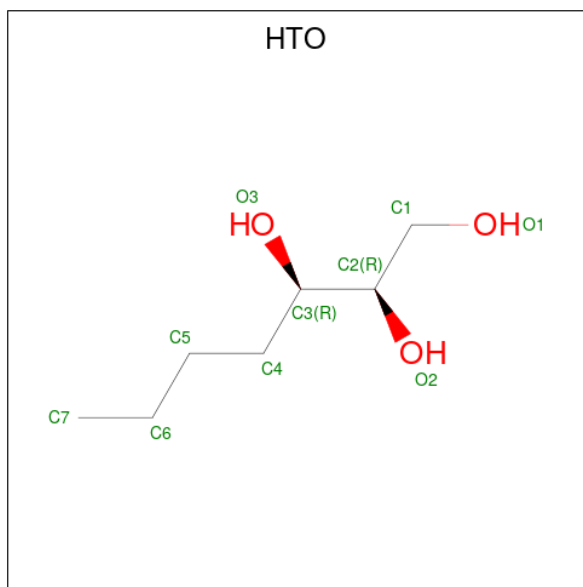
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	O	S	0	0
			19	13	5	1		
10	B	1	Total	C	O	S	0	0
			19	13	5	1		

- Molecule 11 is (3E)-4-(2,6,6-trimethylcyclohex-1-en-1-yl)but-3-en-2-one (CCD ID: ID3) (formula: C₁₃H₂₀O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	A	1	Total	C	O		0	0
			14	13	1			
11	B	1	Total	C	O		0	0
			14	13	1			

- Molecule 12 is HEPTANE-1,2,3-TRIOL (CCD ID: HTO) (formula: C₇H₁₆O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			10	7	3		

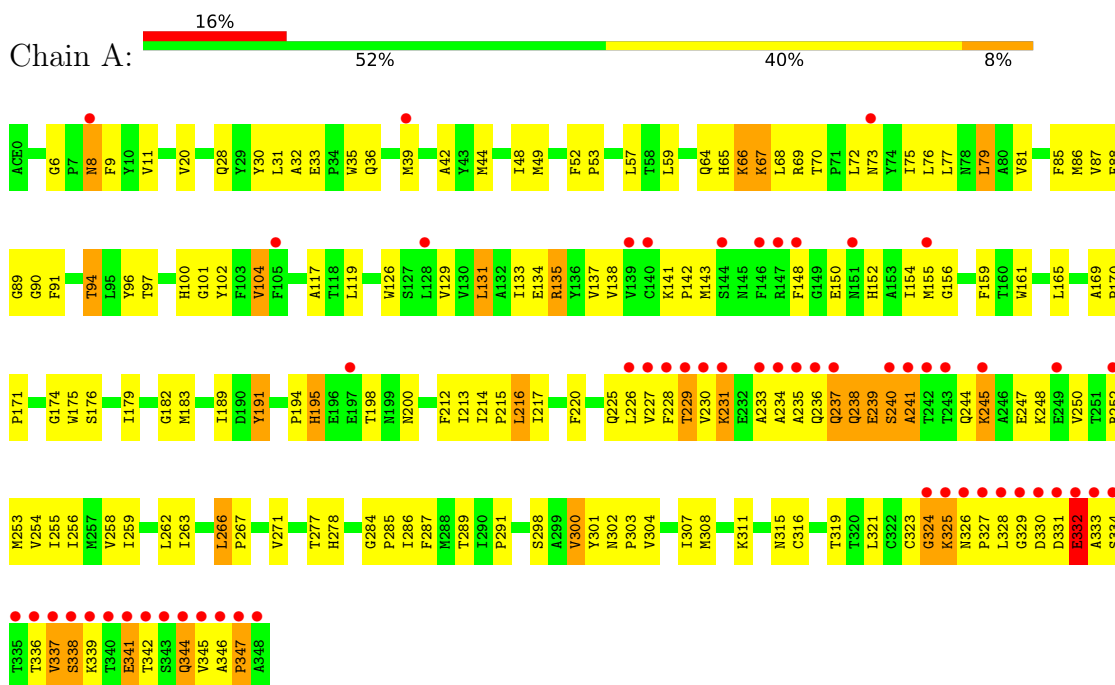
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	57	Total	O	0	0
			57	57		
13	B	48	Total	O	0	0
			48	48		

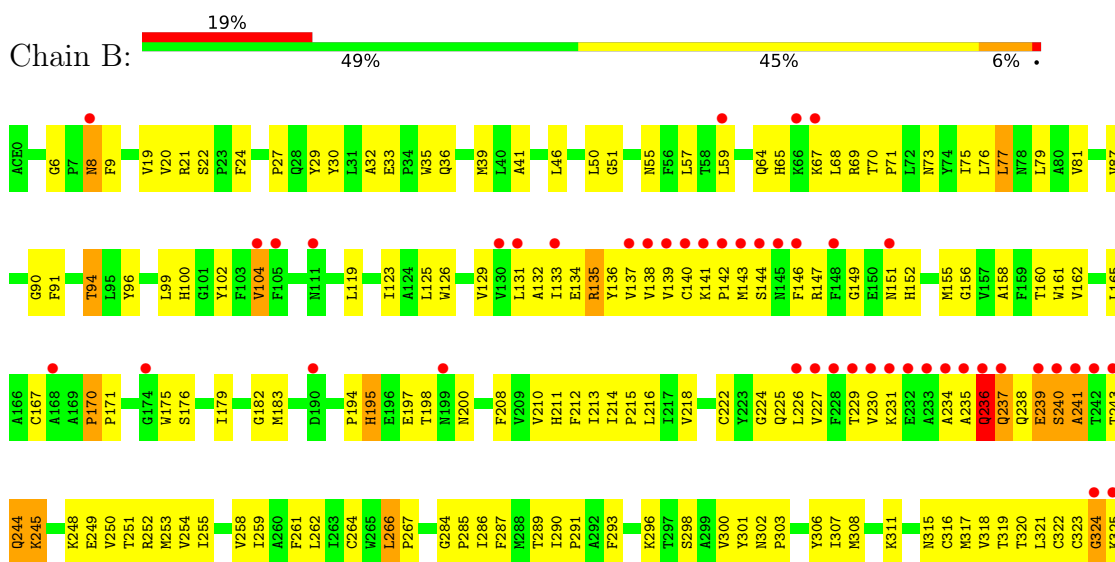
3 Residue-property plots [i](#)

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 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: Rhodopsin



• Molecule 1: Rhodopsin





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



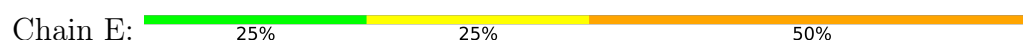
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	96.99Å 96.99Å 149.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.60) 93.6 (50.00-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.262 0.236 , 0.235	Depositor DCC
R_{free} test set	1996 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	52.8	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 59.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6015	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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: BMA, ZN, NAG, 4E6, ID3, HTO, HTG, RET, MAN, ACE, PLM, HG

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	0.57	0/2831	0.94	2/3859 (0.1%)
1	B	0.53	0/2831	0.93	4/3859 (0.1%)
All	All	0.55	0/5662	0.93	6/7718 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	GLY	N-CA-C	5.95	121.76	114.69
1	B	140	CYS	N-CA-C	-5.93	106.58	113.88
1	B	77	LEU	N-CA-C	-5.78	105.06	111.36
1	B	170	PRO	N-CA-C	5.35	117.23	110.70
1	A	191	TYR	N-CA-C	-5.27	106.87	113.72
1	B	285	PRO	N-CA-C	5.22	120.70	113.65

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	2749	0	2706	193	0
1	B	2749	0	2708	225	0
2	C	39	0	34	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	28	0	25	0	0
3	F	28	0	25	0	0
4	E	50	0	43	2	0
5	A	20	0	27	1	0
5	B	20	0	27	0	0
6	A	34	0	62	0	0
6	B	34	0	62	3	0
7	A	3	0	0	0	0
7	B	3	0	0	1	0
8	A	4	0	0	0	0
8	B	3	0	0	0	0
9	A	16	0	27	1	0
9	B	16	0	27	0	0
10	A	38	0	52	1	0
10	B	38	0	52	3	0
11	A	14	0	20	5	0
11	B	14	0	20	9	0
12	B	10	0	16	1	0
13	A	57	0	0	2	0
13	B	48	0	0	3	0
All	All	6015	0	5933	417	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 35.

All (417) 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:65:HIS:HB3	1:A:337:VAL:HG22	1.28	1.15
1:B:346:ALA:H	1:B:347:PRO:HD3	1.02	1.07
1:A:345:VAL:HG12	1:A:347:PRO:HD3	1.32	1.06
1:A:67:LYS:HB2	1:A:337:VAL:HB	1.36	1.06
1:A:341:GLU:HG3	1:A:342:THR:H	1.23	1.00
1:A:183:MET:HE3	1:A:289:THR:HG21	1.46	0.98
1:B:338:SER:HB2	1:B:341:GLU:HG2	1.46	0.96
1:B:346:ALA:H	1:B:347:PRO:CD	1.82	0.93
1:A:284:GLY:H	11:A:6025:ID3:H17A	1.30	0.93
1:A:325:LYS:HG2	1:A:326:ASN:H	1.35	0.91
1:B:143:MET:HG2	1:B:146:PHE:HB2	1.51	0.90
1:B:59:LEU:HD12	1:B:77:LEU:HD11	1.52	0.90
1:B:346:ALA:N	1:B:347:PRO:HD3	1.87	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:GLU:HB3	1:B:244:GLN:HE22	1.39	0.88
1:A:91:PHE:HA	1:A:94:THR:CG2	2.06	0.85
1:A:345:VAL:HG12	1:A:347:PRO:CD	2.07	0.84
1:B:237:GLN:H	1:B:237:GLN:NE2	1.76	0.83
1:B:183:MET:HE3	1:B:289:THR:HG21	1.58	0.83
1:B:245:LYS:HE3	1:B:245:LYS:HA	1.60	0.82
1:B:341:GLU:HG3	1:B:342:THR:N	1.92	0.81
1:B:143:MET:HG2	1:B:146:PHE:CB	2.11	0.81
1:B:230:VAL:HG23	1:B:248:LYS:HD3	1.63	0.81
1:B:239:GLU:HB3	1:B:244:GLN:NE2	1.96	0.80
1:B:67:LYS:HB3	1:B:337:VAL:CG2	2.12	0.79
1:B:64:GLN:HG2	1:B:339:LYS:HB2	1.63	0.79
1:B:332:GLU:HB2	1:B:336:THR:OG1	1.82	0.79
1:A:341:GLU:HG3	1:A:342:THR:N	1.92	0.79
1:B:284:GLY:HA3	11:B:6026:ID3:H4A	1.64	0.78
1:B:316:CYS:SG	1:B:337:VAL:HB	2.22	0.78
1:A:325:LYS:HG2	1:A:326:ASN:N	1.98	0.78
1:A:311:LYS:HE3	1:A:315:ASN:HD21	1.48	0.78
1:A:59:LEU:HD12	1:A:77:LEU:HD11	1.66	0.78
1:A:65:HIS:CG	1:A:338:SER:HA	2.18	0.77
1:B:91:PHE:HA	1:B:94:THR:CG2	2.15	0.76
1:A:338:SER:CB	1:A:341:GLU:HG2	2.16	0.76
1:B:214:ILE:HB	1:B:215:PRO:HD3	1.68	0.76
1:B:284:GLY:CA	11:B:6026:ID3:H4A	2.16	0.75
1:A:183:MET:HE2	1:A:286:ILE:HD13	1.68	0.75
1:B:91:PHE:HA	1:B:94:THR:HG23	1.68	0.75
1:A:331:ASP:O	1:A:332:GLU:HB2	1.86	0.74
1:A:67:LYS:HB2	1:A:337:VAL:CB	2.14	0.74
1:A:332:GLU:OE2	1:A:334:SER:HB2	1.87	0.74
1:B:238:GLN:HG2	1:B:239:GLU:H	1.52	0.74
1:B:341:GLU:HG3	1:B:342:THR:HG22	1.71	0.73
1:A:236:GLN:O	1:A:245:LYS:HD2	1.89	0.73
1:B:255:ILE:O	1:B:259:ILE:HG12	1.89	0.72
1:A:304:VAL:O	1:A:308:MET:HG2	1.90	0.72
1:B:332:GLU:HG3	1:B:336:THR:HA	1.71	0.71
1:B:238:GLN:HG2	1:B:239:GLU:N	2.06	0.71
1:B:67:LYS:HB3	1:B:337:VAL:CG1	2.20	0.70
1:A:195:HIS:HD1	1:A:198:THR:CG2	2.03	0.70
1:B:341:GLU:HG3	1:B:342:THR:H	1.56	0.70
1:B:222:CYS:O	1:B:226:LEU:HD13	1.92	0.70
1:A:66:LYS:N	1:A:66:LYS:HE2	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:GLN:O	1:A:239:GLU:HB2	1.92	0.69
1:A:316:CYS:SG	1:A:337:VAL:HG13	2.31	0.69
1:B:32:ALA:HB1	1:B:36:GLN:OE1	1.92	0.69
1:B:67:LYS:HB3	1:B:337:VAL:HG22	1.73	0.69
9:A:1410:4E6:H8	1:B:46:LEU:HD11	1.75	0.69
1:B:236:GLN:HB2	1:B:237:GLN:NE2	2.08	0.69
1:A:245:LYS:HZ1	1:A:245:LYS:HA	1.58	0.68
1:B:135:ARG:NE	1:B:135:ARG:HA	2.08	0.68
1:A:234:ALA:HB1	1:A:245:LYS:HE2	1.76	0.68
1:B:143:MET:HG3	1:B:144:SER:H	1.59	0.68
1:B:338:SER:HB2	1:B:341:GLU:CG	2.22	0.67
1:A:66:LYS:HE2	1:A:66:LYS:H	1.60	0.67
1:A:161:TRP:O	1:A:165:LEU:HD23	1.94	0.67
1:B:302:ASN:HB2	13:B:2016:HOH:O	1.93	0.67
1:B:239:GLU:HB2	1:B:245:LYS:HD2	1.76	0.67
1:A:237:GLN:H	1:A:237:GLN:NE2	1.93	0.67
1:B:222:CYS:SG	7:B:904:HG:HG	2.11	0.67
1:A:67:LYS:H	1:A:337:VAL:HG23	1.59	0.66
1:B:65:HIS:CE1	1:B:338:SER:HA	2.30	0.66
1:B:239:GLU:CB	1:B:244:GLN:HE22	2.08	0.66
1:A:216:LEU:HD12	1:A:220:PHE:CE2	2.30	0.66
1:B:161:TRP:O	1:B:165:LEU:HD23	1.96	0.66
1:A:239:GLU:HB3	1:A:244:GLN:NE2	2.11	0.66
1:A:59:LEU:CD1	1:A:77:LEU:HD11	2.25	0.66
1:A:91:PHE:HA	1:A:94:THR:HG23	1.77	0.66
1:B:65:HIS:HB3	1:B:337:VAL:CG1	2.26	0.66
1:A:75:ILE:HG13	1:A:131:LEU:HD13	1.77	0.66
1:A:325:LYS:CG	1:A:326:ASN:H	2.03	0.66
1:B:225:GLN:C	1:B:226:LEU:HD12	2.21	0.66
1:B:325:LYS:HE3	1:B:340:THR:O	1.96	0.66
1:A:327:PRO:HB2	1:A:331:ASP:HA	1.77	0.66
1:B:141:LYS:C	1:B:143:MET:H	2.03	0.66
1:A:212:PHE:O	1:A:216:LEU:HD23	1.96	0.65
1:A:346:ALA:N	1:A:347:PRO:HD3	2.12	0.65
1:B:336:THR:HB	1:B:342:THR:CG2	2.26	0.65
1:A:287:PHE:H	11:A:6025:ID3:H16	1.62	0.65
1:A:308:MET:HE1	1:B:41:ALA:HB1	1.77	0.65
1:B:338:SER:CB	1:B:341:GLU:HG2	2.25	0.65
1:B:231:LYS:HB2	1:B:231:LYS:NZ	2.11	0.65
1:A:341:GLU:CD	1:A:342:THR:HG22	2.22	0.64
1:B:96:TYR:O	1:B:100:HIS:HD2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:HIS:CD2	1:B:338:SER:HA	2.33	0.64
1:A:341:GLU:OE1	1:A:342:THR:HG22	1.98	0.63
1:B:230:VAL:HG23	1:B:248:LYS:CD	2.27	0.63
1:A:65:HIS:HB3	1:A:337:VAL:CG2	2.19	0.63
1:B:230:VAL:HA	1:B:248:LYS:HE3	1.81	0.63
1:A:238:GLN:HG2	1:A:239:GLU:N	2.13	0.63
1:A:195:HIS:HD1	1:A:198:THR:HG22	1.62	0.63
10:B:1506:HTG:H61	11:B:6026:ID3:H16B	1.80	0.63
1:A:338:SER:HB2	1:A:341:GLU:HG2	1.80	0.62
1:A:308:MET:CE	1:B:99:LEU:HD21	2.29	0.62
1:B:143:MET:HG3	1:B:144:SER:N	2.13	0.62
1:B:182:GLY:HA2	13:B:2050:HOH:O	1.98	0.62
1:A:183:MET:CE	1:A:289:THR:HG21	2.27	0.62
1:B:315:ASN:O	1:B:318:VAL:HG12	1.99	0.62
1:B:135:ARG:HA	1:B:135:ARG:HE	1.63	0.62
1:B:284:GLY:N	11:B:6026:ID3:H4A	2.15	0.62
1:B:183:MET:HE2	1:B:286:ILE:CD1	2.30	0.62
1:B:287:PHE:HA	11:B:6026:ID3:H8	1.81	0.61
1:A:308:MET:HE1	1:B:99:LEU:HD21	1.82	0.60
1:A:33:GLU:HB2	1:A:36:GLN:HG3	1.83	0.60
1:A:70:THR:H	1:A:73:ASN:HD22	1.48	0.60
1:A:75:ILE:O	1:A:79:LEU:HD22	2.02	0.60
1:A:338:SER:OG	1:A:341:GLU:HG2	2.01	0.60
1:A:234:ALA:HB2	1:A:248:LYS:HD2	1.84	0.60
1:A:198:THR:HG23	1:A:200:ASN:OD1	2.02	0.60
1:A:64:GLN:O	1:A:339:LYS:HB2	2.02	0.60
1:A:239:GLU:HB3	1:A:244:GLN:HE22	1.65	0.59
1:B:135:ARG:O	1:B:139:VAL:HG23	2.01	0.59
1:B:316:CYS:SG	1:B:337:VAL:CB	2.90	0.59
1:A:220:PHE:HZ	1:A:262:LEU:HD11	1.66	0.59
1:A:126:TRP:CH2	1:A:215:PRO:HG3	2.38	0.59
1:B:341:GLU:CG	1:B:342:THR:H	2.15	0.59
1:B:195:HIS:HD1	1:B:198:THR:CG2	2.16	0.59
1:A:170:PRO:HB2	1:A:171:PRO:HD3	1.84	0.58
1:B:195:HIS:HD1	1:B:198:THR:HG22	1.68	0.58
1:B:59:LEU:CD1	1:B:77:LEU:HD11	2.28	0.58
1:A:227:VAL:HG13	1:A:228:PHE:N	2.17	0.58
1:B:250:VAL:O	1:B:254:VAL:HG23	2.03	0.58
1:A:6:GLY:HA3	1:A:9:PHE:CZ	2.39	0.57
1:A:302:ASN:HB2	1:A:303:PRO:HD3	1.85	0.57
1:B:194:PRO:O	1:B:195:HIS:C	2.47	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ILE:O	1:A:263:ILE:HG13	2.04	0.57
1:A:137:VAL:HA	1:A:142:PRO:HD2	1.86	0.57
1:B:248:LYS:O	1:B:252:ARG:HG3	2.03	0.57
1:B:311:LYS:HE3	10:B:1509:HTG:O3	2.05	0.57
1:B:341:GLU:CG	1:B:342:THR:N	2.62	0.57
1:A:155:MET:HA	1:A:155:MET:HE2	1.87	0.57
1:B:267:PRO:HG2	13:B:2019:HOH:O	2.04	0.56
1:A:284:GLY:HA3	11:A:6025:ID3:H2A	1.86	0.56
1:A:287:PHE:N	11:A:6025:ID3:H16	2.20	0.56
1:A:216:LEU:HD12	1:A:220:PHE:HE2	1.68	0.56
1:A:237:GLN:O	1:A:238:GLN:HB3	2.05	0.56
1:B:331:ASP:O	1:B:332:GLU:HB2	2.06	0.56
1:A:64:GLN:HG3	1:A:339:LYS:HE2	1.87	0.56
1:B:208:PHE:O	1:B:213:ILE:HG13	2.05	0.56
1:A:32:ALA:HB1	1:A:36:GLN:OE1	2.05	0.56
1:B:67:LYS:HB3	1:B:337:VAL:HG13	1.85	0.56
1:B:75:ILE:HG13	1:B:131:LEU:CD1	2.36	0.56
1:B:132:ALA:O	1:B:222:CYS:SG	2.63	0.56
1:A:284:GLY:C	11:A:6025:ID3:H16B	2.30	0.56
1:B:336:THR:HG22	1:B:337:VAL:H	1.71	0.56
1:A:88:PHE:HB3	6:B:1323:PLM:HB1	1.87	0.56
1:A:77:LEU:O	1:A:81:VAL:HG23	2.06	0.55
1:A:194:PRO:O	1:A:195:HIS:C	2.49	0.55
1:B:266:LEU:N	1:B:267:PRO:HD2	2.21	0.55
1:A:245:LYS:HA	1:A:245:LYS:NZ	2.21	0.55
1:A:330:ASP:O	1:A:331:ASP:HB3	2.06	0.55
1:A:90:GLY:O	1:A:94:THR:HG22	2.07	0.55
1:B:70:THR:H	1:B:73:ASN:HD22	1.54	0.55
1:B:167:CYS:HB2	1:B:211:HIS:CD2	2.42	0.55
1:A:298:SER:HA	1:A:301:TYR:CE2	2.42	0.55
1:A:330:ASP:C	1:A:332:GLU:H	2.15	0.55
1:B:75:ILE:HG21	1:B:131:LEU:CD1	2.36	0.55
1:B:183:MET:HE2	1:B:286:ILE:HD13	1.88	0.55
1:B:226:LEU:HB3	1:B:230:VAL:CG1	2.36	0.55
1:B:75:ILE:HG13	1:B:131:LEU:HD12	1.88	0.55
1:B:156:GLY:O	1:B:160:THR:HG23	2.06	0.55
1:A:323:CYS:O	1:A:324:GLY:C	2.49	0.54
1:B:151:ASN:HD21	1:B:152:HIS:CE1	2.25	0.54
1:A:28:GLN:HB3	1:A:31:LEU:HD12	1.89	0.54
1:A:337:VAL:C	1:A:338:SER:HG	2.14	0.54
1:A:225:GLN:C	1:A:227:VAL:H	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:LYS:NZ	13:A:2007:HOH:O	2.39	0.54
1:B:87:VAL:O	1:B:91:PHE:HB2	2.08	0.54
1:B:75:ILE:HG21	1:B:131:LEU:HD11	1.89	0.54
1:B:175:TRP:O	1:B:176:SER:HB3	2.07	0.54
1:B:131:LEU:HD23	1:B:254:VAL:HG22	1.88	0.54
1:B:57:LEU:HD11	1:B:317:MET:HG3	1.89	0.54
1:B:253:MET:HE1	1:B:306:TYR:CD1	2.43	0.54
1:A:213:ILE:O	1:A:217:ILE:HG13	2.07	0.53
1:B:332:GLU:O	1:B:333:ALA:HB3	2.08	0.53
1:A:231:LYS:HZ2	1:A:233:ALA:HB3	1.72	0.53
10:B:1506:HTG:C6	11:B:6026:ID3:H16B	2.39	0.53
1:B:65:HIS:NE2	1:B:338:SER:HA	2.23	0.53
1:A:342:THR:HG1	1:A:344:GLN:CD	2.16	0.53
1:A:97:THR:HG23	1:A:102:TYR:C	2.34	0.53
1:A:237:GLN:O	1:A:238:GLN:CB	2.57	0.53
1:A:240:SER:O	1:A:241:ALA:CB	2.56	0.52
1:A:325:LYS:HG2	1:A:327:PRO:HD3	1.90	0.52
1:B:158:ALA:O	1:B:162:VAL:HG23	2.09	0.52
1:A:137:VAL:O	1:A:141:LYS:HA	2.10	0.52
1:B:76:LEU:HD22	1:B:306:TYR:CG	2.43	0.52
1:B:65:HIS:CG	1:B:338:SER:HA	2.45	0.52
1:B:240:SER:O	1:B:241:ALA:HB2	2.08	0.52
1:B:212:PHE:O	1:B:216:LEU:HD23	2.09	0.52
1:A:67:LYS:H	1:A:337:VAL:CG2	2.22	0.52
1:B:239:GLU:HB3	1:B:244:GLN:CD	2.33	0.52
1:A:33:GLU:HB3	1:A:35:TRP:CD1	2.44	0.51
1:A:338:SER:HB2	1:A:341:GLU:CG	2.40	0.51
1:A:227:VAL:CG1	1:A:228:PHE:N	2.72	0.51
1:A:327:PRO:HG3	1:A:331:ASP:OD2	2.11	0.51
1:A:250:VAL:O	1:A:254:VAL:HG23	2.09	0.51
1:A:319:THR:HG23	1:A:325:LYS:HA	1.91	0.51
1:B:152:HIS:O	1:B:155:MET:HB2	2.11	0.51
1:B:234:ALA:HA	1:B:245:LYS:HZ1	1.75	0.51
1:A:42:ALA:HA	12:B:1401:HTO:H72	1.91	0.51
1:B:143:MET:CE	1:B:144:SER:H	2.23	0.51
1:B:141:LYS:N	1:B:142:PRO:HD3	2.26	0.51
1:B:210:VAL:HA	1:B:214:ILE:HD12	1.92	0.51
1:A:152:HIS:O	1:A:155:MET:HB2	2.10	0.50
1:A:342:THR:O	1:A:342:THR:HG23	2.09	0.50
1:B:197:GLU:O	1:B:197:GLU:HG2	2.12	0.50
1:B:237:GLN:H	1:B:237:GLN:HE21	1.57	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:VAL:HG22	1:A:231:LYS:H	1.77	0.50
1:B:6:GLY:HA3	1:B:9:PHE:CZ	2.47	0.50
1:B:249:GLU:HA	1:B:252:ARG:HG3	1.94	0.50
1:B:319:THR:HG21	1:B:338:SER:OG	2.12	0.50
1:A:237:GLN:H	1:A:237:GLN:CD	2.19	0.50
1:B:136:TYR:CE2	1:B:142:PRO:HG2	2.46	0.50
1:A:67:LYS:HB2	1:A:337:VAL:CG2	2.42	0.49
1:B:226:LEU:HD23	1:B:230:VAL:HG11	1.93	0.49
1:B:332:GLU:C	1:B:334:SER:H	2.20	0.49
1:B:346:ALA:N	1:B:347:PRO:CD	2.58	0.49
1:B:241:ALA:HB1	1:B:243:THR:HG22	1.95	0.49
1:A:214:ILE:HB	1:A:215:PRO:HD3	1.94	0.49
1:B:65:HIS:HB3	1:B:337:VAL:HG12	1.94	0.49
1:B:129:VAL:HG13	1:B:218:VAL:HG11	1.93	0.49
1:B:136:TYR:HE1	1:B:225:GLN:HB3	1.77	0.49
1:A:135:ARG:NH2	1:A:138:VAL:HG21	2.27	0.49
1:B:315:ASN:HA	1:B:318:VAL:HG12	1.93	0.49
1:A:135:ARG:HA	1:A:135:ARG:NE	2.28	0.49
1:A:228:PHE:O	1:A:229:THR:C	2.55	0.49
1:B:143:MET:HG2	1:B:146:PHE:HB3	1.93	0.49
1:A:230:VAL:HG22	1:A:231:LYS:N	2.26	0.49
1:A:267:PRO:HG2	13:A:964:HOH:O	2.11	0.49
1:B:65:HIS:HB2	1:B:68:LEU:HD12	1.95	0.49
1:A:308:MET:CE	1:B:41:ALA:HB1	2.41	0.49
1:A:341:GLU:CG	1:A:342:THR:N	2.67	0.49
1:A:176:SER:HA	1:A:200:ASN:OD1	2.13	0.48
1:B:332:GLU:HG3	1:B:336:THR:CA	2.42	0.48
1:A:36:GLN:O	1:A:39:MET:HB2	2.14	0.48
1:A:198:THR:CG2	1:A:200:ASN:OD1	2.62	0.48
1:A:189:ILE:HB	1:A:191:TYR:CE1	2.48	0.48
2:C:1:NAG:H61	2:C:2:NAG:C7	2.44	0.48
1:A:235:ALA:HB3	1:A:239:GLU:OE2	2.13	0.48
1:A:156:GLY:O	1:A:159:PHE:HB3	2.13	0.48
1:B:303:PRO:O	1:B:307:ILE:HG13	2.14	0.48
1:B:21:ARG:NH2	4:E:2:NAG:H61	2.28	0.48
1:A:49:MET:HE3	6:B:1322:PLM:HB2	1.95	0.48
1:A:234:ALA:CB	1:A:248:LYS:HD2	2.44	0.48
1:B:234:ALA:HA	1:B:245:LYS:NZ	2.28	0.48
1:B:300:VAL:O	1:B:303:PRO:HD2	2.13	0.48
1:A:298:SER:HA	1:A:301:TYR:CD2	2.49	0.48
1:A:321:LEU:C	1:A:323:CYS:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:LEU:O	1:B:266:LEU:HB2	2.14	0.48
1:A:254:VAL:O	1:A:258:VAL:HG23	2.14	0.47
1:A:67:LYS:HE3	1:A:344:GLN:O	2.14	0.47
1:B:64:GLN:HG3	1:B:339:LYS:HE2	1.95	0.47
1:B:141:LYS:C	1:B:143:MET:N	2.71	0.47
1:B:64:GLN:HG2	1:B:64:GLN:O	2.13	0.47
1:A:88:PHE:HB2	6:B:1323:PLM:HF2	1.97	0.47
1:A:169:ALA:O	1:A:170:PRO:C	2.58	0.47
1:A:238:GLN:HA	1:A:241:ALA:C	2.40	0.47
1:B:68:LEU:O	1:B:69:ARG:NH1	2.40	0.47
1:B:325:LYS:O	1:B:326:ASN:C	2.58	0.47
1:A:332:GLU:O	1:A:333:ALA:HB3	2.15	0.47
1:A:137:VAL:HA	1:A:142:PRO:CD	2.45	0.47
1:A:267:PRO:O	1:A:271:VAL:HG23	2.15	0.47
1:B:245:LYS:HA	1:B:245:LYS:CE	2.38	0.47
1:B:298:SER:HA	1:B:301:TYR:CD2	2.50	0.46
1:B:311:LYS:HE2	1:B:315:ASN:OD1	2.15	0.46
1:B:33:GLU:HB2	1:B:36:GLN:HG3	1.98	0.46
1:A:238:GLN:HG2	1:A:239:GLU:H	1.80	0.46
1:B:51:GLY:HA2	1:B:300:VAL:HG12	1.97	0.46
1:B:51:GLY:CA	1:B:300:VAL:HG12	2.45	0.46
1:B:137:VAL:HG12	1:B:137:VAL:O	2.15	0.46
1:A:129:VAL:O	1:A:133:ILE:HG12	2.14	0.46
1:B:237:GLN:O	1:B:238:GLN:HB3	2.16	0.46
1:B:290:ILE:HB	1:B:291:PRO:CD	2.46	0.46
1:B:216:LEU:HD11	1:B:262:LEU:HD21	1.98	0.46
1:A:195:HIS:ND1	1:A:198:THR:HG22	2.31	0.46
1:A:96:TYR:O	1:A:100:HIS:HD2	1.99	0.46
1:B:244:GLN:NE2	1:B:245:LYS:N	2.64	0.46
1:B:319:THR:HG23	1:B:325:LYS:HA	1.98	0.46
1:A:308:MET:CE	1:B:41:ALA:CB	2.94	0.46
1:B:237:GLN:NE2	1:B:237:GLN:N	2.57	0.46
1:B:330:ASP:O	1:B:331:ASP:CB	2.64	0.45
1:A:175:TRP:O	1:A:176:SER:HB3	2.16	0.45
1:A:240:SER:O	1:A:241:ALA:HB3	2.15	0.45
1:B:240:SER:O	1:B:241:ALA:CB	2.65	0.45
1:A:65:HIS:ND1	1:A:337:VAL:O	2.49	0.45
1:B:6:GLY:HA3	1:B:9:PHE:CE1	2.52	0.45
1:B:136:TYR:CE1	1:B:225:GLN:HB3	2.52	0.45
1:B:170:PRO:HB2	1:B:171:PRO:HD3	1.98	0.45
1:A:183:MET:HE3	1:A:289:THR:CG2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ALA:HB1	1:A:245:LYS:CE	2.44	0.45
1:B:287:PHE:CA	11:B:6026:ID3:H8	2.46	0.45
1:B:298:SER:HA	1:B:301:TYR:CE2	2.51	0.45
1:B:70:THR:H	1:B:73:ASN:ND2	2.13	0.45
1:A:315:ASN:ND2	1:A:332:GLU:HA	2.32	0.45
1:A:337:VAL:CG2	1:A:338:SER:N	2.80	0.45
1:B:131:LEU:HD23	1:B:254:VAL:HG13	1.98	0.45
1:A:85:PHE:O	1:A:89:GLY:N	2.49	0.45
1:A:326:ASN:O	1:A:328:LEU:HD22	2.17	0.45
1:B:67:LYS:CB	1:B:337:VAL:HG13	2.47	0.45
1:B:332:GLU:O	1:B:332:GLU:OE1	2.34	0.45
1:A:87:VAL:O	1:A:91:PHE:HB2	2.17	0.44
1:B:27:PRO:HB3	1:B:29:TYR:CE2	2.52	0.44
1:B:331:ASP:OD1	1:B:336:THR:OG1	2.31	0.44
1:B:19:VAL:HG22	1:B:19:VAL:O	2.17	0.44
1:B:129:VAL:O	1:B:133:ILE:HG12	2.17	0.44
1:B:210:VAL:O	1:B:215:PRO:HD3	2.17	0.44
1:A:67:LYS:N	1:A:337:VAL:CG2	2.81	0.44
1:B:119:LEU:HD13	1:B:123:ILE:HD12	1.99	0.44
1:B:226:LEU:HB3	1:B:230:VAL:HG12	2.00	0.44
1:B:239:GLU:HG2	1:B:245:LYS:HZ2	1.83	0.44
1:B:336:THR:HB	1:B:342:THR:HG23	1.98	0.44
1:A:96:TYR:O	1:A:100:HIS:CD2	2.70	0.44
1:A:256:ILE:HG13	10:A:1508:HTG:H1'1	2.00	0.44
1:B:67:LYS:CB	1:B:337:VAL:HG22	2.43	0.44
1:B:143:MET:HE3	1:B:144:SER:H	1.82	0.44
1:B:155:MET:HE2	1:B:155:MET:HA	1.99	0.44
1:A:150:GLU:O	1:A:154:ILE:HG13	2.17	0.44
1:B:254:VAL:O	1:B:258:VAL:HG23	2.17	0.44
1:A:8:ASN:HD22	1:A:8:ASN:HA	1.53	0.44
1:A:300:VAL:O	1:A:304:VAL:HG23	2.17	0.44
1:B:146:PHE:HZ	1:B:152:HIS:CD2	2.35	0.44
1:B:195:HIS:HB3	1:B:200:ASN:ND2	2.33	0.44
1:B:135:ARG:NH2	1:B:138:VAL:HG21	2.33	0.44
1:A:238:GLN:CG	1:A:239:GLU:N	2.78	0.43
1:A:303:PRO:O	1:A:307:ILE:HG13	2.18	0.43
1:B:336:THR:HB	1:B:342:THR:HG21	2.00	0.43
4:E:3:BMA:O4	4:E:4:MAN:H61	2.18	0.43
1:B:8:ASN:HD22	1:B:8:ASN:HA	1.53	0.43
1:B:9:PHE:HA	1:B:179:ILE:HD11	2.00	0.43
1:A:134:GLU:HA	1:A:148:PHE:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:TRP:CH2	1:B:215:PRO:HG3	2.53	0.43
1:B:139:VAL:HG11	1:B:230:VAL:HG12	2.01	0.43
1:B:231:LYS:HB2	1:B:231:LYS:HZ3	1.80	0.43
1:A:66:LYS:H	1:A:66:LYS:CE	2.31	0.43
1:A:248:LYS:HB2	1:A:248:LYS:HE3	1.83	0.43
1:A:9:PHE:HA	1:A:179:ILE:HD11	2.00	0.43
1:A:247:GLU:OE1	1:A:247:GLU:HA	2.18	0.43
1:B:161:TRP:O	1:B:165:LEU:CD2	2.67	0.43
1:B:284:GLY:N	11:B:6026:ID3:H3A	2.34	0.43
1:B:293:PHE:HA	1:B:296:LYS:HD2	2.01	0.43
1:A:262:LEU:HB3	1:A:266:LEU:HD22	2.01	0.42
1:B:59:LEU:HD12	1:B:77:LEU:CD1	2.36	0.42
1:B:324:GLY:O	1:B:325:LYS:HG3	2.19	0.42
1:A:183:MET:HE2	1:A:286:ILE:CD1	2.43	0.42
1:A:323:CYS:O	1:A:325:LYS:N	2.52	0.42
1:A:326:ASN:OD1	1:A:328:LEU:HD22	2.20	0.42
1:B:67:LYS:H	1:B:337:VAL:CG1	2.32	0.42
1:B:340:THR:O	1:B:340:THR:HG23	2.19	0.42
1:A:86:MET:HE3	1:A:117:ALA:HA	2.01	0.42
1:A:182:GLY:HA2	1:A:285:PRO:O	2.19	0.42
1:B:143:MET:CG	1:B:144:SER:H	2.30	0.42
1:A:142:PRO:C	1:A:143:MET:HE3	2.44	0.42
1:A:68:LEU:N	1:A:337:VAL:HG21	2.34	0.42
1:A:72:LEU:HD11	1:A:253:MET:HE2	2.01	0.42
1:A:96:TYR:HE2	1:A:104:VAL:CG2	2.32	0.42
1:B:77:LEU:O	1:B:81:VAL:HG23	2.19	0.42
1:B:324:GLY:C	1:B:325:LYS:HG3	2.44	0.42
1:B:135:ARG:HE	1:B:135:ARG:CA	2.30	0.42
1:B:141:LYS:O	1:B:143:MET:N	2.52	0.42
1:B:147:ARG:O	1:B:149:GLY:N	2.52	0.42
1:A:11:VAL:CG1	1:A:31:LEU:HD21	2.49	0.42
1:B:20:VAL:HA	1:B:30:TYR:CZ	2.54	0.42
1:B:224:GLY:O	1:B:227:VAL:HG12	2.20	0.42
1:B:326:ASN:C	1:B:328:LEU:HD22	2.45	0.42
1:B:345:VAL:O	1:B:346:ALA:HB2	2.20	0.42
1:A:308:MET:HE2	1:B:41:ALA:HB3	2.01	0.42
1:A:332:GLU:O	1:A:332:GLU:OE1	2.38	0.42
1:B:90:GLY:O	1:B:94:THR:HG22	2.20	0.42
1:B:131:LEU:O	1:B:135:ARG:HB2	2.20	0.42
1:A:271:VAL:HG21	1:A:291:PRO:HG3	2.03	0.41
1:B:51:GLY:O	1:B:55:ASN:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:LYS:HD2	1:A:339:LYS:HA	2.01	0.41
1:B:102:TYR:CE2	1:B:104:VAL:HA	2.55	0.41
1:B:266:LEU:N	1:B:267:PRO:CD	2.83	0.41
1:A:255:ILE:O	1:A:259:ILE:HG12	2.20	0.41
1:A:101:GLY:O	1:A:102:TYR:HB3	2.21	0.41
1:A:332:GLU:CD	1:A:334:SER:HB2	2.45	0.41
1:A:226:LEU:HD12	1:A:226:LEU:N	2.36	0.41
1:B:239:GLU:HB3	1:B:244:GLN:OE1	2.21	0.41
1:B:336:THR:C	1:B:337:VAL:CG2	2.94	0.41
1:B:22:SER:C	1:B:24:PHE:H	2.29	0.41
1:B:64:GLN:OE1	1:B:320:THR:HG23	2.21	0.41
1:B:322:CYS:O	1:B:324:GLY:N	2.54	0.41
1:A:195:HIS:HD1	1:A:198:THR:HG21	1.84	0.41
1:B:57:LEU:HD21	1:B:321:LEU:HD21	2.03	0.41
1:B:70:THR:HB	1:B:71:PRO:CD	2.51	0.41
1:B:135:ARG:HD3	1:B:251:THR:OG1	2.20	0.41
1:A:44:MET:O	1:A:48:ILE:HG13	2.21	0.40
1:A:52:PHE:HB3	1:A:53:PRO:CD	2.51	0.40
1:A:57:LEU:HD23	1:A:57:LEU:O	2.21	0.40
1:A:66:LYS:CD	1:A:339:LYS:HA	2.52	0.40
1:B:39:MET:HA	1:B:39:MET:HE3	2.04	0.40
1:B:67:LYS:HG2	1:B:337:VAL:HG22	2.04	0.40
1:B:238:GLN:O	1:B:245:LYS:HD2	2.21	0.40
11:B:6026:ID3:H7	11:B:6026:ID3:H19	1.82	0.40
1:A:262:LEU:O	1:A:266:LEU:HB2	2.22	0.40
1:A:96:TYR:HE2	1:A:104:VAL:HG21	1.87	0.40
5:A:1296:RET:H181	5:A:1296:RET:H8	2.03	0.40
1:B:33:GLU:HB3	1:B:35:TRP:CD1	2.56	0.40
1:B:125:LEU:HB2	1:B:261:PHE:CZ	2.57	0.40
1:B:146:PHE:CG	1:B:147:ARG:N	2.89	0.40
1:B:249:GLU:HG3	1:B:250:VAL:N	2.36	0.40
1:A:20:VAL:HG13	1:A:30:TYR:OH	2.22	0.40
1:A:68:LEU:O	1:A:69:ARG:HD3	2.21	0.40
1:A:277:THR:C	1:A:278:HIS:ND1	2.79	0.40
1:A:308:MET:HE2	1:B:41:ALA:CB	2.52	0.40

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	347/349 (99%)	302 (87%)	34 (10%)	11 (3%)	3	5
1	B	347/349 (99%)	300 (86%)	32 (9%)	15 (4%)	2	2
All	All	694/698 (99%)	602 (87%)	66 (10%)	26 (4%)	2	3

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	229	THR
1	A	238	GLN
1	A	241	ALA
1	A	325	LYS
1	B	240	SER
1	B	241	ALA
1	B	332	GLU
1	B	346	ALA
1	A	195	HIS
1	A	324	GLY
1	A	329	GLY
1	A	332	GLU
1	A	347	PRO
1	B	195	HIS
1	B	229	THR
1	B	239	GLU
1	B	323	CYS
1	B	324	GLY
1	B	329	GLY
1	B	340	THR
1	A	240	SER
1	B	236	GLN
1	B	235	ALA
1	B	331	ASP
1	A	338	SER

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Mol	Chain	Res	Type
1	B	347	PRO

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	296/296 (100%)	273 (92%)	23 (8%)	11	26
1	B	296/296 (100%)	280 (95%)	16 (5%)	20	42
All	All	592/592 (100%)	553 (93%)	39 (7%)	15	34

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	66	LYS
1	A	67	LYS
1	A	76	LEU
1	A	79	LEU
1	A	94	THR
1	A	104	VAL
1	A	119	LEU
1	A	131	LEU
1	A	135	ARG
1	A	216	LEU
1	A	231	LYS
1	A	237	GLN
1	A	239	GLU
1	A	245	LYS
1	A	252	ARG
1	A	266	LEU
1	A	300	VAL
1	A	332	GLU
1	A	336	THR
1	A	337	VAL
1	A	341	GLU

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Mol	Chain	Res	Type
1	A	344	GLN
1	B	8	ASN
1	B	50	LEU
1	B	79	LEU
1	B	94	THR
1	B	104	VAL
1	B	134	GLU
1	B	135	ARG
1	B	236	GLN
1	B	237	GLN
1	B	244	GLN
1	B	245	LYS
1	B	264	CYS
1	B	266	LEU
1	B	308	MET
1	B	332	GLU
1	B	337	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	64	GLN
1	A	73	ASN
1	A	152	HIS
1	A	237	GLN
1	A	315	ASN
1	B	8	ASN
1	B	64	GLN
1	B	73	ASN
1	B	100	HIS
1	B	151	ASN
1	B	237	GLN
1	B	244	GLN
1	B	279	GLN
1	B	302	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 ⓘ

11 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	C	1	1,2	14,14,15	0.59	0	17,19,21	0.75	0
2	NAG	C	2	2	14,14,15	0.63	0	17,19,21	0.82	0
2	BMA	C	3	2	11,11,12	0.50	0	15,15,17	0.40	0
3	NAG	D	1	3,1	14,14,15	0.53	0	17,19,21	0.71	0
3	NAG	D	2	3	14,14,15	0.49	0	17,19,21	0.75	1 (5%)
4	NAG	E	1	4,1	14,14,15	0.67	0	17,19,21	0.76	0
4	NAG	E	2	4	14,14,15	0.56	0	17,19,21	0.74	1 (5%)
4	BMA	E	3	4	11,11,12	0.62	0	15,15,17	0.42	0
4	MAN	E	4	4	11,11,12	0.69	0	15,15,17	0.63	1 (6%)
3	NAG	F	1	3,1	14,14,15	0.55	0	17,19,21	0.57	0
3	NAG	F	2	3	14,14,15	0.60	0	17,19,21	0.75	1 (5%)

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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	4/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	D	2	3	-	4/6/23/26	0/1/1/1
4	NAG	E	1	4,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	2	4	-	1/6/23/26	0/1/1/1
4	BMA	E	3	4	-	1/2/19/22	0/1/1/1
4	MAN	E	4	4	-	2/2/19/22	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	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(°)
4	E	2	NAG	C2-N2-C7	-2.29	119.84	122.90
3	D	2	NAG	C2-N2-C7	-2.27	119.86	122.90
3	F	2	NAG	C2-N2-C7	-2.25	119.88	122.90
4	E	4	MAN	C1-O5-C5	2.03	114.90	112.19

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	F	2	NAG	C8-C7-N2-C2
3	F	2	NAG	O7-C7-N2-C2
4	E	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
2	C	3	BMA	O5-C5-C6-O6
4	E	4	MAN	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
3	F	1	NAG	C8-C7-N2-C2
3	D	2	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6

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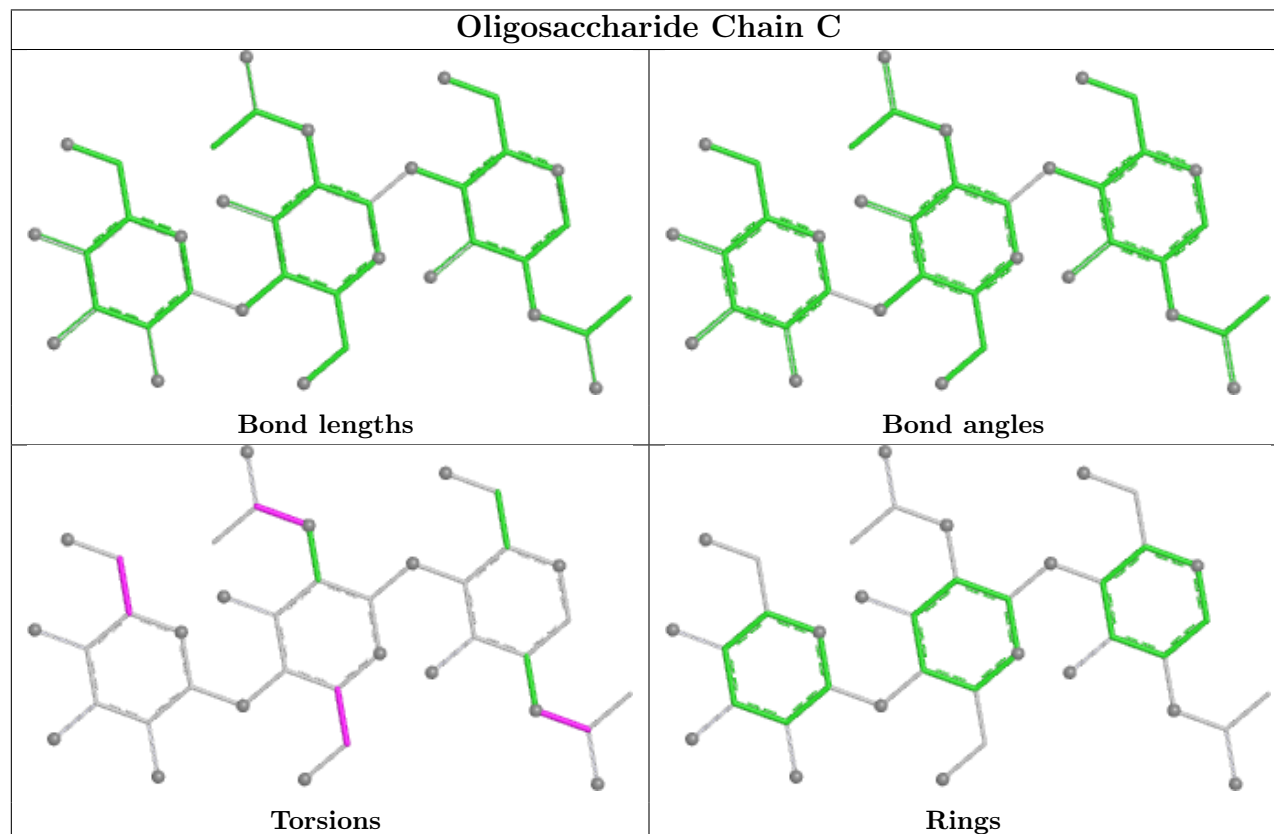
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C4-C5-C6-O6
3	F	1	NAG	O7-C7-N2-C2
4	E	4	MAN	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
4	E	3	BMA	C4-C5-C6-O6
4	E	2	NAG	O5-C5-C6-O6

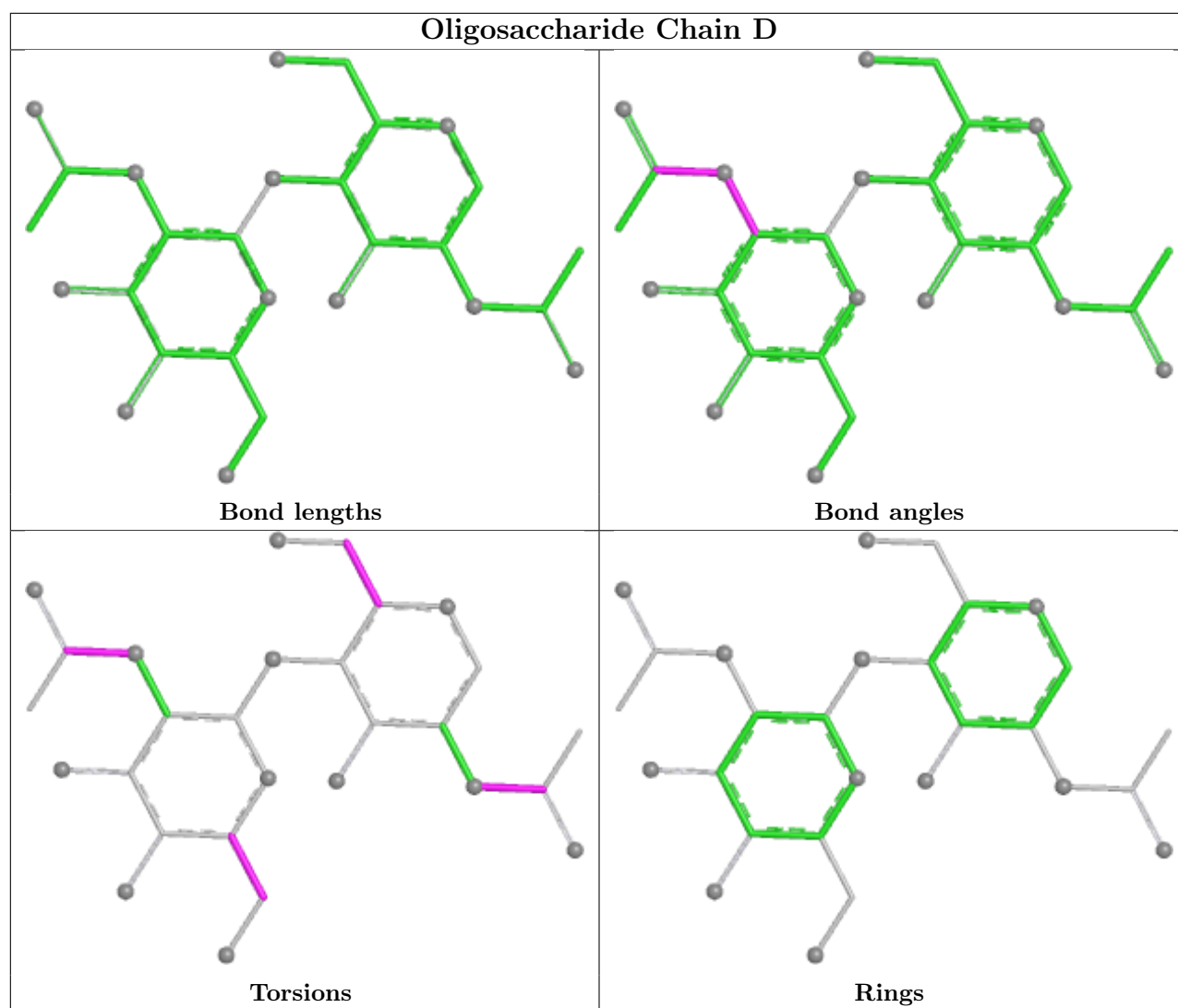
There are no ring outliers.

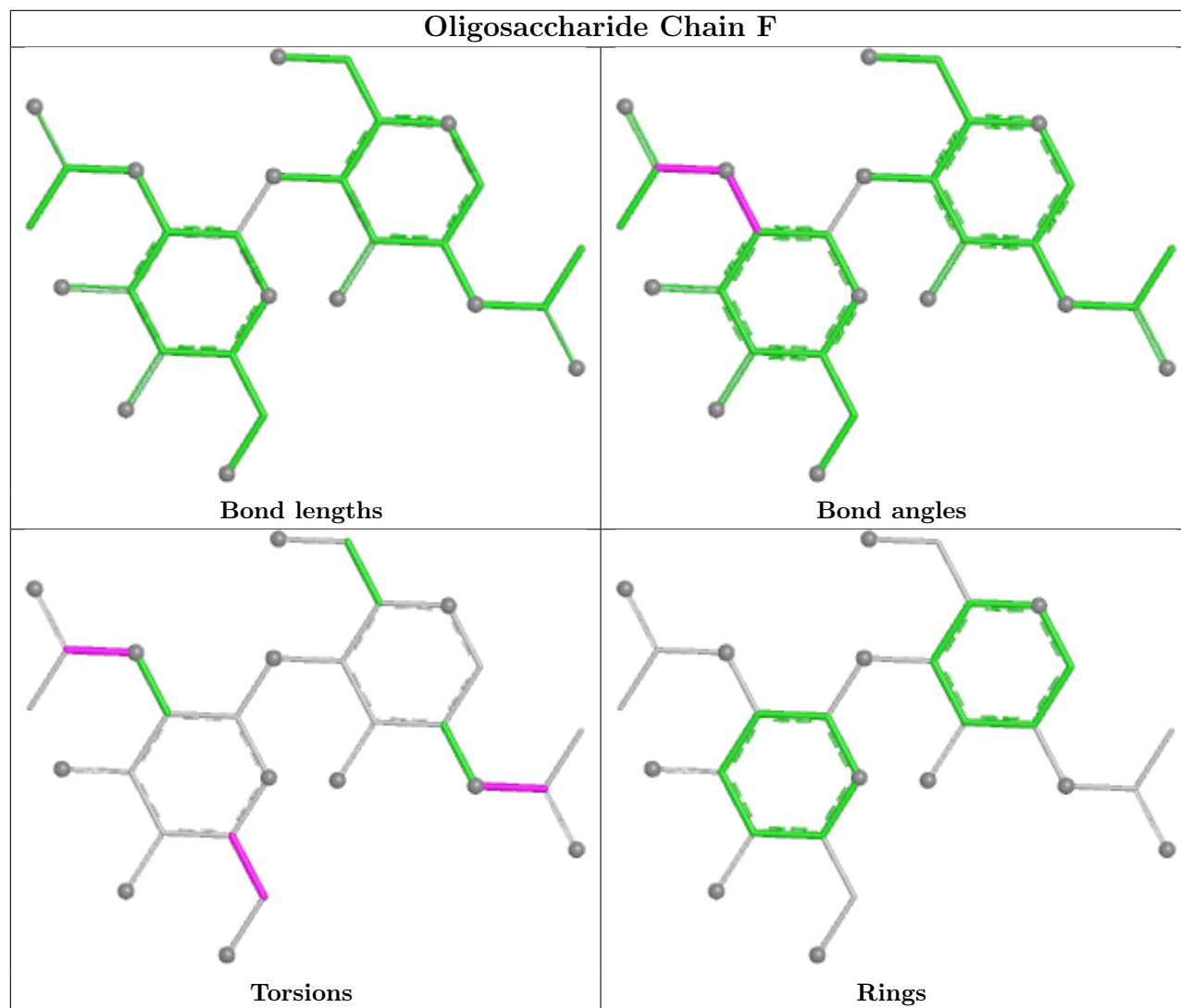
5 monomers are involved in 3 short contacts:

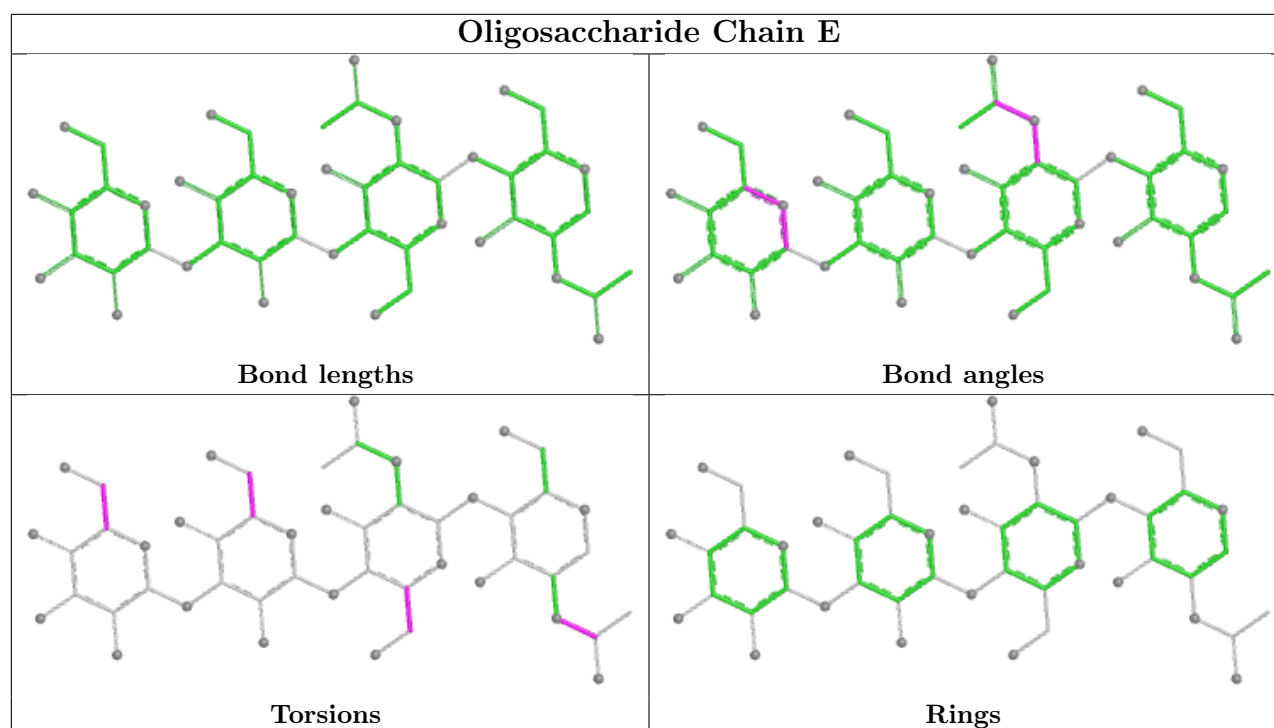
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	4	MAN	1	0
4	E	2	NAG	1	0
2	C	2	NAG	1	0
2	C	1	NAG	1	0
4	E	3	BMA	1	0

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](#)

Of 28 ligands modelled in this entry, 13 are monoatomic - leaving 15 for Mogul analysis.

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$
6	PLM	B	1322	1	15,16,17	0.34	0	14,15,17	0.49	0
10	HTG	B	1509	-	19,19,19	2.75	7 (36%)	23,24,24	1.98	3 (13%)
10	HTG	B	1506	-	19,19,19	2.66	7 (36%)	23,24,24	2.21	4 (17%)
12	HTO	B	1401	-	9,9,9	1.92	2 (22%)	10,10,10	0.90	0
6	PLM	B	1323	1	15,16,17	0.38	0	14,15,17	0.48	0
9	4E6	A	1410	-	15,15,15	1.87	1 (6%)	13,14,14	3.05	5 (38%)
11	ID3	B	6026	-	14,14,14	2.59	4 (28%)	20,20,20	1.56	5 (25%)
10	HTG	A	1508	-	19,19,19	2.43	7 (36%)	23,24,24	1.75	1 (4%)
9	4E6	B	1407	-	15,15,15	1.81	1 (6%)	13,14,14	2.89	6 (46%)
5	RET	B	1296	1	20,20,21	2.20	3 (15%)	27,27,28	1.73	9 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	HTG	A	1507	-	19,19,19	2.78	7 (36%)	23,24,24	1.74	1 (4%)
11	ID3	A	6025	-	14,14,14	2.86	6 (42%)	20,20,20	1.78	5 (25%)
6	PLM	A	1323	1	15,16,17	0.30	0	14,15,17	0.54	0
5	RET	A	1296	1	20,20,21	2.17	3 (15%)	27,27,28	1.71	8 (29%)
6	PLM	A	1322	1	15,16,17	0.29	0	14,15,17	0.56	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
6	PLM	B	1322	1	-	11/14/14/15	-
10	HTG	B	1509	-	-	5/10/30/30	0/1/1/1
10	HTG	B	1506	-	-	2/10/30/30	0/1/1/1
12	HTO	B	1401	-	-	3/10/10/10	-
6	PLM	B	1323	1	-	9/14/14/15	-
9	4E6	A	1410	-	-	3/13/13/13	-
11	ID3	B	6026	-	-	0/5/22/22	0/1/1/1
10	HTG	A	1508	-	-	7/10/30/30	0/1/1/1
9	4E6	B	1407	-	-	3/13/13/13	-
5	RET	B	1296	1	-	1/13/30/31	0/1/1/1
10	HTG	A	1507	-	-	3/10/30/30	0/1/1/1
11	ID3	A	6025	-	-	0/5/22/22	0/1/1/1
6	PLM	A	1323	1	-	10/14/14/15	-
5	RET	A	1296	1	-	1/13/30/31	0/1/1/1
6	PLM	A	1322	1	-	8/14/14/15	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1507	HTG	O5-C1	8.11	1.55	1.42
10	B	1509	HTG	O5-C1	7.97	1.54	1.42
10	B	1506	HTG	O5-C1	7.93	1.54	1.42
11	B	6026	ID3	O1-C9	7.26	1.40	1.24
10	A	1508	HTG	O5-C1	7.05	1.53	1.42
11	A	6025	ID3	O1-C9	7.03	1.40	1.24
9	A	1410	4E6	C12-C11	-6.44	1.23	1.44
9	B	1407	4E6	C12-C11	-6.32	1.24	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1296	RET	C1-C6	5.56	1.60	1.53
5	A	1296	RET	C1-C6	5.08	1.60	1.53
5	B	1296	RET	C5-C6	5.08	1.43	1.34
5	A	1296	RET	C5-C6	5.05	1.43	1.34
12	B	1401	HTO	C3-C2	4.68	1.64	1.53
5	A	1296	RET	C14-C13	4.50	1.36	1.33
10	B	1509	HTG	C4-C5	4.16	1.61	1.53
11	A	6025	ID3	C5-C6	4.08	1.41	1.34
10	A	1507	HTG	C4-C5	3.98	1.61	1.53
10	B	1509	HTG	C1-C2	3.97	1.60	1.53
11	A	6025	ID3	C18-C5	3.84	1.57	1.50
10	B	1506	HTG	C4-C5	3.68	1.60	1.53
5	B	1296	RET	C14-C13	3.67	1.36	1.33
10	A	1508	HTG	C1-C2	3.62	1.59	1.53
10	B	1506	HTG	C1-C2	3.57	1.59	1.53
10	B	1506	HTG	O5-C5	3.54	1.53	1.44
10	A	1507	HTG	C1-S1	3.53	1.86	1.80
10	B	1509	HTG	O5-C5	3.53	1.53	1.44
10	A	1507	HTG	C1-C2	3.52	1.59	1.53
11	B	6026	ID3	C7-C6	3.45	1.56	1.45
10	A	1508	HTG	C4-C5	3.45	1.60	1.53
10	A	1507	HTG	C3-C2	3.34	1.61	1.52
10	B	1506	HTG	C1-S1	3.26	1.86	1.80
10	A	1507	HTG	O5-C5	3.23	1.52	1.44
10	A	1507	HTG	C4-C3	3.21	1.60	1.52
11	A	6025	ID3	C7-C6	3.13	1.55	1.45
10	B	1509	HTG	C3-C2	3.10	1.60	1.52
10	B	1506	HTG	C3-C2	3.09	1.60	1.52
10	B	1509	HTG	C1-S1	3.09	1.85	1.80
10	B	1509	HTG	C4-C3	3.05	1.60	1.52
10	A	1508	HTG	C3-C2	3.02	1.60	1.52
10	A	1508	HTG	O5-C5	2.99	1.51	1.44
10	A	1508	HTG	C4-C3	2.89	1.59	1.52
11	A	6025	ID3	C8-C7	2.88	1.41	1.33
10	B	1506	HTG	C4-C3	2.69	1.59	1.52
10	A	1508	HTG	C1-S1	2.46	1.84	1.80
11	A	6025	ID3	C17-C1	2.18	1.57	1.53
11	B	6026	ID3	C5-C6	2.15	1.38	1.34
12	B	1401	HTO	C4-C3	2.11	1.56	1.52
11	B	6026	ID3	C3-C4	2.00	1.58	1.52

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	1506	HTG	C1'-S1-C1	9.32	120.58	100.45
10	B	1509	HTG	C1'-S1-C1	8.40	118.59	100.45
9	A	1410	4E6	C8-C9-C10	7.63	155.32	112.60
10	A	1508	HTG	C1'-S1-C1	7.46	116.56	100.45
10	A	1507	HTG	C1'-S1-C1	7.19	115.98	100.45
9	B	1407	4E6	C8-C9-C10	6.79	150.61	112.60
9	B	1407	4E6	C11-C12-C13	5.71	156.59	125.30
11	A	6025	ID3	C17-C1-C6	-5.70	101.30	110.24
9	A	1410	4E6	C11-C12-C13	4.93	152.31	125.30
11	B	6026	ID3	C17-C1-C6	-4.17	103.70	110.24
9	A	1410	4E6	C13-C14-C15	-3.58	94.41	112.02
5	B	1296	RET	C20-C13-C12	3.52	123.47	118.09
5	A	1296	RET	C20-C13-C12	3.43	123.32	118.09
9	B	1407	4E6	C13-C14-C15	-3.38	95.40	112.02
5	B	1296	RET	C18-C5-C6	3.36	128.15	124.48
5	A	1296	RET	C18-C5-C6	3.29	128.08	124.48
9	A	1410	4E6	C9-C10-C11	-3.25	109.71	125.66
5	B	1296	RET	C7-C8-C9	2.85	130.46	126.23
5	A	1296	RET	C2-C1-C6	2.71	114.38	110.44
5	A	1296	RET	C7-C8-C9	2.66	130.16	126.23
11	A	6025	ID3	C16-C1-C6	2.58	114.28	110.24
9	A	1410	4E6	C5-C4-C3	2.55	127.26	114.37
10	B	1506	HTG	C2'-C1'-S1	-2.54	103.79	112.36
5	A	1296	RET	C19-C9-C10	2.54	126.93	122.82
5	B	1296	RET	C12-C13-C14	-2.41	112.15	118.55
5	A	1296	RET	C12-C13-C14	-2.36	112.29	118.55
5	B	1296	RET	C2-C1-C6	2.34	113.83	110.44
11	A	6025	ID3	C18-C5-C6	-2.33	121.94	124.48
11	A	6025	ID3	C17-C1-C16	2.31	115.24	108.63
5	B	1296	RET	C19-C9-C10	2.27	126.50	122.82
5	B	1296	RET	C8-C9-C10	-2.24	115.49	119.01
5	A	1296	RET	C8-C9-C10	-2.23	115.50	119.01
10	B	1506	HTG	O5-C1-C2	-2.22	107.25	110.32
5	B	1296	RET	C1-C6-C5	-2.21	119.61	122.64
11	B	6026	ID3	C2-C3-C4	2.21	116.14	111.28
11	A	6025	ID3	C2-C3-C4	2.21	116.14	111.28
9	B	1407	4E6	C9-C10-C11	-2.21	114.81	125.66
11	B	6026	ID3	C2-C1-C6	2.20	113.64	110.44
5	B	1296	RET	C11-C10-C9	-2.19	124.21	127.28
10	B	1506	HTG	O5-C5-C6	2.16	111.80	106.44
9	B	1407	4E6	C7-C8-C9	2.16	124.23	113.86
5	A	1296	RET	C1-C6-C5	-2.14	119.71	122.64
9	B	1407	4E6	C5-C4-C3	2.14	125.17	114.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B	6026	ID3	C7-C8-C9	-2.13	120.60	124.56
10	B	1509	HTG	O5-C5-C6	2.04	111.49	106.44
10	B	1509	HTG	C2'-C1'-S1	-2.01	105.58	112.36
11	B	6026	ID3	C17-C1-C2	-2.01	101.24	108.95

There are no chirality outliers.

All (66) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1296	RET	C10-C11-C12-C13
5	B	1296	RET	C10-C11-C12-C13
6	A	1323	PLM	O2-C1-C2-C3
6	B	1322	PLM	O2-C1-C2-C3
10	B	1509	HTG	O5-C5-C6-O6
10	B	1509	HTG	C4-C5-C6-O6
10	B	1506	HTG	C1'-C2'-C3'-C4'
6	A	1323	PLM	CB-CC-CD-CE
6	A	1323	PLM	C4-C5-C6-C7
6	B	1323	PLM	C6-C7-C8-C9
6	B	1323	PLM	CA-CB-CC-CD
10	A	1507	HTG	C2'-C3'-C4'-C5'
6	A	1323	PLM	C7-C8-C9-CA
6	B	1322	PLM	CC-CD-CE-CF
6	A	1323	PLM	C3-C4-C5-C6
6	B	1323	PLM	C9-CA-CB-CC
10	A	1508	HTG	C2'-C3'-C4'-C5'
6	A	1322	PLM	CC-CD-CE-CF
6	B	1322	PLM	C5-C6-C7-C8
10	B	1509	HTG	C3'-C4'-C5'-C6'
10	B	1506	HTG	C2'-C3'-C4'-C5'
6	B	1323	PLM	C4-C5-C6-C7
6	B	1322	PLM	C3-C4-C5-C6
6	B	1322	PLM	C9-CA-CB-CC
10	A	1508	HTG	C3'-C4'-C5'-C6'
6	A	1323	PLM	C8-C9-CA-CB
6	B	1322	PLM	C8-C9-CA-CB
6	B	1322	PLM	C4-C5-C6-C7
6	A	1322	PLM	CB-CC-CD-CE
6	B	1323	PLM	C8-C9-CA-CB
10	A	1508	HTG	O5-C5-C6-O6
6	A	1322	PLM	C5-C6-C7-C8
10	B	1509	HTG	C2'-C3'-C4'-C5'

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Mol	Chain	Res	Type	Atoms
6	B	1323	PLM	C3-C4-C5-C6
10	A	1508	HTG	C1'-C2'-C3'-C4'
6	B	1323	PLM	CC-CD-CE-CF
10	A	1508	HTG	C4-C5-C6-O6
10	A	1507	HTG	C4'-C5'-C6'-C7'
10	B	1509	HTG	C4'-C5'-C6'-C7'
12	B	1401	HTO	C4-C5-C6-C7
6	A	1322	PLM	C6-C7-C8-C9
6	A	1323	PLM	CA-CB-CC-CD
9	A	1410	4E6	C12-C13-C14-C15
9	B	1407	4E6	C12-C13-C14-C15
10	A	1508	HTG	C4'-C5'-C6'-C7'
6	A	1322	PLM	C8-C9-CA-CB
9	A	1410	4E6	C13-C14-C15-C16
6	A	1323	PLM	CC-CD-CE-CF
12	B	1401	HTO	C1-C2-C3-O3
6	A	1322	PLM	C1-C2-C3-C4
6	A	1323	PLM	C1-C2-C3-C4
6	B	1322	PLM	C7-C8-C9-CA
6	A	1322	PLM	C3-C4-C5-C6
9	A	1410	4E6	C11-C10-C9-C8
9	B	1407	4E6	C13-C14-C15-C16
6	B	1323	PLM	CB-CC-CD-CE
6	A	1323	PLM	C6-C7-C8-C9
12	B	1401	HTO	C3-C4-C5-C6
6	B	1322	PLM	CB-CC-CD-CE
6	B	1323	PLM	C2-C3-C4-C5
6	A	1322	PLM	C9-CA-CB-CC
10	A	1507	HTG	C3'-C4'-C5'-C6'
9	B	1407	4E6	C11-C10-C9-C8
10	A	1508	HTG	C2'-C1'-S1-C1
6	B	1322	PLM	C1-C2-C3-C4
6	B	1322	PLM	CA-CB-CC-CD

There are no ring outliers.

10 monomers are involved in 22 short contacts:

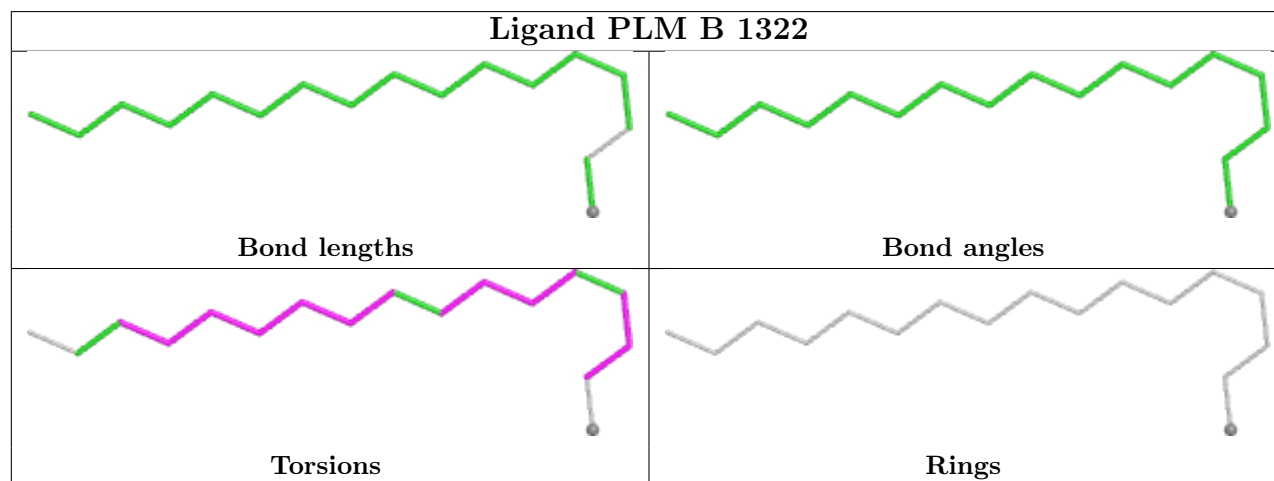
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1322	PLM	1	0
10	B	1509	HTG	1	0
10	B	1506	HTG	2	0
12	B	1401	HTO	1	0

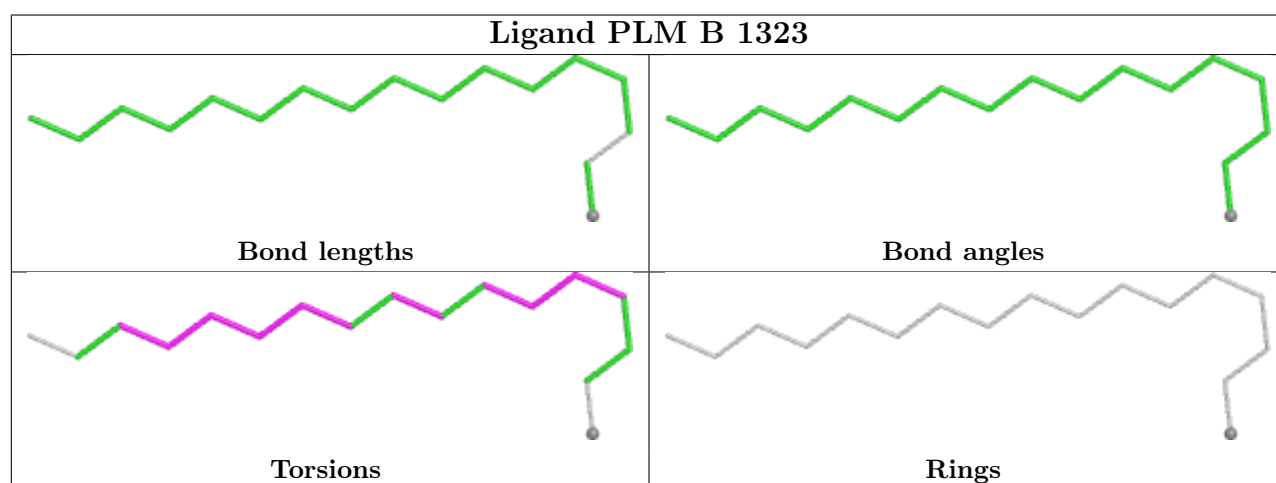
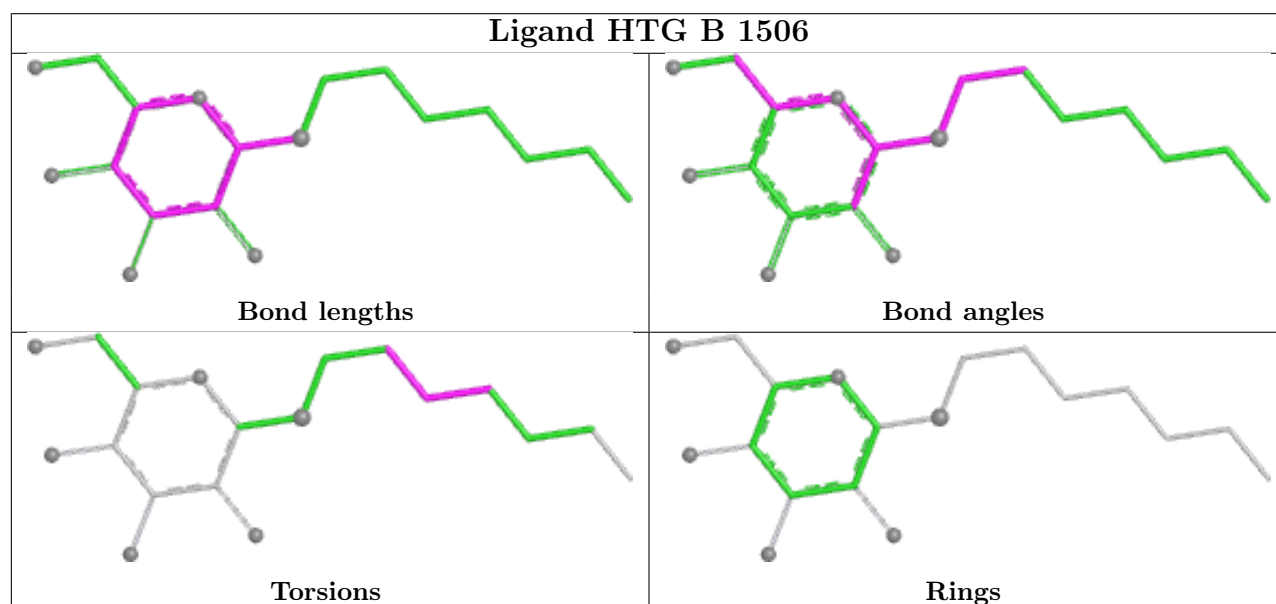
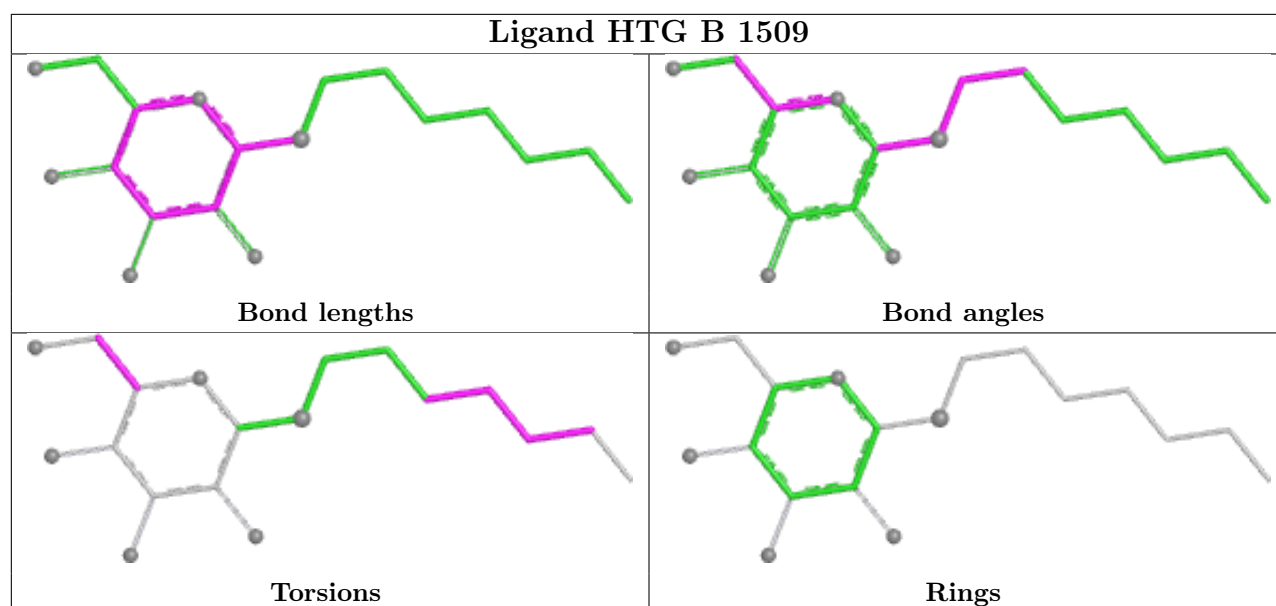
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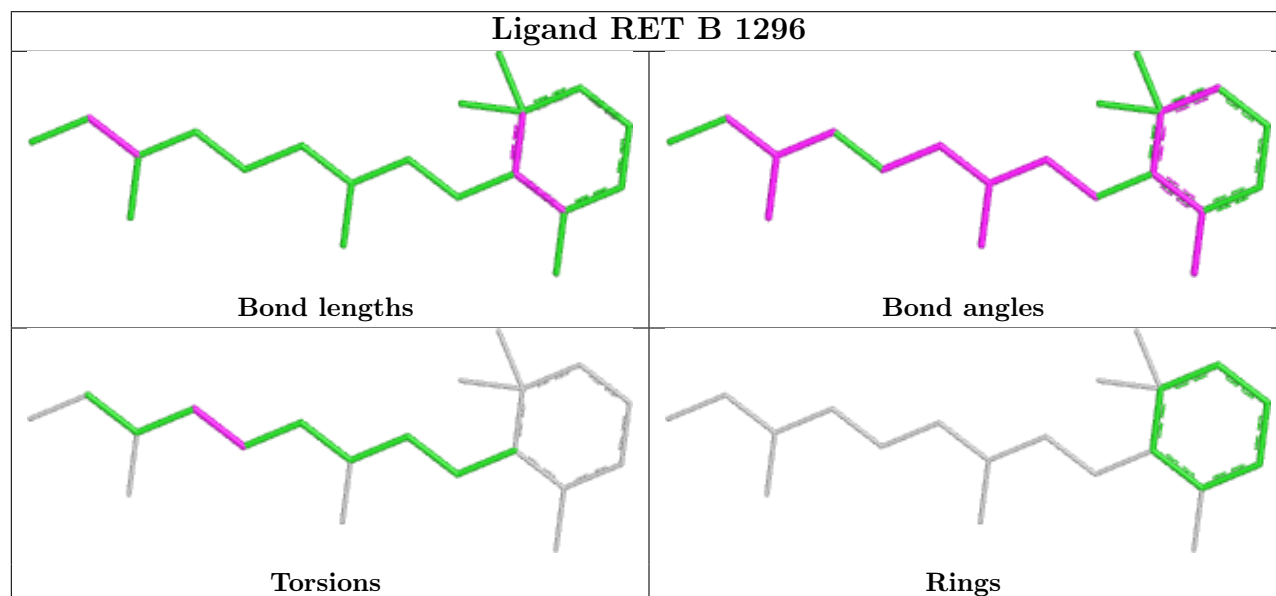
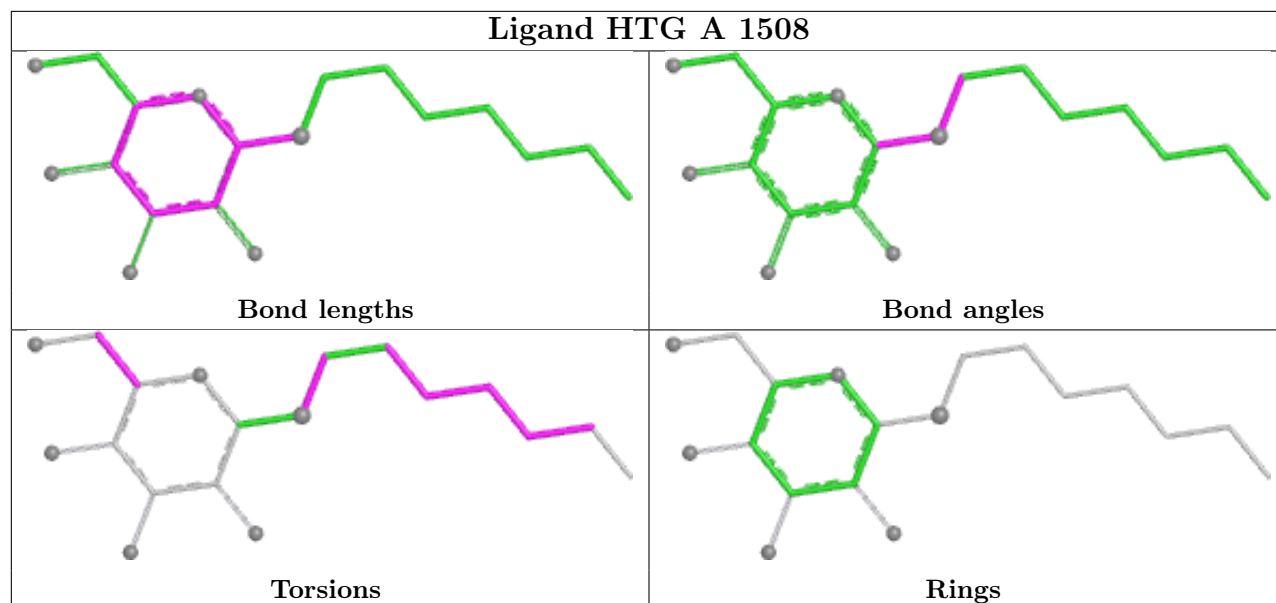
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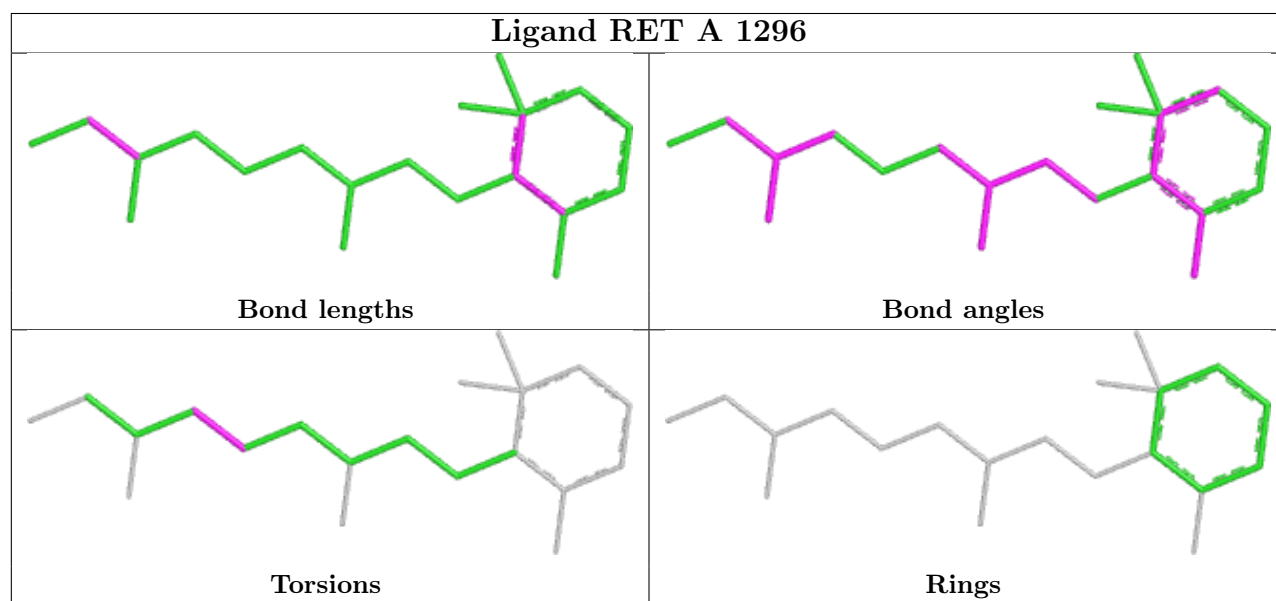
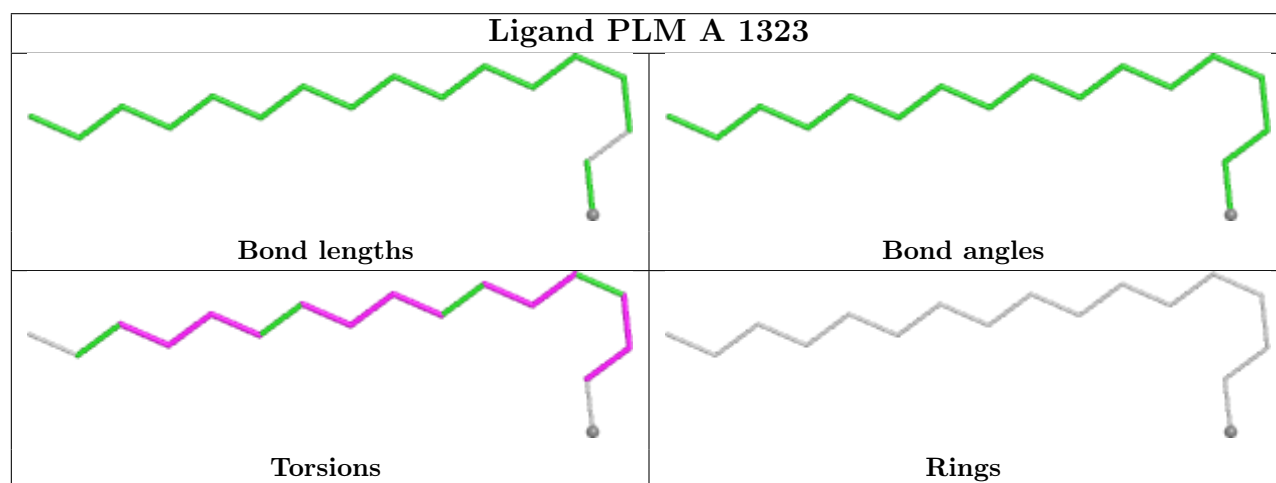
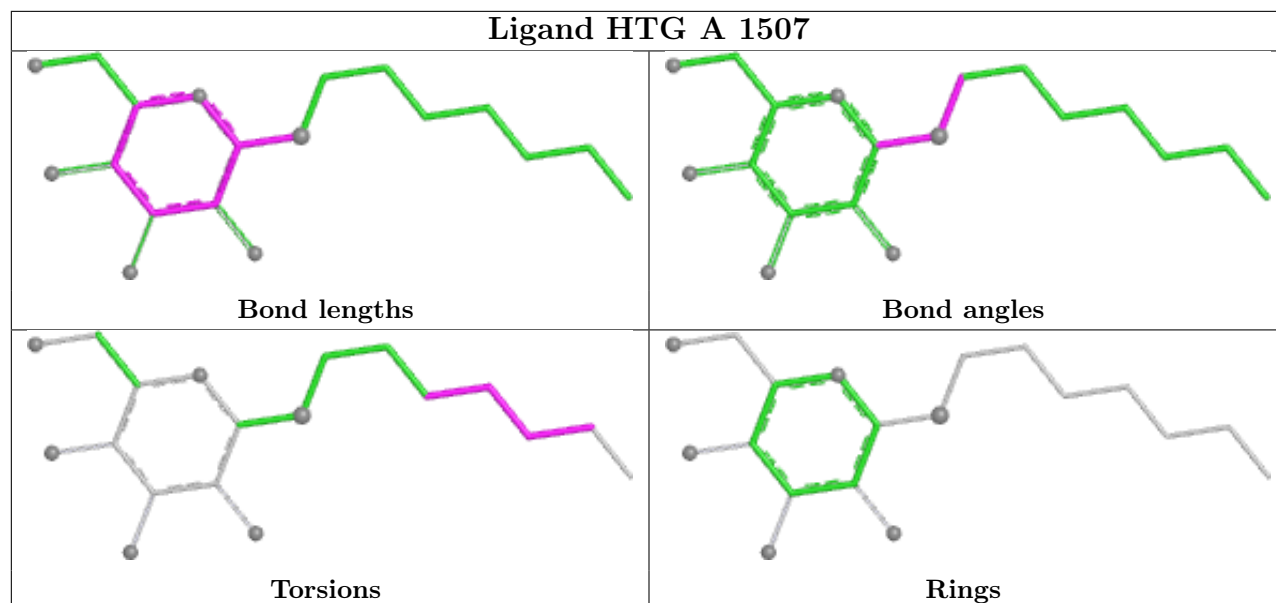
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1323	PLM	2	0
9	A	1410	4E6	1	0
11	B	6026	ID3	9	0
10	A	1508	HTG	1	0
11	A	6025	ID3	5	0
5	A	1296	RET	1	0

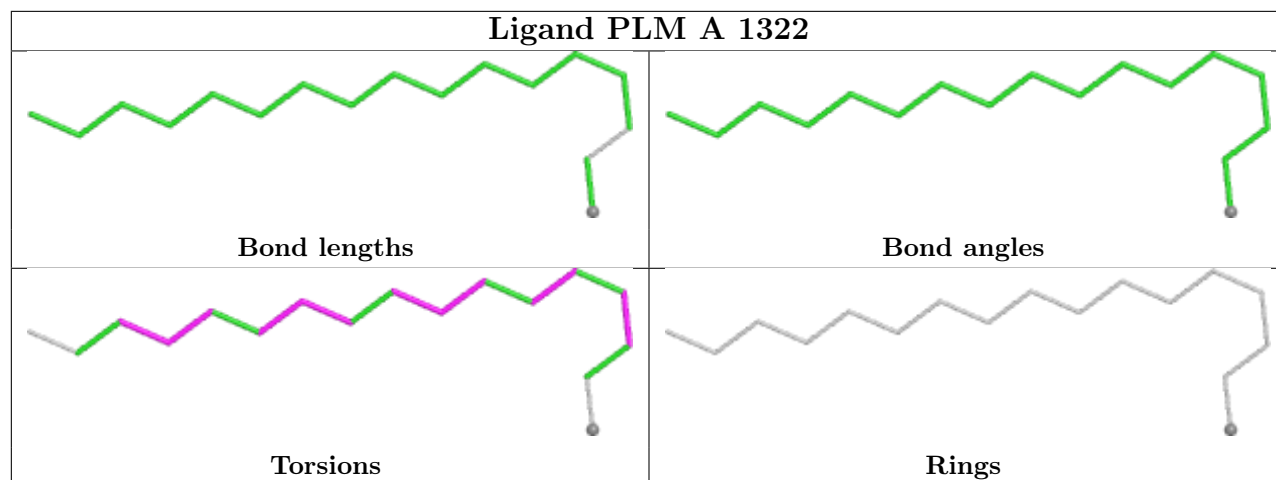
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	348/349 (99%)	0.65	57 (16%) 4 3	42, 56, 138, 155	0
1	B	348/349 (99%)	0.98	67 (19%) 3 2	41, 62, 156, 161	0
All	All	696/698 (99%)	0.82	124 (17%) 4 3	41, 58, 151, 161	0

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	345	VAL	13.6
1	B	344	GLN	12.5
1	B	343	SER	8.5
1	B	327	PRO	8.0
1	B	348	ALA	8.0
1	A	328	LEU	7.9
1	B	335	THR	7.6
1	A	237	GLN	7.3
1	B	341	GLU	7.2
1	B	347	PRO	6.6
1	B	234	ALA	6.5
1	B	233	ALA	6.2
1	A	339	LYS	6.1
1	B	340	THR	6.1
1	A	235	ALA	6.1
1	B	346	ALA	6.0
1	B	339	LYS	5.9
1	A	348	ALA	5.7
1	A	338	SER	5.5
1	B	228	PHE	5.4
1	A	340	THR	5.2
1	B	235	ALA	5.2
1	A	332	GLU	5.2
1	B	333	ALA	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	230	VAL	5.1
1	B	148	PHE	5.0
1	A	236	GLN	4.9
1	A	331	ASP	4.8
1	B	229	THR	4.8
1	A	327	PRO	4.8
1	B	342	THR	4.8
1	B	141	LYS	4.7
1	B	331	ASP	4.6
1	B	142	PRO	4.4
1	B	325	LYS	4.3
1	B	230	VAL	4.2
1	A	347	PRO	4.1
1	A	344	GLN	4.1
1	B	326	ASN	4.1
1	B	334	SER	4.0
1	B	66	LYS	4.0
1	A	336	THR	3.9
1	B	131	LEU	3.9
1	B	146	PHE	3.9
1	A	330	ASP	3.9
1	A	128	LEU	3.9
1	A	337	VAL	3.9
1	B	329	GLY	3.8
1	A	333	ALA	3.8
1	A	346	ALA	3.8
1	B	67	LYS	3.6
1	A	234	ALA	3.5
1	B	337	VAL	3.5
1	A	229	THR	3.5
1	B	241	ALA	3.4
1	B	143	MET	3.4
1	B	242	THR	3.4
1	B	237	GLN	3.4
1	A	146	PHE	3.3
1	A	341	GLU	3.2
1	A	8	ASN	3.2
1	A	147	ARG	3.2
1	B	145	ASN	3.2
1	A	228	PHE	3.2
1	B	133	ILE	3.1
1	A	249	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	345	VAL	3.1
1	A	233	ALA	3.0
1	B	328	LEU	3.0
1	B	243	THR	2.9
1	A	326	ASN	2.9
1	A	335	THR	2.9
1	B	240	SER	2.9
1	A	252	ARG	2.8
1	A	329	GLY	2.8
1	A	227	VAL	2.8
1	B	138	VAL	2.8
1	A	144	SER	2.8
1	B	105	PHE	2.8
1	B	336	THR	2.8
1	A	241	ALA	2.7
1	A	325	LYS	2.7
1	B	231	LYS	2.7
1	A	343	SER	2.7
1	B	227	VAL	2.6
1	B	140	CYS	2.6
1	B	338	SER	2.6
1	A	245	LYS	2.6
1	B	236	GLN	2.6
1	B	239	GLU	2.5
1	B	8	ASN	2.5
1	A	231	LYS	2.5
1	A	148	PHE	2.5
1	B	139	VAL	2.5
1	B	151	ASN	2.5
1	A	240	SER	2.5
1	A	139	VAL	2.4
1	B	137	VAL	2.4
1	B	168	ALA	2.4
1	A	243	THR	2.4
1	A	155	MET	2.4
1	A	334	SER	2.4
1	A	39	MET	2.3
1	A	324	GLY	2.3
1	B	330	ASP	2.3
1	A	151	ASN	2.3
1	B	59	LEU	2.3
1	A	242	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	324	GLY	2.2
1	A	105	PHE	2.2
1	B	199	ASN	2.2
1	B	144	SER	2.2
1	A	140	CYS	2.2
1	B	226	LEU	2.2
1	B	130	VAL	2.1
1	A	342	THR	2.1
1	A	197	GLU	2.1
1	B	190	ASP	2.1
1	A	226	LEU	2.1
1	B	232	GLU	2.0
1	A	73	ASN	2.0
1	B	111	ASN	2.0
1	B	174	GLY	2.0
1	B	104	VAL	2.0

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

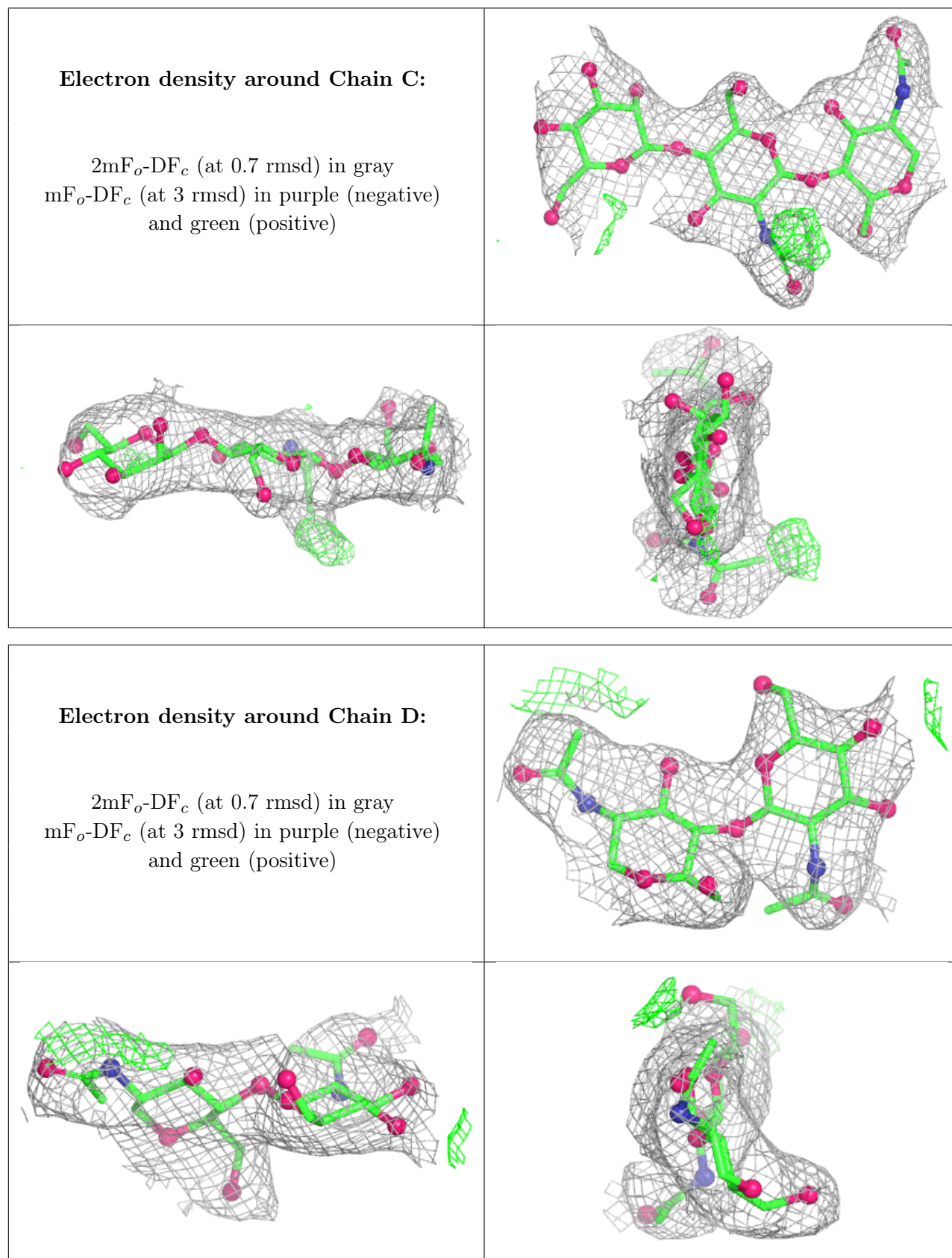
There are no non-standard protein/DNA/RNA residues in this entry.

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.

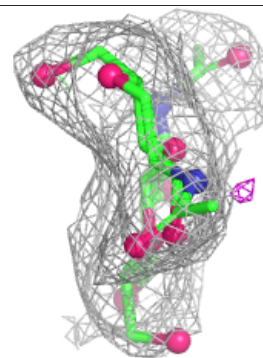
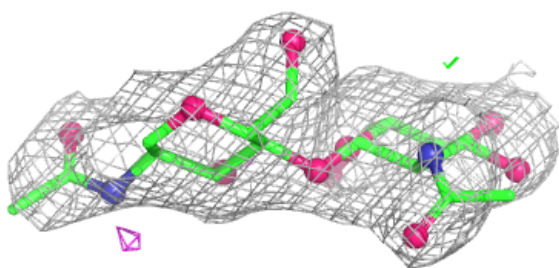
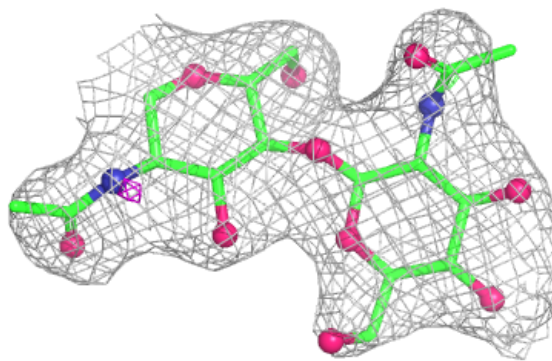
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	E	3	11/12	0.65	0.15	99,105,106,109	0
3	NAG	F	2	14/15	0.69	0.15	81,86,87,88	0
2	BMA	C	3	11/12	0.72	0.15	99,103,106,106	0
4	MAN	E	4	11/12	0.75	0.16	111,113,113,114	0
3	NAG	D	2	14/15	0.81	0.15	85,91,95,96	0
2	NAG	C	2	14/15	0.81	0.14	76,80,86,92	0
3	NAG	D	1	14/15	0.91	0.11	63,68,72,78	0
4	NAG	E	2	14/15	0.91	0.10	72,78,84,92	0
2	NAG	C	1	14/15	0.93	0.11	59,62,67,70	0
4	NAG	E	1	14/15	0.94	0.09	59,63,65,68	0
3	NAG	F	1	14/15	0.95	0.09	63,66,69,75	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.

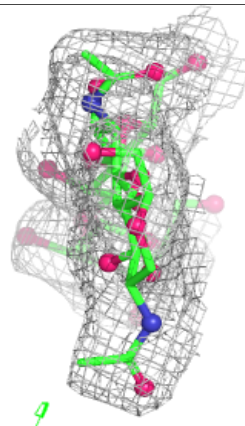
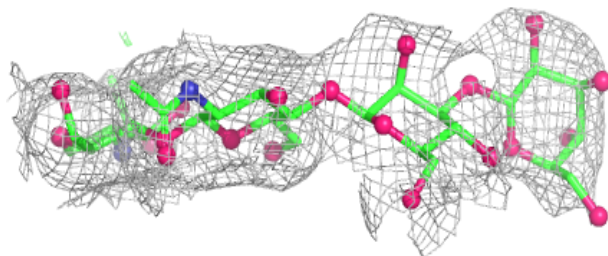
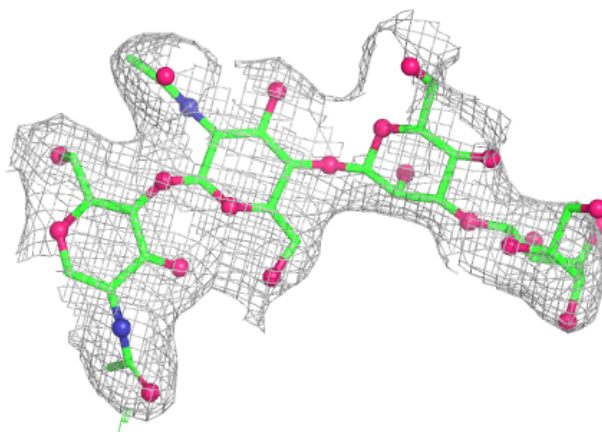


Electron density around Chain F:

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

**Electron density around Chain E:**

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



6.4 Ligands ⓘ

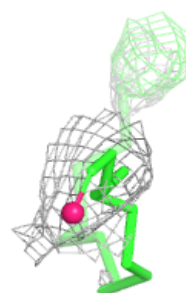
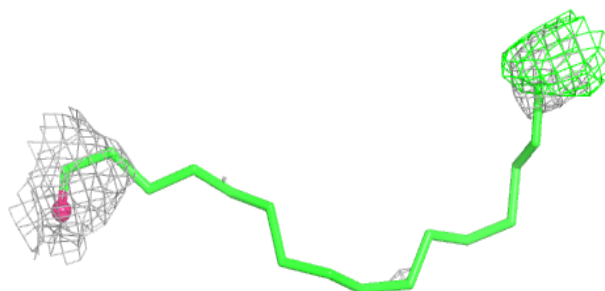
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	PLM	B	1323	17/18	0.72	0.38	115,121,122,122	0
11	ID3	B	6026	14/14	0.75	0.30	69,75,76,78	0
11	ID3	A	6025	14/14	0.76	0.28	64,70,72,72	0
10	HTG	B	1506	19/19	0.80	0.26	97,104,107,107	0
10	HTG	B	1509	19/19	0.80	0.26	101,102,105,105	0
6	PLM	A	1323	17/18	0.82	0.29	100,108,113,113	0
6	PLM	B	1322	17/18	0.84	0.31	102,104,106,106	0
9	4E6	B	1407	16/16	0.84	0.33	83,91,97,97	0
10	HTG	A	1507	19/19	0.86	0.20	95,102,105,105	0
6	PLM	A	1322	17/18	0.87	0.24	88,92,102,103	0
7	HG	B	906	1/1	0.89	0.16	121,121,121,121	1
9	4E6	A	1410	16/16	0.89	0.27	81,83,85,85	0
10	HTG	A	1508	19/19	0.93	0.17	61,76,81,84	0
12	HTO	B	1401	10/10	0.93	0.17	63,67,68,72	0
5	RET	B	1296	20/21	0.94	0.14	43,49,51,51	0
8	ZN	B	963	1/1	0.95	0.09	136,136,136,136	1
8	ZN	A	959	1/1	0.95	0.12	96,96,96,96	1
8	ZN	A	957	1/1	0.96	0.09	53,53,53,53	1
5	RET	A	1296	20/21	0.96	0.11	43,45,48,49	0
8	ZN	A	962	1/1	0.96	0.11	120,120,120,120	1
8	ZN	B	956	1/1	0.96	0.21	70,70,70,70	1
8	ZN	B	958	1/1	0.96	0.06	41,41,41,41	1
8	ZN	A	2011	1/1	0.97	0.12	59,59,59,59	1
7	HG	B	904	1/1	0.98	0.13	98,98,98,98	1
7	HG	A	901	1/1	0.98	0.11	73,73,73,73	1
7	HG	A	905	1/1	0.98	0.10	81,81,81,81	1
7	HG	A	903	1/1	0.99	0.12	82,82,82,82	1
7	HG	B	902	1/1	0.99	0.09	79,79,79,79	1

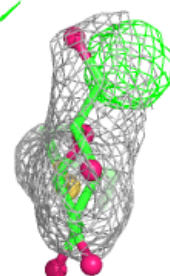
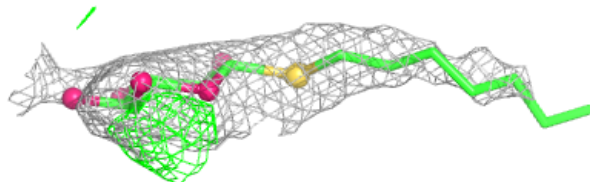
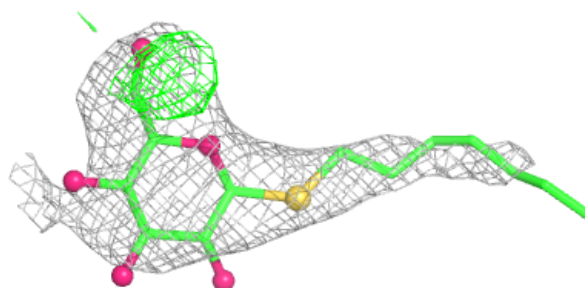
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PLM B 1323:

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

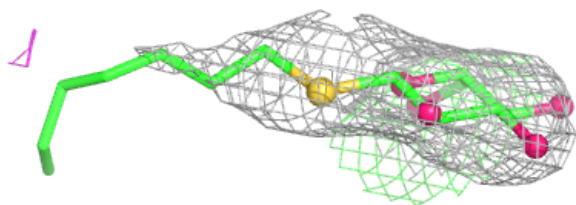
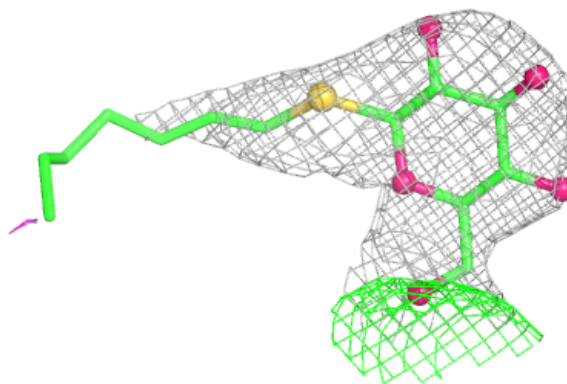
**Electron density around HTG B 1506:**

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

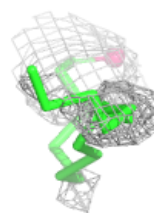
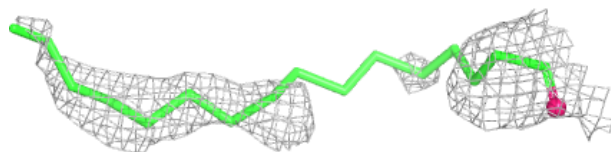
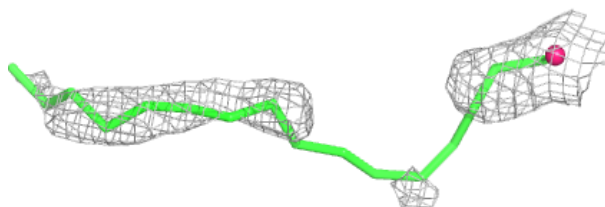


Electron density around HTG B 1509:

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

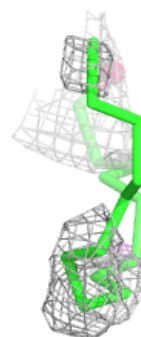
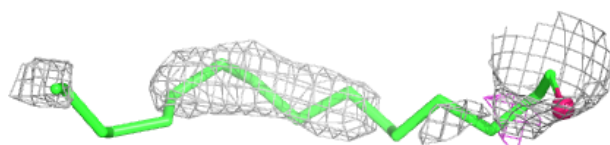
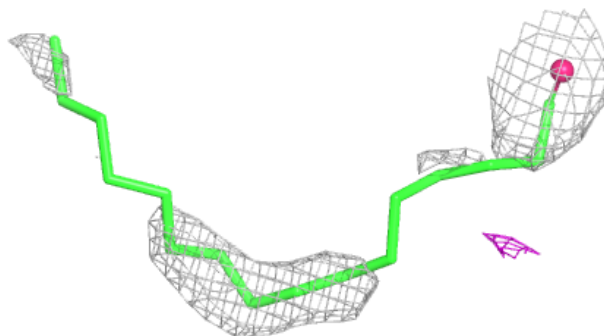
**Electron density around PLM A 1323:**

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

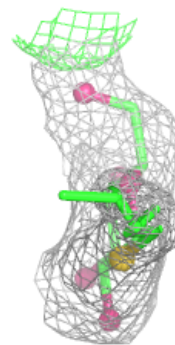
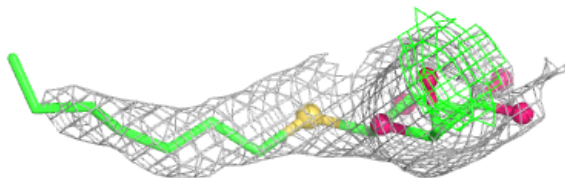
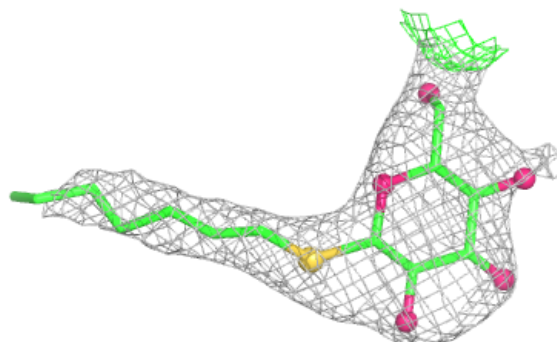


Electron density around PLM B 1322:

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

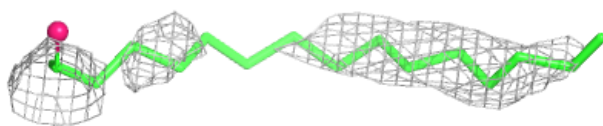
**Electron density around HTG A 1507:**

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

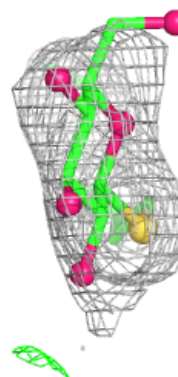
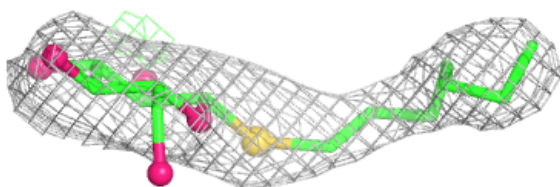
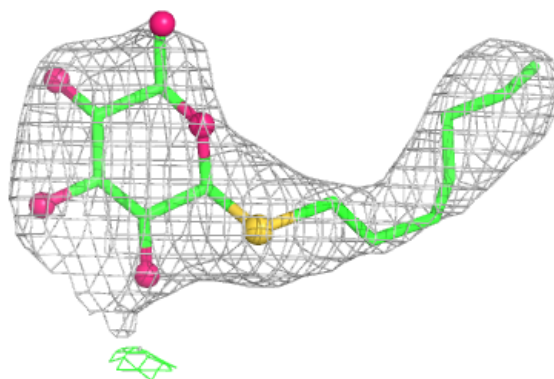


Electron density around PLM A 1322:

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

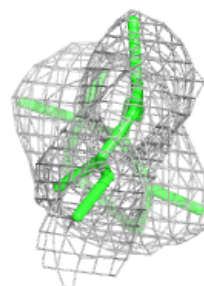
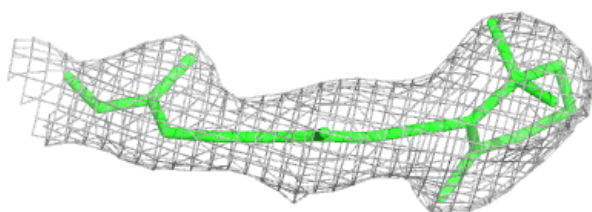
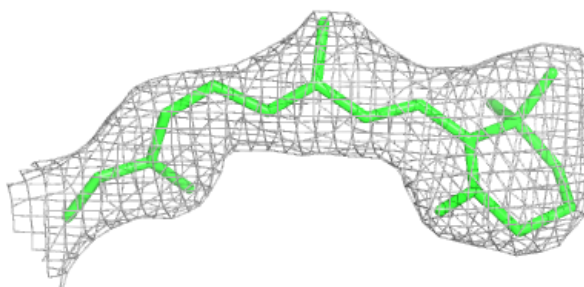
**Electron density around HTG A 1508:**

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

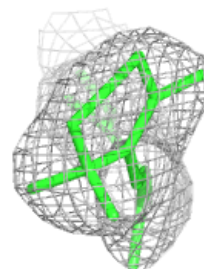
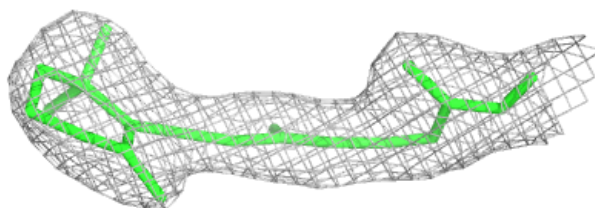
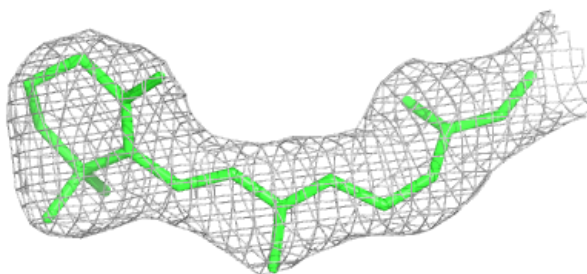


Electron density around RET B 1296:

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

**Electron density around RET A 1296:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.