



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2024 – 03:08 PM EST

PDB ID : 1H1M  
Title : CRYSTAL STRUCTURE OF QUERCETIN 2,3-DIOXYGENASE ANAEROBICALLY COMPLEXED WITH THE SUBSTRATE KAEMPFEROL  
Authors : Steiner, R.A.; Dijkstra, B.W.  
Deposited on : 2002-07-19  
Resolution : 1.90 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](mailto: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>.

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

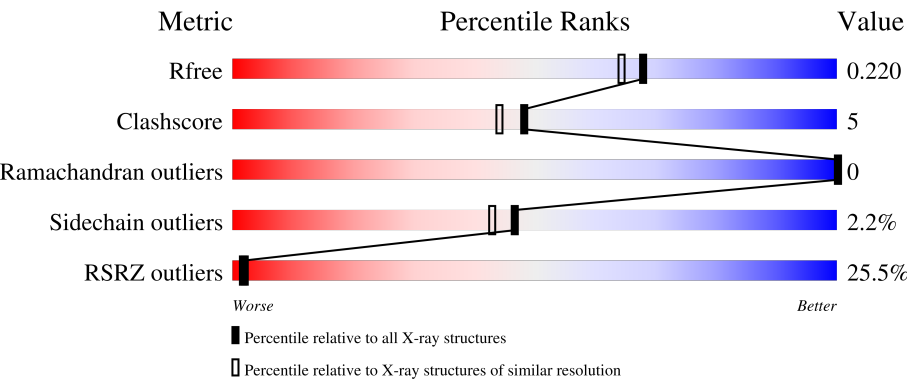
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 1.90 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))
$R_{free}$	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	350	<div><div></div><div></div><div></div><div></div><div></div></div> <div>89%8% ..</div>
1	B	350	<div><div></div><div></div><div></div><div></div><div></div></div> <div>87%11% .</div>
1	C	350	<div><div></div><div></div><div></div><div></div><div></div></div> <div>88%8% ..</div>
1	D	350	<div><div></div><div></div><div></div><div></div><div></div></div> <div>96%89%9% ..</div>
2	E	5	<div><div></div><div></div><div></div><div></div><div></div></div> <div>40%40%20%</div>
3	F	4	<div><div></div><div></div><div></div><div></div><div></div></div> <div>25%50%25%</div>

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Mol	Chain	Length	Quality of chain
3	G	4	
4	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
8	MPD	B	1361	-	-	X	-
8	MPD	C	1360	-	-	X	-

## 2 Entry composition [i](#)

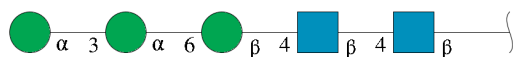
There are 9 unique types of molecules in this entry. The entry contains 12645 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 QUERCETIN 2,3-DIOXYGENASE.

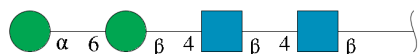
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	5	0
			2657	1682	431	539	5			
1	B	344	Total	C	N	O	S	0	4	0
			2654	1681	431	537	5			
1	C	343	Total	C	N	O	S	0	4	0
			2648	1678	430	535	5			
1	D	343	Total	C	N	O	S	0	5	0
			2648	1678	430	535	5			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-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	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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
3	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

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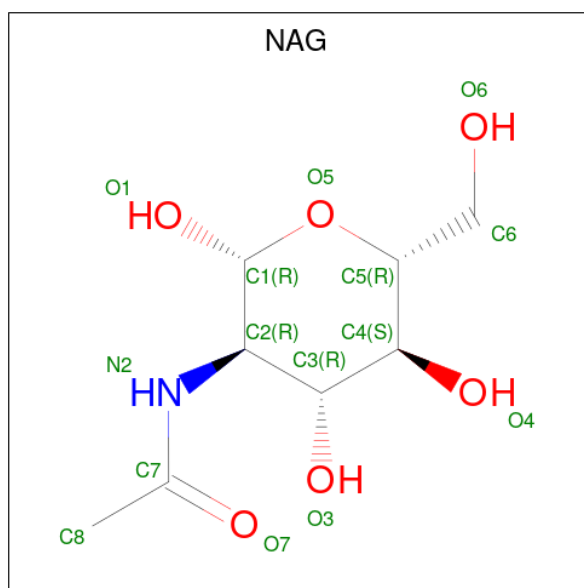
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 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
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



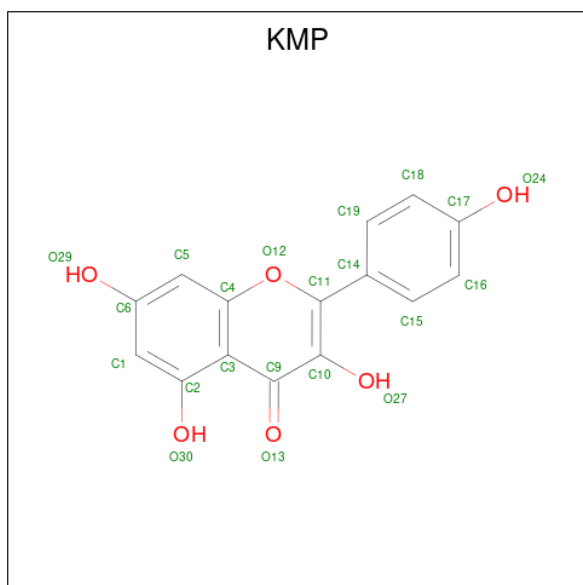
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 6 is 3,5,7-TRIHIDROXY-2-(4-HIDROXYPHENYL)-4H-CHROMEN-4-ONE (three-letter code: KMP) (formula: C<sub>15</sub>H<sub>10</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			21	15	6		
6	B	1	Total	C	O	0	0
			21	15	6		

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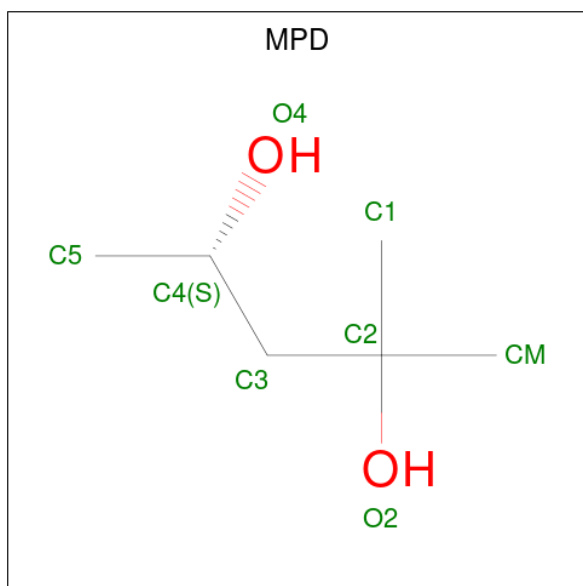
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			21	15	6		
6	D	1	Total	C	O	0	0
			21	15	6		

- Molecule 7 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cu	0	0
			1	1		
7	B	1	Total	Cu	0	0
			1	1		
7	C	1	Total	Cu	0	0
			1	1		
7	D	1	Total	Cu	0	0
			1	1		

- Molecule 8 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			8	6	2		
8	B	1	Total	C	O	0	0
			8	6	2		
8	B	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			8	6	2		

- Molecule 9 is water.

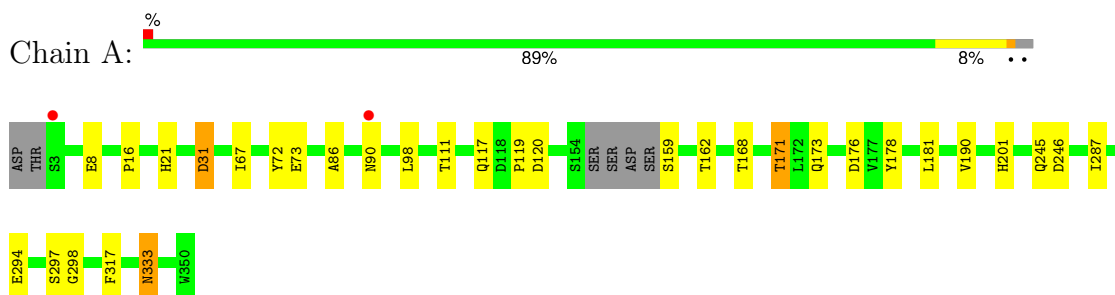
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	416	Total	O	0	0
			416	416		
9	B	387	Total	O	0	0
			387	387		
9	C	381	Total	O	0	0
			381	381		
9	D	363	Total	O	0	0
			363	363		



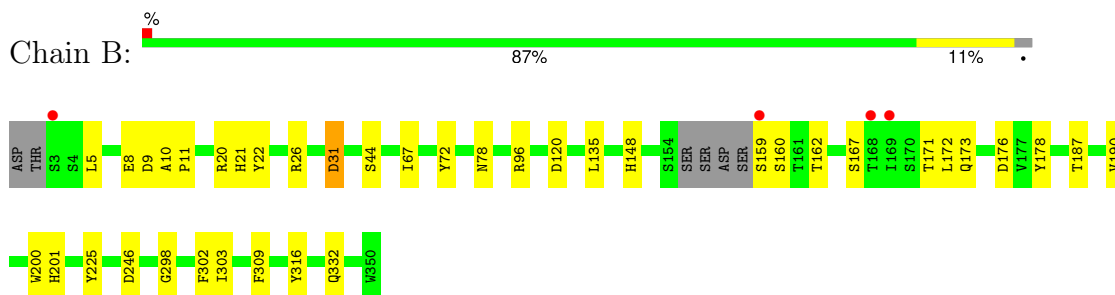
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

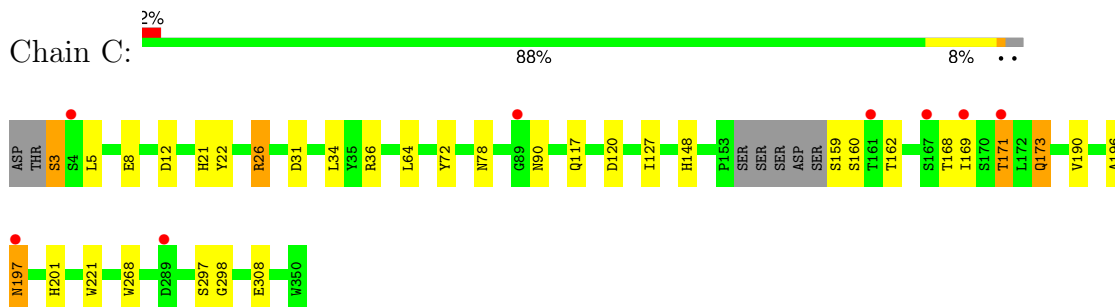
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE



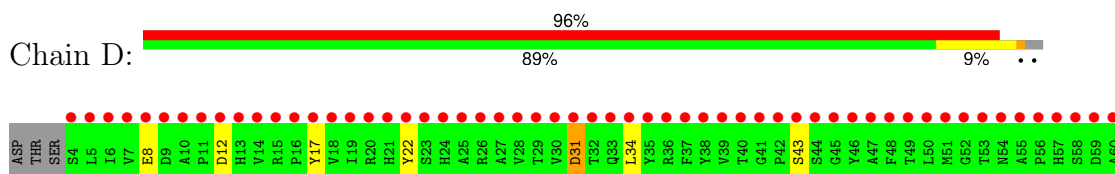
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

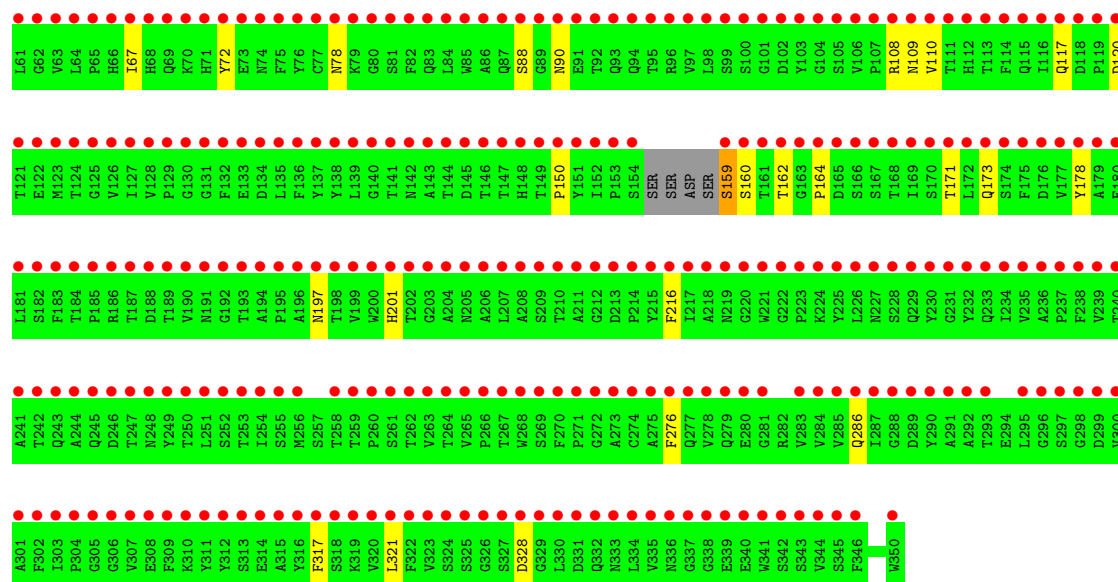


- Molecule 1: QUERCETIN 2,3-DIOXYGENASE



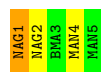
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE





- Molecule 2: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 40% 40% 20%



- Molecule 3: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 25% 50% 25%



- Molecule 3: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 75% 25%



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

Chain H: 50% 50%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.27Å 55.38Å 123.93Å 90.00° 98.33° 90.00°	Depositor
Resolution (Å)	49.39 – 1.90 49.39 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (49.39-1.90) 96.5 (49.39-1.90)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.154 , 0.204 0.180 , 0.220	Depositor DCC
$R_{free}$ test set	5608 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtriage
Anisotropy	0.571	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 43.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	12645	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: CU, MAN, BMA, KMP, MPD, 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	0.95	0/2762	0.94	4/3786 (0.1%)
1	B	0.91	0/2754	0.93	7/3775 (0.2%)
1	C	0.92	0/2748	0.87	2/3767 (0.1%)
1	D	0.90	0/2748	0.88	4/3767 (0.1%)
All	All	0.92	0/11012	0.91	17/15095 (0.1%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	120	ASP	CB-CG-OD2	8.07	125.56	118.30
1	A	246	ASP	CB-CG-OD2	7.70	125.23	118.30
1	B	9	ASP	CB-CG-OD2	7.60	125.14	118.30
1	A	176	ASP	CB-CG-OD2	7.37	124.93	118.30
1	C	120	ASP	CB-CG-OD2	7.01	124.61	118.30
1	D	31	ASP	CB-CG-OD2	6.62	124.25	118.30
1	A	31	ASP	CB-CG-OD2	6.57	124.21	118.30
1	A	120	ASP	CB-CG-OD2	6.44	124.10	118.30
1	D	120	ASP	CB-CG-OD2	6.36	124.02	118.30
1	B	176	ASP	CB-CG-OD2	5.93	123.64	118.30
1	D	328	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	20	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	D	12	ASP	CB-CG-OD2	5.46	123.22	118.30
1	B	31	ASP	CB-CG-OD2	5.46	123.21	118.30
1	C	12	ASP	CB-CG-OD2	5.26	123.04	118.30
1	B	20	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	B	246	ASP	CB-CG-OD2	5.02	122.82	118.30

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	2657	0	2453	32	0
1	B	2654	0	2454	26	0
1	C	2648	0	2449	26	0
1	D	2648	0	2445	25	0
2	E	61	0	52	1	0
3	F	50	0	43	1	0
3	G	50	0	43	1	0
4	H	28	0	25	1	0
5	A	56	0	52	0	0
5	B	42	0	39	0	0
5	C	42	0	39	4	0
5	D	42	0	39	0	0
6	A	21	0	6	1	0
6	B	21	0	6	1	0
6	C	21	0	6	0	0
6	D	21	0	7	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	8	0	14	4	0
8	B	16	0	28	7	0
8	C	8	0	14	6	0
9	A	416	0	0	14	0
9	B	387	0	0	12	0
9	C	381	0	0	6	0
9	D	363	0	0	11	0
All	All	12645	0	10214	115	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 5.

All (115) 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)
8:B:1360:MPD:H32	8:B:1361:MPD:H32	1.26	1.14
1:A:8[A]:GLU:HG2	9:A:2018:HOH:O	1.55	1.05
1:D:117:GLN:HG3	9:D:2141:HOH:O	1.66	0.95
1:D:78[D]:ASN:HB3	9:D:2151:HOH:O	1.66	0.94
8:B:1360:MPD:C3	8:B:1361:MPD:H32	2.02	0.89
1:B:8[A]:GLU:HG2	9:B:2004:HOH:O	1.71	0.89
1:D:78[D]:ASN:CB	9:D:2151:HOH:O	2.20	0.88
1:B:8[A]:GLU:CG	9:B:2004:HOH:O	2.23	0.84
1:D:8[A]:GLU:HG2	9:D:2009:HOH:O	1.81	0.80
8:A:1362:MPD:H32	8:C:1360:MPD:H32	1.65	0.79
9:B:2384:HOH:O	5:C:1355:NAG:H61	1.84	0.77
1:B:8[A]:GLU:OE2	1:B:148:HIS:HE1	1.68	0.77
1:C:78[B]:ASN:ND2	9:C:2117:HOH:O	2.02	0.76
1:B:172:LEU:HA	9:B:2184:HOH:O	1.86	0.74
1:C:8[A]:GLU:HG2	9:C:2009:HOH:O	1.87	0.74
1:C:26:ARG:HG3	1:C:26:ARG:HH11	1.53	0.73
1:D:159:SER:HA	9:D:2182:HOH:O	1.87	0.72
8:A:1362:MPD:C3	8:C:1360:MPD:H32	2.21	0.71
1:D:173:GLN:HG2	1:D:178:TYR:CE2	2.25	0.71
1:B:31:ASP:HB2	1:B:162:THR:HG23	1.73	0.70
8:B:1360:MPD:H12	1:D:201:HIS:CE1	2.26	0.69
1:A:16:PRO:HB3	1:A:287:ILE:HG21	1.74	0.68
1:B:201:HIS:CE1	8:B:1361:MPD:H12	2.29	0.68
1:C:8[A]:GLU:OE2	1:C:148:HIS:HE1	1.76	0.68
1:A:171:THR:CG2	9:A:2215:HOH:O	2.43	0.67
9:B:2384:HOH:O	5:C:1355:NAG:C6	2.43	0.65
1:A:173:GLN:HG3	9:A:2221:HOH:O	1.96	0.63
1:A:201:HIS:HB3	1:C:117:GLN:NE2	2.15	0.62
1:D:31:ASP:HB2	1:D:162:THR:HG23	1.84	0.60
1:A:8[A]:GLU:CG	9:A:2018:HOH:O	2.31	0.59
1:A:201:HIS:CE1	8:A:1362:MPD:H12	2.38	0.59
9:B:2384:HOH:O	5:C:1355:NAG:H4	2.03	0.59
1:A:294:GLU:HG2	9:A:2331:HOH:O	2.03	0.58
1:C:190:VAL:HG11	3:G:1:NAG:H82	1.86	0.58
1:A:117:GLN:HE22	8:C:1360:MPD:HM3	1.69	0.58
1:C:168:THR:O	1:C:171:THR:HB	2.03	0.57
1:C:26:ARG:HH11	1:C:26:ARG:CG	2.18	0.56
1:A:117:GLN:NE2	8:C:1360:MPD:HM3	2.21	0.56
1:D:78[D]:ASN:HB2	9:D:2151:HOH:O	1.97	0.56
1:A:117:GLN:HG3	9:A:2165:HOH:O	2.06	0.55
1:D:108:ARG:O	1:D:109[A]:ASN:HB2	2.05	0.55
8:B:1360:MPD:H4	8:B:1361:MPD:HM1	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:GLN:HG2	1:A:178:TYR:CE2	2.42	0.55
1:B:171:THR:HG22	1:B:171:THR:O	2.07	0.54
1:D:171:THR:HG22	1:D:171:THR:O	2.08	0.54
1:C:196:ALA:O	1:C:197:ASN:CB	2.53	0.54
1:B:167:SER:HB3	9:B:2182:HOH:O	2.08	0.54
1:A:90:ASN:HA	9:A:2129:HOH:O	2.09	0.53
1:C:171:THR:HG23	9:C:2202:HOH:O	2.09	0.53
1:A:173:GLN:HG3	9:A:2218:HOH:O	2.09	0.53
6:B:1358:KMP:H19	6:B:1358:KMP:O27	2.09	0.52
1:A:31:ASP:HB2	1:A:162:THR:HG23	1.92	0.52
1:C:5:LEU:HD22	9:C:2309:HOH:O	2.10	0.52
1:A:171:THR:HG22	9:A:2215:HOH:O	2.07	0.52
1:A:168:THR:O	1:A:171:THR:HB	2.10	0.51
1:C:8[A]:GLU:OE2	1:C:148:HIS:CE1	2.61	0.51
1:A:297:SER:HB2	9:A:2111:HOH:O	2.10	0.51
1:C:196:ALA:O	1:C:197:ASN:HB2	2.11	0.51
1:B:332:GLN:NE2	9:B:2346:HOH:O	2.44	0.51
1:B:135:LEU:HD11	1:B:172:LEU:HD13	1.93	0.49
8:B:1360:MPD:H32	8:B:1361:MPD:C3	2.18	0.49
1:D:34:LEU:C	1:D:34:LEU:HD23	2.33	0.49
1:D:173:GLN:NE2	9:D:2195:HOH:O	2.46	0.49
1:A:21:HIS:CG	1:A:298:GLY:HA3	2.49	0.48
1:D:164:PRO:HD2	9:D:2185:HOH:O	2.14	0.48
1:B:8[A]:GLU:OE2	1:B:148:HIS:CE1	2.58	0.48
1:D:8[A]:GLU:CG	9:D:2009:HOH:O	2.48	0.48
1:B:190:VAL:HG11	3:F:1:NAG:H82	1.94	0.48
1:C:31:ASP:HB2	1:C:162:THR:HG23	1.96	0.48
1:D:173:GLN:HG2	1:D:178:TYR:CD2	2.49	0.48
1:D:197:ASN:CG	1:D:197:ASN:O	2.52	0.48
1:A:333[A]:ASN:ND2	9:A:2376:HOH:O	1.96	0.47
1:D:88:SER:HB2	1:D:110:VAL:HG22	1.97	0.47
1:C:173:GLN:H	1:C:173:GLN:HG2	1.45	0.46
1:A:67:ILE:HG12	1:A:178:TYR:HB2	1.96	0.46
1:D:286:GLN:HA	9:D:2293:HOH:O	2.16	0.46
1:B:78[B]:ASN:ND2	9:B:2094:HOH:O	2.48	0.45
1:A:317:PHE:HB3	1:C:22:TYR:CE2	2.52	0.45
8:A:1362:MPD:H31	8:C:1360:MPD:H32	1.99	0.45
1:B:332:GLN:NE2	9:B:2347:HOH:O	2.50	0.45
1:C:90:ASN:ND2	9:C:2132:HOH:O	2.50	0.45
9:B:2384:HOH:O	5:C:1355:NAG:C5	2.65	0.45
1:D:17:TYR:CE2	1:D:43[A]:SER:OG	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:216:PHE:CD1	1:D:216:PHE:N	2.85	0.45
1:A:245:GLN:HG3	9:A:2293:HOH:O	2.17	0.44
1:A:73:GLU:OE2	6:A:1360:KMP:O27	2.36	0.44
1:C:3:SER:N	9:C:2001:HOH:O	2.50	0.44
1:A:171:THR:HG23	9:A:2216:HOH:O	2.18	0.44
1:A:86:ALA:HA	1:A:111:THR:O	2.17	0.43
1:C:127:ILE:HD12	1:C:127:ILE:N	2.33	0.43
1:D:197:ASN:HB3	9:D:2215:HOH:O	2.18	0.43
1:A:117:GLN:HB2	9:A:2162:HOH:O	2.18	0.43
1:B:187:THR:HB	4:H:2:NAG:O3	2.18	0.43
1:B:22:TYR:CE2	1:D:317:PHE:HB3	2.54	0.43
1:B:5:LEU:HD11	9:B:2295:HOH:O	2.18	0.42
1:B:173:GLN:HG2	1:B:178:TYR:CD2	2.54	0.42
1:A:16:PRO:HB3	1:A:287:ILE:CG2	2.47	0.42
1:A:98:LEU:HD12	1:A:98:LEU:N	2.35	0.42
1:A:201:HIS:HB3	1:C:117:GLN:HE22	1.85	0.42
1:A:119:PRO:HD3	1:C:221:TRP:CE2	2.55	0.41
1:B:316:TYR:HB2	1:D:22:TYR:HB2	2.03	0.41
1:B:10:ALA:HA	1:B:11:PRO:HD3	1.90	0.41
1:B:225:TYR:CD1	1:B:225:TYR:N	2.89	0.41
1:C:201:HIS:CE1	8:C:1360:MPD:H12	2.55	0.41
1:D:276:PHE:HA	1:D:321:LEU:O	2.21	0.41
1:B:21:HIS:CG	1:B:298:GLY:HA3	2.56	0.41
1:B:201:HIS:ND1	8:B:1361:MPD:H12	2.36	0.41
1:C:268:TRP:O	1:C:308:GLU:HA	2.21	0.41
1:C:64:LEU:HB2	1:C:169:ILE:HD13	2.03	0.40
1:B:303:ILE:HG21	1:B:309:PHE:CD1	2.57	0.40
1:C:21:HIS:CG	1:C:298:GLY:HA3	2.56	0.40
1:C:34:LEU:HD22	1:C:36:ARG:NH1	2.37	0.40
1:A:190:VAL:HG11	2:E:1:NAG:H82	2.03	0.40
1:B:44:SER:HA	1:B:302:PHE:CZ	2.56	0.40
1:B:96:ARG:HD2	1:B:200:TRP:CD2	2.56	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	345/350 (99%)	333 (96%)	12 (4%)	0	100	100
1	B	344/350 (98%)	332 (96%)	12 (4%)	0	100	100
1	C	343/350 (98%)	334 (97%)	9 (3%)	0	100	100
1	D	343/350 (98%)	334 (97%)	9 (3%)	0	100	100
All	All	1375/1400 (98%)	1333 (97%)	42 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	293/294 (100%)	287 (98%)	6 (2%)	50	47
1	B	292/294 (99%)	287 (98%)	5 (2%)	56	54
1	C	291/294 (99%)	282 (97%)	9 (3%)	35	29
1	D	291/294 (99%)	285 (98%)	6 (2%)	48	45
All	All	1167/1176 (99%)	1141 (98%)	26 (2%)	47	43

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	TYR
1	A	159	SER
1	A	171	THR
1	A	181	LEU
1	A	333[A]	ASN
1	A	333[B]	ASN
1	B	26	ARG
1	B	67	ILE

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Mol	Chain	Res	Type
1	B	72	TYR
1	B	159	SER
1	B	160	SER
1	C	3	SER
1	C	26	ARG
1	C	72	TYR
1	C	159	SER
1	C	160	SER
1	C	171	THR
1	C	173	GLN
1	C	197	ASN
1	C	297	SER
1	D	67	ILE
1	D	72	TYR
1	D	90	ASN
1	D	150	PRO
1	D	159	SER
1	D	160	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	117	GLN
1	A	332	GLN
1	B	83	GLN
1	B	117	GLN
1	B	148	HIS
1	B	286	GLN
1	B	332	GLN
1	C	83	GLN
1	C	117	GLN
1	C	148	HIS
1	C	336	ASN
1	D	83	GLN
1	D	90	ASN
1	D	173	GLN
1	D	336	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 ⓘ

15 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	E	1	1,2	14,14,15	0.89	1 (7%)	17,19,21	1.25	2 (11%)
2	NAG	E	2	2	14,14,15	0.69	0	17,19,21	1.19	2 (11%)
2	BMA	E	3	2	11,11,12	0.92	0	15,15,17	0.92	0
2	MAN	E	4	2	11,11,12	0.58	0	15,15,17	1.35	1 (6%)
2	MAN	E	5	2	11,11,12	0.76	0	15,15,17	0.78	0
3	NAG	F	1	1,3	14,14,15	0.88	1 (7%)	17,19,21	1.52	1 (5%)
3	NAG	F	2	3	14,14,15	0.61	0	17,19,21	1.94	6 (35%)
3	BMA	F	3	3	11,11,12	0.70	0	15,15,17	1.59	2 (13%)
3	MAN	F	4	3	11,11,12	0.83	0	15,15,17	1.01	0
3	NAG	G	1	1,3	14,14,15	0.46	0	17,19,21	1.59	5 (29%)
3	NAG	G	2	3	14,14,15	0.48	0	17,19,21	1.52	4 (23%)
3	BMA	G	3	3	11,11,12	1.06	1 (9%)	15,15,17	0.92	0
3	MAN	G	4	3	11,11,12	0.67	0	15,15,17	1.03	1 (6%)
4	NAG	H	1	1,4	14,14,15	0.79	1 (7%)	17,19,21	0.99	1 (5%)
4	NAG	H	2	4	14,14,15	0.89	0	17,19,21	1.83	4 (23%)

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	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4	2	-	2/2/19/22	0/1/1/1
2	MAN	E	5	2	-	2/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	1/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	0/2/19/22	0/1/1/1
4	NAG	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	3	BMA	O5-C1	-2.82	1.39	1.43
2	E	1	NAG	C1-C2	2.43	1.55	1.52
4	H	1	NAG	C1-C2	2.42	1.55	1.52
3	F	1	NAG	C1-C2	2.19	1.55	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	NAG	C1-O5-C5	5.38	119.40	112.19
3	F	2	NAG	C1-O5-C5	4.55	118.28	112.19
4	H	2	NAG	O7-C7-C8	-4.29	114.41	122.05
3	F	3	BMA	C1-O5-C5	4.24	117.86	112.19
2	E	4	MAN	C1-O5-C5	4.17	117.78	112.19
3	G	2	NAG	O5-C1-C2	-3.70	105.56	111.29
4	H	2	NAG	C1-C2-N2	3.31	115.65	110.43
4	H	2	NAG	C8-C7-N2	3.03	121.15	116.12
3	G	1	NAG	O5-C1-C2	-2.96	106.72	111.29
4	H	2	NAG	C1-O5-C5	2.95	116.14	112.19
2	E	2	NAG	C1-O5-C5	2.92	116.10	112.19
3	F	2	NAG	O6-C6-C5	-2.86	101.61	111.33
2	E	1	NAG	O5-C1-C2	-2.81	106.94	111.29
3	G	4	MAN	O5-C5-C6	2.73	112.98	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	NAG	C8-C7-N2	-2.67	111.69	116.12
3	F	2	NAG	C3-C4-C5	2.59	114.93	110.23
3	G	1	NAG	O7-C7-C8	-2.45	117.68	122.05
3	G	2	NAG	C1-C2-N2	2.45	114.30	110.43
3	G	1	NAG	O5-C5-C6	2.36	112.26	107.66
3	F	2	NAG	O7-C7-N2	2.27	126.00	121.98
3	G	2	NAG	O7-C7-N2	2.26	125.98	121.98
4	H	1	NAG	C8-C7-N2	2.23	119.82	116.12
3	G	2	NAG	O4-C4-C3	-2.23	105.12	110.38
3	F	3	BMA	C3-C4-C5	2.22	114.25	110.23
3	G	1	NAG	O6-C6-C5	-2.21	103.81	111.33
3	G	1	NAG	C4-C3-C2	2.18	114.21	111.02
3	F	2	NAG	C6-C5-C4	-2.11	107.85	113.02
2	E	2	NAG	O5-C1-C2	-2.05	108.13	111.29
2	E	1	NAG	C4-C3-C2	-2.01	108.07	111.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

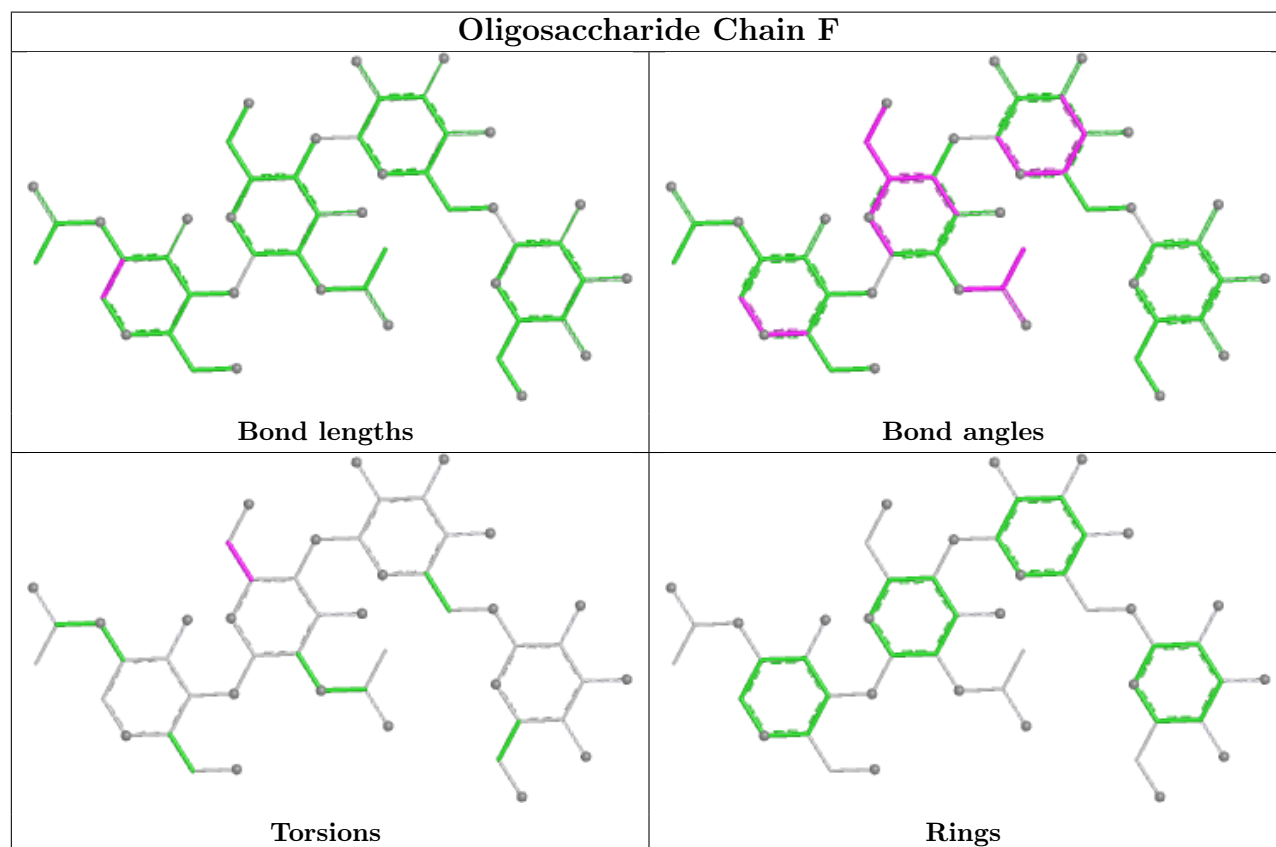
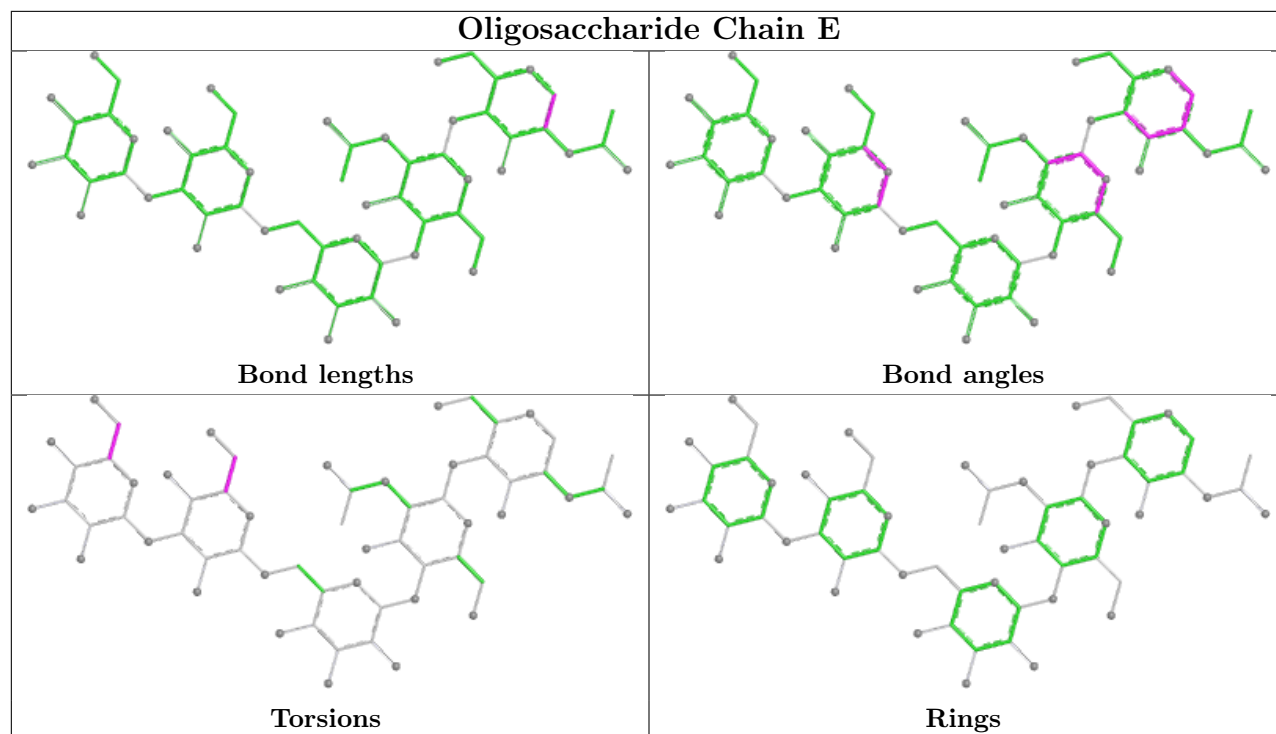
Mol	Chain	Res	Type	Atoms
2	E	5	MAN	O5-C5-C6-O6
2	E	5	MAN	C4-C5-C6-O6
2	E	4	MAN	C4-C5-C6-O6
2	E	4	MAN	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6

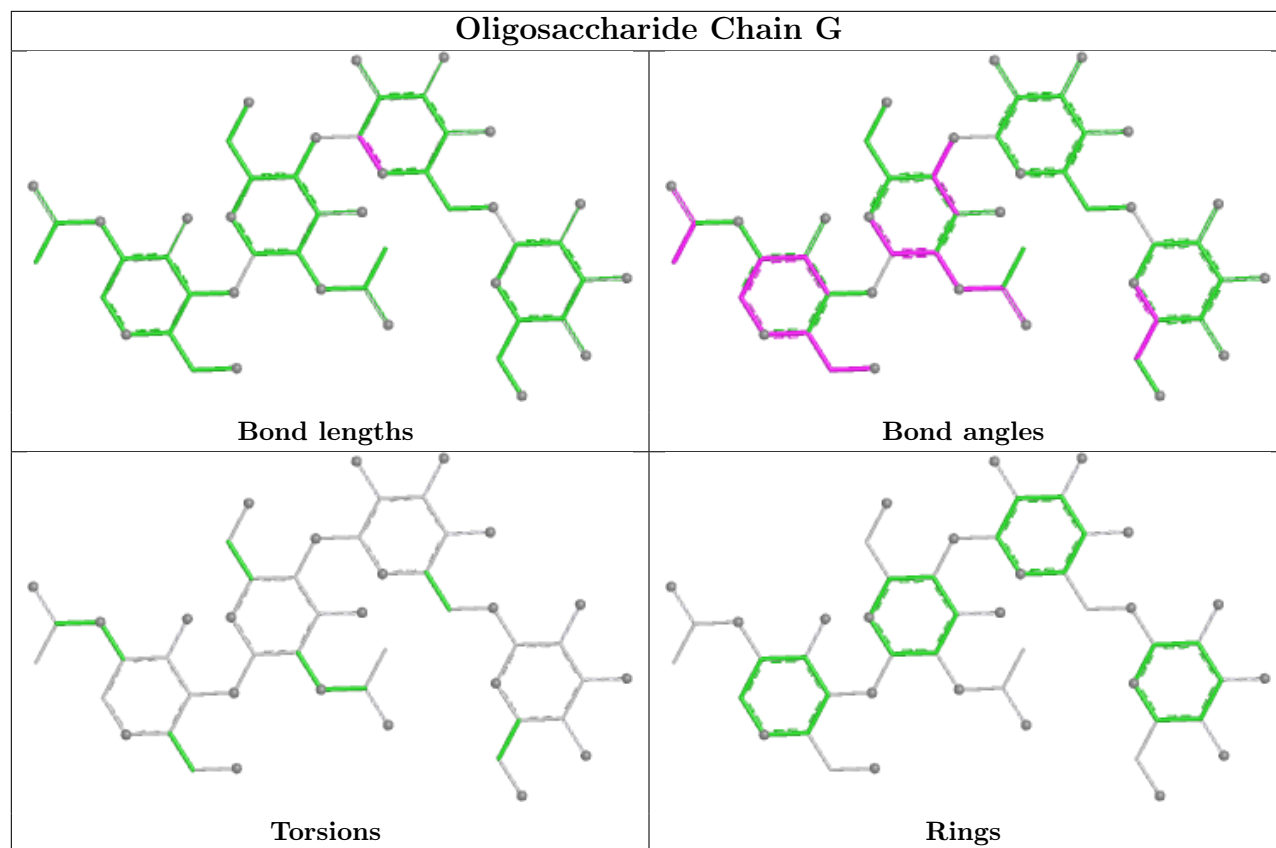
There are no ring outliers.

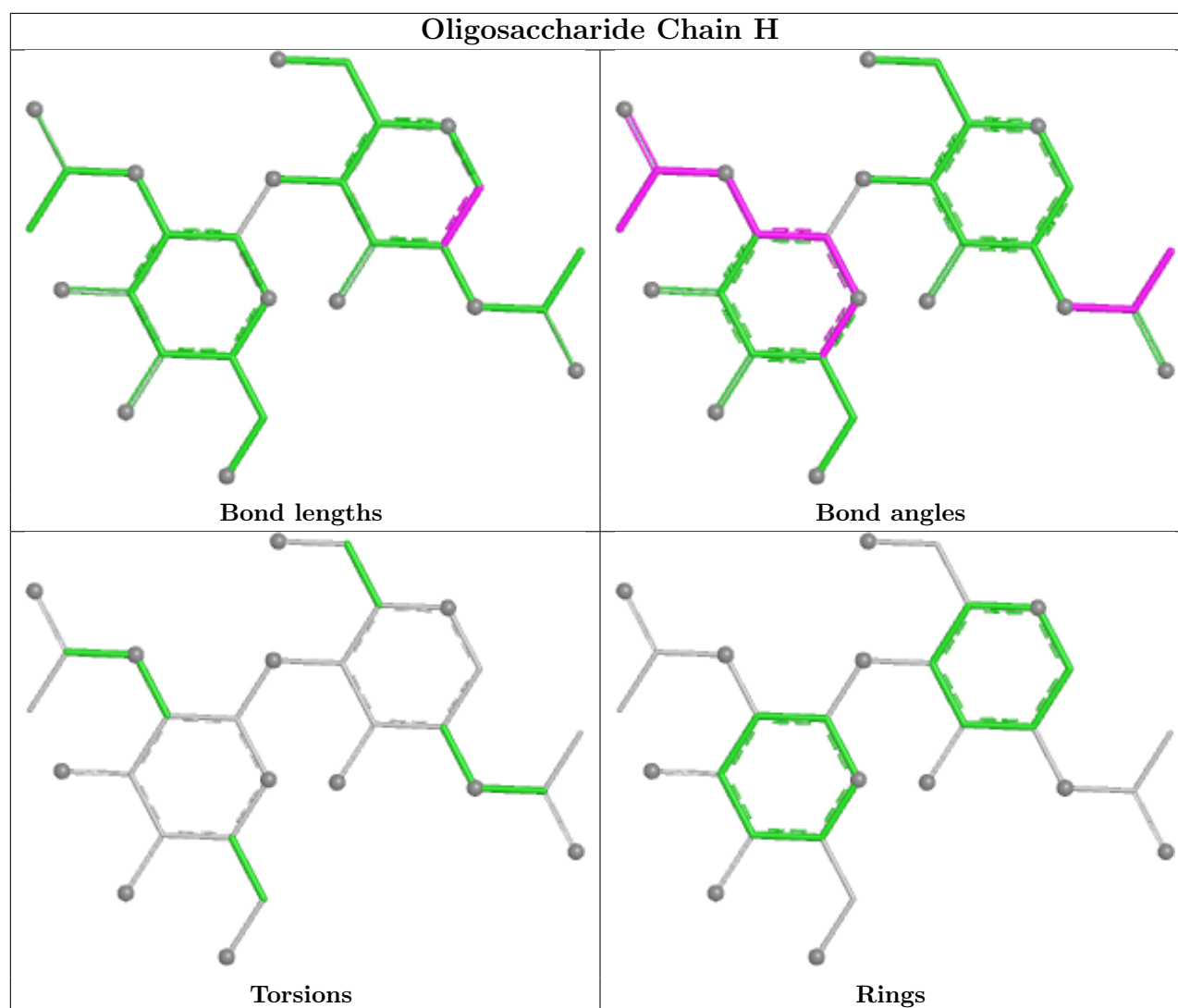
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0
3	F	1	NAG	1	0
3	G	1	NAG	1	0
4	H	2	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](#)

Of 25 ligands modelled in this entry, 4 are monoatomic - leaving 21 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	$\# Z  > 2$
5	NAG	A	1356	1	14,14,15	0.96	0	17,19,21	1.48	1 (5%)
5	NAG	A	1355	1	14,14,15	1.03	1 (7%)	17,19,21	1.51	3 (17%)
6	KMP	B	1358	7	19,23,23	2.06	5 (26%)	25,34,34	1.68	6 (24%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	KMP	C	1358	7	19,23,23	2.31	3 (15%)	25,34,34	1.61	6 (24%)
5	NAG	D	1354	1	14,14,15	1.12	1 (7%)	17,19,21	1.93	2 (11%)
5	NAG	C	1354	1	14,14,15	0.96	1 (7%)	17,19,21	1.38	3 (17%)
5	NAG	C	1355	1	14,14,15	0.76	0	17,19,21	2.02	5 (29%)
8	MPD	B	1360	-	7,7,7	0.62	0	9,10,10	2.02	3 (33%)
5	NAG	D	1355	1	14,14,15	0.88	1 (7%)	17,19,21	1.68	3 (17%)
5	NAG	A	1351	1	14,14,15	0.66	0	17,19,21	1.04	1 (5%)
5	NAG	B	1351	1	14,14,15	0.48	0	17,19,21	1.00	1 (5%)
8	MPD	A	1362	-	7,7,7	0.74	0	9,10,10	1.85	1 (11%)
5	NAG	D	1351	1	14,14,15	0.83	1 (7%)	17,19,21	1.49	3 (17%)
5	NAG	C	1351	1	14,14,15	0.52	0	17,19,21	1.04	0
8	MPD	C	1360	-	7,7,7	0.64	0	9,10,10	1.48	1 (11%)
5	NAG	A	1354	1	14,14,15	0.74	0	17,19,21	1.55	3 (17%)
5	NAG	B	1354	1	14,14,15	0.76	0	17,19,21	1.25	3 (17%)
6	KMP	A	1360	7	19,23,23	2.16	5 (26%)	25,34,34	2.12	5 (20%)
8	MPD	B	1361	-	7,7,7	0.70	0	9,10,10	1.87	2 (22%)
5	NAG	B	1355	1	14,14,15	0.79	1 (7%)	17,19,21	1.22	2 (11%)
6	KMP	D	1356	7	19,23,23	2.63	3 (15%)	25,34,34	1.75	5 (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
5	NAG	A	1356	1	-	5/6/23/26	0/1/1/1
5	NAG	A	1355	1	-	2/6/23/26	0/1/1/1
6	KMP	B	1358	7	-	0/0/4/4	0/3/3/3
6	KMP	C	1358	7	-	0/0/4/4	0/3/3/3
5	NAG	D	1354	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1354	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1355	1	-	1/6/23/26	0/1/1/1
8	MPD	B	1360	-	-	1/5/5/5	-
5	NAG	D	1355	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1351	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1351	1	-	0/6/23/26	0/1/1/1
8	MPD	A	1362	-	-	1/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	D	1351	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1351	1	-	0/6/23/26	0/1/1/1
8	MPD	C	1360	-	-	3/5/5/5	-
5	NAG	A	1354	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1354	1	-	2/6/23/26	0/1/1/1
6	KMP	A	1360	7	-	0/0/4/4	0/3/3/3
8	MPD	B	1361	-	-	3/5/5/5	-
5	NAG	B	1355	1	-	0/6/23/26	0/1/1/1
6	KMP	D	1356	7	-	0/0/4/4	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	1356	KMP	O12-C11	7.54	1.48	1.36
6	D	1356	KMP	C3-C4	6.47	1.49	1.41
6	C	1358	KMP	C3-C4	6.31	1.48	1.41
6	C	1358	KMP	O12-C11	5.73	1.45	1.36
6	B	1358	KMP	C3-C4	5.40	1.47	1.41
6	A	1360	KMP	O12-C11	5.26	1.44	1.36
6	A	1360	KMP	C3-C4	5.10	1.47	1.41
6	B	1358	KMP	O12-C11	4.60	1.43	1.36
6	A	1360	KMP	C2-C3	3.18	1.48	1.43
5	D	1354	NAG	C1-C2	3.04	1.56	1.52
5	C	1354	NAG	C1-C2	2.99	1.56	1.52
6	D	1356	KMP	C2-C3	2.94	1.48	1.43
6	B	1358	KMP	C2-C3	2.90	1.48	1.43
5	D	1355	NAG	C1-C2	2.79	1.56	1.52
6	B	1358	KMP	C1-C6	2.73	1.43	1.39
6	C	1358	KMP	C2-C3	2.73	1.47	1.43
5	A	1355	NAG	C1-C2	2.63	1.55	1.52
6	A	1360	KMP	O24-C17	-2.27	1.31	1.37
6	B	1358	KMP	O29-C6	-2.23	1.32	1.37
5	D	1351	NAG	C1-C2	2.19	1.55	1.52
5	B	1355	NAG	C1-C2	2.17	1.55	1.52
6	A	1360	KMP	C1-C2	2.07	1.42	1.37

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1360	KMP	O12-C4-C5	5.12	121.93	115.95
5	D	1354	NAG	O5-C1-C2	-5.03	103.51	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1356	NAG	C1-O5-C5	4.92	118.78	112.19
6	D	1356	KMP	O12-C4-C5	4.79	121.56	115.95
5	C	1355	NAG	C1-O5-C5	-4.75	105.82	112.19
6	A	1360	KMP	C5-C4-C3	-4.70	118.06	123.11
8	A	1362	MPD	CM-C2-C1	-4.61	100.29	110.63
5	D	1354	NAG	C1-O5-C5	4.49	118.20	112.19
8	B	1361	MPD	CM-C2-C1	-4.40	100.77	110.63
6	A	1360	KMP	C4-O12-C11	4.36	123.93	120.25
8	B	1360	MPD	CM-C2-C1	-4.15	101.33	110.63
6	B	1358	KMP	C4-O12-C11	4.10	123.71	120.25
6	C	1358	KMP	O12-C4-C5	3.81	120.40	115.95
5	A	1354	NAG	C2-N2-C7	-3.76	117.86	122.90
5	D	1355	NAG	C2-N2-C7	-3.75	117.88	122.90
5	D	1351	NAG	C1-O5-C5	3.71	117.16	112.19
6	A	1360	KMP	C15-C16-C17	-3.71	116.07	120.08
6	C	1358	KMP	C1-C2-C3	-3.65	116.58	120.55
5	D	1355	NAG	O5-C1-C2	-3.65	105.65	111.29
6	B	1358	KMP	C1-C2-C3	-3.57	116.68	120.55
5	A	1355	NAG	C1-O5-C5	3.48	116.85	112.19
8	C	1360	MPD	CM-C2-C1	-3.45	102.90	110.63
5	B	1355	NAG	C2-N2-C7	3.44	127.51	122.90
5	D	1355	NAG	C1-O5-C5	3.27	116.57	112.19
5	A	1354	NAG	O5-C1-C2	-3.26	106.24	111.29
5	C	1355	NAG	C6-C5-C4	3.24	120.97	113.02
6	C	1358	KMP	C2-C1-C6	3.17	122.62	119.68
6	B	1358	KMP	O12-C4-C3	-3.16	118.36	121.12
6	B	1358	KMP	O12-C4-C5	3.15	119.63	115.95
6	D	1356	KMP	O12-C4-C3	-3.08	118.43	121.12
5	C	1354	NAG	C2-N2-C7	-3.06	118.79	122.90
5	C	1355	NAG	O4-C4-C3	-3.06	103.16	110.38
6	D	1356	KMP	C5-C4-C3	-2.89	120.01	123.11
5	A	1355	NAG	O7-C7-C8	-2.85	116.98	122.05
6	D	1356	KMP	C19-C18-C17	2.77	123.07	120.08
6	D	1356	KMP	C5-C6-C1	2.72	123.27	120.82
8	B	1360	MPD	O2-C2-CM	-2.70	99.57	107.99
8	B	1361	MPD	O2-C2-C1	2.65	116.23	107.99
8	B	1360	MPD	O2-C2-C1	2.59	116.04	107.99
5	C	1355	NAG	C2-N2-C7	-2.57	119.46	122.90
6	C	1358	KMP	C4-O12-C11	2.52	122.37	120.25
6	C	1358	KMP	C5-C4-C3	-2.52	120.41	123.11
5	C	1355	NAG	O5-C5-C4	-2.51	104.72	110.83
5	B	1351	NAG	C3-C4-C5	-2.37	105.94	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1354	NAG	C2-N2-C7	-2.35	119.75	122.90
5	C	1354	NAG	O5-C1-C2	-2.34	107.67	111.29
5	B	1354	NAG	O5-C1-C2	-2.30	107.73	111.29
6	B	1358	KMP	C5-C6-C1	2.24	122.84	120.82
6	C	1358	KMP	O12-C4-C3	-2.21	119.19	121.12
5	D	1351	NAG	C2-N2-C7	-2.21	119.93	122.90
5	D	1351	NAG	O7-C7-C8	-2.15	118.23	122.05
5	A	1355	NAG	O5-C1-C2	-2.12	108.00	111.29
5	B	1355	NAG	O5-C1-C2	-2.10	108.04	111.29
5	A	1351	NAG	O6-C6-C5	-2.09	104.20	111.33
5	C	1354	NAG	O5-C5-C6	2.08	111.71	107.66
6	B	1358	KMP	C2-C1-C6	2.07	121.60	119.68
5	A	1354	NAG	O5-C5-C4	-2.06	105.81	110.83
6	A	1360	KMP	O29-C6-C5	-2.06	115.11	121.07
5	B	1354	NAG	O5-C5-C6	2.00	111.56	107.66

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	1361	MPD	C2-C3-C4-C5
5	D	1351	NAG	O5-C5-C6-O6
5	A	1355	NAG	C4-C5-C6-O6
5	D	1351	NAG	C4-C5-C6-O6
5	D	1351	NAG	C8-C7-N2-C2
5	A	1355	NAG	O5-C5-C6-O6
5	A	1356	NAG	O5-C5-C6-O6
5	D	1351	NAG	O7-C7-N2-C2
5	C	1354	NAG	C4-C5-C6-O6
5	C	1354	NAG	O5-C5-C6-O6
5	A	1356	NAG	C8-C7-N2-C2
5	A	1356	NAG	C3-C2-N2-C7
5	C	1355	NAG	C4-C5-C6-O6
5	A	1356	NAG	O7-C7-N2-C2
5	A	1356	NAG	C4-C5-C6-O6
5	B	1354	NAG	C4-C5-C6-O6
8	B	1361	MPD	C1-C2-C3-C4
8	C	1360	MPD	C1-C2-C3-C4
5	D	1354	NAG	O7-C7-N2-C2
5	D	1354	NAG	C3-C2-N2-C7
8	C	1360	MPD	C2-C3-C4-C5
5	B	1354	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	D	1355	NAG	C8-C7-N2-C2
5	D	1354	NAG	C8-C7-N2-C2
5	D	1355	NAG	O7-C7-N2-C2
8	A	1362	MPD	C1-C2-C3-C4
8	B	1360	MPD	C1-C2-C3-C4
8	B	1361	MPD	CM-C2-C3-C4
8	C	1360	MPD	CM-C2-C3-C4

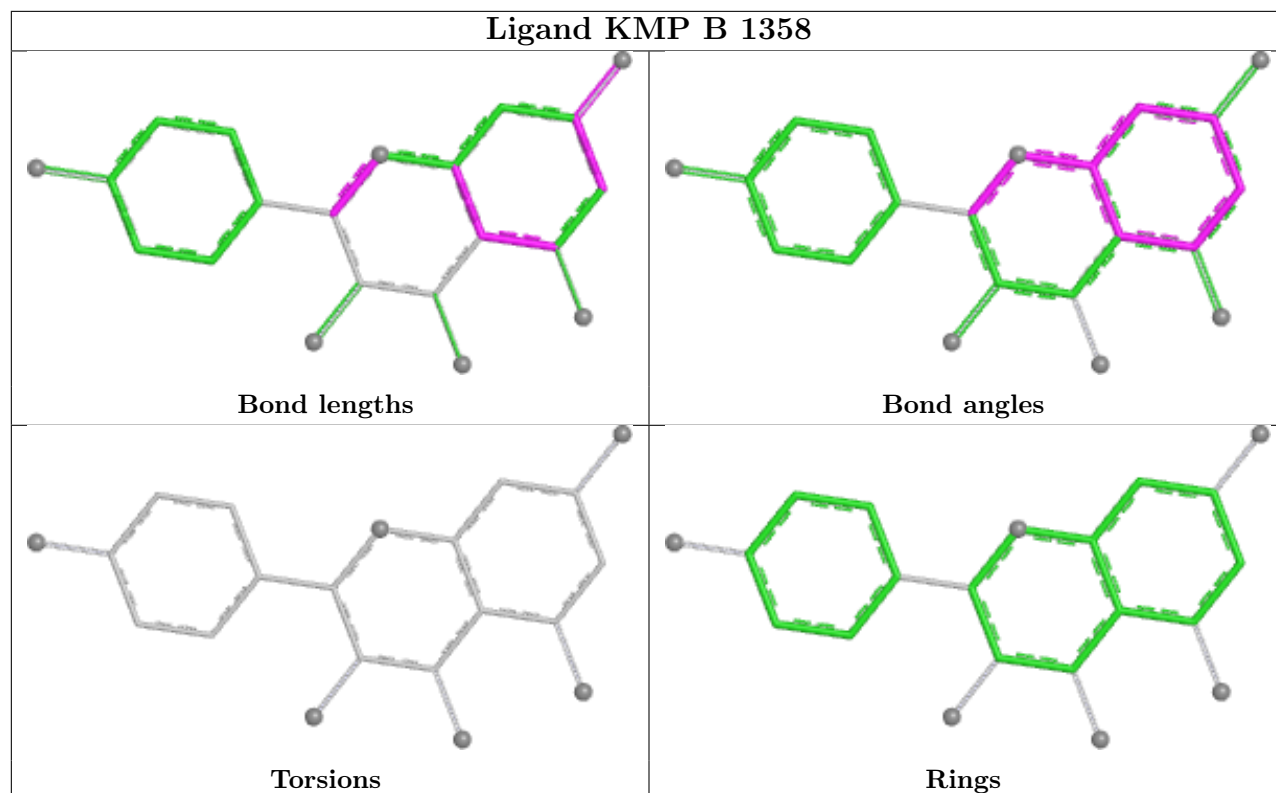
There are no ring outliers.

7 monomers are involved in 20 short contacts:

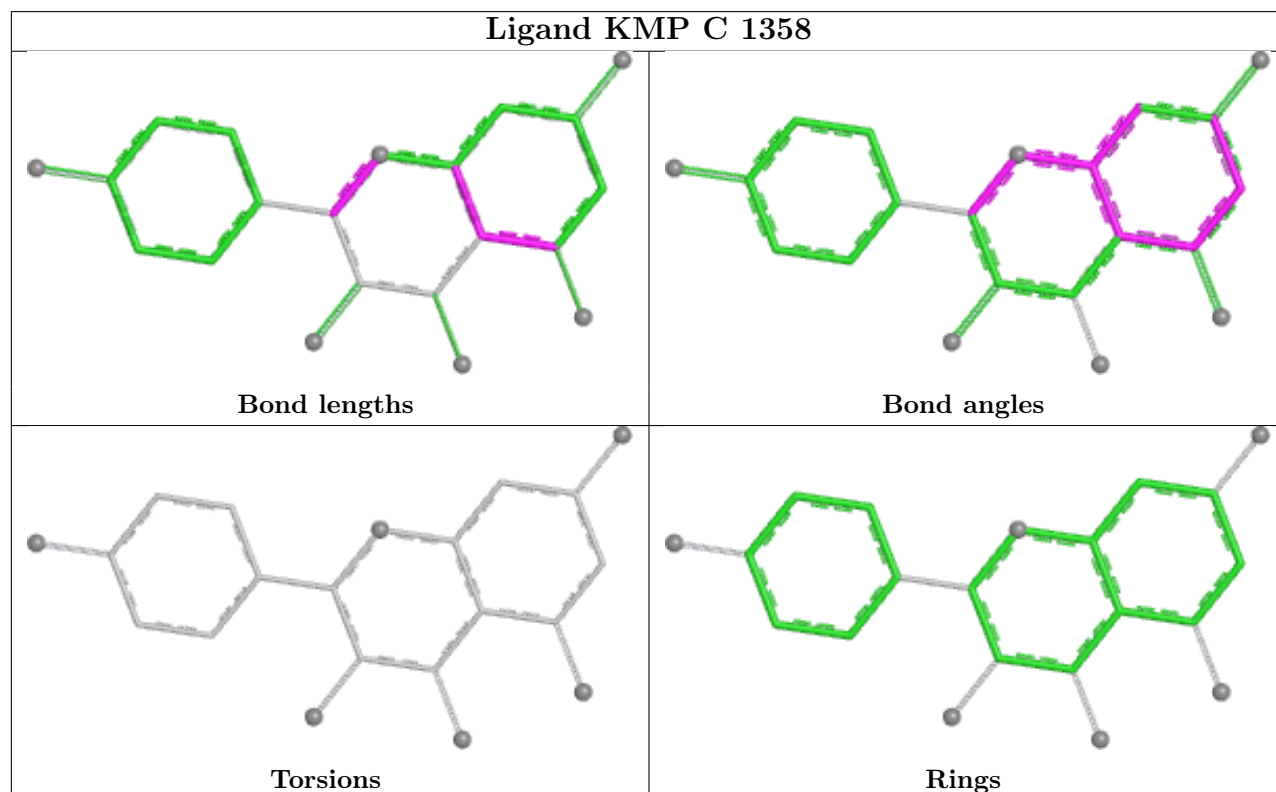
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1358	KMP	1	0
5	C	1355	NAG	4	0
8	B	1360	MPD	5	0
8	A	1362	MPD	4	0
8	C	1360	MPD	6	0
6	A	1360	KMP	1	0
8	B	1361	MPD	6	0

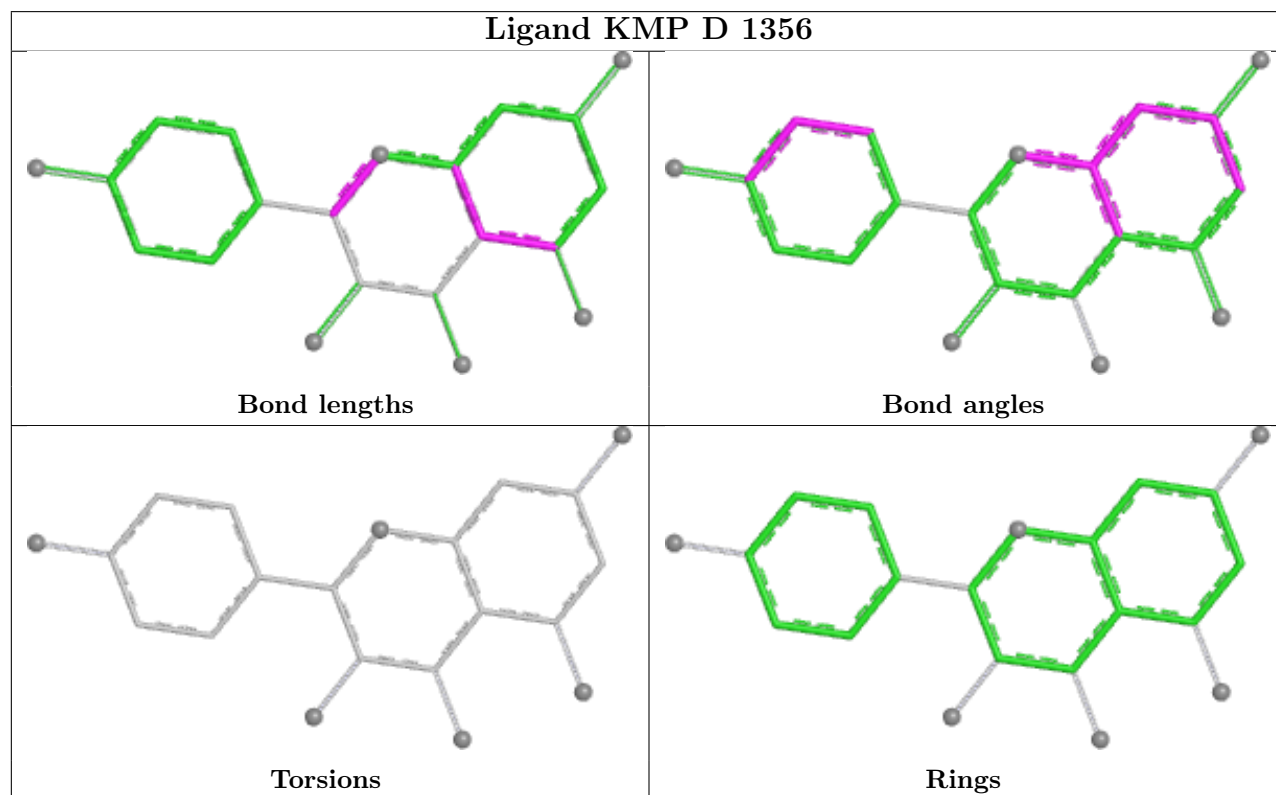
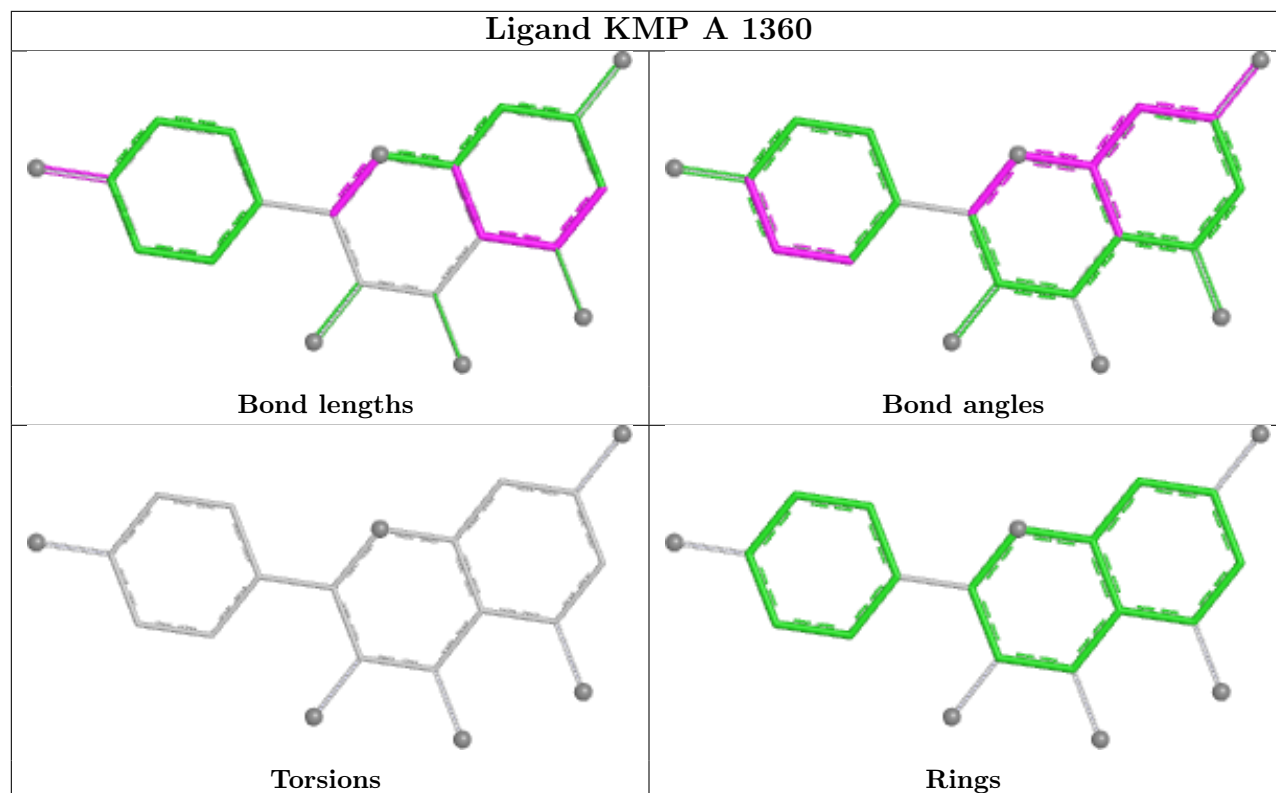
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 KMP B 1358



## Ligand KMP C 1358





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

**Warning:** The R factor obtained from EDS is 0.2613, which does not match the depositor's R factor of 0.154. Please interpret the results in this section carefully.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	344/350 (98%)	-0.23	2 (0%) 85 87	4, 9, 16, 30	5 (1%)
1	B	344/350 (98%)	-0.13	4 (1%) 76 78	3, 9, 17, 31	4 (1%)
1	C	343/350 (98%)	-0.07	8 (2%) 61 63	3, 9, 17, 31	4 (1%)
1	D	343/350 (98%)	4.88	337 (98%) 0 0	4, 9, 16, 31	5 (1%)
All	All	1374/1400 (98%)	1.11	351 (25%) 2 2	3, 9, 17, 31	18 (1%)

All (351) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	159	SER	17.8
1	D	160	SER	17.6
1	D	4	SER	13.2
1	D	262	THR	11.9
1	D	166	SER	11.6
1	D	154	SER	10.8
1	D	171	THR	10.3
1	D	70	LYS	9.9
1	D	162	THR	9.9
1	D	169	ILE	9.6
1	D	163	GLY	8.5
1	D	261	SER	8.3
1	D	168	THR	8.1
1	D	181	LEU	8.1
1	D	165	ASP	8.0
1	D	289	ASP	8.0
1	D	80	GLY	7.7
1	D	31	ASP	7.6
1	D	164	PRO	7.6

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Mol	Chain	Res	Type	RSRZ
1	D	190	VAL	7.5
1	D	161	THR	7.4
1	D	170	SER	7.4
1	D	77	CYS	7.4
1	D	115	GLN	7.3
1	D	117	GLN	7.3
1	D	217	ILE	7.3
1	D	97	VAL	7.2
1	D	263	VAL	7.2
1	D	64	LEU	7.2
1	D	58	SER	7.2
1	D	37	PHE	7.2
1	D	78[D]	ASN	7.1
1	D	138	TYR	7.1
1	D	67	ILE	7.0
1	D	116	ILE	7.0
1	D	172	LEU	7.0
1	D	196	ALA	6.9
1	D	29	THR	6.9
1	D	137	TYR	6.9
1	D	143	ALA	6.6
1	D	22	TYR	6.6
1	D	51	MET	6.6
1	D	216	PHE	6.6
1	D	127	ILE	6.5
1	D	82	PHE	6.5
1	D	182	SER	6.5
1	D	60	ALA	6.5
1	D	183	PHE	6.5
1	D	167	SER	6.5
1	D	34	LEU	6.5
1	D	173	GLN	6.4
1	D	75	PHE	6.4
1	D	35	TYR	6.4
1	D	90	ASN	6.4
1	D	120	ASP	6.4
1	D	114	PHE	6.3
1	D	177	VAL	6.3
1	D	225	TYR	6.3
1	D	153	PRO	6.3
1	D	132	PHE	6.3
1	D	98	LEU	6.3

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Mol	Chain	Res	Type	RSRZ
1	D	189	THR	6.3
1	D	350	TRP	6.3
1	D	152	ILE	6.3
1	D	124	THR	6.1
1	D	207	LEU	6.1
1	D	61	LEU	6.0
1	D	135	LEU	6.0
1	D	141	THR	6.0
1	D	109[A]	ASN	5.9
1	D	28	VAL	5.9
1	D	76	TYR	5.9
1	D	128	VAL	5.9
1	D	230	TYR	5.9
1	D	175	PHE	5.9
1	D	63	VAL	5.9
1	D	323	VAL	5.9
1	D	59	ASP	5.9
1	D	47	ALA	5.8
1	D	113	THR	5.8
1	D	151	TYR	5.8
1	D	184	THR	5.8
1	D	211	ALA	5.8
1	D	53	THR	5.8
1	D	291	ALA	5.7
1	D	199	VAL	5.7
1	D	85	TRP	5.7
1	D	32	THR	5.6
1	D	55	ALA	5.6
1	D	81	SER	5.6
1	D	106	VAL	5.6
1	D	215	TYR	5.6
1	D	218	ALA	5.6
1	D	30	VAL	5.6
1	D	38	TYR	5.5
1	D	89	GLY	5.5
1	D	110	VAL	5.5
1	D	241	ALA	5.5
1	D	73	GLU	5.5
1	D	69	GLN	5.5
1	D	43[A]	SER	5.5
1	D	210	THR	5.5
1	D	84	LEU	5.4

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Mol	Chain	Res	Type	RSRZ
1	D	23	SER	5.4
1	D	14	VAL	5.4
1	D	111	THR	5.4
1	D	214	PRO	5.4
1	D	208	ALA	5.4
1	D	321	LEU	5.3
1	D	54	ASN	5.3
1	D	288	GLY	5.3
1	D	27	ALA	5.3
1	D	146	THR	5.3
1	D	328	ASP	5.3
1	D	269	SER	5.3
1	D	6	ILE	5.3
1	D	95	THR	5.3
1	D	194	ALA	5.3
1	D	86	ALA	5.2
1	D	17	TYR	5.2
1	D	136	PHE	5.2
1	D	187	THR	5.2
1	D	39	VAL	5.1
1	D	126	VAL	5.1
1	D	178	TYR	5.1
1	D	68	HIS	5.1
1	D	121	THR	5.1
1	D	188	ASP	5.1
1	D	276	PHE	5.0
1	D	209	SER	5.0
1	D	123	MET	5.0
1	D	25	ALA	5.0
1	D	308	GLU	5.0
1	D	57	HIS	4.9
1	D	100	SER	4.9
1	D	286	GLN	4.9
1	D	56	PRO	4.9
1	D	62	GLY	4.9
1	D	193	THR	4.9
1	D	198	THR	4.9
1	D	310	LYS	4.9
1	D	8[A]	GLU	4.8
1	D	202	THR	4.8
1	D	247	THR	4.8
1	D	278	VAL	4.8

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Mol	Chain	Res	Type	RSRZ
1	D	48	PHE	4.8
1	D	131	GLY	4.8
1	D	197	ASN	4.8
1	D	24	HIS	4.8
1	D	249	TYR	4.8
1	D	50	LEU	4.8
1	D	142	ASN	4.8
1	D	236	ALA	4.8
1	D	340	GLU	4.7
1	D	139	LEU	4.7
1	D	191	ASN	4.7
1	D	99	SER	4.7
1	D	342[A]	SER	4.7
1	D	134	ASP	4.7
1	D	238	PHE	4.6
1	D	83	GLN	4.6
1	D	179	ALA	4.6
1	D	212	GLY	4.6
1	D	254	ILE	4.6
1	D	245	GLN	4.6
1	D	150	PRO	4.6
1	D	309	PHE	4.6
1	D	72	TYR	4.6
1	D	40	THR	4.5
1	D	46	TYR	4.5
1	D	221	TRP	4.5
1	D	219	ASN	4.5
1	D	33	GLN	4.5
1	D	326	GLY	4.5
1	D	329	GLY	4.5
1	D	49	THR	4.5
1	D	87	GLN	4.5
1	D	195	PRO	4.4
1	D	300	VAL	4.4
1	D	101	GLY	4.4
1	D	213	ASP	4.4
1	D	239	VAL	4.4
1	D	71	HIS	4.4
1	D	149	THR	4.4
1	D	66	HIS	4.4
1	D	335	VAL	4.4
1	D	118	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	253	THR	4.3
1	D	103	TYR	4.3
1	D	180	GLU	4.3
1	D	229	GLN	4.3
1	D	140	GLY	4.3
1	D	192	GLY	4.3
1	D	200	TRP	4.3
1	D	144	THR	4.3
1	D	234	ILE	4.3
1	D	292	ALA	4.3
1	D	45	GLY	4.3
1	D	102	ASP	4.3
1	D	5	LEU	4.3
1	D	293	THR	4.3
1	D	327	SER	4.2
1	D	301	ALA	4.2
1	D	104	GLY	4.2
1	D	130	GLY	4.2
1	D	264	THR	4.2
1	D	41	GLY	4.2
1	D	244	ALA	4.2
1	D	251	LEU	4.2
1	D	147	THR	4.2
1	D	250	THR	4.2
1	D	344	VAL	4.2
1	D	74	ASN	4.2
1	D	79	LYS	4.2
1	D	185	PRO	4.2
1	D	298	GLY	4.2
1	D	268	TRP	4.2
1	D	92	THR	4.2
1	D	65	PRO	4.2
1	D	252	SER	4.1
1	D	312	TYR	4.1
1	D	176	ASP	4.1
1	D	119	PRO	4.1
1	D	52	GLY	4.1
1	D	9	ASP	4.0
1	D	246	ASP	4.0
1	D	275	ALA	4.0
1	D	297	SER	4.0
1	D	93	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
1	D	10	ALA	4.0
1	D	112	HIS	4.0
1	D	274	CYS	4.0
1	D	322	PHE	4.0
1	D	91	GLU	4.0
1	D	125	GLY	4.0
1	D	122	GLU	3.9
1	D	317	PHE	3.9
1	D	129	PRO	3.9
1	D	307	VAL	3.9
1	D	273	ALA	3.9
1	D	299	ASP	3.9
1	D	26	ARG	3.9
1	D	242	THR	3.9
1	D	36	ARG	3.8
1	D	302	PHE	3.8
1	D	324	SER	3.8
1	D	96	ARG	3.8
1	D	320	VAL	3.8
1	D	290	TYR	3.8
1	D	224	LYS	3.8
1	D	223	PRO	3.8
1	D	12	ASP	3.8
1	D	88	SER	3.8
1	D	334	LEU	3.8
1	D	204	ALA	3.8
1	D	240	THR	3.8
1	D	325	SER	3.7
1	D	205	ASN	3.7
1	D	270	PHE	3.7
1	D	19	ILE	3.7
1	D	222	GLY	3.7
1	D	303	ILE	3.7
1	D	174	SER	3.7
1	D	235	VAL	3.7
1	D	107	PRO	3.7
1	D	314	GLU	3.7
1	D	201	HIS	3.7
1	D	186	ARG	3.7
1	D	206	ALA	3.7
1	D	341	TRP	3.7
1	D	336	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	296	GLY	3.7
1	D	319	LYS	3.7
1	C	197	ASN	3.6
1	D	259	THR	3.6
1	D	287	ILE	3.6
1	D	145	ASP	3.6
1	D	21	HIS	3.6
1	D	260	PRO	3.5
1	D	330	LEU	3.5
1	D	338	GLY	3.4
1	D	11	PRO	3.4
1	D	13	HIS	3.4
1	D	42	PRO	3.4
1	D	237	PRO	3.4
1	D	232	TYR	3.4
1	D	265	VAL	3.4
1	A	90	ASN	3.3
1	D	256	MET	3.3
1	D	7	VAL	3.2
1	D	304	PRO	3.2
1	D	243	GLN	3.2
1	D	305	GLY	3.2
1	D	105	SER	3.2
1	D	295	LEU	3.2
1	D	345	SER	3.2
1	D	228	SER	3.1
1	D	318	SER	3.1
1	D	44	SER	3.1
1	D	94	GLN	3.1
1	D	248	ASN	3.1
1	D	15	ARG	3.1
1	D	220	GLY	3.1
1	D	281	GLY	3.1
1	D	279	GLN	3.1
1	D	333	ASN	3.0
1	D	311	TYR	3.0
1	D	133	GLU	3.0
1	D	266	PRO	3.0
1	B	159	SER	3.0
1	D	226	LEU	3.0
1	D	258	THR	3.0
1	D	271	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	203	GLY	2.9
1	D	283	VAL	2.9
1	D	255	SER	2.9
1	D	337	GLY	2.8
1	D	284	VAL	2.8
1	D	331	ASP	2.8
1	D	108	ARG	2.8
1	D	332	GLN	2.8
1	C	4	SER	2.8
1	D	231	GLY	2.7
1	A	3	SER	2.7
1	D	272	GLY	2.7
1	D	339	GLU	2.7
1	D	18	VAL	2.7
1	D	285	VAL	2.7
1	C	289	ASP	2.7
1	D	148	HIS	2.6
1	D	306	GLY	2.6
1	B	3	SER	2.6
1	C	161	THR	2.6
1	D	267	THR	2.5
1	D	16	PRO	2.5
1	C	169	ILE	2.5
1	D	315	ALA	2.5
1	D	277	GLN	2.5
1	D	227	ASN	2.5
1	D	346	PHE	2.5
1	D	20	ARG	2.4
1	B	168	THR	2.4
1	D	313	SER	2.3
1	C	171	THR	2.2
1	D	343	SER	2.2
1	C	167	SER	2.2
1	D	316	TYR	2.2
1	D	280	GLU	2.1
1	B	169	ILE	2.1
1	D	233	GLN	2.0
1	C	89	GLY	2.0

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

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

## 6.3 Carbohydrates

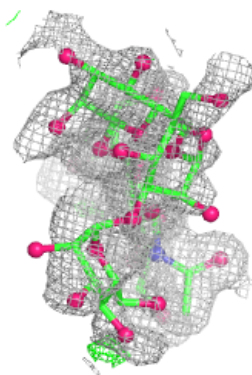
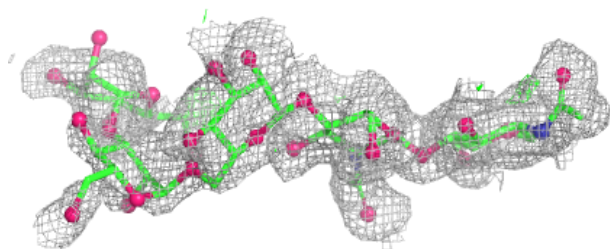
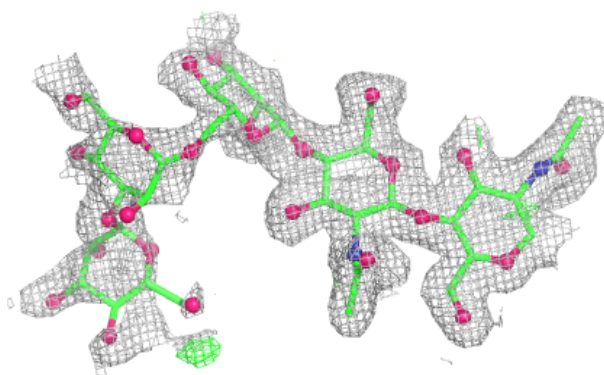
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MAN	E	5	11/12	0.34	0.21	67,68,68,69	0
3	MAN	F	4	11/12	0.53	0.18	61,62,64,65	0
2	MAN	E	4	11/12	0.58	0.18	60,61,62,65	0
3	BMA	F	3	11/12	0.66	0.14	46,48,54,59	0
3	MAN	G	4	11/12	0.66	0.15	43,46,48,49	0
2	BMA	E	3	11/12	0.67	0.15	45,48,54,58	0
3	NAG	F	2	14/15	0.79	0.12	24,32,40,44	0
3	BMA	G	3	11/12	0.82	0.11	35,41,43,44	0
4	NAG	H	2	14/15	0.86	0.10	18,29,34,35	0
2	NAG	E	1	14/15	0.87	0.09	19,25,28,30	0
3	NAG	F	1	14/15	0.87	0.09	21,24,29,31	0
3	NAG	G	1	14/15	0.90	0.09	19,23,34,36	0
2	NAG	E	2	14/15	0.90	0.09	24,29,35,39	0
4	NAG	H	1	14/15	0.91	0.08	20,25,31,33	0
3	NAG	G	2	14/15	0.91	0.08	21,25,30,33	0

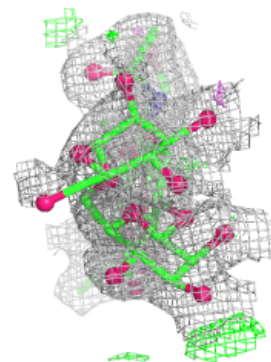
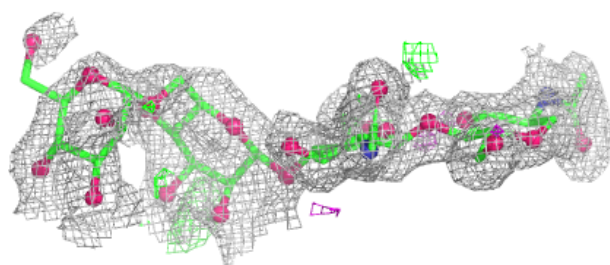
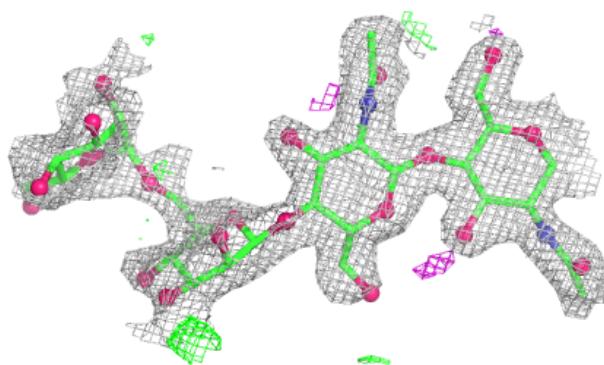
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain E:**

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

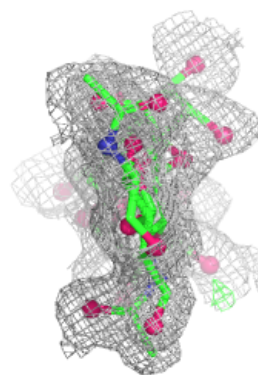
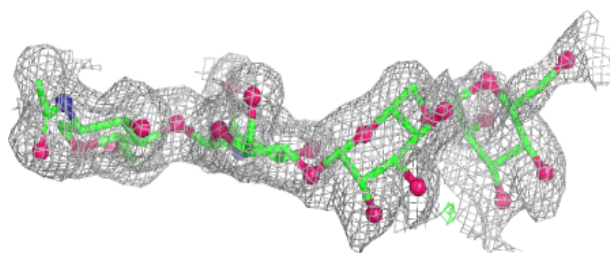
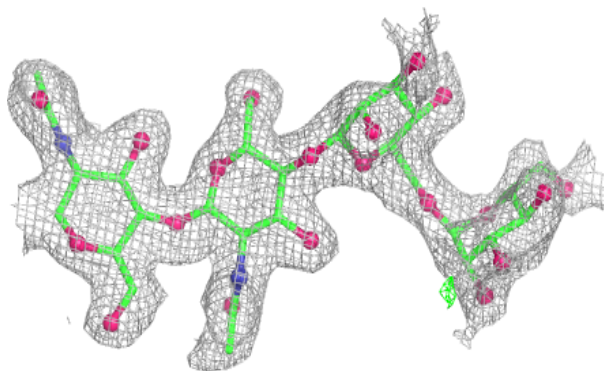
**Electron density around Chain F:**

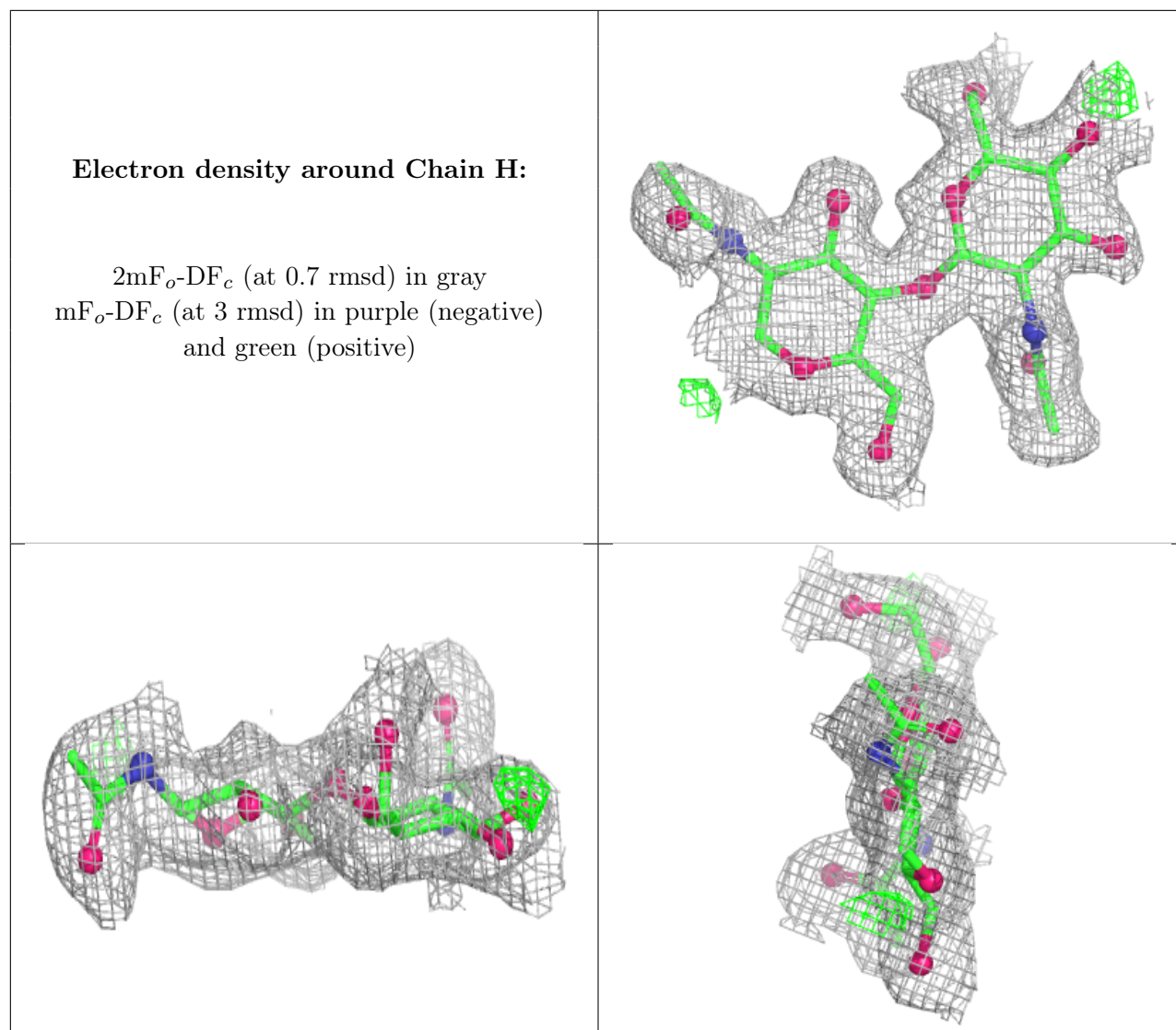
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain G:**

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





## 6.4 Ligands [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	KMP	D	1356	21/21	0.39	0.31	12,16,18,19	0
7	CU	D	1357	1/1	0.48	0.45	11,11,11,11	0
5	NAG	B	1355	14/15	0.70	0.14	31,41,44,47	0
5	NAG	C	1355	14/15	0.70	0.17	34,44,49,49	0
8	MPD	B	1360	8/8	0.75	0.15	24,34,37,39	0
5	NAG	A	1356	14/15	0.76	0.12	26,33,36,39	0
5	NAG	D	1355	14/15	0.77	0.13	27,35,44,46	0

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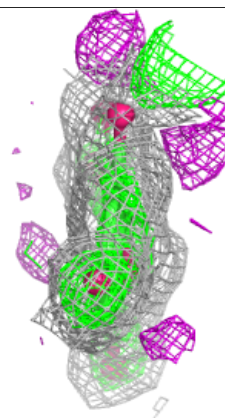
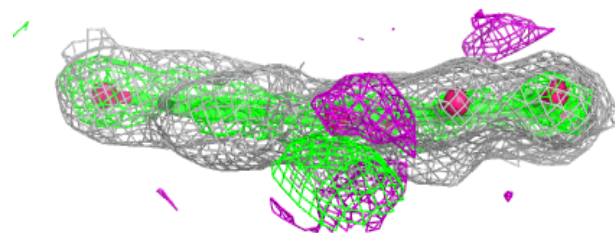
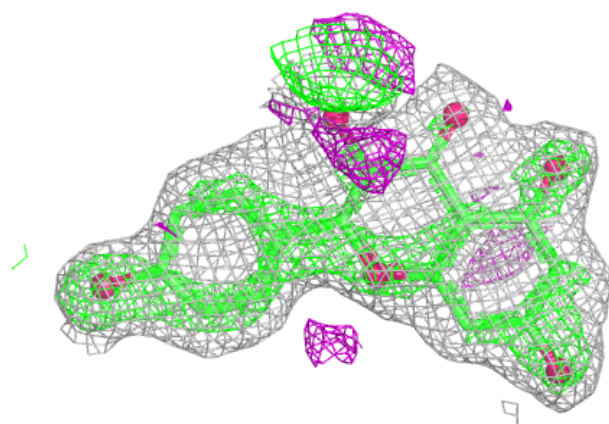
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	1355	14/15	0.79	0.12	28,37,44,46	0
5	NAG	D	1351	14/15	0.80	0.12	30,40,42,44	0
5	NAG	C	1354	14/15	0.81	0.12	28,36,46,47	0
8	MPD	B	1361	8/8	0.81	0.16	26,36,39,43	0
5	NAG	C	1351	14/15	0.82	0.12	27,34,40,43	0
8	MPD	A	1362	8/8	0.82	0.15	20,29,31,34	0
8	MPD	C	1360	8/8	0.82	0.15	24,34,38,42	0
5	NAG	D	1354	14/15	0.84	0.10	22,28,32,36	0
5	NAG	A	1351	14/15	0.85	0.10	26,32,39,39	0
5	NAG	B	1351	14/15	0.86	0.10	23,32,34,35	0
5	NAG	A	1354	14/15	0.88	0.10	20,32,41,41	0
6	KMP	A	1360	21/21	0.89	0.09	11,14,19,20	0
5	NAG	B	1354	14/15	0.90	0.09	22,31,42,43	0
6	KMP	B	1358	21/21	0.91	0.07	15,18,21,21	0
6	KMP	C	1358	21/21	0.91	0.07	17,18,20,23	0
7	CU	B	1359	1/1	0.99	0.03	10,10,10,10	0
7	CU	C	1359	1/1	1.00	0.06	11,11,11,11	0
7	CU	A	1361	1/1	1.00	0.03	9,9,9,9	0

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

**Electron density around KMP D 1356:**

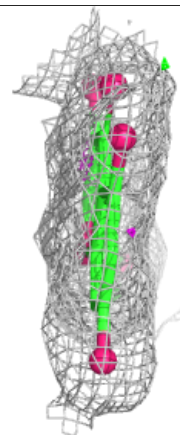
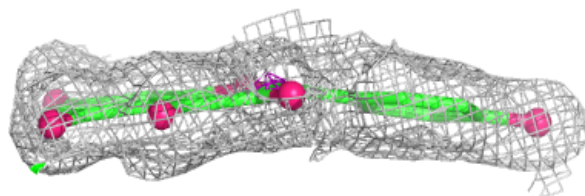
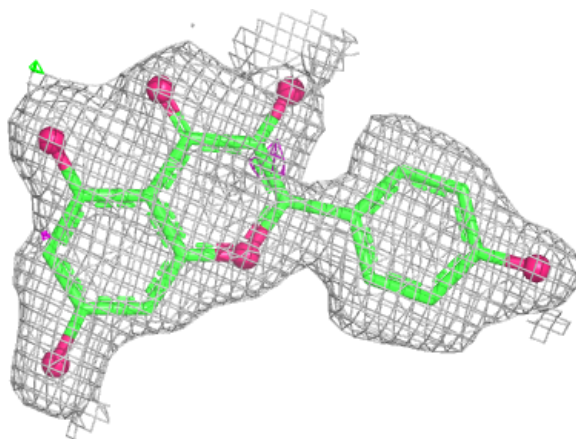
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around KMP A 1360:**

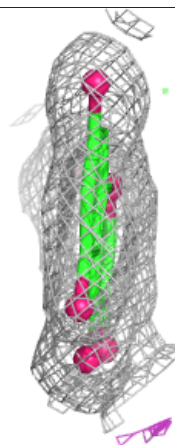
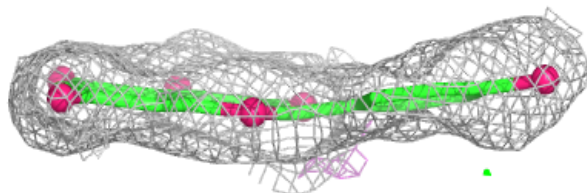
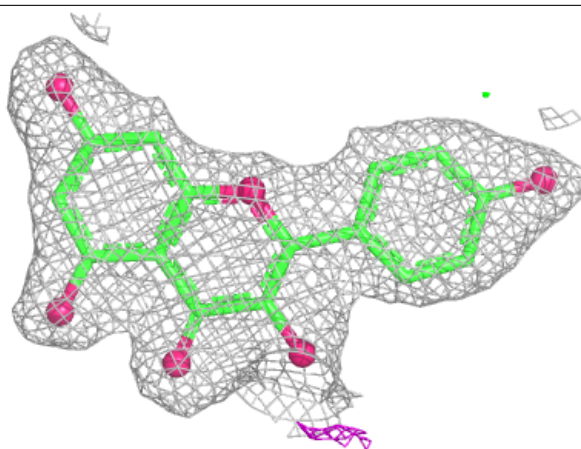
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





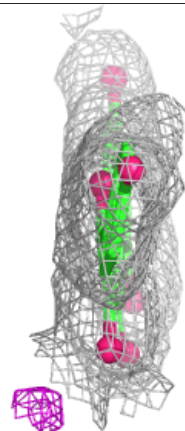
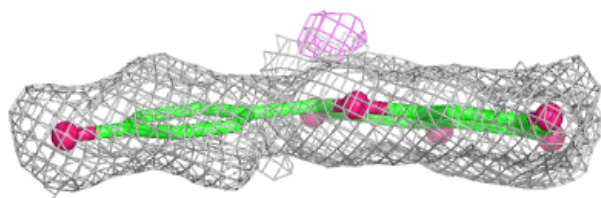
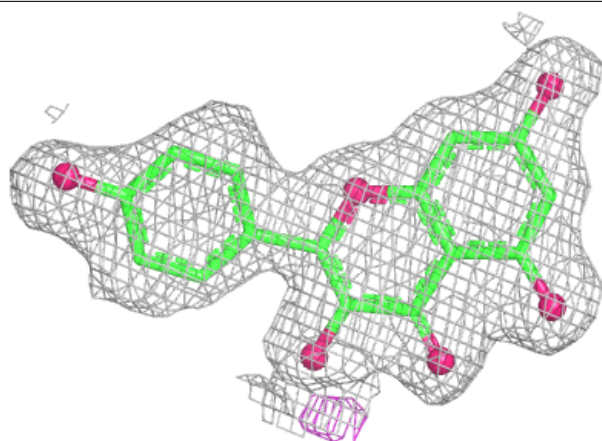
**Electron density around KMP B 1358:**

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



**Electron density around KMP C 1358:**

$2mF_o - DF_c$  (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.