



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:49 AM UTC

PDB ID : 7FQK / pdb_00007fqk
Title : Crystal Structure of human Legumain in complex with (2S)-N-[(3S)-5-amino-1-(1,3-oxazol-2-yl)-5-oxopent-1-yn-3-yl]-1-[1-[4-(trifluoromethoxy)phenyl]cyclopropanecarbonyl]pyrrolidine-2-carboxamide
Authors : Ehler, A.; Benz, J.; Bartels, B.; Rudolph, M.G.
Deposited on : 2022-10-05
Resolution : 1.97 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:

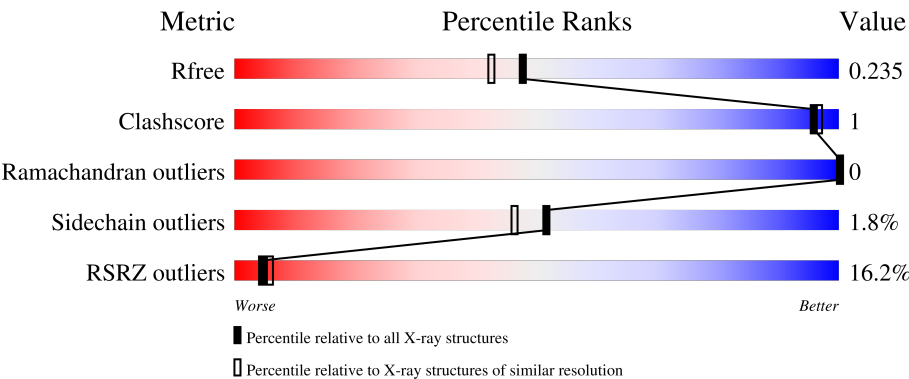
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

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

The reported resolution of this entry is 1.97 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	444	10% 55% 41%
1	B	444	10% 55% 41%
1	C	444	8% 54% 5% 41%
1	D	444	10% 54% 5% 41%

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Mol	Chain	Length	Quality of chain
2	E	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9215 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 Legumain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2114	1335	361	403	15			
1	B	261	Total	C	N	O	S	0	0	0
			2094	1323	355	401	15			
1	C	262	Total	C	N	O	S	0	0	0
			2103	1329	357	402	15			
1	D	262	Total	C	N	O	S	0	2	0
			2117	1338	361	403	15			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q99538
A	1	LYS	-	expression tag	UNP Q99538
A	2	LEU	-	expression tag	UNP Q99538
A	3	CYS	-	expression tag	UNP Q99538
A	4	ILE	-	expression tag	UNP Q99538
A	5	LEU	-	expression tag	UNP Q99538
A	6	LEU	-	expression tag	UNP Q99538
A	7	ALA	-	expression tag	UNP Q99538
A	8	VAL	-	expression tag	UNP Q99538
A	9	VAL	-	expression tag	UNP Q99538
A	10	ALA	-	expression tag	UNP Q99538
A	11	PHE	-	expression tag	UNP Q99538
A	12	VAL	-	expression tag	UNP Q99538
A	13	GLY	-	expression tag	UNP Q99538
A	14	LEU	-	expression tag	UNP Q99538
A	15	SER	-	expression tag	UNP Q99538
A	16	LEU	-	expression tag	UNP Q99538
A	17	GLY	-	expression tag	UNP Q99538
A	147	SNN	ASP	conflict	UNP Q99538
A	272	GLN	ASN	conflict	UNP Q99538
A	434	VAL	-	expression tag	UNP Q99538

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Chain	Residue	Modelled	Actual	Comment	Reference
A	435	ASP	-	expression tag	UNP Q99538
A	436	HIS	-	expression tag	UNP Q99538
A	437	HIS	-	expression tag	UNP Q99538
A	438	HIS	-	expression tag	UNP Q99538
A	439	HIS	-	expression tag	UNP Q99538
A	440	HIS	-	expression tag	UNP Q99538
A	441	HIS	-	expression tag	UNP Q99538
A	442	HIS	-	expression tag	UNP Q99538
A	443	HIS	-	expression tag	UNP Q99538
B	0	MET	-	initiating methionine	UNP Q99538
B	1	LYS	-	expression tag	UNP Q99538
B	2	LEU	-	expression tag	UNP Q99538
B	3	CYS	-	expression tag	UNP Q99538
B	4	ILE	-	expression tag	UNP Q99538
B	5	LEU	-	expression tag	UNP Q99538
B	6	LEU	-	expression tag	UNP Q99538
B	7	ALA	-	expression tag	UNP Q99538
B	8	VAL	-	expression tag	UNP Q99538
B	9	VAL	-	expression tag	UNP Q99538
B	10	ALA	-	expression tag	UNP Q99538
B	11	PHE	-	expression tag	UNP Q99538
B	12	VAL	-	expression tag	UNP Q99538
B	13	GLY	-	expression tag	UNP Q99538
B	14	LEU	-	expression tag	UNP Q99538
B	15	SER	-	expression tag	UNP Q99538
B	16	LEU	-	expression tag	UNP Q99538
B	17	GLY	-	expression tag	UNP Q99538
B	147	SNN	ASP	conflict	UNP Q99538
B	272	GLN	ASN	conflict	UNP Q99538
B	434	VAL	-	expression tag	UNP Q99538
B	435	ASP	-	expression tag	UNP Q99538
B	436	HIS	-	expression tag	UNP Q99538
B	437	HIS	-	expression tag	UNP Q99538
B	438	HIS	-	expression tag	UNP Q99538
B	439	HIS	-	expression tag	UNP Q99538
B	440	HIS	-	expression tag	UNP Q99538
B	441	HIS	-	expression tag	UNP Q99538
B	442	HIS	-	expression tag	UNP Q99538
B	443	HIS	-	expression tag	UNP Q99538
C	0	MET	-	initiating methionine	UNP Q99538
C	1	LYS	-	expression tag	UNP Q99538
C	2	LEU	-	expression tag	UNP Q99538

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Chain	Residue	Modelled	Actual	Comment	Reference
C	3	CYS	-	expression tag	UNP Q99538
C	4	ILE	-	expression tag	UNP Q99538
C	5	LEU	-	expression tag	UNP Q99538
C	6	LEU	-	expression tag	UNP Q99538
C	7	ALA	-	expression tag	UNP Q99538
C	8	VAL	-	expression tag	UNP Q99538
C	9	VAL	-	expression tag	UNP Q99538
C	10	ALA	-	expression tag	UNP Q99538
C	11	PHE	-	expression tag	UNP Q99538
C	12	VAL	-	expression tag	UNP Q99538
C	13	GLY	-	expression tag	UNP Q99538
C	14	LEU	-	expression tag	UNP Q99538
C	15	SER	-	expression tag	UNP Q99538
C	16	LEU	-	expression tag	UNP Q99538
C	17	GLY	-	expression tag	UNP Q99538
C	147	SNN	ASP	conflict	UNP Q99538
C	272	GLN	ASN	conflict	UNP Q99538
C	434	VAL	-	expression tag	UNP Q99538
C	435	ASP	-	expression tag	UNP Q99538
C	436	HIS	-	expression tag	UNP Q99538
C	437	HIS	-	expression tag	UNP Q99538
C	438	HIS	-	expression tag	UNP Q99538
C	439	HIS	-	expression tag	UNP Q99538
C	440	HIS	-	expression tag	UNP Q99538
C	441	HIS	-	expression tag	UNP Q99538
C	442	HIS	-	expression tag	UNP Q99538
C	443	HIS	-	expression tag	UNP Q99538
D	0	MET	-	initiating methionine	UNP Q99538
D	1	LYS	-	expression tag	UNP Q99538
D	2	LEU	-	expression tag	UNP Q99538
D	3	CYS	-	expression tag	UNP Q99538
D	4	ILE	-	expression tag	UNP Q99538
D	5	LEU	-	expression tag	UNP Q99538
D	6	LEU	-	expression tag	UNP Q99538
D	7	ALA	-	expression tag	UNP Q99538
D	8	VAL	-	expression tag	UNP Q99538
D	9	VAL	-	expression tag	UNP Q99538
D	10	ALA	-	expression tag	UNP Q99538
D	11	PHE	-	expression tag	UNP Q99538
D	12	VAL	-	expression tag	UNP Q99538
D	13	GLY	-	expression tag	UNP Q99538
D	14	LEU	-	expression tag	UNP Q99538

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Chain	Residue	Modelled	Actual	Comment	Reference
D	15	SER	-	expression tag	UNP Q99538
D	16	LEU	-	expression tag	UNP Q99538
D	17	GLY	-	expression tag	UNP Q99538
D	147	SNN	ASP	conflict	UNP Q99538
D	272	GLN	ASN	conflict	UNP Q99538
D	434	VAL	-	expression tag	UNP Q99538
D	435	ASP	-	expression tag	UNP Q99538
D	436	HIS	-	expression tag	UNP Q99538
D	437	HIS	-	expression tag	UNP Q99538
D	438	HIS	-	expression tag	UNP Q99538
D	439	HIS	-	expression tag	UNP Q99538
D	440	HIS	-	expression tag	UNP Q99538
D	441	HIS	-	expression tag	UNP Q99538
D	442	HIS	-	expression tag	UNP Q99538
D	443	HIS	-	expression tag	UNP Q99538

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



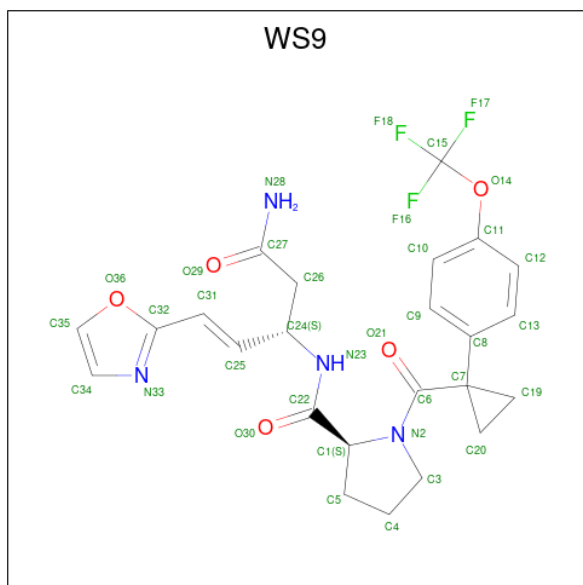
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



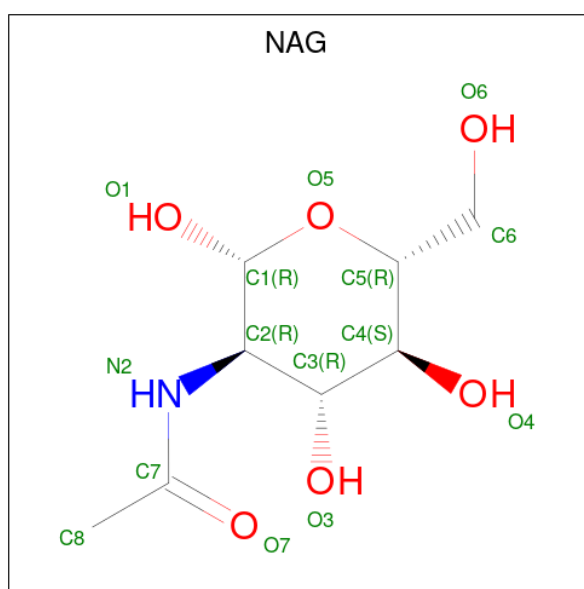
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is N-[(1E,3R)-5-amino-1-(1,3-oxazol-2-yl)-5-oxopent-1-en-3-yl]-1-{1-[4-(trifluoromethoxy)phenyl]cyclopropane-1-carbonyl}-L-prolinamide (CCD ID: WS9) (formula: $C_{24}H_{25}F_3N_4O_5$) (labeled as "Ligand of Interest" by depositor).



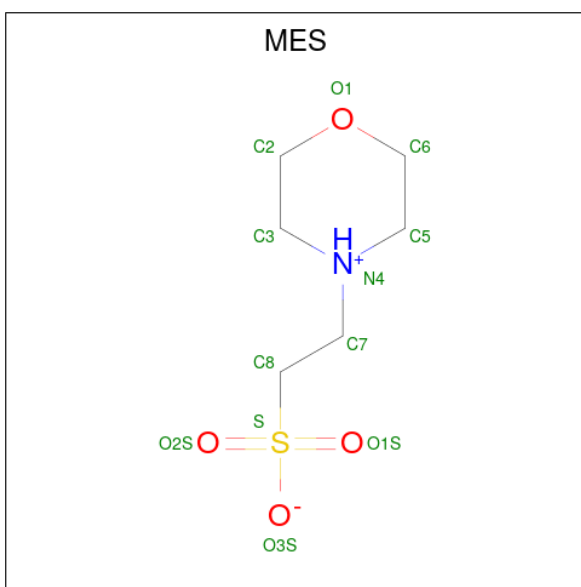
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			36	24	3	4	5		
4	B	1	Total	C	F	N	O	0	0
			36	24	3	4	5		
4	C	1	Total	C	F	N	O	0	0
			36	24	3	4	5		
4	D	1	Total	C	F	N	O	0	0
			36	24	3	4	5		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: 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	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	D	1	Total	C	N	O	0	0
			14	8	1	5		

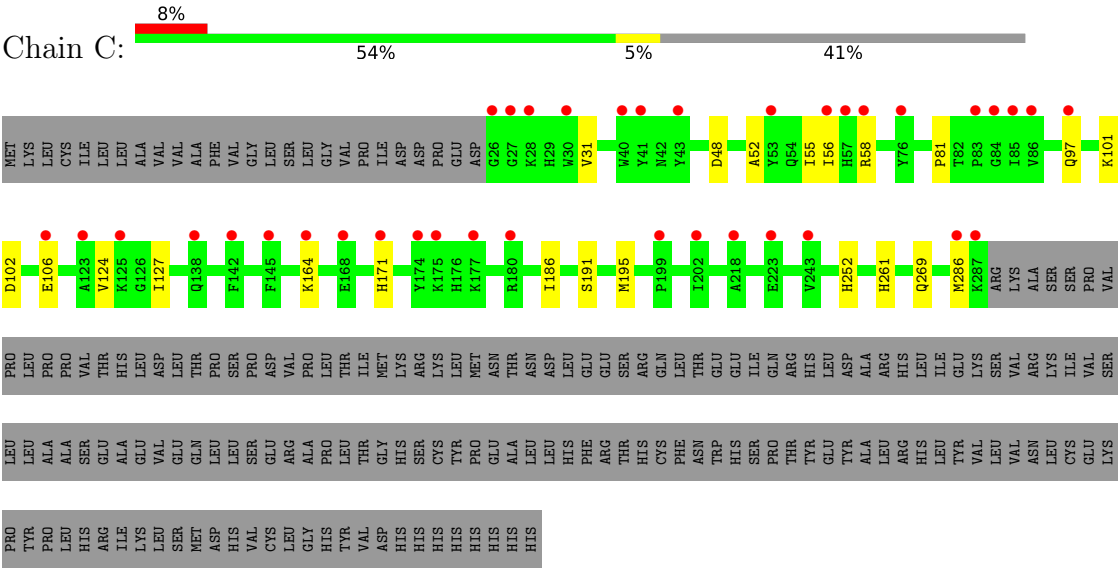
- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



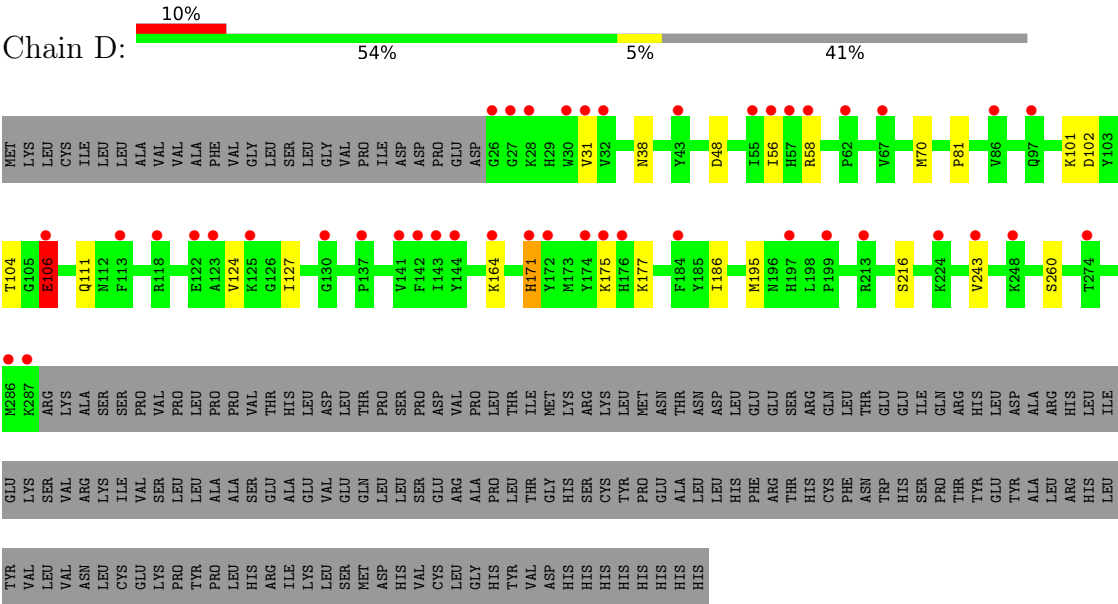
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is water.

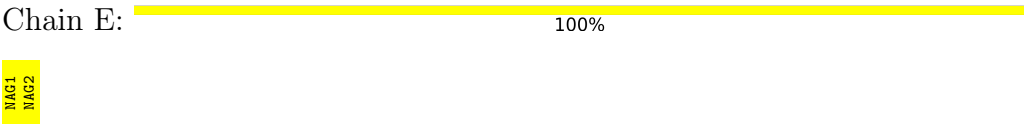
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	136	Total	O	0	0
			136	136		
7	B	126	Total	O	0	0
			126	126		
7	C	141	Total	O	0	0
			141	141		
7	D	134	Total	O	0	0
			134	134		



● Molecule 1: Legumain



● Molecule 2: 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 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.49Å 102.49Å 330.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.13 – 1.97 87.13 – 1.97	Depositor EDS
% Data completeness (in resolution range)	41.7 (87.13-1.97) 41.7 (87.13-1.97)	Depositor EDS
R_{merge}	0.53	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.194 , 0.233 0.199 , 0.235	Depositor DCC
R_{free} test set	2736 reflections (2.18%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9215	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.25% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: WS9, EDO, MES, SNN, 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	1.21	8/2163 (0.4%)	1.22	1/2932 (0.0%)
1	B	1.15	4/2143 (0.2%)	1.23	3/2907 (0.1%)
1	C	1.21	10/2152 (0.5%)	1.22	1/2918 (0.0%)
1	D	1.18	8/2172 (0.4%)	1.22	2/2945 (0.1%)
All	All	1.19	30/8630 (0.3%)	1.22	7/11702 (0.1%)

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	252	HIS	CE1-NE2	8.60	1.41	1.32
1	C	252	HIS	CE1-NE2	8.25	1.40	1.32
1	B	58	ARG	C-O	-7.16	1.15	1.24
1	C	261	HIS	CE1-NE2	7.01	1.39	1.32
1	B	81	PRO	C-O	-6.98	1.15	1.24
1	D	243	VAL	C-O	-6.89	1.17	1.24
1	C	58	ARG	C-O	-6.67	1.16	1.24
1	A	58	ARG	C-O	-6.42	1.16	1.24
1	D	58	ARG	C-O	-6.40	1.16	1.24
1	A	261	HIS	CE1-NE2	6.32	1.38	1.32
1	C	102	ASP	C-O	-6.07	1.17	1.24
1	D	81	PRO	C-O	-5.95	1.16	1.24
1	C	55	ILE	C-O	-5.70	1.17	1.24
1	B	265	SER	C-O	5.58	1.30	1.23
1	B	267	VAL	C-O	-5.57	1.18	1.24
1	C	81	PRO	C-O	-5.57	1.17	1.24
1	D	102	ASP	C-O	-5.57	1.17	1.24
1	A	40	TRP	C-O	-5.56	1.17	1.24
1	A	183	VAL	C-O	-5.54	1.18	1.24
1	C	97	GLN	C-O	-5.48	1.17	1.24
1	D	175	LYS	C-O	-5.43	1.17	1.24
1	C	269	GLN	C-O	-5.34	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	52	ALA	C-O	-5.29	1.18	1.24
1	D	171	HIS	CG-ND1	5.24	1.44	1.38
1	A	102	ASP	C-O	-5.23	1.18	1.24
1	D	38	ASN	C-O	-5.21	1.17	1.23
1	A	171	HIS	CG-ND1	5.14	1.44	1.38
1	D	260	SER	C-O	-5.11	1.17	1.24
1	A	81	PRO	C-O	-5.06	1.17	1.24
1	C	171	HIS	CG-ND1	5.06	1.43	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	48	ASP	CA-CB-CG	7.24	119.84	112.60
1	A	48	ASP	CA-CB-CG	7.09	119.69	112.60
1	D	106	GLU	CB-CG-CD	6.82	124.19	112.60
1	B	282	GLN	CB-CG-CD	-6.04	102.33	112.60
1	B	48	ASP	CA-CB-CG	5.68	118.28	112.60
1	D	48	ASP	CA-CB-CG	5.34	117.94	112.60
1	B	285	GLY	CA-C-O	-5.09	116.60	121.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2114	0	1997	4	0
1	B	2094	0	1971	4	0
1	C	2103	0	1984	3	0
1	D	2117	0	2005	7	0
2	E	28	0	25	0	0
3	A	4	0	6	0	0
3	B	4	0	6	0	0
3	D	4	0	6	0	0
4	A	36	0	0	0	0
4	B	36	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	36	0	0	0	0
4	D	36	0	0	0	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
5	D	14	0	13	0	0
6	B	12	0	13	0	0
6	D	12	0	13	0	0
7	A	136	0	0	1	0
7	B	126	0	0	0	0
7	C	141	0	0	0	0
7	D	134	0	0	1	0
All	All	9215	0	8065	18	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 1.

All (18) 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:B:28:LYS:HA	1:B:286:MET:HE1	1.88	0.56
1:A:124:VAL:HA	1:A:127:ILE:HD12	1.92	0.52
1:D:106:GLU:H	1:D:106:GLU:CD	2.18	0.51
1:B:124:VAL:HA	1:B:127:ILE:HD12	1.94	0.50
1:B:31:VAL:HG21	1:B:56:ILE:HD12	1.92	0.50
1:C:124:VAL:HA	1:C:127:ILE:HD12	1.94	0.50
1:A:31:VAL:HG21	1:A:56:ILE:HD12	1.95	0.48
1:D:124:VAL:HA	1:D:127:ILE:HD12	1.95	0.48
1:D:111[B]:GLN:NE2	1:D:111[B]:GLN:H	2.11	0.47
1:C:186:ILE:HD11	1:C:195:MET:HE3	1.97	0.46
1:C:31:VAL:HG21	1:C:56:ILE:HD12	1.97	0.46
1:D:31:VAL:HG21	1:D:56:ILE:HD12	1.98	0.46
1:A:131:LYS:NZ	7:A:604:HOH:O	2.50	0.44
1:A:186:ILE:HD11	1:A:195:MET:HE3	2.00	0.44
1:D:186:ILE:HD11	1:D:195:MET:HE3	1.99	0.44
1:D:171:HIS:HB3	7:D:713:HOH:O	2.18	0.44
1:B:186:ILE:HD11	1:B:195:MET:HE3	2.00	0.43
1:D:70:MET:O	1:D:104:THR:HA	2.21	0.41

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	260/444 (59%)	255 (98%)	5 (2%)	0	100	100
1	B	258/444 (58%)	254 (98%)	4 (2%)	0	100	100
1	C	259/444 (58%)	253 (98%)	6 (2%)	0	100	100
1	D	261/444 (59%)	256 (98%)	5 (2%)	0	100	100
All	All	1038/1776 (58%)	1018 (98%)	20 (2%)	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	229/396 (58%)	226 (99%)	3 (1%)	61	57
1	B	227/396 (57%)	224 (99%)	3 (1%)	61	57
1	C	228/396 (58%)	223 (98%)	5 (2%)	45	38
1	D	230/396 (58%)	225 (98%)	5 (2%)	45	38
All	All	914/1584 (58%)	898 (98%)	16 (2%)	51	46

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LYS
1	A	106	GLU

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Mol	Chain	Res	Type
1	A	164	LYS
1	B	101	LYS
1	B	164	LYS
1	B	177	LYS
1	C	101	LYS
1	C	106	GLU
1	C	164	LYS
1	C	191	SER
1	C	286	MET
1	D	101	LYS
1	D	106	GLU
1	D	164	LYS
1	D	177	LYS
1	D	216	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	57	HIS
1	A	158	ASN
1	A	254	GLN
1	A	269	GLN
1	A	284	GLN
1	B	254	GLN
1	B	269	GLN
1	B	284	GLN
1	C	111	GLN
1	C	138	GLN
1	C	254	GLN
1	C	284	GLN
1	D	57	HIS
1	D	254	GLN
1	D	269	GLN
1	D	284	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SNN	A	147	1	5,6,8	1.11	0	1,6,11	0.10	0
1	SNN	D	147	1	5,6,8	1.07	0	1,6,11	0.79	0
1	SNN	C	147	1	5,6,8	1.03	0	1,6,11	0.44	0
1	SNN	B	147	1	5,6,8	1.26	0	1,6,11	0.25	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
1	SNN	A	147	1	-	2/3/5/12	-
1	SNN	D	147	1	-	3/3/5/12	-
1	SNN	C	147	1	-	3/3/5/12	-
1	SNN	B	147	1	-	3/3/5/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	147	SNN	C5-C4-CA-N
1	A	147	SNN	CA-C4-C5-O5
1	B	147	SNN	O-C-CA-C4
1	B	147	SNN	C5-C4-CA-N
1	B	147	SNN	CA-C4-C5-O5
1	C	147	SNN	O-C-CA-C4
1	C	147	SNN	C5-C4-CA-N

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Mol	Chain	Res	Type	Atoms
1	C	147	SNN	CA-C4-C5-O5
1	D	147	SNN	O-C-CA-C4
1	D	147	SNN	CA-C4-C5-O5
1	D	147	SNN	C5-C4-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

2 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	2,1	14,14,15	1.13	0	17,19,21	1.70	4 (23%)
2	NAG	E	2	2	14,14,15	1.84	2 (14%)	17,19,21	1.19	2 (11%)

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	2,1	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	NAG	C1-C2	4.16	1.58	1.52
2	E	2	NAG	C4-C5	2.77	1.58	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	NAG	C1-O5-C5	3.10	116.34	112.19
2	E	1	NAG	C1-C2-N2	-2.80	106.02	110.43
2	E	1	NAG	C2-N2-C7	-2.73	119.24	122.90
2	E	1	NAG	O4-C4-C3	-2.62	104.20	110.38
2	E	2	NAG	C2-N2-C7	-2.47	119.59	122.90
2	E	2	NAG	O4-C4-C5	2.13	114.57	109.32

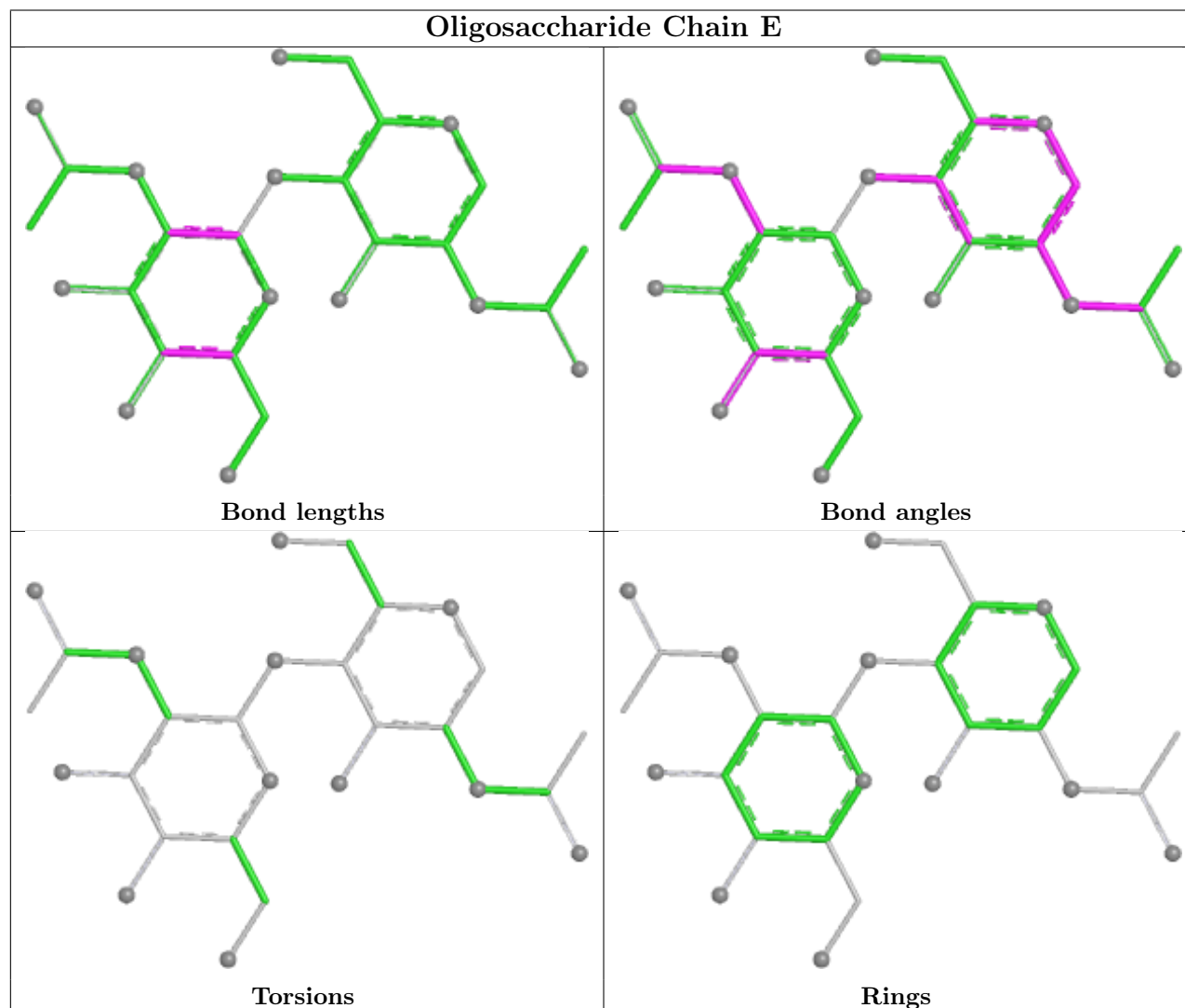
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

12 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	501	-	3,3,3	0.42	0	2,2,2	0.27	0
3	EDO	D	502	-	3,3,3	0.86	0	2,2,2	0.68	0
4	WS9	B	502	1	39,39,39	1.16	1 (2%)	50,57,57	1.73	4 (8%)
5	NAG	B	503	1	14,14,15	1.05	0	17,19,21	1.47	3 (17%)
6	MES	D	501	-	12,12,12	0.57	0	15,16,16	0.53	0
6	MES	B	504	-	12,12,12	0.63	0	15,16,16	0.58	0
3	EDO	B	501	-	3,3,3	0.49	0	2,2,2	0.34	0
5	NAG	A	503	1	14,14,15	0.84	0	17,19,21	1.90	2 (11%)
5	NAG	D	504	1	14,14,15	1.27	1 (7%)	17,19,21	1.80	3 (17%)
4	WS9	A	502	1	39,39,39	0.99	3 (7%)	50,57,57	2.06	10 (20%)
4	WS9	C	501	1	39,39,39	0.83	2 (5%)	50,57,57	2.02	7 (14%)
4	WS9	D	503	1	39,39,39	1.08	1 (2%)	50,57,57	1.71	5 (10%)

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
3	EDO	A	501	-	-	0/1/1/1	-
3	EDO	D	502	-	-	1/1/1/1	-
4	WS9	B	502	1	-	6/38/52/52	0/4/4/4
5	NAG	B	503	1	-	4/6/23/26	0/1/1/1
6	MES	D	501	-	-	3/6/14/14	0/1/1/1
6	MES	B	504	-	-	3/6/14/14	0/1/1/1
3	EDO	B	501	-	-	0/1/1/1	-
5	NAG	A	503	1	-	2/6/23/26	0/1/1/1
5	NAG	D	504	1	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	WS9	A	502	1	-	0/38/52/52	0/4/4/4
4	WS9	C	501	1	-	6/38/52/52	0/4/4/4
4	WS9	D	503	1	-	4/38/52/52	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	502	WS9	C32-N33	6.59	1.37	1.30
4	D	503	WS9	C32-N33	5.96	1.36	1.30
4	A	502	WS9	C32-N33	4.40	1.35	1.30
4	C	501	WS9	F16-C15	2.74	1.44	1.32
4	A	502	WS9	F16-C15	2.68	1.44	1.32
5	D	504	NAG	C3-C2	2.34	1.57	1.52
4	C	501	WS9	C32-N33	2.28	1.33	1.30
4	A	502	WS9	C31-C25	2.00	1.36	1.32

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	501	WS9	C24-C25-C31	-9.52	108.92	125.84
4	B	502	WS9	C24-C25-C31	-8.15	111.35	125.84
4	D	503	WS9	C24-C25-C31	-8.05	111.53	125.84
4	A	502	WS9	C24-C25-C31	-7.65	112.24	125.84
4	A	502	WS9	C19-C7-C8	7.29	127.09	118.58
4	B	502	WS9	C25-C24-N23	-7.20	96.87	110.36
4	C	501	WS9	C25-C24-N23	-6.86	97.51	110.36
5	A	503	NAG	C1-O5-C5	6.43	120.80	112.19
5	D	504	NAG	C1-O5-C5	5.80	119.95	112.19
4	A	502	WS9	C25-C24-N23	-5.73	99.62	110.36
4	D	503	WS9	C25-C24-N23	-5.66	99.77	110.36
4	C	501	WS9	O36-C32-N33	-4.91	108.97	114.71
4	C	501	WS9	C19-C7-C8	4.76	124.13	118.58
4	A	502	WS9	O36-C32-N33	-4.21	109.78	114.71
4	D	503	WS9	C25-C31-C32	3.29	127.91	123.24
5	B	503	NAG	C4-C3-C2	3.05	115.49	111.02
4	D	503	WS9	C19-C7-C8	3.05	122.14	118.58
5	B	503	NAG	C1-C2-N2	-3.02	105.68	110.43
5	B	503	NAG	C1-O5-C5	2.96	116.15	112.19
4	A	502	WS9	F17-C15-O14	-2.79	99.64	111.74
5	D	504	NAG	C4-C3-C2	2.70	114.97	111.02
4	B	502	WS9	C25-C31-C32	2.69	127.06	123.24
5	D	504	NAG	O5-C1-C2	2.56	115.26	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	502	WS9	C19-C7-C8	2.52	121.52	118.58
5	A	503	NAG	C2-N2-C7	-2.42	119.66	122.90
4	C	501	WS9	C31-C32-N33	2.35	132.00	127.15
4	A	502	WS9	F16-C15-O14	2.27	121.56	111.74
4	D	503	WS9	O21-C6-C7	-2.14	118.06	121.57
4	A	502	WS9	C19-C7-C6	2.10	117.35	114.50
4	A	502	WS9	C20-C7-C8	-2.08	116.16	118.58
4	C	501	WS9	F17-C15-O14	-2.06	102.81	111.74
4	A	502	WS9	F18-C15-O14	-2.05	102.85	111.74
4	A	502	WS9	C25-C31-C32	2.03	126.13	123.24
4	C	501	WS9	F16-C15-O14	2.01	120.42	111.74

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	502	WS9	C25-C31-C32-N33
4	B	502	WS9	C25-C31-C32-O36
4	C	501	WS9	C6-C7-C8-C13
4	C	501	WS9	C25-C31-C32-N33
4	C	501	WS9	C25-C31-C32-O36
6	B	504	MES	C7-C8-S-O2S
6	D	501	MES	C7-C8-S-O2S
5	B	503	NAG	C4-C5-C6-O6
5	B	503	NAG	O5-C5-C6-O6
6	D	501	MES	C7-C8-S-O3S
5	A	503	NAG	O5-C5-C6-O6
5	D	504	NAG	C4-C5-C6-O6
5	A	503	NAG	C4-C5-C6-O6
5	B	503	NAG	C8-C7-N2-C2
5	D	504	NAG	C8-C7-N2-C2
6	B	504	MES	C7-C8-S-O3S
5	D	504	NAG	O5-C5-C6-O6
4	B	502	WS9	C19-C7-C8-C13
4	B	502	WS9	C19-C7-C8-C9
4	D	503	WS9	C19-C7-C8-C13
4	D	503	WS9	C19-C7-C8-C9
6	B	504	MES	C7-C8-S-O1S
6	D	501	MES	C7-C8-S-O1S
4	B	502	WS9	C6-C7-C8-C13
4	B	502	WS9	C6-C7-C8-C9
4	C	501	WS9	C6-C7-C8-C9

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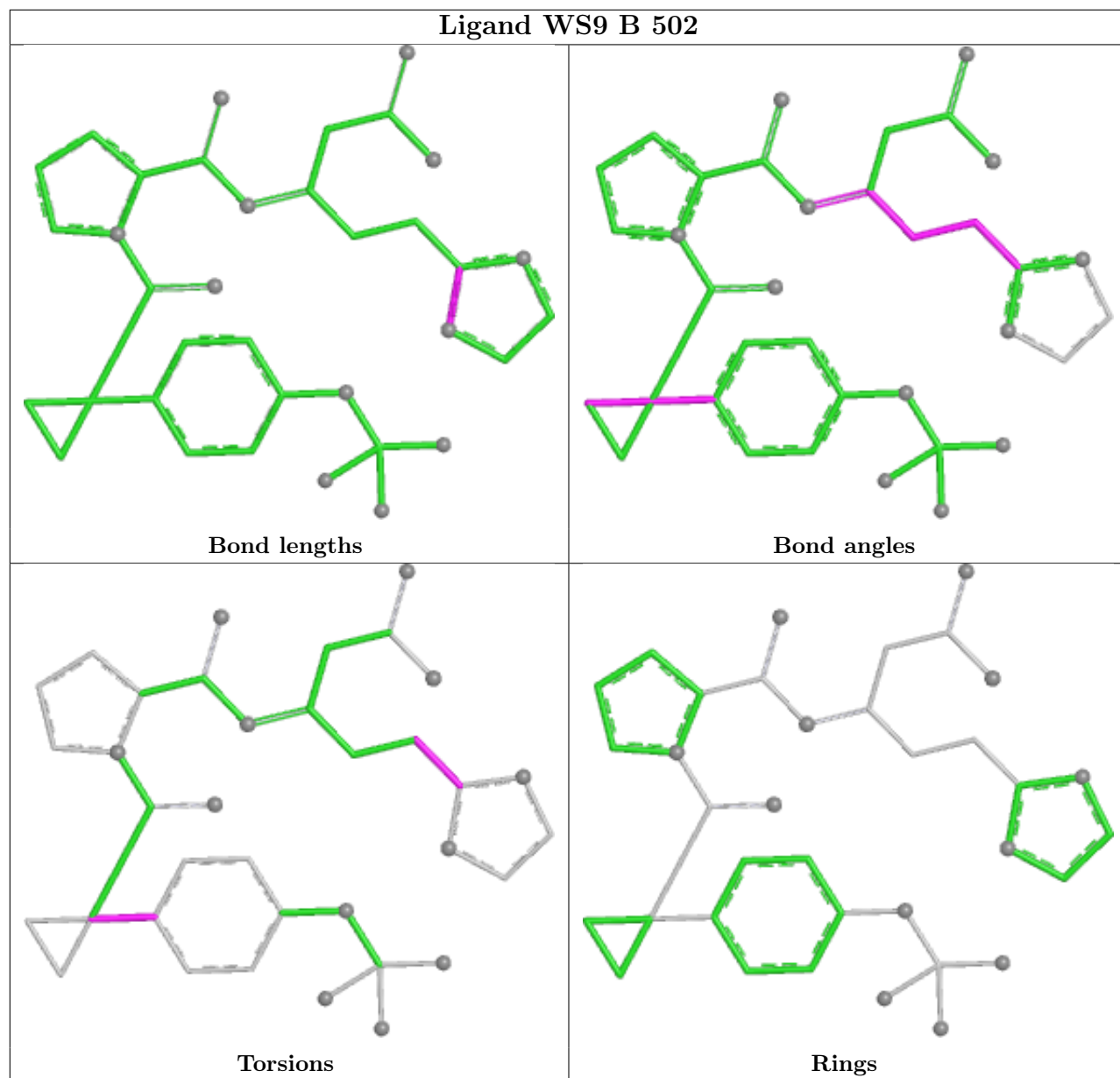
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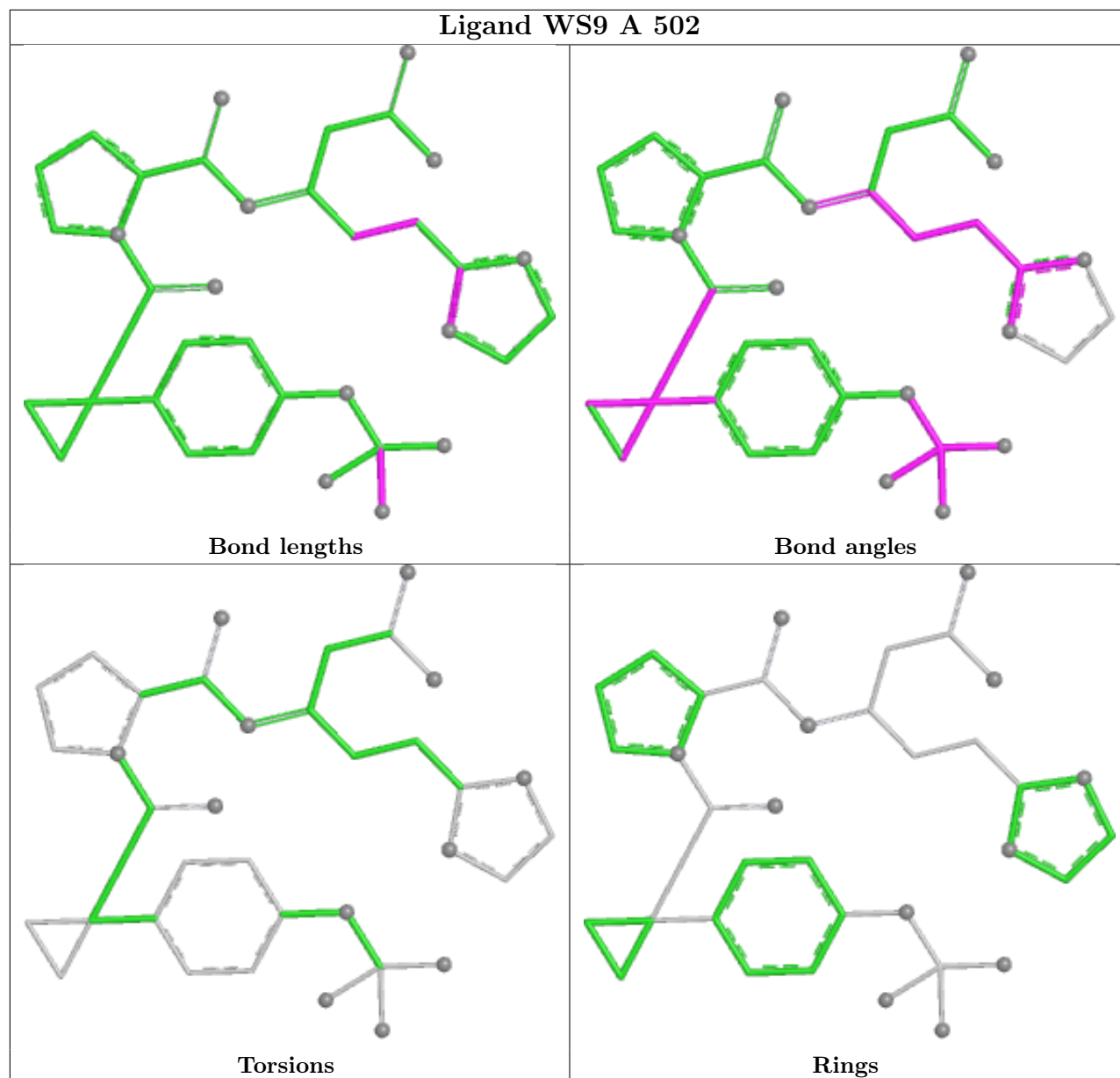
Mol	Chain	Res	Type	Atoms
4	D	503	WS9	C6-C7-C8-C13
4	D	503	WS9	C6-C7-C8-C9
4	C	501	WS9	C19-C7-C8-C13
4	C	501	WS9	C19-C7-C8-C9
5	B	503	NAG	O7-C7-N2-C2
3	D	502	EDO	O1-C1-C2-O2
5	D	504	NAG	O7-C7-N2-C2

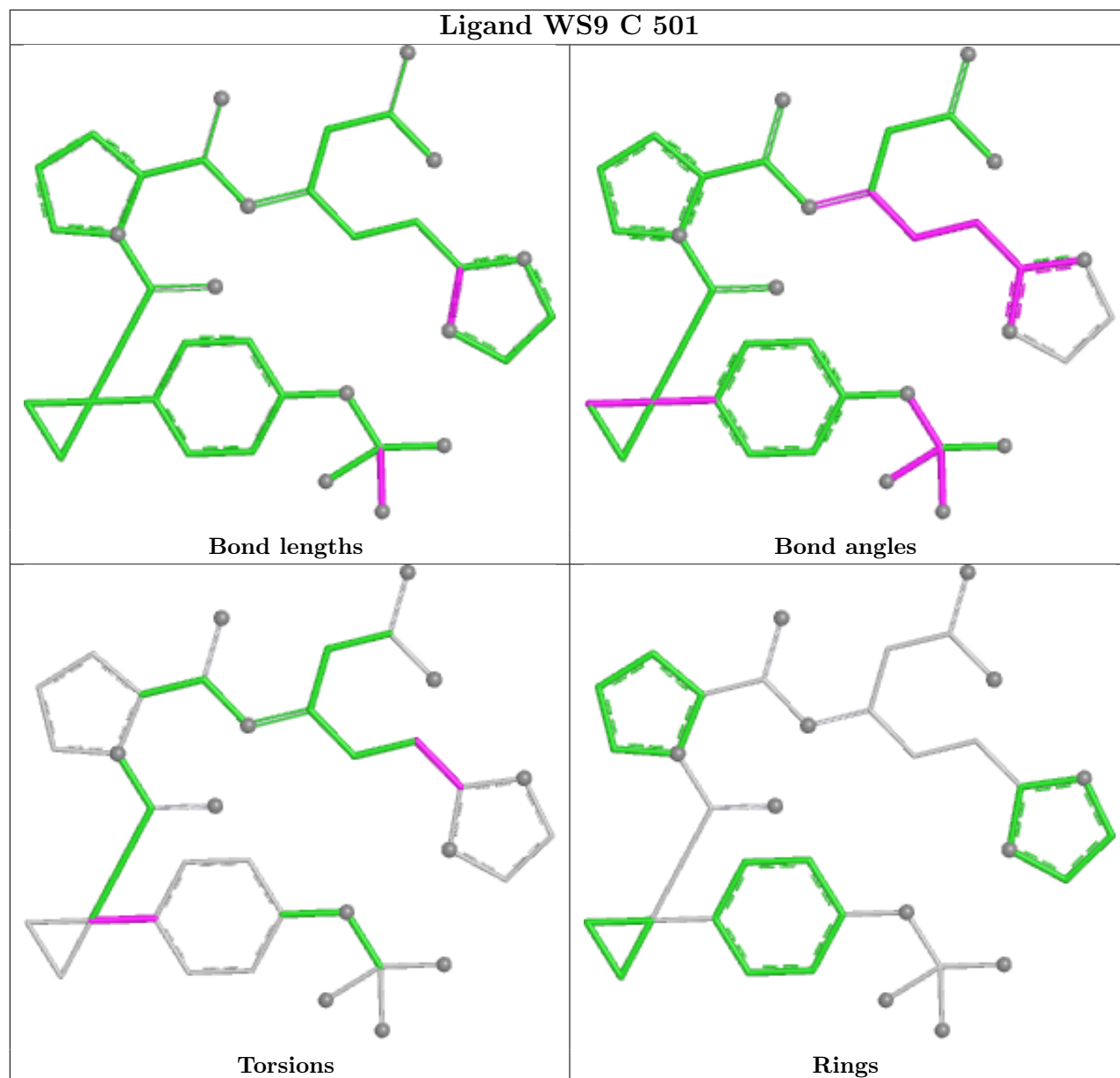
There are no ring outliers.

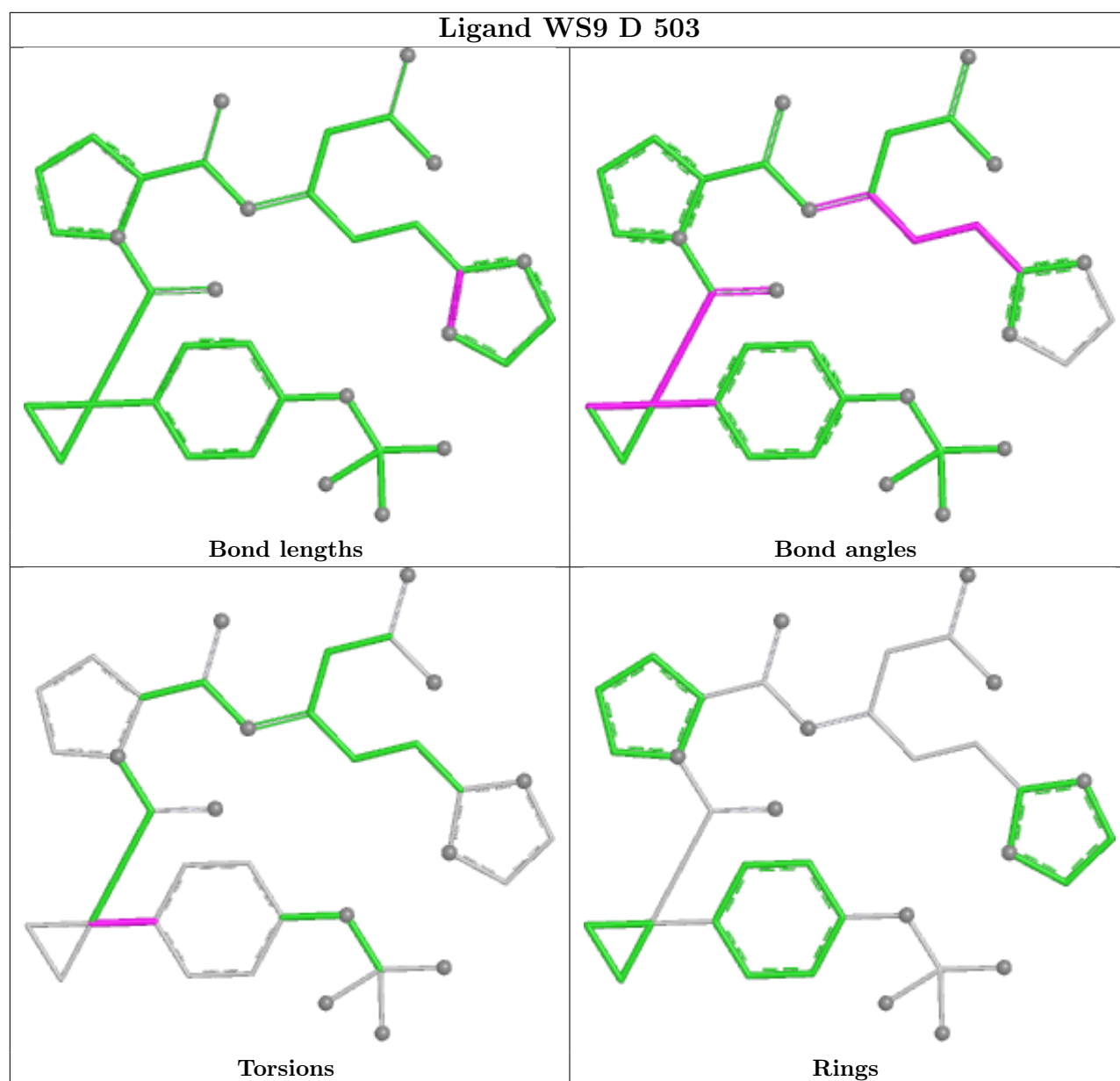
No monomer is involved in short contacts.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	146:THR	C	147:SNN	N	1.61

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

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

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	262/444 (59%)	1.10	45 (17%) 4 5	33, 38, 63, 93	0
1	B	260/444 (58%)	1.07	44 (16%) 4 5	33, 40, 70, 89	0
1	C	261/444 (58%)	1.05	37 (14%) 6 8	32, 39, 62, 94	0
1	D	261/444 (58%)	1.15	43 (16%) 4 5	21, 39, 64, 90	2 (0%)
All	All	1044/1776 (58%)	1.09	169 (16%) 4 6	21, 39, 66, 94	2 (0%)

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	26	GLY	7.5
1	C	26	GLY	6.4
1	A	40	TRP	5.5
1	C	287	LYS	5.1
1	A	41	TYR	4.9
1	A	56	ILE	4.9
1	D	287	LYS	4.9
1	A	26	GLY	4.5
1	D	175	LYS	4.4
1	A	52	ALA	4.3
1	B	26	GLY	4.1
1	B	286	MET	4.1
1	A	58	ARG	4.0
1	B	243	VAL	4.0
1	C	41	TYR	3.9
1	D	31	VAL	3.9
1	C	27	GLY	3.7
1	A	47	ALA	3.7
1	A	49	ALA	3.7
1	B	113	PHE	3.7
1	D	30	TRP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	53	TYR	3.6
1	B	177	LYS	3.6
1	C	171	HIS	3.6
1	B	125	LYS	3.5
1	D	174	TYR	3.4
1	B	224	LYS	3.4
1	B	122	GLU	3.4
1	C	286	MET	3.4
1	D	224	LYS	3.3
1	A	55	ILE	3.3
1	C	40	TRP	3.3
1	A	287	LYS	3.3
1	A	57	HIS	3.3
1	A	27	GLY	3.3
1	C	76	TYR	3.3
1	A	134	LYS	3.3
1	B	171	HIS	3.3
1	B	30	TRP	3.3
1	C	56	ILE	3.2
1	D	28	LYS	3.2
1	C	58	ARG	3.2
1	C	218	ALA	3.2
1	C	28	LYS	3.2
1	D	171	HIS	3.2
1	C	85	ILE	3.1
1	C	175	LYS	3.1
1	D	32	VAL	3.1
1	D	243	VAL	3.1
1	A	288	ARG	3.1
1	B	121	ALA	3.1
1	B	27	GLY	3.0
1	A	91	ASN	3.0
1	A	45	HIS	3.0
1	A	97	GLN	3.0
1	B	175	LYS	3.0
1	D	86	VAL	2.9
1	D	142	PHE	2.9
1	C	97	GLN	2.9
1	A	224	LYS	2.9
1	B	172	TYR	2.8
1	A	143	ILE	2.8
1	A	51	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	175	LYS	2.8
1	B	151	THR	2.8
1	A	42	ASN	2.7
1	B	184	PHE	2.7
1	C	223	GLU	2.7
1	D	213	ARG	2.7
1	C	177	LYS	2.7
1	C	142	PHE	2.7
1	A	180	ARG	2.7
1	D	123	ALA	2.7
1	B	134	LYS	2.7
1	D	125	LYS	2.7
1	D	143	ILE	2.7
1	D	130	GLY	2.6
1	A	48	ASP	2.6
1	D	144	TYR	2.6
1	D	113	PHE	2.6
1	D	56	ILE	2.6
1	A	54	GLN	2.6
1	A	113	PHE	2.6
1	A	90	PRO	2.6
1	C	202	ILE	2.6
1	A	89	ARG	2.6
1	B	213	ARG	2.6
1	B	124	VAL	2.6
1	D	141	VAL	2.6
1	C	164	LYS	2.6
1	C	174	TYR	2.6
1	A	168	GLU	2.6
1	D	106	GLU	2.6
1	A	286	MET	2.5
1	C	30	TRP	2.5
1	B	56	ILE	2.5
1	B	143	ILE	2.5
1	D	57	HIS	2.5
1	D	58	ARG	2.5
1	A	223	GLU	2.5
1	D	199	PRO	2.5
1	A	125	LYS	2.5
1	C	168	GLU	2.5
1	D	97	GLN	2.5
1	B	28	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	125	LYS	2.5
1	C	84	GLY	2.4
1	B	91	ASN	2.4
1	B	117	LEU	2.4
1	A	221	TYR	2.4
1	B	170	ILE	2.4
1	B	126	GLY	2.4
1	D	172	TYR	2.4
1	A	142	PHE	2.4
1	B	66	ILE	2.4
1	B	123	ALA	2.4
1	B	168	GLU	2.4
1	A	138	GLN	2.4
1	B	176	HIS	2.4
1	B	142	PHE	2.3
1	C	57	HIS	2.3
1	B	164	LYS	2.3
1	A	213	ARG	2.3
1	B	198	LEU	2.3
1	C	138	GLN	2.3
1	C	43	TYR	2.3
1	C	123	ALA	2.3
1	D	137	PRO	2.3
1	D	286	MET	2.3
1	D	197	HIS	2.3
1	C	145	PHE	2.3
1	D	248	LYS	2.3
1	B	137	PRO	2.3
1	D	118	ARG	2.3
1	B	141	VAL	2.3
1	B	131	LYS	2.3
1	A	126	GLY	2.2
1	D	184	PHE	2.2
1	B	138	GLN	2.2
1	B	158	ASN	2.2
1	A	117	LEU	2.2
1	B	174	TYR	2.2
1	D	62	PRO	2.2
1	A	43	TYR	2.2
1	C	53	TYR	2.2
1	D	164	LYS	2.2
1	D	122	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	282	GLN	2.2
1	D	176	HIS	2.1
1	B	127	ILE	2.1
1	C	86	VAL	2.1
1	C	243	VAL	2.1
1	D	27	GLY	2.1
1	C	180	ARG	2.1
1	A	106	GLU	2.1
1	D	43	TYR	2.1
1	D	67	VAL	2.1
1	A	248	LYS	2.1
1	A	50	CYS	2.1
1	D	55	ILE	2.1
1	C	106	GLU	2.1
1	D	274	THR	2.1
1	A	243	VAL	2.1
1	C	83	PRO	2.1
1	C	199	PRO	2.1
1	B	180	ARG	2.0
1	B	130	GLY	2.0
1	B	62	PRO	2.0
1	B	204	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SNN	D	147	7/8	0.90	0.14	30,31,31,33	0
1	SNN	A	147	7/8	0.93	0.14	21,24,25,25	0
1	SNN	C	147	7/8	0.94	0.11	23,24,26,27	0
1	SNN	B	147	7/8	0.94	0.10	31,34,35,35	0

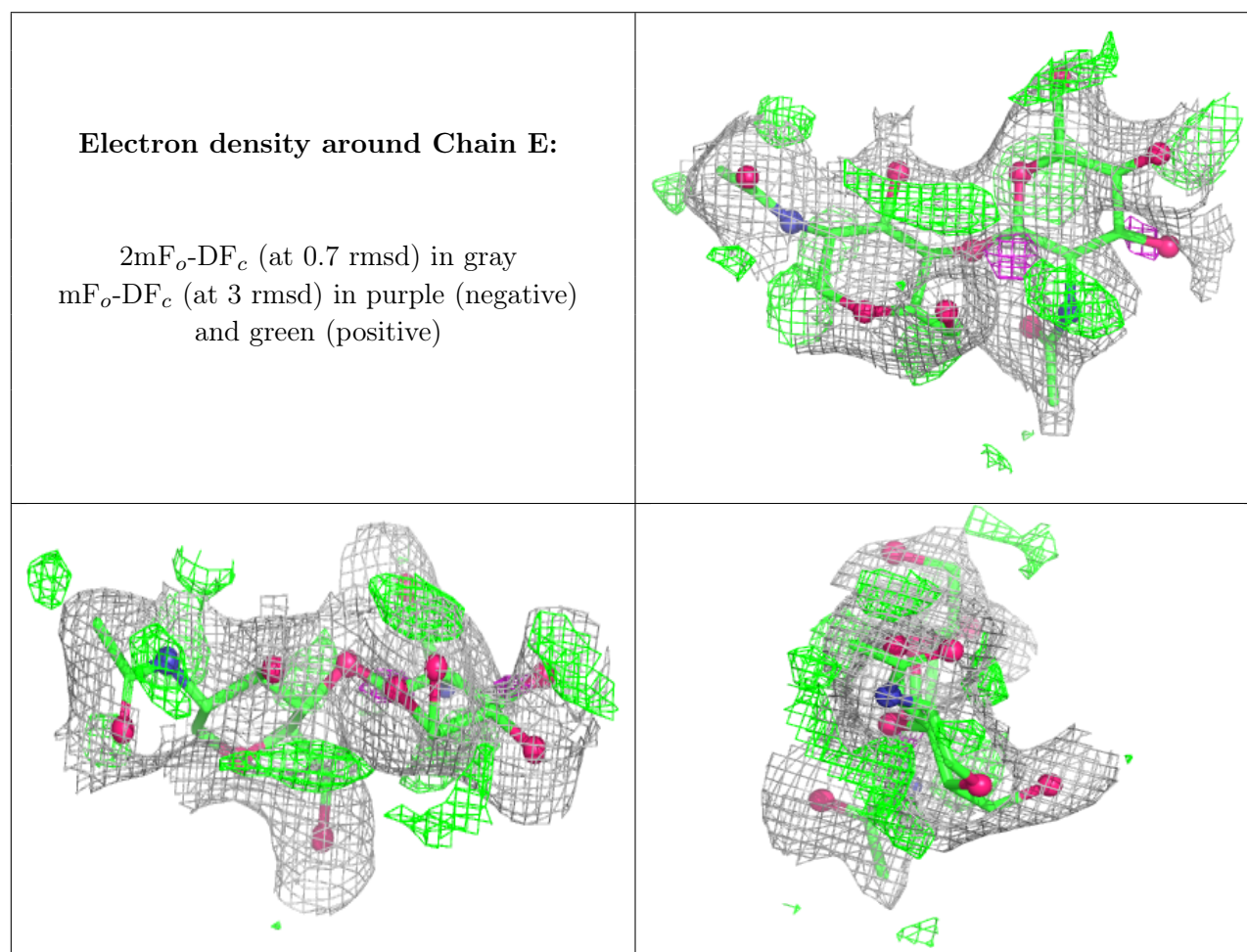
6.3 Carbohydrates [i](#)

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($\text{\AA}^2$)	Q<0.9
2	NAG	E	2	14/15	0.61	0.22	50,55,64,65	0
2	NAG	E	1	14/15	0.77	0.16	47,52,55,56	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.



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.

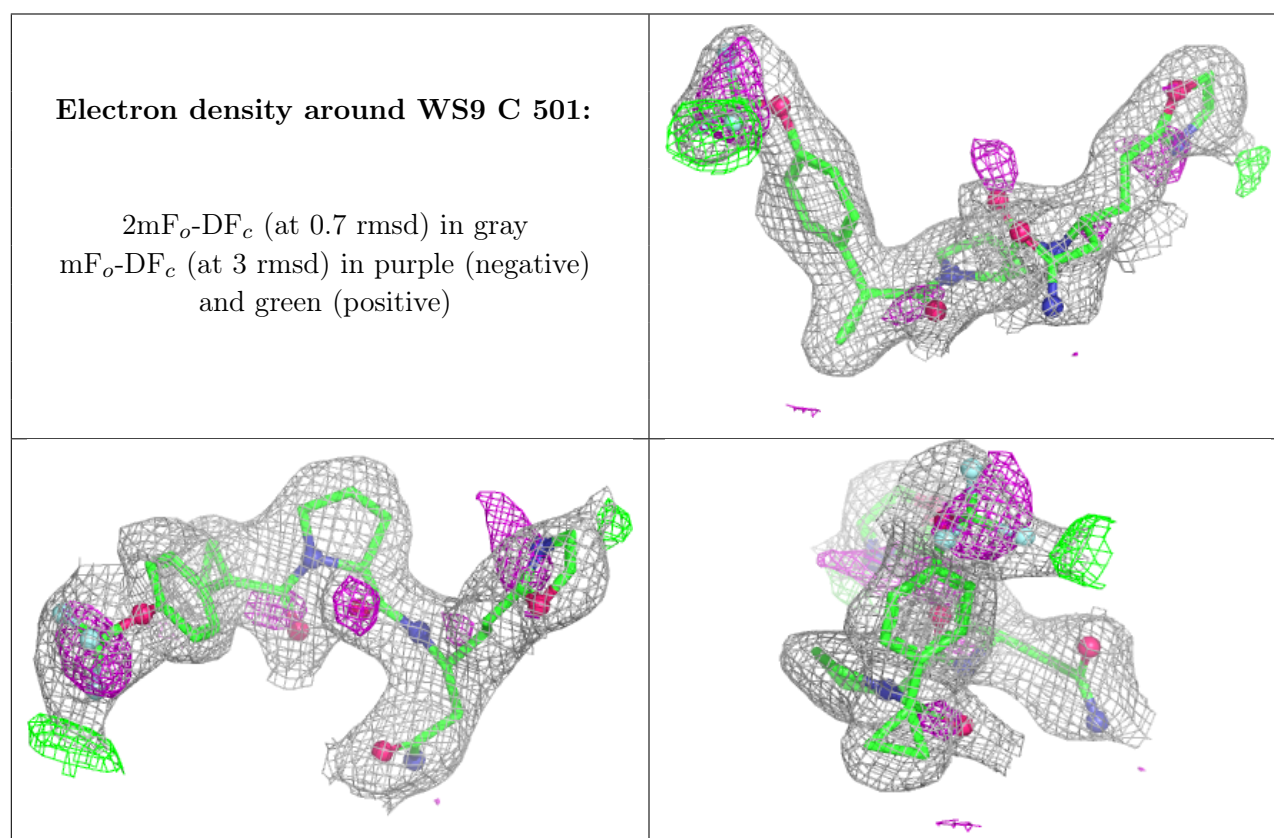
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	D	504	14/15	0.68	0.21	69,77,83,85	0
5	NAG	B	503	14/15	0.74	0.20	73,78,83,83	0

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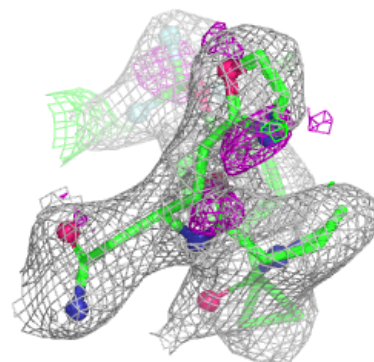
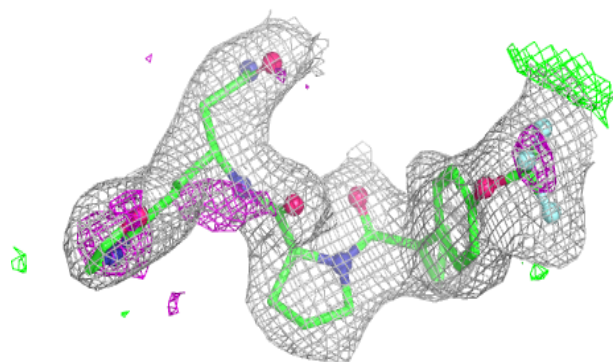
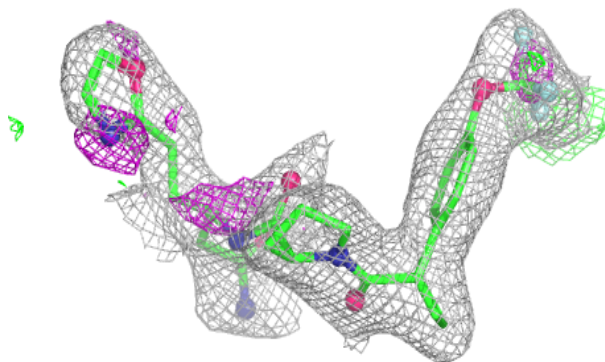
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	D	502	4/4	0.75	0.30	53,58,58,61	0
6	MES	B	504	12/12	0.76	0.28	70,73,76,76	0
5	NAG	A	503	14/15	0.82	0.16	48,50,53,54	0
6	MES	D	501	12/12	0.83	0.22	61,63,70,77	0
3	EDO	B	501	4/4	0.86	0.25	52,55,57,58	0
4	WS9	C	501	36/36	0.91	0.10	25,28,42,45	0
3	EDO	A	501	4/4	0.91	0.15	42,42,43,45	0
4	WS9	A	502	36/36	0.91	0.10	25,30,47,52	0
4	WS9	D	503	36/36	0.93	0.09	21,27,43,45	0
4	WS9	B	502	36/36	0.93	0.09	22,28,44,46	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.

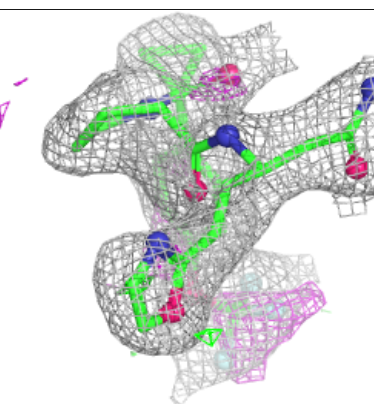
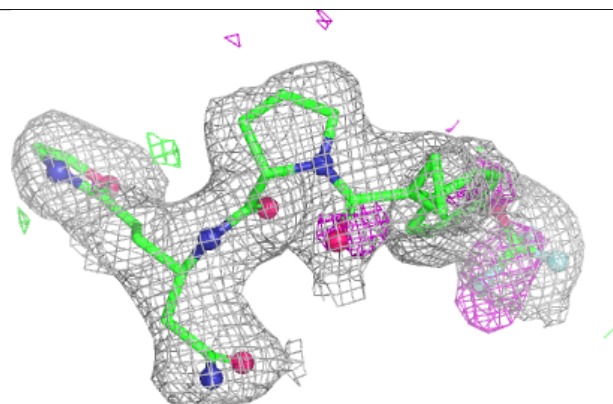
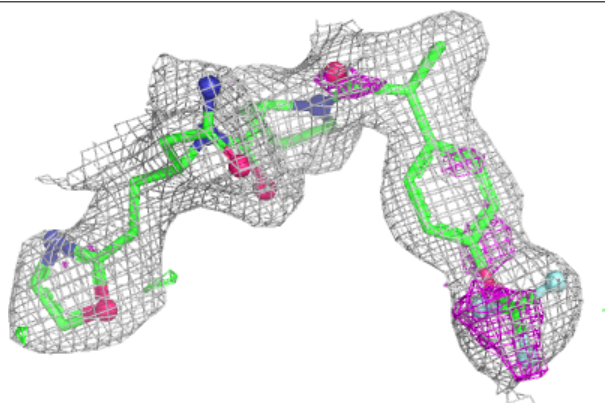


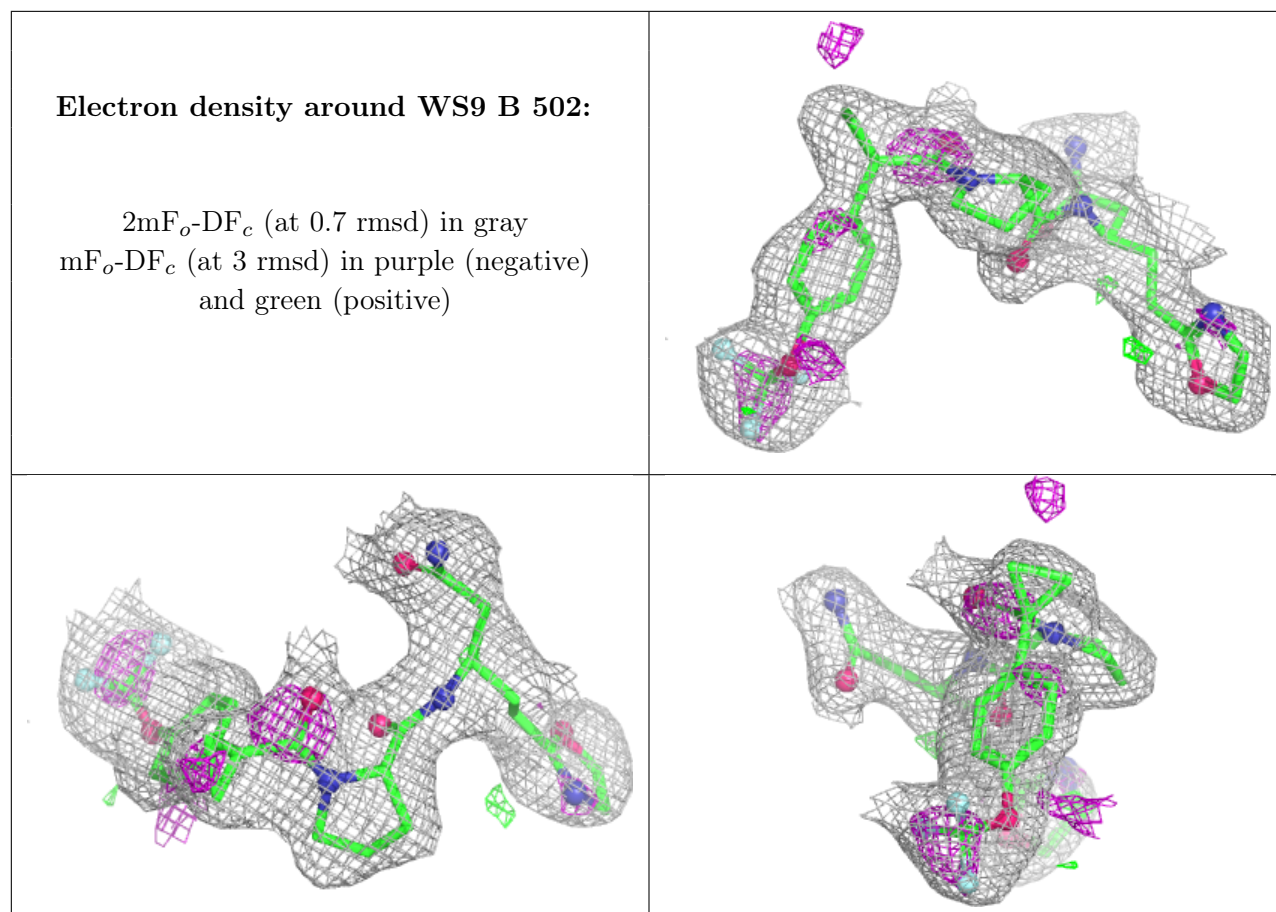
Electron density around WS9 A 502:

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

**Electron density around WS9 D 503:**

$2mF_o-DF_c$ (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.