



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 14, 2024 – 08:38 AM EST

PDB ID : 7FQL
Title : Crystal Structure of human Legumain in complex with (2S)-N-[(1S)-3-amino-1-cyano-3-oxopropyl]-1-[1-[4-[(2,4-difluorophenyl)methoxy]phenyl]cyclopropa-1,2-dicarbonyl]pyrrolidine-2-carboxamide
Authors : Ehler, A.; Benz, J.; Bartels, B.; Rudolph, M.G.
Deposited on : 2022-10-05
Resolution : 2.53 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-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

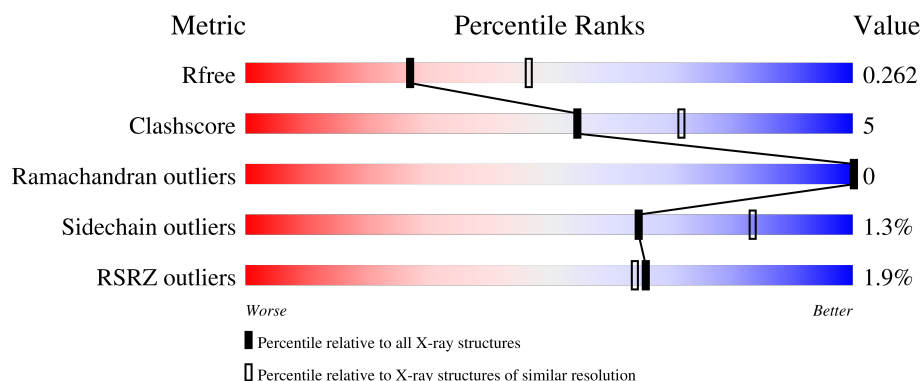
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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	6935 (2.54-2.50)
Clashscore	180529	7778 (2.54-2.50)
Ramachandran outliers	177936	7674 (2.54-2.50)
Sidechain outliers	177891	7676 (2.54-2.50)
RSRZ outliers	164620	6935 (2.54-2.50)

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	<div> <div>2%</div> <div>48%11%41%</div> </div>
1	B	444	<div> <div>50%9%40%</div> </div>
1	C	444	<div> <div>51%8%41%</div> </div>
1	D	444	<div> <div>2%</div> <div>50%8%41%</div> </div>

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Mol	Chain	Length	Quality of chain
1	E	444	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>51%8%41%</div></div></div>
1	F	444	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>49%10%41%</div></div></div>
1	G	444	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>51%8%41%</div></div></div>
1	H	444	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>53%6%41%</div></div></div>
2	I	2	<div><div><div></div><div></div><div></div></div><div>100%</div></div>
2	J	2	<div><div><div></div><div></div><div></div></div><div>50%50%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17343 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	260	Total	C	N	O	S	0	0	0
			2090	1321	354	400	15			
1	B	265	Total	C	N	O	S	0	1	0
			2137	1352	364	406	15			
1	C	261	Total	C	N	O	S	0	1	0
			2108	1335	356	402	15			
1	D	260	Total	C	N	O	S	0	0	0
			2090	1321	354	400	15			
1	E	264	Total	C	N	O	S	0	0	0
			2124	1342	363	404	15			
1	F	260	Total	C	N	O	S	0	0	0
			2090	1321	354	400	15			
1	G	260	Total	C	N	O	S	0	0	0
			2090	1321	354	400	15			
1	H	260	Total	C	N	O	S	0	0	0
			2090	1321	354	400	15			

There are 240 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

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

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

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

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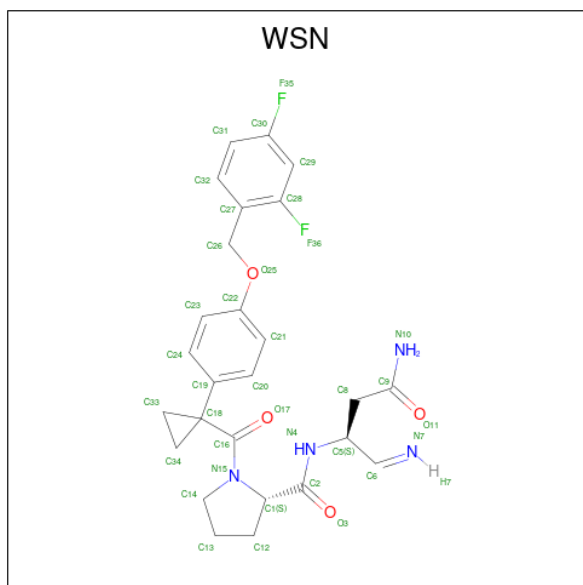
Chain	Residue	Modelled	Actual	Comment	Reference
H	13	GLY	-	expression tag	UNP Q99538
H	14	LEU	-	expression tag	UNP Q99538
H	15	SER	-	expression tag	UNP Q99538
H	16	LEU	-	expression tag	UNP Q99538
H	17	GLY	-	expression tag	UNP Q99538
H	147	SNN	ASP	conflict	UNP Q99538
H	272	GLN	ASN	conflict	UNP Q99538
H	434	VAL	-	expression tag	UNP Q99538
H	435	ASP	-	expression tag	UNP Q99538
H	436	HIS	-	expression tag	UNP Q99538
H	437	HIS	-	expression tag	UNP Q99538
H	438	HIS	-	expression tag	UNP Q99538
H	439	HIS	-	expression tag	UNP Q99538
H	440	HIS	-	expression tag	UNP Q99538
H	441	HIS	-	expression tag	UNP Q99538
H	442	HIS	-	expression tag	UNP Q99538
H	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	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is N-[(2R)-4-amino-1-imino-4-oxobutan-2-yl]-1-(1-{4-[(2,4-difluorophenyl)methoxy]phenyl}cyclopropane-1-carbonyl)-L-prolinamide (three-letter code: WSN) (formula: C₂₆H₂₈F₂N₄O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	B	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	C	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	D	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	E	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	F	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	G	1	Total 36	C 26	F 2	N 4	O 4	0	0
3	H	1	Total 36	C 26	F 2	N 4	O 4	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	H	1	Total	C	N	O	0	0
			14	8	1	5		
4	H	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

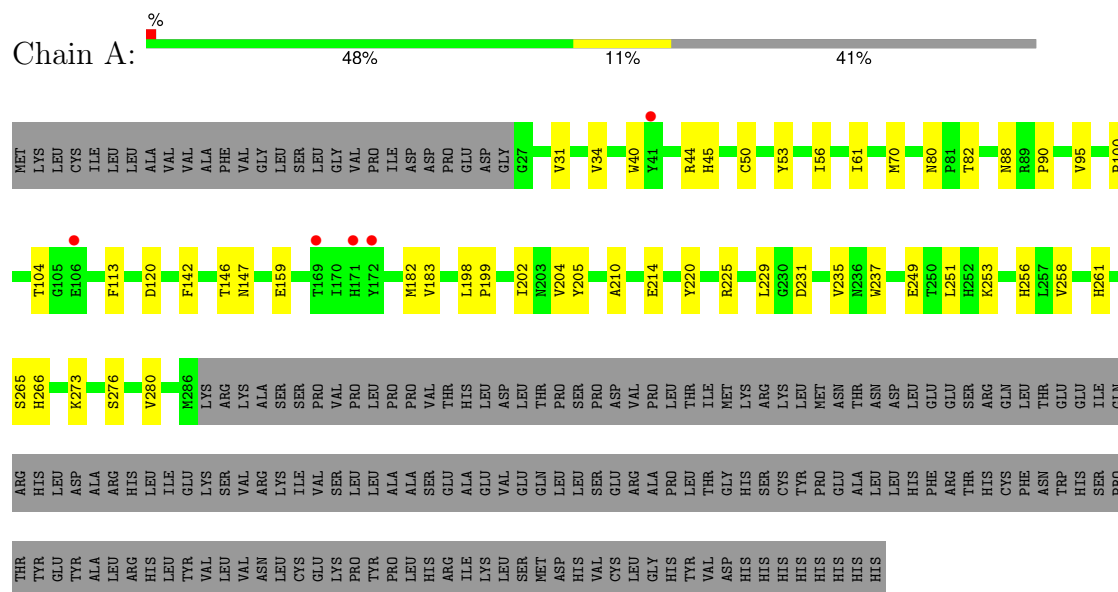


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		

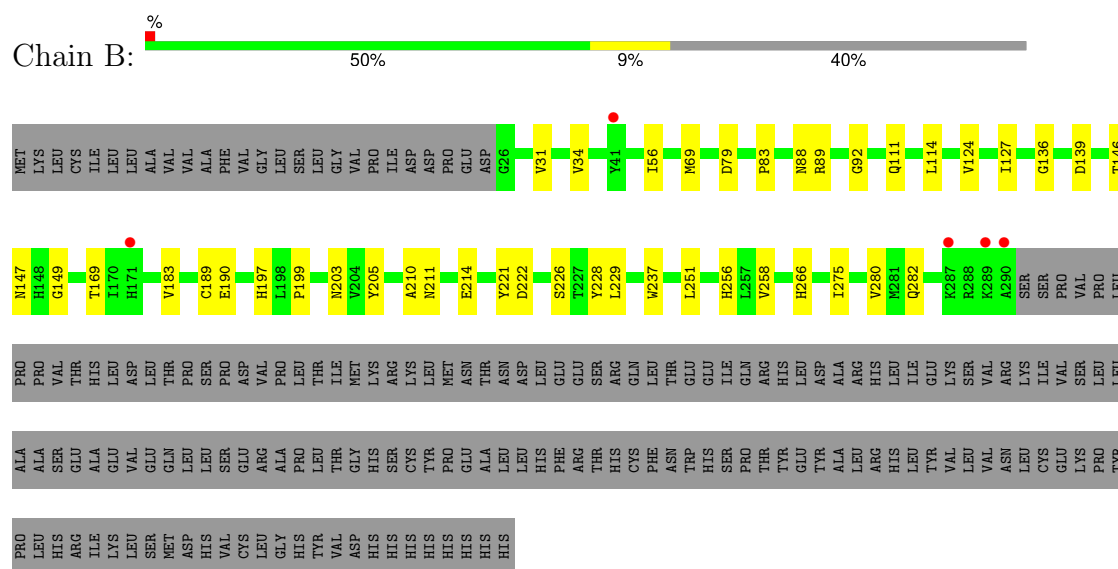
3 Residue-property plots [i](#)

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

• Molecule 1: Legumain

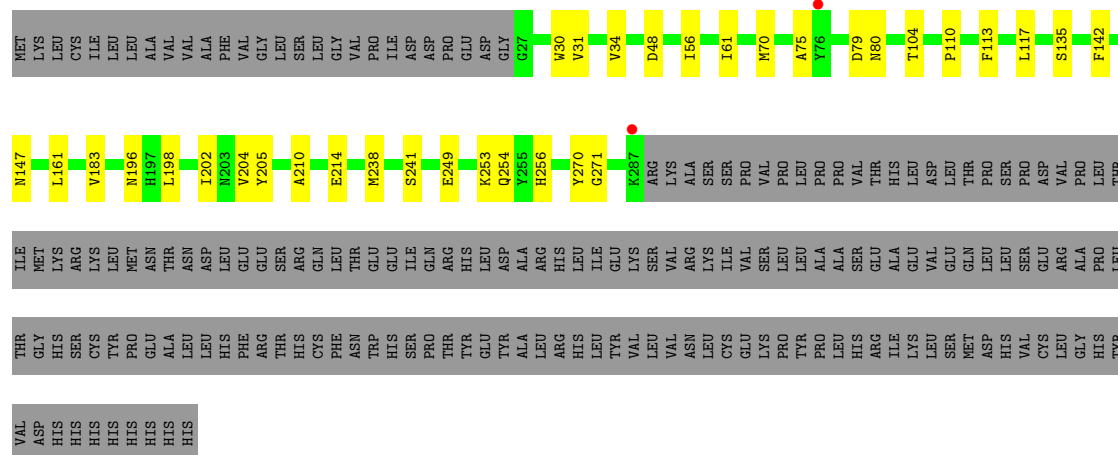


• Molecule 1: Legumain



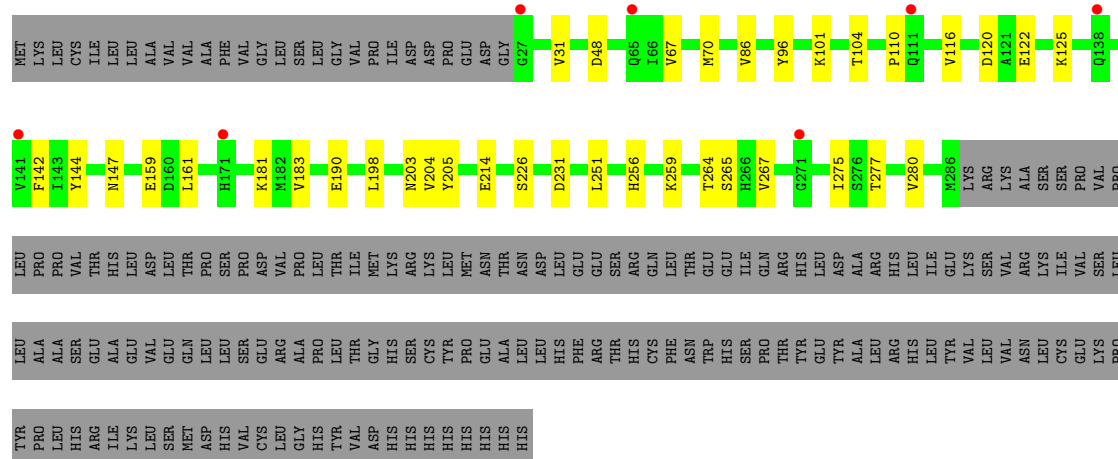
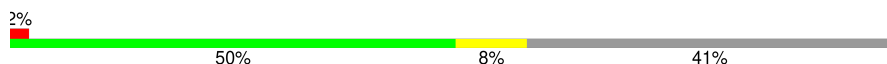
• Molecule 1: Legumain

Chain C:



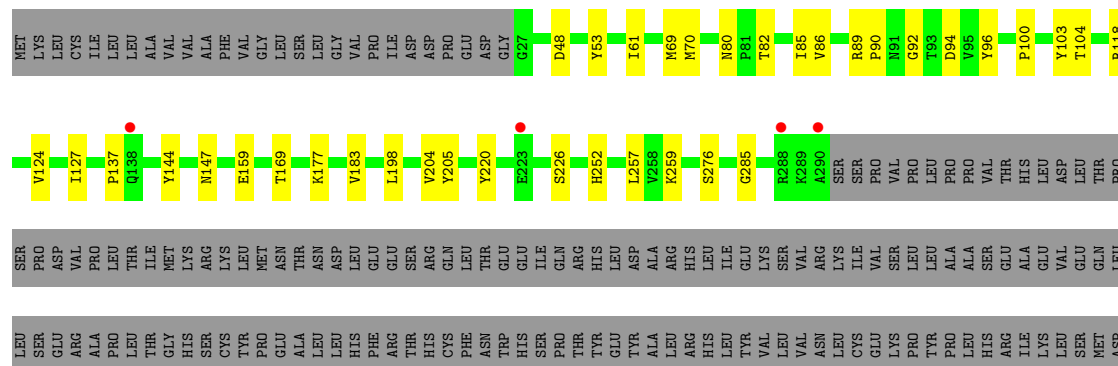
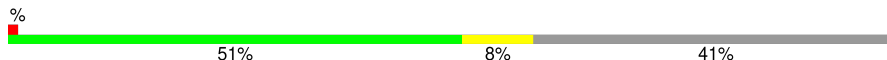
- Molecule 1: Legumain

Chain D:



- Molecule 1: Legumain

Chain E:



ASN	THR	ASN	ASP	LEU	GLY	SER	ARG	GLN	THR	GLY	ILE	GLN	ARG	HIS	LEU	ASP	ALA	ARG	HIS	LEU	ILE	GLY	LYS	SER	VAL	ARG	LYS	ILE	VAL	SER	LEU	ALA	ALA	SER	GLY	ALA	GLY	VAL	GLY	GLN	LEU	LEU	SER	GLY	ARG	PRO	THR	GLY	HIS	SER	CYS	Tyr	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU
ALA
LEU
LEU
HIS
PHE
ARG
THR
HIS
CYS
PHE
ASN
TRP
HIS
SER
PRO
THR
TYR
GLU
GLY
ALA
ALA
ARG
ARG
HIS
LEU
TYR
VAL
VAL
ASN
LEU
CYS
GLU
LYS
PRO
TYR
PRO
LEU
HIS
HIS
ARG
ILE
LYS
LEU
SER
MET
ASP
HIS
VAL
CYS
LEU
GLY
HIS
TYR
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ASP
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HIS
HIS
HIS

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

Chain I: 100%

NAG1
NAG2

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

Chain J: 50% 50%

NAG1
NAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.30Å 131.94Å 117.68Å 90.00° 90.25° 90.00°	Depositor
Resolution (Å)	49.03 – 2.53 49.03 – 2.53	Depositor EDS
% Data completeness (in resolution range)	51.5 (49.03-2.53) 49.9 (49.03-2.53)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.55Å)	Xtriage
Refinement program	PHENIX dev_4230	Depositor
R, R_{free}	0.192 , 0.252 0.201 , 0.262	Depositor DCC
R_{free} test set	4482 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.867	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 28.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-l	Xtriage
F_o, F_c correlation	0.74	EDS
Total number of atoms	17343	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.42% 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: SNN, NAG, SO4, WSN

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	0.25	0/2139	0.47	0/2902
1	B	0.26	0/2190	0.47	0/2968
1	C	0.26	0/2161	0.47	0/2931
1	D	0.25	0/2139	0.46	0/2902
1	E	0.25	0/2173	0.47	0/2945
1	F	0.26	0/2139	0.46	0/2902
1	G	0.25	0/2139	0.46	0/2902
1	H	0.25	0/2139	0.48	0/2902
All	All	0.25	0/17219	0.47	0/23354

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	146	THR	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2090	0	1968	24	0
1	B	2137	0	2024	23	0
1	C	2108	0	1990	18	0
1	D	2090	0	1968	19	0
1	E	2124	0	2011	18	0
1	F	2090	0	1967	30	0
1	G	2090	0	1967	18	0
1	H	2090	0	1967	12	0
2	I	28	0	25	3	0
2	J	28	0	25	0	0
3	A	36	0	0	1	0
3	B	36	0	0	0	0
3	C	36	0	0	0	0
3	D	36	0	0	2	0
3	E	36	0	0	0	0
3	F	36	0	0	0	0
3	G	36	0	0	0	0
3	H	36	0	0	1	0
4	A	14	0	13	0	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
4	E	14	0	13	0	0
4	F	28	0	26	0	0
4	G	28	0	26	0	0
4	H	28	0	26	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	E	5	0	0	0	0
5	F	10	0	0	0	0
5	G	10	0	0	0	0
5	H	5	0	0	0	0
All	All	17343	0	16042	158	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.

The worst 5 of 158 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:197:HIS:HB3	2:I:1:NAG:H3	1.64	0.78
1:F:214:GLU:OE2	1:F:266:HIS:ND1	2.24	0.68
1:A:249:GLU:HG3	1:A:253:LYS:HD3	1.75	0.66
1:F:210:ALA:HB1	1:F:214:GLU:HB3	1.76	0.66
1:H:214:GLU:OE2	1:H:266:HIS:ND1	2.22	0.66

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	257/444 (58%)	250 (97%)	7 (3%)	0	100	100
1	B	263/444 (59%)	256 (97%)	7 (3%)	0	100	100
1	C	259/444 (58%)	255 (98%)	4 (2%)	0	100	100
1	D	257/444 (58%)	251 (98%)	6 (2%)	0	100	100
1	E	261/444 (59%)	256 (98%)	5 (2%)	0	100	100
1	F	257/444 (58%)	251 (98%)	6 (2%)	0	100	100
1	G	257/444 (58%)	253 (98%)	4 (2%)	0	100	100
1	H	257/444 (58%)	250 (97%)	7 (3%)	0	100	100
All	All	2068/3552 (58%)	2022 (98%)	46 (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	227/396 (57%)	221 (97%)	6 (3%)	41	66
1	B	231/396 (58%)	228 (99%)	3 (1%)	65	83
1	C	229/396 (58%)	228 (100%)	1 (0%)	89	96
1	D	227/396 (57%)	222 (98%)	5 (2%)	47	71
1	E	230/396 (58%)	228 (99%)	2 (1%)	75	89
1	F	227/396 (57%)	226 (100%)	1 (0%)	89	96
1	G	227/396 (57%)	225 (99%)	2 (1%)	75	89
1	H	227/396 (57%)	224 (99%)	3 (1%)	65	83
All	All	1825/3168 (58%)	1802 (99%)	23 (1%)	65	83

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	277	THR
1	F	261	HIS
1	E	226	SER
1	G	214	GLU
1	B	111	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	211	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	E	147	1	5,6,8	2.34	1 (20%)	1,6,11	1.59	0
1	SNN	A	147	1	5,6,8	2.27	1 (20%)	1,6,11	1.60	0
1	SNN	G	147	1	5,6,8	2.35	1 (20%)	1,6,11	1.67	0
1	SNN	C	147	1	5,6,8	2.33	1 (20%)	1,6,11	1.52	0
1	SNN	D	147	1	5,6,8	2.29	1 (20%)	1,6,11	1.55	0
1	SNN	B	147	1	5,6,8	2.27	1 (20%)	1,6,11	1.55	0
1	SNN	H	147	1	5,6,8	2.32	1 (20%)	1,6,11	1.71	0
1	SNN	F	147	1	5,6,8	2.28	1 (20%)	1,6,11	1.48	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	E	147	1	-	2/3/5/12	-
1	SNN	A	147	1	-	3/3/5/12	-
1	SNN	G	147	1	-	3/3/5/12	-
1	SNN	C	147	1	-	3/3/5/12	-
1	SNN	D	147	1	-	2/3/5/12	-
1	SNN	B	147	1	-	2/3/5/12	-
1	SNN	H	147	1	-	3/3/5/12	-
1	SNN	F	147	1	-	2/3/5/12	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	147	SNN	C4-C5	5.19	1.63	1.50
1	C	147	SNN	C4-C5	5.13	1.63	1.50
1	E	147	SNN	C4-C5	5.12	1.63	1.50
1	H	147	SNN	C4-C5	5.10	1.63	1.50
1	D	147	SNN	C4-C5	5.06	1.63	1.50

There are no bond angle outliers.

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NAG	I	1	2,1	14,14,15	0.69	1 (7%)	17,19,21	0.58	0
2	NAG	I	2	2	14,14,15	0.93	1 (7%)	17,19,21	1.01	2 (11%)
2	NAG	J	1	2,1	14,14,15	0.80	1 (7%)	17,19,21	0.79	0
2	NAG	J	2	2	14,14,15	0.67	0	17,19,21	0.46	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	I	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	J	2	2	-	3/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	2	NAG	C1-C2	2.95	1.56	1.52
2	J	1	NAG	O5-C1	-2.85	1.38	1.43
2	I	1	NAG	O5-C1	-2.17	1.40	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	2	NAG	C1-O5-C5	2.40	115.41	112.19
2	I	2	NAG	C2-N2-C7	2.24	125.90	122.90

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

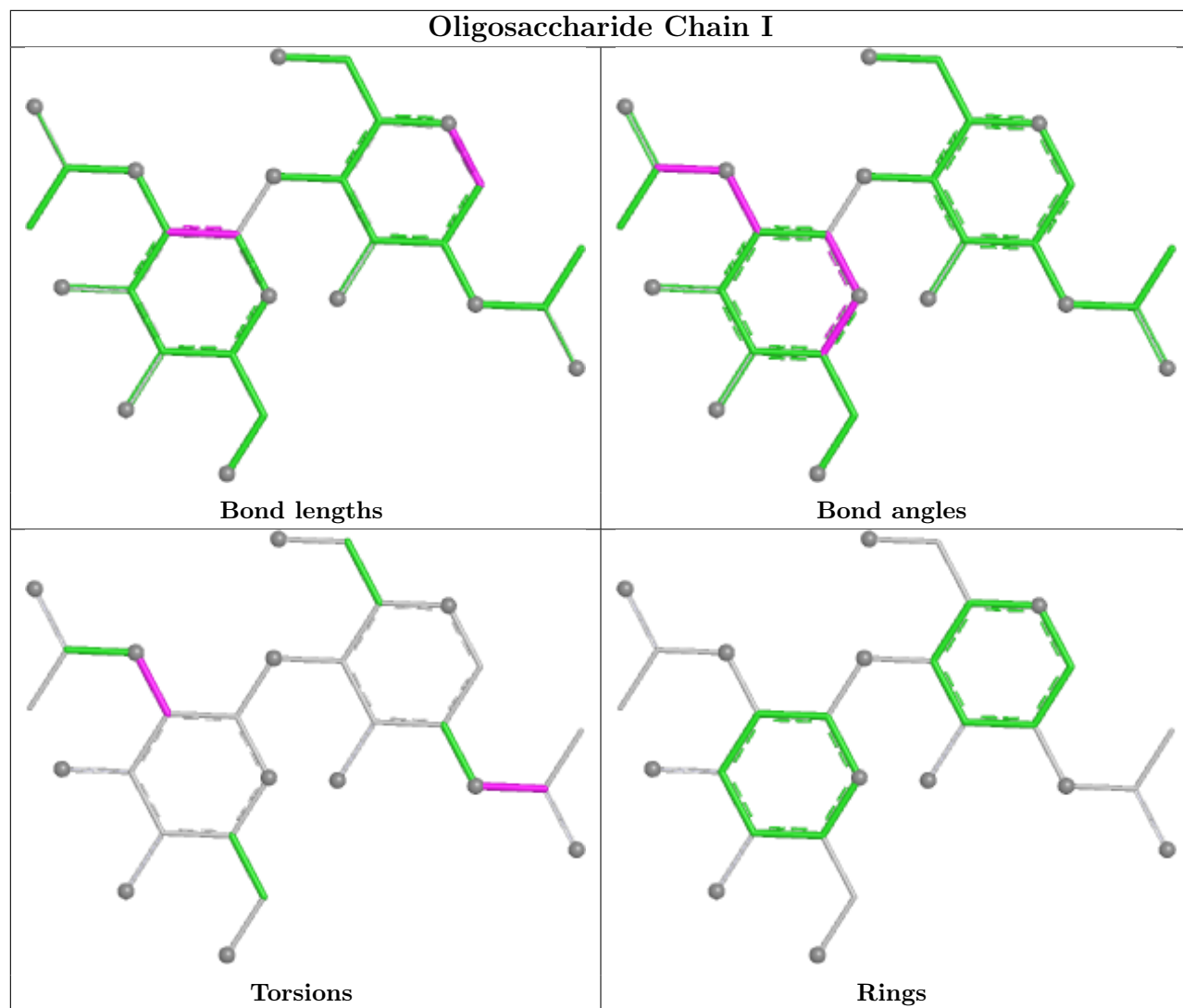
Mol	Chain	Res	Type	Atoms
2	I	2	NAG	C1-C2-N2-C7
2	I	1	NAG	C8-C7-N2-C2
2	I	1	NAG	O7-C7-N2-C2
2	J	2	NAG	O5-C5-C6-O6
2	J	2	NAG	C4-C5-C6-O6

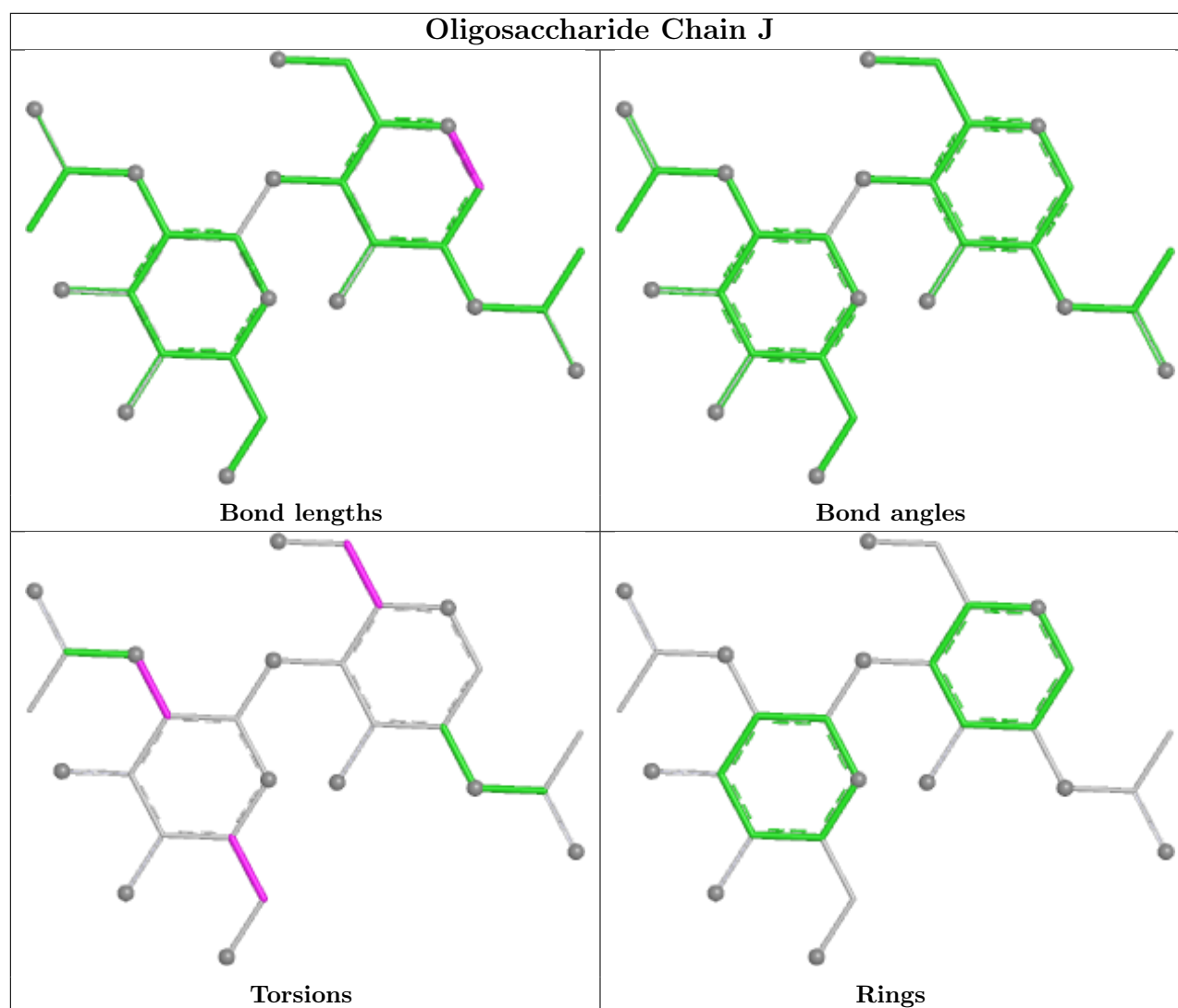
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	2	NAG	2	0
2	I	1	NAG	2	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](#)

26 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	WSN	B	501	-	37,39,39	0.23	0	52,56,56	0.68	1 (1%)
4	NAG	A	502	1	14,14,15	0.21	0	17,19,21	0.38	0
3	WSN	H	501	-	37,39,39	0.27	0	52,56,56	0.72	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	B	502	-	4,4,4	0.23	0	6,6,6	0.13	0
4	NAG	E	502	1	14,14,15	0.30	0	17,19,21	0.51	0
4	NAG	C	501	1	14,14,15	0.29	0	17,19,21	0.37	0
4	NAG	G	503	1	14,14,15	0.17	0	17,19,21	0.51	0
3	WSN	A	501	-	37,39,39	0.27	0	52,56,56	1.00	1 (1%)
4	NAG	F	503	1	14,14,15	0.22	0	17,19,21	0.35	0
3	WSN	G	502	-	37,39,39	0.27	0	52,56,56	0.62	1 (1%)
5	SO4	C	503	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	G	504	-	4,4,4	0.23	0	6,6,6	0.09	0
4	NAG	H	503	1	14,14,15	0.33	0	17,19,21	0.73	1 (5%)
3	WSN	D	501	-	37,39,39	0.27	0	52,56,56	1.07	1 (1%)
5	SO4	H	504	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	E	503	-	4,4,4	0.24	0	6,6,6	0.08	0
3	WSN	C	502	-	37,39,39	0.23	0	52,56,56	0.72	1 (1%)
3	WSN	E	501	-	37,39,39	0.24	0	52,56,56	0.71	1 (1%)
5	SO4	F	504	-	4,4,4	0.24	0	6,6,6	0.14	0
4	NAG	F	501	1	14,14,15	0.61	1 (7%)	17,19,21	0.52	0
4	NAG	G	501	1	14,14,15	0.35	0	17,19,21	0.61	0
5	SO4	G	505	-	4,4,4	0.23	0	6,6,6	0.13	0
4	NAG	H	502	1	14,14,15	0.52	0	17,19,21	0.43	0
4	NAG	D	502	1	14,14,15	0.25	0	17,19,21	0.62	0
5	SO4	F	505	-	4,4,4	0.23	0	6,6,6	0.06	0
3	WSN	F	502	-	37,39,39	0.27	0	52,56,56	0.75	1 (1%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	501	1	-	3/6/23/26	0/1/1/1
4	NAG	G	503	1	-	0/6/23/26	0/1/1/1
3	WSN	B	501	-	-	4/33/49/49	0/4/4/4
3	WSN	A	501	-	-	9/33/49/49	0/4/4/4
3	WSN	E	501	-	-	1/33/49/49	0/4/4/4
3	WSN	G	502	-	-	6/33/49/49	0/4/4/4
4	NAG	F	503	1	-	1/6/23/26	0/1/1/1
4	NAG	A	502	1	-	0/6/23/26	0/1/1/1
3	WSN	D	501	-	-	6/33/49/49	0/4/4/4
4	NAG	H	502	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	502	1	-	0/6/23/26	0/1/1/1
4	NAG	H	503	1	-	2/6/23/26	0/1/1/1
3	WSN	H	501	-	-	4/33/49/49	0/4/4/4
4	NAG	F	501	1	-	0/6/23/26	0/1/1/1
4	NAG	G	501	1	-	2/6/23/26	0/1/1/1
3	WSN	C	502	-	-	5/33/49/49	0/4/4/4
3	WSN	F	502	-	-	1/33/49/49	0/4/4/4
4	NAG	E	502	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	501	NAG	C1-C2	2.15	1.55	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	501	WSN	C33-C18-C19	6.46	126.11	118.58
3	A	501	WSN	C33-C18-C19	5.98	125.56	118.58
3	F	502	WSN	C33-C18-C19	4.71	124.07	118.58
3	C	502	WSN	C33-C18-C19	4.64	123.99	118.58
3	H	501	WSN	C33-C18-C19	4.62	123.97	118.58

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

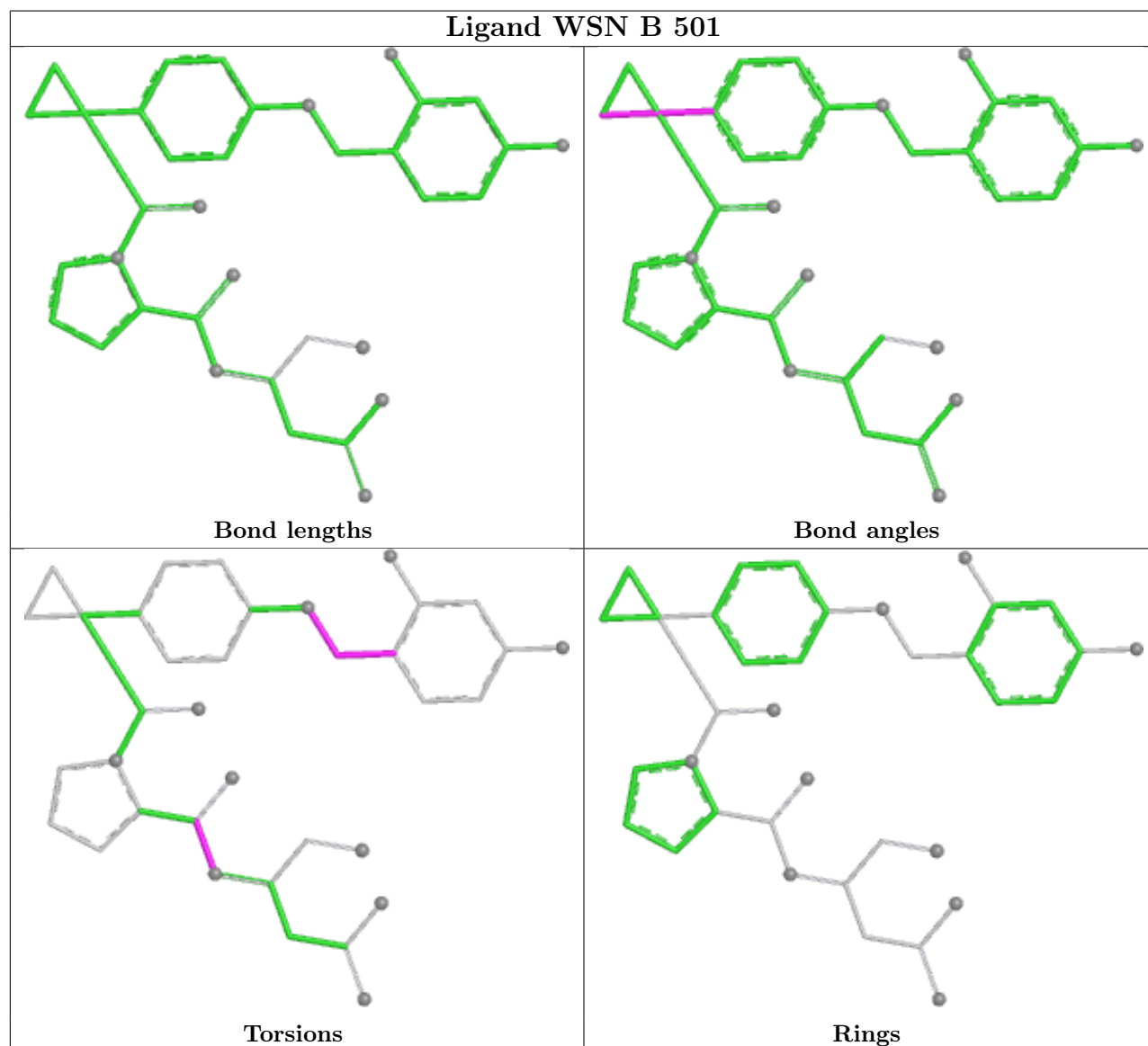
Mol	Chain	Res	Type	Atoms
3	A	501	WSN	O25-C26-C27-C28
3	G	502	WSN	C16-C18-C19-C24
3	H	501	WSN	C16-C18-C19-C24
3	C	502	WSN	C1-C2-N4-C5
3	C	502	WSN	O3-C2-N4-C5

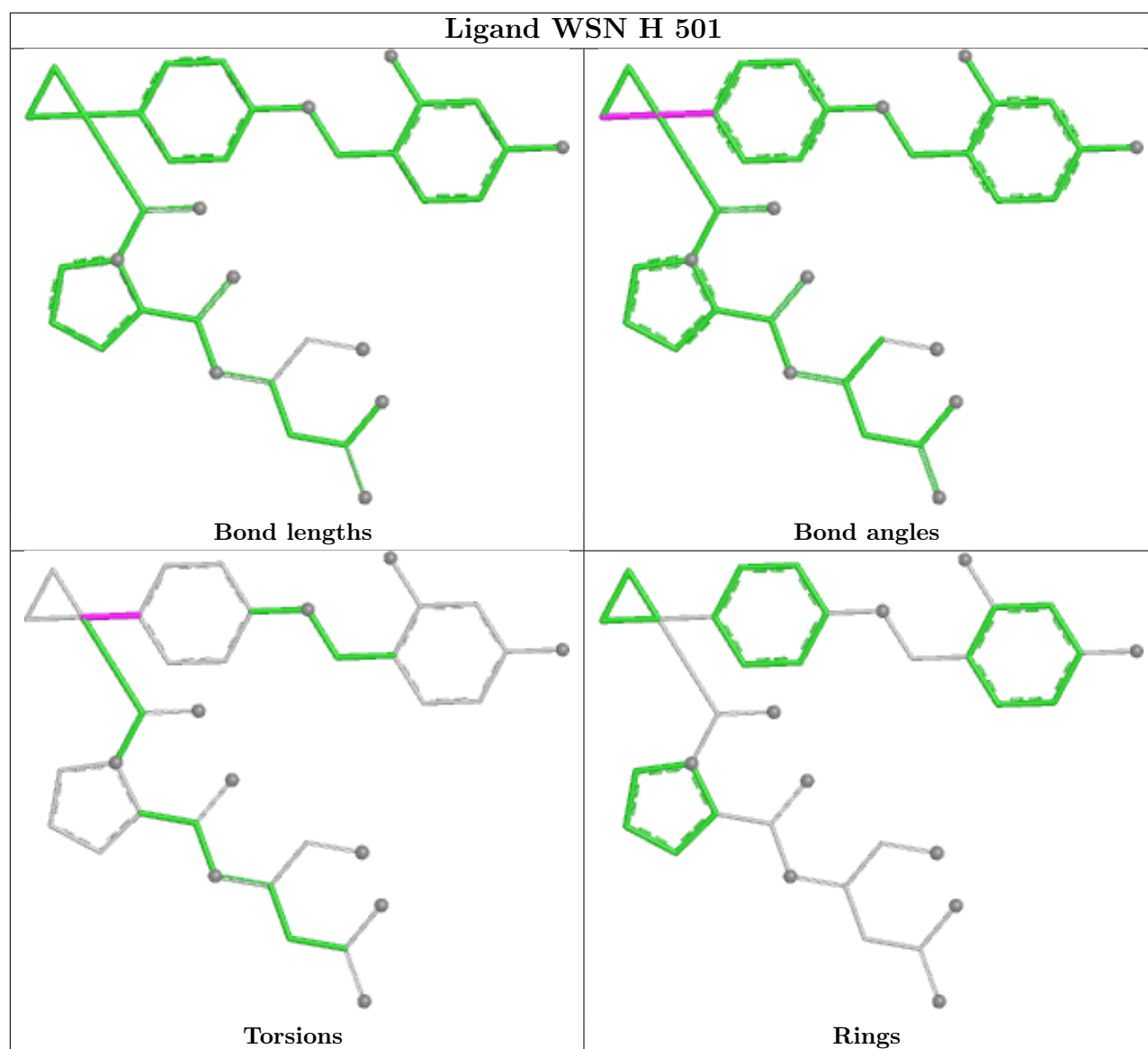
There are no ring outliers.

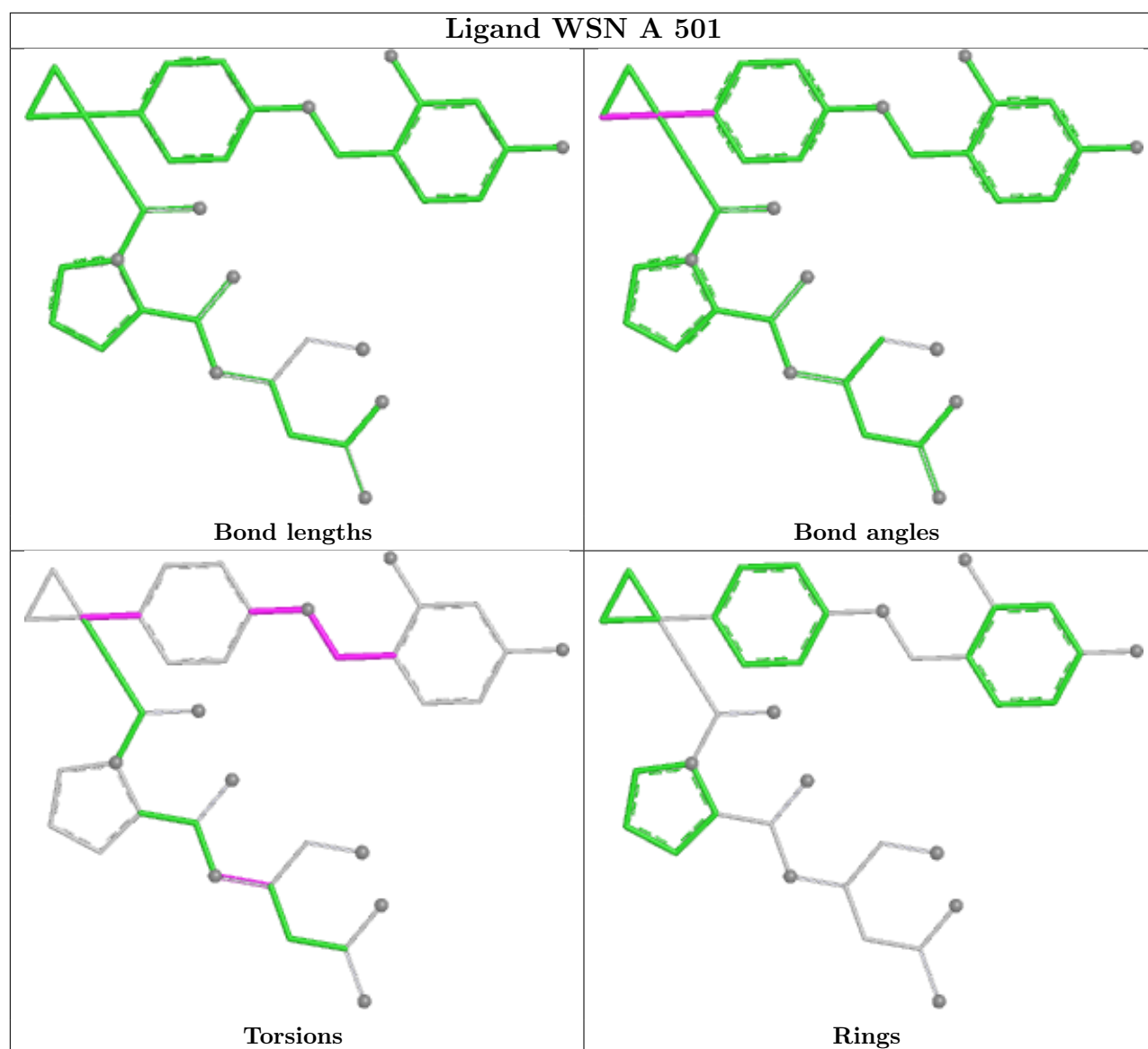
3 monomers are involved in 4 short contacts:

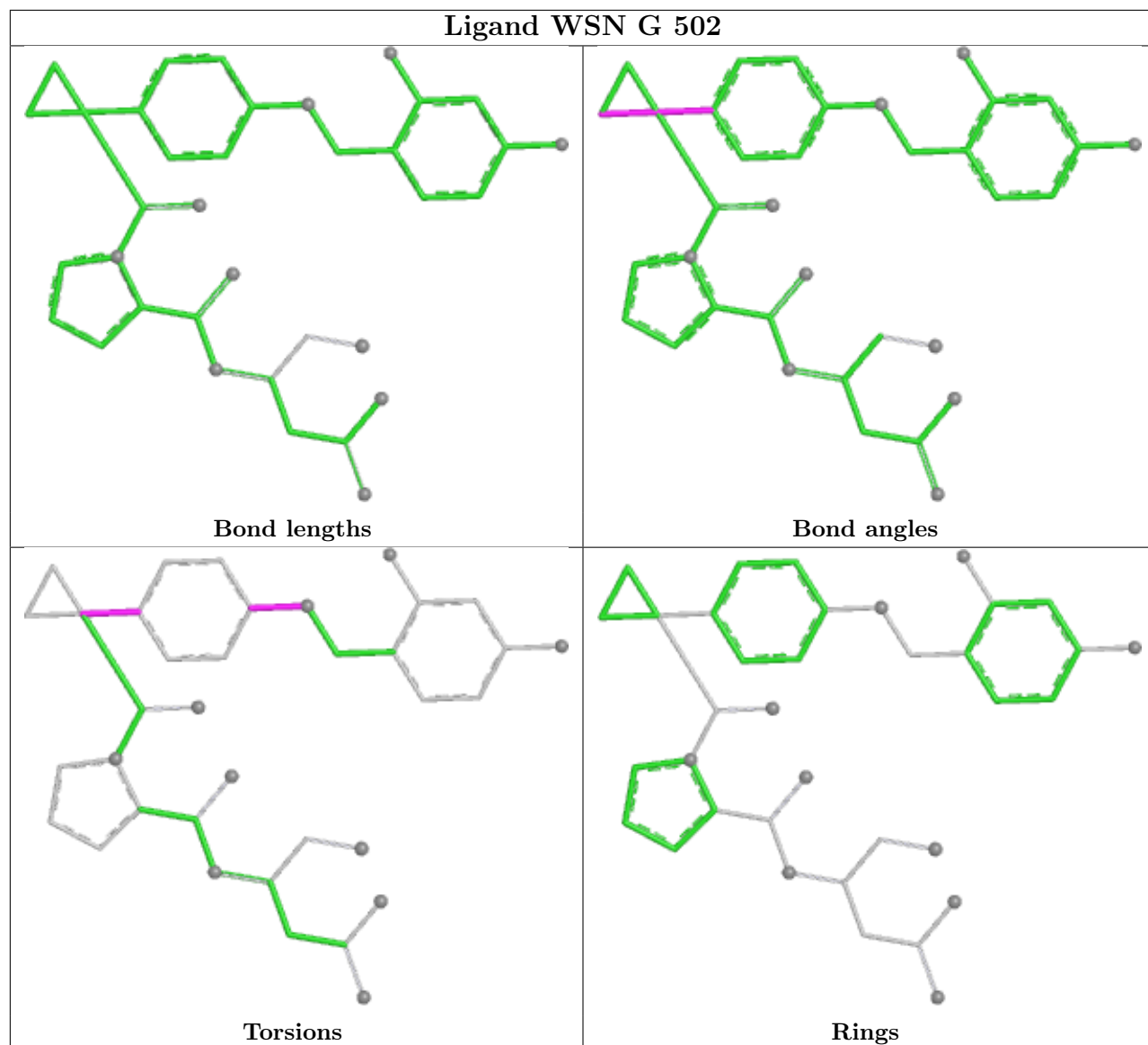
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	501	WSN	1	0
3	A	501	WSN	1	0
3	D	501	WSN	2	0

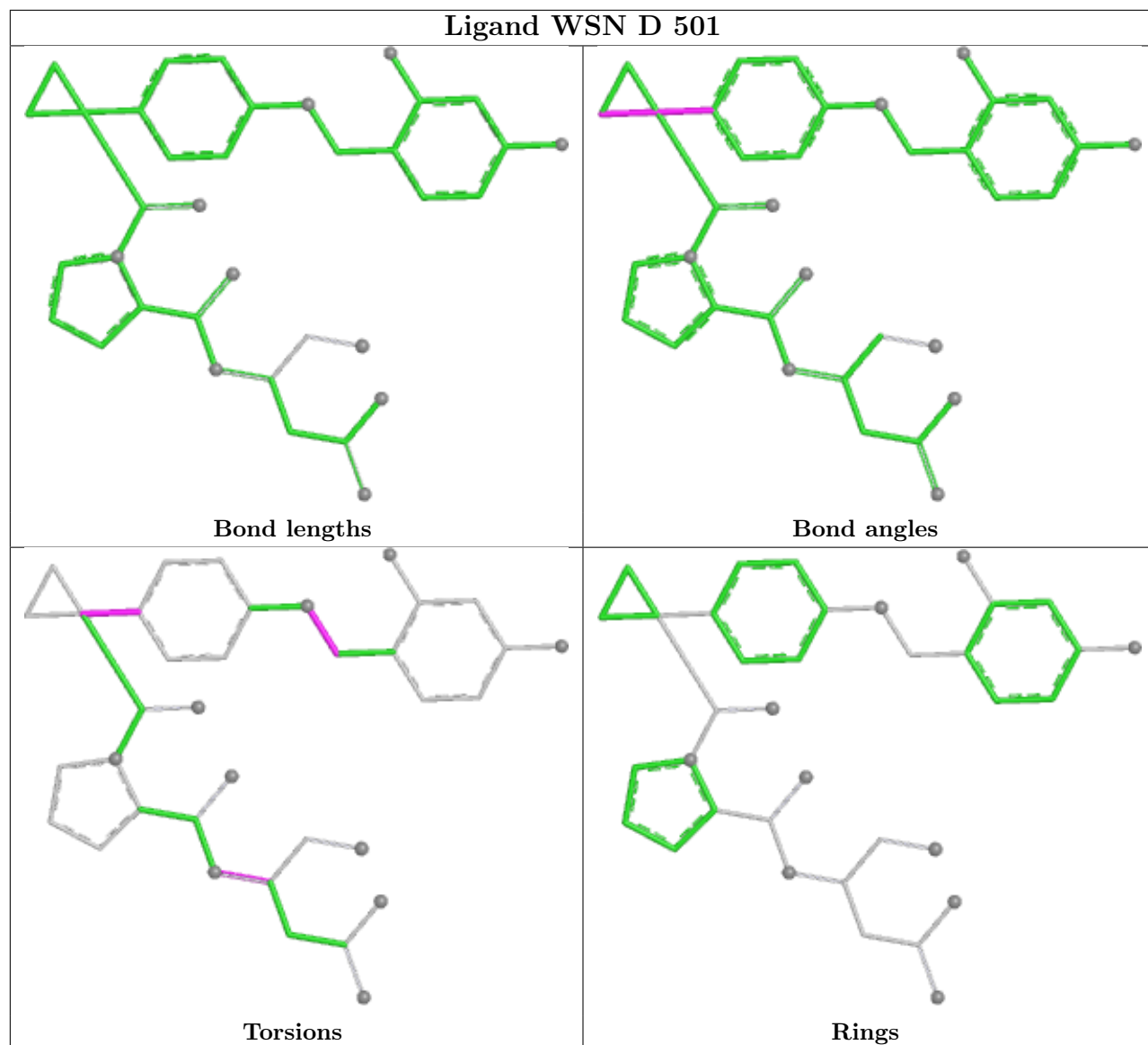
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

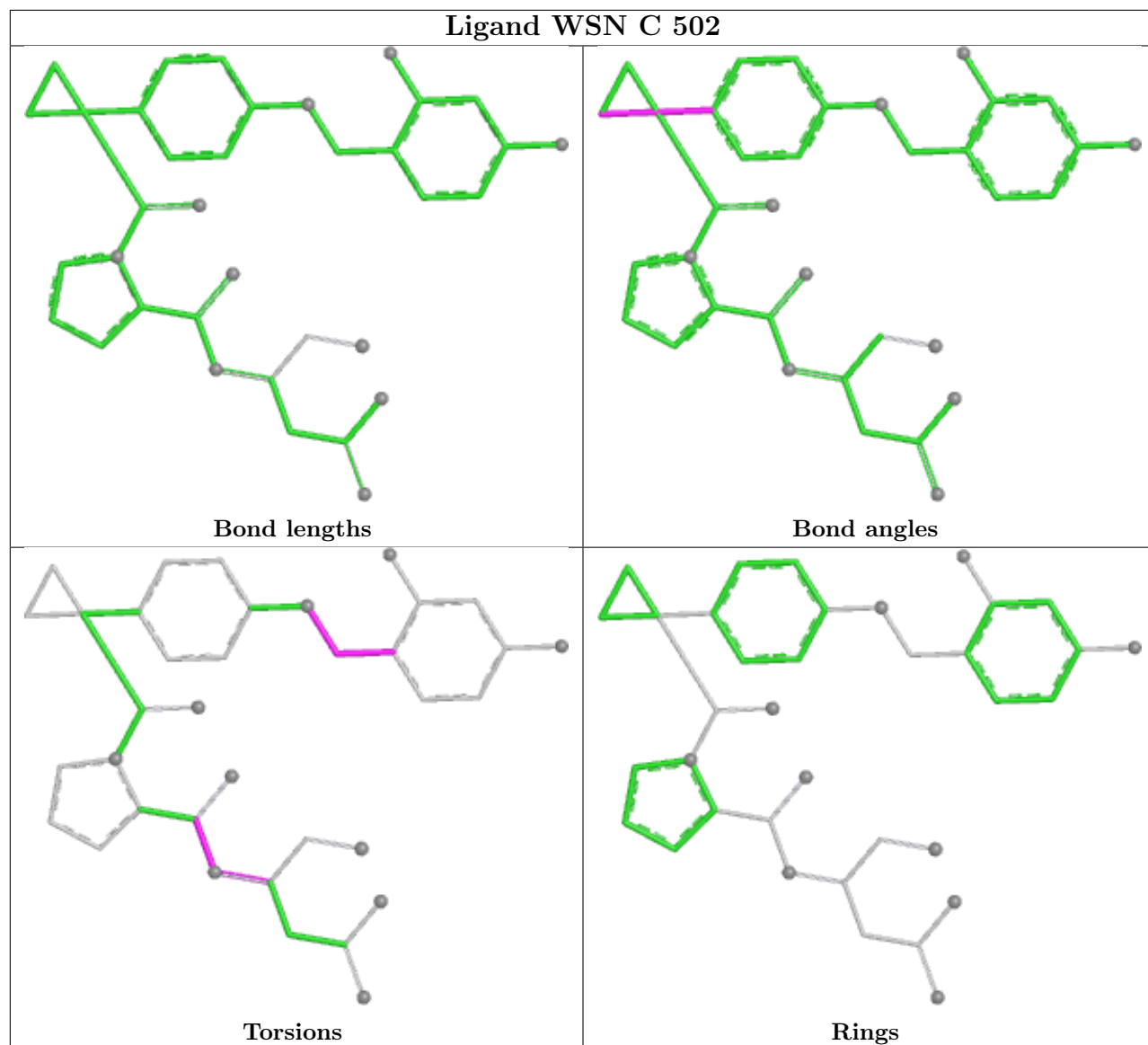


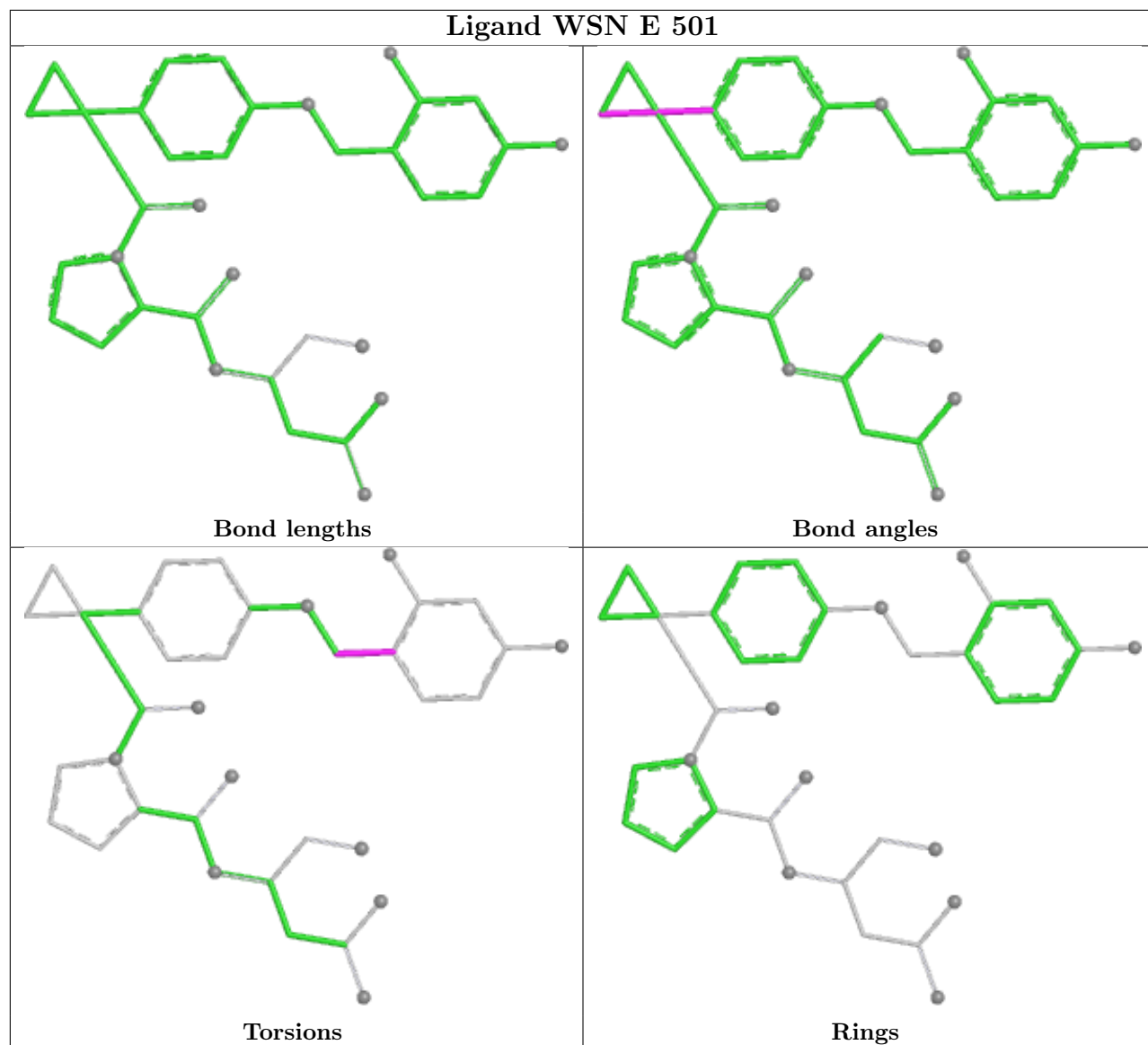


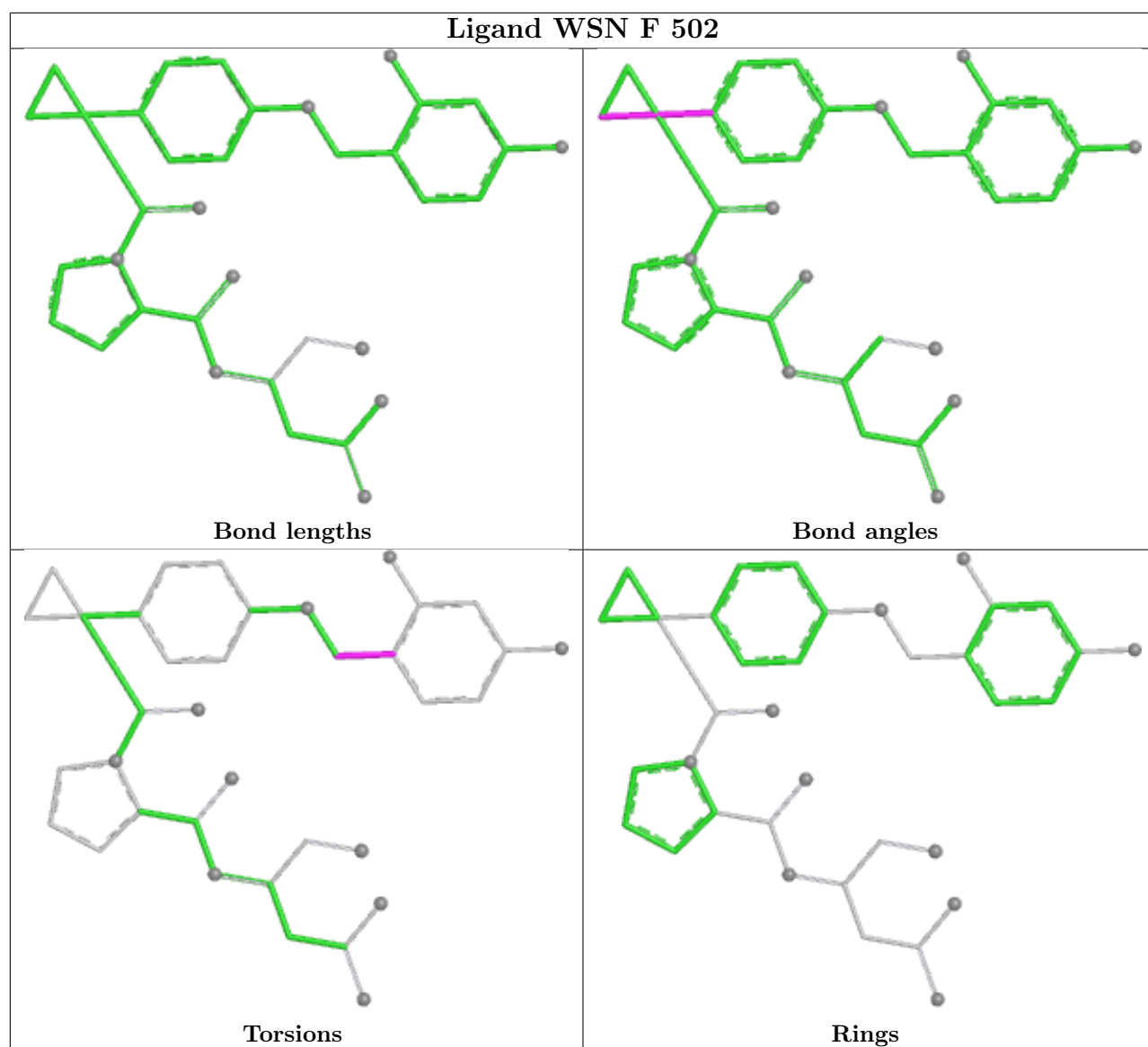












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	259/444 (58%)	0.18	5 (1%) 66 64	21, 38, 55, 71	0
1	B	264/444 (59%)	0.36	5 (1%) 66 64	19, 41, 69, 90	1 (0%)
1	C	260/444 (58%)	0.17	2 (0%) 82 81	19, 38, 57, 73	1 (0%)
1	D	259/444 (58%)	0.31	7 (2%) 56 54	24, 40, 59, 76	0
1	E	263/444 (59%)	0.28	4 (1%) 71 69	23, 42, 66, 103	0
1	F	259/444 (58%)	0.34	4 (1%) 71 69	26, 43, 68, 99	0
1	G	259/444 (58%)	0.42	6 (2%) 61 59	30, 47, 68, 89	0
1	H	259/444 (58%)	0.51	6 (2%) 61 59	32, 51, 78, 96	0
All	All	2082/3552 (58%)	0.32	39 (1%) 66 64	19, 42, 67, 103	2 (0%)

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	290	ALA	5.3
1	B	290	ALA	4.0
1	H	41	TYR	3.8
1	A	171	HIS	3.4
1	B	41[A]	TYR	3.4

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	E	147	7/8	0.91	0.10	30,34,35,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	SNN	G	147	7/8	0.91	0.13	53,55,57,59	0
1	SNN	C	147	7/8	0.93	0.08	27,28,29,31	0
1	SNN	A	147	7/8	0.94	0.09	24,28,30,33	0
1	SNN	D	147	7/8	0.95	0.11	23,27,30,32	0
1	SNN	H	147	7/8	0.95	0.10	37,38,42,50	0
1	SNN	B	147	7/8	0.97	0.06	32,33,36,37	0
1	SNN	F	147	7/8	0.97	0.07	29,31,33,36	0

6.3 Carbohydrates

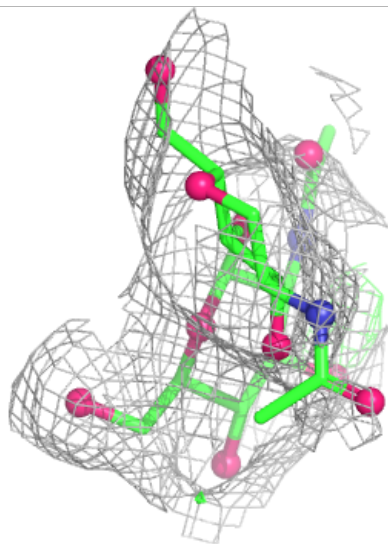
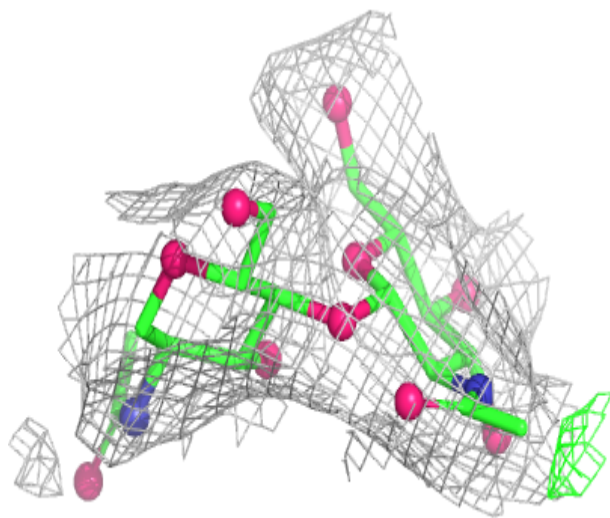
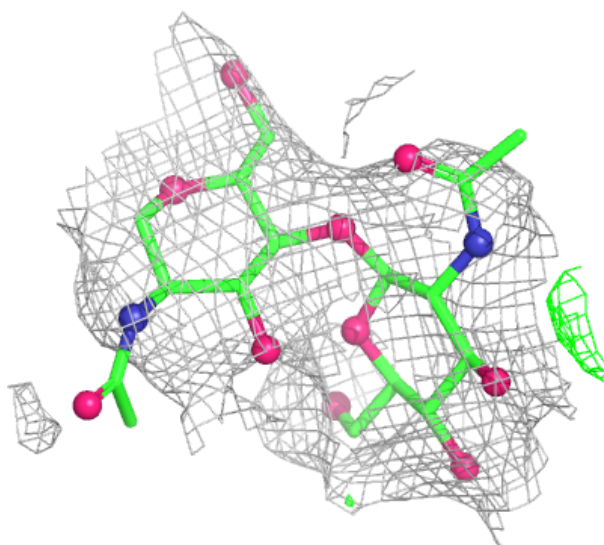
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

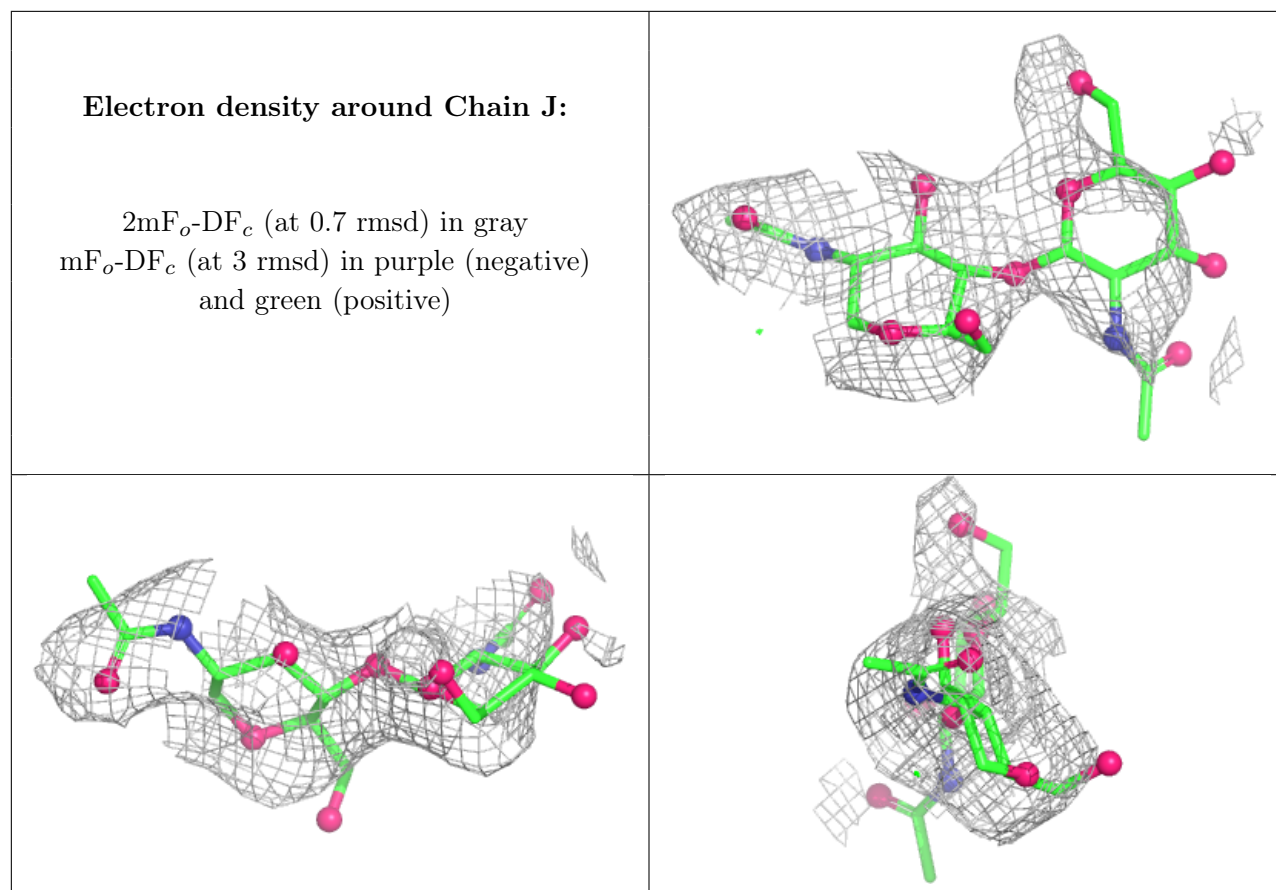
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	J	2	14/15	0.58	0.18	84,98,114,117	0
2	NAG	I	2	14/15	0.68	0.13	51,60,63,63	0
2	NAG	J	1	14/15	0.85	0.12	54,76,85,93	0
2	NAG	I	1	14/15	0.86	0.12	43,57,71,72	0

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 I:

$2mF_o-DF_c$ (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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	C	501	14/15	0.67	0.17	54,60,67,72	0
4	NAG	A	502	14/15	0.71	0.14	60,70,75,76	0
4	NAG	F	501	14/15	0.71	0.14	48,64,76,79	0
4	NAG	D	502	14/15	0.72	0.14	49,60,66,66	0
4	NAG	G	501	14/15	0.77	0.13	52,67,72,73	0
4	NAG	H	503	14/15	0.77	0.12	56,70,78,80	0
5	SO4	B	502	5/5	0.81	0.14	62,65,85,85	0
5	SO4	G	505	5/5	0.82	0.10	56,75,80,80	0
5	SO4	F	505	5/5	0.85	0.08	59,59,72,76	0
3	WSN	D	501	36/36	0.87	0.14	26,35,46,56	0
5	SO4	F	504	5/5	0.87	0.12	55,55,59,78	0
5	SO4	C	503	5/5	0.88	0.09	52,58,72,74	0
3	WSN	E	501	36/36	0.88	0.13	25,31,51,74	0

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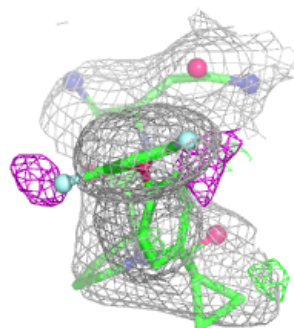
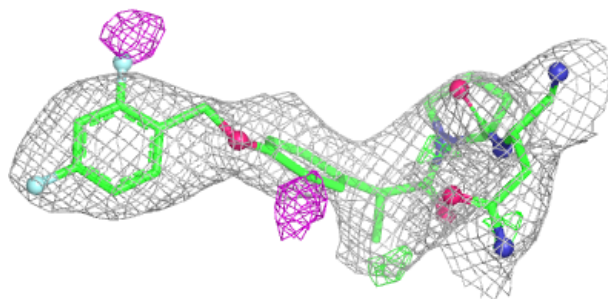
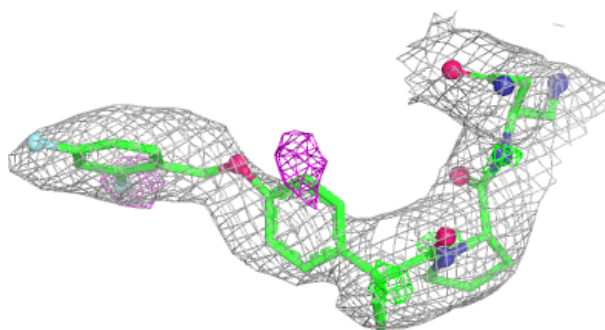
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	WSN	A	501	36/36	0.89	0.11	27,35,40,44	0
3	WSN	B	501	36/36	0.90	0.11	27,36,45,58	0
5	SO4	E	503	5/5	0.90	0.13	54,54,59,72	0
4	NAG	G	503	14/15	0.90	0.10	24,29,38,41	0
4	NAG	E	502	14/15	0.90	0.10	28,35,42,43	0
3	WSN	H	501	36/36	0.90	0.14	29,36,74,82	0
3	WSN	G	502	36/36	0.91	0.13	28,38,61,64	0
3	WSN	C	502	36/36	0.91	0.10	28,36,45,52	0
4	NAG	F	503	14/15	0.93	0.10	27,35,43,43	0
4	NAG	H	502	14/15	0.93	0.09	24,30,40,41	0
3	WSN	F	502	36/36	0.93	0.11	24,33,54,59	0
5	SO4	G	504	5/5	0.95	0.10	43,50,53,59	0
5	SO4	H	504	5/5	0.95	0.11	43,52,57,60	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.

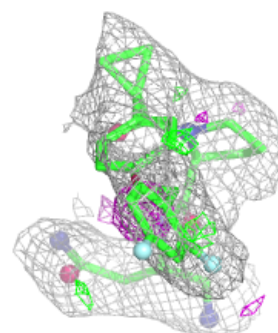
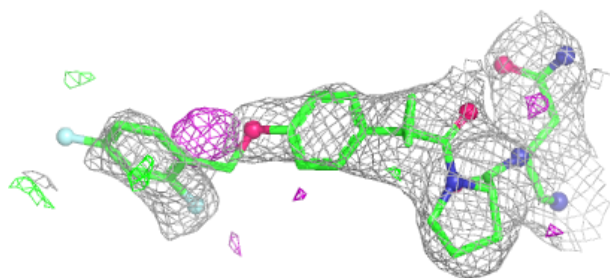
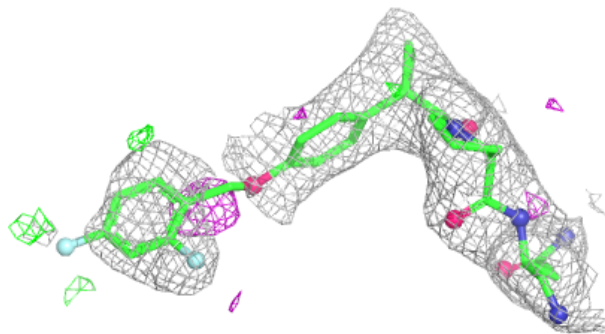
Electron density around WSN D 501:

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

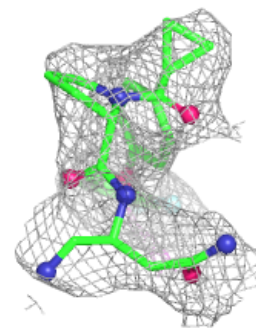
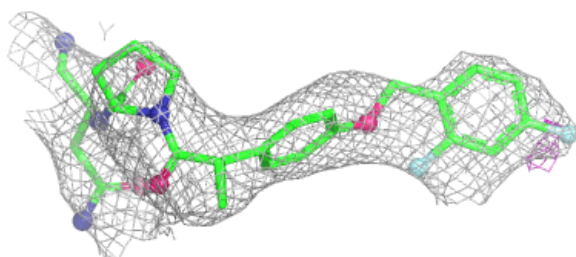
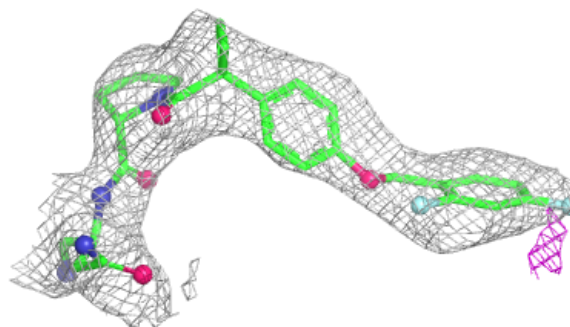


Electron density around WSN E 501:

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

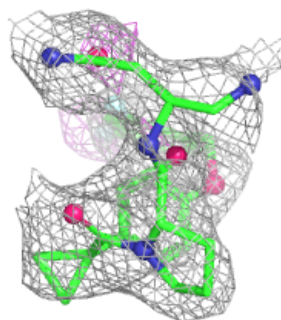
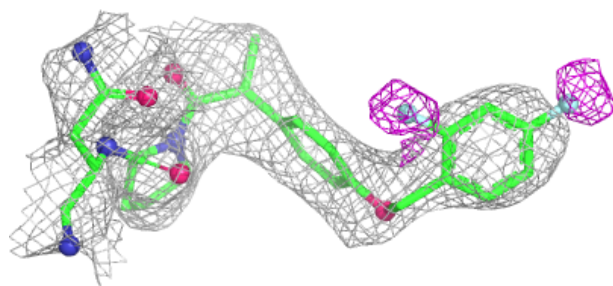
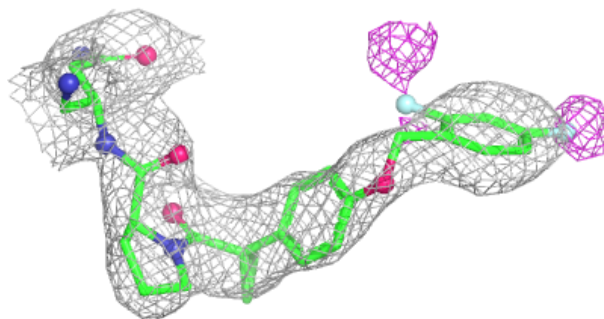
**Electron density around WSN A 501:**

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

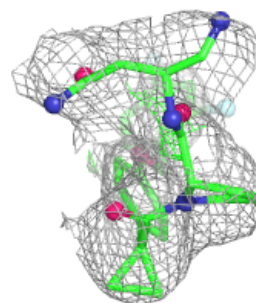
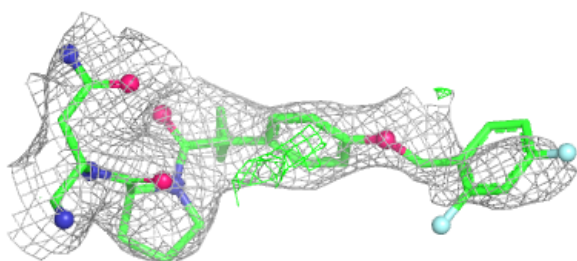
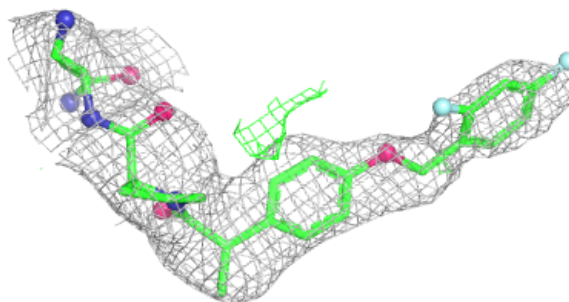


Electron density around WSN B 501:

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

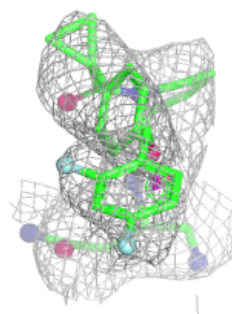
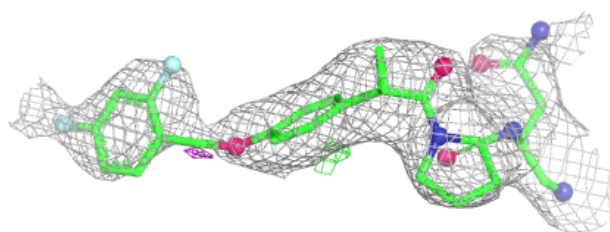
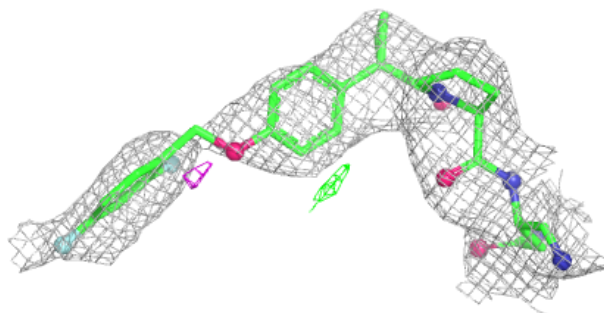
**Electron density around WSN H 501:**

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

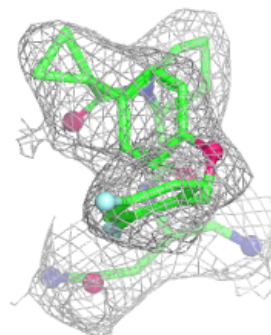
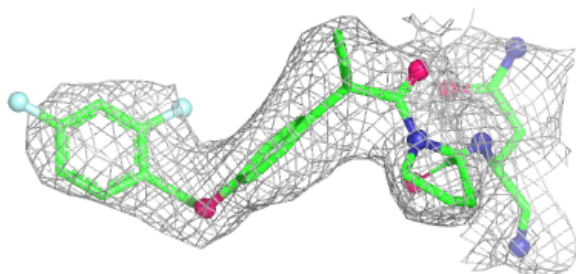
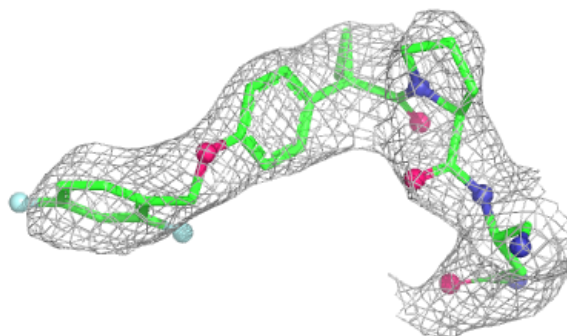


Electron density around WSN G 502:

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

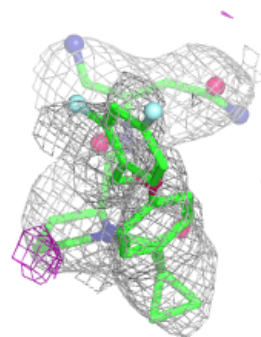
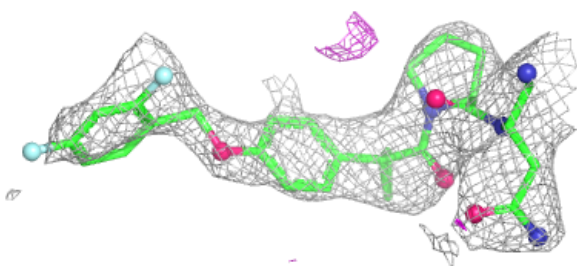
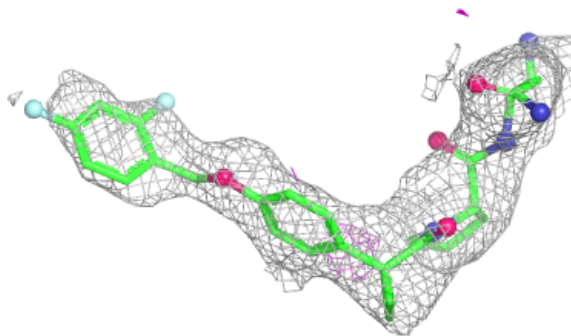
**Electron density around WSN C 502:**

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



Electron density around WSN F 502:

$2mF_o - DF_c$ (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.