



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 12:50 PM BST

PDB ID : 5IJC
Title : The crystal structure of mouse TLR4/MD-2/neoseptin-3 complex
Authors : Wang, Y.; Su, L.; Morin, M.D.; Jones, B.T.; Whitby, L.R.; Surakattula, M.; Huang, H.; Shi, H.; Choi, J.H.; Wang, K.; Moresco, E.M.; Berger, M.; Zhan, X.; Zhang, H.; Boger, D.L.; Beutler, B.
Deposited on : 2016-03-01
Resolution : 2.57 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

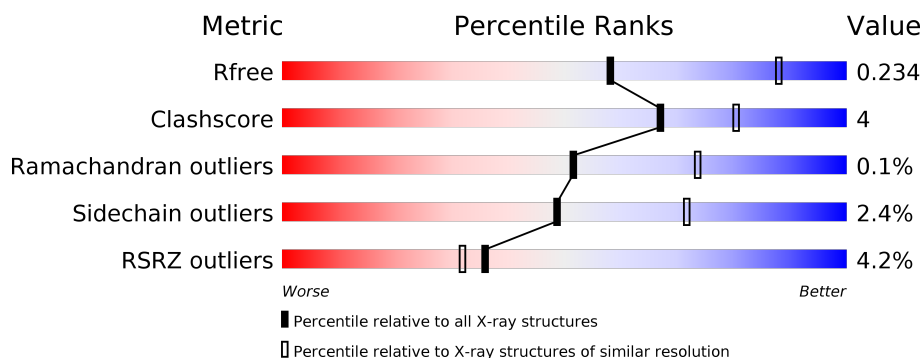
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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.




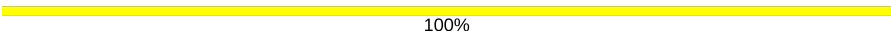

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	635	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>7%</div> </div> </div>
1	B	635	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
2	C	191	<div> <div>%</div> <div> <div></div> <div>55%</div> <div>16%</div> <div>29%</div> </div> </div>
2	D	191	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>10%</div> <div>29%</div> </div> </div>
3	E	2	<div> <div></div> <div>100%</div> </div>
3	F	2	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	2	 50%50%
3	H	2	 100%
3	I	2	 100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12280 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 Toll-like receptor 4, Variable lymphocyte receptor B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	1	0
			4699	3005	782	887	25			
1	B	593	Total	C	N	O	S	0	0	0
			4720	3018	784	893	25			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	expression tag	UNP Q9QUK6
A	-14	LEU	-	expression tag	UNP Q9QUK6
A	-13	LEU	-	expression tag	UNP Q9QUK6
A	-12	VAL	-	expression tag	UNP Q9QUK6
A	-11	ASN	-	expression tag	UNP Q9QUK6
A	-10	GLN	-	expression tag	UNP Q9QUK6
A	-9	SER	-	expression tag	UNP Q9QUK6
A	-8	HIS	-	expression tag	UNP Q9QUK6
A	-7	GLN	-	expression tag	UNP Q9QUK6
A	-6	GLY	-	expression tag	UNP Q9QUK6
A	-5	PHE	-	expression tag	UNP Q9QUK6
A	-4	ASN	-	expression tag	UNP Q9QUK6
A	-3	LYS	-	expression tag	UNP Q9QUK6
A	-2	GLU	-	expression tag	UNP Q9QUK6
A	-1	HIS	-	expression tag	UNP Q9QUK6
A	0	THR	-	expression tag	UNP Q9QUK6
A	1	SER	-	expression tag	UNP Q9QUK6
A	2	LYS	-	expression tag	UNP Q9QUK6
A	3	MET	-	expression tag	UNP Q9QUK6
A	4	VAL	-	expression tag	UNP Q9QUK6
A	5	SER	-	expression tag	UNP Q9QUK6
A	6	ALA	-	expression tag	UNP Q9QUK6
A	7	ILE	-	expression tag	UNP Q9QUK6
A	8	VAL	-	expression tag	UNP Q9QUK6
A	9	LEU	-	expression tag	UNP Q9QUK6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	10	TYR	-	expression tag	UNP Q9QUK6
A	11	VAL	-	expression tag	UNP Q9QUK6
A	12	LEU	-	expression tag	UNP Q9QUK6
A	13	LEU	-	expression tag	UNP Q9QUK6
A	14	ALA	-	expression tag	UNP Q9QUK6
A	15	ALA	-	expression tag	UNP Q9QUK6
A	16	ALA	-	expression tag	UNP Q9QUK6
A	17	ALA	-	expression tag	UNP Q9QUK6
A	18	HIS	-	expression tag	UNP Q9QUK6
A	19	SER	-	expression tag	UNP Q9QUK6
A	20	ALA	-	expression tag	UNP Q9QUK6
A	21	PHE	-	expression tag	UNP Q9QUK6
A	22	ALA	-	expression tag	UNP Q9QUK6
A	23	ALA	-	expression tag	UNP Q9QUK6
A	24	ASP	-	expression tag	UNP Q9QUK6
A	25	PRO	-	expression tag	UNP Q9QUK6
B	-15	MET	-	expression tag	UNP Q9QUK6
B	-14	LEU	-	expression tag	UNP Q9QUK6
B	-13	LEU	-	expression tag	UNP Q9QUK6
B	-12	VAL	-	expression tag	UNP Q9QUK6
B	-11	ASN	-	expression tag	UNP Q9QUK6
B	-10	GLN	-	expression tag	UNP Q9QUK6
B	-9	SER	-	expression tag	UNP Q9QUK6
B	-8	HIS	-	expression tag	UNP Q9QUK6
B	-7	GLN	-	expression tag	UNP Q9QUK6
B	-6	GLY	-	expression tag	UNP Q9QUK6
B	-5	PHE	-	expression tag	UNP Q9QUK6
B	-4	ASN	-	expression tag	UNP Q9QUK6
B	-3	LYS	-	expression tag	UNP Q9QUK6
B	-2	GLU	-	expression tag	UNP Q9QUK6
B	-1	HIS	-	expression tag	UNP Q9QUK6
B	0	THR	-	expression tag	UNP Q9QUK6
B	1	SER	-	expression tag	UNP Q9QUK6
B	2	LYS	-	expression tag	UNP Q9QUK6
B	3	MET	-	expression tag	UNP Q9QUK6
B	4	VAL	-	expression tag	UNP Q9QUK6
B	5	SER	-	expression tag	UNP Q9QUK6
B	6	ALA	-	expression tag	UNP Q9QUK6
B	7	ILE	-	expression tag	UNP Q9QUK6
B	8	VAL	-	expression tag	UNP Q9QUK6
B	9	LEU	-	expression tag	UNP Q9QUK6
B	10	TYR	-	expression tag	UNP Q9QUK6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	11	VAL	-	expression tag	UNP Q9QUK6
B	12	LEU	-	expression tag	UNP Q9QUK6
B	13	LEU	-	expression tag	UNP Q9QUK6
B	14	ALA	-	expression tag	UNP Q9QUK6
B	15	ALA	-	expression tag	UNP Q9QUK6
B	16	ALA	-	expression tag	UNP Q9QUK6
B	17	ALA	-	expression tag	UNP Q9QUK6
B	18	HIS	-	expression tag	UNP Q9QUK6
B	19	SER	-	expression tag	UNP Q9QUK6
B	20	ALA	-	expression tag	UNP Q9QUK6
B	21	PHE	-	expression tag	UNP Q9QUK6
B	22	ALA	-	expression tag	UNP Q9QUK6
B	23	ALA	-	expression tag	UNP Q9QUK6
B	24	ASP	-	expression tag	UNP Q9QUK6
B	25	PRO	-	expression tag	UNP Q9QUK6

- Molecule 2 is a protein called Lymphocyte antigen 96.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	136	Total	C	N	O	S	0	0	0
			1103	712	186	198	7			
2	D	136	Total	C	N	O	S	0	1	0
			1111	717	189	198	7			

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	MET	-	expression tag	UNP Q9JHF9
C	-21	LEU	-	expression tag	UNP Q9JHF9
C	-20	LEU	-	expression tag	UNP Q9JHF9
C	-19	VAL	-	expression tag	UNP Q9JHF9
C	-18	ASN	-	expression tag	UNP Q9JHF9
C	-17	GLN	-	expression tag	UNP Q9JHF9
C	-16	SER	-	expression tag	UNP Q9JHF9
C	-15	HIS	-	expression tag	UNP Q9JHF9
C	-14	GLN	-	expression tag	UNP Q9JHF9
C	-13	GLY	-	expression tag	UNP Q9JHF9
C	-12	PHE	-	expression tag	UNP Q9JHF9
C	-11	ASN	-	expression tag	UNP Q9JHF9
C	-10	LYS	-	expression tag	UNP Q9JHF9
C	-9	GLU	-	expression tag	UNP Q9JHF9
C	-8	HIS	-	expression tag	UNP Q9JHF9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	THR	-	expression tag	UNP Q9JHF9
C	-6	SER	-	expression tag	UNP Q9JHF9
C	-5	LYS	-	expression tag	UNP Q9JHF9
C	-4	MET	-	expression tag	UNP Q9JHF9
C	-3	VAL	-	expression tag	UNP Q9JHF9
C	-2	SER	-	expression tag	UNP Q9JHF9
C	-1	ALA	-	expression tag	UNP Q9JHF9
C	0	ILE	-	expression tag	UNP Q9JHF9
C	1	VAL	-	expression tag	UNP Q9JHF9
C	2	LEU	-	expression tag	UNP Q9JHF9
C	3	TYR	-	expression tag	UNP Q9JHF9
C	4	VAL	-	expression tag	UNP Q9JHF9
C	5	LEU	-	expression tag	UNP Q9JHF9
C	6	LEU	-	expression tag	UNP Q9JHF9
C	7	ALA	-	expression tag	UNP Q9JHF9
C	8	ALA	-	expression tag	UNP Q9JHF9
C	9	ALA	-	expression tag	UNP Q9JHF9
C	10	ALA	-	expression tag	UNP Q9JHF9
C	11	HIS	-	expression tag	UNP Q9JHF9
C	12	SER	-	expression tag	UNP Q9JHF9
C	13	ALA	-	expression tag	UNP Q9JHF9
C	14	PHE	-	expression tag	UNP Q9JHF9
C	15	ALA	-	expression tag	UNP Q9JHF9
C	16	ALA	-	expression tag	UNP Q9JHF9
C	17	ASP	-	expression tag	UNP Q9JHF9
C	18	PRO	-	expression tag	UNP Q9JHF9
C	161	LYS	-	expression tag	UNP Q9JHF9
C	162	GLY	-	expression tag	UNP Q9JHF9
C	163	GLU	-	expression tag	UNP Q9JHF9
C	164	ASN	-	expression tag	UNP Q9JHF9
C	165	LEU	-	expression tag	UNP Q9JHF9
C	166	TYR	-	expression tag	UNP Q9JHF9
C	167	PHE	-	expression tag	UNP Q9JHF9
C	168	GLN	-	expression tag	UNP Q9JHF9
D	-22	MET	-	expression tag	UNP Q9JHF9
D	-21	LEU	-	expression tag	UNP Q9JHF9
D	-20	LEU	-	expression tag	UNP Q9JHF9
D	-19	VAL	-	expression tag	UNP Q9JHF9
D	-18	ASN	-	expression tag	UNP Q9JHF9
D	-17	GLN	-	expression tag	UNP Q9JHF9
D	-16	SER	-	expression tag	UNP Q9JHF9
D	-15	HIS	-	expression tag	UNP Q9JHF9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-14	GLN	-	expression tag	UNP Q9JHF9
D	-13	GLY	-	expression tag	UNP Q9JHF9
D	-12	PHE	-	expression tag	UNP Q9JHF9
D	-11	ASN	-	expression tag	UNP Q9JHF9
D	-10	LYS	-	expression tag	UNP Q9JHF9
D	-9	GLU	-	expression tag	UNP Q9JHF9
D	-8	HIS	-	expression tag	UNP Q9JHF9
D	-7	THR	-	expression tag	UNP Q9JHF9
D	-6	SER	-	expression tag	UNP Q9JHF9
D	-5	LYS	-	expression tag	UNP Q9JHF9
D	-4	MET	-	expression tag	UNP Q9JHF9
D	-3	VAL	-	expression tag	UNP Q9JHF9
D	-2	SER	-	expression tag	UNP Q9JHF9
D	-1	ALA	-	expression tag	UNP Q9JHF9
D	0	ILE	-	expression tag	UNP Q9JHF9
D	1	VAL	-	expression tag	UNP Q9JHF9
D	2	LEU	-	expression tag	UNP Q9JHF9
D	3	TYR	-	expression tag	UNP Q9JHF9
D	4	VAL	-	expression tag	UNP Q9JHF9
D	5	LEU	-	expression tag	UNP Q9JHF9
D	6	LEU	-	expression tag	UNP Q9JHF9
D	7	ALA	-	expression tag	UNP Q9JHF9
D	8	ALA	-	expression tag	UNP Q9JHF9
D	9	ALA	-	expression tag	UNP Q9JHF9
D	10	ALA	-	expression tag	UNP Q9JHF9
D	11	HIS	-	expression tag	UNP Q9JHF9
D	12	SER	-	expression tag	UNP Q9JHF9
D	13	ALA	-	expression tag	UNP Q9JHF9
D	14	PHE	-	expression tag	UNP Q9JHF9
D	15	ALA	-	expression tag	UNP Q9JHF9
D	16	ALA	-	expression tag	UNP Q9JHF9
D	17	ASP	-	expression tag	UNP Q9JHF9
D	18	PRO	-	expression tag	UNP Q9JHF9
D	161	LYS	-	expression tag	UNP Q9JHF9
D	162	GLY	-	expression tag	UNP Q9JHF9
D	163	GLU	-	expression tag	UNP Q9JHF9
D	164	ASN	-	expression tag	UNP Q9JHF9
D	165	LEU	-	expression tag	UNP Q9JHF9
D	166	TYR	-	expression tag	UNP Q9JHF9
D	167	PHE	-	expression tag	UNP Q9JHF9
D	168	GLN	-	expression tag	UNP Q9JHF9

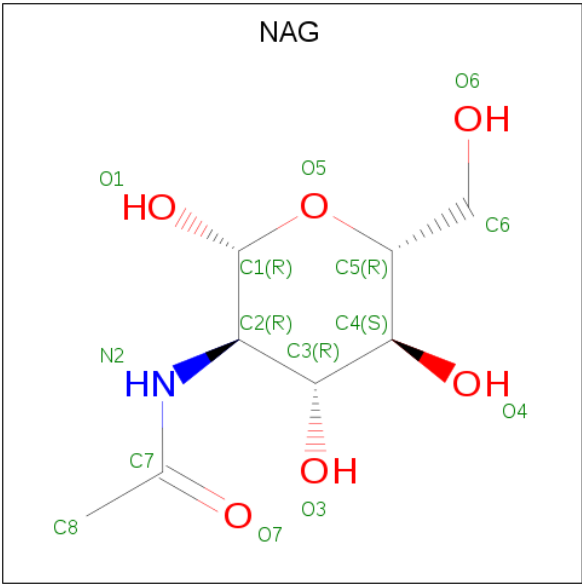
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a

cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



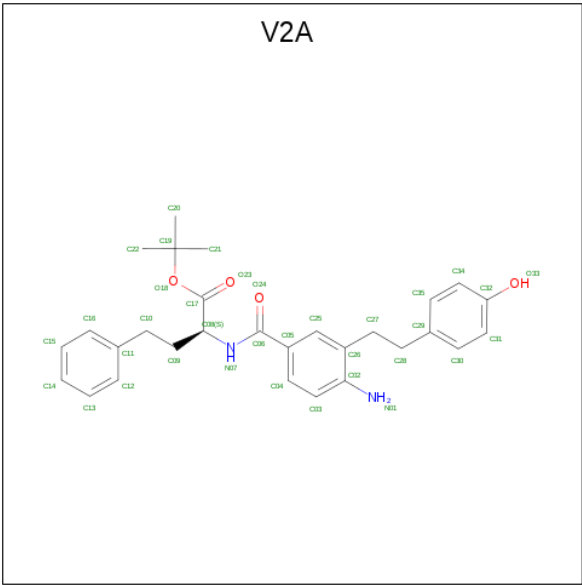
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

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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	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	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	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is neoseptin 3 (three-letter code: V2A) (formula: C₂₉H₃₄N₂O₄) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			35	29	2	4		
5	B	1	Total	C	N	O	0	0
			35	29	2	4		
5	B	1	Total	C	N	O	0	0
			35	29	2	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			35	29	2	4		

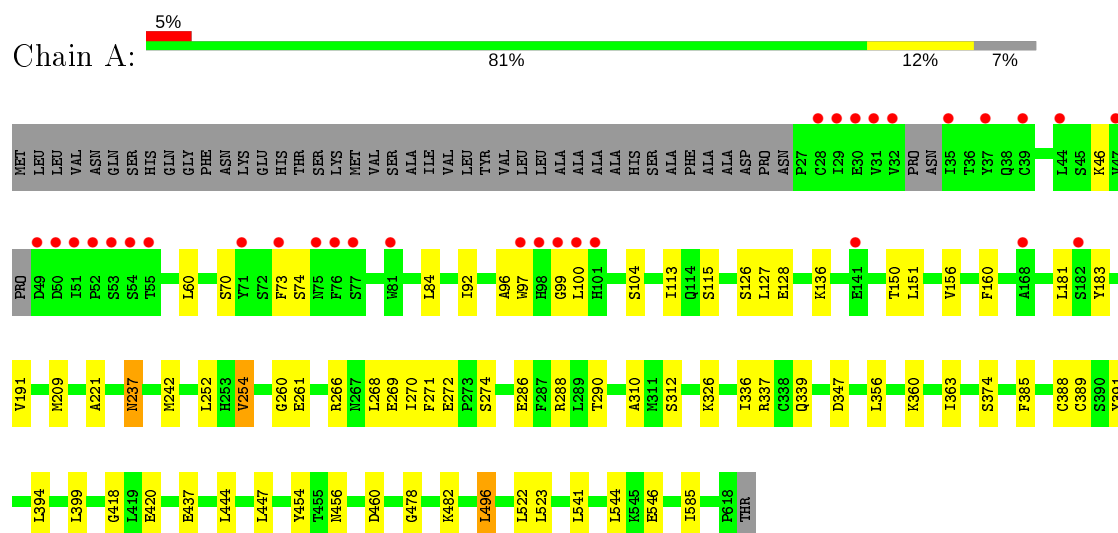
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	88	Total	O	0	0
			88	88		
6	C	21	Total	O	0	0
			21	21		
6	B	85	Total	O	0	0
			85	85		
6	D	19	Total	O	0	0
			19	19		

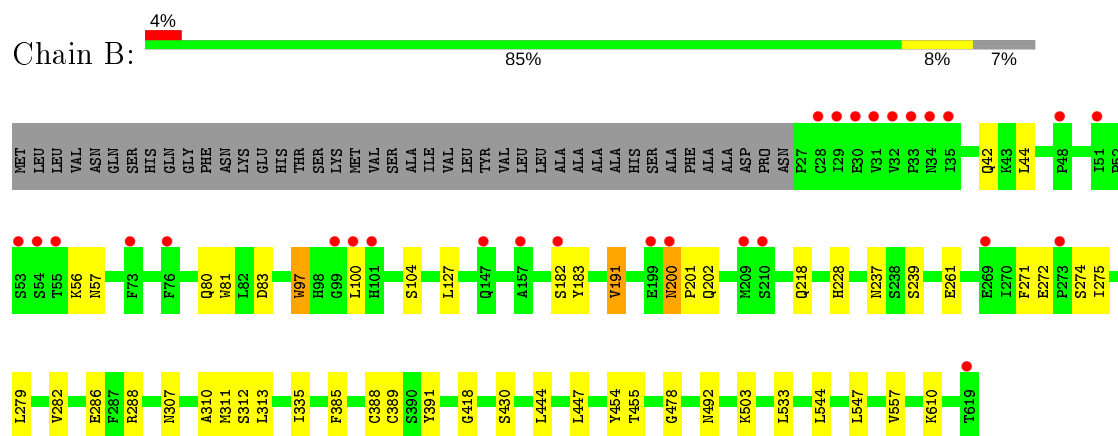
3 Residue-property plots [i](#)

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.

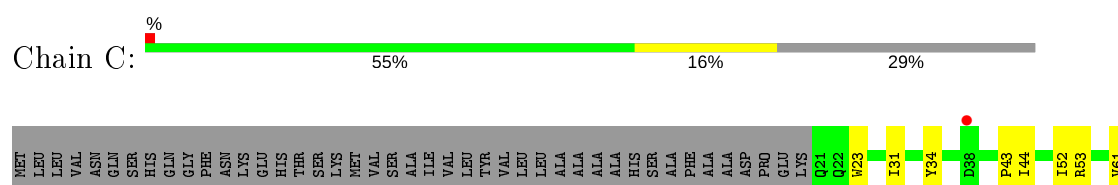
- Molecule 1: Toll-like receptor 4,Variable lymphocyte receptor B



- Molecule 1: Toll-like receptor 4,Variable lymphocyte receptor B

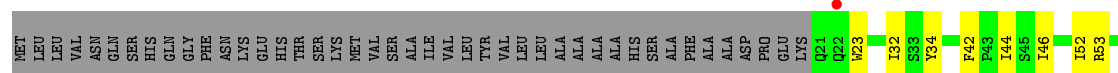


- Molecule 2: Lymphocyte antigen 96





- Molecule 2: Lymphocyte antigen 96



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



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



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



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



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



2019
MAG

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.75Å 148.56Å 131.72Å 90.00° 98.30° 90.00°	Depositor
Resolution (Å)	42.36 – 2.57 42.36 – 2.57	Depositor EDS
% Data completeness (in resolution range)	85.3 (42.36-2.57) 85.3 (42.36-2.57)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472, PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.193 , 0.234 0.194 , 0.234	Depositor DCC
R_{free} test set	2000 reflections (2.73%)	wwPDB-VP
Wilson B-factor (Å ²)	38.9	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.9	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	0.93	EDS
Total number of atoms	12280	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 3.04% 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: V2A, 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	0.25	0/4799	0.46	0/6497
1	B	0.25	0/4821	0.44	0/6534
2	C	0.26	0/1134	0.47	0/1533
2	D	0.26	0/1145	0.46	0/1547
All	All	0.25	0/11899	0.45	0/16111

There are no bond length outliers.

There are no bond angle outliers.

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	4699	0	4682	40	0
1	B	4720	0	4699	25	0
2	C	1103	0	1062	15	0
2	D	1111	0	1075	13	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	1	0
3	H	28	0	25	2	0
3	I	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	56	0	52	2	0
4	B	56	0	52	2	0
4	C	14	0	13	0	0
4	D	28	0	26	0	0
5	A	35	0	0	0	0
5	B	70	0	0	1	0
5	D	35	0	0	2	0
6	A	88	0	0	0	0
6	B	85	0	0	0	0
6	C	21	0	0	0	0
6	D	19	0	0	0	0
All	All	12280	0	11786	93	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 4.

All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:SER:HA	1:A:96:ALA:HA	1.66	0.77
2:C:128:LYS:HE3	2:C:156:ARG:HB2	1.64	0.77
1:A:237:ASN:OD1	1:A:266:ARG:HB2	1.91	0.71
1:B:97:TRP:HB3	1:B:100:LEU:HD12	1.78	0.66
1:A:391:TYR:HB2	1:A:418:GLY:HA3	1.80	0.63
1:A:128:GLU:HA	1:A:151:LEU:HA	1.80	0.63
1:A:336:ILE:HG22	1:A:337:ARG:HG3	1.82	0.61
1:A:460:ASP:HB3	1:A:482:LYS:HB2	1.84	0.59
3:G:1:NAG:H3	3:G:1:NAG:H83	1.85	0.58
2:D:90[B]:ARG:NH1	5:D:201:V2A:O24	2.35	0.58
2:D:90[B]:ARG:HH12	5:D:201:V2A:C06	2.17	0.57
4:A:704:NAG:H3	4:A:704:NAG:H83	1.87	0.57
1:A:113:ILE:O	1:A:115:SER:N	2.36	0.56
4:B:704:NAG:H83	4:B:704:NAG:H3	1.88	0.56
1:B:279:LEU:HA	1:B:282:VAL:HG12	1.87	0.56
1:A:104:SER:HA	1:A:127:LEU:HA	1.87	0.55
2:D:46:ILE:HG12	2:D:63:VAL:HG22	1.87	0.55
2:C:31:ILE:HG12	2:C:154:ILE:HB	1.88	0.55
1:A:286:GLU:HG2	1:A:310:ALA:HB3	1.89	0.54
1:A:191:VAL:HG12	1:A:221:ALA:HA	1.89	0.54
1:B:239:SER:HB3	1:B:275:ILE:HD11	1.90	0.53
2:C:67:PRO:HD2	2:C:111:GLU:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:SER:HA	1:A:150:THR:HG21	1.91	0.53
1:A:288:ARG:HG3	1:A:312:SER:HB3	1.90	0.52
2:C:76:PHE:HE2	2:C:94:LEU:HD12	1.75	0.52
1:B:272:GLU:HG3	1:B:274:SER:H	1.75	0.52
1:A:252:LEU:HD11	1:A:254:VAL:HG13	1.94	0.50
1:A:339:GLN:HG2	1:A:360:LYS:HD2	1.91	0.50
1:A:522:LEU:HD13	1:A:546:GLU:HB2	1.94	0.50
1:B:182:SER:OG	2:D:106:ARG:NH2	2.45	0.49
1:A:73:PHE:HB3	1:A:100:LEU:HD21	1.95	0.49
1:B:503:LYS:NZ	3:H:2:NAG:H81	2.27	0.49
2:C:52:ILE:HG21	5:B:701:V2A:C16	2.44	0.48
1:B:313:LEU:HD12	1:B:335:ILE:HD12	1.95	0.48
1:A:266:ARG:HH11	4:A:703:NAG:H82	1.78	0.48
1:A:437:GLU:O	2:D:90[A]:ARG:NH2	2.47	0.48
1:A:269:GLU:HG2	1:A:270:ILE:HG12	1.96	0.47
2:D:32:ILE:HD13	2:D:52:ILE:HB	1.96	0.47
1:B:288:ARG:HH21	2:D:99:ASP:CG	2.18	0.47
1:A:374:SER:HA	1:A:399:LEU:HA	1.97	0.47
1:B:444:LEU:HB3	1:B:447:LEU:HB2	1.95	0.47
1:B:288:ARG:HG3	1:B:312:SER:HB3	1.97	0.47
1:B:311:MET:HB2	1:B:311:MET:HE2	1.72	0.47
1:B:430:SER:O	1:B:455:THR:HA	2.14	0.47
2:D:42:PHE:CD2	2:D:68:ARG:HG3	2.50	0.46
1:B:454:TYR:CD1	1:B:478:GLY:HA3	2.50	0.46
1:B:81:TRP:CZ3	1:B:83:ASP:HB2	2.50	0.46
3:H:1:NAG:H61	3:H:2:NAG:C7	2.45	0.46
2:D:141:ASP:N	2:D:141:ASP:OD1	2.41	0.46
1:B:544:LEU:HD21	1:B:547:LEU:HB2	1.98	0.46
1:A:136:LYS:HG2	1:A:160:PHE:HE2	1.81	0.46
1:B:388:CYS:HA	1:B:389:CYS:HA	1.70	0.46
1:A:181:LEU:HB2	1:A:209:MET:HE1	1.99	0.45
2:D:23:TRP:HB3	2:D:34:TYR:CE1	2.52	0.45
2:D:67:PRO:HD2	2:D:111:GLU:O	2.17	0.45
1:A:444:LEU:HB3	1:A:447:LEU:HB2	1.99	0.44
1:A:156:VAL:HG23	1:A:181:LEU:HD23	2.00	0.44
1:B:391:TYR:HB2	1:B:418:GLY:HA3	1.99	0.44
2:C:66:ILE:O	2:C:68:ARG:NH1	2.50	0.44
2:C:155:HIS:O	2:C:156:ARG:HB3	2.17	0.44
2:C:79:PHE:HE1	2:C:89:LYS:HD3	1.83	0.44
1:B:286:GLU:HG2	1:B:310:ALA:HB3	1.99	0.44
1:B:56:LYS:HD3	1:B:80:GLN:OE1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:106:ARG:NH1	2:C:111:GLU:OE1	2.52	0.43
1:A:541:LEU:HB3	1:A:544:LEU:HB2	2.00	0.43
1:A:74:SER:HA	1:A:99:GLY:HA3	2.00	0.43
1:B:200:ASN:HB3	1:B:202:GLN:OE1	2.19	0.43
1:A:388:CYS:HA	1:A:389:CYS:HA	1.79	0.43
1:B:228:HIS:NE2	4:B:703:NAG:H3	2.34	0.43
2:D:80:ILE:HD12	2:D:90[A]:ARG:NH1	2.34	0.42
1:A:242:MET:SD	1:A:268:LEU:HD11	2.59	0.42
1:A:454:TYR:CD1	1:A:478:GLY:HA3	2.54	0.42
1:B:42:GLN:HB2	1:B:44:LEU:HG	2.02	0.42
2:D:44:ILE:HG13	2:D:65:PHE:HB3	2.00	0.42
1:A:181:LEU:HD12	1:A:209:MET:HE1	2.01	0.42
2:C:23:TRP:HB3	2:C:34:TYR:CE2	2.54	0.42
1:A:46:LYS:HA	1:A:46:LYS:HD2	1.78	0.42
1:A:60:LEU:HB3	1:A:84:LEU:HD23	2.02	0.42
1:B:191:VAL:HG13	1:B:218:GLN:OE1	2.20	0.42
1:B:533:LEU:HD12	1:B:557:VAL:HG12	2.01	0.42
2:C:44:ILE:HG13	2:C:65:PHE:HB3	2.01	0.41
1:A:272:GLU:HG2	1:A:274:SER:H	1.85	0.41
1:A:326:LYS:NZ	1:A:347:ASP:HB3	2.35	0.41
1:A:522:LEU:HD12	1:A:523:LEU:N	2.35	0.41
1:A:496:LEU:HA	1:A:496:LEU:HD12	1.86	0.41
1:A:288:ARG:HD3	2:C:99:ASP:OD2	2.21	0.41
2:C:43:PRO:HD2	2:C:68:ARG:NH2	2.35	0.41
1:A:394:LEU:HD13	1:A:399:LEU:HD22	2.03	0.41
1:B:104:SER:HA	1:B:127:LEU:HA	2.03	0.41
2:C:61:VAL:HG23	2:C:119:PHE:CD2	2.55	0.41
1:A:260:GLY:HA3	1:A:290:THR:OG1	2.21	0.41
2:C:72:LYS:HD3	2:C:73:TYR:CE2	2.56	0.40
1:A:92:ILE:HD13	1:A:97:TRP:CH2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	584/635 (92%)	559 (96%)	25 (4%)	0	100	100
1	B	591/635 (93%)	560 (95%)	30 (5%)	1 (0%)	47	69
2	C	134/191 (70%)	130 (97%)	4 (3%)	0	100	100
2	D	135/191 (71%)	131 (97%)	4 (3%)	0	100	100
All	All	1444/1652 (87%)	1380 (96%)	63 (4%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	201	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	547/583 (94%)	535 (98%)	12 (2%)	52	74
1	B	550/583 (94%)	538 (98%)	12 (2%)	52	74
2	C	123/168 (73%)	118 (96%)	5 (4%)	30	54
2	D	124/168 (74%)	121 (98%)	3 (2%)	49	72
All	All	1344/1502 (90%)	1312 (98%)	32 (2%)	49	72

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	TYR
1	A	237	ASN
1	A	254	VAL
1	A	261	GLU
1	A	271	PHE
1	A	356	LEU
1	A	363	ILE

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Mol	Chain	Res	Type
1	A	385	PHE
1	A	420	GLU
1	A	456	ASN
1	A	496	LEU
1	A	585	ILE
2	C	53	ARG
2	C	81	SER
2	C	90	ARG
2	C	130	HIS
2	C	131	TYR
1	B	57	ASN
1	B	97	TRP
1	B	183	TYR
1	B	191	VAL
1	B	200	ASN
1	B	237	ASN
1	B	261	GLU
1	B	271	PHE
1	B	307	ASN
1	B	385	PHE
1	B	492	ASN
1	B	610	LYS
2	D	53	ARG
2	D	131	TYR
2	D	134	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

10 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	$\# Z > 2$
3	NAG	E	1	1,3	14,14,15	0.30	0	17,19,21	0.41	0
3	NAG	E	2	3	14,14,15	0.24	0	17,19,21	0.51	0
3	NAG	F	1	1,3	14,14,15	0.37	0	17,19,21	0.48	0
3	NAG	F	2	3	14,14,15	0.24	0	17,19,21	0.61	0
3	NAG	G	1	3,2	14,14,15	0.24	0	17,19,21	1.33	2 (11%)
3	NAG	G	2	3	14,14,15	0.34	0	17,19,21	0.52	0
3	NAG	H	1	1,3	14,14,15	0.30	0	17,19,21	0.44	0
3	NAG	H	2	3	14,14,15	0.32	0	17,19,21	0.39	0
3	NAG	I	1	1,3	14,14,15	0.39	0	17,19,21	0.74	0
3	NAG	I	2	3	14,14,15	0.21	0	17,19,21	0.70	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
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	NAG	G	1	3,2	-	5/6/23/26	0/1/1/1
3	NAG	G	2	3	-	3/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1	NAG	C2-N2-C7	4.33	129.07	122.90
3	G	1	NAG	C1-C2-N2	2.10	114.07	110.49

There are no chirality outliers.

All (21) torsion outliers are listed below:

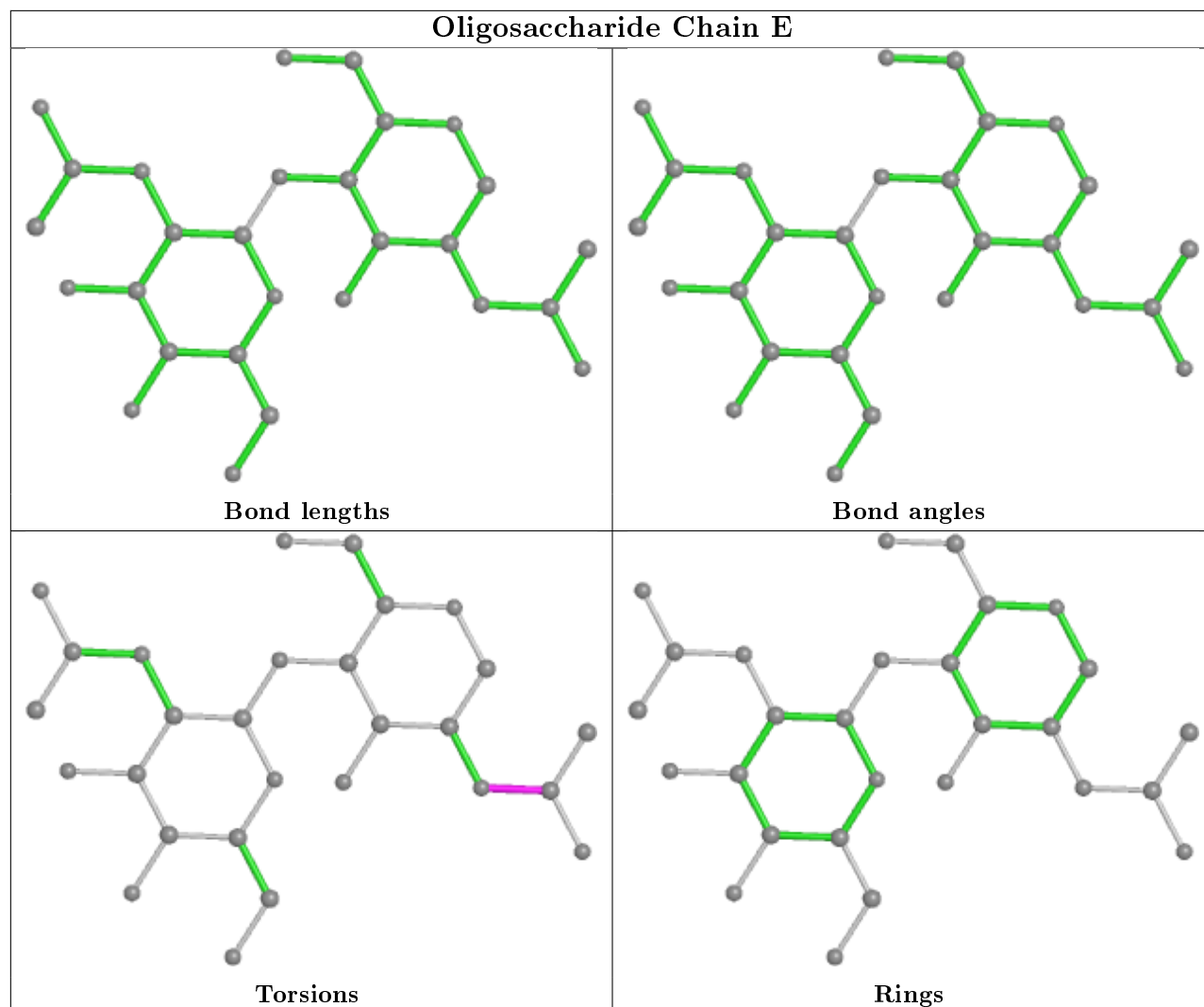
Mol	Chain	Res	Type	Atoms
3	F	1	NAG	O5-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2
3	E	1	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	F	1	NAG	C8-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
3	G	2	NAG	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	I	2	NAG	C1-C2-N2-C7
3	G	1	NAG	C3-C2-N2-C7
3	G	2	NAG	C3-C2-N2-C7
3	I	2	NAG	C3-C2-N2-C7

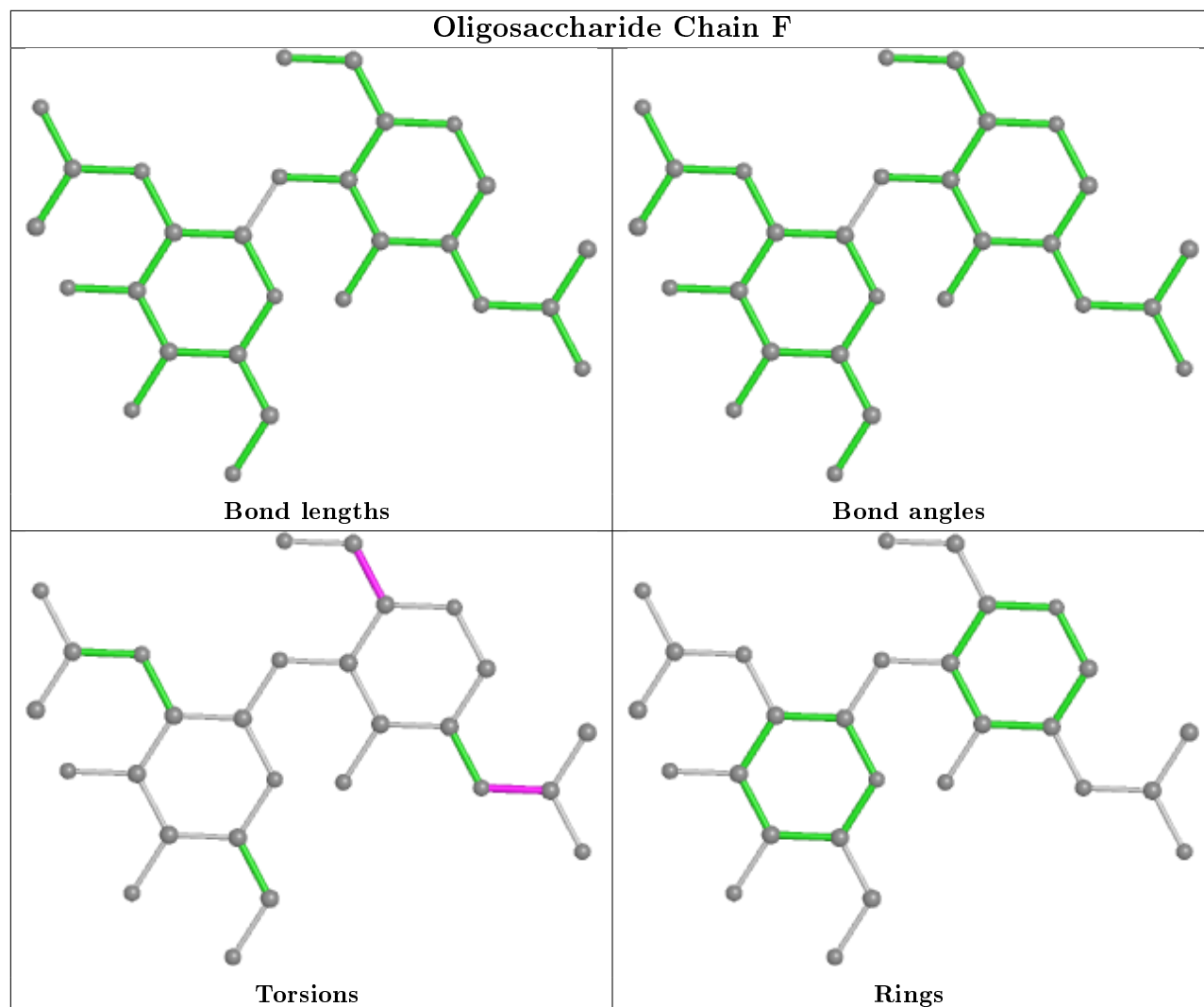
There are no ring outliers.

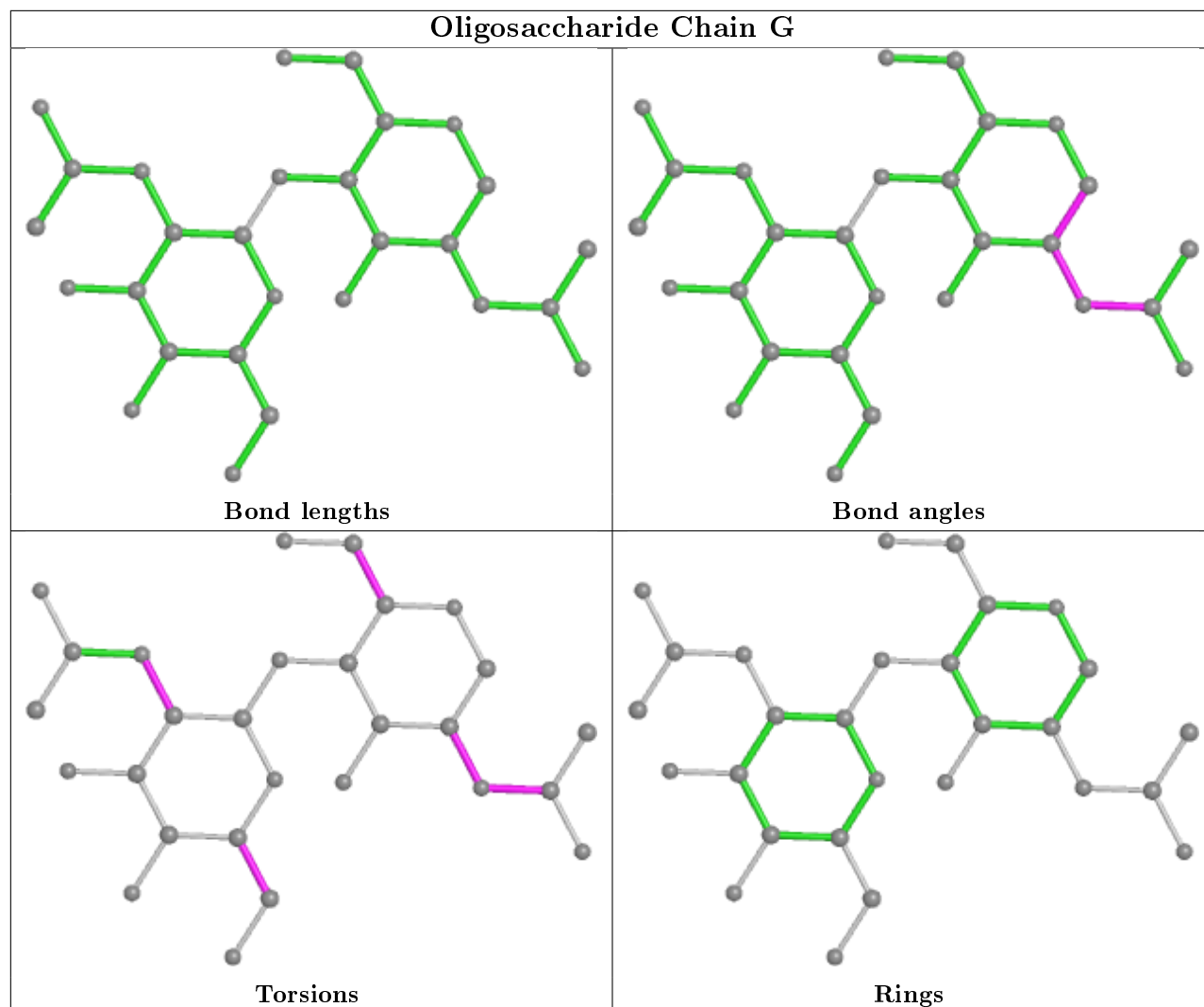
3 monomers are involved in 3 short contacts:

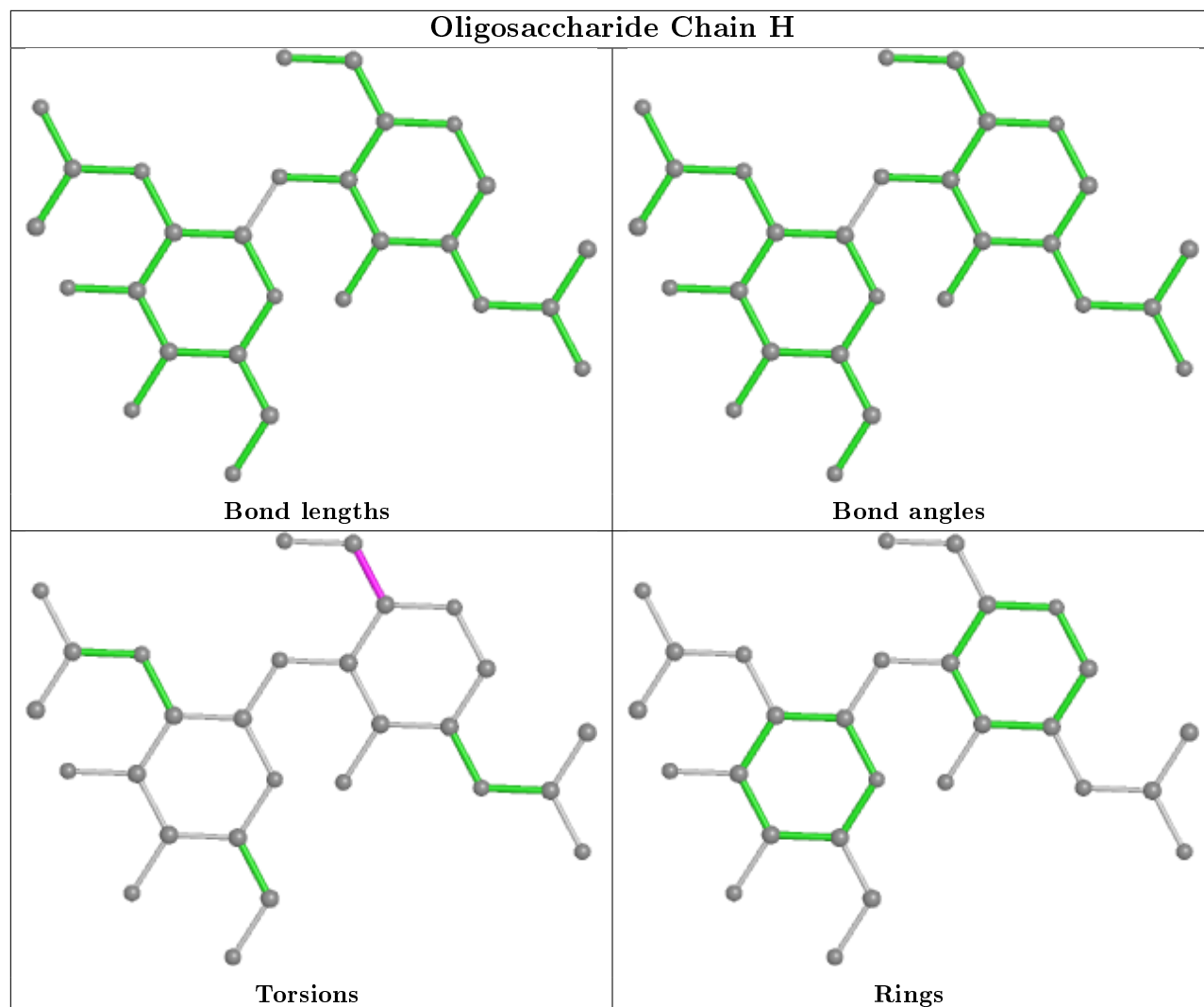
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1	NAG	1	0
3	H	1	NAG	1	0
3	H	2	NAG	2	0

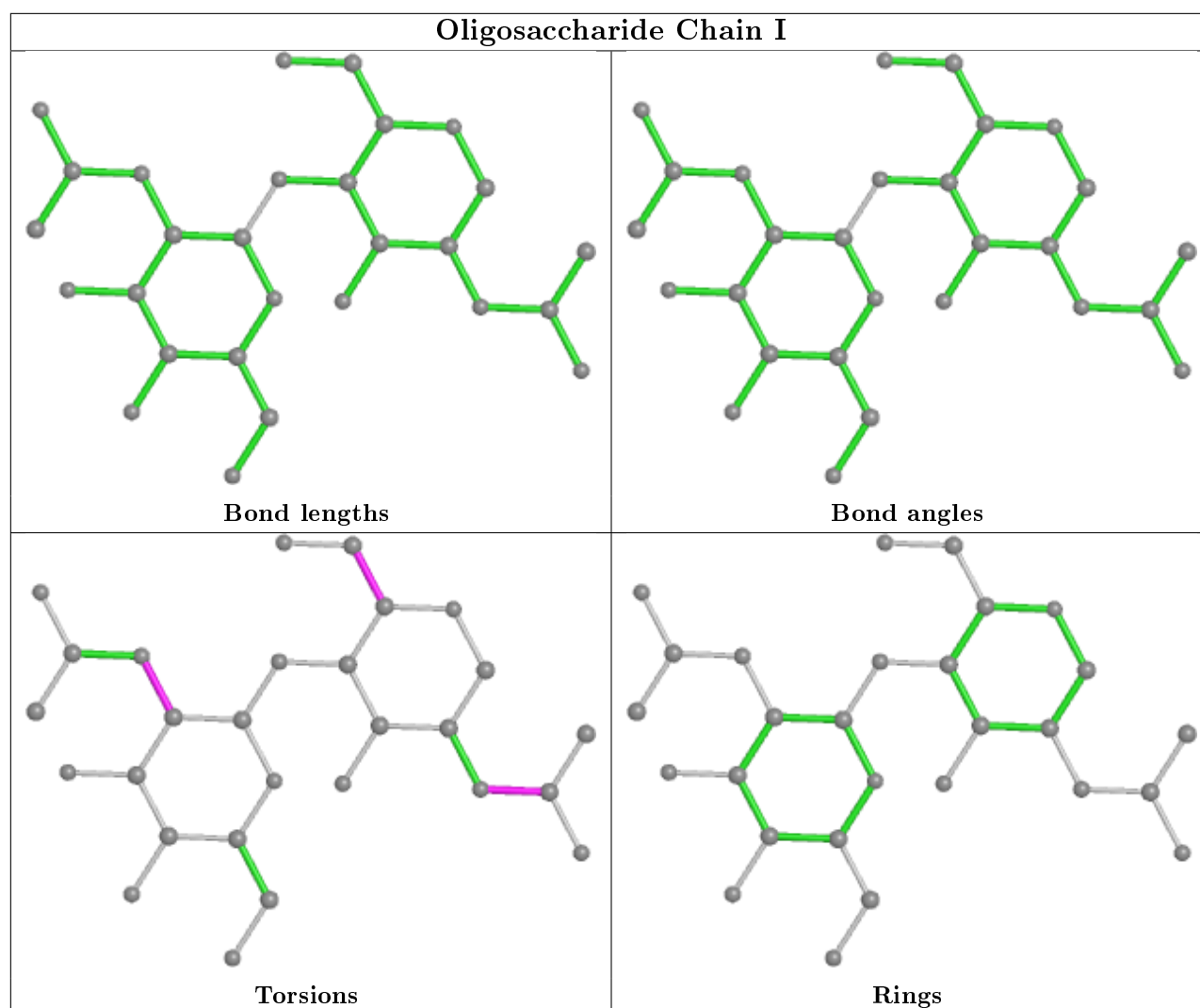
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry ⓘ

15 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	V2A	A	709	-	37,37,37	1.60	5 (13%)	51,51,51	1.19	2 (3%)
4	NAG	A	706	1	14,14,15	0.57	0	17,19,21	0.51	0
4	NAG	B	704	1	14,14,15	0.61	0	17,19,21	1.48	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	703	1	14,14,15	0.47	0	17,19,21	0.53	0
4	NAG	A	703	1	14,14,15	0.44	0	17,19,21	0.58	0
4	NAG	C	203	2	14,14,15	0.43	0	17,19,21	0.92	0
4	NAG	B	706	1	14,14,15	0.42	0	17,19,21	0.44	0
5	V2A	B	702	-	37,37,37	1.62	6 (16%)	51,51,51	1.12	2 (3%)
4	NAG	A	704	1	14,14,15	0.43	0	17,19,21	1.26	1 (5%)
4	NAG	D	203	2	14,14,15	0.31	0	17,19,21	0.56	0
4	NAG	A	705	1	14,14,15	0.41	0	17,19,21	0.39	0
5	V2A	D	201	-	37,37,37	1.61	5 (13%)	51,51,51	1.08	4 (7%)
4	NAG	B	705	1	14,14,15	0.42	0	17,19,21	0.62	0
4	NAG	D	202	2	14,14,15	0.28	0	17,19,21	0.50	0
5	V2A	B	701	-	37,37,37	1.61	5 (13%)	51,51,51	1.21	3 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	V2A	A	709	-	-	3/27/27/27	0/3/3/3
4	NAG	A	706	1	-	4/6/23/26	0/1/1/1
4	NAG	B	704	1	-	3/6/23/26	0/1/1/1
4	NAG	B	703	1	-	2/6/23/26	0/1/1/1
4	NAG	A	703	1	-	2/6/23/26	0/1/1/1
4	NAG	C	203	2	-	3/6/23/26	0/1/1/1
4	NAG	B	706	1	-	2/6/23/26	0/1/1/1
5	V2A	B	702	-	-	10/27/27/27	0/3/3/3
4	NAG	A	704	1	-	3/6/23/26	0/1/1/1
4	NAG	D	203	2	-	1/6/23/26	0/1/1/1
4	NAG	A	705	1	-	3/6/23/26	0/1/1/1
5	V2A	D	201	-	-	4/27/27/27	0/3/3/3
4	NAG	B	705	1	-	3/6/23/26	0/1/1/1
4	NAG	D	202	2	-	0/6/23/26	0/1/1/1
5	V2A	B	701	-	-	1/27/27/27	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	702	V2A	C06-N07	5.81	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	201	V2A	C06-N07	5.66	1.46	1.34
5	B	701	V2A	C06-N07	5.52	1.46	1.34
5	A	709	V2A	C06-N07	5.51	1.46	1.34
5	A	709	V2A	O18-C17	5.04	1.41	1.33
5	B	701	V2A	O18-C17	5.00	1.41	1.33
5	D	201	V2A	O18-C17	4.93	1.41	1.33
5	B	702	V2A	O18-C17	4.83	1.41	1.33
5	D	201	V2A	O18-C19	-3.93	1.41	1.48
5	B	701	V2A	O18-C19	-3.91	1.41	1.48
5	A	709	V2A	O18-C19	-3.88	1.41	1.48
5	B	702	V2A	O18-C19	-3.86	1.41	1.48
5	B	702	V2A	C02-N01	2.46	1.46	1.37
5	B	701	V2A	C02-N01	2.45	1.46	1.37
5	D	201	V2A	C02-N01	2.45	1.46	1.37
5	A	709	V2A	C02-N01	2.43	1.45	1.37
5	B	701	V2A	O24-C06	-2.39	1.18	1.23
5	A	709	V2A	O24-C06	-2.30	1.18	1.23
5	B	702	V2A	O24-C06	-2.26	1.18	1.23
5	D	201	V2A	O24-C06	-2.20	1.18	1.23
5	B	702	V2A	C05-C06	2.06	1.54	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	701	V2A	O18-C17-C08	5.45	118.23	110.40
5	A	709	V2A	O18-C17-C08	5.24	117.94	110.40
5	B	702	V2A	O18-C17-C08	4.71	117.17	110.40
4	A	704	NAG	C2-N2-C7	4.30	129.03	122.90
4	B	704	NAG	C2-N2-C7	4.28	128.99	122.90
5	D	201	V2A	O18-C17-C08	3.52	115.45	110.40
4	B	704	NAG	C1-O5-C5	3.24	116.58	112.19
5	D	201	V2A	C05-C06-N07	2.70	122.25	117.06
5	B	701	V2A	C27-C26-C02	-2.54	118.15	122.67
5	B	702	V2A	C27-C26-C02	-2.40	118.39	122.67
5	A	709	V2A	C27-C26-C02	-2.29	118.59	122.67
4	B	704	NAG	C1-C2-N2	2.22	114.28	110.49
5	D	201	V2A	C08-N07-C06	-2.18	116.27	121.60
5	D	201	V2A	O24-C06-N07	-2.05	118.67	122.45
5	B	701	V2A	O23-C17-C08	-2.01	117.92	123.92

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	702	V2A	C08-C17-O18-C19
5	B	702	V2A	O23-C17-O18-C19
4	A	706	NAG	O5-C5-C6-O6
4	C	203	NAG	C4-C5-C6-O6
5	B	702	V2A	C22-C19-O18-C17
5	B	702	V2A	C21-C19-O18-C17
4	B	706	NAG	O5-C5-C6-O6
4	B	706	NAG	C4-C5-C6-O6
5	B	702	V2A	C20-C19-O18-C17
4	C	203	NAG	O5-C5-C6-O6
4	A	706	NAG	C4-C5-C6-O6
4	A	706	NAG	C8-C7-N2-C2
4	A	706	NAG	O7-C7-N2-C2
4	B	704	NAG	C8-C7-N2-C2
4	B	704	NAG	O7-C7-N2-C2
4	B	703	NAG	C8-C7-N2-C2
4	B	703	NAG	O7-C7-N2-C2
4	A	704	NAG	C8-C7-N2-C2
4	A	704	NAG	O7-C7-N2-C2
4	A	705	NAG	C8-C7-N2-C2
4	A	705	NAG	O7-C7-N2-C2
4	B	705	NAG	O5-C5-C6-O6
4	A	705	NAG	O5-C5-C6-O6
4	A	703	NAG	C1-C2-N2-C7
5	B	702	V2A	C08-C09-C10-C11
4	B	705	NAG	C4-C5-C6-O6
5	D	201	V2A	C17-C08-C09-C10
5	D	201	V2A	N07-C08-C09-C10
5	A	709	V2A	C17-C08-C09-C10
5	A	709	V2A	C25-C26-C27-C28
4	A	703	NAG	C3-C2-N2-C7
4	C	203	NAG	C3-C2-N2-C7
4	B	705	NAG	C3-C2-N2-C7
5	A	709	V2A	C02-C26-C27-C28
5	B	702	V2A	C27-C28-C29-C30
5	B	702	V2A	C27-C28-C29-C35
5	D	201	V2A	C27-C28-C29-C30
5	D	201	V2A	C27-C28-C29-C35
5	B	702	V2A	C09-C10-C11-C12
4	B	704	NAG	C3-C2-N2-C7
4	A	704	NAG	C3-C2-N2-C7
5	B	702	V2A	C09-C10-C11-C16
4	D	203	NAG	O5-C5-C6-O6

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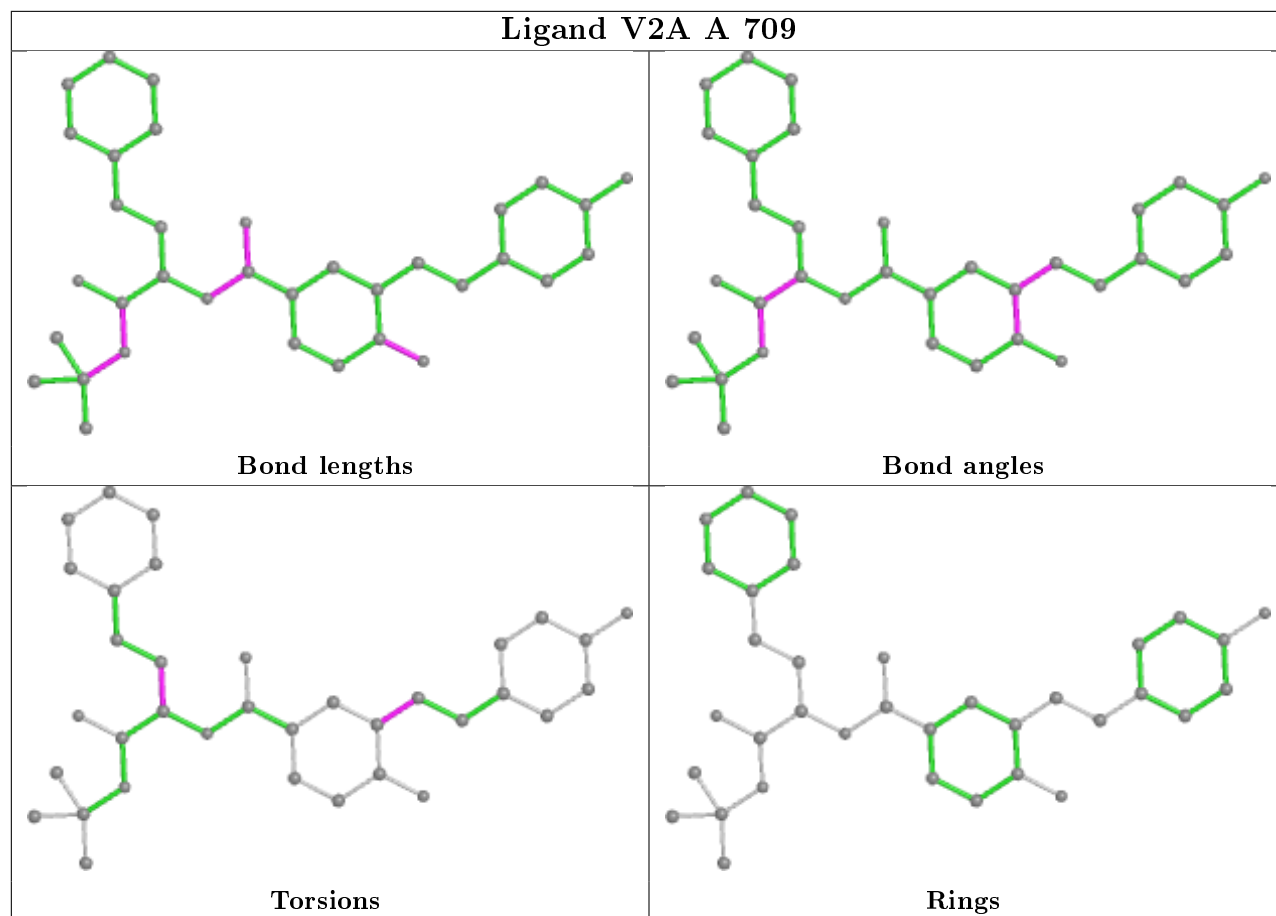
Mol	Chain	Res	Type	Atoms
5	B	701	V2A	C25-C26-C27-C28

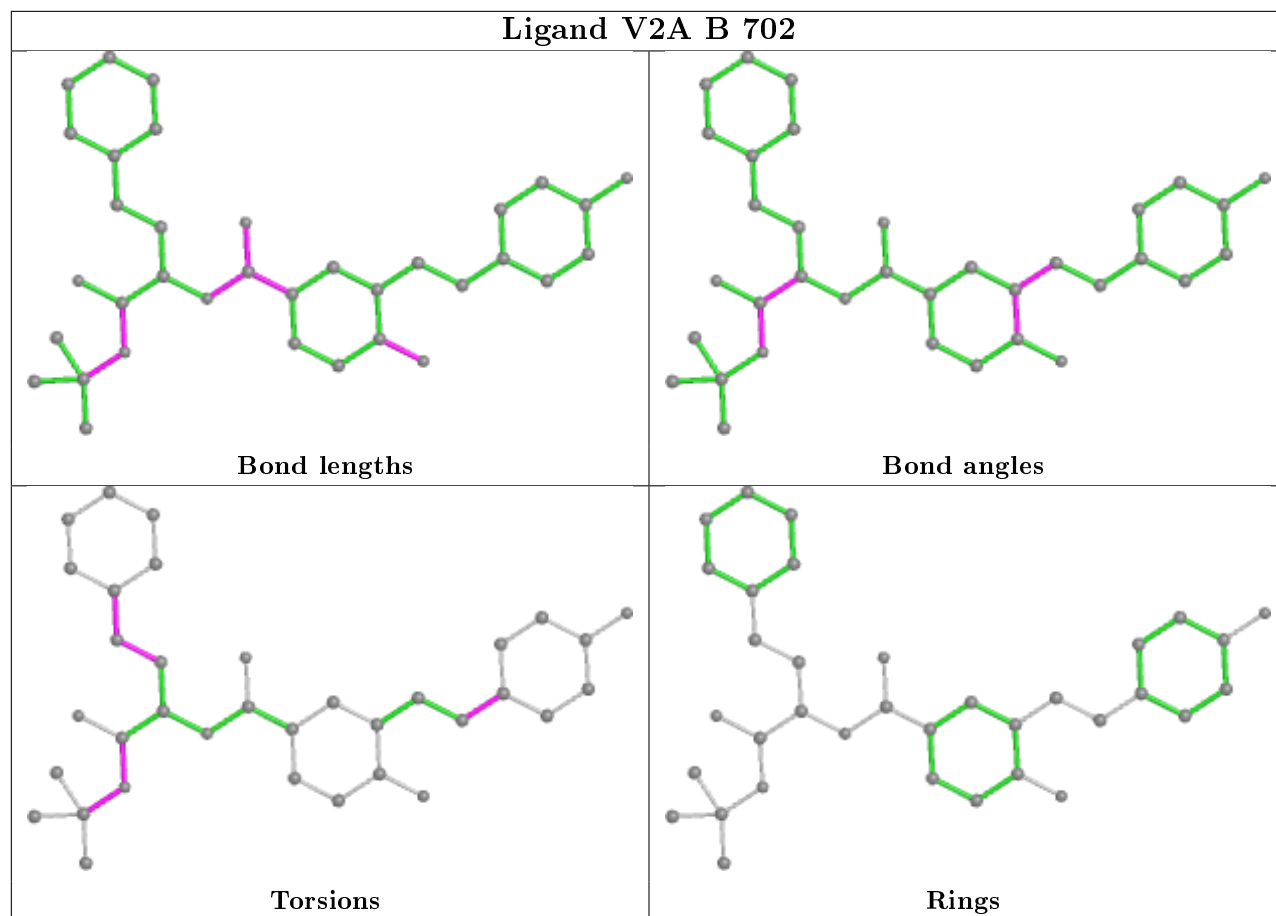
There are no ring outliers.

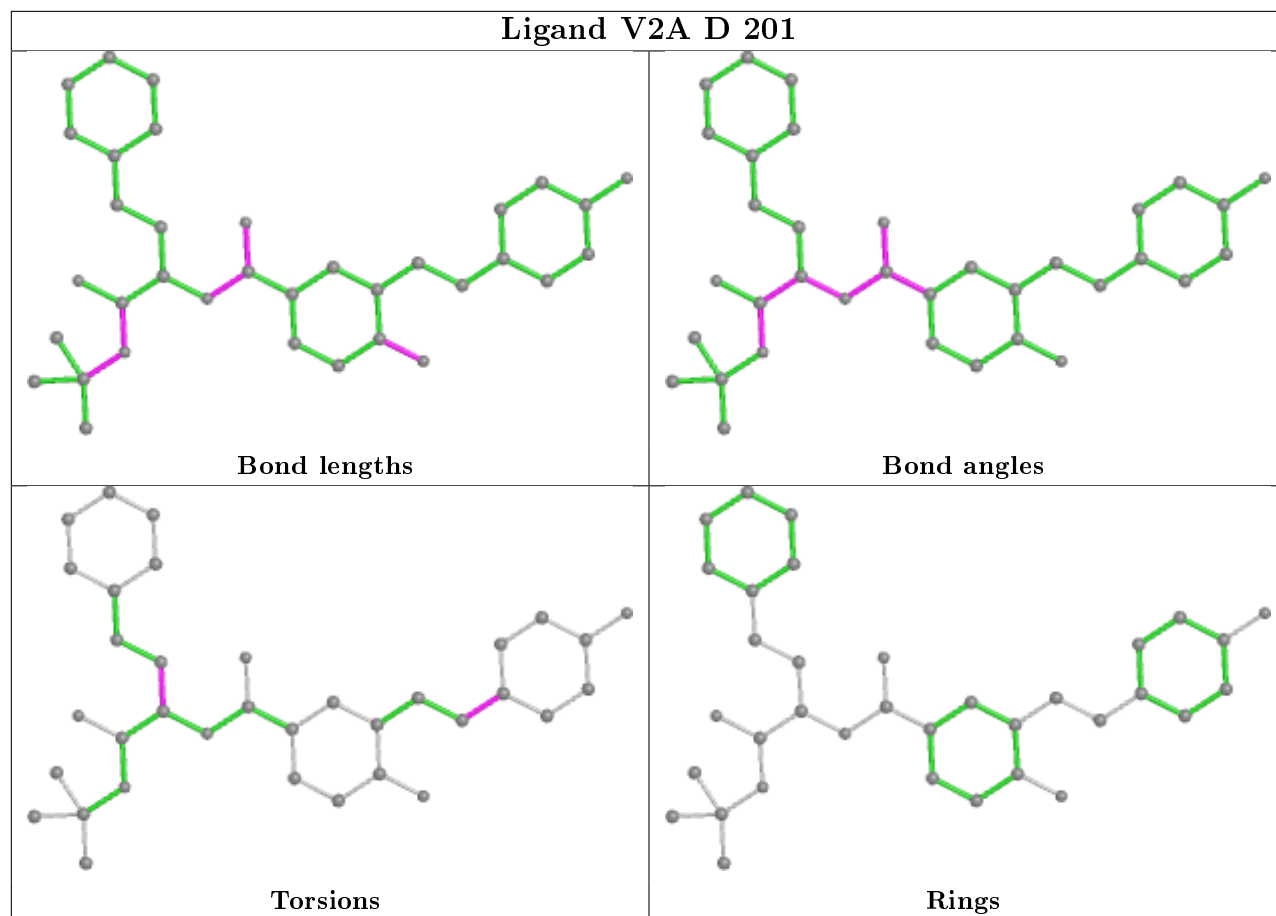
6 monomers are involved in 7 short contacts:

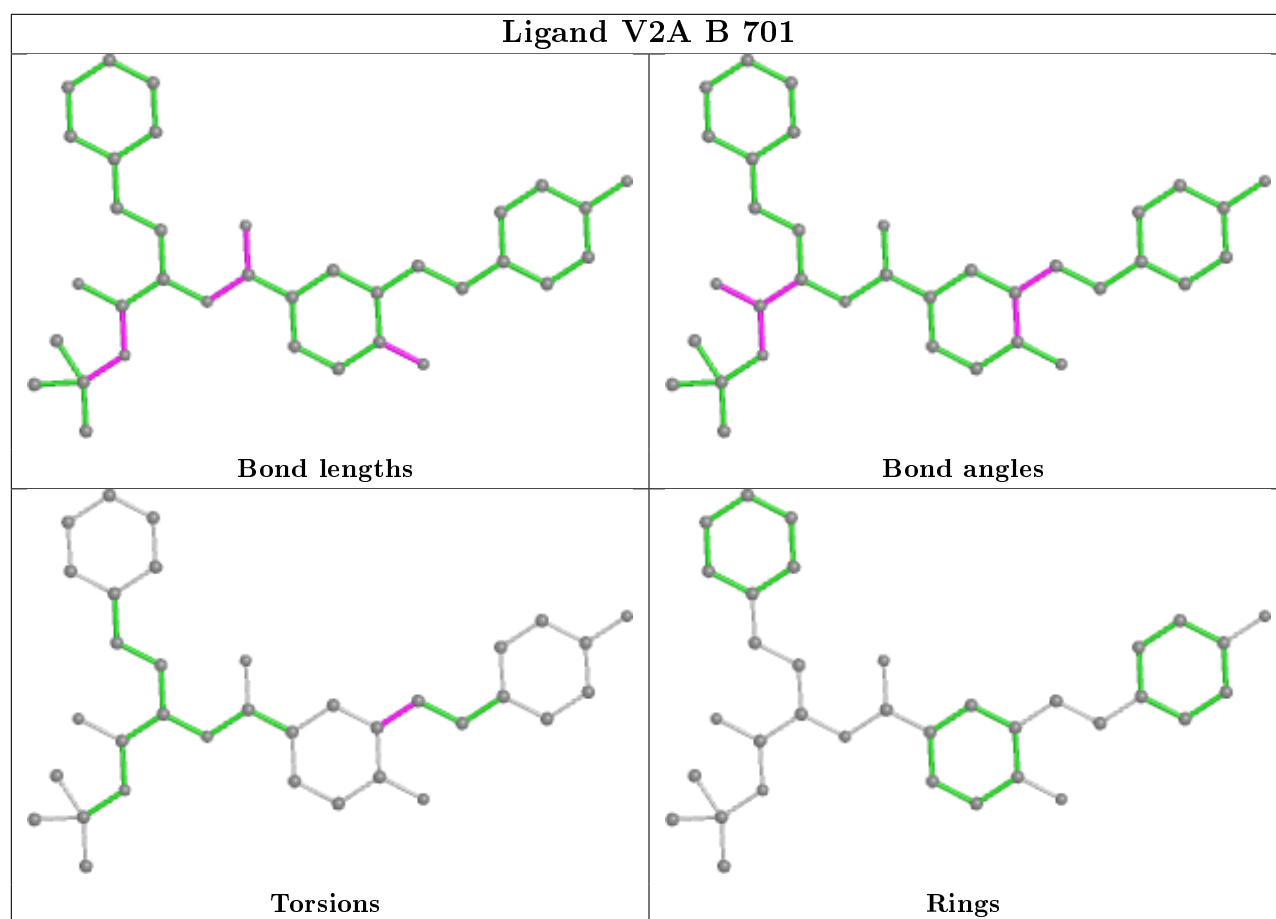
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	704	NAG	1	0
4	B	703	NAG	1	0
4	A	703	NAG	1	0
4	A	704	NAG	1	0
5	D	201	V2A	2	0
5	B	701	V2A	1	0

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	589/635 (92%)	0.04	31 (5%) 26 22	11, 40, 89, 129	0
1	B	593/635 (93%)	0.11	28 (4%) 31 28	12, 41, 80, 115	0
2	C	136/191 (71%)	-0.11	1 (0%) 87 86	20, 40, 66, 76	2 (1%)
2	D	136/191 (71%)	-0.14	1 (0%) 87 86	27, 40, 61, 73	0
All	All	1454/1652 (88%)	0.04	61 (4%) 36 32	11, 40, 80, 129	2 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	THR	4.8
1	B	31	VAL	4.7
1	A	50	ASP	4.3
1	A	101	HIS	4.3
1	A	31	VAL	4.2
1	A	35	ILE	4.1
1	A	77	SER	4.0
1	B	99	GLY	3.9
1	A	73	PHE	3.9
1	A	28	CYS	3.8
1	B	55	THR	3.8
1	A	51	ILE	3.8
1	B	35	ILE	3.7
1	B	200	ASN	3.5
1	B	29	ILE	3.4
1	B	619	THR	3.3
1	A	49	ASP	3.3
1	B	147	GLN	3.3
1	A	54	SER	3.2
1	A	71	TYR	3.2
1	B	33	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	75	ASN	3.1
1	B	32	VAL	3.1
1	A	32	VAL	2.9
1	A	76	PHE	2.9
1	A	53	SER	2.8
1	B	101	HIS	2.8
1	A	30	GLU	2.8
1	A	52	PRO	2.7
1	A	98	HIS	2.6
1	B	199	GLU	2.6
1	B	34	ASN	2.6
1	B	48	PRO	2.6
1	B	73	PHE	2.6
1	B	76	PHE	2.5
1	A	81	TRP	2.5
1	A	37	TYR	2.5
1	A	44	LEU	2.5
1	A	39	CYS	2.5
1	B	209	MET	2.4
1	B	269	GLU	2.4
1	B	54	SER	2.4
1	B	53	SER	2.4
1	A	100	LEU	2.3
1	A	97	TRP	2.3
1	B	157	ALA	2.3
1	A	141	GLU	2.3
1	B	51	ILE	2.3
1	B	30	GLU	2.3
1	B	182	SER	2.2
1	B	100	LEU	2.2
1	A	47	VAL	2.1
1	B	273	PRO	2.1
1	A	99	GLY	2.1
1	B	210	SER	2.1
1	A	29	ILE	2.1
1	A	182	SER	2.1
1	A	168	ALA	2.1
2	C	38	ASP	2.1
2	D	22	GLN	2.0
1	B	28	CYS	2.0

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

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

6.3 Carbohydrates [i](#)

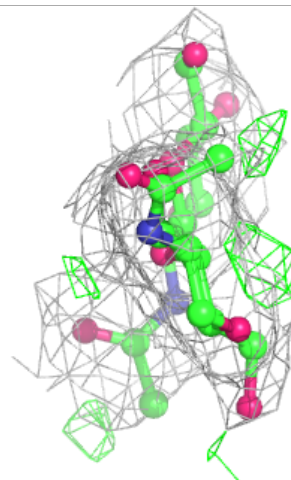
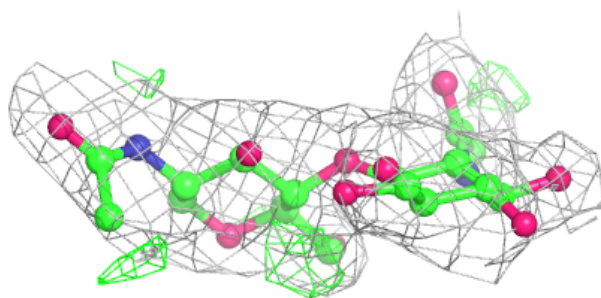
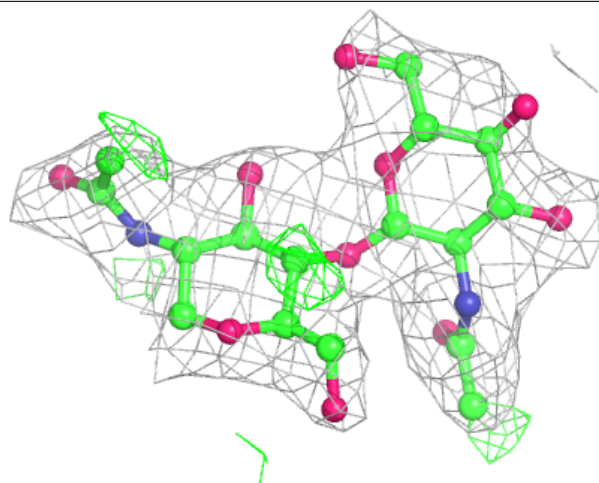
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	I	2	14/15	0.81	0.26	69,90,99,107	0
3	NAG	I	1	14/15	0.81	0.21	66,89,93,102	0
3	NAG	G	2	14/15	0.85	0.29	60,85,96,97	0
3	NAG	H	2	14/15	0.86	0.35	53,76,90,90	0
3	NAG	E	2	14/15	0.89	0.14	47,73,87,96	0
3	NAG	F	2	14/15	0.89	0.20	63,75,79,80	0
3	NAG	E	1	14/15	0.90	0.15	32,56,74,81	0
3	NAG	F	1	14/15	0.94	0.12	21,35,51,55	0
3	NAG	G	1	14/15	0.94	0.17	25,43,71,74	0
3	NAG	H	1	14/15	0.96	0.15	15,34,47,49	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.

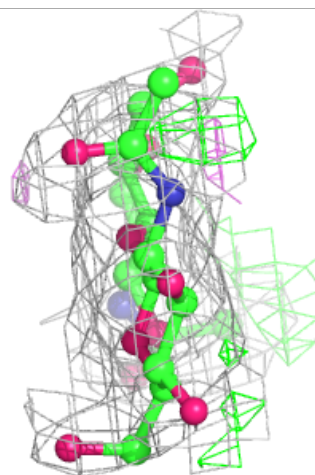
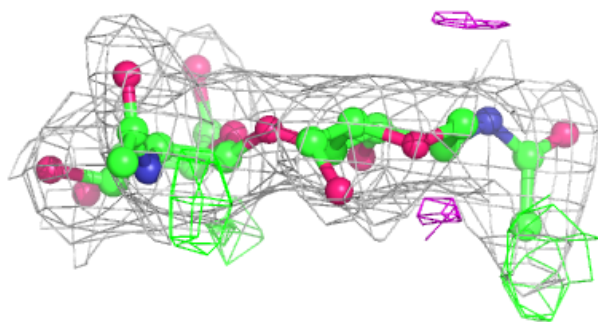
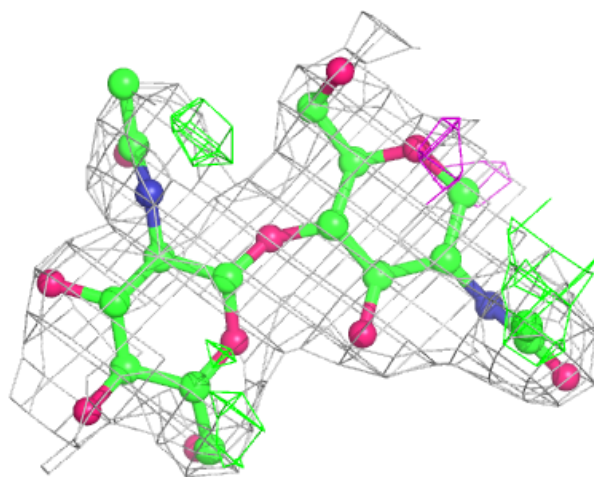
Electron density around Chain E:

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



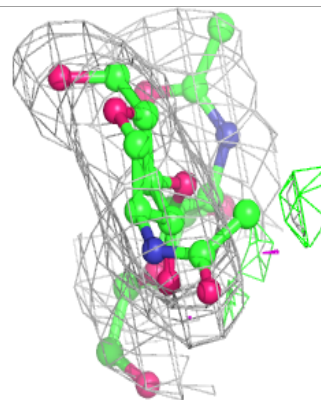
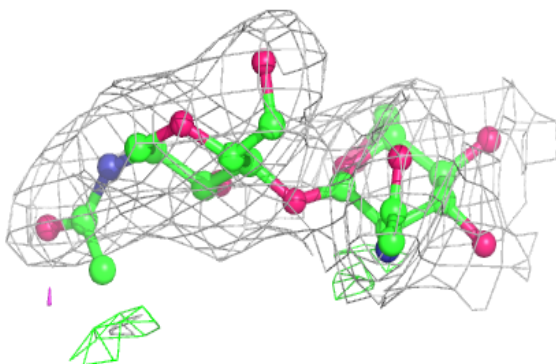
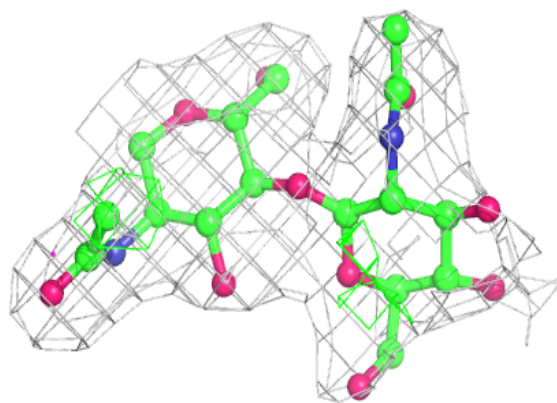
Electron density around Chain F:

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



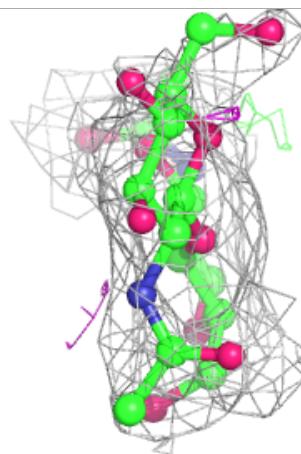
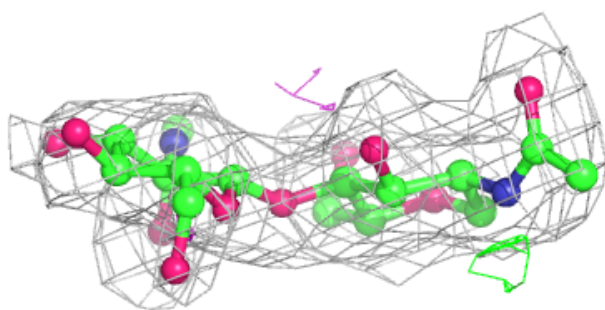
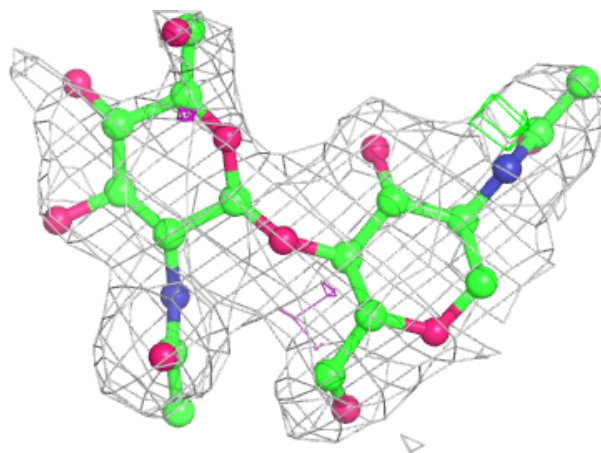
Electron density around Chain G:

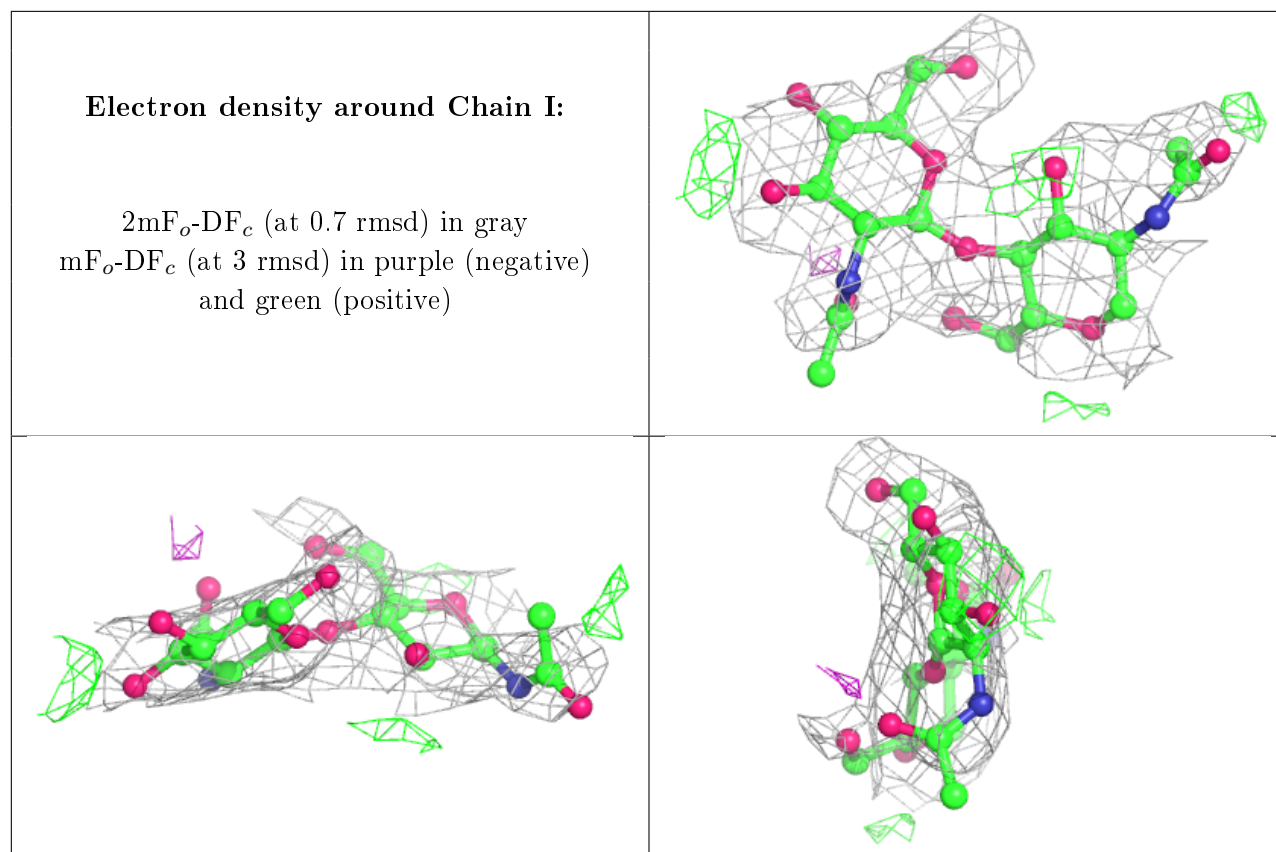
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (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	A	706	14/15	0.67	0.32	76,90,96,99	0
4	NAG	A	704	14/15	0.69	0.27	71,88,104,106	0
4	NAG	B	705	14/15	0.70	0.26	68,93,105,109	0
4	NAG	A	705	14/15	0.73	0.17	62,74,81,85	0
4	NAG	B	704	14/15	0.77	0.28	67,97,103,106	0
4	NAG	B	706	14/15	0.79	0.17	64,76,92,96	0
4	NAG	A	703	14/15	0.80	0.21	85,91,99,99	0
4	NAG	B	703	14/15	0.83	0.18	55,69,85,93	0
4	NAG	D	202	14/15	0.85	0.19	53,76,91,94	0
4	NAG	C	203	14/15	0.87	0.31	57,82,87,90	0
4	NAG	D	203	14/15	0.92	0.17	30,45,63,63	0
5	V2A	B	702	35/35	0.94	0.19	28,44,56,57	0
5	V2A	A	709	35/35	0.96	0.14	29,34,45,48	0
5	V2A	D	201	35/35	0.96	0.16	29,44,59,68	0

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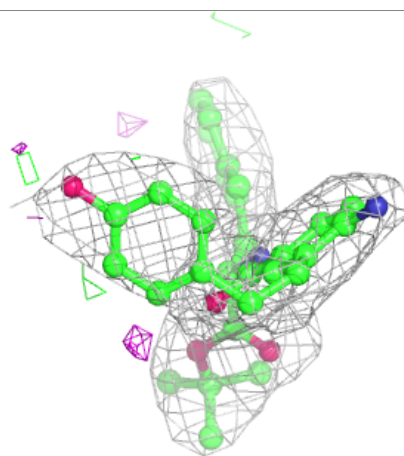
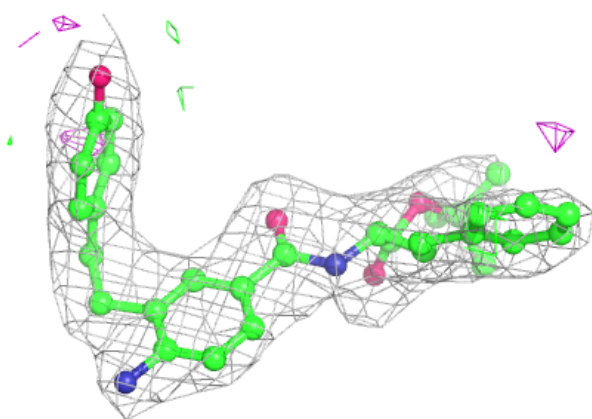
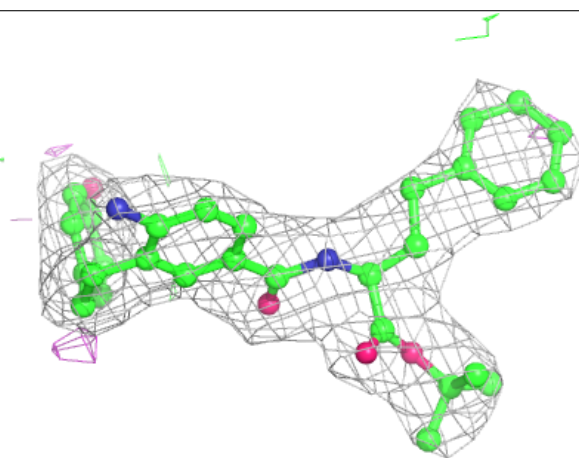
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	V2A	B	701	35/35	0.96	0.15	25,33,45,51	0

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.

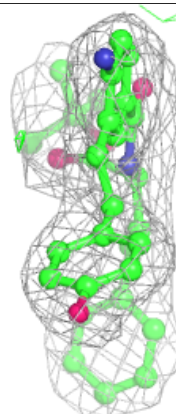
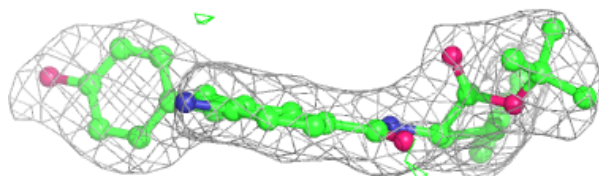
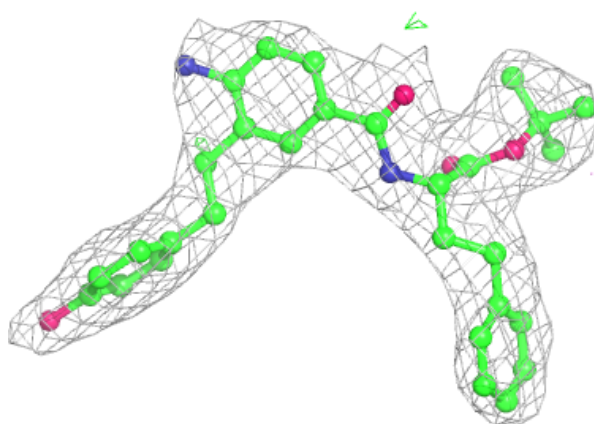
Electron density around V2A B 702:

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



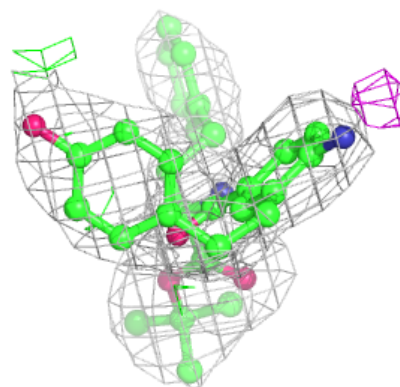
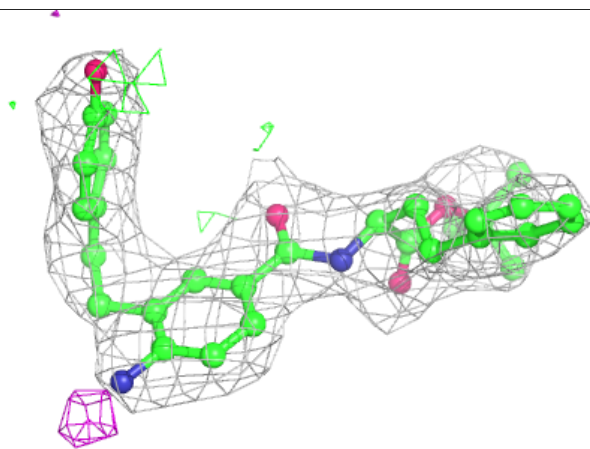
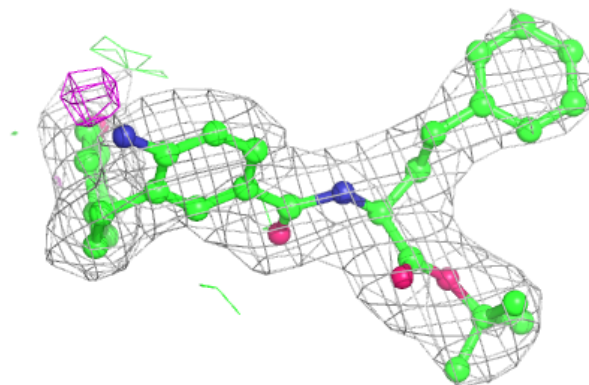
Electron density around V2A A 709:

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



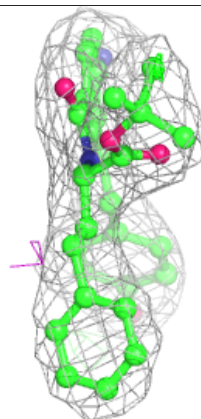
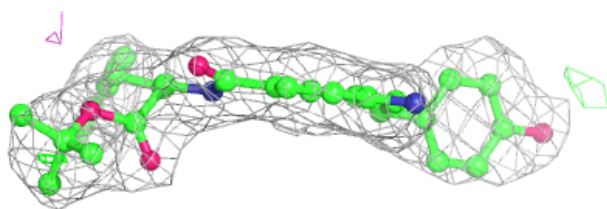
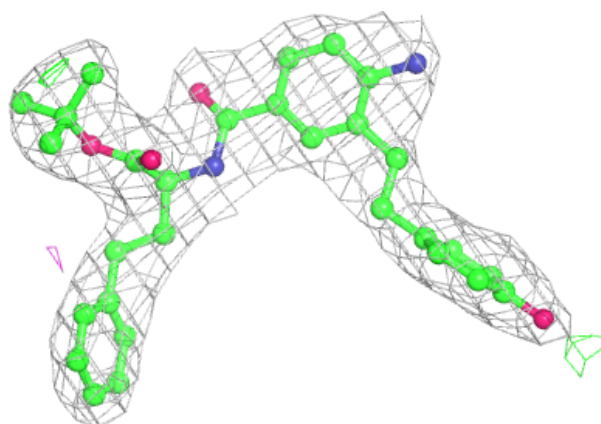
Electron density around V2A D 201:

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



Electron density around V2A B 701:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.