



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:35 AM UTC

PDB ID : 3DMK / pdb_00003dmk
Title : Crystal structure of Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains
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Deposited on : 2008-07-01
Resolution : 4.19 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

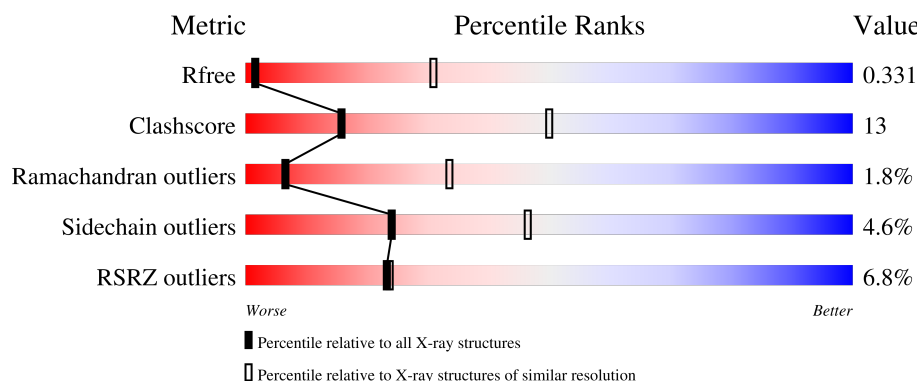
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.19 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



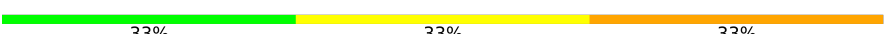
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	816	5% 66% 27% • 5%
1	B	816	% 60% 22% • 17%
1	C	816	11% 59% 23% • 17%
2	D	2	50% 50%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 50% 50%
2	I	2	 50% 50%
3	G	3	 33% 67%
3	H	3	 33% 67%
3	J	3	 33% 33% 33%
3	K	3	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	G	1	X	-	-	-
3	NAG	H	1	X	-	-	-
3	NAG	K	1	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16740 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 Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	775	Total	C	N	O	S	0	0	0
			5985	3778	1035	1147	25			
1	B	676	Total	C	N	O	S	0	0	0
			5223	3295	908	998	22			
1	C	676	Total	C	N	O	S	0	0	0
			5223	3295	908	998	22			

There are 18 discrepancies between the modelled and reference sequences:

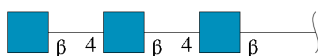
Chain	Residue	Modelled	Actual	Comment	Reference
A	776	HIS	-	expression tag	PDB 3DMK
A	777	HIS	-	expression tag	PDB 3DMK
A	778	HIS	-	expression tag	PDB 3DMK
A	779	HIS	-	expression tag	PDB 3DMK
A	780	HIS	-	expression tag	PDB 3DMK
A	781	HIS	-	expression tag	PDB 3DMK
B	776	HIS	-	expression tag	PDB 3DMK
B	777	HIS	-	expression tag	PDB 3DMK
B	778	HIS	-	expression tag	PDB 3DMK
B	779	HIS	-	expression tag	PDB 3DMK
B	780	HIS	-	expression tag	PDB 3DMK
B	781	HIS	-	expression tag	PDB 3DMK
C	776	HIS	-	expression tag	PDB 3DMK
C	777	HIS	-	expression tag	PDB 3DMK
C	778	HIS	-	expression tag	PDB 3DMK
C	779	HIS	-	expression tag	PDB 3DMK
C	780	HIS	-	expression tag	PDB 3DMK
C	781	HIS	-	expression tag	PDB 3DMK

- 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	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



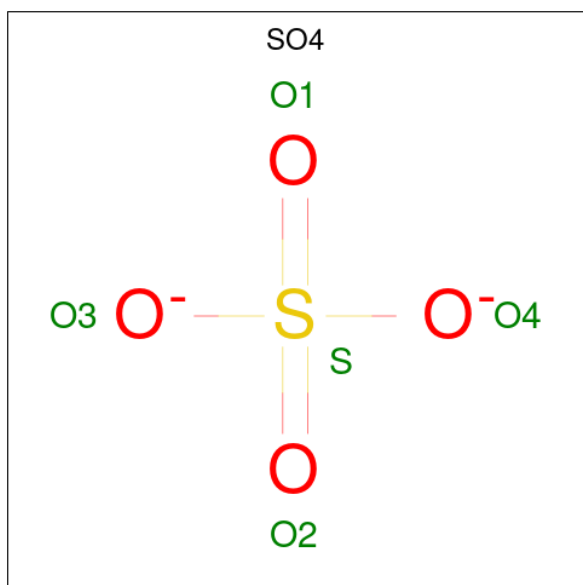
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	3	Total	C	N	O	0	0	0
			42	24	3	15			
3	H	3	Total	C	N	O	0	0	0
			42	24	3	15			
3	J	3	Total	C	N	O	0	0	0
			42	24	3	15			
3	K	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

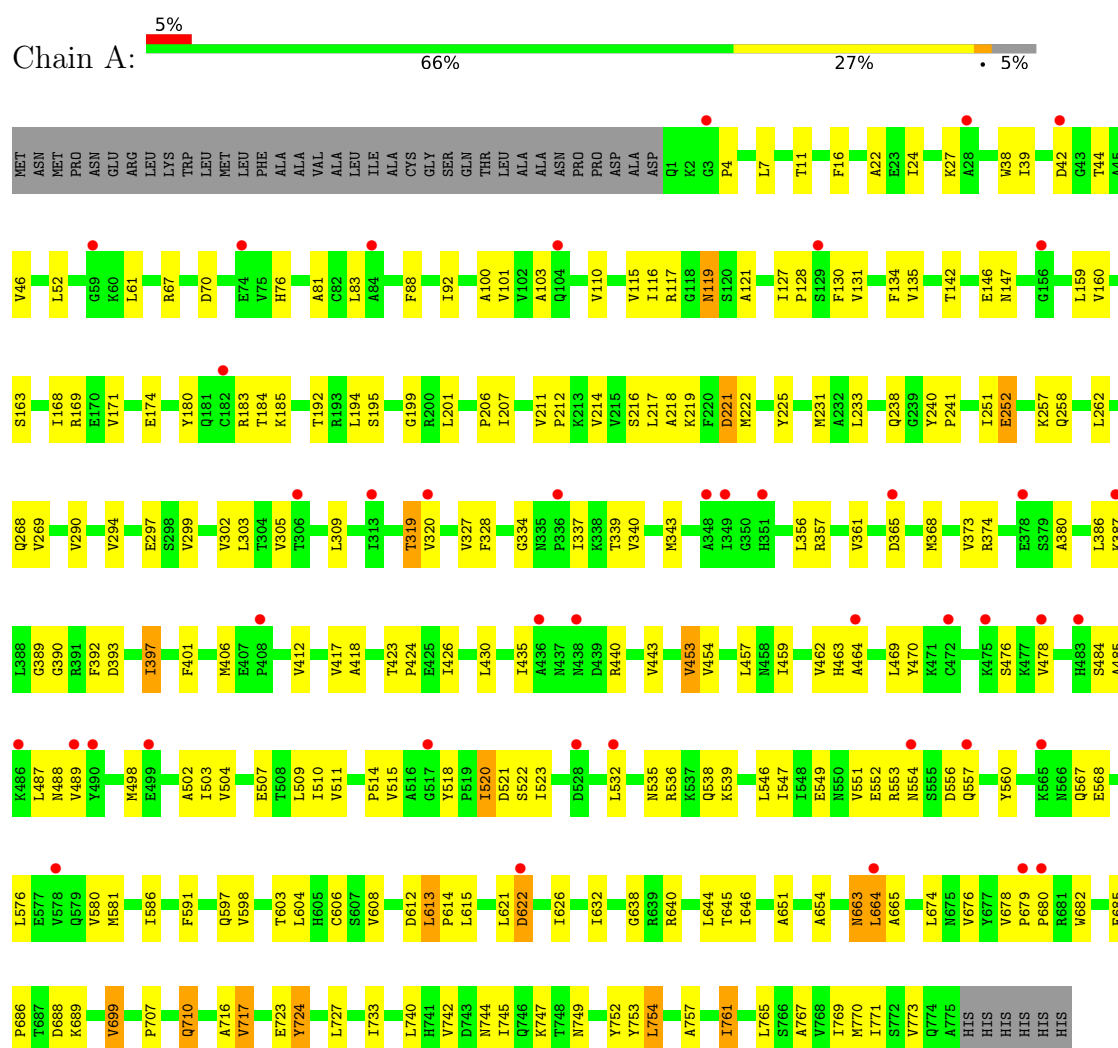


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		

3 Residue-property plots

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.

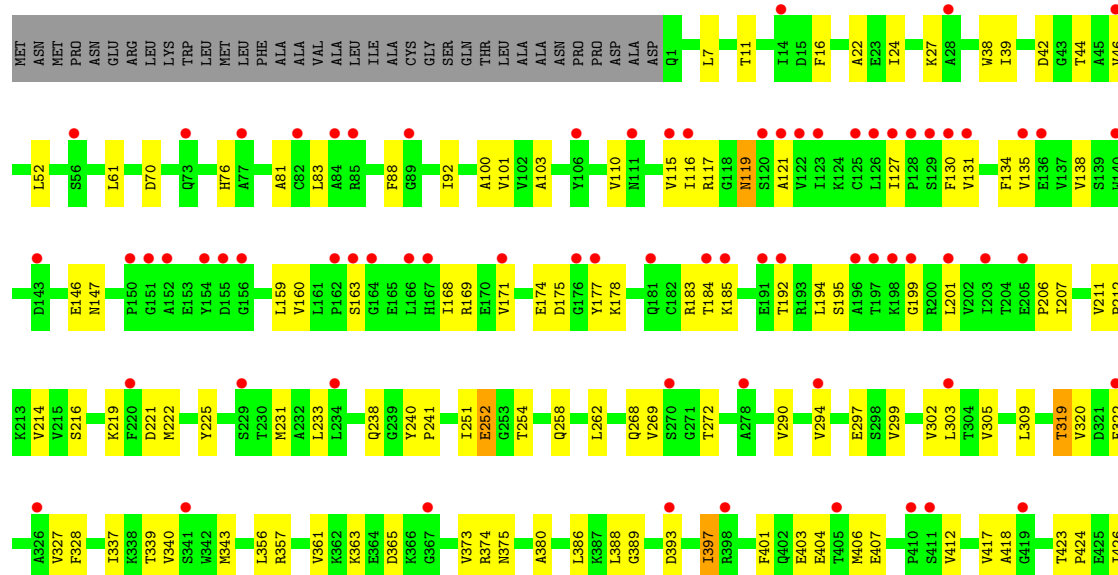
- Molecule 1: Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains

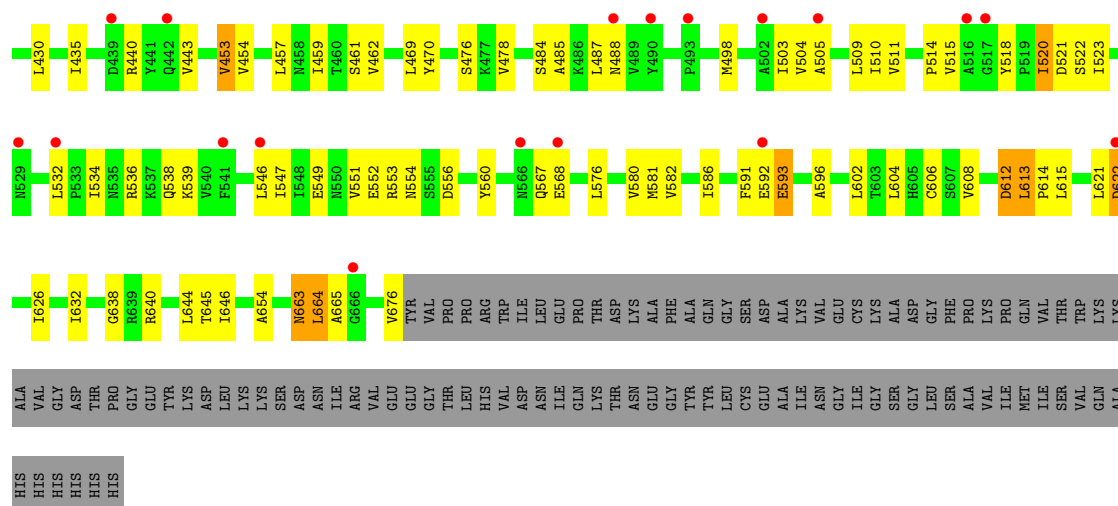


- Molecule 1: Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains



- Molecule 1: Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains





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

Chain D:  50%



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

Chain E:  50%



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

Chain F:  50%



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

Chain I:  50%



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

Chain G:  33%

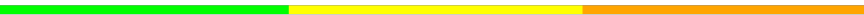


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  33% 67%



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

Chain J:  33% 33% 33%



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

Chain K:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	118.46Å 177.61Å 434.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 4.19 12.00 – 4.19	Depositor EDS
% Data completeness (in resolution range)	99.4 (12.00-4.19) 95.1 (12.00-4.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 4.19Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.280 , 0.327 0.284 , 0.331	Depositor DCC
R_{free} test set	1618 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	99.4	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , 104.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	16740	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, 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	0.45	0/6113	0.70	3/8303 (0.0%)
1	B	0.48	0/5334	0.73	2/7246 (0.0%)
1	C	0.45	1/5334 (0.0%)	0.70	0/7246
All	All	0.46	1/16781 (0.0%)	0.71	5/22795 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	178	LYS	C-N	-5.38	1.25	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	685	GLU	CA-C-N	6.06	126.41	119.92
1	A	685	GLU	C-N-CA	6.06	126.41	119.92
1	A	717	VAL	N-CA-C	5.93	116.00	110.42
1	B	532	LEU	CA-C-N	-5.63	112.81	119.84
1	B	532	LEU	C-N-CA	-5.63	112.81	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5985	0	5928	182	0
1	B	5223	0	5172	132	1
1	C	5223	0	5174	138	1
2	D	28	0	25	2	0
2	E	28	0	25	1	0
2	F	28	0	25	1	0
2	I	28	0	25	0	0
3	G	42	0	37	0	0
3	H	42	0	37	0	0
3	J	42	0	37	1	0
3	K	42	0	37	0	0
4	A	12	0	16	0	0
4	B	12	0	16	0	0
5	B	5	0	0	0	0
All	All	16740	0	16554	444	1

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 13.

All (444) 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:654:ALA:HB2	1:A:676:VAL:HG12	1.38	1.00
1:A:733:ILE:HG23	1:A:742:VAL:HG22	1.46	0.97
1:B:412:VAL:HB	1:B:459:ILE:HG22	1.53	0.90
1:C:412:VAL:HB	1:C:459:ILE:HG22	1.56	0.87
1:C:504:VAL:HG12	1:C:581:MET:HB2	1.56	0.87
1:C:401:PHE:CE2	1:C:485:ALA:HB3	2.11	0.86
1:A:412:VAL:HB	1:A:459:ILE:HG22	1.58	0.85
1:B:654:ALA:HB2	1:B:676:VAL:HG12	1.59	0.85
1:A:654:ALA:HB2	1:A:676:VAL:CG1	2.08	0.84
1:B:320:VAL:HG21	1:B:361:VAL:HG21	1.61	0.82
1:A:320:VAL:HG21	1:A:361:VAL:HG21	1.62	0.82
1:A:401:PHE:CE2	1:A:485:ALA:HB3	2.14	0.82
1:B:401:PHE:CE2	1:B:485:ALA:HB3	2.15	0.81
1:C:320:VAL:HG21	1:C:361:VAL:HG21	1.62	0.81
1:A:217:LEU:HD23	1:B:217:LEU:HD23	1.62	0.81
1:A:218:ALA:HA	1:B:217:LEU:HD21	1.66	0.78
1:A:217:LEU:HD21	1:B:218:ALA:HA	1.64	0.78
1:C:417:VAL:HG22	1:C:454:VAL:HG22	1.65	0.77
1:A:699:VAL:HG13	1:A:740:LEU:HB3	1.65	0.77
1:C:596:ALA:HB2	1:C:602:LEU:HD21	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:VAL:HG22	1:A:454:VAL:HG22	1.68	0.76
1:C:504:VAL:HG11	1:C:665:ALA:HB3	1.67	0.75
1:B:503:ILE:HG21	1:B:551:VAL:HG21	1.70	0.74
1:A:217:LEU:HD23	1:B:217:LEU:CD2	2.17	0.74
1:A:217:LEU:CD2	1:B:217:LEU:HD23	2.18	0.74
1:B:417:VAL:HG22	1:B:454:VAL:HG22	1.70	0.74
1:C:373:VAL:HG23	1:C:380:ALA:HB3	1.69	0.74
1:B:76:HIS:HB3	1:B:100:ALA:HB3	1.68	0.74
1:C:532:LEU:HD23	1:C:546:LEU:HD13	1.68	0.73
1:A:373:VAL:HG23	1:A:380:ALA:HB3	1.70	0.73
1:B:127:ILE:HD13	1:B:135:VAL:HG12	1.71	0.72
1:A:651:ALA:HA	1:A:676:VAL:HG11	1.72	0.71
1:A:503:ILE:HG21	1:A:551:VAL:HG21	1.72	0.71
1:B:373:VAL:HG23	1:B:380:ALA:HB3	1.71	0.71
1:A:532:LEU:HD21	1:A:546:LEU:HD22	1.71	0.71
1:C:76:HIS:HB3	1:C:100:ALA:HB3	1.71	0.71
1:B:632:ILE:CG2	1:B:644:LEU:HD11	2.21	0.71
1:C:503:ILE:HG21	1:C:551:VAL:HG21	1.71	0.71
1:A:76:HIS:HB3	1:A:100:ALA:HB3	1.73	0.71
1:C:632:ILE:CG2	1:C:644:LEU:HD11	2.20	0.71
1:A:225:TYR:HB2	1:A:231:MET:HE3	1.72	0.70
1:A:597:GLN:OE1	1:A:761:ILE:HG22	1.91	0.70
1:C:127:ILE:HD13	1:C:135:VAL:HG12	1.73	0.70
1:A:532:LEU:CD2	1:A:546:LEU:HD22	2.22	0.70
1:B:535:ASN:C	1:B:535:ASN:HD22	2.00	0.69
1:C:430:LEU:HD12	1:C:470:TYR:CZ	2.28	0.69
1:B:412:VAL:HB	1:B:459:ILE:CG2	2.22	0.69
1:A:612:ASP:O	1:A:614:PRO:HD2	1.93	0.69
1:B:612:ASP:O	1:B:614:PRO:HD2	1.93	0.68
1:C:504:VAL:HG13	1:C:581:MET:HE3	1.75	0.68
1:A:586:ILE:HA	1:A:608:VAL:HG22	1.76	0.67
1:B:586:ILE:HA	1:B:608:VAL:HG22	1.76	0.67
1:A:632:ILE:CG2	1:A:644:LEU:HD11	2.24	0.67
1:C:612:ASP:O	1:C:614:PRO:HD2	1.94	0.67
1:A:67:ARG:HH11	2:D:1:NAG:H81	1.60	0.67
1:A:319:THR:HG22	1:A:389:GLY:CA	2.24	0.67
1:C:225:TYR:HB2	1:C:231:MET:HE3	1.77	0.67
1:A:127:ILE:HD13	1:A:135:VAL:HG12	1.76	0.66
1:B:476:SER:OG	1:B:478:VAL:HG12	1.96	0.66
1:C:231:MET:HE1	1:C:305:VAL:HG22	1.78	0.66
1:A:717:VAL:H	1:A:723:GLU:CD	2.03	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:TYR:HB2	1:B:231:MET:HE3	1.78	0.65
1:C:532:LEU:CD2	1:C:546:LEU:HD13	2.26	0.65
1:C:592:GLU:O	1:C:593:GLU:C	2.40	0.64
1:A:532:LEU:HD21	1:A:546:LEU:CD2	2.27	0.64
1:A:430:LEU:HD12	1:A:470:TYR:CZ	2.33	0.64
1:B:430:LEU:HD12	1:B:470:TYR:CZ	2.32	0.64
1:B:168:ILE:HD12	1:B:201:LEU:HD11	1.80	0.64
1:C:476:SER:OG	1:C:478:VAL:HG12	1.98	0.64
1:B:502:ALA:HB1	1:B:581:MET:HE2	1.80	0.63
1:C:231:MET:CE	1:C:305:VAL:HG22	2.29	0.63
1:A:211:VAL:HG22	1:A:294:VAL:CG1	2.29	0.63
1:A:476:SER:OG	1:A:478:VAL:HG12	1.99	0.63
1:B:406:MET:HE3	1:B:487:LEU:HD11	1.80	0.63
1:C:168:ILE:HD12	1:C:201:LEU:HD11	1.80	0.63
1:A:231:MET:CE	1:A:305:VAL:HG22	2.29	0.63
1:A:412:VAL:HB	1:A:459:ILE:CG2	2.28	0.63
1:A:532:LEU:O	1:A:538:GLN:OE1	2.17	0.63
1:A:676:VAL:HG13	1:A:676:VAL:O	1.99	0.62
1:A:231:MET:HE1	1:A:305:VAL:HG22	1.81	0.62
1:B:211:VAL:HG22	1:B:294:VAL:CG1	2.30	0.62
1:C:412:VAL:HB	1:C:459:ILE:CG2	2.27	0.62
1:B:146:GLU:C	1:B:147:ASN:HD22	2.08	0.61
1:B:251:ILE:HD11	1:B:258:GLN:HG3	1.81	0.61
1:A:110:VAL:HG12	1:A:199:GLY:HA3	1.82	0.61
1:C:110:VAL:HG12	1:C:199:GLY:HA3	1.83	0.61
1:C:211:VAL:HG22	1:C:294:VAL:CG1	2.30	0.61
1:A:222:MET:HE3	1:A:302:VAL:HG11	1.83	0.61
1:C:222:MET:HE3	1:C:302:VAL:HG11	1.81	0.61
1:B:222:MET:HE3	1:B:302:VAL:HG11	1.82	0.61
1:A:146:GLU:C	1:A:147:ASN:HD22	2.09	0.61
1:A:423:THR:CG2	1:A:453:VAL:HG23	2.31	0.60
1:A:168:ILE:HD12	1:A:201:LEU:HD11	1.83	0.60
1:A:406:MET:HE3	1:A:487:LEU:HD11	1.83	0.60
1:B:110:VAL:HG12	1:B:199:GLY:HA3	1.83	0.60
1:C:251:ILE:HD11	1:C:258:GLN:HG3	1.82	0.59
1:B:231:MET:HE1	1:B:305:VAL:HG22	1.83	0.59
1:A:251:ILE:HD11	1:A:258:GLN:HG3	1.84	0.59
1:A:747:LYS:HA	1:A:773:VAL:HG21	1.84	0.59
1:B:231:MET:CE	1:B:305:VAL:HG22	2.32	0.59
1:C:146:GLU:C	1:C:147:ASN:HD22	2.11	0.59
1:C:423:THR:CG2	1:C:453:VAL:HG23	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:LEU:HD13	1:B:92:ILE:CG2	2.33	0.58
1:A:707:PRO:CD	1:A:761:ILE:HD11	2.33	0.58
1:C:504:VAL:CG1	1:C:581:MET:HE3	2.33	0.58
1:A:591:PHE:CE1	1:A:604:LEU:HD13	2.39	0.58
1:B:340:VAL:HG22	1:B:373:VAL:HG12	1.86	0.58
1:C:262:LEU:HD21	1:C:268:GLN:HB2	1.86	0.58
1:A:262:LEU:HD21	1:A:268:GLN:HB2	1.85	0.57
1:C:121:ALA:HB2	1:C:171:VAL:HG21	1.86	0.57
1:A:185:LYS:HB2	1:A:192:THR:HG22	1.87	0.57
1:B:121:ALA:HB2	1:B:171:VAL:HG21	1.87	0.57
1:A:678:VAL:HG13	1:A:679:PRO:HD2	1.87	0.57
1:B:262:LEU:HD21	1:B:268:GLN:HB2	1.87	0.56
1:B:488:ASN:HB3	1:B:518:TYR:HB2	1.86	0.56
1:B:532:LEU:CD2	1:B:546:LEU:HD22	2.36	0.56
1:A:511:VAL:HG21	1:A:576:LEU:HD22	1.87	0.56
1:B:423:THR:CG2	1:B:453:VAL:HG23	2.35	0.56
1:C:551:VAL:HG12	1:C:580:VAL:HG13	1.87	0.56
1:C:586:ILE:HD11	1:C:606:CYS:SG	2.45	0.56
1:C:83:LEU:HD13	1:C:92:ILE:CG2	2.36	0.56
1:C:254:THR:HG22	1:C:593:GLU:O	2.05	0.56
1:A:121:ALA:HB2	1:A:171:VAL:HG21	1.88	0.56
1:A:504:VAL:HG11	1:A:665:ALA:O	2.06	0.56
1:C:511:VAL:HG21	1:C:576:LEU:HD22	1.88	0.56
1:A:83:LEU:HB2	1:A:92:ILE:HG22	1.88	0.55
1:A:488:ASN:HB3	1:A:518:TYR:HB2	1.88	0.55
1:A:680:PRO:HB2	1:A:765:LEU:HD13	1.87	0.55
1:A:211:VAL:HG22	1:A:294:VAL:HG12	1.87	0.55
1:B:211:VAL:HG22	1:B:294:VAL:HG12	1.89	0.55
1:C:488:ASN:HB3	1:C:518:TYR:HB2	1.88	0.55
1:C:586:ILE:HA	1:C:608:VAL:HG22	1.87	0.55
1:A:83:LEU:HD13	1:A:92:ILE:CG2	2.37	0.55
1:C:498:MET:HE3	1:C:514:PRO:HD3	1.87	0.55
1:B:240:TYR:HA	1:B:241:PRO:C	2.32	0.55
1:A:340:VAL:HG22	1:A:373:VAL:HG12	1.89	0.55
1:A:654:ALA:CB	1:A:676:VAL:HG12	2.26	0.55
1:B:185:LYS:HB2	1:B:192:THR:HG22	1.89	0.55
1:B:83:LEU:HB2	1:B:92:ILE:HG22	1.88	0.55
1:A:498:MET:HE3	1:A:514:PRO:HD3	1.89	0.54
1:B:591:PHE:CE1	1:B:604:LEU:HD13	2.43	0.54
1:A:418:ALA:CB	1:A:426:ILE:HD11	2.37	0.54
1:C:83:LEU:HB2	1:C:92:ILE:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LEU:CD2	1:B:217:LEU:CD2	2.84	0.54
1:B:397:ILE:HD12	1:B:397:ILE:O	2.08	0.54
1:C:211:VAL:HG22	1:C:294:VAL:HG12	1.88	0.54
1:C:663:ASN:O	1:C:664:LEU:C	2.51	0.54
1:C:654:ALA:HB2	1:C:676:VAL:HG12	1.89	0.54
1:B:83:LEU:HD13	1:B:92:ILE:HG23	1.90	0.54
1:C:175:ASP:C	1:C:177:TYR:H	2.15	0.54
1:C:322:PHE:O	1:C:478:VAL:HG23	2.08	0.54
1:B:418:ALA:CB	1:B:426:ILE:HD11	2.38	0.53
1:B:518:TYR:O	1:B:518:TYR:CD1	2.61	0.53
1:C:185:LYS:HB2	1:C:192:THR:HG22	1.90	0.53
1:C:212:PRO:HA	1:C:238:GLN:O	2.09	0.53
1:B:663:ASN:O	1:B:664:LEU:C	2.51	0.53
1:A:504:VAL:CG1	1:A:665:ALA:HB1	2.39	0.53
1:C:340:VAL:HG22	1:C:373:VAL:HG12	1.90	0.53
1:A:532:LEU:CD2	1:A:546:LEU:HD13	2.38	0.53
1:B:206:PRO:O	1:B:207:ILE:HD13	2.09	0.53
1:B:567:GLN:O	1:B:568:GLU:HG3	2.09	0.53
1:C:406:MET:HE3	1:C:487:LEU:HD11	1.91	0.53
1:B:498:MET:HE3	1:B:514:PRO:HD3	1.89	0.52
1:C:418:ALA:CB	1:C:426:ILE:HD11	2.39	0.52
1:C:532:LEU:CD2	1:C:546:LEU:HD22	2.38	0.52
1:A:397:ILE:HD12	1:A:397:ILE:O	2.09	0.52
1:B:38:TRP:O	1:B:46:VAL:HG22	2.09	0.52
1:B:212:PRO:HA	1:B:238:GLN:O	2.08	0.52
1:C:518:TYR:CD1	1:C:518:TYR:O	2.62	0.52
1:A:240:TYR:HA	1:A:241:PRO:C	2.34	0.52
1:B:406:MET:SD	1:B:462:VAL:HG11	2.49	0.52
1:B:520:ILE:HD13	1:B:521:ASP:N	2.25	0.52
1:B:328:PHE:HD2	1:B:356:LEU:HD12	1.74	0.52
1:C:591:PHE:CZ	1:C:604:LEU:HD13	2.43	0.52
1:B:169:ARG:NH2	1:B:269:VAL:HG13	2.25	0.52
1:B:430:LEU:HD23	1:B:430:LEU:C	2.35	0.52
1:A:225:TYR:HD1	1:A:231:MET:HE2	1.75	0.52
1:C:397:ILE:O	1:C:397:ILE:HD12	2.09	0.52
1:C:591:PHE:CE1	1:C:604:LEU:HD13	2.44	0.52
1:A:551:VAL:HG12	1:A:580:VAL:HG13	1.91	0.52
1:A:716:ALA:HA	1:A:723:GLU:CG	2.40	0.52
1:B:515:VAL:HG21	1:B:523:ILE:HD11	1.91	0.52
1:A:319:THR:HG22	1:A:389:GLY:N	2.24	0.52
1:A:212:PRO:HA	1:A:238:GLN:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:LEU:HD12	1:B:457:LEU:C	2.35	0.51
1:C:101:VAL:HG21	1:C:134:PHE:CZ	2.46	0.51
1:C:240:TYR:HA	1:C:241:PRO:C	2.35	0.51
1:C:520:ILE:HD13	1:C:521:ASP:N	2.25	0.51
1:C:430:LEU:C	1:C:430:LEU:HD23	2.36	0.51
1:A:598:VAL:CG1	1:A:678:VAL:HG22	2.40	0.51
1:C:83:LEU:HD13	1:C:92:ILE:HG23	1.92	0.51
1:B:511:VAL:HG21	1:B:576:LEU:HD22	1.93	0.51
1:A:520:ILE:HD13	1:A:521:ASP:N	2.26	0.51
1:A:688:ASP:N	1:A:769:ILE:HD11	2.26	0.51
1:A:83:LEU:HD13	1:A:92:ILE:HG23	1.93	0.50
1:A:211:VAL:HG22	1:A:294:VAL:HG11	1.93	0.50
1:C:328:PHE:HD2	1:C:356:LEU:HD12	1.76	0.50
1:A:532:LEU:HD23	1:A:546:LEU:HD13	1.93	0.50
1:B:211:VAL:HG22	1:B:294:VAL:HG11	1.93	0.50
1:C:505:ALA:HB2	1:C:582:VAL:HA	1.93	0.50
1:A:621:LEU:O	1:A:622:ASP:C	2.54	0.50
1:B:535:ASN:O	1:B:536:ARG:C	2.54	0.50
1:C:309:LEU:HD22	1:C:337:ILE:CD1	2.42	0.50
1:A:754:LEU:C	1:A:754:LEU:CD2	2.85	0.50
1:B:309:LEU:HD22	1:B:337:ILE:CD1	2.41	0.50
1:A:603:THR:HG21	1:B:607:SER:CB	2.42	0.50
1:A:257:LYS:HE3	2:E:2:NAG:H81	1.94	0.50
1:C:169:ARG:NH2	1:C:269:VAL:HG13	2.27	0.50
1:A:7:LEU:HD12	1:A:27:LYS:HE3	1.94	0.50
1:A:67:ARG:NH1	2:D:1:NAG:H81	2.26	0.50
1:A:328:PHE:HD2	1:A:356:LEU:HD12	1.77	0.50
1:B:7:LEU:HD12	1:B:27:LYS:HE3	1.93	0.50
1:A:309:LEU:HD22	1:A:337:ILE:CD1	2.41	0.49
1:A:430:LEU:C	1:A:430:LEU:HD23	2.37	0.49
1:B:42:ASP:OD1	1:B:44:THR:HG22	2.12	0.49
1:A:101:VAL:HG21	1:A:134:PHE:CZ	2.48	0.49
1:A:183:ARG:HG3	1:A:194:LEU:HD23	1.94	0.49
1:A:663:ASN:O	1:A:664:LEU:C	2.55	0.49
1:A:515:VAL:HG21	1:A:523:ILE:HD11	1.93	0.49
1:B:532:LEU:O	1:B:538:GLN:OE1	2.30	0.49
1:A:327:VAL:HG22	1:A:357:ARG:CD	2.43	0.49
1:B:535:ASN:C	1:B:535:ASN:ND2	2.67	0.49
1:A:682:TRP:CD1	1:A:765:LEU:HD23	2.48	0.49
1:B:116:ILE:O	1:B:117:ARG:C	2.55	0.49
1:B:183:ARG:HG3	1:B:194:LEU:HD23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:505:ALA:CB	1:C:582:VAL:HA	2.43	0.49
1:A:753:TYR:CD2	1:A:771:ILE:HD12	2.48	0.49
1:B:101:VAL:HG21	1:B:134:PHE:CZ	2.47	0.49
1:A:518:TYR:C	1:A:520:ILE:H	2.20	0.49
1:B:532:LEU:O	1:B:532:LEU:HD12	2.13	0.49
1:A:689:LYS:O	1:A:771:ILE:HA	2.13	0.48
1:C:38:TRP:O	1:C:46:VAL:HG22	2.13	0.48
1:C:42:ASP:OD1	1:C:44:THR:HG22	2.13	0.48
1:C:632:ILE:HG23	1:C:646:ILE:HG12	1.93	0.48
1:C:621:LEU:O	1:C:622:ASP:C	2.55	0.48
1:A:42:ASP:OD1	1:A:44:THR:HG22	2.13	0.48
1:A:169:ARG:NH2	1:A:269:VAL:HG13	2.27	0.48
1:A:682:TRP:NE1	1:A:765:LEU:HD23	2.28	0.48
1:C:532:LEU:HD21	1:C:546:LEU:CD2	2.44	0.48
1:A:233:LEU:HD21	1:A:303:LEU:HD13	1.95	0.48
1:C:211:VAL:HG22	1:C:294:VAL:HG11	1.94	0.48
1:B:327:VAL:HG22	1:B:357:ARG:CD	2.44	0.48
1:B:615:LEU:HD13	1:B:640:ARG:HB2	1.94	0.48
1:C:327:VAL:HG22	1:C:357:ARG:CD	2.44	0.48
1:B:621:LEU:O	1:B:622:ASP:C	2.55	0.47
1:C:532:LEU:HD21	1:C:546:LEU:HD22	1.95	0.47
1:A:214:VAL:HG13	1:A:297:GLU:HG2	1.95	0.47
1:A:632:ILE:HG23	1:A:646:ILE:HG12	1.96	0.47
1:A:686:PRO:HG2	1:A:769:ILE:HD13	1.96	0.47
1:B:92:ILE:HD11	1:B:343:MET:SD	2.54	0.47
1:C:363:LYS:HA	1:C:388:LEU:HD11	1.96	0.47
1:C:532:LEU:O	1:C:538:GLN:OE1	2.32	0.47
1:A:319:THR:CG2	1:A:389:GLY:O	2.62	0.47
1:A:761:ILE:CD1	1:A:761:ILE:N	2.78	0.47
1:B:532:LEU:HD23	1:B:546:LEU:HD13	1.95	0.47
1:B:214:VAL:HG13	1:B:297:GLU:HG2	1.97	0.47
1:B:632:ILE:HG23	1:B:646:ILE:HG12	1.95	0.47
1:C:7:LEU:HD12	1:C:27:LYS:HE3	1.94	0.47
1:A:319:THR:HG22	1:A:389:GLY:O	2.14	0.47
1:A:664:LEU:O	1:A:665:ALA:HB3	2.15	0.47
1:B:290:VAL:HG12	1:B:297:GLU:O	2.14	0.47
1:B:518:TYR:C	1:B:520:ILE:H	2.22	0.47
1:A:551:VAL:HG12	1:A:580:VAL:CG1	2.45	0.47
1:A:733:ILE:HG12	1:A:742:VAL:HG13	1.96	0.47
1:B:418:ALA:HB2	1:B:426:ILE:HD11	1.97	0.47
1:B:365:ASP:O	1:B:386:LEU:HD23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:469:LEU:HD11	1:B:484:SER:HB3	1.96	0.47
1:A:258:GLN:HE21	1:A:710:GLN:CD	2.22	0.46
1:A:390:GLY:C	1:A:392:PHE:N	2.72	0.46
1:A:115:VAL:HG11	1:A:121:ALA:HB2	1.97	0.46
1:A:532:LEU:HD11	1:A:560:TYR:HE2	1.80	0.46
1:A:603:THR:HG21	1:B:607:SER:HB3	1.97	0.46
1:C:206:PRO:O	1:C:207:ILE:HD13	2.15	0.46
1:A:116:ILE:O	1:A:117:ARG:C	2.59	0.46
1:A:615:LEU:HD13	1:A:640:ARG:HB2	1.97	0.46
1:A:757:ALA:HB3	1:A:765:LEU:HB2	1.97	0.46
1:B:130:PHE:CD1	1:B:131:VAL:HG13	2.51	0.46
1:B:515:VAL:HG11	1:B:523:ILE:CD1	2.46	0.46
1:C:518:TYR:C	1:C:520:ILE:H	2.24	0.46
1:A:327:VAL:HG22	1:A:357:ARG:HD3	1.97	0.46
1:A:406:MET:SD	1:A:462:VAL:HG11	2.55	0.46
1:C:115:VAL:HG21	1:C:171:VAL:HG11	1.98	0.46
1:A:206:PRO:O	1:A:207:ILE:HD13	2.15	0.46
1:A:567:GLN:O	1:A:568:GLU:HG3	2.15	0.46
1:A:591:PHE:CZ	1:A:674:LEU:HD12	2.51	0.46
1:C:457:LEU:HD12	1:C:457:LEU:C	2.40	0.46
1:C:613:LEU:CB	1:C:614:PRO:CD	2.94	0.46
1:C:621:LEU:HD23	1:C:622:ASP:N	2.31	0.46
1:A:502:ALA:HB1	1:A:581:MET:HE1	1.98	0.46
1:C:130:PHE:CD1	1:C:131:VAL:HG13	2.51	0.46
1:B:233:LEU:HD21	1:B:303:LEU:HD13	1.97	0.46
1:C:52:LEU:HD21	1:C:70:ASP:HB3	1.98	0.46
1:C:365:ASP:O	1:C:386:LEU:HD23	2.16	0.46
1:C:615:LEU:HD13	1:C:640:ARG:HB2	1.97	0.46
1:A:38:TRP:O	1:A:46:VAL:HG22	2.16	0.46
1:A:365:ASP:O	1:A:386:LEU:HD23	2.16	0.46
1:A:745:ILE:HD12	1:A:749:ASN:HD22	1.81	0.46
1:C:183:ARG:HG3	1:C:194:LEU:HD23	1.97	0.46
1:B:83:LEU:HD13	1:B:92:ILE:HG22	1.98	0.46
1:B:121:ALA:HB3	1:B:168:ILE:HB	1.98	0.46
1:C:532:LEU:HD11	1:C:560:TYR:CE2	2.51	0.46
1:A:557:GLN:HB2	1:A:580:VAL:HB	1.96	0.45
1:B:534:ILE:HD11	1:B:538:GLN:HE22	1.80	0.45
1:A:52:LEU:HD21	1:A:70:ASP:HB3	1.99	0.45
1:B:443:VAL:HG22	1:B:457:LEU:HD13	1.98	0.45
1:B:613:LEU:CB	1:B:614:PRO:CD	2.94	0.45
1:C:430:LEU:HD12	1:C:470:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:532:LEU:HD11	1:C:560:TYR:HE2	1.80	0.45
1:C:567:GLN:O	1:C:568:GLU:HG3	2.15	0.45
1:A:586:ILE:HD11	1:A:606:CYS:SG	2.57	0.45
1:A:613:LEU:CB	1:A:614:PRO:CD	2.94	0.45
1:B:535:ASN:O	1:B:535:ASN:ND2	2.49	0.45
1:A:621:LEU:HD23	1:A:622:ASP:N	2.32	0.45
1:C:233:LEU:HD21	1:C:303:LEU:HD13	1.97	0.45
1:C:327:VAL:HG22	1:C:357:ARG:HD3	1.99	0.45
1:B:225:TYR:HD1	1:B:231:MET:HE2	1.82	0.45
1:A:443:VAL:HG22	1:A:457:LEU:HD13	1.98	0.45
1:C:92:ILE:HD11	1:C:343:MET:SD	2.57	0.45
1:A:231:MET:CE	1:A:303:LEU:HD21	2.47	0.45
1:B:251:ILE:O	1:B:252:GLU:C	2.60	0.45
1:B:327:VAL:HG22	1:B:357:ARG:HD3	1.99	0.45
1:B:591:PHE:CZ	1:B:674:LEU:HD12	2.51	0.45
1:C:214:VAL:HG13	1:C:297:GLU:HG2	1.99	0.45
1:C:539:LYS:HB2	1:C:547:ILE:HG23	1.99	0.45
1:A:707:PRO:HD2	1:A:761:ILE:HD11	1.99	0.45
1:A:518:TYR:O	1:A:518:TYR:CD1	2.69	0.45
1:B:52:LEU:HD21	1:B:70:ASP:HB3	1.98	0.45
1:B:309:LEU:HD11	1:B:375:ASN:ND2	2.32	0.44
1:A:539:LYS:HB2	1:A:547:ILE:HG23	1.99	0.44
1:C:373:VAL:CG2	1:C:380:ALA:HB3	2.44	0.44
1:C:418:ALA:HB2	1:C:426:ILE:HD11	2.00	0.44
1:A:130:PHE:CD1	1:A:131:VAL:HG13	2.52	0.44
1:C:251:ILE:O	1:C:252:GLU:C	2.60	0.44
1:C:254:THR:HG22	1:C:593:GLU:C	2.43	0.44
1:C:469:LEU:HD11	1:C:484:SER:HB3	2.00	0.44
1:A:115:VAL:HG21	1:A:171:VAL:HG11	1.99	0.44
1:A:319:THR:HG22	1:A:389:GLY:HA2	1.98	0.44
1:A:251:ILE:O	1:A:252:GLU:C	2.60	0.44
1:B:231:MET:CE	1:B:303:LEU:HD21	2.47	0.44
1:B:664:LEU:O	1:B:665:ALA:HB3	2.17	0.44
1:A:24:ILE:HD11	1:A:61:LEU:HD23	2.00	0.44
1:A:551:VAL:CG1	1:A:580:VAL:HG13	2.48	0.44
1:B:290:VAL:HG13	1:B:290:VAL:O	2.17	0.44
1:A:119:ASN:N	1:A:119:ASN:HD22	2.16	0.44
1:A:184:THR:O	1:A:192:THR:HA	2.18	0.44
1:A:225:TYR:CD1	1:A:231:MET:HE2	2.51	0.44
1:A:469:LEU:HD11	1:A:484:SER:HB3	1.99	0.44
1:B:119:ASN:HD22	1:B:119:ASN:N	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:621:LEU:HD23	1:B:622:ASP:N	2.33	0.44
1:A:319:THR:HG23	1:A:387:LYS:HB3	2.00	0.44
1:C:184:THR:O	1:C:192:THR:HA	2.18	0.43
1:C:219:LYS:HA	1:C:299:VAL:HG12	2.00	0.43
1:C:225:TYR:HD1	1:C:231:MET:HE2	1.83	0.43
1:C:417:VAL:CG2	1:C:454:VAL:HG22	2.42	0.43
1:C:116:ILE:O	1:C:117:ARG:C	2.60	0.43
1:C:115:VAL:HG11	1:C:121:ALA:HB2	2.00	0.43
1:A:598:VAL:HG11	1:A:678:VAL:HG22	2.01	0.43
1:A:457:LEU:C	1:A:457:LEU:HD12	2.43	0.43
1:C:24:ILE:HD11	1:C:61:LEU:HD23	2.00	0.43
1:C:515:VAL:HG21	1:C:523:ILE:HD11	1.99	0.43
1:B:184:THR:O	1:B:192:THR:HA	2.18	0.43
1:C:363:LYS:HA	1:C:388:LEU:CD1	2.48	0.43
1:A:159:LEU:HD12	1:A:160:VAL:N	2.34	0.43
1:A:418:ALA:HB2	1:A:426:ILE:HD11	1.99	0.43
1:A:507:GLU:O	1:A:551:VAL:HG23	2.19	0.43
1:A:723:GLU:O	1:A:724:TYR:C	2.61	0.43
1:C:309:LEU:HD11	1:C:375:ASN:ND2	2.34	0.43
1:A:92:ILE:HD11	1:A:343:MET:SD	2.58	0.42
1:A:231:MET:HE2	1:A:303:LEU:HD11	2.00	0.42
1:B:219:LYS:HA	1:B:299:VAL:HG12	2.00	0.42
1:B:586:ILE:HD11	1:B:606:CYS:SG	2.58	0.42
1:B:632:ILE:HG22	1:B:644:LEU:HD11	2.00	0.42
1:C:83:LEU:HD13	1:C:92:ILE:HG22	2.01	0.42
1:C:231:MET:CE	1:C:303:LEU:HD21	2.49	0.42
1:C:319:THR:HG22	1:C:389:GLY:CA	2.49	0.42
1:C:664:LEU:O	1:C:665:ALA:HB3	2.19	0.42
1:A:290:VAL:HG12	1:A:297:GLU:O	2.19	0.42
1:B:231:MET:HE2	1:B:303:LEU:HD11	2.01	0.42
1:C:443:VAL:HG22	1:C:457:LEU:HD13	2.01	0.42
1:A:319:THR:HG23	1:A:387:LYS:CB	2.49	0.42
1:A:418:ALA:HB3	1:A:426:ILE:HD11	2.02	0.42
1:B:233:LEU:O	1:B:272:THR:HG23	2.20	0.42
1:A:478:VAL:HG22	1:A:478:VAL:O	2.19	0.42
1:B:373:VAL:CG2	1:B:380:ALA:HB3	2.44	0.42
1:B:507:GLU:O	1:B:551:VAL:HG23	2.19	0.42
1:C:632:ILE:HG22	1:C:644:LEU:HD11	2.00	0.42
1:B:159:LEU:HD12	1:B:160:VAL:N	2.35	0.42
1:C:119:ASN:N	1:C:119:ASN:HD22	2.17	0.42
1:C:290:VAL:HG13	1:C:290:VAL:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:PRO:O	1:A:453:VAL:HG21	2.19	0.42
1:B:424:PRO:O	1:B:453:VAL:HG21	2.19	0.42
1:B:115:VAL:HG21	1:B:171:VAL:HG11	2.02	0.42
1:C:147:ASN:HD22	1:C:147:ASN:N	2.18	0.42
1:C:168:ILE:CD1	1:C:201:LEU:HD11	2.49	0.42
1:C:290:VAL:HG12	1:C:297:GLU:O	2.19	0.42
1:A:16:PHE:CG	1:A:22:ALA:HB2	2.55	0.41
1:A:128:PRO:HB2	1:A:131:VAL:HG22	2.02	0.41
1:A:515:VAL:HG11	1:A:523:ILE:CD1	2.50	0.41
1:B:539:LYS:HB2	1:B:547:ILE:HG23	2.02	0.41
1:C:159:LEU:HD12	1:C:160:VAL:N	2.35	0.41
1:A:221:ASP:HB2	1:B:217:LEU:HG	2.02	0.41
1:A:707:PRO:HD3	1:A:761:ILE:HD11	2.02	0.41
1:B:16:PHE:CG	1:B:22:ALA:HB2	2.54	0.41
1:B:225:TYR:CD1	1:B:231:MET:HE2	2.55	0.41
1:C:16:PHE:CG	1:C:22:ALA:HB2	2.56	0.41
1:A:258:GLN:NE2	1:A:710:GLN:OE1	2.53	0.41
1:C:101:VAL:HG21	1:C:134:PHE:CE2	2.55	0.41
1:C:138:VAL:HG21	1:C:185:LYS:HB2	2.02	0.41
1:A:463:HIS:O	1:A:489:VAL:HG11	2.20	0.41
1:B:551:VAL:CG1	1:B:580:VAL:HG22	2.50	0.41
1:C:406:MET:SD	1:C:462:VAL:HG11	2.60	0.41
1:C:461:SER:O	1:C:462:VAL:C	2.64	0.41
1:A:754:LEU:HD23	1:A:767:ALA:O	2.20	0.41
1:B:19:SER:OG	2:F:1:NAG:N2	2.54	0.41
1:A:219:LYS:HA	1:A:299:VAL:HG12	2.02	0.41
1:A:290:VAL:HG13	1:A:290:VAL:O	2.20	0.41
1:A:423:THR:HA	1:A:424:PRO:HD3	1.96	0.41
1:A:752:TYR:CE1	1:A:770:MET:HE2	2.56	0.41
1:B:14:ILE:HD13	1:B:14:ILE:HA	1.97	0.41
1:B:233:LEU:HD12	1:B:273:LEU:HD23	2.03	0.41
1:B:403:GLU:HG3	1:B:404:GLU:N	2.36	0.41
1:B:532:LEU:HD21	1:B:546:LEU:CD2	2.51	0.41
1:C:39:ILE:HG13	1:C:81:ALA:HB3	2.02	0.41
1:C:478:VAL:HG22	1:C:478:VAL:O	2.20	0.41
1:A:727:LEU:HD23	1:A:733:ILE:HG21	2.03	0.41
1:C:322:PHE:CB	1:C:478:VAL:HG22	2.51	0.41
1:A:83:LEU:HD13	1:A:92:ILE:HG22	2.02	0.40
1:A:142:THR:HG22	1:A:180:TYR:HD1	1.86	0.40
1:C:322:PHE:HB3	1:C:478:VAL:HG22	2.02	0.40
1:C:424:PRO:O	1:C:453:VAL:HG21	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:VAL:CG2	1:A:454:VAL:HG22	2.45	0.40
1:B:478:VAL:O	1:B:478:VAL:HG22	2.21	0.40
1:A:309:LEU:HD23	1:A:334:GLY:HA3	2.04	0.40
1:A:716:ALA:HA	1:A:723:GLU:HG3	2.03	0.40
1:A:752:TYR:HA	1:A:769:ILE:O	2.21	0.40
1:A:39:ILE:HG13	1:A:81:ALA:HB3	2.03	0.40
1:A:373:VAL:CG2	1:A:380:ALA:HB3	2.45	0.40
1:B:461:SER:O	1:B:462:VAL:C	2.64	0.40
1:C:231:MET:HE2	1:C:303:LEU:HD11	2.03	0.40
1:C:233:LEU:O	1:C:272:THR:HG23	2.20	0.40
1:C:403:GLU:HG3	1:C:404:GLU:N	2.35	0.40
1:A:4:PRO:O	1:A:368:MET:HE2	2.21	0.40
1:B:430:LEU:HD12	1:B:470:TYR:CE2	2.57	0.40
3:J:1:NAG:O3	3:J:2:NAG:O5	2.33	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:492:LEU:N	1:C:407:GLU:OE1[8_455]	2.04	0.16

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	773/816 (95%)	696 (90%)	64 (8%)	13 (2%)	7	35
1	B	674/816 (83%)	605 (90%)	56 (8%)	13 (2%)	6	32
1	C	674/816 (83%)	600 (89%)	62 (9%)	12 (2%)	6	33
All	All	2121/2448 (87%)	1901 (90%)	182 (9%)	38 (2%)	6	33

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	613	LEU
1	A	626	ILE
1	B	613	LEU
1	B	626	ILE
1	C	613	LEU
1	C	626	ILE
1	A	216	SER
1	A	638	GLY
1	A	724	TYR
1	B	216	SER
1	B	392	PHE
1	B	638	GLY
1	C	216	SER
1	C	638	GLY
1	A	103	ALA
1	A	174	GLU
1	A	252	GLU
1	A	622	ASP
1	A	664	LEU
1	B	103	ALA
1	B	252	GLU
1	B	622	ASP
1	B	664	LEU
1	C	103	ALA
1	C	174	GLU
1	C	252	GLU
1	C	593	GLU
1	C	622	ASP
1	C	664	LEU
1	A	744	ASN
1	B	174	GLU
1	B	464	ALA
1	B	612	ASP
1	C	612	ASP
1	A	464	ALA
1	A	553	ARG
1	B	553	ARG
1	C	553	ARG

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	654/687 (95%)	624 (95%)	30 (5%)	24	46
1	B	572/687 (83%)	546 (96%)	26 (4%)	24	47
1	C	572/687 (83%)	546 (96%)	26 (4%)	24	47
All	All	1798/2061 (87%)	1716 (95%)	82 (5%)	24	46

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	THR
1	A	88	PHE
1	A	119	ASN
1	A	163	SER
1	A	195	SER
1	A	221	ASP
1	A	319	THR
1	A	339	THR
1	A	374	ARG
1	A	393	ASP
1	A	397	ILE
1	A	435	ILE
1	A	440	ARG
1	A	453	VAL
1	A	509	LEU
1	A	510	ILE
1	A	520	ILE
1	A	522	SER
1	A	535	ASN
1	A	536	ARG
1	A	549	GLU
1	A	552	GLU
1	A	554	ASN
1	A	556	ASP
1	A	645	THR
1	A	663	ASN
1	A	699	VAL
1	A	710	GLN
1	A	754	LEU
1	A	761	ILE

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Mol	Chain	Res	Type
1	B	11	THR
1	B	88	PHE
1	B	119	ASN
1	B	163	SER
1	B	195	SER
1	B	221	ASP
1	B	319	THR
1	B	339	THR
1	B	374	ARG
1	B	393	ASP
1	B	397	ILE
1	B	435	ILE
1	B	440	ARG
1	B	453	VAL
1	B	509	LEU
1	B	510	ILE
1	B	520	ILE
1	B	522	SER
1	B	535	ASN
1	B	536	ARG
1	B	549	GLU
1	B	552	GLU
1	B	554	ASN
1	B	556	ASP
1	B	645	THR
1	B	663	ASN
1	C	11	THR
1	C	88	PHE
1	C	119	ASN
1	C	163	SER
1	C	195	SER
1	C	221	ASP
1	C	319	THR
1	C	339	THR
1	C	374	ARG
1	C	393	ASP
1	C	397	ILE
1	C	435	ILE
1	C	440	ARG
1	C	453	VAL
1	C	509	LEU
1	C	510	ILE

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Mol	Chain	Res	Type
1	C	520	ILE
1	C	522	SER
1	C	534	ILE
1	C	536	ARG
1	C	549	GLU
1	C	552	GLU
1	C	554	ASN
1	C	556	ASP
1	C	645	THR
1	C	663	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	147	ASN
1	A	258	GLN
1	A	402	GLN
1	A	465	ASN
1	A	550	ASN
1	A	554	ASN
1	A	616	ASN
1	A	732	ASN
1	A	749	ASN
1	B	31	ASN
1	B	147	ASN
1	B	402	GLN
1	B	465	ASN
1	B	554	ASN
1	B	616	ASN
1	C	31	ASN
1	C	147	ASN
1	C	167	HIS
1	C	268	GLN
1	C	402	GLN
1	C	465	ASN
1	C	550	ASN
1	C	554	ASN
1	C	579	GLN
1	C	616	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

20 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	D	1	1,2	14,14,15	0.41	0	17,19,21	1.54	2 (11%)
2	NAG	D	2	2	14,14,15	0.51	0	17,19,21	0.77	0
2	NAG	E	1	1,2	14,14,15	0.69	1 (7%)	17,19,21	1.79	3 (17%)
2	NAG	E	2	2	14,14,15	0.50	0	17,19,21	0.87	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.59	0	17,19,21	1.30	1 (5%)
2	NAG	F	2	2	14,14,15	0.78	0	17,19,21	1.16	1 (5%)
3	NAG	G	1	1,3	14,14,15	0.54	0	17,19,21	1.28	2 (11%)
3	NAG	G	2	3	14,14,15	0.46	0	17,19,21	1.21	2 (11%)
3	NAG	G	3	3	14,14,15	0.56	0	17,19,21	0.79	0
3	NAG	H	1	1,3	14,14,15	0.82	0	17,19,21	2.00	4 (23%)
3	NAG	H	2	3	14,14,15	0.72	0	17,19,21	1.49	3 (17%)
3	NAG	H	3	3	14,14,15	0.56	0	17,19,21	0.74	0
2	NAG	I	1	1,2	14,14,15	0.80	1 (7%)	17,19,21	1.40	2 (11%)
2	NAG	I	2	2	14,14,15	0.60	0	17,19,21	0.87	0
3	NAG	J	1	1,3	14,14,15	0.33	0	17,19,21	1.59	2 (11%)
3	NAG	J	2	3	14,14,15	0.58	0	17,19,21	0.83	0
3	NAG	J	3	3	14,14,15	0.51	0	17,19,21	0.83	0
3	NAG	K	1	1,3	14,14,15	0.42	0	17,19,21	1.42	2 (11%)
3	NAG	K	2	3	14,14,15	0.61	0	17,19,21	1.12	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	K	3	3	14,14,15	0.65	0	17,19,21	1.01	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	4/6/23/26	0/1/1/1
3	NAG	G	1	1,3	1/1/5/7	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1
3	NAG	G	3	3	-	5/6/23/26	0/1/1/1
3	NAG	H	1	1,3	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
3	NAG	H	3	3	-	3/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	I	2	2	-	3/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	NAG	J	3	3	-	2/6/23/26	0/1/1/1
3	NAG	K	1	1,3	1/1/5/7	4/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1
3	NAG	K	3	3	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	NAG	C1-C2	2.21	1.55	1.52
2	E	1	NAG	C1-C2	2.15	1.55	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	NAG	O5-C1-C2	-5.39	102.95	111.29
3	J	1	NAG	C1-O5-C5	4.79	118.61	112.19
3	H	1	NAG	C4-C3-C2	4.71	117.92	111.02
2	D	1	NAG	O5-C1-C2	-4.38	104.51	111.29
2	I	1	NAG	C4-C3-C2	4.37	117.42	111.02
2	F	1	NAG	O5-C1-C2	-4.34	104.58	111.29
3	H	2	NAG	C4-C3-C2	4.12	117.05	111.02
3	K	1	NAG	C1-O5-C5	3.83	117.32	112.19
3	H	1	NAG	C2-N2-C7	3.82	128.02	122.90
3	K	1	NAG	O5-C1-C2	-3.78	105.44	111.29
3	K	2	NAG	C4-C3-C2	3.48	116.12	111.02
2	F	2	NAG	C4-C3-C2	3.46	116.09	111.02
3	J	1	NAG	C4-C3-C2	-3.37	106.08	111.02
3	H	1	NAG	C3-C4-C5	3.36	116.33	110.23
2	D	1	NAG	C1-O5-C5	3.35	116.68	112.19
2	E	1	NAG	C1-C2-N2	3.32	115.66	110.43
3	G	2	NAG	C2-N2-C7	-3.09	118.75	122.90
3	G	1	NAG	C1-O5-C5	2.97	116.17	112.19
3	G	2	NAG	O5-C1-C2	-2.89	106.82	111.29
3	H	2	NAG	C1-O5-C5	-2.65	108.64	112.19
3	G	1	NAG	C1-C2-N2	2.55	114.45	110.43
2	I	1	NAG	O5-C1-C2	-2.32	107.70	111.29
3	H	1	NAG	O7-C7-N2	2.16	125.81	121.98
3	H	2	NAG	C1-C2-N2	-2.15	107.04	110.43
2	E	1	NAG	C1-O5-C5	2.14	115.06	112.19
2	E	2	NAG	C1-O5-C5	2.05	114.94	112.19
3	K	3	NAG	C4-C3-C2	2.05	114.02	111.02

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	G	1	NAG	C1
3	H	1	NAG	C1
3	K	1	NAG	C1

All (59) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	E	1	NAG	C8-C7-N2-C2

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

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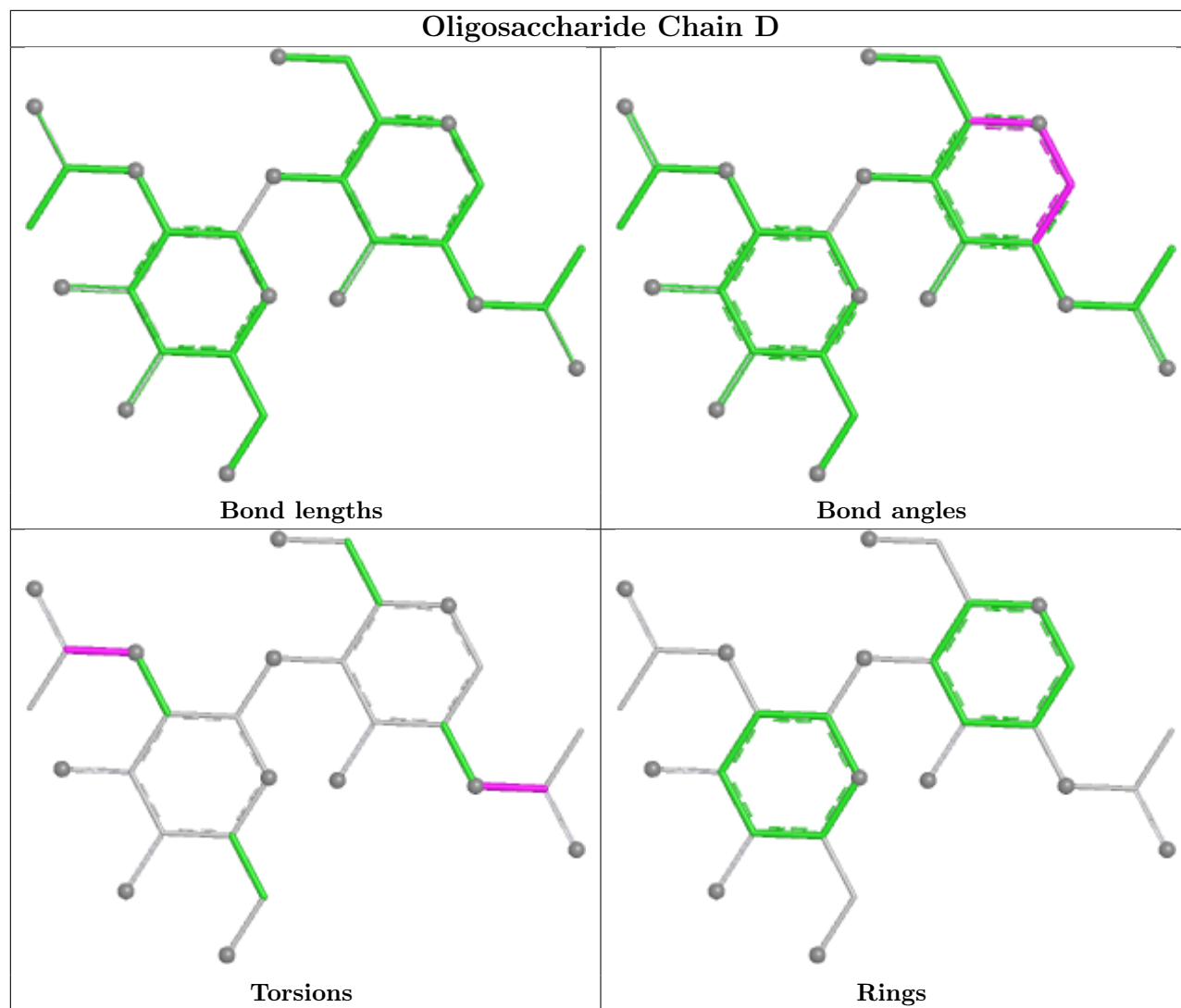
Mol	Chain	Res	Type	Atoms
3	K	1	NAG	C4-C5-C6-O6
3	G	1	NAG	O7-C7-N2-C2
3	G	2	NAG	O5-C5-C6-O6
3	G	3	NAG	C4-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
3	K	3	NAG	C4-C5-C6-O6
3	H	3	NAG	O5-C5-C6-O6
2	I	2	NAG	O5-C5-C6-O6
3	K	3	NAG	O5-C5-C6-O6
3	H	1	NAG	C1-C2-N2-C7
3	G	1	NAG	O5-C5-C6-O6
3	G	3	NAG	C1-C2-N2-C7

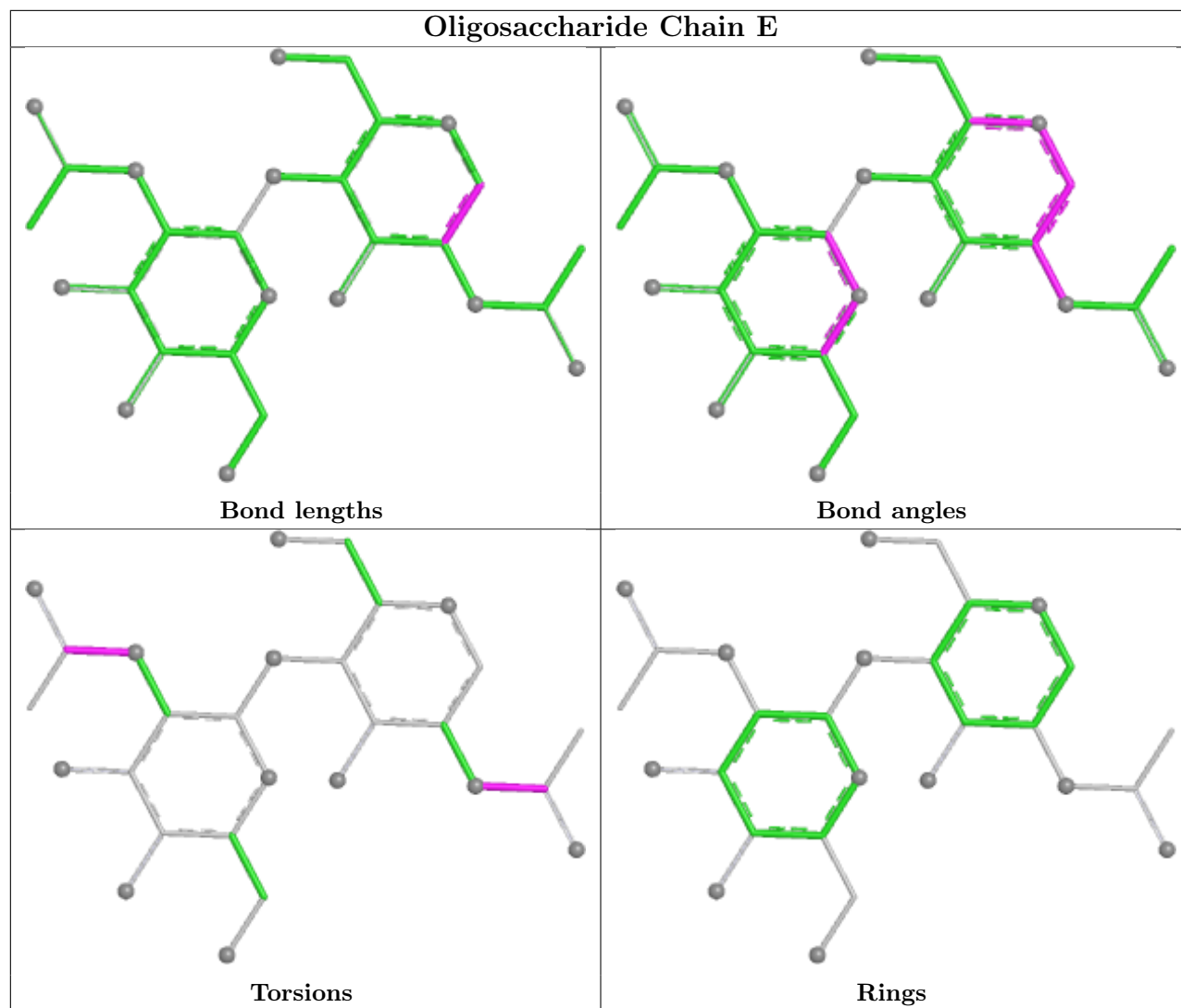
There are no ring outliers.

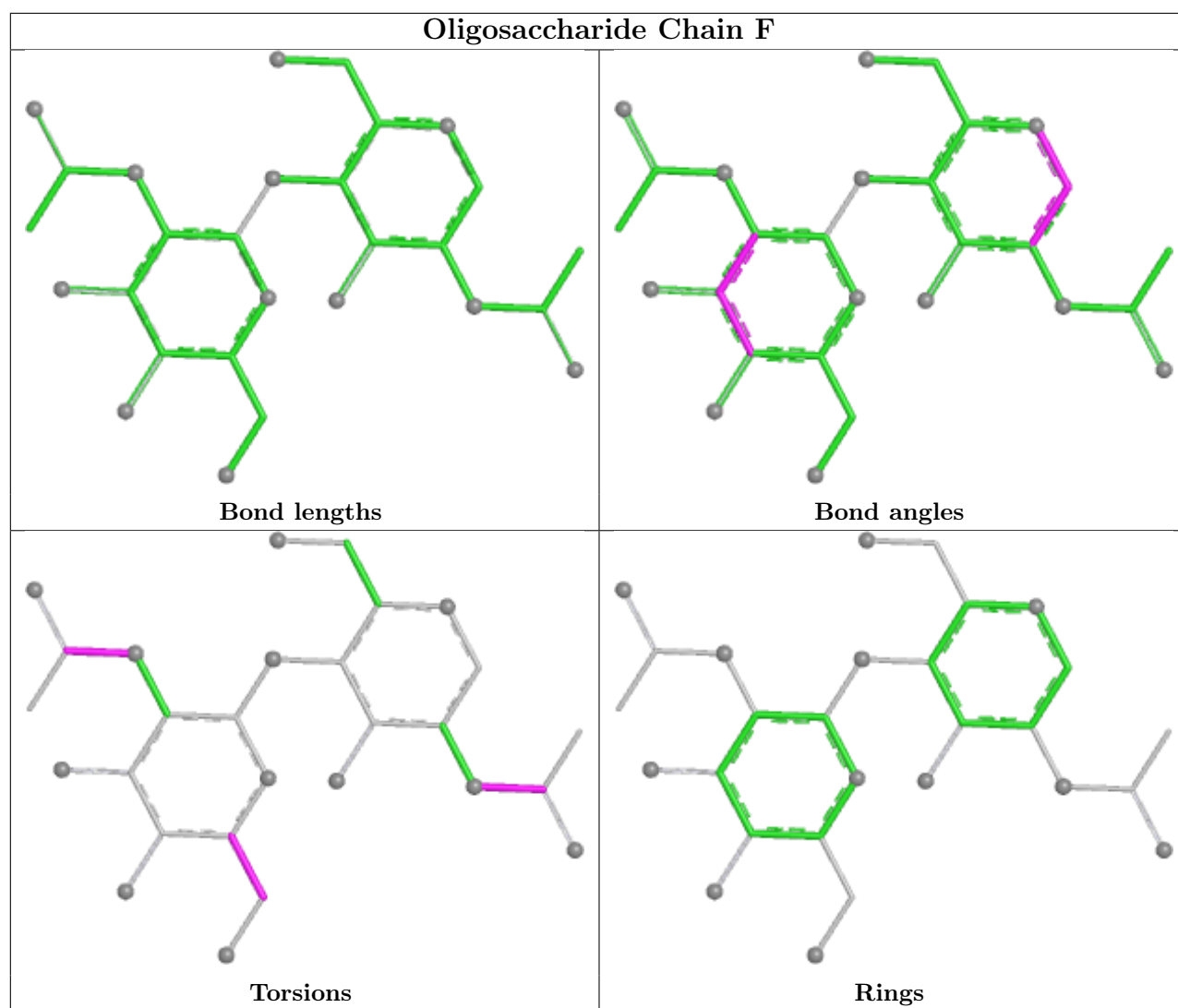
5 monomers are involved in 5 short contacts:

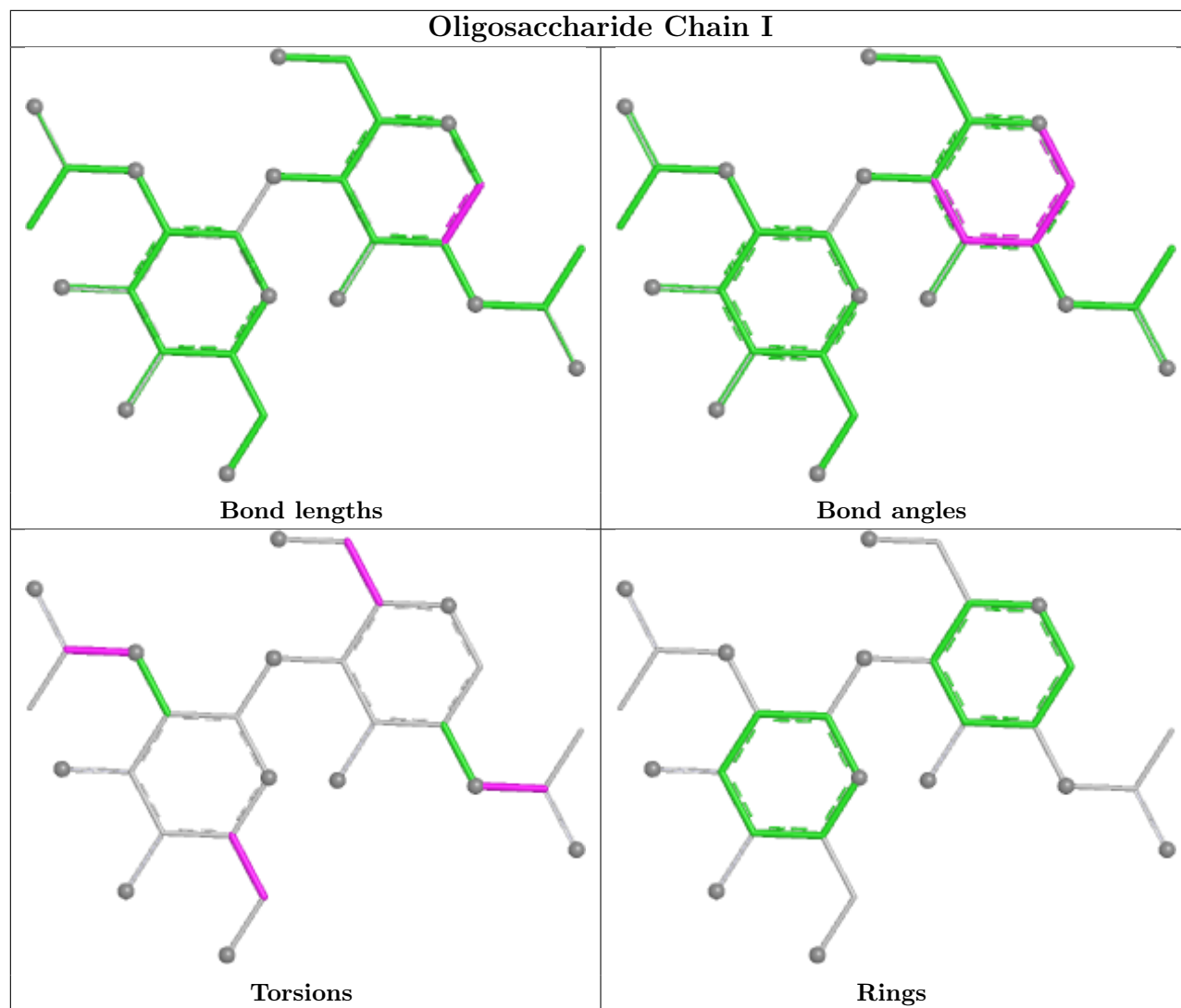
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	NAG	1	0
2	D	1	NAG	2	0
3	J	2	NAG	1	0
2	F	1	NAG	1	0
3	J	1	NAG	1	0

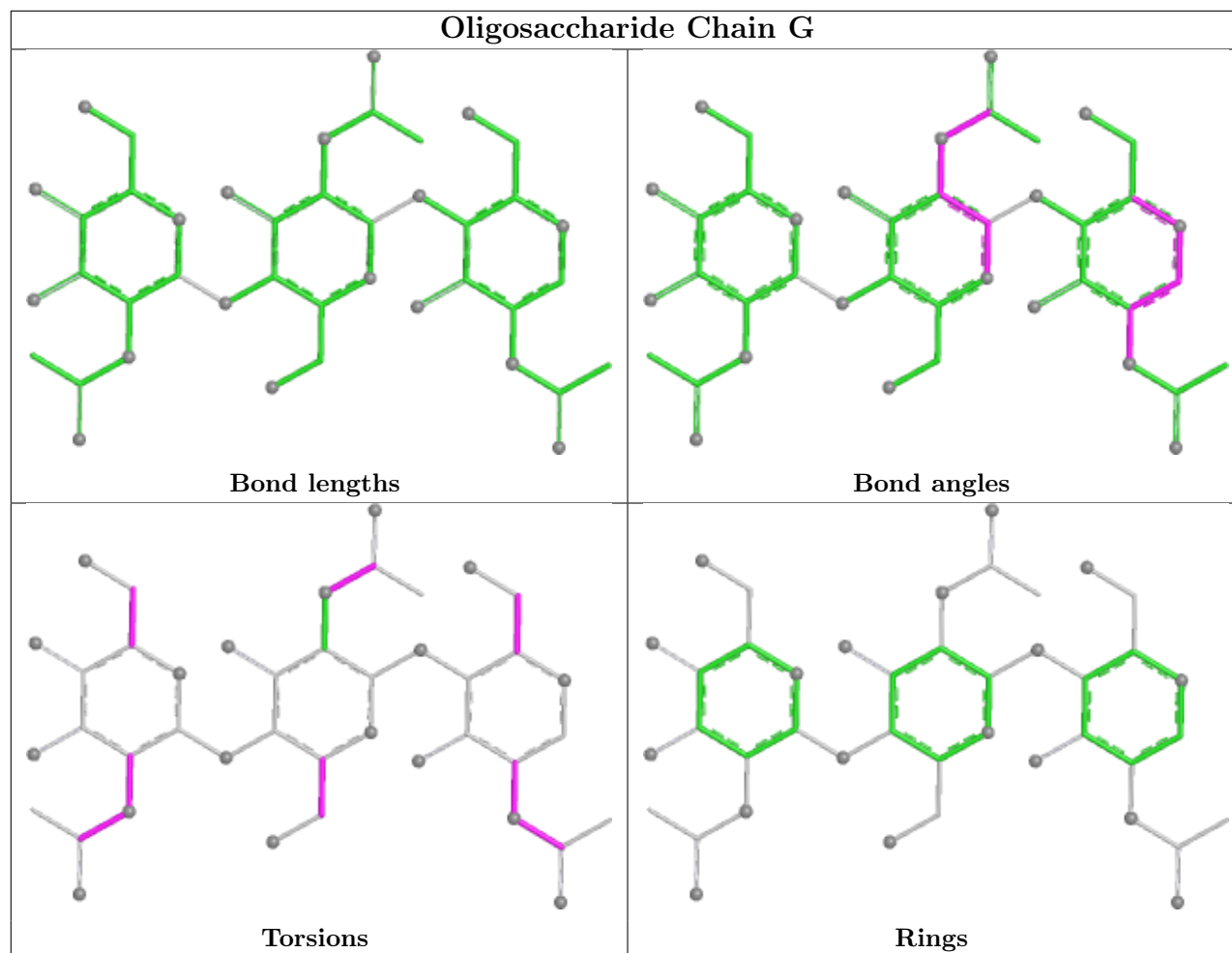
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

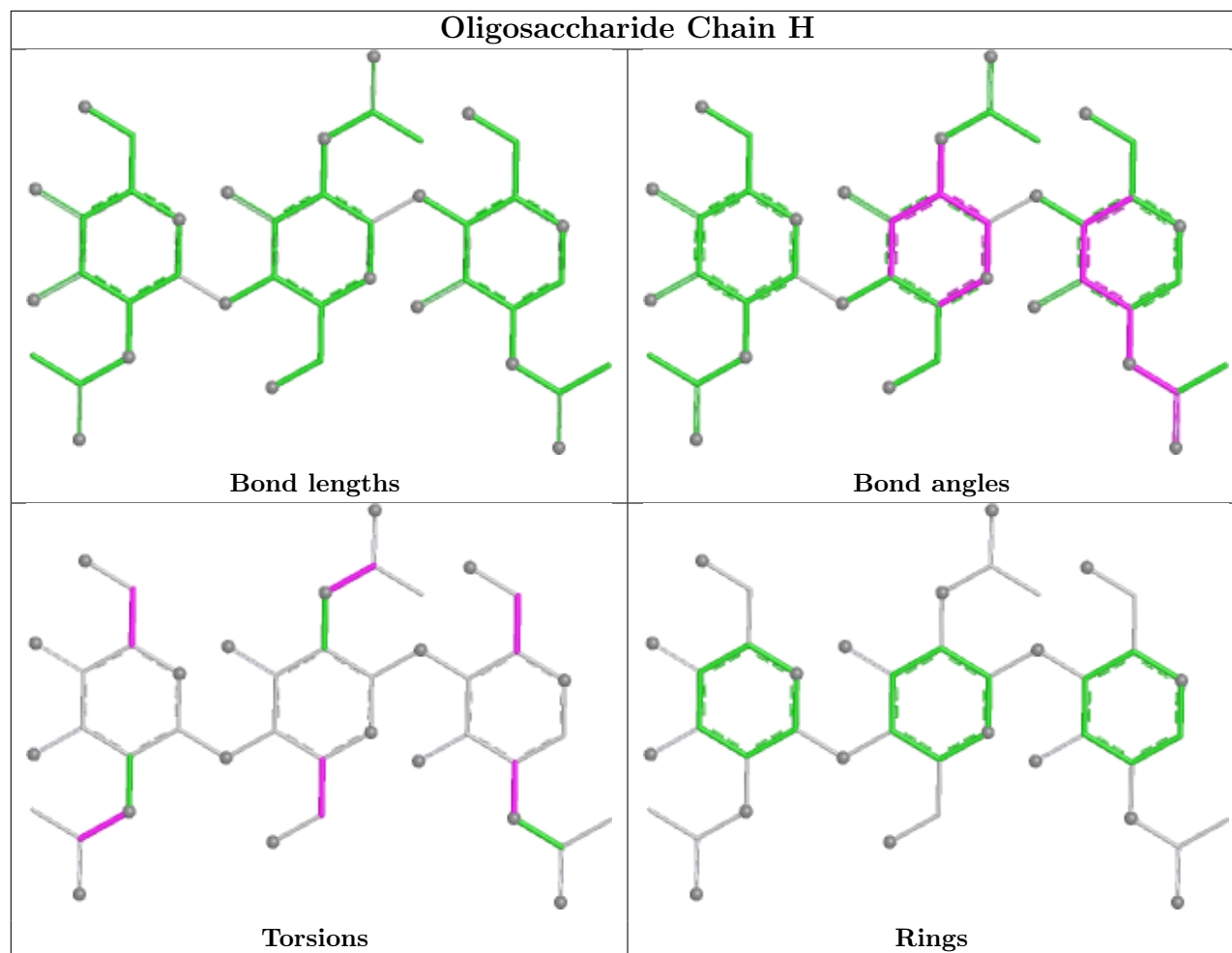


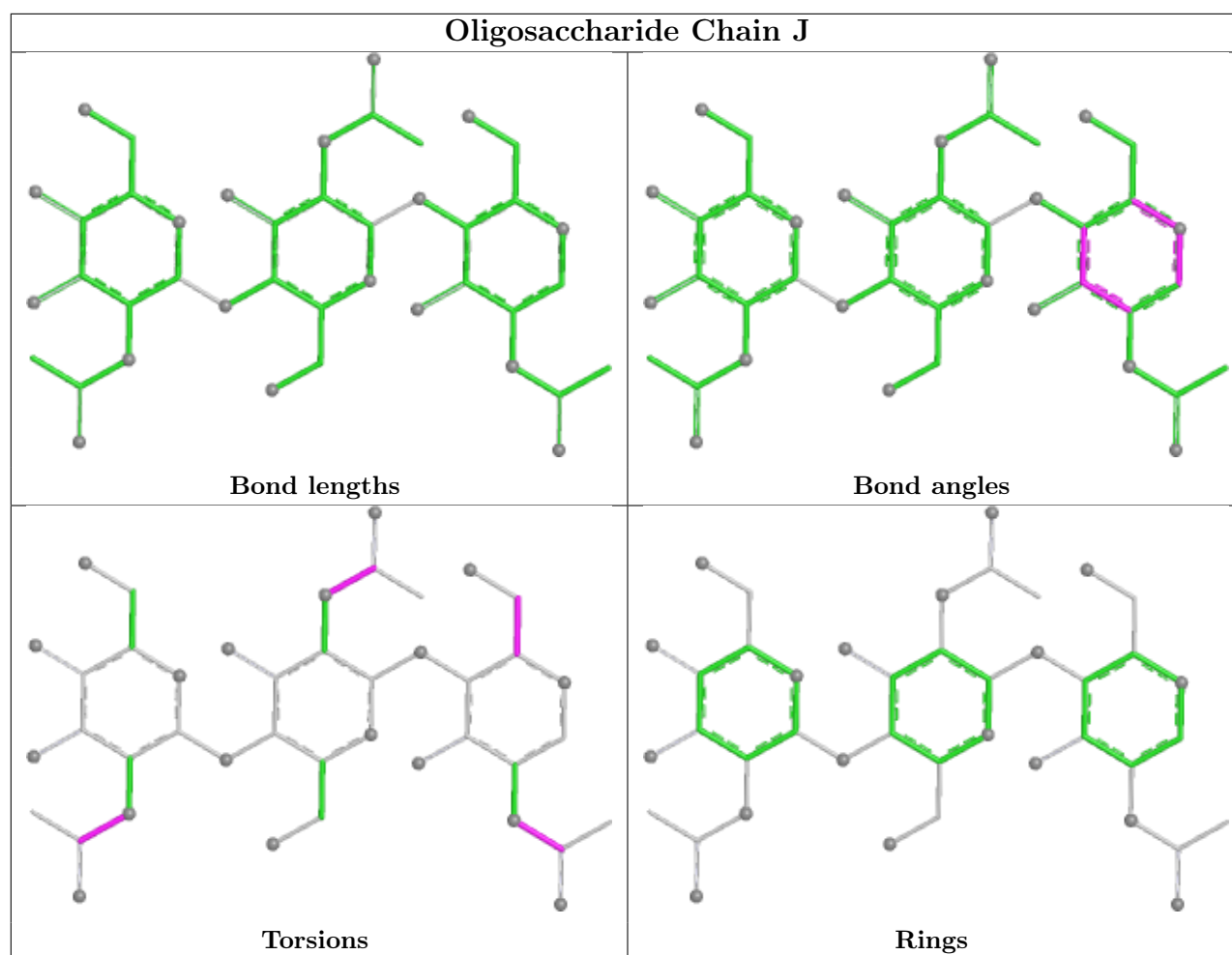


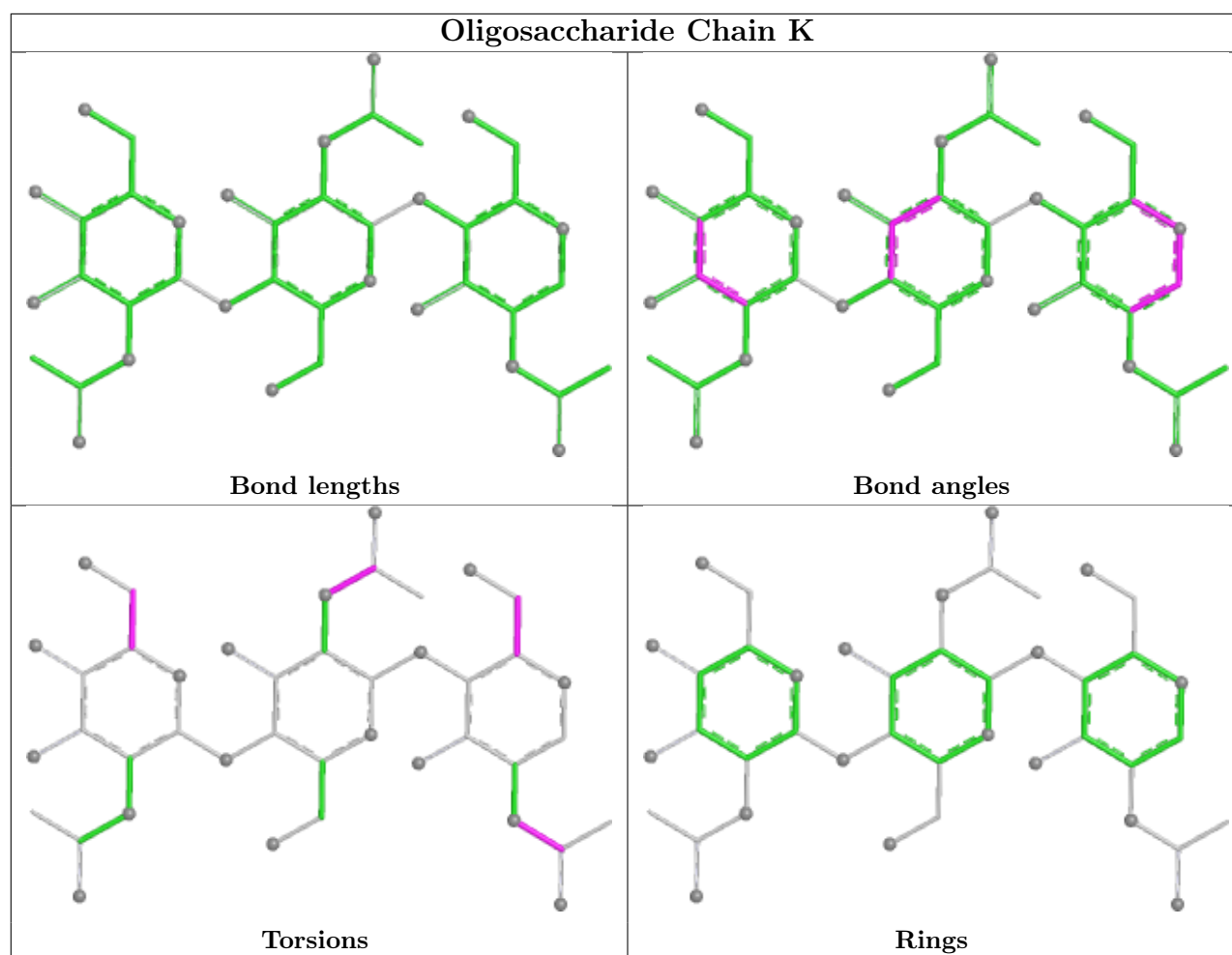












5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
4	GOL	B	793	-	5,5,5	0.40	0	5,5,5	0.20	0
4	GOL	A	786	-	5,5,5	0.36	0	5,5,5	0.38	0
5	SO4	B	792	-	4,4,4	0.22	0	6,6,6	0.13	0
4	GOL	A	787	-	5,5,5	0.40	0	5,5,5	0.28	0
4	GOL	B	794	-	5,5,5	0.45	0	5,5,5	0.24	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
4	GOL	B	793	-	-	0/4/4/4	-
4	GOL	A	787	-	-	2/4/4/4	-
4	GOL	B	794	-	-	4/4/4/4	-
4	GOL	A	786	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	786	GOL	C1-C2-C3-O3
4	A	787	GOL	C1-C2-C3-O3
4	B	794	GOL	O1-C1-C2-C3
4	B	794	GOL	C1-C2-C3-O3
4	A	787	GOL	O2-C2-C3-O3
4	B	794	GOL	O1-C1-C2-O2
4	B	794	GOL	O2-C2-C3-O3
4	A	786	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	775/816 (94%)	0.60	43 (5%)	30 28	27, 55, 89, 101	0
1	B	676/816 (82%)	0.29	11 (1%)	70 54	16, 42, 82, 93	0
1	C	676/816 (82%)	0.87	90 (13%)	7 11	25, 53, 101, 108	0
All	All	2127/2448 (86%)	0.59	144 (6%)	23 24	16, 50, 93, 108	0

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	184	THR	5.9
1	A	313	ILE	5.1
1	A	320	VAL	5.1
1	C	77	ALA	5.0
1	C	198	LYS	4.8
1	A	472	CYS	4.7
1	C	163	SER	4.6
1	C	541	PHE	4.4
1	C	529	ASN	4.4
1	C	162	PRO	4.4
1	C	367	GLY	4.3
1	C	199	GLY	4.1
1	C	156	GLY	4.0
1	C	164	GLY	3.9
1	C	152	ALA	3.8
1	C	14	ILE	3.8
1	C	123	ILE	3.8
1	A	517	GLY	3.8
1	C	122	VAL	3.7
1	A	438	ASN	3.6
1	C	129	SER	3.6
1	A	532	LEU	3.6
1	C	171	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	680	PRO	3.5
1	C	136	GLU	3.5
1	C	167	HIS	3.4
1	C	28	ALA	3.4
1	A	408	PRO	3.4
1	A	486	LYS	3.3
1	B	594	GLY	3.3
1	C	410	PRO	3.2
1	C	326	ALA	3.2
1	C	155	ASP	3.2
1	A	365	ASP	3.2
1	C	185	LYS	3.1
1	B	367	GLY	3.1
1	C	203	ILE	3.0
1	C	127	ILE	2.9
1	C	270	SER	2.9
1	A	489	VAL	2.9
1	C	111	ASN	2.9
1	B	550	ASN	2.9
1	C	419	GLY	2.9
1	C	488	ASN	2.8
1	A	74	GLU	2.8
1	A	348	ALA	2.8
1	C	278	ALA	2.8
1	C	341	SER	2.8
1	C	176	GLY	2.8
1	C	505	ALA	2.8
1	C	125	CYS	2.8
1	A	436	ALA	2.8
1	C	201	LEU	2.7
1	C	128	PRO	2.7
1	C	196	ALA	2.7
1	A	59	GLY	2.7
1	C	166	LEU	2.7
1	C	143	ASP	2.7
1	C	151	GLY	2.7
1	A	387	LYS	2.6
1	C	532	LEU	2.6
1	C	56	SER	2.6
1	C	121	ALA	2.6
1	A	499	GLU	2.6
1	C	85	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	490	TYR	2.6
1	C	442	GLN	2.6
1	C	229	SER	2.6
1	A	182	CYS	2.6
1	C	303	LEU	2.6
1	B	663	ASN	2.5
1	C	220	PHE	2.5
1	B	436	ALA	2.5
1	C	131	VAL	2.5
1	C	135	VAL	2.5
1	C	516	ALA	2.5
1	C	120	SER	2.5
1	A	378	GLU	2.5
1	C	191	GLU	2.5
1	A	3	GLY	2.5
1	A	104	GLN	2.5
1	A	349	ILE	2.5
1	A	679	PRO	2.4
1	A	483	HIS	2.4
1	C	405	THR	2.4
1	C	89	GLY	2.4
1	A	578	VAL	2.4
1	C	130	PHE	2.4
1	C	622	ASP	2.4
1	C	116	ILE	2.4
1	C	140	TRP	2.4
1	C	566	ASN	2.4
1	C	126	LEU	2.4
1	C	181	GLN	2.3
1	C	568	GLU	2.3
1	A	565	LYS	2.3
1	C	234	LEU	2.3
1	A	42	ASP	2.3
1	A	475	LYS	2.3
1	B	27	LYS	2.3
1	A	129	SER	2.3
1	C	106	TYR	2.3
1	A	557	GLN	2.3
1	C	197	THR	2.3
1	B	544	GLY	2.3
1	A	28	ALA	2.3
1	C	177	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	192	THR	2.3
1	A	478	VAL	2.3
1	B	568	GLU	2.2
1	C	82	CYS	2.2
1	A	351	HIS	2.2
1	A	306	THR	2.2
1	A	622	ASP	2.2
1	C	205	GLU	2.2
1	C	294	VAL	2.2
1	A	336	PRO	2.2
1	B	508	THR	2.2
1	C	411	SER	2.2
1	C	46	VAL	2.2
1	C	592	GLU	2.1
1	C	154	TYR	2.1
1	B	599	GLY	2.1
1	C	84	ALA	2.1
1	C	502	ALA	2.1
1	C	150	PRO	2.1
1	A	528	ASP	2.1
1	A	554	ASN	2.1
1	A	84	ALA	2.1
1	C	666	GLY	2.1
1	A	664	LEU	2.1
1	C	439	ASP	2.1
1	C	398	ARG	2.1
1	A	464	ALA	2.1
1	C	546	LEU	2.1
1	C	493	PRO	2.1
1	C	322	PHE	2.1
1	C	73	GLN	2.1
1	B	552	GLU	2.1
1	C	115	VAL	2.1
1	C	393	ASP	2.0
1	A	156	GLY	2.0
1	A	490	TYR	2.0
1	C	517	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

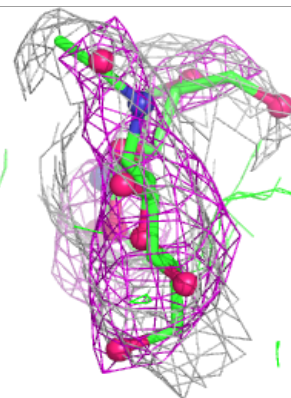
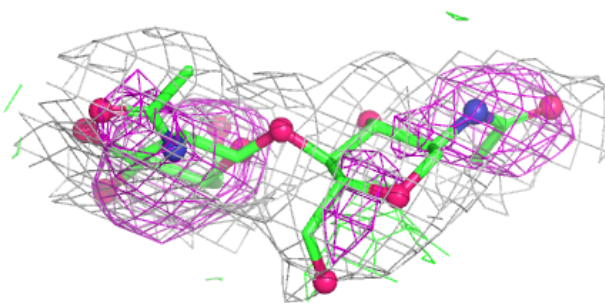
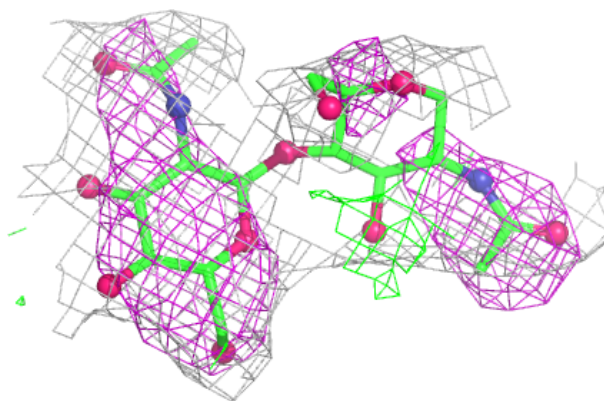
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	K	2	14/15	0.40	0.15	66,66,67,67	0
3	NAG	K	1	14/15	0.43	0.15	63,64,67,67	0
3	NAG	G	3	14/15	0.50	0.18	52,53,54,54	0
3	NAG	G	2	14/15	0.52	0.17	44,50,51,51	0
3	NAG	H	3	14/15	0.52	0.13	83,84,85,86	0
3	NAG	K	3	14/15	0.54	0.16	66,67,67,67	0
3	NAG	J	3	14/15	0.60	0.13	53,53,55,55	0
2	NAG	I	1	14/15	0.60	0.29	64,66,68,70	0
3	NAG	H	2	14/15	0.70	0.13	77,80,81,81	0
2	NAG	I	2	14/15	0.70	0.25	71,72,73,73	0
3	NAG	G	1	14/15	0.71	0.14	38,44,48,48	0
3	NAG	H	1	14/15	0.71	0.15	60,64,68,72	0
2	NAG	E	1	14/15	0.72	0.31	62,65,66,66	0
3	NAG	J	1	14/15	0.74	0.13	42,45,46,46	0
2	NAG	E	2	14/15	0.75	0.22	66,66,67,67	0
2	NAG	F	2	14/15	0.75	0.24	54,56,59,59	0
2	NAG	D	2	14/15	0.75	0.24	52,53,53,54	0
3	NAG	J	2	14/15	0.78	0.11	46,49,50,51	0
2	NAG	D	1	14/15	0.81	0.18	50,52,52,53	0
2	NAG	F	1	14/15	0.82	0.20	46,47,49,51	0

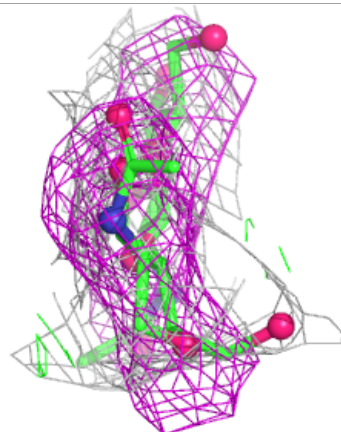
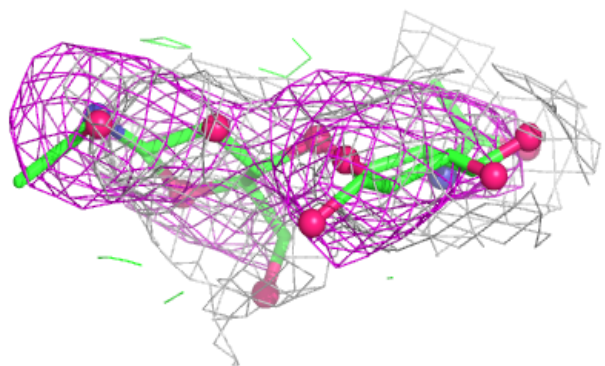
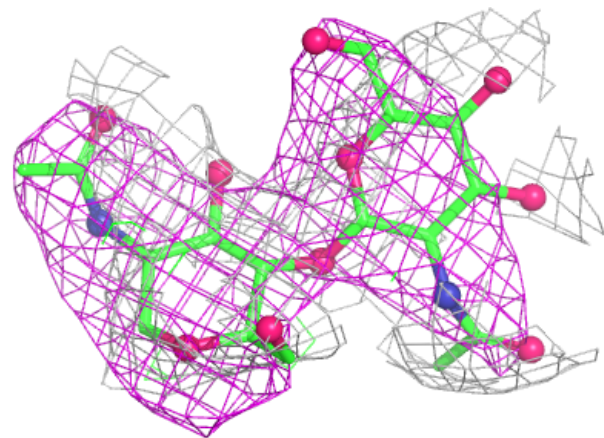
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

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

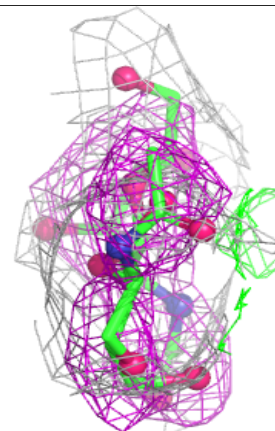
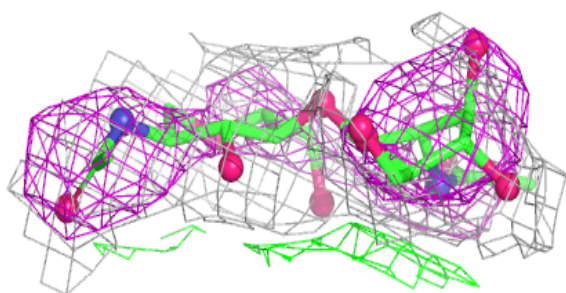
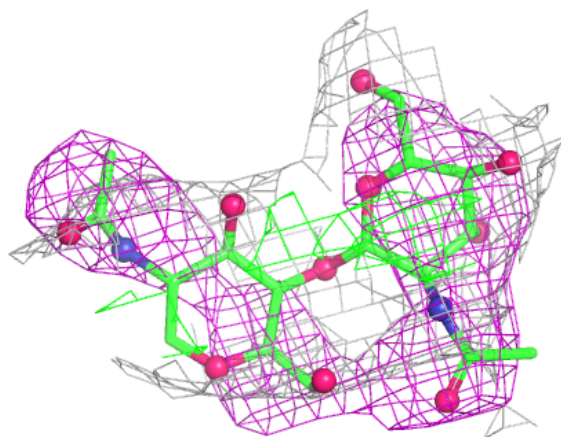
**Electron density around Chain E:**

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



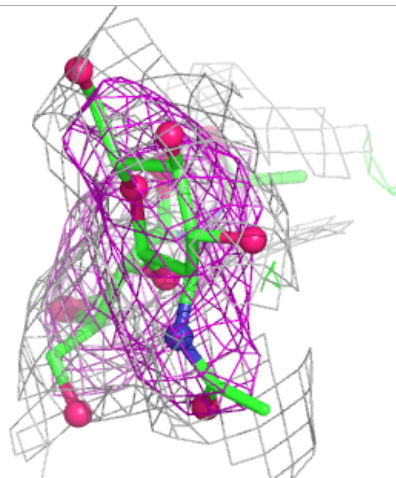
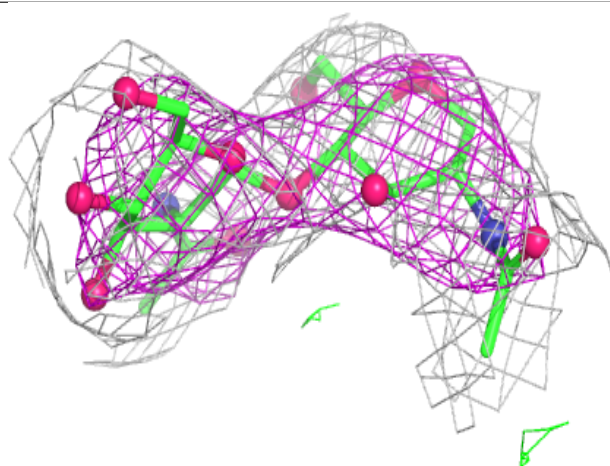
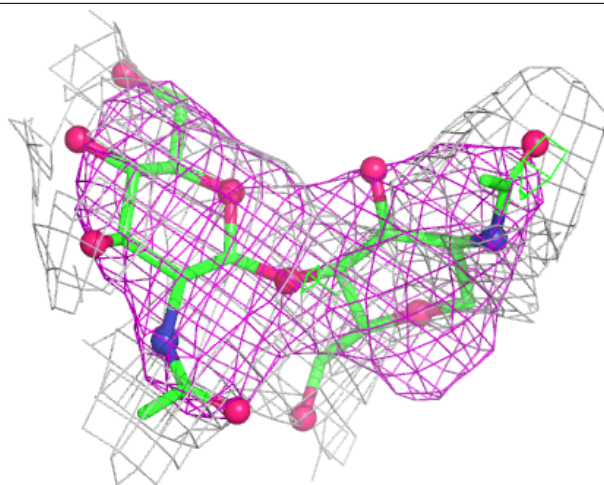
Electron density around Chain F:

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



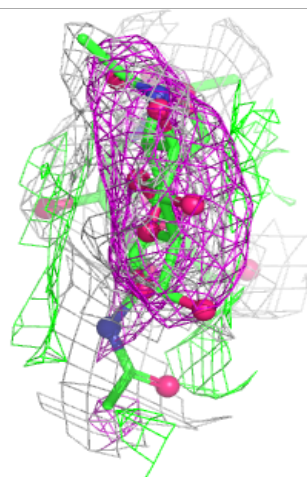
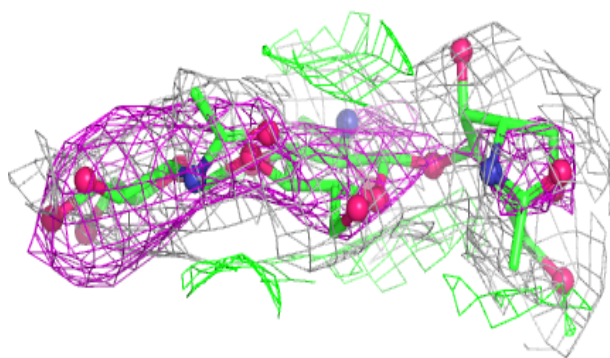
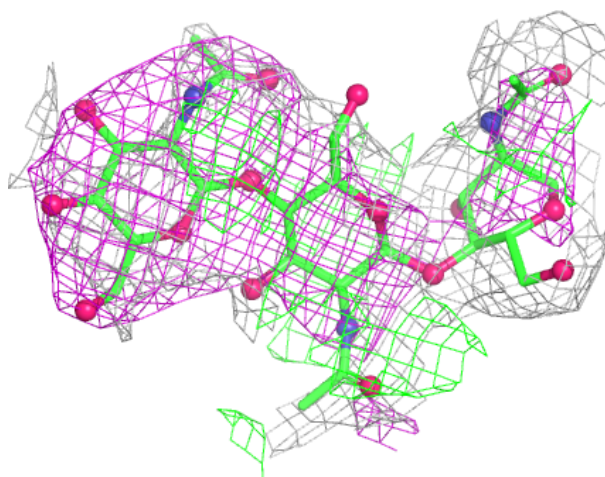
Electron density around Chain I:

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



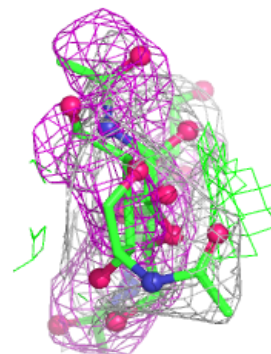
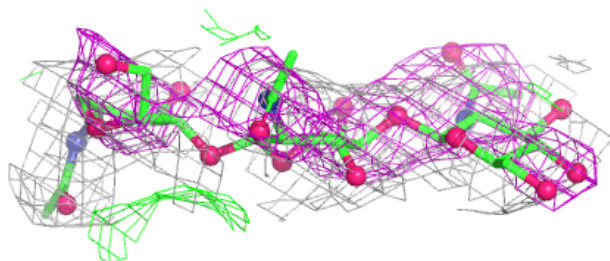
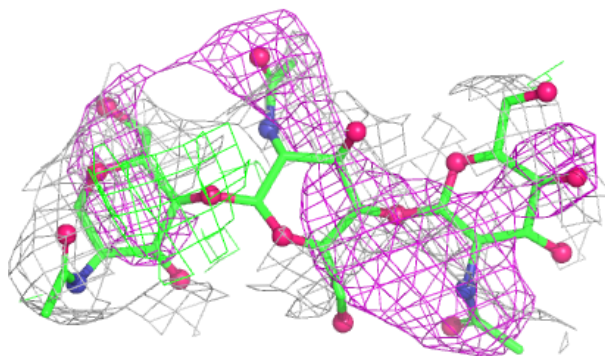
Electron density around Chain G:

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



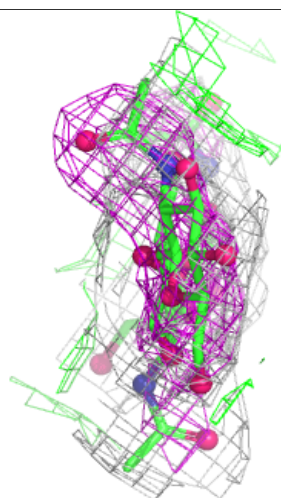
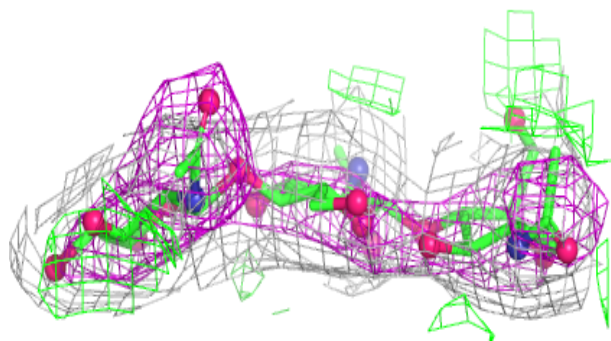
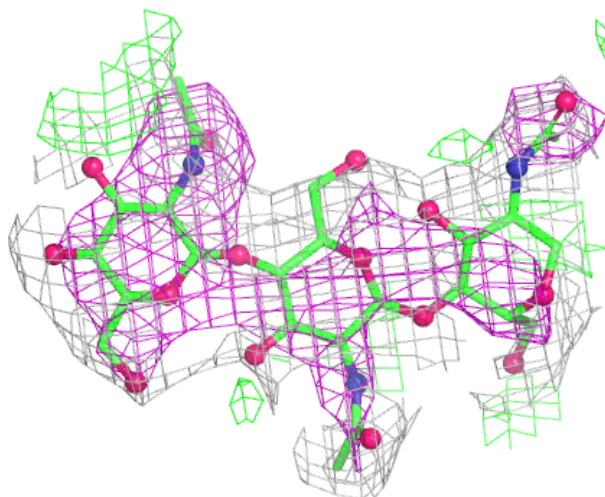
Electron density around Chain H:

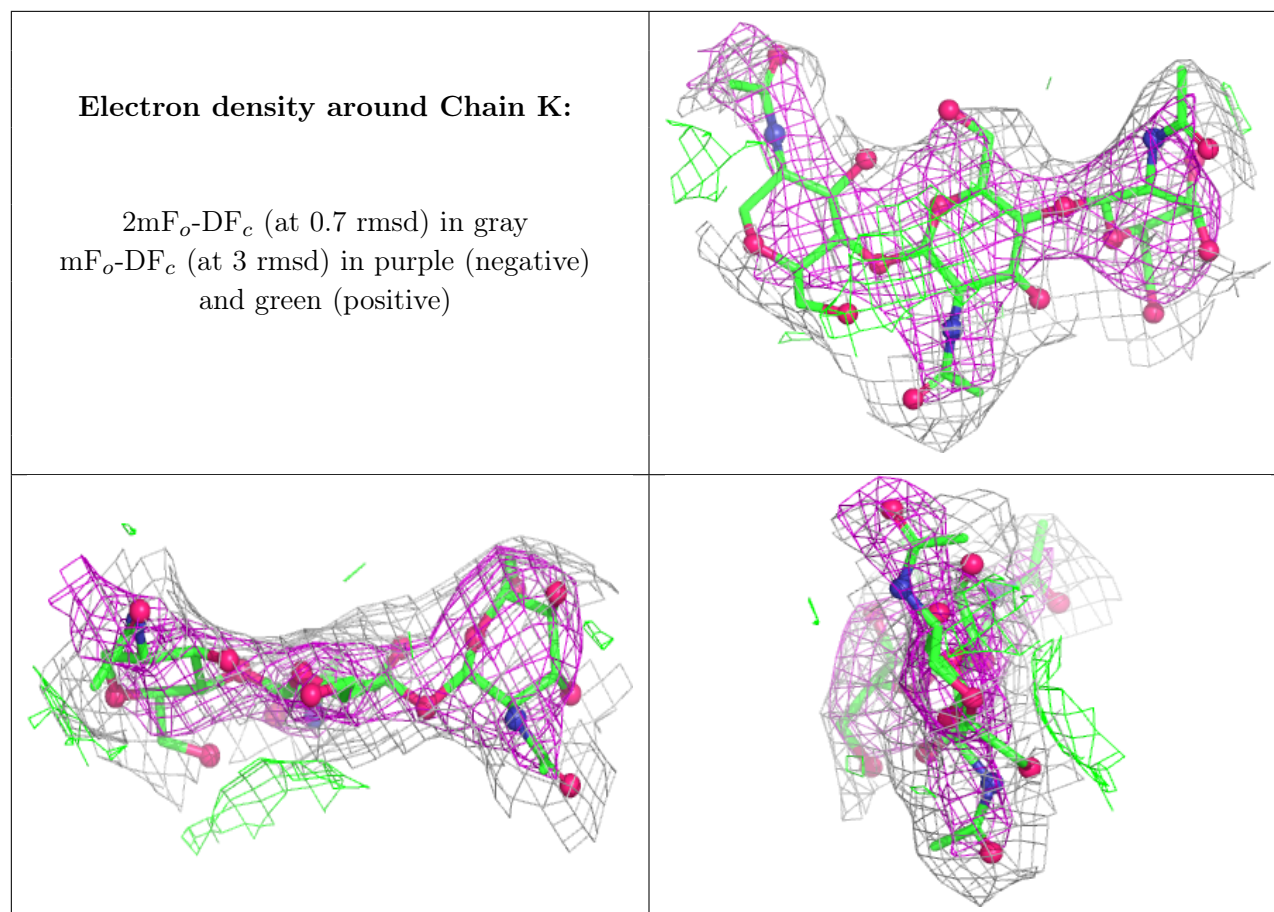
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain J:

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
4	GOL	A	787	6/6	0.75	0.35	22,22,22,23	0
4	GOL	B	793	6/6	0.81	0.34	23,23,24,24	0
4	GOL	A	786	6/6	0.84	0.23	25,27,27,27	0
4	GOL	B	794	6/6	0.84	0.29	41,41,42,44	0
5	SO4	B	792	5/5	0.93	0.23	20,21,21,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.