



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2021 – 07:53 PM EDT

PDB ID : 3H9Z
Title : Crystal structure of the IgE-Fc3-4 domains
Authors : Wurzburg, B.A.
Deposited on : 2009-04-30
Resolution : 2.45 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 : 2.23.2
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) : 2.23.2

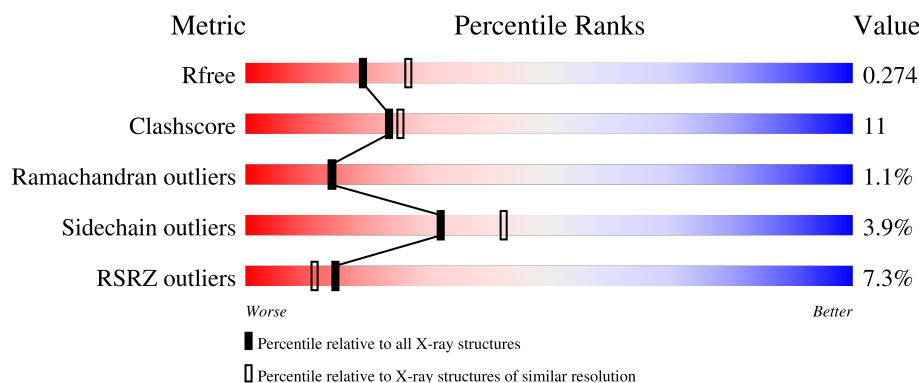
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	223	<div> <div>7%</div> <div> <div></div> <div>77%</div> <div>15%</div> <div>• 6%</div> </div> </div>
1	B	223	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>17%</div> <div>• 6%</div> </div> </div>
1	C	223	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>17%</div> <div>• 6%</div> </div> </div>
1	D	223	<div> <div>8%</div> <div> <div></div> <div>74%</div> <div>18%</div> <div>• 6%</div> </div> </div>
2	E	5	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	5	<div><div></div><div>40%</div><div></div><div>60%</div><div></div></div>
2	G	5	<div><div></div><div>20%</div><div></div><div>80%</div><div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6954 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.

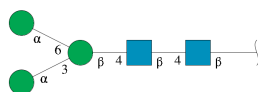
- Molecule 1 is a protein called Ig epsilon chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1656	1037	305	308	6			
1	B	209	Total	C	N	O	S	0	0	0
			1656	1037	305	308	6			
1	C	209	Total	C	N	O	S	0	0	0
			1656	1037	305	308	6			
1	D	209	Total	C	N	O	S	0	0	0
			1656	1037	305	308	6			

There are 20 discrepancies between the modelled and reference sequences:

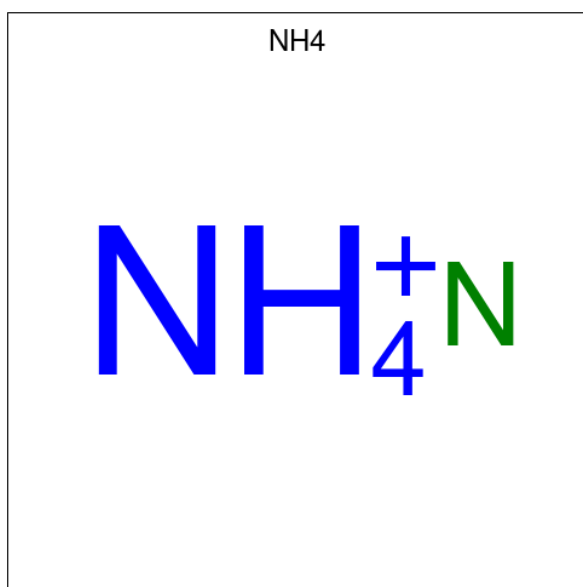
Chain	Residue	Modelled	Actual	Comment	Reference
A	325	ALA	-	expression tag	UNP P01854
A	326	ASP	-	expression tag	UNP P01854
A	327	PRO	-	expression tag	UNP P01854
A	371	GLN	ASN	engineered mutation	UNP P01854
A	383	GLN	ASN	engineered mutation	UNP P01854
B	325	ALA	-	expression tag	UNP P01854
B	326	ASP	-	expression tag	UNP P01854
B	327	PRO	-	expression tag	UNP P01854
B	371	GLN	ASN	engineered mutation	UNP P01854
B	383	GLN	ASN	engineered mutation	UNP P01854
C	325	ALA	-	expression tag	UNP P01854
C	326	ASP	-	expression tag	UNP P01854
C	327	PRO	-	expression tag	UNP P01854
C	371	GLN	ASN	engineered mutation	UNP P01854
C	383	GLN	ASN	engineered mutation	UNP P01854
D	325	ALA	-	expression tag	UNP P01854
D	326	ASP	-	expression tag	UNP P01854
D	327	PRO	-	expression tag	UNP P01854
D	371	GLN	ASN	engineered mutation	UNP P01854
D	383	GLN	ASN	engineered mutation	UNP P01854

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	F	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is AMMONIUM ION (three-letter code: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	N	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	31	Total	O	0	0
			31	31		
4	B	38	Total	O	0	0
			38	38		

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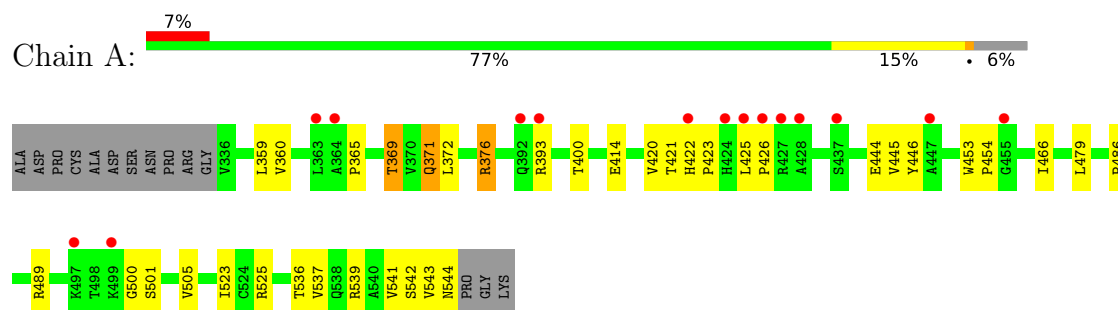
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	47	Total	O	0	0
			47	47		
4	D	30	Total	O	0	0
			30	30		

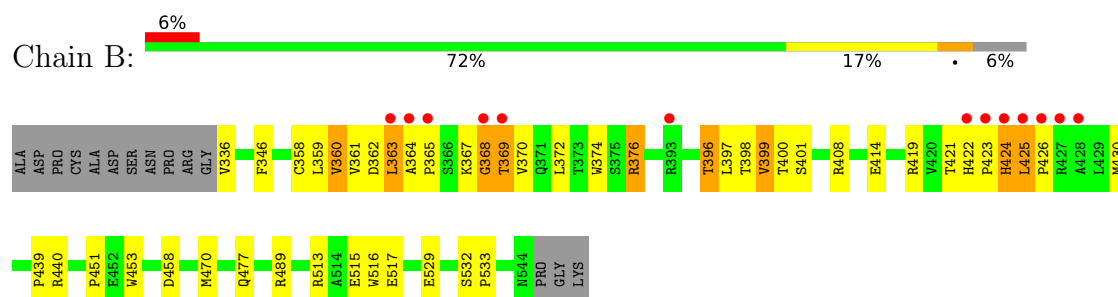
3 Residue-property plots [i](#)

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.

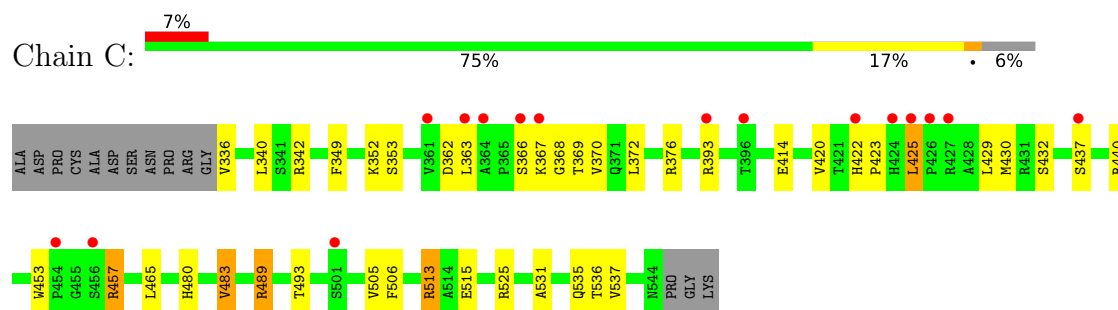
- Molecule 1: Ig epsilon chain C region



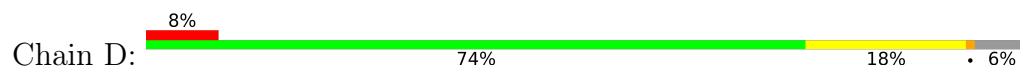
- Molecule 1: Ig epsilon chain C region

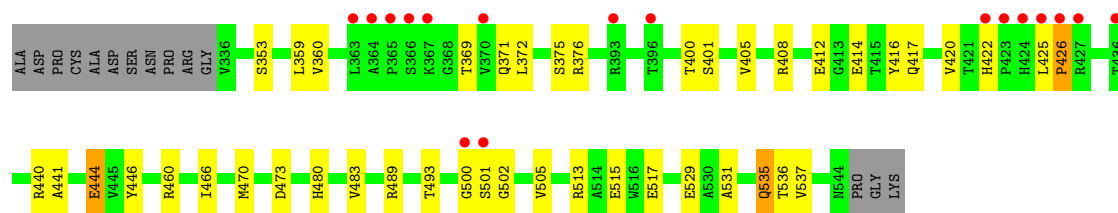


- Molecule 1: Ig epsilon chain C region



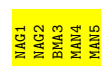
- Molecule 1: Ig epsilon chain C region





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

Chain E: 100%



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

Chain F: 40%



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

Chain G: 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.66Å 99.35Å 77.64Å 90.00° 97.40° 90.00°	Depositor
Resolution (Å)	28.71 – 2.45 28.71 – 2.45	Depositor EDS
% Data completeness (in resolution range)	98.8 (28.71-2.45) 98.8 (28.71-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.45Å)	Xtriage
Refinement program	REFMAC, CNS	Depositor
R, R_{free}	0.229 , 0.277 0.229 , 0.274	Depositor DCC
R_{free} test set	1824 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6954	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.3678e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MAN, BMA, NAG, NH4

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	0.51	0/1698	0.73	1/2311 (0.0%)
1	B	0.50	0/1698	0.74	1/2311 (0.0%)
1	C	0.49	0/1698	0.71	0/2311
1	D	0.52	0/1698	0.72	0/2311
All	All	0.51	0/6792	0.72	2/9244 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	376	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	A	376	ARG	NE-CZ-NH2	-5.49	117.55	120.30

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	1656	0	1642	34	0
1	B	1656	0	1641	49	0
1	C	1656	0	1641	34	0
1	D	1656	0	1641	40	0
2	E	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	61	0	52	3	0
2	G	61	0	52	0	0
3	C	1	0	0	1	0
4	A	31	0	0	1	0
4	B	38	0	0	0	0
4	C	47	0	0	1	0
4	D	30	0	0	4	0
All	All	6954	0	6721	151	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 11.

All (151) 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:425:LEU:HD12	1:A:425:LEU:O	1.31	1.30
1:B:425:LEU:HD12	1:B:425:LEU:O	1.50	1.09
1:A:369:THR:HG21	1:D:369:THR:HG21	1.46	0.97
1:C:425:LEU:HD12	1:C:425:LEU:O	1.66	0.94
1:B:369:THR:HG22	1:B:369:THR:O	1.71	0.91
1:B:363:LEU:HD11	1:B:422:HIS:CE1	2.11	0.85
1:D:372:LEU:HD22	1:D:420:VAL:HG22	1.57	0.84
1:A:425:LEU:O	1:A:425:LEU:CD1	2.24	0.84
1:B:359:LEU:HD13	1:B:400:THR:HG22	1.64	0.78
1:A:425:LEU:HD12	1:A:425:LEU:C	2.05	0.77
1:D:372:LEU:CD2	1:D:420:VAL:HG22	2.14	0.77
1:D:531:ALA:HB1	1:D:537:VAL:HG23	1.69	0.74
1:D:422:HIS:HB3	1:D:425:LEU:HB2	1.70	0.73
1:B:425:LEU:HD12	1:B:425:LEU:C	2.08	0.73
1:B:364:ALA:HB3	1:B:365:PRO:HD3	1.71	0.73
1:A:369:THR:CG2	1:D:369:THR:HG21	2.18	0.72
1:D:470:MET:HE1	1:D:501:SER:O	1.89	0.71
1:C:489:ARG:NH2	1:C:515:GLU:OE1	2.22	0.71
1:A:445:VAL:HG22	1:A:466:ILE:HD12	1.72	0.70
1:A:369:THR:HG21	1:D:369:THR:CG2	2.22	0.70
1:A:376:ARG:HD2	1:A:414:GLU:OE2	1.91	0.70
1:C:457:ARG:O	1:C:513:ARG:NH1	2.25	0.69
1:D:489:ARG:NH2	1:D:515:GLU:OE1	2.25	0.69
1:B:422:HIS:CG	1:B:423:PRO:HD2	2.30	0.66
1:D:425:LEU:HD12	1:D:426:PRO:HD2	1.79	0.65
1:C:363:LEU:CD2	2:F:1:NAG:H83	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:480:HIS:O	1:C:483:VAL:CG1	2.45	0.64
1:C:342:ARG:O	3:C:548:NH4:N	2.31	0.64
1:D:531:ALA:O	1:D:535:GLN:HA	1.97	0.64
1:B:376:ARG:HD2	1:B:414:GLU:OE2	1.98	0.63
1:B:424:HIS:CD2	1:B:424:HIS:O	2.51	0.63
1:D:513:ARG:O	1:D:517:GLU:HB2	1.99	0.63
1:C:493:THR:O	1:C:505:VAL:HG23	1.99	0.62
1:A:444:GLU:HG2	1:B:453:TRP:CE2	2.35	0.61
1:D:473:ASP:CG	4:D:18:HOH:O	2.37	0.61
1:A:371:GLN:HB2	1:A:421:THR:HB	1.82	0.60
1:B:425:LEU:C	1:B:425:LEU:CD1	2.69	0.60
1:C:369:THR:HG23	1:C:369:THR:O	2.01	0.60
1:B:422:HIS:ND1	1:B:423:PRO:HD2	2.18	0.59
1:B:359:LEU:HD13	1:B:400:THR:CG2	2.31	0.59
1:C:480:HIS:O	1:C:483:VAL:HG13	2.02	0.59
1:C:531:ALA:O	1:C:535:GLN:HA	2.01	0.59
1:A:445:VAL:HG13	1:A:466:ILE:CD1	2.33	0.59
1:B:419:ARG:HG3	1:B:430:MET:HG2	1.83	0.59
1:B:369:THR:O	1:B:369:THR:CG2	2.43	0.59
1:A:422:HIS:CG	1:A:423:PRO:HD2	2.38	0.58
1:A:466:ILE:HB	1:A:505:VAL:HG12	1.85	0.58
1:B:346:PHE:HE1	1:B:477:GLN:HE22	1.50	0.58
1:B:424:HIS:O	1:B:424:HIS:HD2	1.87	0.57
1:A:372:LEU:HD22	1:A:420:VAL:HG22	1.86	0.57
1:B:513:ARG:HG3	1:B:517:GLU:HG3	1.86	0.57
1:A:445:VAL:HG13	1:A:466:ILE:HD11	1.85	0.57
1:B:346:PHE:CE1	1:B:477:GLN:NE2	2.73	0.57
1:B:361:VAL:HG12	1:B:362:ASP:N	2.20	0.57
1:B:363:LEU:HD21	1:B:422:HIS:ND1	2.21	0.56
1:D:359:LEU:HD13	1:D:400:THR:HG22	1.87	0.55
1:A:359:LEU:CD1	1:A:400:THR:HG22	2.36	0.55
1:A:425:LEU:CD1	1:A:425:LEU:C	2.72	0.54
1:D:537:VAL:HG22	4:D:179:HOH:O	2.07	0.54
1:B:489:ARG:NH2	1:B:515:GLU:OE1	2.39	0.54
1:B:359:LEU:CD1	1:B:400:THR:HG22	2.36	0.54
1:A:359:LEU:HD13	1:A:400:THR:HG22	1.91	0.53
1:C:372:LEU:HD22	1:C:420:VAL:HG22	1.91	0.53
1:B:422:HIS:CE1	1:B:423:PRO:HD2	2.44	0.53
1:A:360:VAL:HG21	1:A:372:LEU:HD21	1.91	0.53
1:C:425:LEU:HD12	1:C:425:LEU:C	2.30	0.52
1:B:364:ALA:HB3	1:B:365:PRO:CD	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:470:MET:HE1	1:D:501:SER:C	2.30	0.52
1:C:525:ARG:HD2	1:C:536:THR:CG2	2.39	0.52
1:A:421:THR:HG23	1:A:425:LEU:CD2	2.40	0.51
1:B:396:THR:HG23	1:B:397:LEU:N	2.26	0.51
1:C:336:VAL:HG22	1:C:362:ASP:OD1	2.10	0.51
1:C:480:HIS:O	1:C:483:VAL:HG12	2.09	0.51
1:B:372:LEU:HD23	1:B:401:SER:CB	2.40	0.51
1:D:360:VAL:HG21	1:D:372:LEU:HD21	1.91	0.51
1:C:393:ARG:HG3	4:C:235:HOH:O	2.10	0.51
1:C:349:PHE:HB3	1:C:535:GLN:HG3	1.92	0.51
1:A:479:LEU:HD21	1:A:525:ARG:NH2	2.27	0.50
1:B:372:LEU:HD23	1:B:401:SER:HB2	1.92	0.50
1:D:359:LEU:CD1	1:D:400:THR:HG22	2.41	0.50
1:C:493:THR:O	1:C:505:VAL:CG2	2.60	0.50
1:A:421:THR:HG23	1:A:425:LEU:HD21	1.92	0.49
1:D:441:ALA:HB3	1:D:470:MET:HG2	1.95	0.49
1:D:375:SER:OG	1:D:417:GLN:HG3	2.14	0.48
1:D:470:MET:HE2	1:D:502:GLY:HA2	1.94	0.48
1:C:366:SER:O	1:C:368:GLY:N	2.46	0.48
1:C:363:LEU:HD21	2:F:1:NAG:H83	1.95	0.48
1:C:453:TRP:CE2	1:D:444:GLU:HB3	2.49	0.48
1:B:422:HIS:HD2	1:B:424:HIS:CD2	2.31	0.48
1:C:340:LEU:HD23	1:C:432:SER:C	2.34	0.47
1:A:444:GLU:O	1:A:466:ILE:HA	2.15	0.47
1:D:376:ARG:HD2	1:D:414:GLU:OE2	2.14	0.47
1:B:513:ARG:HA	1:B:516:TRP:CD2	2.50	0.47
1:C:370:VAL:HG22	1:C:422:HIS:CD2	2.50	0.47
1:C:368:GLY:HA3	1:C:423:PRO:HG2	1.97	0.47
1:C:493:THR:HG21	1:D:493:THR:HG21	1.96	0.47
1:D:473:ASP:HB2	4:D:18:HOH:O	2.14	0.47
1:D:473:ASP:CB	4:D:18:HOH:O	2.63	0.46
1:D:493:THR:O	1:D:505:VAL:CG2	2.64	0.46
1:A:422:HIS:N	1:A:425:LEU:HD23	2.31	0.46
1:B:440:ARG:NH1	1:B:529:GLU:OE2	2.47	0.46
1:D:408:ARG:NE	1:D:412:GLU:OE2	2.48	0.46
1:C:525:ARG:HD2	1:C:536:THR:HG21	1.97	0.46
1:D:493:THR:O	1:D:505:VAL:HG23	2.15	0.46
1:B:367:LYS:HB3	1:B:423:PRO:HG2	1.98	0.46
2:F:3:BMA:H61	2:F:5:MAN:H2	1.53	0.46
1:C:531:ALA:HB1	1:C:537:VAL:HG23	1.97	0.45
1:D:470:MET:CE	1:D:501:SER:C	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:VAL:CG1	1:B:362:ASP:N	2.79	0.45
1:D:359:LEU:HD13	1:D:400:THR:CG2	2.46	0.45
1:A:466:ILE:HB	1:A:505:VAL:CG1	2.47	0.45
1:C:420:VAL:HB	1:C:429:LEU:HB2	1.99	0.45
1:A:523:ILE:HD12	4:A:181:HOH:O	2.16	0.45
1:B:439:PRO:HG2	1:B:470:MET:HE1	1.98	0.45
1:C:370:VAL:HG22	1:C:422:HIS:HD2	1.81	0.44
1:D:372:LEU:HD12	1:D:401:SER:HB2	1.98	0.44
1:B:424:HIS:CD2	1:B:424:HIS:C	2.91	0.44
1:D:531:ALA:CB	1:D:537:VAL:HG23	2.43	0.44
1:A:525:ARG:HD2	1:A:536:THR:HG23	1.98	0.44
1:D:440:ARG:NH1	1:D:529:GLU:OE2	2.51	0.44
1:A:486:PRO:O	1:A:489:ARG:HB2	2.18	0.44
1:A:453:TRP:O	1:A:454:PRO:C	2.57	0.44
1:D:444:GLU:OE1	1:D:446:TYR:OH	2.28	0.43
1:B:422:HIS:CD2	1:B:424:HIS:CD2	3.06	0.43
1:B:363:LEU:HD23	1:B:370:VAL:HG21	2.01	0.43
1:B:422:HIS:CG	1:B:423:PRO:CD	2.99	0.43
1:B:358:CYS:HB2	1:B:374:TRP:CH2	2.53	0.43
1:D:480:HIS:O	1:D:483:VAL:HG12	2.19	0.43
1:C:425:LEU:O	1:C:425:LEU:CD1	2.52	0.43
1:A:446:TYR:CD2	1:B:451:PRO:HD2	2.53	0.43
1:B:368:GLY:O	1:B:369:THR:OG1	2.31	0.43
1:B:513:ARG:CG	1:B:517:GLU:HG3	2.49	0.43
1:C:376:ARG:HD2	1:C:414:GLU:OE2	2.18	0.43
1:B:513:ARG:HA	1:B:516:TRP:CE2	2.53	0.43
1:A:422:HIS:HB3	1:A:425:LEU:HB3	2.01	0.42
1:B:532:SER:HA	1:B:533:PRO:HA	1.85	0.42
1:D:470:MET:CE	1:D:502:GLY:HA2	2.49	0.42
1:C:425:LEU:C	1:C:425:LEU:CD1	2.87	0.42
1:C:349:PHE:O	1:C:352:LYS:NZ	2.53	0.42
1:A:371:GLN:HE21	1:A:371:GLN:HA	1.85	0.42
1:B:376:ARG:HD3	1:B:414:GLU:HG2	2.01	0.41
1:B:360:VAL:HG13	1:B:399:VAL:HG13	2.02	0.41
1:B:458:ASP:OD1	1:B:513:ARG:NH1	2.53	0.41
1:A:543:VAL:O	1:A:544:ASN:HB2	2.20	0.41
1:B:336:VAL:HG22	1:B:363:LEU:HD13	2.01	0.41
1:D:422:HIS:HB3	1:D:425:LEU:CB	2.46	0.41
1:D:466:ILE:HB	1:D:505:VAL:HG12	2.03	0.41
1:A:541:VAL:HG22	1:A:542:SER:N	2.36	0.40
1:D:405:VAL:HG12	1:D:416:TYR:CE2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:421:THR:HA	1:B:425:LEU:HD23	2.04	0.40
1:C:465:LEU:HD13	1:C:506:PHE:CE2	2.57	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	207/223 (93%)	197 (95%)	7 (3%)	3 (1%)	11	9
1	B	207/223 (93%)	193 (93%)	11 (5%)	3 (1%)	11	9
1	C	207/223 (93%)	199 (96%)	7 (3%)	1 (0%)	29	34
1	D	207/223 (93%)	197 (95%)	8 (4%)	2 (1%)	15	16
All	All	828/892 (93%)	786 (95%)	33 (4%)	9 (1%)	14	14

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	368	GLY
1	C	367	LYS
1	A	500	GLY
1	B	369	THR
1	D	500	GLY
1	B	426	PRO
1	A	426	PRO
1	A	365	PRO
1	D	426	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	185/195 (95%)	179 (97%)	6 (3%)	39	50
1	B	185/195 (95%)	177 (96%)	8 (4%)	29	38
1	C	185/195 (95%)	176 (95%)	9 (5%)	25	32
1	D	185/195 (95%)	179 (97%)	6 (3%)	39	50
All	All	740/780 (95%)	711 (96%)	29 (4%)	32	42

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	THR
1	A	371	GLN
1	A	393	ARG
1	A	501	SER
1	A	537	VAL
1	A	539	ARG
1	B	360	VAL
1	B	363	LEU
1	B	396	THR
1	B	398	THR
1	B	399	VAL
1	B	408	ARG
1	B	424	HIS
1	B	425	LEU
1	C	353	SER
1	C	425	LEU
1	C	430	MET
1	C	437	SER
1	C	440	ARG
1	C	457	ARG
1	C	483	VAL
1	C	489	ARG
1	C	513	ARG
1	D	353	SER

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Mol	Chain	Res	Type
1	D	371	GLN
1	D	444	GLU
1	D	460	ARG
1	D	535	GLN
1	D	536	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	371	GLN
1	A	484	GLN
1	A	490	HIS
1	B	422	HIS
1	B	424	HIS
1	B	544	ASN
1	C	417	GLN
1	C	484	GLN
1	C	535	GLN
1	D	371	GLN
1	D	384	HIS
1	D	392	GLN
1	D	484	GLN
1	D	535	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

15 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	1,2	14,14,15	0.52	0	17,19,21	1.46	2 (11%)
2	NAG	E	2	2	14,14,15	0.57	0	17,19,21	1.38	2 (11%)
2	BMA	E	3	2	11,11,12	0.71	0	15,15,17	2.17	3 (20%)
2	MAN	E	4	2	11,11,12	0.61	0	15,15,17	1.59	4 (26%)
2	MAN	E	5	2	11,11,12	0.64	0	15,15,17	1.56	3 (20%)
2	NAG	F	1	1,2	14,14,15	0.51	0	17,19,21	1.18	2 (11%)
2	NAG	F	2	2	14,14,15	0.45	0	17,19,21	1.30	1 (5%)
2	BMA	F	3	2	11,11,12	0.59	0	15,15,17	2.12	3 (20%)
2	MAN	F	4	2	11,11,12	0.59	0	15,15,17	1.25	1 (6%)
2	MAN	F	5	2	11,11,12	0.75	0	15,15,17	1.48	3 (20%)
2	NAG	G	1	1,2	14,14,15	0.52	0	17,19,21	1.26	2 (11%)
2	NAG	G	2	2	14,14,15	0.57	0	17,19,21	0.74	0
2	BMA	G	3	2	11,11,12	0.64	0	15,15,17	1.41	2 (13%)
2	MAN	G	4	2	11,11,12	0.60	0	15,15,17	1.29	2 (13%)
2	MAN	G	5	2	11,11,12	0.58	0	15,15,17	1.40	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	E	2	2	-	1/6/23/26	0/1/1/1
2	BMA	E	3	2	-	2/2/19/22	0/1/1/1
2	MAN	E	4	2	-	1/2/19/22	0/1/1/1
2	MAN	E	5	2	-	2/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	BMA	F	3	2	-	1/2/19/22	0/1/1/1
2	MAN	F	4	2	-	2/2/19/22	0/1/1/1
2	MAN	F	5	2	-	2/2/19/22	0/1/1/1
2	NAG	G	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
2	MAN	G	4	2	-	2/2/19/22	0/1/1/1
2	MAN	G	5	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	3	BMA	O5-C5-C6	6.43	117.29	107.20
2	F	3	BMA	O5-C5-C6	6.11	116.78	107.20
2	E	1	NAG	O5-C5-C6	3.78	113.14	107.20
2	F	2	NAG	C1-O5-C5	3.66	117.16	112.19
2	G	3	BMA	O5-C5-C6	3.65	112.92	107.20
2	G	5	MAN	O5-C1-C2	-3.38	105.56	110.77
2	E	4	MAN	O5-C1-C2	-3.28	105.71	110.77
2	E	5	MAN	O5-C1-C2	-3.27	105.73	110.77
2	F	3	BMA	O3-C3-C4	-3.26	102.82	110.35
2	G	1	NAG	O5-C1-C2	-3.22	106.20	111.29
2	E	3	BMA	O3-C3-C4	-3.09	103.21	110.35
2	E	5	MAN	C3-C4-C5	3.03	115.64	110.24
2	E	3	BMA	C6-C5-C4	-2.99	106.01	113.00
2	F	4	MAN	O5-C1-C2	-2.84	106.39	110.77
2	E	2	NAG	C1-O5-C5	2.83	116.03	112.19
2	G	4	MAN	O5-C5-C6	2.79	111.57	107.20
2	E	4	MAN	C3-C4-C5	-2.76	105.32	110.24
2	E	5	MAN	O4-C4-C3	-2.53	104.51	110.35
2	G	5	MAN	C1-C2-C3	-2.41	106.70	109.67
2	E	1	NAG	O5-C1-C2	-2.35	107.58	111.29
2	E	4	MAN	C2-C3-C4	-2.34	106.84	110.89
2	F	3	BMA	C3-C4-C5	2.33	114.40	110.24
2	G	3	BMA	C2-C3-C4	-2.33	106.87	110.89
2	G	4	MAN	C1-C2-C3	-2.29	106.85	109.67
2	F	1	NAG	O5-C5-C6	2.23	110.70	107.20
2	F	1	NAG	C1-O5-C5	2.22	115.21	112.19
2	G	1	NAG	C6-C5-C4	-2.17	107.92	113.00
2	F	5	MAN	C1-O5-C5	2.14	115.10	112.19
2	F	5	MAN	O4-C4-C3	-2.08	105.53	110.35
2	E	4	MAN	C1-C2-C3	-2.05	107.14	109.67
2	E	2	NAG	O5-C5-C6	2.01	110.36	107.20
2	F	5	MAN	O5-C1-C2	2.00	113.86	110.77

There are no chirality outliers.

All (24) torsion outliers are listed below:

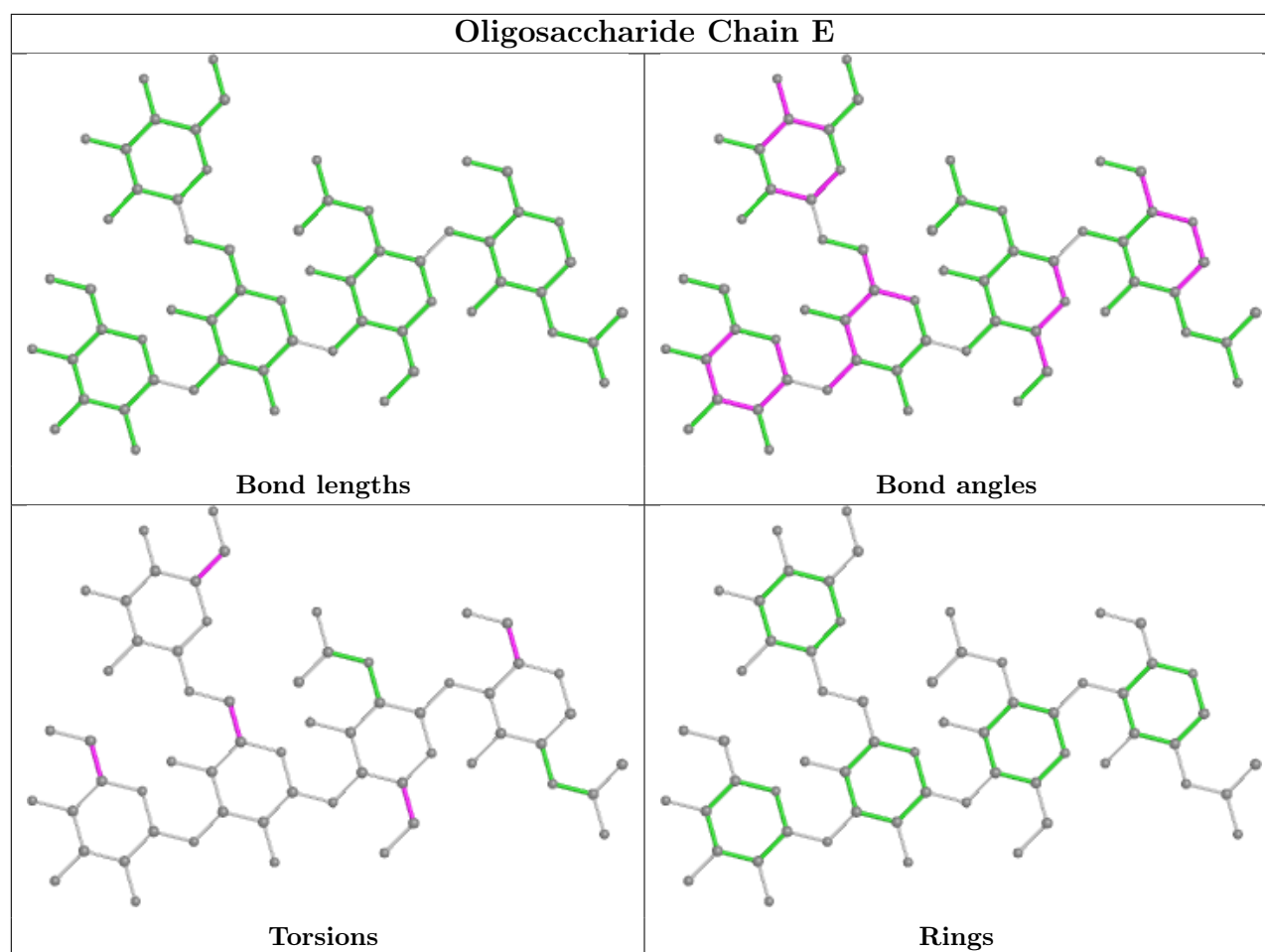
Mol	Chain	Res	Type	Atoms
2	F	2	NAG	O5-C5-C6-O6
2	E	5	MAN	O5-C5-C6-O6
2	F	4	MAN	O5-C5-C6-O6
2	G	1	NAG	O5-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	E	5	MAN	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
2	G	5	MAN	O5-C5-C6-O6
2	G	1	NAG	C4-C5-C6-O6
2	G	5	MAN	C4-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	F	5	MAN	O5-C5-C6-O6
2	G	4	MAN	C4-C5-C6-O6
2	G	3	BMA	C4-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
2	F	3	BMA	O5-C5-C6-O6
2	F	4	MAN	C4-C5-C6-O6
2	F	5	MAN	C4-C5-C6-O6
2	G	4	MAN	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
2	E	4	MAN	C4-C5-C6-O6

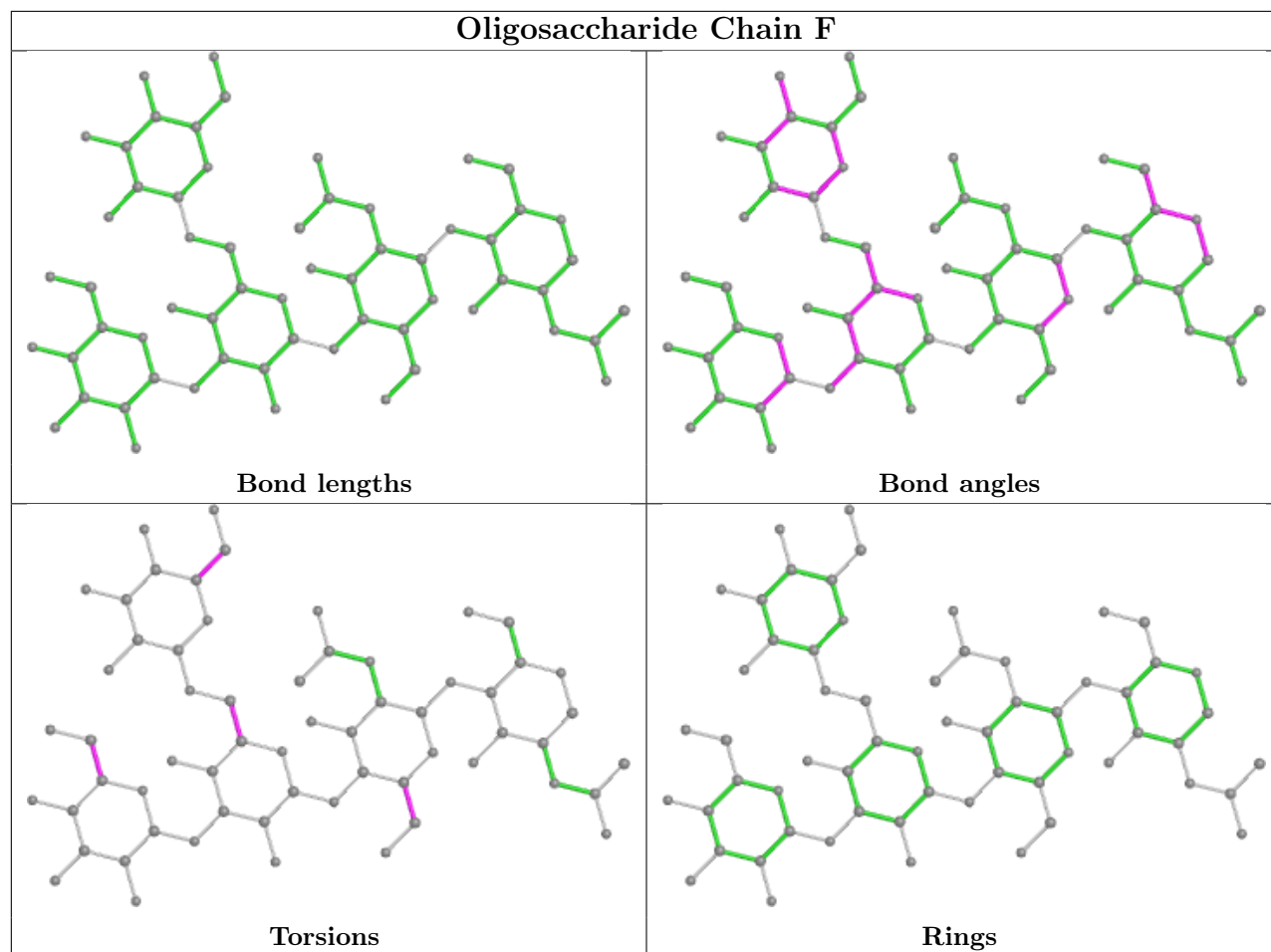
There are no ring outliers.

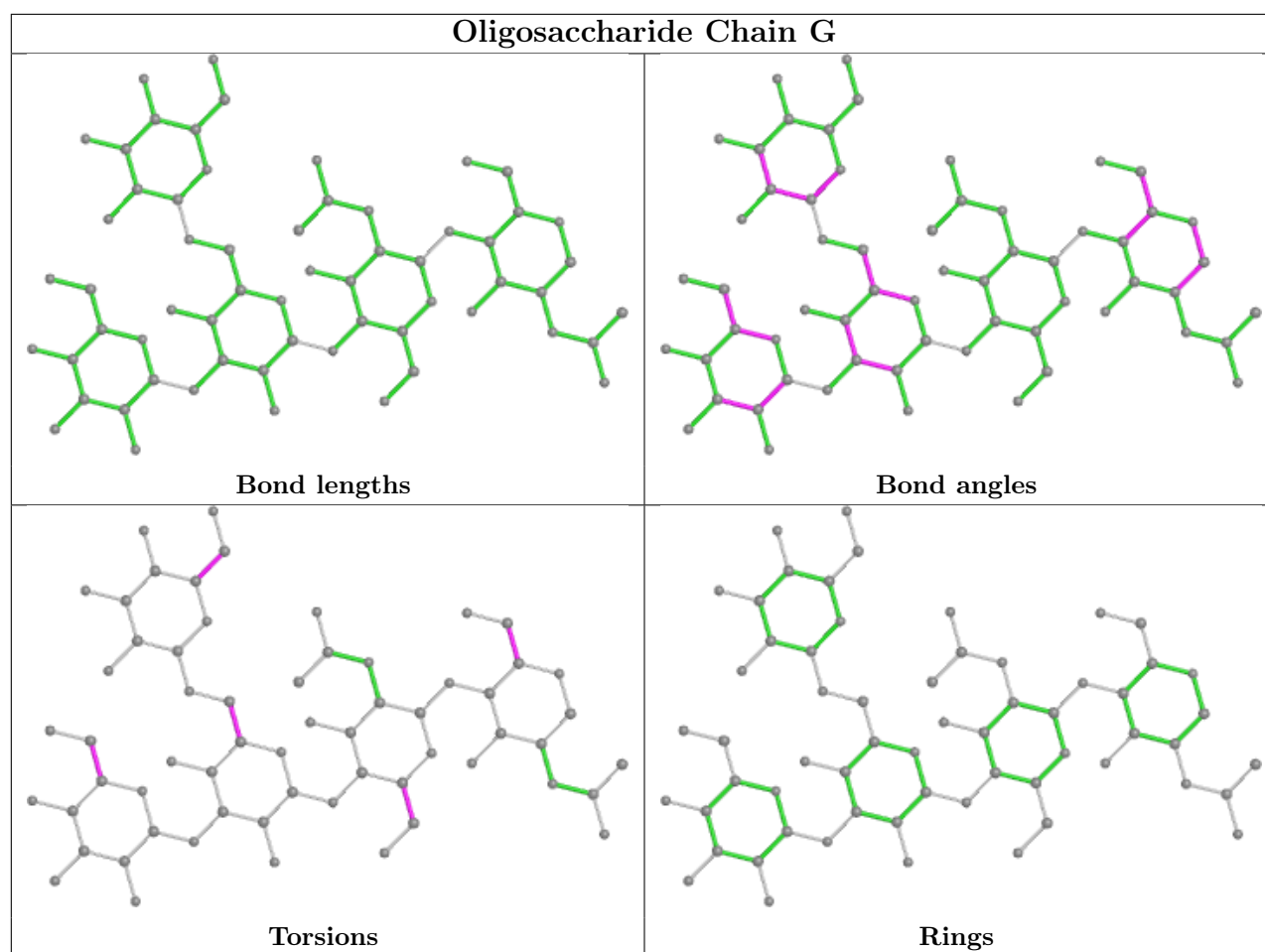
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	NAG	2	0
2	F	3	BMA	1	0
2	F	5	MAN	1	0

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







5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

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	209/223 (93%)	0.26	15 (7%) 15 11	18, 33, 59, 70	0
1	B	209/223 (93%)	0.24	13 (6%) 20 17	18, 32, 65, 74	0
1	C	209/223 (93%)	0.26	16 (7%) 13 10	16, 33, 61, 72	0
1	D	209/223 (93%)	0.28	17 (8%) 12 9	18, 33, 66, 77	0
All	All	836/892 (93%)	0.26	61 (7%) 15 11	16, 33, 64, 77	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	364	ALA	6.7
1	C	363	LEU	6.6
1	C	422	HIS	6.5
1	B	368	GLY	6.4
1	B	422	HIS	6.4
1	C	424	HIS	5.7
1	D	501	SER	5.0
1	B	393	ARG	4.9
1	D	422	HIS	4.9
1	A	437	SER	4.7
1	B	423	PRO	4.7
1	A	363	LEU	4.7
1	C	426	PRO	4.6
1	C	425	LEU	4.5
1	C	367	LYS	4.3
1	B	427	ARG	4.3
1	D	436	THR	4.2
1	A	455	GLY	4.0
1	D	363	LEU	3.9
1	A	426	PRO	3.8
1	A	424	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	426	PRO	3.7
1	D	367	LYS	3.7
1	B	363	LEU	3.6
1	B	426	PRO	3.5
1	B	424	HIS	3.5
1	D	393	ARG	3.5
1	B	425	LEU	3.5
1	D	364	ALA	3.4
1	B	369	THR	3.4
1	D	427	ARG	3.3
1	A	393	ARG	3.1
1	D	366	SER	3.1
1	A	427	ARG	3.1
1	A	499	LYS	2.9
1	B	364	ALA	2.9
1	B	428	ALA	2.9
1	B	365	PRO	2.9
1	D	365	PRO	2.8
1	C	454	PRO	2.8
1	C	393	ARG	2.7
1	C	361	VAL	2.5
1	A	364	ALA	2.5
1	A	428	ALA	2.5
1	D	370	VAL	2.4
1	D	396	THR	2.4
1	D	423	PRO	2.3
1	C	437	SER	2.3
1	C	427	ARG	2.3
1	D	500	GLY	2.3
1	A	425	LEU	2.3
1	A	422	HIS	2.2
1	D	424	HIS	2.2
1	D	425	LEU	2.2
1	C	501	SER	2.1
1	C	396	THR	2.1
1	A	497	LYS	2.1
1	C	456	SER	2.1
1	C	366	SER	2.1
1	A	392	GLN	2.1
1	A	447	ALA	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 ⓘ

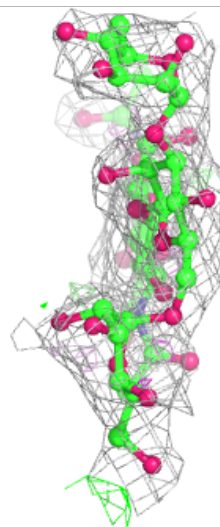
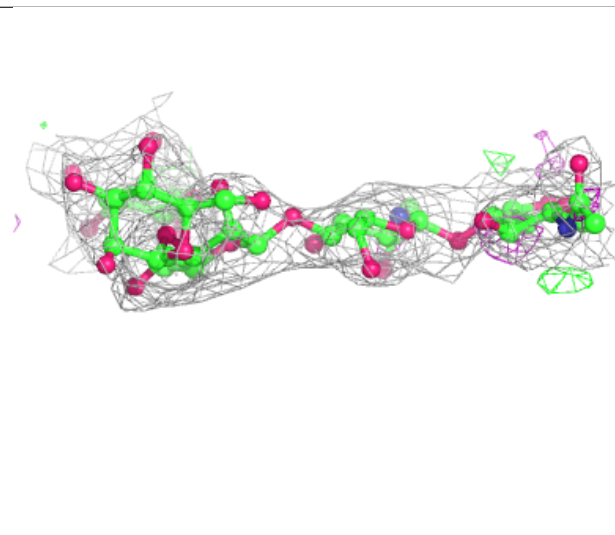
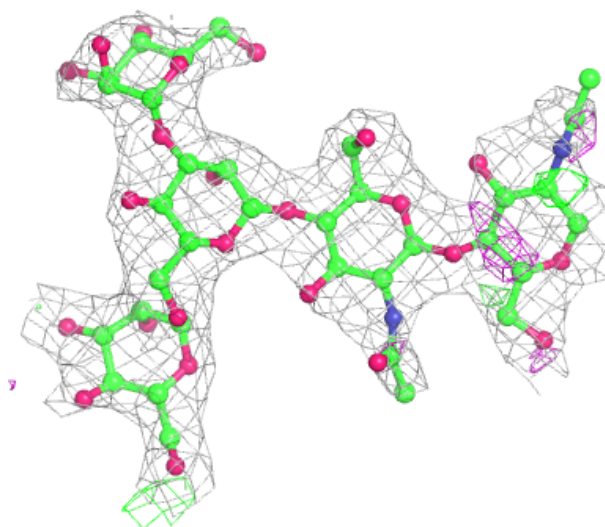
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MAN	F	4	11/12	0.69	0.28	72,74,75,75	0
2	MAN	G	5	11/12	0.69	0.33	74,75,76,77	0
2	NAG	G	1	14/15	0.79	0.35	58,60,61,63	0
2	MAN	E	5	11/12	0.79	0.17	68,69,70,70	0
2	NAG	E	1	14/15	0.80	0.33	63,64,64,64	0
2	NAG	F	1	14/15	0.82	0.32	57,60,61,61	0
2	BMA	G	3	11/12	0.83	0.23	67,69,71,72	0
2	MAN	F	5	11/12	0.84	0.20	60,61,62,62	0
2	NAG	F	2	14/15	0.84	0.28	59,61,62,63	0
2	MAN	G	4	11/12	0.86	0.30	72,73,73,74	0
2	NAG	G	2	14/15	0.88	0.24	64,65,66,67	0
2	MAN	E	4	11/12	0.88	0.34	69,69,70,70	0
2	NAG	E	2	14/15	0.89	0.30	62,65,66,67	0
2	BMA	E	3	11/12	0.90	0.13	66,67,68,69	0
2	BMA	F	3	11/12	0.92	0.17	63,64,66,69	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.

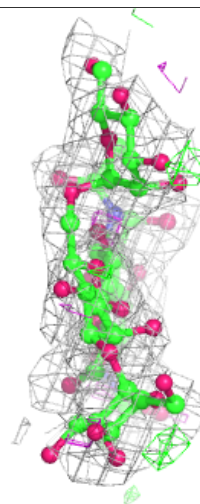
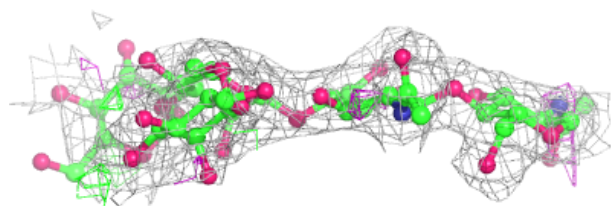
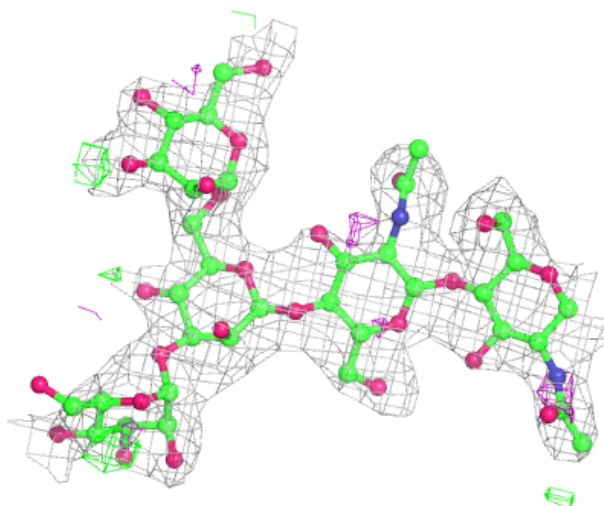
Electron density around Chain E:

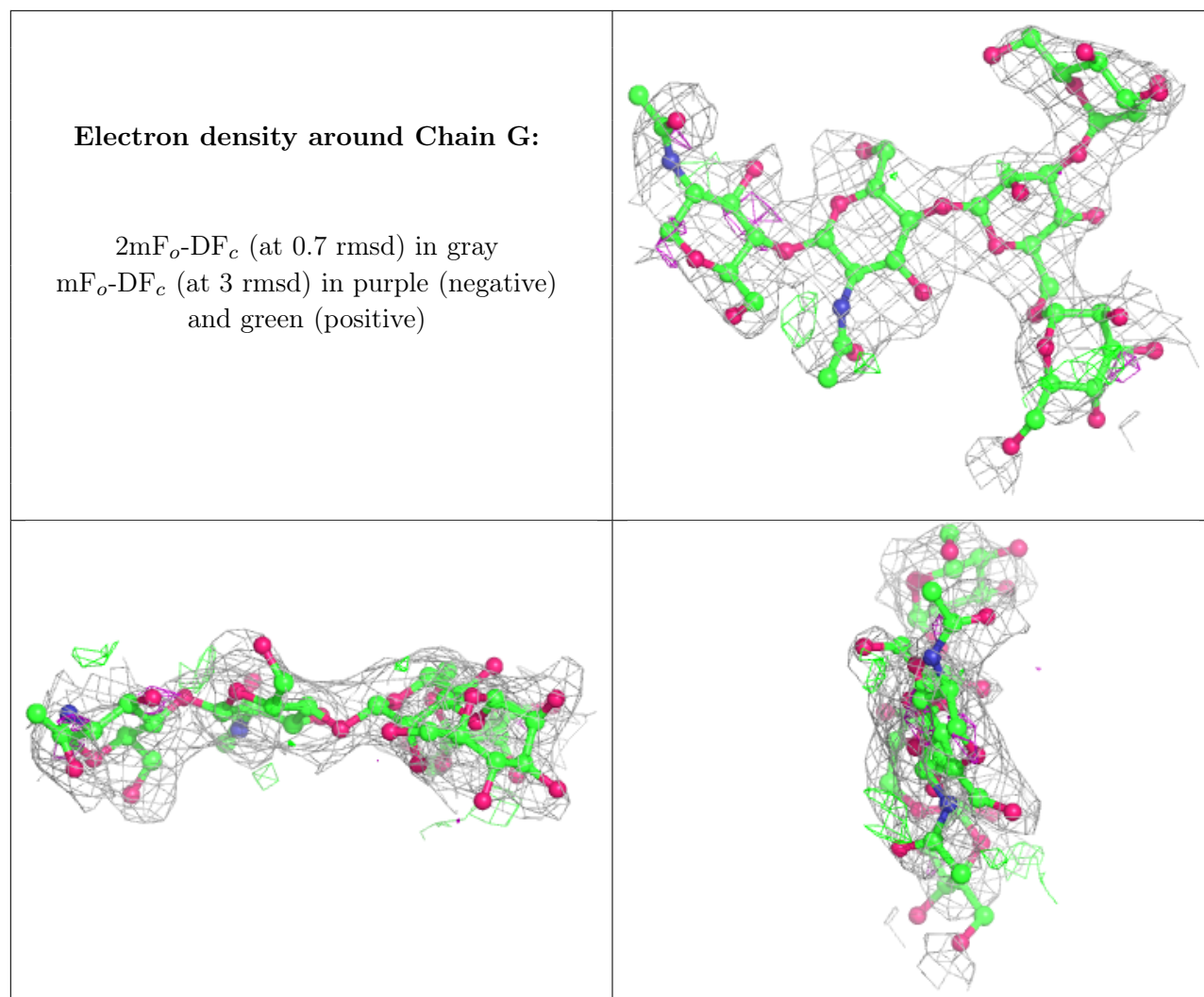
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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(\AA^2)	Q<0.9
3	NH4	C	548	1/1	0.94	0.16	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.