



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 07:34 PM BST

PDB ID : 5LGK
Title : Crystal structure of the human IgE-Fc bound to its B cell receptor derCD23
Authors : Dhaliwal, B.; Pang, M.O.Y.; Sutton, B.J.
Deposited on : 2016-07-07
Resolution : 3.50 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
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

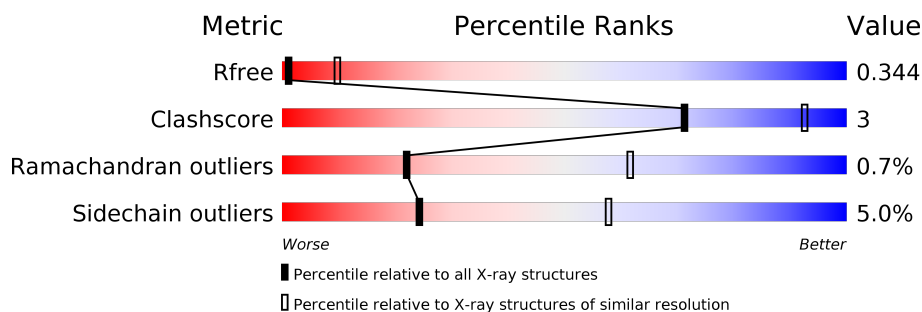
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	307	89% 10% .
1	B	307	88% 9% ..
1	C	307	89% 10% .
1	D	307	87% 11% ..
2	E	120	82% 6% 13%
2	F	120	82% 5% . 12%
3	G	3	100%

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Mol	Chain	Length	Quality of chain
3	H	3	 33% 67%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11420 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	307	Total	C	N	O	S	0	0	0
			2406	1499	430	466	11			
1	B	304	Total	C	N	O	S	0	0	0
			2386	1485	427	463	11			
1	C	306	Total	C	N	O	S	14	0	0
			2399	1494	429	465	11			
1	D	304	Total	C	N	O	S	0	0	0
			2386	1485	427	463	11			

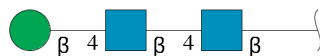
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P01854
A	265	GLN	ASN	conflict	UNP P01854
A	371	GLN	ASN	conflict	UNP P01854
A	383	GLN	ASN	conflict	UNP P01854
B	?	-	LEU	deletion	UNP P01854
B	265	GLN	ASN	conflict	UNP P01854
B	371	GLN	ASN	conflict	UNP P01854
B	383	GLN	ASN	conflict	UNP P01854
C	?	-	LEU	deletion	UNP P01854
C	265	GLN	ASN	conflict	UNP P01854
C	371	GLN	ASN	conflict	UNP P01854
C	383	GLN	ASN	conflict	UNP P01854
D	?	-	LEU	deletion	UNP P01854
D	265	GLN	ASN	conflict	UNP P01854
D	371	GLN	ASN	conflict	UNP P01854
D	383	GLN	ASN	conflict	UNP P01854

- Molecule 2 is a protein called Low affinity immunoglobulin epsilon Fc receptor.

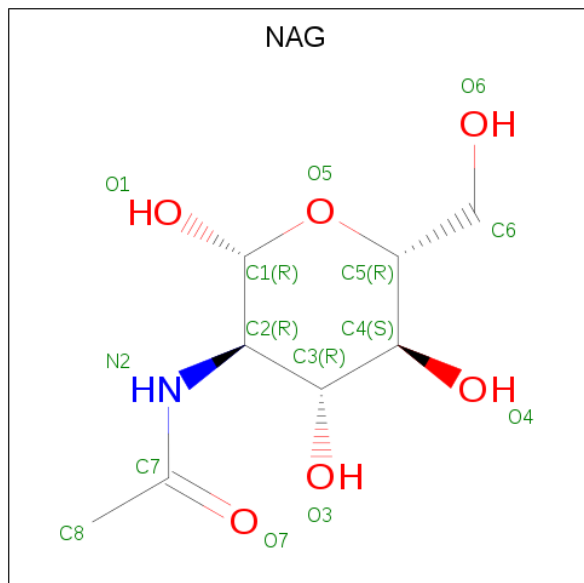
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	105	Total	C	N	O	S	0	0	0
			864	546	156	154	8			
2	F	106	Total	C	N	O	S	0	0	0
			873	551	157	157	8			

- Molecule 3 is an oligosaccharide called 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
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

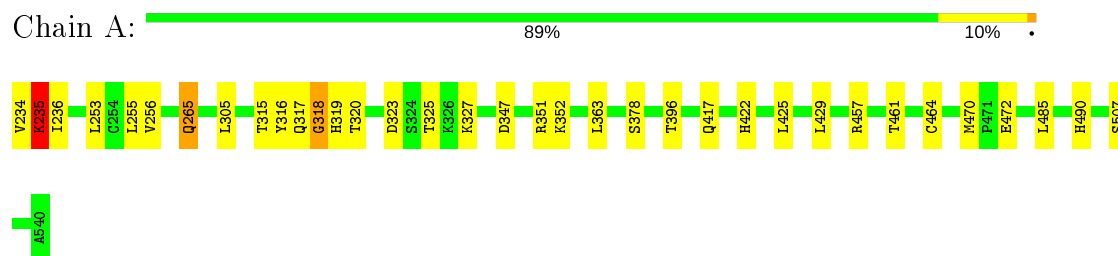


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		

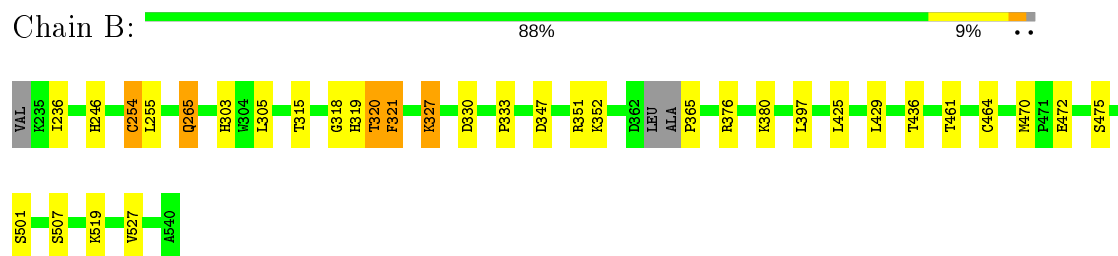
3 Residue-property plots [i](#)

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. 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. 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.

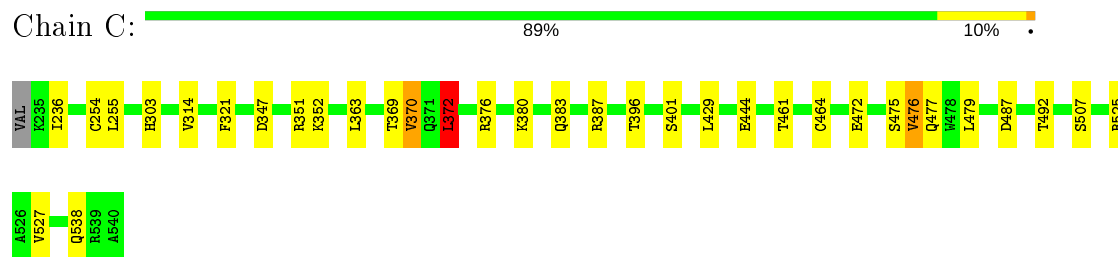
- Molecule 1: Ig epsilon chain C region



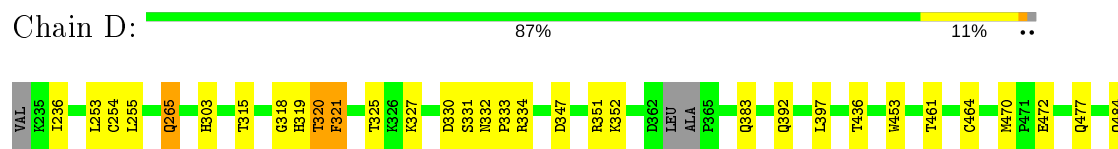
- Molecule 1: Ig epsilon chain C region



- Molecule 1: Ig epsilon chain C region



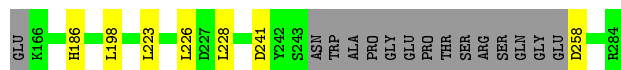
- Molecule 1: Ig epsilon chain C region





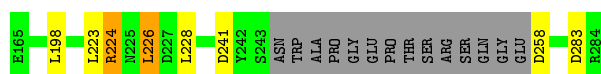
- Molecule 2: Low affinity immunoglobulin epsilon Fc receptor

Chain E: 82% 6% 13%



- Molecule 2: Low affinity immunoglobulin epsilon Fc receptor

Chain F: 82% 5% 12%



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

Chain G: 100%



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

Chain H: 33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	80.52Å 85.32Å 88.23Å 117.87° 90.32° 112.62°	Depositor
Resolution (Å)	75.96 – 3.50 75.96 – 3.50	Depositor EDS
% Data completeness (in resolution range)	88.8 (75.96-3.50) 74.9 (75.96-3.50)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 3.49Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.0	Depositor
R, R_{free}	0.266 , 0.278 0.322 , 0.344	Depositor DCC
R_{free} test set	1087 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , -28.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.58	EDS
Total number of atoms	11420	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% 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: BMA, 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	0.40	0/2464	0.58	1/3354 (0.0%)
1	B	0.37	0/2443	0.55	0/3322
1	C	0.37	0/2457	0.55	1/3344 (0.0%)
1	D	0.37	0/2443	0.54	0/3322
2	E	0.34	0/889	0.49	0/1196
2	F	0.34	0/898	0.49	0/1208
All	All	0.37	0/11594	0.55	2/15746 (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	A	318	GLY	N-CA-C	-5.55	99.21	113.10
1	C	372	LEU	CA-CB-CG	5.49	127.92	115.30

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	2406	0	2356	17	0
1	B	2386	0	2331	20	0
1	C	2399	0	2345	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2386	0	2331	17	0
2	E	864	0	802	1	0
2	F	873	0	808	1	0
3	G	39	0	34	0	0
3	H	39	0	34	3	0
4	A	14	0	13	0	0
4	C	14	0	13	0	0
All	All	11420	0	11067	78	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 3.

All (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:THR:HG23	1:B:320:THR:O	1.62	0.99
1:B:319:HIS:O	1:B:320:THR:HG22	1.63	0.99
1:C:372:LEU:HD23	1:C:401:SER:CB	1.95	0.97
1:D:332:ASN:ND2	1:D:334:ARG:O	2.01	0.93
1:C:372:LEU:CD2	1:C:401:SER:HB2	1.98	0.93
1:A:234:VAL:O	1:A:235:LYS:HB2	1.76	0.85
1:C:372:LEU:HD23	1:C:401:SER:HB2	1.57	0.85
1:B:320:THR:CG2	1:B:320:THR:O	2.30	0.80
1:B:319:HIS:O	1:B:320:THR:CG2	2.30	0.79
1:B:321:PHE:CD2	1:B:321:PHE:N	2.53	0.73
1:C:372:LEU:HD23	1:C:401:SER:HB3	1.69	0.71
1:A:317:GLN:O	1:A:318:GLY:C	2.30	0.70
1:D:321:PHE:N	1:D:321:PHE:CD2	2.59	0.69
1:C:369:THR:OG1	1:C:370:VAL:N	2.25	0.68
1:B:321:PHE:HD2	1:B:321:PHE:N	1.91	0.67
1:B:319:HIS:O	1:B:320:THR:CB	2.44	0.65
1:D:392:GLN:HG3	3:H:1:NAG:H61	1.79	0.65
1:C:370:VAL:HB	1:C:387:ARG:HH21	1.64	0.63
1:D:331:SER:OG	1:D:332:ASN:N	2.30	0.61
1:B:236:ILE:HG23	1:B:254:CYS:H	1.65	0.61
1:D:236:ILE:HG23	1:D:254:CYS:H	1.65	0.60
1:C:236:ILE:HG23	1:C:254:CYS:H	1.66	0.60
1:D:477:GLN:HE21	1:D:484:GLN:HE21	1.51	0.59
1:C:372:LEU:CD2	1:C:401:SER:CB	2.65	0.58
1:A:319:HIS:O	1:A:320:THR:HG22	2.08	0.54
1:A:422:HIS:HB3	1:A:425:LEU:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:321:PHE:HD2	1:D:321:PHE:H	1.56	0.53
1:B:319:HIS:C	1:B:320:THR:HG22	2.28	0.52
1:C:314:VAL:HB	1:C:321:PHE:HB2	1.90	0.52
1:D:321:PHE:HD2	1:D:321:PHE:N	2.05	0.51
1:A:265:GLN:HB3	1:A:315:THR:HB	1.93	0.51
1:C:370:VAL:CB	1:C:387:ARG:HH21	2.24	0.51
1:C:369:THR:C	1:C:370:VAL:HG23	2.30	0.51
1:D:265:GLN:HB3	1:D:315:THR:HB	1.93	0.50
1:C:525:ARG:HD3	1:C:538:GLN:HB3	1.93	0.50
1:C:370:VAL:CG2	1:C:387:ARG:HH21	2.24	0.50
1:A:316:TYR:O	1:A:317:GLN:C	2.49	0.50
1:B:265:GLN:HB3	1:B:315:THR:HB	1.94	0.50
1:D:392:GLN:HE21	3:H:1:NAG:H61	1.77	0.49
1:A:464:CYS:HB3	1:A:507:SER:HB3	1.96	0.48
1:B:305:LEU:HG	1:B:327:LYS:HD2	1.96	0.48
1:B:464:CYS:HB3	1:B:507:SER:HB3	1.96	0.48
1:C:369:THR:C	1:C:370:VAL:CG2	2.82	0.48
1:D:320:THR:OG1	1:D:320:THR:O	2.33	0.47
1:C:464:CYS:HB3	1:C:507:SER:HB3	1.96	0.47
1:D:464:CYS:HB3	1:D:507:SER:HB3	1.96	0.47
1:B:319:HIS:O	1:B:320:THR:HB	2.15	0.46
1:C:369:THR:HG23	1:C:370:VAL:N	2.30	0.46
1:A:305:LEU:HG	1:A:327:LYS:HD2	1.97	0.46
1:A:235:LYS:HA	1:A:235:LYS:HD3	1.69	0.45
1:C:476:VAL:HG21	1:C:492:THR:HG21	1.96	0.45
1:A:417:GLN:HB3	1:B:246:HIS:CD2	2.51	0.45
1:B:330:ASP:HB2	1:B:333:PRO:HG3	1.98	0.45
2:F:224:ARG:HH21	2:F:226:LEU:HD12	1.82	0.45
1:B:365:PRO:HG3	1:B:397:LEU:HB2	1.99	0.44
1:D:319:HIS:O	1:D:320:THR:OG1	2.30	0.44
1:A:363:LEU:HA	1:A:396:THR:HG22	1.99	0.44
1:B:347:ASP:HA	1:B:351:ARG:HB3	1.99	0.44
1:A:347:ASP:HA	1:A:351:ARG:HB3	2.00	0.44
1:C:477:GLN:HB2	1:C:525:ARG:HB3	2.00	0.44
1:C:347:ASP:HA	1:C:351:ARG:HB3	2.00	0.44
1:A:236:ILE:HG13	1:A:323:ASP:OD1	2.17	0.43
1:D:392:GLN:HG3	3:H:1:NAG:C6	2.46	0.43
1:C:363:LEU:HA	1:C:396:THR:HG22	2.01	0.43
1:D:347:ASP:HA	1:D:351:ARG:HB3	1.99	0.42
1:C:475:SER:HB2	1:C:527:VAL:HB	2.00	0.42
1:A:378:SER:HB3	2:E:186:HIS:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:444:GLU:HG2	1:D:453:TRP:CE2	2.55	0.41
1:B:318:GLY:O	1:B:319:HIS:CD2	2.73	0.41
1:B:475:SER:HB2	1:B:527:VAL:HB	2.02	0.41
1:A:234:VAL:HG11	1:A:256:VAL:HG13	2.03	0.41
1:B:376:ARG:HD2	1:B:380:LYS:HB2	2.02	0.41
1:C:376:ARG:HD2	1:C:380:LYS:HB2	2.02	0.41
1:C:370:VAL:CG2	1:C:387:ARG:NH2	2.84	0.41
1:C:370:VAL:HG23	1:C:387:ARG:NH2	2.35	0.41
1:A:253:LEU:HD22	1:A:325:THR:HG21	2.03	0.40
1:D:253:LEU:HD22	1:D:325:THR:HG21	2.04	0.40
1:A:317:GLN:O	1:A:318:GLY:O	2.38	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	305/307 (99%)	281 (92%)	23 (8%)	1 (0%)	41	75
1	B	300/307 (98%)	276 (92%)	21 (7%)	3 (1%)	15	54
1	C	304/307 (99%)	284 (93%)	19 (6%)	1 (0%)	41	75
1	D	300/307 (98%)	276 (92%)	19 (6%)	5 (2%)	9	42
2	E	101/120 (84%)	92 (91%)	9 (9%)	0	100	100
2	F	102/120 (85%)	93 (91%)	9 (9%)	0	100	100
All	All	1412/1468 (96%)	1302 (92%)	100 (7%)	10 (1%)	22	61

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	333	PRO

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Mol	Chain	Res	Type
1	B	320	THR
1	C	370	VAL
1	D	320	THR
1	A	235	LYS
1	B	254	CYS
1	B	436	THR
1	D	436	THR
1	D	500	GLY
1	D	318	GLY

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	271/271 (100%)	260 (96%)	11 (4%)	30	63
1	B	269/271 (99%)	256 (95%)	13 (5%)	25	60
1	C	270/271 (100%)	259 (96%)	11 (4%)	30	63
1	D	269/271 (99%)	255 (95%)	14 (5%)	23	56
2	E	90/102 (88%)	84 (93%)	6 (7%)	16	48
2	F	91/102 (89%)	83 (91%)	8 (9%)	10	38
All	All	1260/1288 (98%)	1197 (95%)	63 (5%)	24	58

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	LYS
1	A	255	LEU
1	A	265	GLN
1	A	352	LYS
1	A	429	LEU
1	A	457	ARG
1	A	461	THR
1	A	470	MET
1	A	472	GLU

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Mol	Chain	Res	Type
1	A	485	LEU
1	A	490	HIS
1	B	255	LEU
1	B	265	GLN
1	B	303	HIS
1	B	321	PHE
1	B	327	LYS
1	B	352	LYS
1	B	425	LEU
1	B	429	LEU
1	B	461	THR
1	B	470	MET
1	B	472	GLU
1	B	501	SER
1	B	519	LYS
1	C	255	LEU
1	C	303	HIS
1	C	352	LYS
1	C	372	LEU
1	C	383	GLN
1	C	429	LEU
1	C	461	THR
1	C	472	GLU
1	C	476	VAL
1	C	479	LEU
1	C	487	ASP
1	D	255	LEU
1	D	265	GLN
1	D	303	HIS
1	D	321	PHE
1	D	327	LYS
1	D	330	ASP
1	D	352	LYS
1	D	383	GLN
1	D	397	LEU
1	D	461	THR
1	D	470	MET
1	D	472	GLU
1	D	487	ASP
1	D	501	SER
2	E	198	LEU
2	E	223	LEU

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Mol	Chain	Res	Type
2	E	226	LEU
2	E	228	LEU
2	E	241	ASP
2	E	258	ASP
2	F	198	LEU
2	F	223	LEU
2	F	224	ARG
2	F	226	LEU
2	F	228	LEU
2	F	241	ASP
2	F	258	ASP
2	F	283	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	246	HIS
1	B	319	HIS
1	B	392	GLN
1	B	490	HIS
1	C	490	HIS
1	D	246	HIS
1	D	392	GLN
1	D	477	GLN
1	D	490	HIS

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 ⓘ

6 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	G	1	1,3	14,14,15	0.27	0	17,19,21	0.56	0
3	NAG	G	2	3	14,14,15	0.28	0	17,19,21	0.75	0
3	BMA	G	3	3	11,11,12	0.32	0	15,15,17	0.61	0
3	NAG	H	1	1,3	14,14,15	0.30	0	17,19,21	0.42	0
3	NAG	H	2	3	14,14,15	0.30	0	17,19,21	0.90	1 (5%)
3	BMA	H	3	3	11,11,12	0.29	0	15,15,17	0.49	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	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	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	BMA	H	3	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	NAG	C1-O5-C5	2.87	116.08	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

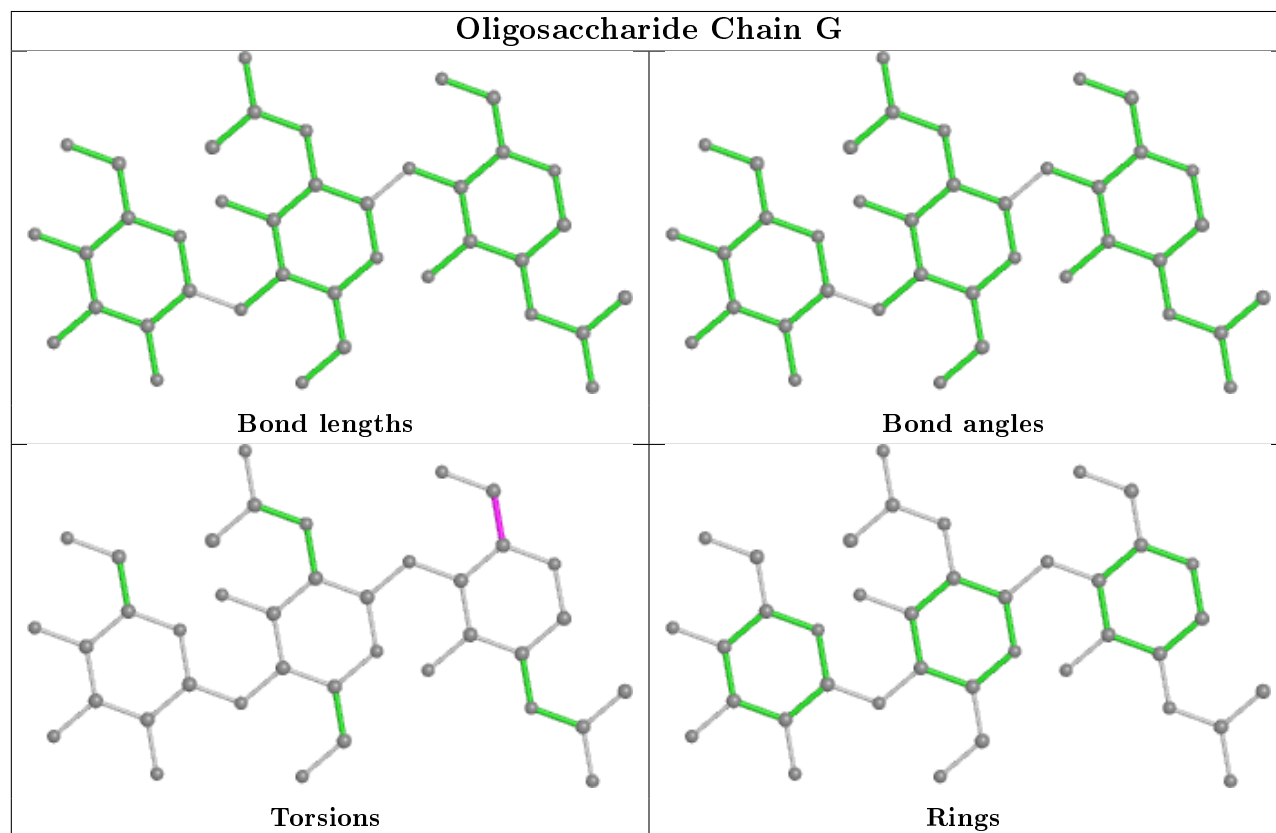
Mol	Chain	Res	Type	Atoms
3	H	1	NAG	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6

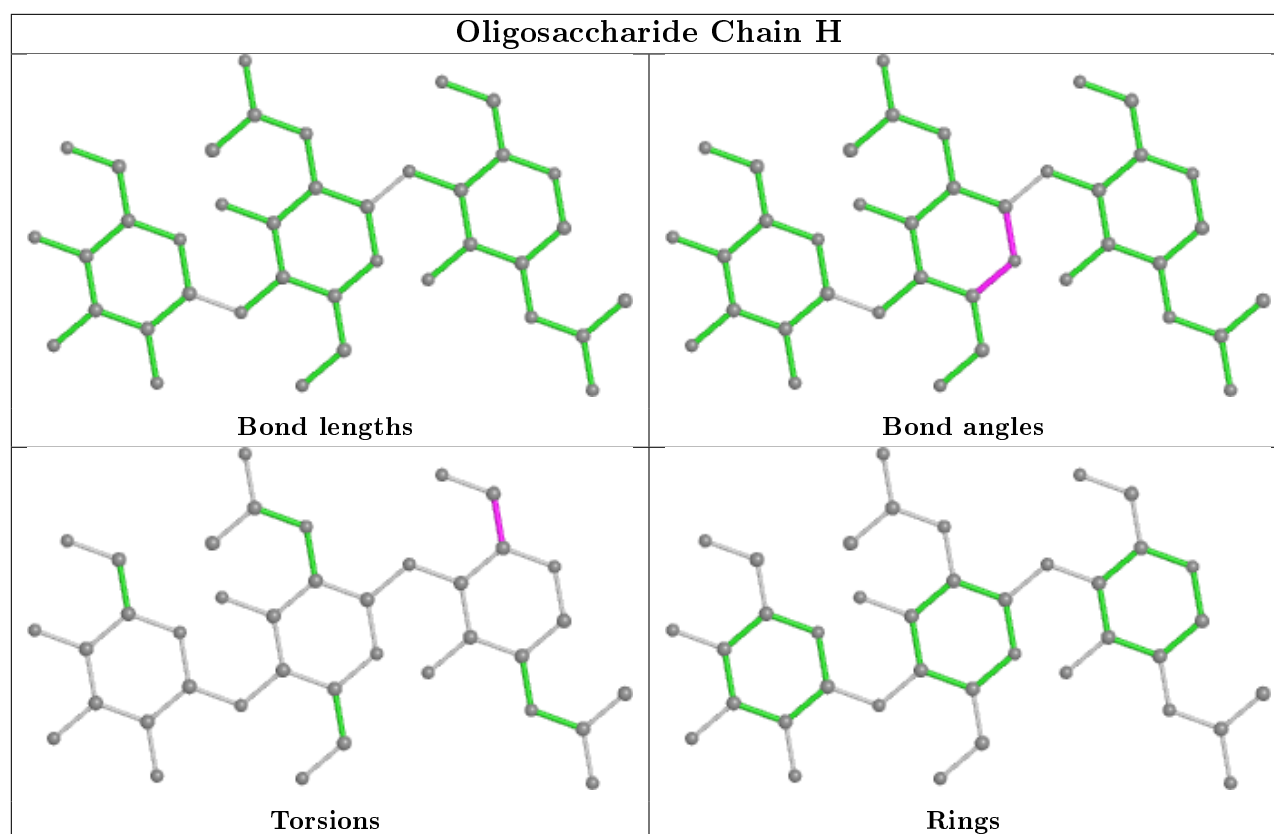
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	3	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](#)

2 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	NAG	C	601	1	14,14,15	0.27	0	17,19,21	0.53	0
4	NAG	A	601	1	14,14,15	0.26	0	17,19,21	0.55	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	NAG	C	601	1	-	1/6/23/26	0/1/1/1
4	NAG	A	601	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	NAG	O5-C5-C6-O6
4	C	601	NAG	O5-C5-C6-O6

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 [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

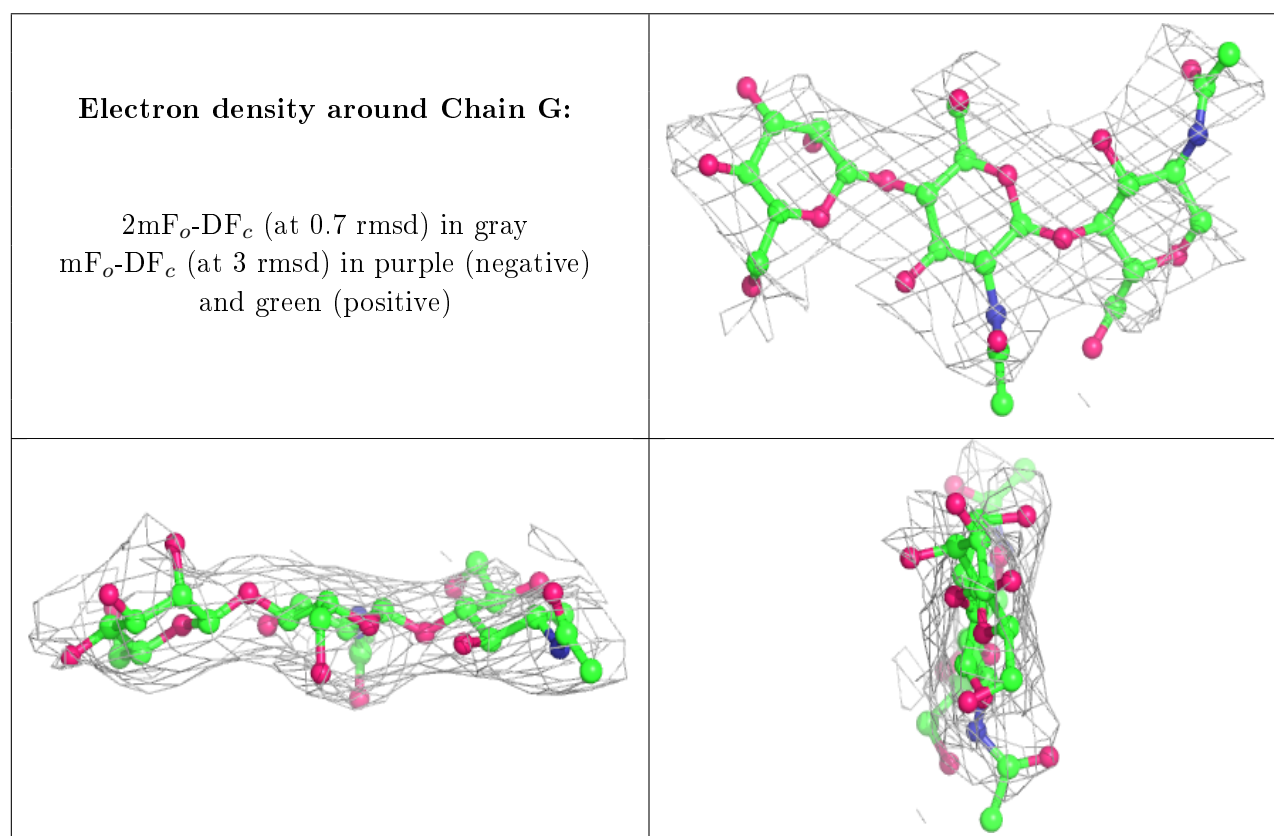
6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

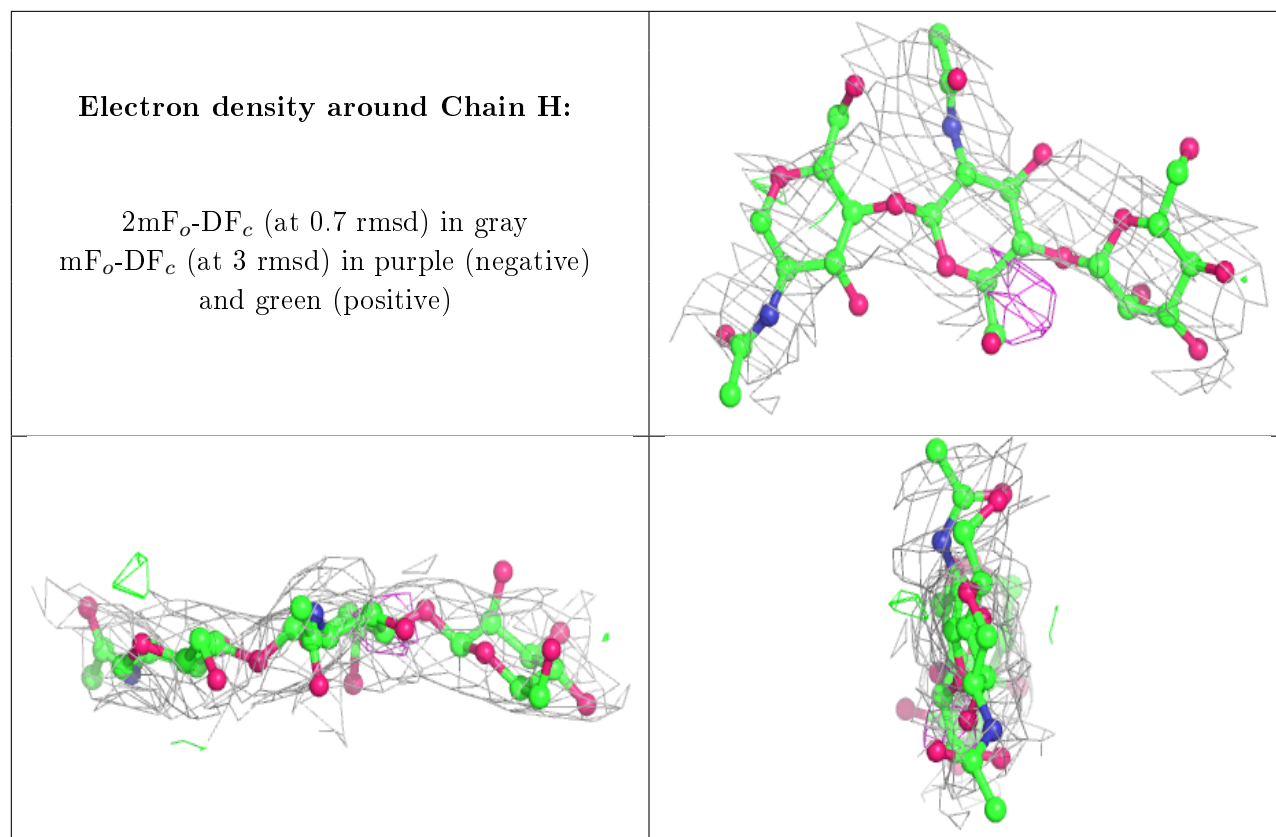
Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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





6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.