



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:13 PM UTC

PDB ID : 8ISN / pdb_00008isn
Title : HLA-A24 in complex with modified 9mer WT1 peptide
Authors : Bekker, G.J.; Numoto, N.; Kawasaki, M.; Hayashi, T.; Yabuno, S.; Kozono, Y.; Shimizu, T.; Kozono, H.; Ito, N.; Oda, M.; Kamiya, N.
Deposited on : 2023-03-21
Resolution : 2.48 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:

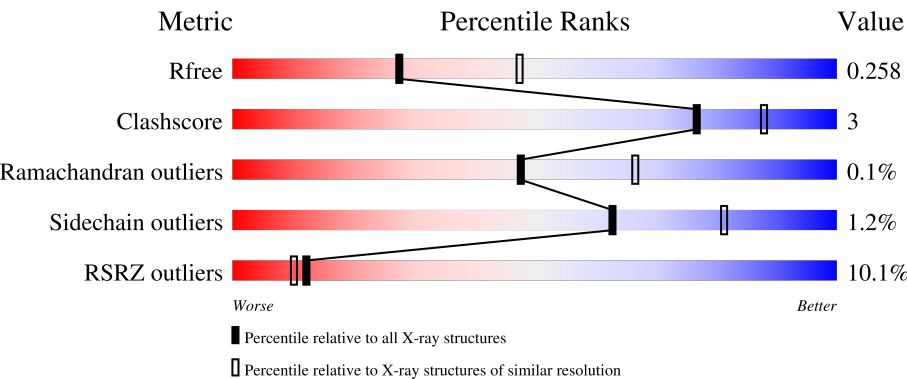
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	305	2% 83% 7% 10%
1	D	305	9% 82% 8% 10%
2	B	99	93% 7%
2	E	99	42% 92% 8%
3	C	9	11% 67% 22% 11%

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Mol	Chain	Length	Quality of chain
3	F	9	11% 78% 22%
4	G	4	50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6495 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2221	1382	403	426	10			
1	D	274	Total	C	N	O	S	0	0	0
			2221	1382	403	426	10			

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	277	GLY	-	expression tag	UNP D9UAY1
A	278	ALA	-	expression tag	UNP D9UAY1
A	279	SER	-	expression tag	UNP D9UAY1
A	280	GLY	-	expression tag	UNP D9UAY1
A	281	ASP	-	expression tag	UNP D9UAY1
A	282	TYR	-	expression tag	UNP D9UAY1
A	283	LYS	-	expression tag	UNP D9UAY1
A	284	ASP	-	expression tag	UNP D9UAY1
A	285	ASP	-	expression tag	UNP D9UAY1
A	286	ASP	-	expression tag	UNP D9UAY1
A	287	ASP	-	expression tag	UNP D9UAY1
A	288	LYS	-	expression tag	UNP D9UAY1
A	289	GLY	-	expression tag	UNP D9UAY1
A	290	GLY	-	expression tag	UNP D9UAY1
A	291	GLY	-	expression tag	UNP D9UAY1
A	292	GLY	-	expression tag	UNP D9UAY1
A	293	LEU	-	expression tag	UNP D9UAY1
A	294	ASN	-	expression tag	UNP D9UAY1
A	295	ASP	-	expression tag	UNP D9UAY1
A	296	ILE	-	expression tag	UNP D9UAY1
A	297	PHE	-	expression tag	UNP D9UAY1
A	298	GLU	-	expression tag	UNP D9UAY1
A	299	ALA	-	expression tag	UNP D9UAY1
A	300	GLN	-	expression tag	UNP D9UAY1
A	301	LYS	-	expression tag	UNP D9UAY1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	302	ILE	-	expression tag	UNP D9UAY1
A	303	GLU	-	expression tag	UNP D9UAY1
A	304	TRP	-	expression tag	UNP D9UAY1
A	305	HIS	-	expression tag	UNP D9UAY1
D	277	GLY	-	expression tag	UNP D9UAY1
D	278	ALA	-	expression tag	UNP D9UAY1
D	279	SER	-	expression tag	UNP D9UAY1
D	280	GLY	-	expression tag	UNP D9UAY1
D	281	ASP	-	expression tag	UNP D9UAY1
D	282	TYR	-	expression tag	UNP D9UAY1
D	283	LYS	-	expression tag	UNP D9UAY1
D	284	ASP	-	expression tag	UNP D9UAY1
D	285	ASP	-	expression tag	UNP D9UAY1
D	286	ASP	-	expression tag	UNP D9UAY1
D	287	ASP	-	expression tag	UNP D9UAY1
D	288	LYS	-	expression tag	UNP D9UAY1
D	289	GLY	-	expression tag	UNP D9UAY1
D	290	GLY	-	expression tag	UNP D9UAY1
D	291	GLY	-	expression tag	UNP D9UAY1
D	292	GLY	-	expression tag	UNP D9UAY1
D	293	LEU	-	expression tag	UNP D9UAY1
D	294	ASN	-	expression tag	UNP D9UAY1
D	295	ASP	-	expression tag	UNP D9UAY1
D	296	ILE	-	expression tag	UNP D9UAY1
D	297	PHE	-	expression tag	UNP D9UAY1
D	298	GLU	-	expression tag	UNP D9UAY1
D	299	ALA	-	expression tag	UNP D9UAY1
D	300	GLN	-	expression tag	UNP D9UAY1
D	301	LYS	-	expression tag	UNP D9UAY1
D	302	ILE	-	expression tag	UNP D9UAY1
D	303	GLU	-	expression tag	UNP D9UAY1
D	304	TRP	-	expression tag	UNP D9UAY1
D	305	HIS	-	expression tag	UNP D9UAY1

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	E	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called CYS-TYR-THR-TRP-ASN-GLN-MET-ASN-LEU.

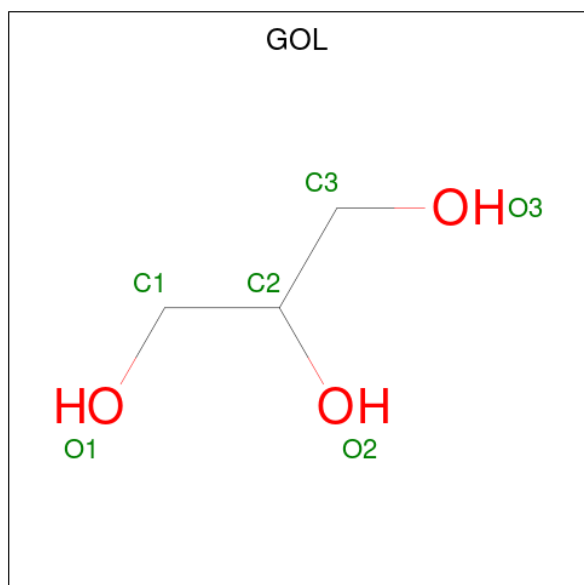
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total 81	C 51	N 13	O 15	S 2	0	0	0
3	F	9	Total 81	C 51	N 13	O 15	S 2	0	0	0

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranoside-(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
4	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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

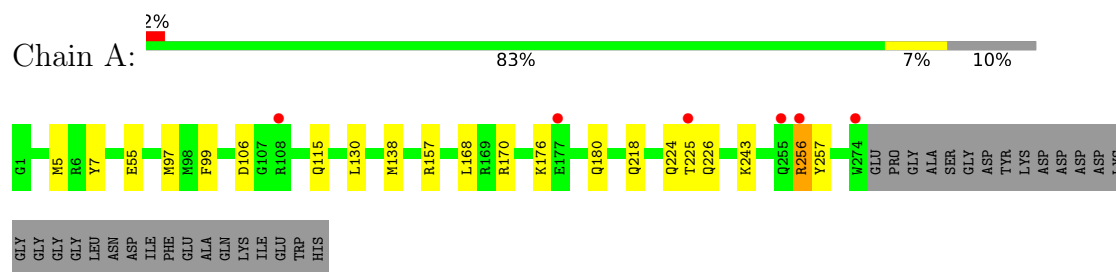
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	79	Total	O	0	0
			79	79		
6	B	36	Total	O	0	0
			36	36		
6	C	1	Total	O	0	0
			1	1		
6	D	32	Total	O	0	0
			32	32		
6	E	5	Total	O	0	0
			5	5		

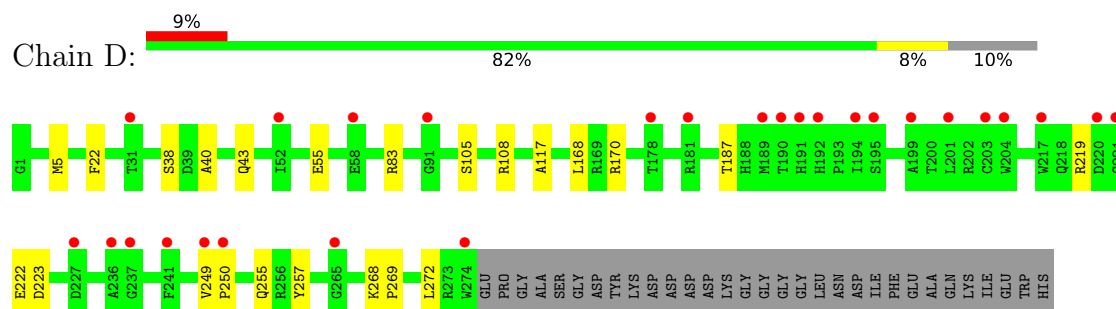
3 Residue-property plots

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.

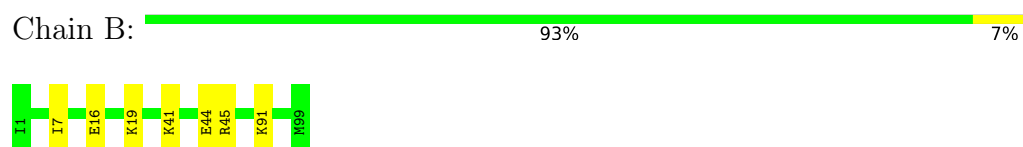
- Molecule 1: MHC class I antigen



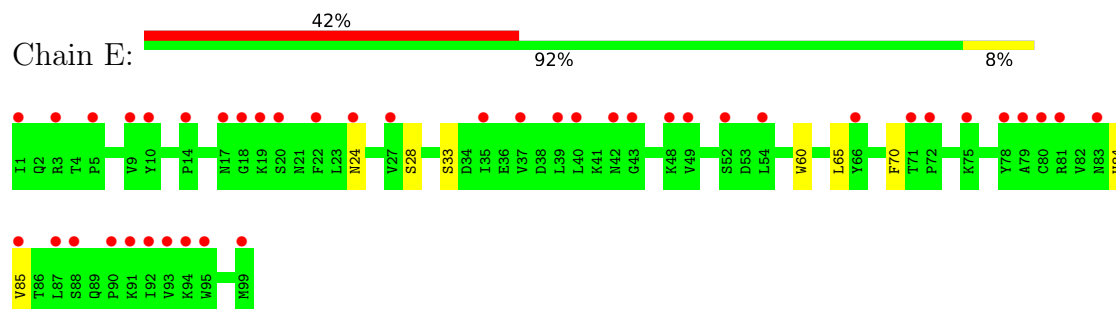
- Molecule 1: MHC class I antigen



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: CYS-TYR-THR-TRP-ASN-GLN-MET-ASN-LEU

Chain C: 



- Molecule 3: CYS-TYR-THR-TRP-ASN-GLN-MET-ASN-LEU

Chain F: 



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

Chain G: 



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	161.40Å 166.13Å 180.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.24 – 2.48 49.24 – 2.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.24-2.48) 91.3 (49.24-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.25	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.74 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.222 , 0.258 0.223 , 0.258	Depositor DCC
R_{free} test set	2014 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6495	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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: NAG, BMA, GOL, MAN

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	0.10	0/2281	0.27	0/3092
1	D	0.11	0/2281	0.29	0/3092
2	B	0.09	0/852	0.27	0/1152
2	E	0.10	0/852	0.29	0/1152
3	C	0.11	0/83	0.26	0/111
3	F	0.20	0/83	0.24	0/111
All	All	0.10	0/6432	0.28	0/8710

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2221	0	2081	15	0
1	D	2221	0	2082	12	0
2	B	829	0	794	5	0
2	E	829	0	794	3	0
3	C	81	0	73	3	0
3	F	81	0	73	1	0
4	G	50	0	43	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	18	0	24	0	0
5	B	12	0	16	2	0
6	A	79	0	0	1	0
6	B	36	0	0	1	0
6	C	1	0	0	0	0
6	D	32	0	0	2	0
6	E	5	0	0	0	0
All	All	6495	0	5980	36	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 (36) 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)
2:B:41:LYS:NZ	6:B:202:HOH:O	2.33	0.61
2:B:44:GLU:HA	5:B:102:GOL:H31	1.83	0.60
1:D:83:ARG:NH1	6:D:402:HOH:O	2.37	0.57
1:A:7:TYR:OH	3:C:1:CYS:N	2.37	0.57
2:B:7:ILE:HD12	2:B:91:LYS:HD3	1.89	0.55
1:A:5:MET:HE2	1:A:7:TYR:CE2	2.44	0.53
3:F:5:ASN:HA	3:F:7:MET:HE3	1.91	0.53
1:D:55:GLU:OE1	1:D:170:ARG:NH2	2.42	0.52
1:D:5:MET:HB2	1:D:168:LEU:HD13	1.92	0.52
1:D:40:ALA:O	1:D:43:GLN:NE2	2.40	0.52
1:D:268:LYS:HG3	1:D:269:PRO:HD2	1.93	0.51
1:D:219:ARG:HG3	1:D:257:TYR:CZ	2.47	0.49
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.47	0.49
1:A:115:GLN:NE2	6:A:507:HOH:O	2.46	0.48
1:A:97:MET:HE2	1:A:99:PHE:CD2	2.49	0.48
1:D:222:GLU:O	1:D:223:ASP:HB2	2.14	0.48
3:C:5:ASN:HA	3:C:7:MET:HE3	1.96	0.47
1:D:249:VAL:HG12	1:D:250:PRO:O	2.15	0.47
2:E:84:HIS:CE1	2:E:85:VAL:HG12	2.51	0.46
1:A:176:LYS:HA	1:A:180:GLN:HG3	1.97	0.46
2:E:24:ASN:HB3	2:E:65:LEU:HD11	1.97	0.46
1:A:224:GLN:O	1:A:226:GLN:N	2.48	0.45
1:A:106:ASP:OD1	1:A:106:ASP:N	2.38	0.44
1:A:5:MET:HE2	1:A:7:TYR:HE2	1.83	0.43
1:A:138:MET:HE2	1:A:138:MET:HB3	1.87	0.42
2:B:45:ARG:H	5:B:102:GOL:H12	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:GLN:O	1:A:257:TYR:HA	2.20	0.42
1:A:55:GLU:CD	1:A:170:ARG:HH21	2.28	0.42
2:B:16:GLU:HB3	2:B:19:LYS:HG3	2.02	0.42
1:D:255:GLN:NE2	6:D:404:HOH:O	2.54	0.41
1:A:256:ARG:H	1:A:256:ARG:HG2	1.44	0.41
1:D:187:THR:HB	1:D:272:LEU:HD21	2.03	0.41
1:A:97:MET:HE1	3:C:5:ASN:OD1	2.21	0.41
1:D:22:PHE:HB3	1:D:38:SER:HB3	2.03	0.41
1:A:5:MET:HB2	1:A:168:LEU:HD13	2.03	0.40
1:A:130:LEU:HD13	1:A:157:ARG:HG3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/305 (89%)	264 (97%)	7 (3%)	1 (0%)	30	46
1	D	272/305 (89%)	262 (96%)	10 (4%)	0	100	100
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
2	E	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
3	C	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	752/826 (91%)	724 (96%)	27 (4%)	1 (0%)	48	66

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	THR

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	230/253 (91%)	228 (99%)	2 (1%)	70	86
1	D	230/253 (91%)	228 (99%)	2 (1%)	70	86
2	B	94/94 (100%)	94 (100%)	0	100	100
2	E	94/94 (100%)	91 (97%)	3 (3%)	34	58
3	C	9/9 (100%)	8 (89%)	1 (11%)	6	11
3	F	9/9 (100%)	9 (100%)	0	100	100
All	All	666/712 (94%)	658 (99%)	8 (1%)	63	81

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	243	LYS
1	A	256	ARG
3	C	1	CYS
1	D	105	SER
1	D	108	ARG
2	E	28	SER
2	E	33	SER
2	E	70	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	HIS
1	A	180	GLN
2	B	13	HIS
3	C	8	ASN
1	D	72	GLN
1	D	151	HIS
1	D	156	GLN
1	D	197	HIS
1	D	255	GLN

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Mol	Chain	Res	Type
3	F	8	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 ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	G	1	4,1	14,14,15	0.24	0	17,19,21	0.48	0
4	NAG	G	2	4	14,14,15	0.23	0	17,19,21	0.67	0
4	BMA	G	3	4	11,11,12	1.36	2 (18%)	15,15,17	1.46	4 (26%)
4	MAN	G	4	4	11,11,12	0.95	1 (9%)	15,15,17	1.38	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
4	NAG	G	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	2/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	3	BMA	C2-C3	2.86	1.56	1.52
4	G	4	MAN	C1-C2	2.77	1.58	1.52
4	G	3	BMA	C1-C2	2.51	1.58	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	4	MAN	C1-O5-C5	3.70	117.14	112.19
4	G	3	BMA	C1-C2-C3	3.58	114.86	109.64
4	G	4	MAN	O2-C2-C3	-2.15	105.69	110.15
4	G	3	BMA	C2-C3-C4	2.05	114.47	110.86
4	G	3	BMA	C1-O5-C5	2.04	114.92	112.19
4	G	3	BMA	O5-C5-C4	-2.01	105.94	110.83

There are no chirality outliers.

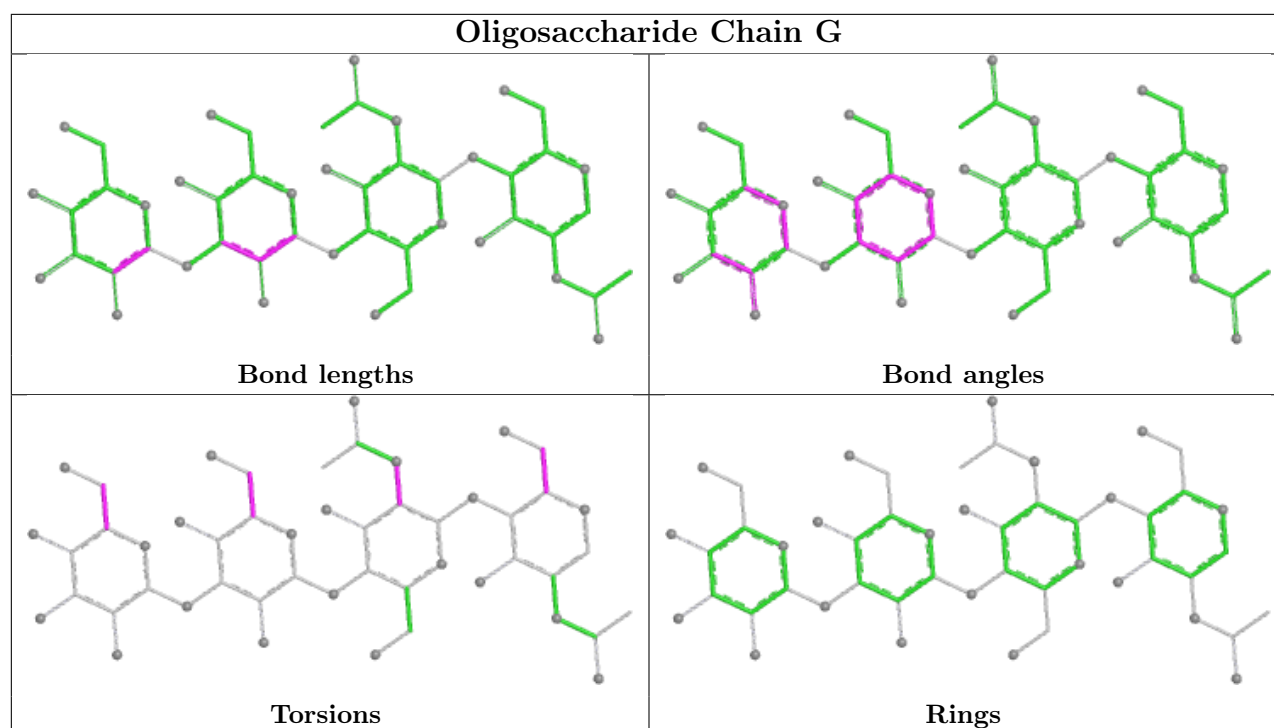
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	4	MAN	O5-C5-C6-O6
4	G	4	MAN	C4-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6
4	G	3	BMA	O5-C5-C6-O6
4	G	2	NAG	C1-C2-N2-C7
4	G	3	BMA	C4-C5-C6-O6
4	G	2	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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	$\# Z > 2$
5	GOL	B	102	-	5,5,5	0.99	0	5,5,5	1.02	0
5	GOL	A	402	-	5,5,5	0.93	0	5,5,5	1.07	0
5	GOL	B	101	-	5,5,5	0.96	0	5,5,5	1.02	0
5	GOL	A	403	-	5,5,5	1.02	0	5,5,5	0.99	0
5	GOL	A	401	-	5,5,5	0.97	0	5,5,5	1.04	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
5	GOL	B	102	-	-	0/4/4/4	-
5	GOL	A	402	-	-	0/4/4/4	-
5	GOL	B	101	-	-	0/4/4/4	-
5	GOL	A	403	-	-	2/4/4/4	-
5	GOL	A	401	-	-	0/4/4/4	-

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
5	A	403	GOL	O1-C1-C2-C3
5	A	403	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	102	GOL	2	0

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	274/305 (89%)	0.33	6 (2%) 62 59	32, 49, 73, 99	0
1	D	274/305 (89%)	0.92	27 (9%) 13 10	40, 68, 101, 120	0
2	B	99/99 (100%)	0.00	0 100 100	32, 44, 69, 93	0
2	E	99/99 (100%)	1.89	42 (42%) 0 0	56, 88, 106, 109	0
3	C	9/9 (100%)	0.61	1 (11%) 10 8	43, 46, 51, 56	0
3	F	9/9 (100%)	0.54	1 (11%) 10 8	45, 50, 54, 55	0
All	All	764/826 (92%)	0.71	77 (10%) 12 10	32, 57, 98, 120	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	178	THR	5.3
2	E	95	TRP	3.8
2	E	14	PRO	3.8
2	E	1	ILE	3.7
2	E	79	ALA	3.6
2	E	75	LYS	3.5
1	D	190	THR	3.4
2	E	87	LEU	3.3
1	A	177	GLU	3.2
1	D	274	TRP	3.1
2	E	10	TYR	3.0
2	E	88	SER	3.0
2	E	91	LYS	3.0
2	E	80	CYS	3.0
2	E	52	SER	2.9
2	E	39	LEU	2.9
3	C	1	CYS	2.9
2	E	93	VAL	2.8
1	D	221	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	52	ILE	2.8
2	E	78	TYR	2.8
2	E	99	MET	2.8
2	E	90	PRO	2.7
2	E	9	VAL	2.7
2	E	43	GLY	2.6
1	D	227	ASP	2.6
2	E	19	LYS	2.6
2	E	72	PRO	2.5
1	D	194	ILE	2.5
2	E	37	VAL	2.5
2	E	18	GLY	2.4
1	D	91	GLY	2.4
2	E	92	ILE	2.4
1	D	249	VAL	2.4
1	D	199	ALA	2.4
1	D	195	SER	2.4
1	D	265	GLY	2.4
2	E	5	PRO	2.3
1	D	181	ARG	2.3
1	D	237	GLY	2.3
2	E	81	ARG	2.3
2	E	71	THR	2.3
1	D	204	TRP	2.3
2	E	66	TYR	2.3
1	D	31	THR	2.3
1	D	192	HIS	2.2
2	E	40	LEU	2.2
2	E	54	LEU	2.2
1	D	236	ALA	2.2
1	D	201	LEU	2.2
1	A	256	ARG	2.2
1	A	274	TRP	2.2
2	E	85	VAL	2.2
2	E	94	LYS	2.2
1	A	255	GLN	2.1
1	D	189	MET	2.1
2	E	83	ASN	2.1
1	A	108	ARG	2.1
1	D	58	GLU	2.1
2	E	20	SER	2.1
2	E	48	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	35	ILE	2.1
1	D	203	CYS	2.1
1	D	220	ASP	2.1
2	E	27	VAL	2.1
2	E	49	VAL	2.1
2	E	17	ASN	2.1
2	E	24	ASN	2.0
1	A	225	THR	2.0
1	D	217	TRP	2.0
3	F	1	CYS	2.0
1	D	241	PHE	2.0
2	E	3	ARG	2.0
2	E	22	PHE	2.0
2	E	42	ASN	2.0
1	D	250	PRO	2.0
1	D	191	HIS	2.0

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

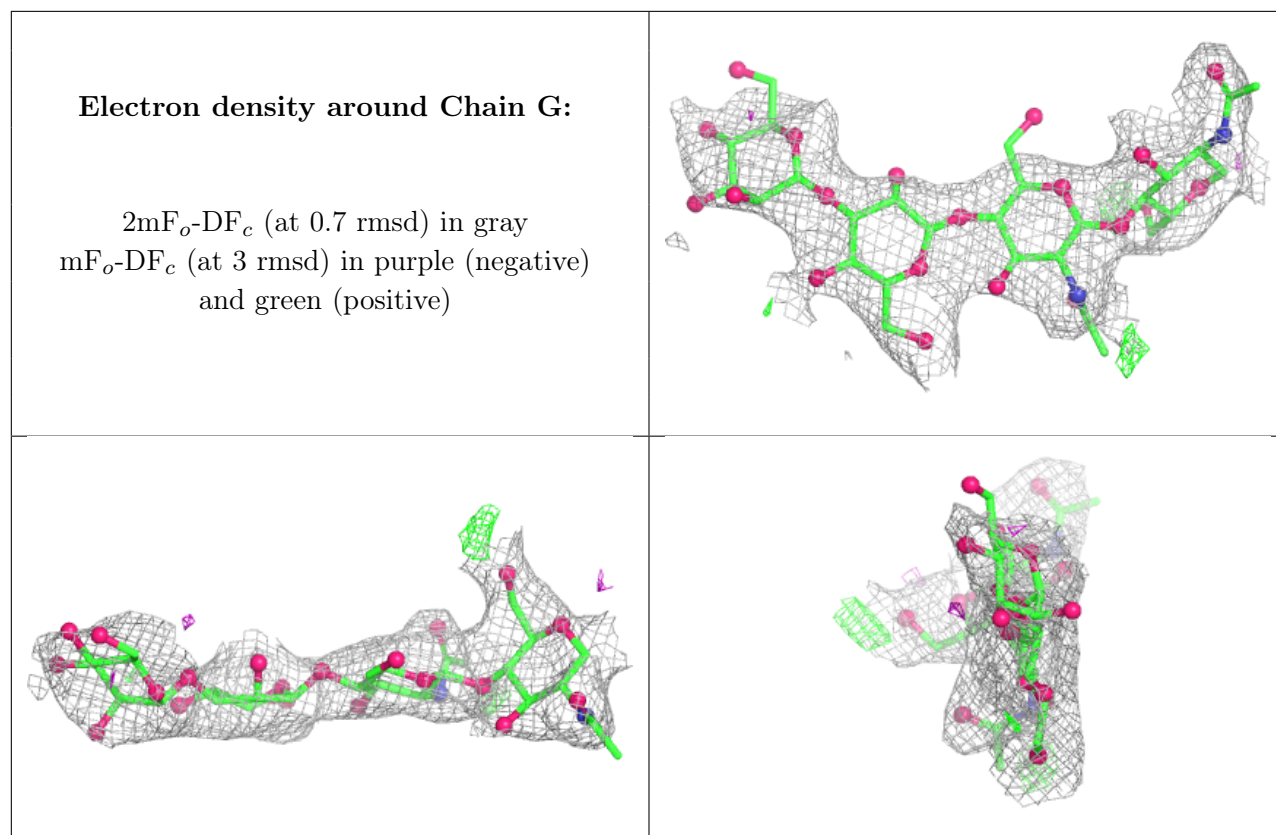
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	G	4	11/12	0.55	0.17	114,121,126,128	0
4	BMA	G	3	11/12	0.62	0.14	86,102,112,114	0
4	NAG	G	1	14/15	0.64	0.15	91,100,105,110	0
4	NAG	G	2	14/15	0.66	0.16	109,112,114,115	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.



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
5	GOL	B	102	6/6	0.76	0.16	60,62,63,64	0
5	GOL	A	403	6/6	0.85	0.14	39,45,46,51	0
5	GOL	A	402	6/6	0.86	0.15	46,49,57,58	0
5	GOL	B	101	6/6	0.87	0.19	53,53,58,64	0
5	GOL	A	401	6/6	0.91	0.14	53,55,58,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.