



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:42 PM UTC

PDB ID : 1MMX / pdb_00001mmx
Title : Crystal structure of galactose mutarotase from *Lactococcus lactis* complexed with D-fucose
Authors : Thoden, J.B.; Kim, J.; Raushel, F.M.; Holden, H.M.
Deposited on : 2002-09-04
Resolution : 1.80 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

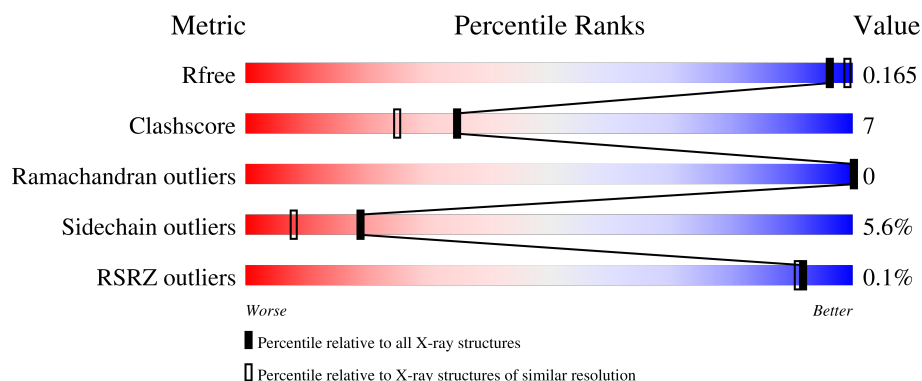
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	347	 76% 18% . .
1	B	347	 81% 16% .

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
2	FUC	A	348[A]	X	-	-	-
2	FUC	A	348[B]	X	-	-	-
2	FUC	B	348[A]	X	-	-	-
2	FUC	B	348[B]	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5937 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.

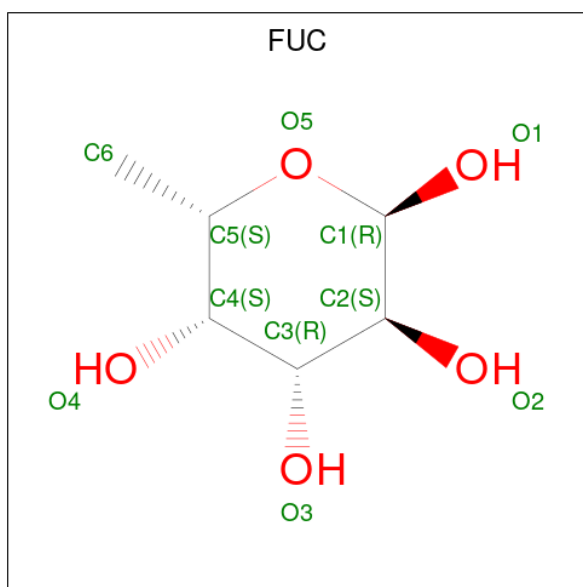
- Molecule 1 is a protein called Aldose 1-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	5	0
			2666	1683	449	531	3			
1	B	346	Total	C	N	O	S	0	5	0
			2740	1726	467	543	4			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	GLU	engineered mutation	UNP Q9ZB17
A	340	LEU	-	expression tag	UNP Q9ZB17
A	341	GLU	-	expression tag	UNP Q9ZB17
A	342	HIS	-	expression tag	UNP Q9ZB17
A	343	HIS	-	expression tag	UNP Q9ZB17
A	344	HIS	-	expression tag	UNP Q9ZB17
A	345	HIS	-	expression tag	UNP Q9ZB17
A	346	HIS	-	expression tag	UNP Q9ZB17
A	347	HIS	-	expression tag	UNP Q9ZB17
B	2	SER	GLU	engineered mutation	UNP Q9ZB17
B	340	LEU	-	expression tag	UNP Q9ZB17
B	341	GLU	-	expression tag	UNP Q9ZB17
B	342	HIS	-	expression tag	UNP Q9ZB17
B	343	HIS	-	expression tag	UNP Q9ZB17
B	344	HIS	-	expression tag	UNP Q9ZB17
B	345	HIS	-	expression tag	UNP Q9ZB17
B	346	HIS	-	expression tag	UNP Q9ZB17
B	347	HIS	-	expression tag	UNP Q9ZB17

- Molecule 2 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	1
			12	6	6		
2	B	1	Total	C	O	0	1
			12	6	6		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

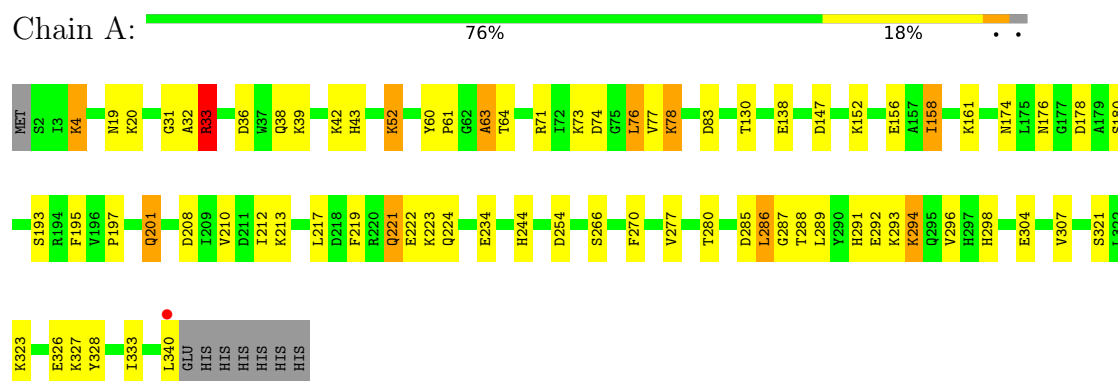
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	234	Total	O	0	0
			234	234		
4	B	272	Total	O	0	0
			272	272		

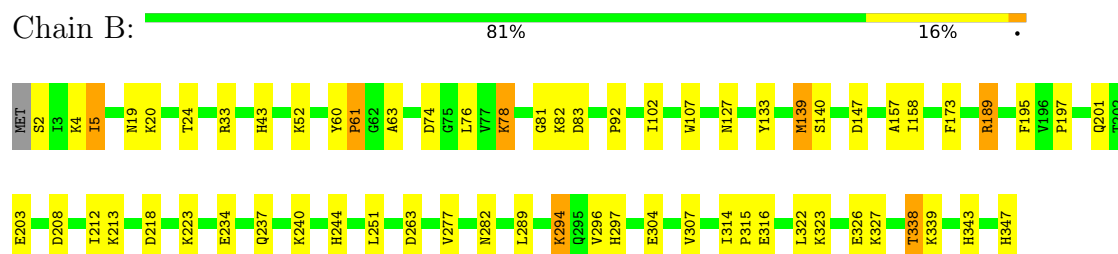
3 Residue-property plots

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: Aldose 1-epimerase



- Molecule 1: Aldose 1-epimerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.90Å 76.30Å 210.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.80 30.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.5 (30.00-1.80) 97.5 (30.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.36 (at 1.71Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.168 , 0.229 0.164 , 0.165	Depositor DCC
R_{free} test set	7403 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 90.1	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	0.97	EDS
Total number of atoms	5937	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% 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: NA, FUC

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	1.07	0/2738	1.47	11/3703 (0.3%)
1	B	1.12	1/2818 (0.0%)	1.47	17/3811 (0.4%)
All	All	1.10	1/5556 (0.0%)	1.47	28/7514 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	244	HIS	CA-C	-6.11	1.45	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	244	HIS	O-C-N	7.75	127.31	121.65
1	A	33	ARG	N-CA-CB	-6.97	98.68	111.37
1	B	33	ARG	N-CA-C	6.89	120.91	109.95
1	B	33	ARG	N-CA-CB	-6.87	99.86	110.85
1	A	307	VAL	N-CA-C	-6.87	99.83	108.89
1	A	76	LEU	N-CA-C	6.82	119.85	108.73
1	B	173	PHE	CA-CB-CG	-6.75	107.05	113.80
1	A	210	VAL	N-CA-C	6.54	117.90	108.48
1	A	38	GLN	N-CA-C	6.16	118.78	109.23
1	B	347	HIS	CA-CB-CG	-6.13	107.67	113.80
1	B	76	LEU	N-CA-C	6.13	118.72	108.73
1	B	307	VAL	N-CA-C	-6.11	100.83	108.89
1	A	33	ARG	N-CA-C	6.03	119.02	109.50
1	A	63	ALA	N-CA-C	6.01	118.66	110.55
1	B	61	PRO	N-CA-CB	5.92	109.47	103.25
1	A	244	HIS	O-C-N	5.65	125.81	121.85
1	B	244	HIS	CB-CA-C	-5.53	101.39	109.97
1	B	244	HIS	N-CA-C	5.52	114.65	108.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	LEU	CB-CA-C	5.42	119.49	110.81
1	B	173	PHE	CB-CA-C	-5.41	100.87	109.80
1	B	63	ALA	N-CA-C	5.39	117.48	110.53
1	B	43	HIS	CB-CA-C	-5.36	101.32	109.89
1	B	203	GLU	N-CA-C	5.31	119.71	113.23
1	B	133	TYR	N-CA-C	5.26	116.28	109.65
1	B	296	VAL	CB-CA-C	-5.19	104.33	111.49
1	B	102	ILE	N-CA-C	5.02	118.09	111.17
1	A	64	THR	N-CA-C	-5.01	100.99	108.96
1	A	244	HIS	CB-CA-C	-5.00	101.70	109.55

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	2666	0	2608	43	0
1	B	2740	0	2652	38	0
2	A	12	0	4	0	0
2	B	12	0	4	0	0
3	A	1	0	0	0	0
4	A	234	0	0	6	0
4	B	272	0	0	4	0
All	All	5937	0	5268	80	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 7.

All (80) 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:189:ARG:HH11	1:B:189:ARG:HG2	1.24	1.01
1:B:78[B]:LYS:HE2	1:B:81:GLY:HA2	1.50	0.93
1:B:78[B]:LYS:HE2	1:B:81:GLY:CA	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:GLN:NE2	1:A:201:GLN:H	1.78	0.82
1:B:237:GLN:HG2	4:B:566:HOH:O	1.86	0.76
1:B:218:ASP:O	1:B:223:LYS:HE3	1.85	0.76
1:B:338:THR:HG22	1:B:339:LYS:HG3	1.72	0.71
1:A:234:GLU:HG2	4:A:567:HOH:O	1.92	0.69
1:A:180:SER:HA	1:A:296:VAL:HG13	1.75	0.69
1:B:78[B]:LYS:HE2	1:B:81:GLY:N	2.07	0.68
1:B:78[B]:LYS:HE2	1:B:81:GLY:H	1.58	0.67
1:A:161:LYS:HE3	4:A:561:HOH:O	1.96	0.65
1:B:189:ARG:HG2	1:B:189:ARG:NH1	2.00	0.64
1:B:263:ASP:H	1:B:343:HIS:HD1	1.45	0.64
1:A:174:ASN:OD1	1:A:176:ASN:HB2	1.98	0.64
1:A:156:GLU:OE2	1:A:327:LYS:NZ	2.31	0.62
1:A:152:LYS:HG3	1:A:333:ILE:HG12	1.81	0.62
1:B:158:ILE:HD11	1:B:327:LYS:HB2	1.82	0.60
1:B:322:LEU:HD12	1:B:326[B]:GLU:HG2	1.82	0.60
1:B:338:THR:CG2	1:B:339:LYS:HG3	2.31	0.59
1:B:78[A]:LYS:HG3	1:B:83:ASP:OD1	2.03	0.59
1:B:158:ILE:HD13	1:B:327:LYS:HA	1.85	0.58
1:A:156:GLU:HB3	1:A:327:LYS:HZ2	1.70	0.56
1:A:73[B]:LYS:NZ	1:A:74:ASP:OD2	2.37	0.56
1:A:138:GLU:HG3	4:A:397:HOH:O	2.07	0.54
1:A:156:GLU:CD	1:A:327:LYS:HZ1	2.16	0.54
1:A:197:PRO:HD2	1:A:208:ASP:O	2.08	0.54
1:B:158:ILE:HD11	1:B:327:LYS:CB	2.39	0.53
1:B:322:LEU:CD1	1:B:326[B]:GLU:HG2	2.39	0.53
1:A:19:ASN:HB2	1:A:147:ASP:OD1	2.08	0.53
1:B:197:PRO:HD2	1:B:208:ASP:O	2.10	0.52
1:A:321:SER:HB2	4:A:479:HOH:O	2.08	0.52
1:B:289:LEU:HD23	1:B:294:LYS:HA	1.92	0.52
1:B:140:SER:HB3	4:B:597:HOH:O	2.10	0.51
1:B:4:LYS:C	1:B:5:ILE:HG12	2.36	0.50
1:A:193:SER:HB3	1:A:213:LYS:HE3	1.94	0.50
1:B:78[B]:LYS:CE	1:B:81:GLY:H	2.24	0.50
1:A:289:LEU:HD23	1:A:294:LYS:HA	1.93	0.50
1:A:78:LYS:HE3	1:A:83:ASP:OD1	2.12	0.49
1:A:156:GLU:HB3	1:A:327:LYS:NZ	2.27	0.49
1:A:201:GLN:H	1:A:201:GLN:CD	2.21	0.49
1:B:24:THR:HB	4:B:522:HOH:O	2.13	0.48
1:A:130:THR:HG23	1:B:127:ASN:HB2	1.95	0.48
1:A:254:ASP:OD1	1:A:254:ASP:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:HIS:O	1:A:292[B]:GLU:HB2	2.13	0.47
1:A:270:PHE:HB2	1:A:333:ILE:HB	1.96	0.47
1:A:52:LYS:HB2	4:A:491:HOH:O	2.15	0.46
1:A:212:ILE:HD12	1:A:217:LEU:O	2.14	0.46
1:B:158:ILE:CD1	1:B:327:LYS:HA	2.46	0.46
1:A:221:GLN:O	1:A:222:GLU:C	2.55	0.46
1:B:60:TYR:N	1:B:61:PRO:CD	2.78	0.46
1:B:107:TRP:CH2	1:B:139[A]:MET:CE	2.99	0.46
1:A:33:ARG:HB2	1:A:63:ALA:HA	1.98	0.46
1:B:157:ALA:C	1:B:158:ILE:HG12	2.41	0.45
1:A:219:PHE:CD2	1:A:223:LYS:HG2	2.52	0.45
1:B:251:LEU:N	1:B:251:LEU:HD23	2.32	0.45
1:B:277:VAL:HB	1:B:304:GLU:HB2	1.98	0.44
1:A:280:THR:O	1:A:298:HIS:HA	2.18	0.44
1:A:71:ARG:HD2	4:A:416:HOH:O	2.17	0.44
1:A:36:ASP:OD1	1:A:43:HIS:ND1	2.50	0.43
1:A:178:ASP:OD2	1:A:293:LYS:HE2	2.17	0.43
1:A:277:VAL:HB	1:A:304:GLU:HB2	2.00	0.43
1:A:4[A]:LYS:HB3	1:A:4[A]:LYS:HE3	1.74	0.43
1:B:314:ILE:HA	1:B:315:PRO:HD2	1.74	0.43
1:A:76:LEU:HD23	1:A:77:VAL:N	2.34	0.42
1:A:156:GLU:HA	1:A:328:TYR:O	2.18	0.42
1:B:2:SER:N	4:B:444:HOH:O	2.53	0.42
1:A:285:ASP:O	1:A:286:LEU:C	2.62	0.42
1:A:158:ILE:HD11	1:A:327:LYS:HB2	2.01	0.41
1:A:201:GLN:NE2	1:A:201:GLN:N	2.58	0.41
1:B:74:ASP:HA	1:B:92:PRO:O	2.20	0.41
1:B:282:ASN:HA	1:B:297:HIS:CE1	2.55	0.41
1:A:60:TYR:N	1:A:61:PRO:CD	2.83	0.41
1:B:19:ASN:HB2	1:B:147:ASP:OD1	2.20	0.41
1:A:31:GLY:O	1:A:32:ALA:C	2.64	0.41
1:A:180:SER:O	1:A:296:VAL:HG11	2.21	0.40
1:B:78[A]:LYS:HD2	1:B:83:ASP:OD1	2.21	0.40
1:A:287:GLY:O	1:A:288:THR:C	2.60	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	342/347 (99%)	321 (94%)	21 (6%)	0	100	100
1	B	349/347 (101%)	332 (95%)	17 (5%)	0	100	100
All	All	691/694 (100%)	653 (94%)	38 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	297/300 (99%)	279 (94%)	18 (6%)	17	6
1	B	304/300 (101%)	286 (94%)	18 (6%)	18	7
All	All	601/600 (100%)	565 (94%)	36 (6%)	19	7

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4[A]	LYS
1	A	4[B]	LYS
1	A	20	LYS
1	A	33	ARG
1	A	39	LYS
1	A	42	LYS
1	A	52	LYS
1	A	78	LYS

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Mol	Chain	Res	Type
1	A	158	ILE
1	A	195	PHE
1	A	201	GLN
1	A	221	GLN
1	A	224	GLN
1	A	266	SER
1	A	294	LYS
1	A	323	LYS
1	A	326	GLU
1	A	340	LEU
1	B	5	ILE
1	B	20	LYS
1	B	52	LYS
1	B	78[A]	LYS
1	B	78[B]	LYS
1	B	82	LYS
1	B	139[A]	MET
1	B	139[B]	MET
1	B	189	ARG
1	B	195	PHE
1	B	201	GLN
1	B	212	ILE
1	B	213	LYS
1	B	234	GLU
1	B	240	LYS
1	B	294	LYS
1	B	323	LYS
1	B	338	THR

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

Mol	Chain	Res	Type
1	A	38	GLN
1	A	201	GLN
1	A	227	ASN
1	B	38	GLN
1	B	224	GLN
1	B	227	ASN
1	B	295	GLN
1	B	306	GLN
1	B	344	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	FUC	B	348[A]	-	11,11,11	0.69	0	16,16,16	1.25	2 (12%)
2	FUC	A	348[B]	-	11,11,11	0.50	0	16,16,16	1.08	1 (6%)
2	FUC	B	348[B]	-	11,11,11	0.63	0	16,16,16	1.25	2 (12%)
2	FUC	A	348[A]	-	11,11,11	0.48	0	16,16,16	1.07	1 (6%)

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	FUC	B	348[A]	-	5/5/5/5	-	0/1/1/1
2	FUC	A	348[B]	-	5/5/5/5	-	0/1/1/1
2	FUC	B	348[B]	-	5/5/5/5	-	0/1/1/1
2	FUC	A	348[A]	-	5/5/5/5	-	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	348[A]	FUC	C4-C3-C2	-2.64	106.19	110.83
2	B	348[B]	FUC	C4-C3-C2	-2.64	106.19	110.83
2	A	348[A]	FUC	O2-C2-C1	2.17	114.25	109.25
2	A	348[B]	FUC	O2-C2-C1	2.17	114.25	109.25
2	B	348[A]	FUC	C3-C4-C5	-2.15	106.54	109.81
2	B	348[B]	FUC	C3-C4-C5	-2.15	106.54	109.81

All (20) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	348[A]	FUC	C5
2	A	348[A]	FUC	C4
2	A	348[A]	FUC	C2
2	A	348[A]	FUC	C3
2	A	348[A]	FUC	C1
2	A	348[B]	FUC	C5
2	A	348[B]	FUC	C4
2	A	348[B]	FUC	C2
2	A	348[B]	FUC	C3
2	A	348[B]	FUC	C1
2	B	348[A]	FUC	C5
2	B	348[A]	FUC	C4
2	B	348[A]	FUC	C2
2	B	348[A]	FUC	C3
2	B	348[A]	FUC	C1
2	B	348[B]	FUC	C5
2	B	348[B]	FUC	C4
2	B	348[B]	FUC	C2
2	B	348[B]	FUC	C3
2	B	348[B]	FUC	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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 [i](#)

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

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	339/347 (97%)	-0.52	1 (0%) 90 90	11, 23, 54, 92	5 (1%)
1	B	346/347 (99%)	-0.71	0 100 100	11, 20, 44, 60	5 (1%)
All	All	685/694 (98%)	-0.62	1 (0%) 92 91	11, 21, 52, 92	10 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	340	LEU	3.1

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](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NA	A	349	1/1	0.92	0.18	28,28,28,28	0
2	FUC	A	348[B]	11/11	0.98	0.04	11,17,22,26	1
2	FUC	B	348[A]	11/11	0.98	0.04	7,18,22,26	1
2	FUC	B	348[B]	11/11	0.98	0.04	15,19,24,26	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FUC	A	348[A]	11/11	0.98	0.04	11,18,22,26	1

6.5 Other polymers [i](#)

There are no such residues in this entry.