



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:02 PM GMT

PDB ID : 4UO2
Title : Structure of the A_Equine_Richmond_07 H3 haemagglutinin in complex with Sialyl Lewis X
Authors : Vachieri, S.G.; Collins, P.J.; Haire, L.F.; Ogrodowicz, R.W.; Martin, S.R.; Walker, P.A.; Xiong, X.; Gamblin, S.J.; Skehel, J.J.
Deposited on : 2014-05-31
Resolution : 2.70 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

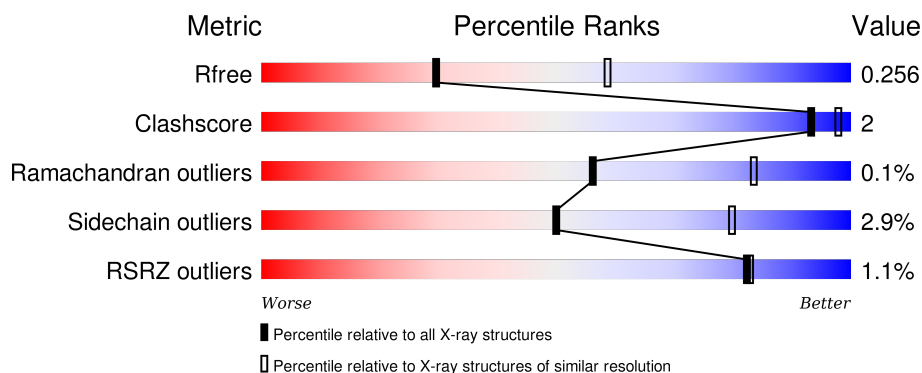
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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. 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	329	<div> <div></div> <div>91% 7% .</div> </div>
1	C	329	<div> <div></div> <div>89% 8% .</div> </div>
1	E	329	<div> <div>3%</div> <div>90% 9% .</div> </div>
2	B	172	<div> <div></div> <div>95% 5%</div> </div>
2	D	172	<div> <div></div> <div>94% 6% .</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	172	

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
10	NAG	C	422	-	-	-	X
11	FUC	D	200	X	-	-	-
11	NAG	D	201	-	-	-	X
11	FUC	F	200	X	-	-	X
3	NAG	A	621	X	-	-	-
6	FUC	A	600	X	-	-	-
8	FUC	E	704	X	-	-	-
9	FUC	B	200	X	-	-	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 12916 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 H3 HAEMAGGLUTININ HA1 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	0	0
			2529	1581	446	487	15			
1	C	320	Total	C	N	O	S	0	0	0
			2493	1558	441	479	15			
1	E	325	Total	C	N	O	S	0	0	0
			2530	1580	447	488	15			

- Molecule 2 is a protein called H3 HAEMAGGLUTININ HA2 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1399	873	242	278	6			
2	D	171	Total	C	N	O	S	0	0	0
			1394	869	243	276	6			
2	F	172	Total	C	N	O	S	0	0	0
			1403	874	245	278	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	5	Total	C	N	O	0	0
			61	34	2	25		
4	C	5	Total	C	N	O	0	0
			61	34	2	25		
4	E	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		
5	C	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	2	Total	C	N	O	0	0
			28	16	2	10		
5	E	2	Total	C	N	O	0	0
			28	16	2	10		
5	E	2	Total	C	N	O	0	0
			28	16	2	10		
5	E	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 7 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	3	Total	C	N	O	0	0
			39	22	2	15		
7	C	3	Total	C	N	O	0	0
			39	22	2	15		
7	C	3	Total	C	N	O	0	0
			39	22	2	15		
7	C	3	Total	C	N	O	0	0
			39	22	2	15		
7	E	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	4	Total	C	N	O	0	0
			56	31	2	23		
8	C	4	Total	C	N	O	0	0
			56	31	2	23		
8	E	4	Total	C	N	O	0	0
			56	31	2	23		

- Molecule 9 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 10 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	C	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 11 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	D	3	Total	C	N	O	0	0
			38	22	2	14		
11	F	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	50	Total	O	0	0
			50	50		
12	B	29	Total	O	0	0
			29	29		
12	C	46	Total	O	0	0
			46	46		
12	D	27	Total	O	0	0
			27	27		
12	E	28	Total	O	0	0
			28	28		
12	F	19	Total	O	0	0
			19	19		

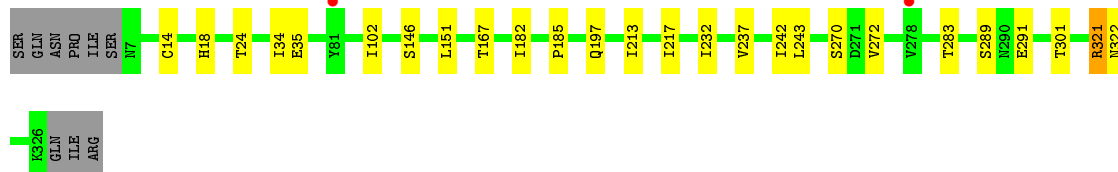
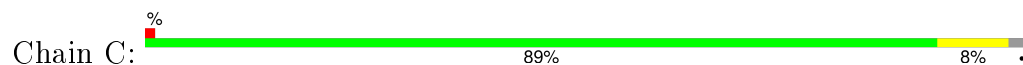
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

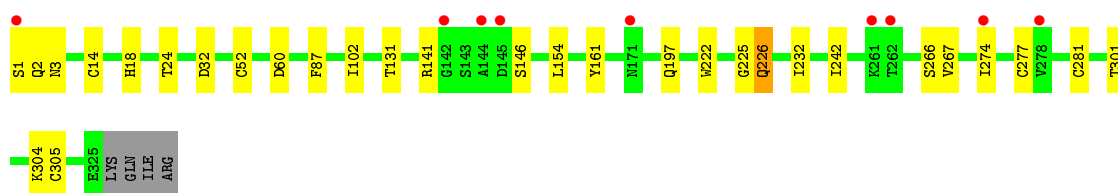
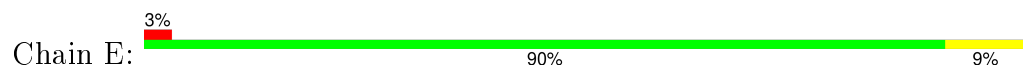
- Molecule 1: H3 HAEMAGGLUTININ HA1 CHAIN



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- Molecule 1: H3 HAEMAGGLUTININ HA1 CHAIN

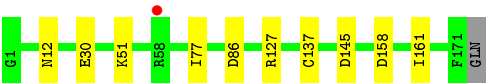


- Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN

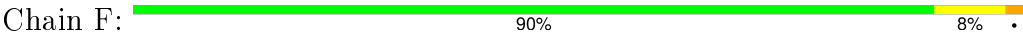


- Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN





● Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.30Å 129.79Å 193.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	107.81 – 2.70 48.41 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (107.81-2.70) 98.8 (48.41-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.198 , 0.256 0.197 , 0.256	Depositor DCC
R_{free} test set	2789 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	47.4	Xtriage
Anisotropy	0.672	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 34.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 55072 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12916	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BMA, NAG, SIA, GAL, FUC, 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	0.32	0/2583	0.51	0/3507
1	C	0.32	0/2546	0.51	0/3456
1	E	0.32	0/2584	0.51	0/3509
2	B	0.35	0/1424	0.51	0/1915
2	D	0.36	0/1419	0.50	0/1908
2	F	0.35	0/1428	0.52	0/1920
All	All	0.33	0/11984	0.51	0/16215

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	A	1	0
8	E	1	0
9	B	1	0
11	D	1	0
11	F	1	0
All	All	5	0

There are no bond length outliers.

There are no bond angle outliers.

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	600	FUC	C1
9	B	200	FUC	C1
11	D	200	FUC	C1
8	E	704	FUC	C5

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Mol	Chain	Res	Type	Atom
11	F	200	FUC	C1

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	2529	0	2472	10	0
1	C	2493	0	2436	13	0
1	E	2530	0	2471	12	0
2	B	1399	0	1317	3	0
2	D	1394	0	1316	3	0
2	F	1403	0	1324	8	0
3	A	42	0	39	0	0
3	E	14	0	13	0	0
4	A	61	0	52	0	0
4	C	61	0	52	0	0
4	E	61	0	52	0	0
5	A	28	0	25	0	0
5	C	28	0	25	0	0
5	E	112	0	100	1	0
6	A	49	0	43	0	0
7	A	39	0	34	0	0
7	C	117	0	102	0	0
7	E	39	0	34	0	0
8	A	56	0	49	0	0
8	C	56	0	49	0	0
8	E	56	0	49	0	0
9	B	24	0	22	0	0
10	C	50	0	43	0	0
11	D	38	0	34	0	0
11	F	38	0	34	0	0
12	A	50	0	0	0	0
12	B	29	0	0	0	0
12	C	46	0	0	0	0
12	D	27	0	0	0	0
12	E	28	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	F	19	0	0	1	0
All	All	12916	0	12187	48	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 2.

All (48) 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:C:289:SER:OG	1:C:291:GLU:HG2	1.91	0.70
1:C:102:ILE:HG12	1:C:232:ILE:HB	1.74	0.68
1:E:226:GLN:HE21	1:E:226:GLN:HA	1.58	0.68
1:A:203:THR:HG23	1:A:212:THR:HG22	1.85	0.58
1:C:237:VAL:HG21	1:C:243:LEU:HB2	1.85	0.57
2:F:43:THR:HG22	2:F:47:GLN:HE21	1.72	0.55
1:C:34:ILE:HD11	1:C:321:ARG:HD2	1.87	0.55
2:F:144:CYS:HG	2:F:148:CYS:HG	1.52	0.54
1:A:175:ASP:OD1	1:A:239:PRO:HD3	2.08	0.53
1:C:167:THR:OG1	1:C:242:ILE:HD11	2.09	0.52
1:C:289:SER:HG	1:C:291:GLU:HG2	1.75	0.51
1:A:283:THR:HG22	1:A:301:THR:HG22	1.91	0.51
1:A:180:TRP:HB3	1:A:254:PRO:HG3	1.93	0.51
1:C:35:GLU:HG2	1:C:322:ASN:HB3	1.94	0.50
2:F:53:ASN:N	2:F:53:ASN:HD22	2.10	0.50
1:E:102:ILE:HG12	1:E:232:ILE:HB	1.95	0.49
1:C:34:ILE:HD11	1:C:321:ARG:CD	2.44	0.48
1:A:15:LEU:HD22	2:B:119:PHE:HA	1.96	0.48
1:E:301:THR:HB	1:E:305:CYS:SG	2.55	0.47
1:E:161:TYR:HB3	1:E:197:GLN:HE22	1.80	0.47
1:C:283:THR:HG22	1:C:301:THR:HG22	1.97	0.46
2:B:19:ASP:N	2:B:19:ASP:OD1	2.49	0.46
1:C:182:ILE:HD13	1:C:213:ILE:HG22	1.97	0.46
2:D:158:ASP:HB3	2:D:161:ILE:HD12	1.99	0.44
2:D:30:GLU:OE2	2:D:145:ASP:HB2	2.18	0.44
1:A:301:THR:HB	1:A:305:CYS:SG	2.58	0.44
5:E:442:NAG:H83	5:E:442:NAG:H3	2.00	0.44
2:F:163:ARG:HG2	2:F:167:LEU:HD22	1.99	0.44
1:E:52:CYS:HB3	1:E:277:CYS:O	2.18	0.43
1:E:60:ASP:HB2	1:E:274:ILE:HD12	2.01	0.43
1:E:1:SER:N	1:E:2:GLN:HA	2.34	0.43
1:E:281:CYS:HB2	1:E:304:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:11:GLU:HB2	12:F:2002:HOH:O	2.19	0.42
2:B:9:PHE:O	2:B:135:GLY:HA2	2.19	0.42
2:F:78:GLN:HA	2:F:81:GLU:OE1	2.19	0.42
1:C:14:CYS:HA	2:D:137:CYS:HA	2.02	0.42
1:A:208:ARG:O	1:A:209:SER:HB3	2.18	0.42
1:A:281:CYS:HB2	1:A:304:LYS:O	2.20	0.42
1:E:87:PHE:HB3	1:E:267:VAL:HG23	2.01	0.42
1:A:152:ASN:HB3	1:A:253:ALA:HB3	2.00	0.42
1:C:270:SER:OG	1:C:272:VAL:HG22	2.19	0.42
2:F:144:CYS:SG	2:F:148:CYS:SG	3.11	0.42
1:E:222:TRP:CE2	1:E:225:GLY:HA2	2.56	0.41
1:E:141:ARG:HB3	1:E:146:SER:CB	2.49	0.41
1:C:185:PRO:HG2	1:C:217:ILE:HG12	2.02	0.40
1:A:272:VAL:HA	1:A:273:PRO:HD3	1.87	0.40
1:E:14:CYS:HB3	12:E:2001:HOH:O	2.21	0.40
2:F:129:ASN:HA	2:F:166:ALA:HB1	2.04	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	323/329 (98%)	304 (94%)	18 (6%)	1 (0%)	46	75
1	C	318/329 (97%)	304 (96%)	14 (4%)	0	100	100
1	E	323/329 (98%)	310 (96%)	12 (4%)	1 (0%)	46	75
2	B	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
2	D	169/172 (98%)	159 (94%)	10 (6%)	0	100	100
2	F	170/172 (99%)	156 (92%)	14 (8%)	0	100	100
All	All	1473/1503 (98%)	1394 (95%)	77 (5%)	2 (0%)	56	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	SER
1	E	3	ASN

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	287/292 (98%)	280 (98%)	7 (2%)	57	85
1	C	282/292 (97%)	276 (98%)	6 (2%)	61	87
1	E	287/292 (98%)	279 (97%)	8 (3%)	51	81
2	B	145/146 (99%)	141 (97%)	4 (3%)	51	81
2	D	145/146 (99%)	140 (97%)	5 (3%)	44	75
2	F	146/146 (100%)	138 (94%)	8 (6%)	27	55
All	All	1292/1314 (98%)	1254 (97%)	38 (3%)	50	80

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	24	THR
1	A	40	THR
1	A	47	SER
1	A	146	SER
1	A	264	LYS
1	A	326	LYS
2	B	12	ASN
2	B	86	ASP
2	B	110	LEU
2	B	168	ASN
1	C	18	HIS
1	C	24	THR
1	C	146	SER
1	C	151	LEU

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Mol	Chain	Res	Type
1	C	197	GLN
1	C	321	ARG
2	D	12	ASN
2	D	51	LYS
2	D	77	ILE
2	D	86	ASP
2	D	127	ARG
1	E	18	HIS
1	E	24	THR
1	E	32	ASP
1	E	131	THR
1	E	154	LEU
1	E	226	GLN
1	E	242	ILE
1	E	266	SER
2	F	11	GLU
2	F	12	ASN
2	F	53	ASN
2	F	55	VAL
2	F	60	ASN
2	F	86	ASP
2	F	110	LEU
2	F	167	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	188	ASN
2	B	47	GLN
2	B	168	ASN
1	C	248	ASN
2	D	12	ASN
1	E	3	ASN
1	E	18	HIS
1	E	159	ASN
1	E	197	GLN
1	E	226	GLN
2	F	12	ASN
2	F	47	GLN
2	F	53	ASN
2	F	65	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 ⓘ

70 carbohydrates 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	A	431	1,4	14,14,15	0.52	0	15,19,21	0.61	0
4	NAG	A	432	4	14,14,15	0.47	0	15,19,21	0.86	0
4	BMA	A	433	4	11,11,12	0.68	0	14,15,17	1.98	2 (14%)
4	MAN	A	434	4	11,11,12	0.53	0	14,15,17	1.21	2 (14%)
4	MAN	A	437	4	11,11,12	0.61	0	14,15,17	1.25	1 (7%)
5	NAG	A	441	1,5	14,14,15	0.47	0	15,19,21	1.55	2 (13%)
5	NAG	A	442	5	14,14,15	0.60	0	15,19,21	1.27	2 (13%)
6	FUC	A	600	6	10,10,11	0.64	0	14,14,16	0.95	1 (7%)
6	NAG	A	601	1,6	14,14,15	0.61	0	15,19,21	1.15	2 (13%)
6	NAG	A	602	6	14,14,15	0.46	0	15,19,21	0.56	0
6	BMA	A	603	6	11,11,12	0.47	0	14,15,17	0.83	1 (7%)
7	NAG	A	631	1,7	14,14,15	0.49	0	15,19,21	0.84	0
7	NAG	A	632	7	14,14,15	0.50	0	15,19,21	1.14	1 (6%)
7	BMA	A	633	7	11,11,12	0.54	0	14,15,17	0.67	0
8	SIA	A	701	8	16,20,21	0.28	0	18,28,31	1.14	2 (11%)
8	GAL	A	702	8	11,11,12	0.60	0	14,15,17	1.10	1 (7%)
8	NAG	A	703	8	15,15,15	0.50	0	17,21,21	1.62	3 (17%)
8	FUC	A	704	8	10,10,11	0.61	0	14,14,16	1.00	1 (7%)
9	FUC	B	200	9	10,10,11	0.70	0	14,14,16	1.11	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	B	201	9,2	14,14,15	0.53	0	15,19,21	1.06	0
7	NAG	C	411	1,7	14,14,15	0.53	0	15,19,21	0.98	0
7	NAG	C	412	7	14,14,15	0.50	0	15,19,21	1.07	2 (13%)
7	BMA	C	413	7	11,11,12	0.46	0	14,15,17	1.18	2 (14%)
10	NAG	C	421	1,10	14,14,15	0.60	0	15,19,21	1.61	3 (20%)
10	NAG	C	422	10	14,14,15	0.66	0	15,19,21	1.40	2 (13%)
10	BMA	C	423	10	11,11,12	0.42	0	14,15,17	2.01	3 (21%)
10	MAN	C	424	10	11,11,12	0.66	0	14,15,17	1.12	2 (14%)
4	NAG	C	431	1,4	14,14,15	0.52	0	15,19,21	0.66	0
4	NAG	C	432	4	14,14,15	0.50	0	15,19,21	0.63	0
4	BMA	C	433	4	11,11,12	0.54	0	14,15,17	1.56	2 (14%)
4	MAN	C	434	4	11,11,12	0.59	0	14,15,17	1.02	1 (7%)
4	MAN	C	437	4	11,11,12	0.58	0	14,15,17	0.98	1 (7%)
5	NAG	C	441	1,5	14,14,15	0.46	0	15,19,21	1.03	0
5	NAG	C	442	5	14,14,15	0.54	0	15,19,21	0.99	0
7	NAG	C	621	1,7	14,14,15	0.49	0	15,19,21	0.86	1 (6%)
7	NAG	C	622	7	14,14,15	0.52	0	15,19,21	1.06	1 (6%)
7	BMA	C	623	7	11,11,12	0.56	0	14,15,17	1.67	3 (21%)
7	NAG	C	631	1,7	14,14,15	0.57	0	15,19,21	1.69	2 (13%)
7	NAG	C	632	7	14,14,15	0.57	0	15,19,21	0.92	1 (6%)
7	BMA	C	633	7	11,11,12	0.60	0	14,15,17	0.95	1 (7%)
8	SIA	C	701	8	16,20,21	0.32	0	18,28,31	1.08	2 (11%)
8	GAL	C	702	8	11,11,12	0.59	0	14,15,17	0.81	0
8	NAG	C	703	8	15,15,15	0.44	0	17,21,21	0.66	0
8	FUC	C	704	8	10,10,11	0.57	0	14,14,16	0.99	1 (7%)
11	FUC	D	200	11	10,10,11	0.61	0	14,14,16	1.21	2 (14%)
11	NAG	D	201	11,2	14,14,15	0.51	0	15,19,21	1.37	3 (20%)
11	NAG	D	202	11	14,14,15	0.49	0	15,19,21	1.06	1 (6%)
5	NAG	E	411	1,5	14,14,15	0.54	0	15,19,21	2.07	2 (13%)
5	NAG	E	412	5	14,14,15	0.49	0	15,19,21	0.87	0
5	NAG	E	421	1,5	14,14,15	0.33	0	15,19,21	2.14	1 (6%)
5	NAG	E	422	5	14,14,15	0.52	0	15,19,21	1.00	1 (6%)
4	NAG	E	431	1,4	14,14,15	0.50	0	15,19,21	0.74	0
4	NAG	E	432	4	14,14,15	0.46	0	15,19,21	0.92	1 (6%)
4	BMA	E	433	4	11,11,12	0.49	0	14,15,17	1.36	1 (7%)
4	MAN	E	434	4	11,11,12	0.63	0	14,15,17	1.49	2 (14%)
4	MAN	E	437	4	11,11,12	0.65	0	14,15,17	1.07	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	E	441	1,5	14,14,15	0.42	0	15,19,21	1.42	2 (13%)
5	NAG	E	442	5	14,14,15	0.68	0	15,19,21	2.26	4 (26%)
5	NAG	E	601	1,5	14,14,15	0.45	0	15,19,21	1.33	1 (6%)
5	NAG	E	602	5	14,14,15	0.43	0	15,19,21	0.76	0
7	NAG	E	631	1,7	14,14,15	0.73	0	15,19,21	1.42	1 (6%)
7	NAG	E	632	7	14,14,15	0.55	0	15,19,21	1.95	3 (20%)
7	BMA	E	633	7	11,11,12	0.41	0	14,15,17	0.78	1 (7%)
8	SIA	E	701	8	16,20,21	0.51	0	18,28,31	1.37	3 (16%)
8	GAL	E	702	8	11,11,12	0.65	0	14,15,17	1.21	1 (7%)
8	NAG	E	703	8	15,15,15	0.49	0	17,21,21	1.18	1 (5%)
8	FUC	E	704	8	10,10,11	0.70	0	14,14,16	0.90	0
11	FUC	F	200	11	10,10,11	0.66	0	14,14,16	0.99	0
11	NAG	F	201	11,2	14,14,15	0.48	0	15,19,21	1.03	0
11	NAG	F	202	11	14,14,15	0.40	0	15,19,21	2.17	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	A	431	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	432	4	-	0/6/23/26	0/1/1/1
4	BMA	A	433	4	-	0/2/19/22	0/1/1/1
4	MAN	A	434	4	-	0/2/19/22	0/1/1/1
4	MAN	A	437	4	-	0/2/19/22	0/1/1/1
5	NAG	A	441	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	442	5	-	0/6/23/26	0/1/1/1
6	FUC	A	600	6	1/1/4/5	0/0/17/20	0/1/1/1
6	NAG	A	601	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	602	6	-	0/6/23/26	0/1/1/1
6	BMA	A	603	6	-	0/2/19/22	0/1/1/1
7	NAG	A	631	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	632	7	-	0/6/23/26	0/1/1/1
7	BMA	A	633	7	-	0/2/19/22	0/1/1/1
8	SIA	A	701	8	-	0/14/34/38	0/1/1/1
8	GAL	A	702	8	-	0/2/19/22	0/1/1/1
8	NAG	A	703	8	-	0/6/26/26	0/1/1/1
8	FUC	A	704	8	-	0/0/17/20	0/1/1/1
9	FUC	B	200	9	1/1/4/5	0/0/17/20	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	B	201	9,2	-	0/6/23/26	0/1/1/1
7	NAG	C	411	1,7	-	0/6/23/26	0/1/1/1
7	NAG	C	412	7	-	0/6/23/26	0/1/1/1
7	BMA	C	413	7	-	0/2/19/22	0/1/1/1
10	NAG	C	421	1,10	-	0/6/23/26	0/1/1/1
10	NAG	C	422	10	-	0/6/23/26	0/1/1/1
10	BMA	C	423	10	-	0/2/19/22	0/1/1/1
10	MAN	C	424	10	-	0/2/19/22	0/1/1/1
4	NAG	C	431	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	432	4	-	0/6/23/26	0/1/1/1
4	BMA	C	433	4	-	0/2/19/22	0/1/1/1
4	MAN	C	434	4	-	0/2/19/22	0/1/1/1
4	MAN	C	437	4	-	0/2/19/22	0/1/1/1
5	NAG	C	441	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	442	5	-	0/6/23/26	0/1/1/1
7	NAG	C	621	1,7	-	0/6/23/26	0/1/1/1
7	NAG	C	622	7	-	0/6/23/26	0/1/1/1
7	BMA	C	623	7	-	0/2/19/22	0/1/1/1
7	NAG	C	631	1,7	-	0/6/23/26	0/1/1/1
7	NAG	C	632	7	-	0/6/23/26	0/1/1/1
7	BMA	C	633	7	-	0/2/19/22	0/1/1/1
8	SIA	C	701	8	-	0/14/34/38	0/1/1/1
8	GAL	C	702	8	-	0/2/19/22	0/1/1/1
8	NAG	C	703	8	-	0/6/26/26	0/1/1/1
8	FUC	C	704	8	-	0/0/17/20	0/1/1/1
11	FUC	D	200	11	1/1/4/5	0/0/17/20	0/1/1/1
11	NAG	D	201	11,2	-	0/6/23/26	0/1/1/1
11	NAG	D	202	11	-	0/6/23/26	0/1/1/1
5	NAG	E	411	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	412	5	-	0/6/23/26	0/1/1/1
5	NAG	E	421	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	422	5	-	0/6/23/26	0/1/1/1
4	NAG	E	431	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	432	4	-	0/6/23/26	0/1/1/1
4	BMA	E	433	4	-	0/2/19/22	0/1/1/1
4	MAN	E	434	4	-	0/2/19/22	0/1/1/1
4	MAN	E	437	4	-	0/2/19/22	0/1/1/1
5	NAG	E	441	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	442	5	-	0/6/23/26	0/1/1/1
5	NAG	E	601	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	602	5	-	0/6/23/26	0/1/1/1
7	NAG	E	631	1,7	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	E	632	7	-	0/6/23/26	0/1/1/1
7	BMA	E	633	7	-	0/2/19/22	0/1/1/1
8	SIA	E	701	8	-	0/14/34/38	0/1/1/1
8	GAL	E	702	8	-	0/2/19/22	0/1/1/1
8	NAG	E	703	8	-	0/6/26/26	0/1/1/1
8	FUC	E	704	8	1/1/4/5	0/0/17/20	0/1/1/1
11	FUC	F	200	11	1/1/4/5	0/0/17/20	0/1/1/1
11	NAG	F	201	11,2	-	0/6/23/26	0/1/1/1
11	NAG	F	202	11	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (86) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	441	NAG	C3-C4-C5	-3.24	104.55	110.20
5	A	441	NAG	C4-C3-C2	-2.87	106.78	111.23
11	D	200	FUC	C1-C2-C3	-2.58	106.49	109.54
5	E	442	NAG	O7-C7-C8	-2.48	117.50	122.06
8	E	701	SIA	C7-C6-C5	-2.46	110.59	114.32
4	C	437	MAN	O5-C1-C2	-2.25	107.20	110.86
8	A	701	SIA	C7-C6-C5	-2.15	111.06	114.32
8	C	701	SIA	C7-C6-C5	-2.06	111.20	114.32
8	E	701	SIA	C6-C5-N5	-2.04	107.51	111.07
5	E	441	NAG	C4-C3-C2	-2.00	108.12	111.23
5	E	422	NAG	C4-C3-C2	2.01	114.35	111.23
5	E	442	NAG	C4-C3-C2	2.01	114.35	111.23
4	A	434	MAN	C3-C4-C5	2.01	113.71	110.20
7	E	632	NAG	C4-C3-C2	2.02	114.37	111.23
7	C	413	BMA	C1-O5-C5	2.04	114.83	112.25
7	C	412	NAG	C4-C3-C2	2.06	114.43	111.23
4	E	434	MAN	C3-C4-C5	2.07	113.80	110.20
5	E	411	NAG	C2-N2-C7	2.07	125.70	123.04
11	D	201	NAG	O6-C6-C5	2.07	118.18	111.33
7	C	412	NAG	C1-O5-C5	2.08	114.89	112.25
10	C	421	NAG	C3-C4-C5	2.09	113.85	110.20
8	A	703	NAG	C1-O5-C5	2.15	117.45	113.47
6	A	603	BMA	C1-C2-C3	2.16	112.10	109.54
6	A	601	NAG	O6-C6-C5	2.18	118.54	111.33
10	C	424	MAN	C3-C4-C5	2.19	114.01	110.20
8	C	701	SIA	O6-C6-C5	2.21	112.10	108.48
10	C	424	MAN	C1-C2-C3	2.22	112.17	109.54
7	C	632	NAG	C4-C3-C2	2.22	114.68	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	702	GAL	C1-C2-C3	2.28	112.24	109.54
6	A	601	NAG	C6-C5-C4	2.29	118.66	113.02
7	C	623	BMA	C1-C2-C3	2.32	112.29	109.54
7	E	633	BMA	C1-O5-C5	2.32	115.20	112.25
7	C	623	BMA	O5-C5-C6	2.32	112.38	107.35
8	A	701	SIA	O6-C6-C5	2.37	112.36	108.48
4	E	432	NAG	C1-O5-C5	2.39	115.28	112.25
4	C	433	BMA	C2-C3-C4	2.39	115.11	111.04
7	C	621	NAG	C1-O5-C5	2.44	115.34	112.25
10	C	423	BMA	C3-C4-C5	2.46	114.49	110.20
9	B	200	FUC	C3-C4-C5	2.51	113.95	109.72
7	C	633	BMA	C1-C2-C3	2.55	112.56	109.54
6	A	600	FUC	O5-C5-C6	2.66	110.53	106.13
11	F	202	NAG	C3-C4-C5	2.68	114.87	110.20
5	A	442	NAG	C3-C4-C5	2.70	114.90	110.20
4	C	434	MAN	C1-O5-C5	2.70	115.67	112.25
7	C	413	BMA	C1-C2-C3	2.71	112.75	109.54
7	C	631	NAG	C3-C4-C5	2.75	114.98	110.20
10	C	423	BMA	C1-C2-C3	2.76	112.81	109.54
11	D	201	NAG	O5-C5-C6	2.77	113.34	107.35
5	A	442	NAG	C4-C3-C2	2.80	115.59	111.23
8	C	704	FUC	O5-C5-C6	2.83	110.81	106.13
8	A	704	FUC	C1-O5-C5	2.84	116.77	112.38
11	D	202	NAG	C1-O5-C5	2.86	115.88	112.25
7	A	632	NAG	C4-C3-C2	2.92	115.77	111.23
11	D	201	NAG	C1-O5-C5	2.96	116.01	112.25
11	D	200	FUC	O5-C5-C6	3.06	111.19	106.13
10	C	422	NAG	C3-C4-C5	3.06	115.54	110.20
4	E	437	MAN	C3-C4-C5	3.10	115.59	110.20
5	E	442	NAG	C8-C7-N2	3.13	122.09	116.11
7	C	622	NAG	C1-O5-C5	3.21	116.33	112.25
4	A	433	BMA	C2-C3-C4	3.26	116.59	111.04
4	A	434	MAN	C1-O5-C5	3.36	116.51	112.25
4	E	433	BMA	C1-C2-C3	3.38	113.54	109.54
4	A	437	MAN	C1-O5-C5	3.46	116.64	112.25
10	C	421	NAG	C4-C3-C2	3.49	116.66	111.23
10	C	421	NAG	C1-O5-C5	3.49	116.68	112.25
10	C	422	NAG	C4-C3-C2	3.49	116.66	111.23
5	E	601	NAG	C1-O5-C5	3.58	116.80	112.25
8	E	703	NAG	C4-C3-C2	3.64	115.48	110.43
8	E	702	GAL	C1-C2-C3	3.77	114.00	109.54
8	A	703	NAG	O5-C5-C4	3.83	116.86	109.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	632	NAG	O4-C4-C5	3.91	119.61	109.24
8	E	701	SIA	O6-C6-C5	3.99	115.02	108.48
4	C	433	BMA	C1-C2-C3	4.02	114.29	109.54
7	E	631	NAG	C4-C3-C2	4.10	117.61	111.23
8	A	703	NAG	C3-C4-C5	4.17	117.46	110.20
4	E	434	MAN	C1-C2-C3	4.19	114.50	109.54
5	E	441	NAG	C1-O5-C5	4.22	117.60	112.25
7	C	631	NAG	C1-O5-C5	4.45	117.89	112.25
7	C	623	BMA	C1-O5-C5	4.63	118.12	112.25
7	E	632	NAG	C1-O5-C5	5.74	119.54	112.25
10	C	423	BMA	C1-O5-C5	6.04	119.91	112.25
4	A	433	BMA	C1-C2-C3	6.05	116.70	109.54
5	E	411	NAG	C1-O5-C5	6.55	120.56	112.25
5	E	442	NAG	C2-N2-C7	7.07	132.12	123.04
11	F	202	NAG	C1-O5-C5	7.68	121.99	112.25
5	E	421	NAG	C1-O5-C5	7.90	122.28	112.25

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	D	200	FUC	C1
9	B	200	FUC	C1
6	A	600	FUC	C1
11	F	200	FUC	C1
8	E	704	FUC	C5

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	442	NAG	1	0

5.6 Ligand geometry ⓘ

4 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	$\# Z > 2$
3	NAG	A	411	1	14,14,15	0.53	0	15,19,21	1.22	1 (6%)
3	NAG	A	421	1	14,14,15	0.60	0	15,19,21	0.90	0
3	NAG	A	621	1	14,14,15	0.54	0	15,19,21	1.09	0
3	NAG	E	621	1	14,14,15	0.43	0	15,19,21	1.95	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
3	NAG	A	411	1	-	0/6/23/26	0/1/1/1
3	NAG	A	421	1	-	0/6/23/26	0/1/1/1
3	NAG	A	621	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	E	621	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	411	NAG	C2-N2-C7	3.75	127.86	123.04
3	E	621	NAG	C1-O5-C5	6.67	120.72	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	621	NAG	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 ⓘ

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	325/329 (98%)	-0.14	3 (0%) 85 86	33, 54, 83, 97	0
1	C	320/329 (97%)	-0.23	2 (0%) 90 91	34, 52, 73, 95	0
1	E	325/329 (98%)	0.07	9 (2%) 56 57	38, 70, 99, 128	0
2	B	172/172 (100%)	-0.23	1 (0%) 90 91	31, 47, 66, 83	0
2	D	171/172 (99%)	-0.17	1 (0%) 90 91	31, 48, 67, 103	0
2	F	172/172 (100%)	-0.20	0 100 100	31, 47, 72, 107	0
All	All	1485/1503 (98%)	-0.13	16 (1%) 82 83	31, 53, 86, 128	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	81	TYR	4.9
1	A	276	ILE	4.0
1	E	142	GLY	3.3
1	A	278	VAL	2.9
1	E	144	ALA	2.8
2	B	172	GLN	2.7
1	E	274	ILE	2.7
1	A	277	CYS	2.7
1	E	278	VAL	2.5
1	E	1	SER	2.3
1	C	278	VAL	2.3
1	E	262	THR	2.2
1	E	171	ASN	2.2
1	E	261	LYS	2.1
1	E	145	ASP	2.1
2	D	58	ARG	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
10	NAG	C	422	14/15	0.81	0.43	8.14	107,110,115,117	0
11	NAG	D	201	14/15	0.81	0.25	6.03	81,87,94,95	0
11	FUC	F	200	10/11	0.87	0.26	3.63	99,103,105,107	0
7	NAG	C	621	14/15	0.84	0.28	1.39	96,109,120,130	0
4	NAG	A	432	14/15	0.93	0.22	0.75	81,88,95,100	0
8	SIA	C	701	20/21	0.93	0.17	0.59	58,64,73,76	0
8	SIA	E	701	20/21	0.88	0.21	0.42	101,108,113,116	0
8	SIA	A	701	20/21	0.90	0.16	0.39	53,58,69,74	0
6	NAG	A	601	14/15	0.90	0.14	0.33	76,84,96,103	0
7	NAG	C	631	14/15	0.95	0.14	-0.50	59,62,67,75	0
8	NAG	A	703	15/15	0.89	0.16	-0.50	73,80,86,88	0
4	NAG	E	432	14/15	0.94	0.15	-0.52	69,77,81,85	0
7	NAG	C	632	14/15	0.82	0.20	-	82,89,98,98	0
4	BMA	E	433	11/12	0.91	0.12	-	88,93,97,100	0
7	BMA	C	633	11/12	0.74	0.20	-	101,104,109,110	0
7	NAG	C	411	14/15	0.79	0.35	-	95,104,110,116	0
7	BMA	A	633	11/12	0.72	0.40	-	98,112,117,121	0
10	BMA	C	423	11/12	0.66	0.36	-	112,116,119,122	0
8	GAL	E	702	11/12	0.93	0.21	-	111,113,120,121	0
9	FUC	B	200	10/11	0.87	0.39	-	99,106,109,114	0
5	NAG	E	601	14/15	0.69	0.26	-	91,96,99,103	0
5	NAG	E	442	14/15	0.50	0.39	-	111,118,121,126	0
11	NAG	F	202	14/15	0.73	0.38	-	103,113,119,124	0
6	NAG	A	602	14/15	0.88	0.18	-	97,102,111,113	0
7	BMA	C	413	11/12	0.80	0.21	-	121,130,132,137	0
4	NAG	E	431	14/15	0.95	0.12	-	70,72,74,75	0
4	NAG	A	431	14/15	0.93	0.18	-	76,79,83,83	0
5	NAG	C	442	14/15	0.66	0.35	-	113,118,122,123	0
10	MAN	C	424	11/12	0.68	0.57	-	109,113,118,119	0
5	NAG	E	441	14/15	0.86	0.18	-	89,97,102,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
11	NAG	D	202	14/15	0.76	0.40	-	94,102,106,108	0
7	NAG	C	622	14/15	0.76	0.41	-	132,141,150,153	0
7	NAG	A	631	14/15	0.82	0.28	-	74,83,88,92	0
4	NAG	C	432	14/15	0.94	0.17	-	62,70,79,81	0
5	NAG	E	602	14/15	0.76	0.28	-	105,111,115,117	0
8	NAG	E	703	15/15	0.70	0.33	-	123,126,135,136	0
8	GAL	A	702	11/12	0.96	0.11	-	65,67,69,70	0
4	MAN	E	437	11/12	0.82	0.18	-	101,105,109,110	0
8	FUC	A	704	10/11	0.91	0.22	-	84,87,91,92	0
6	FUC	A	600	10/11	0.87	0.37	-	105,111,116,116	0
7	NAG	C	412	14/15	0.81	0.38	-	116,122,125,127	0
4	MAN	C	437	11/12	0.82	0.23	-	106,111,115,116	0
8	FUC	C	704	10/11	0.91	0.23	-	88,89,93,94	0
5	NAG	E	422	14/15	0.60	0.41	-	127,137,143,145	0
11	FUC	D	200	10/11	0.85	0.25	-	96,100,103,105	0
7	NAG	E	632	14/15	0.73	0.33	-	96,104,110,116	0
6	BMA	A	603	11/12	0.74	0.36	-	119,126,132,134	0
4	BMA	C	433	11/12	0.89	0.18	-	87,94,100,104	0
7	NAG	A	632	14/15	0.78	0.45	-	98,104,110,111	0
5	NAG	E	411	14/15	0.79	0.43	-	131,141,146,146	0
4	BMA	A	433	11/12	0.73	0.13	-	104,109,116,116	0
11	NAG	F	201	14/15	0.89	0.25	-	81,94,98,102	0
8	NAG	C	703	15/15	0.90	0.22	-	84,92,101,103	0
4	MAN	C	434	11/12	0.58	0.26	-	97,103,110,112	0
9	NAG	B	201	14/15	0.87	0.28	-	81,90,95,97	0
4	MAN	A	434	11/12	0.72	0.31	-	115,124,135,140	0
5	NAG	E	412	14/15	0.68	0.49	-	147,156,158,162	0
10	NAG	C	421	14/15	0.87	0.25	-	94,102,105,106	0
7	BMA	E	633	11/12	0.80	0.23	-	118,119,126,127	0
4	MAN	A	437	11/12	0.92	0.20	-	111,118,126,132	0
5	NAG	C	441	14/15	0.84	0.18	-	78,87,94,105	0
7	BMA	C	623	11/12	0.77	0.60	-	154,157,158,159	0
4	NAG	C	431	14/15	0.95	0.14	-	60,64,66,66	0
8	GAL	C	702	11/12	0.95	0.08	-	74,75,79,80	0
8	FUC	E	704	10/11	0.78	0.28	-	117,120,122,123	0
5	NAG	A	441	14/15	0.87	0.20	-	76,84,89,97	0
5	NAG	A	442	14/15	0.66	0.36	-	95,107,113,114	0
7	NAG	E	631	14/15	0.91	0.19	-	70,76,81,90	0
5	NAG	E	421	14/15	0.76	0.39	-	111,117,124,128	0
4	MAN	E	434	11/12	0.67	0.26	-	100,104,110,111	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	A	411	14/15	0.84	0.31	-	109,112,117,121	0
3	NAG	E	621	14/15	0.69	0.39	-	89,93,100,103	0
3	NAG	A	621	14/15	0.63	0.30	-	100,104,108,111	0
3	NAG	A	421	14/15	0.79	0.32	-	88,96,98,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.