



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 03:02 PM GMT

PDB ID : 3W3G
Title : Crystal structure of human TLR8 (unliganded form)
Authors : Tanji, H.; Ohto, U.; Shimizu, T.
Deposited on : 2012-12-21
Resolution : 2.30 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

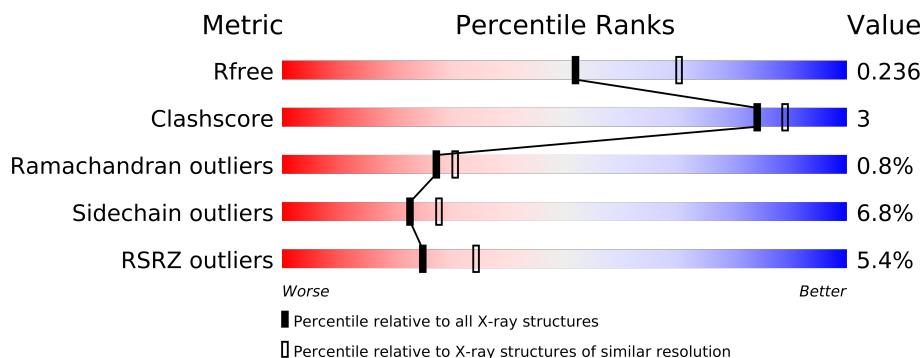
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	811	
1	B	811	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	A	1004	-	X
3	NAG	A	1008	-	X
3	NAG	A	1012	-	X
3	NAG	A	1014	-	X
3	NAG	A	1015	-	X
3	NAG	B	1003	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	B	1007	-	X
4	BU3	A	1016	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12865 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Toll-like receptor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	752	Total	C	N	O	S	0	0	0
			6055	3873	1029	1134	19			
1	B	743	Total	C	N	O	S	0	0	0
			5985	3828	1019	1119	19			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
A	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
A	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
A	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
A	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
A	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	833	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	24	SER	-	EXPRESSION TAG	UNP Q9NR97
B	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
B	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
B	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
B	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
B	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
B	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	833	ARG	-	EXPRESSION TAG	UNP Q9NR97

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

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

There are 50 discrepancies between the modelled and reference sequences:

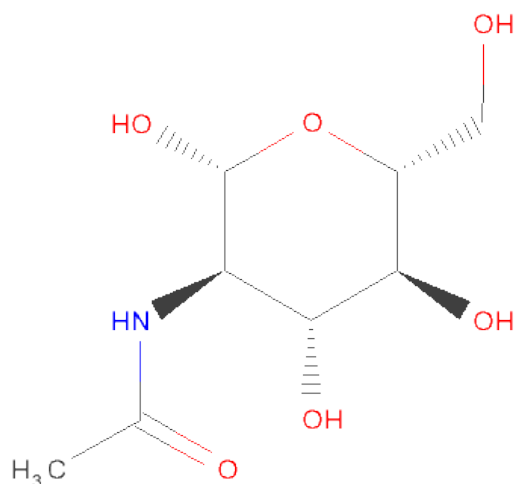
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
A	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
A	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
A	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
A	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
A	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	833	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
A	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
A	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
A	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
A	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
A	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	833	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
A	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
A	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
A	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
A	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
A	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	833	ARG	-	EXPRESSION TAG	UNP Q9NR97

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Chain	Residue	Modelled	Actual	Comment	Reference
B	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	24	SER	-	EXPRESSION TAG	UNP Q9NR97
B	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
B	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
B	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
B	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
B	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
B	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	833	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	24	SER	-	EXPRESSION TAG	UNP Q9NR97
B	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
B	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
B	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
B	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
B	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
B	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	833	ARG	-	EXPRESSION TAG	UNP Q9NR97

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



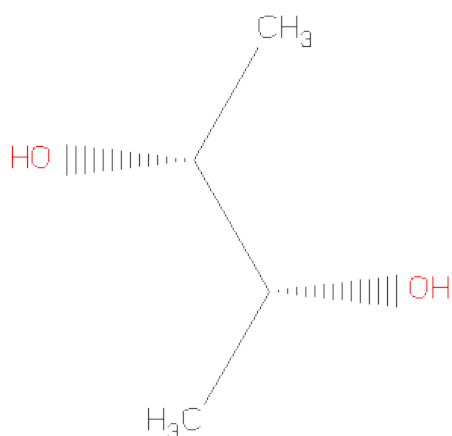
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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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	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	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is (R,R)-2,3-BUTANEDIOL (three-letter code: BU3) (formula: C₄H₁₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	4	2		

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

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

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
B	24	SER	-	EXPRESSION TAG	UNP Q9NR97
B	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
B	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
B	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
B	830	LEU	-	EXPRESSION TAG	UNP Q9NR97
B	831	VAL	-	EXPRESSION TAG	UNP Q9NR97
B	832	PRO	-	EXPRESSION TAG	UNP Q9NR97
B	833	ARG	-	EXPRESSION TAG	UNP Q9NR97

- Molecule 6 is water.

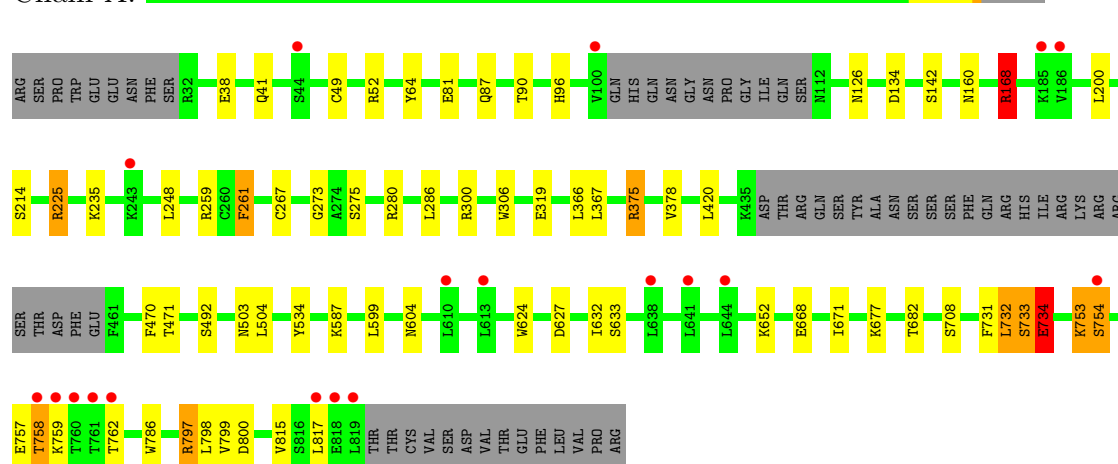
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	299	Total	O	0	0
			299	299		
6	B	157	Total	O	0	0
			157	157		

3 Residue-property plots

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.

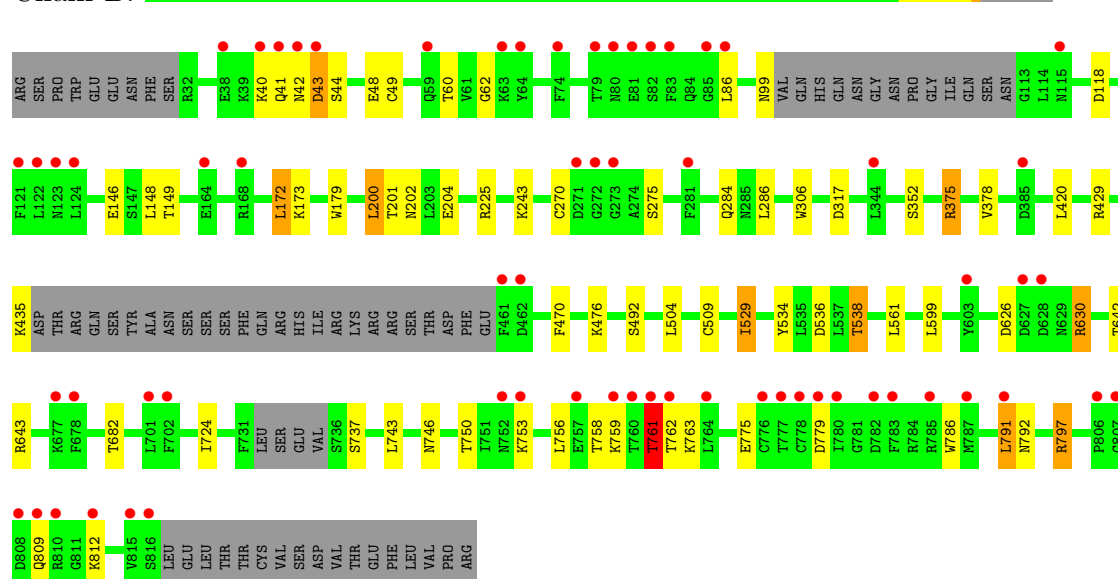
• Molecule 1: Toll-like receptor 8

Chain A:



• Molecule 1: Toll-like receptor 8

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	137.53Å 101.97Å 141.34Å 90.00° 104.75° 90.00°	Depositor
Resolution (Å)	34.38 – 2.30 34.38 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (34.38-2.30) 99.6 (34.38-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.182 , 0.236 0.182 , 0.236	Depositor DCC
R_{free} test set	4191 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 83847 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12865	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BU3, 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	0.71	3/6179 (0.0%)	0.80	6/8380 (0.1%)
1	B	0.61	3/6108 (0.0%)	0.72	4/8281 (0.0%)
All	All	0.66	6/12287 (0.0%)	0.76	10/16661 (0.1%)

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
1	A	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	179	TRP	CD2-CE2	5.42	1.47	1.41
1	A	624	TRP	CD2-CE2	5.42	1.47	1.41
1	A	786	TRP	CD2-CE2	5.25	1.47	1.41
1	B	306	TRP	CD2-CE2	5.24	1.47	1.41
1	A	306	TRP	CD2-CE2	5.20	1.47	1.41
1	B	786	TRP	CD2-CE2	5.07	1.47	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	791	LEU	CA-CB-CG	7.00	131.41	115.30
1	B	375	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	A	375	ARG	NE-CZ-NH2	-6.57	117.01	120.30
1	A	259	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	300	ARG	NE-CZ-NH2	-5.33	117.63	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	319	GLU	CB-CA-C	-5.13	100.14	110.40
1	A	168	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	B	43	ASP	N-CA-C	5.06	124.67	111.00
1	B	643	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	734	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6055	0	0	18	0
1	B	5985	0	0	17	0
2	A	117	0	0	0	0
2	B	78	0	0	0	0
3	A	84	0	0	0	0
3	B	56	0	0	0	0
4	A	6	0	0	1	0
5	B	28	0	0	0	0
6	A	299	0	0	7	0
6	B	157	0	0	4	0
All	All	12865	0	0	36	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (36) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:708:SER:CB	1:A:734:GLU:O	2.32	0.77
1:A:375:ARG:CD	6:A:1191:HOH:O	2.32	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:96:HIS:CD2	1:A:134:ASP:OD2	2.57	0.58
1:A:731:PHE:O	1:A:733:SER:N	2.38	0.57
1:B:626:ASP:OD2	1:B:630:ARG:NH1	2.39	0.56
1:A:731:PHE:C	1:A:733:SER:N	2.59	0.55
1:A:604:ASN:ND2	6:A:1206:HOH:O	2.40	0.54
1:A:87:GLN:O	1:A:126:ASN:ND2	2.40	0.54
1:A:753:LYS:O	1:A:754:SER:OG	2.26	0.53
1:A:797:ARG:O	1:A:800:ASP:N	2.41	0.53
1:A:225:ARG:NH1	6:A:1214:HOH:O	2.42	0.53
1:B:200:LEU:O	1:B:202:ASN:N	2.43	0.52
1:B:626:ASP:OD1	1:B:630:ARG:NH1	2.43	0.52
1:B:172:LEU:CB	6:B:1233:HOH:O	2.58	0.52
1:B:630:ARG:CG	1:B:630:ARG:NH1	2.73	0.51
1:B:41:GLN:N	1:B:44:SER:O	2.44	0.51
1:A:38:GLU:OE1	1:A:64:TYR:OH	2.30	0.50
1:A:168:ARG:NH1	1:A:168:ARG:CG	2.77	0.48
1:B:743:LEU:O	1:B:746:ASN:ND2	2.46	0.48
1:B:797:ARG:CG	1:B:797:ARG:NH1	2.78	0.46
1:B:375:ARG:CD	6:B:1130:HOH:O	2.63	0.45
1:B:626:ASP:CG	1:B:630:ARG:NH1	2.70	0.45
1:B:173:LYS:O	1:B:204:GLU:N	2.51	0.44
1:B:761:THR:OG1	1:B:762:THR:N	2.50	0.44
1:A:261:PHE:C	1:A:261:PHE:CD1	2.91	0.44
1:A:753:LYS:O	1:A:754:SER:CB	2.66	0.43
1:B:529:ILE:N	1:B:529:ILE:CD1	2.82	0.43
1:B:536:ASP:OD1	1:B:538:THR:CB	2.66	0.43
1:A:503:ASN:N	6:A:1394:HOH:O	2.51	0.43
1:A:267:CYS:CB	6:A:1248:HOH:O	2.66	0.42
1:B:746:ASN:CA	6:B:1249:HOH:O	2.67	0.42
1:B:809:GLN:O	1:B:812:LYS:N	2.53	0.42
1:A:758:THR:OG1	1:A:758:THR:O	2.37	0.42
1:A:41:GLN:N	6:A:1330:HOH:O	2.53	0.41
4:A:1016:BU3:C4	6:A:1204:HOH:O	2.67	0.41
1:B:270:CYS:N	6:B:1122:HOH:O	2.53	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	746/811 (92%)	691 (93%)	49 (7%)	6 (1%)	27	30
1	B	735/811 (91%)	677 (92%)	52 (7%)	6 (1%)	27	30
All	All	1481/1622 (91%)	1368 (92%)	101 (7%)	12 (1%)	27	30

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	733	SER
1	A	273	GLY
1	A	732	LEU
1	A	754	SER
1	B	42	ASN
1	B	43	ASP
1	B	201	THR
1	B	761	THR
1	A	378	VAL
1	A	762	THR
1	B	378	VAL
1	B	62	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	699/755 (93%)	654 (94%)	45 (6%)	25	31
1	B	690/755 (91%)	641 (93%)	49 (7%)	21	26
All	All	1389/1510 (92%)	1295 (93%)	94 (7%)	22	28

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	CYS
1	A	52	ARG
1	A	81	GLU
1	A	90	THR
1	A	142	SER
1	A	160	ASN
1	A	168	ARG
1	A	200	LEU
1	A	214	SER
1	A	225	ARG
1	A	235	LYS
1	A	248	LEU
1	A	261	PHE
1	A	275	SER
1	A	280	ARG
1	A	286	LEU
1	A	366	LEU
1	A	367	LEU
1	A	420	LEU
1	A	470	PHE
1	A	471	THR
1	A	492	SER
1	A	504	LEU
1	A	534	TYR
1	A	587	LYS
1	A	599	LEU
1	A	627	ASP
1	A	632	ILE
1	A	633	SER
1	A	652	LYS
1	A	668	GLU
1	A	671	ILE
1	A	677	LYS
1	A	682	THR
1	A	732	LEU
1	A	734	GLU
1	A	753	LYS
1	A	757	GLU
1	A	758	THR
1	A	759	LYS
1	A	797	ARG
1	A	798	LEU

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Mol	Chain	Res	Type
1	A	799	VAL
1	A	815	VAL
1	A	817	LEU
1	B	40	LYS
1	B	48	GLU
1	B	49	CYS
1	B	60	THR
1	B	86	LEU
1	B	99	ASN
1	B	118	ASP
1	B	146	GLU
1	B	148	LEU
1	B	149	THR
1	B	172	LEU
1	B	200	LEU
1	B	225	ARG
1	B	243	LYS
1	B	275	SER
1	B	284	GLN
1	B	286	LEU
1	B	317	ASP
1	B	352	SER
1	B	420	LEU
1	B	429	ARG
1	B	435	LYS
1	B	470	PHE
1	B	476	LYS
1	B	492	SER
1	B	504	LEU
1	B	509	CYS
1	B	529	ILE
1	B	534	TYR
1	B	538	THR
1	B	561	LEU
1	B	599	LEU
1	B	630	ARG
1	B	642	THR
1	B	682	THR
1	B	724	ILE
1	B	737	SER
1	B	750	THR
1	B	753	LYS

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Mol	Chain	Res	Type
1	B	756	LEU
1	B	758	THR
1	B	759	LYS
1	B	761	THR
1	B	763	LYS
1	B	775	GLU
1	B	779	ASP
1	B	791	LEU
1	B	792	ASN
1	B	797	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

17 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	$\# Z > 2$
2	NAG	A	1001	1,2	12,14,15	1.15	1 (8%)	15,19,21	1.70	1 (6%)
2	NAG	A	1002	2	12,14,15	0.84	0	15,19,21	2.50	3 (20%)
2	BMA	A	1003	2	10,11,12	0.51	0	11,15,17	0.87	1 (9%)
2	NAG	A	1005	1,2	12,14,15	1.08	2 (16%)	15,19,21	1.15	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1006	2	12,14,15	0.76	0	15,19,21	2.40	5 (33%)
2	BMA	A	1007	2	10,11,12	0.55	0	11,15,17	1.37	2 (18%)
2	NAG	A	1009	1,2	12,14,15	0.88	1 (8%)	15,19,21	2.06	6 (40%)
2	NAG	A	1010	2	12,14,15	1.13	1 (8%)	15,19,21	2.33	7 (46%)
2	BMA	A	1011	2	10,11,12	0.65	0	11,15,17	2.19	2 (18%)
5	NAG	B	1001	1,5	12,14,15	0.69	0	15,19,21	1.90	4 (26%)
5	NAG	B	1002	5	12,14,15	0.54	0	15,19,21	1.55	2 (13%)
2	NAG	B	1004	1,2	12,14,15	0.69	0	15,19,21	0.75	0
2	NAG	B	1005	2	12,14,15	0.62	0	15,19,21	2.08	3 (20%)
2	BMA	B	1006	2	10,11,12	0.62	0	11,15,17	1.59	2 (18%)
2	NAG	B	1008	1,2	12,14,15	0.94	1 (8%)	15,19,21	1.75	2 (13%)
2	NAG	B	1009	2	12,14,15	0.65	0	15,19,21	1.56	3 (20%)
2	BMA	B	1010	2	10,11,12	0.51	0	11,15,17	0.86	1 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1001	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1002	2	-	0/6/23/26	0/1/1/1
2	BMA	A	1003	2	-	0/2/19/22	0/1/1/1
2	NAG	A	1005	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1006	2	-	0/6/23/26	0/1/1/1
2	BMA	A	1007	2	-	0/2/19/22	0/1/1/1
2	NAG	A	1009	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1010	2	-	0/6/23/26	0/1/1/1
2	BMA	A	1011	2	-	0/2/19/22	0/1/1/1
5	NAG	B	1001	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	1002	5	-	0/6/23/26	0/1/1/1
2	NAG	B	1004	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1005	2	-	0/6/23/26	0/1/1/1
2	BMA	B	1006	2	-	0/2/19/22	0/1/1/1
2	NAG	B	1008	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1009	2	-	0/6/23/26	0/1/1/1
2	BMA	B	1010	2	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1010	NAG	O5-C5	-3.11	1.39	1.45
2	A	1001	NAG	C2-N2	-2.90	1.42	1.46
2	A	1005	NAG	O5-C5	-2.70	1.40	1.45
2	A	1005	NAG	C2-N2	-2.19	1.43	1.46
2	A	1009	NAG	O5-C5	-2.14	1.41	1.45
2	B	1008	NAG	O5-C5	-2.08	1.41	1.45

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1002	NAG	O5-C5-C6	6.64	113.95	106.98
2	A	1011	BMA	O5-C5-C6	5.84	113.11	106.98
2	A	1002	NAG	C3-C2-N2	-5.60	103.24	111.76
2	A	1006	NAG	O5-C5-C4	5.36	117.45	110.65
2	B	1005	NAG	O5-C5-C4	5.15	117.19	110.65
2	A	1009	NAG	C3-C2-N2	-5.04	104.09	111.76
2	A	1001	NAG	C3-C2-N2	-4.70	104.60	111.76
2	A	1010	NAG	O6-C6-C5	-4.51	95.84	111.36
2	B	1008	NAG	O5-C5-C4	-4.24	105.27	110.65
2	B	1006	BMA	O5-C5-C6	4.20	111.39	106.98
2	A	1006	NAG	O5-C5-C6	-4.19	102.58	106.98
2	B	1005	NAG	C3-C2-N2	-4.14	105.46	111.76
2	A	1010	NAG	O5-C5-C6	-4.01	102.77	106.98
2	A	1010	NAG	C3-C2-N2	-3.69	106.14	111.76
5	B	1001	NAG	O5-C5-C4	3.55	115.16	110.65
5	B	1002	NAG	O5-C5-C6	3.48	110.64	106.98
5	B	1001	NAG	C3-C2-N2	-3.48	106.46	111.76
2	A	1006	NAG	C6-C5-C4	-3.47	104.61	113.00
2	A	1009	NAG	O5-C5-C6	3.45	110.60	106.98
5	B	1002	NAG	C3-C2-N2	-3.24	106.82	111.76
2	B	1008	NAG	C3-C2-N2	-3.21	106.87	111.76
2	A	1010	NAG	C6-C5-C4	-3.03	105.68	113.00
2	B	1009	NAG	O5-C5-C4	3.01	114.47	110.65
2	B	1005	NAG	C6-C5-C4	-2.90	105.99	113.00
5	B	1001	NAG	O6-C6-C5	-2.84	101.58	111.36
2	B	1009	NAG	C6-C5-C4	-2.80	106.23	113.00
2	B	1009	NAG	O5-C5-C6	-2.75	104.10	106.98
2	A	1005	NAG	O5-C5-C6	2.73	109.84	106.98
2	A	1011	BMA	O3-C3-C2	2.73	114.92	109.94
2	A	1006	NAG	O3-C3-C4	-2.71	104.28	110.35
2	A	1002	NAG	C2-N2-C7	-2.53	118.84	123.09
2	A	1010	NAG	O3-C3-C4	-2.45	104.87	110.35
2	A	1007	BMA	C3-C4-C5	2.43	114.54	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1009	NAG	O4-C4-C3	-2.42	104.92	110.35
5	B	1001	NAG	O3-C3-C2	-2.41	104.03	109.09
2	A	1003	BMA	O5-C5-C6	2.38	109.48	106.98
2	A	1009	NAG	C8-C7-N2	2.38	120.75	116.11
2	A	1007	BMA	O5-C5-C4	2.38	113.67	110.65
2	A	1009	NAG	C3-C4-C5	-2.37	105.97	110.20
2	B	1010	BMA	O5-C5-C6	2.34	109.44	106.98
2	A	1010	NAG	O5-C5-C4	2.30	113.58	110.65
2	B	1006	BMA	O5-C5-C4	-2.12	107.96	110.65
2	A	1010	NAG	C2-N2-C7	-2.08	119.60	123.09
2	A	1006	NAG	O6-C6-C5	-2.07	104.23	111.36
2	A	1009	NAG	O7-C7-N2	-2.03	117.66	121.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry ⓘ

11 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	1004	1	12,14,15	0.89	1 (8%)	15,19,21	1.19	1 (6%)
3	NAG	A	1008	1	12,14,15	0.76	0	15,19,21	1.00	0
3	NAG	A	1012	1	12,14,15	0.68	0	15,19,21	1.17	1 (6%)
3	NAG	A	1013	1	12,14,15	0.89	1 (8%)	15,19,21	1.60	5 (33%)
3	NAG	A	1014	1	12,14,15	0.58	0	15,19,21	2.06	3 (20%)
3	NAG	A	1015	1	12,14,15	0.65	0	15,19,21	0.76	0
4	BU3	A	1016	-	5,5,5	0.50	0	6,6,6	0.55	0
3	NAG	B	1003	1	12,14,15	0.65	0	15,19,21	1.07	1 (6%)
3	NAG	B	1007	1	12,14,15	0.68	0	15,19,21	1.12	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	1011	1	12,14,15	0.59	0	15,19,21	0.82	0
3	NAG	B	1012	1	12,14,15	0.76	1 (8%)	15,19,21	0.97	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	1004	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1008	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1012	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1013	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1014	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1015	1	-	0/6/23/26	0/1/1/1
4	BU3	A	1016	-	-	0/4/4/4	0/0/0/0
3	NAG	B	1003	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1007	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1011	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1012	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1004	NAG	O5-C5	-2.56	1.40	1.45
3	A	1013	NAG	O3-C3	-2.24	1.37	1.43
3	B	1012	NAG	O5-C5	-2.12	1.41	1.45

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1014	NAG	O5-C5-C6	6.77	114.08	106.98
3	A	1012	NAG	O5-C5-C6	3.62	110.78	106.98
3	A	1004	NAG	O5-C5-C4	-2.96	106.90	110.65
3	A	1013	NAG	C6-C5-C4	-2.71	106.46	113.00
3	A	1013	NAG	O4-C4-C3	-2.70	104.29	110.35
3	A	1014	NAG	C3-C2-N2	-2.59	107.82	111.76
3	A	1013	NAG	O5-C5-C6	2.52	109.63	106.98
3	B	1007	NAG	C3-C2-N2	-2.50	107.96	111.76
3	B	1012	NAG	O5-C5-C4	-2.27	107.77	110.65
3	A	1014	NAG	C3-C4-C5	-2.23	106.22	110.20
3	A	1013	NAG	O6-C6-C5	-2.17	103.89	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1003	NAG	C8-C7-N2	2.10	120.22	116.11
3	A	1013	NAG	C3-C2-N2	-2.09	108.57	111.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	752/811 (92%)	-0.10	19 (2%) 54 65	14, 27, 61, 139	0
1	B	743/811 (91%)	0.35	64 (8%) 11 17	17, 44, 102, 137	0
All	All	1495/1622 (92%)	0.12	83 (5%) 25 33	14, 33, 92, 139	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	ASN	6.4
1	B	273	GLY	6.1
1	A	762	THR	6.1
1	A	819	LEU	5.8
1	B	41	GLN	5.8
1	A	760	THR	5.7
1	B	760	THR	5.4
1	B	83	PHE	5.3
1	B	778	CYS	5.3
1	B	783	PHE	4.8
1	B	806	PRO	4.8
1	B	780	ILE	4.7
1	B	812	LYS	4.3
1	A	761	THR	4.0
1	B	810	ARG	3.9
1	A	185	LYS	3.9
1	B	461	PHE	3.8
1	B	808	ASP	3.8
1	B	785	ARG	3.7
1	B	816	SER	3.7
1	B	701	LEU	3.7
1	A	641	LEU	3.7
1	B	124	LEU	3.7
1	B	81	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	123	ASN	3.5
1	B	757	GLU	3.5
1	B	40	LYS	3.5
1	B	782	ASP	3.5
1	B	121	PHE	3.4
1	B	281	PHE	3.4
1	A	817	LEU	3.4
1	B	753	LYS	3.4
1	B	43	ASP	3.3
1	B	791	LEU	3.3
1	B	807	GLY	3.2
1	B	777	THR	3.1
1	B	759	LYS	3.1
1	B	761	THR	3.1
1	B	815	VAL	3.0
1	B	776	CYS	3.0
1	B	74	PHE	2.9
1	B	809	GLN	2.9
1	B	86	LEU	2.8
1	A	758	THR	2.8
1	A	644	LEU	2.8
1	B	779	ASP	2.7
1	B	627	ASP	2.7
1	B	85	GLY	2.7
1	B	764	LEU	2.6
1	A	100	VAL	2.6
1	A	613	LEU	2.6
1	A	759	LYS	2.6
1	B	385	ASP	2.6
1	B	762	THR	2.6
1	B	64	TYR	2.5
1	B	122	LEU	2.5
1	B	462	ASP	2.5
1	A	638	LEU	2.5
1	A	243	LYS	2.5
1	B	59	GLN	2.4
1	B	82	SER	2.4
1	B	271	ASP	2.4
1	A	186	VAL	2.4
1	B	38	GLU	2.4
1	B	677	LYS	2.3
1	B	272	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	754	SER	2.2
1	B	678	PHE	2.2
1	A	818	GLU	2.2
1	B	702	PHE	2.2
1	B	79	THR	2.1
1	B	752	ASN	2.1
1	B	603	TYR	2.1
1	B	164	GLU	2.1
1	B	168	ARG	2.1
1	A	44	SER	2.1
1	B	628	ASP	2.1
1	B	344	LEU	2.1
1	B	115	ASN	2.1
1	A	610	LEU	2.0
1	B	80	ASN	2.0
1	B	787	MET	2.0
1	B	63	LYS	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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	B	1001	14/15	0.14	-0.13	26,30,34,39	0
2	NAG	A	1002	14/15	0.09	-0.41	16,20,28,35	0
2	NAG	A	1006	14/15	0.14	-0.46	31,36,45,52	0
2	NAG	A	1001	14/15	0.09	-0.60	14,16,18,19	0
2	NAG	B	1005	14/15	0.15	-0.62	35,44,63,63	0
2	NAG	A	1010	14/15	0.10	-1.01	21,23,27,29	0
2	NAG	A	1009	14/15	0.09	-1.10	15,18,19,22	0
5	NAG	B	1002	14/15	0.10	-1.17	34,37,48,49	0
2	NAG	A	1005	14/15	0.09	-1.17	17,21,24,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	B	1004	14/15	0.08	-1.31	22,24,26,30	0
2	NAG	B	1009	14/15	0.08	-1.49	27,29,35,42	0
2	NAG	B	1008	14/15	0.08	-1.76	19,22,23,25	0
2	BMA	A	1003	11/12	0.21	-	45,57,64,68	0
2	BMA	B	1006	11/12	0.29	-	66,70,75,80	0
2	BMA	A	1011	11/12	0.18	-	31,37,40,47	0
2	BMA	B	1010	11/12	0.19	-	42,51,55,57	0
2	BMA	A	1007	11/12	0.28	-	51,60,64,69	0

6.4 Ligands

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	1008	14/15	0.28	35.42	40,47,55,56	0
3	NAG	B	1003	14/15	0.29	11.26	59,69,73,76	0
3	NAG	B	1007	14/15	0.25	10.45	51,63,70,71	0
3	NAG	A	1015	14/15	0.21	3.48	55,64,69,70	0
3	NAG	A	1012	14/15	0.23	2.87	44,47,49,49	0
4	BU3	A	1016	6/6	0.33	2.75	49,55,58,69	0
3	NAG	A	1004	14/15	0.20	2.43	37,44,49,50	0
3	NAG	A	1014	14/15	0.22	2.13	42,50,56,57	0
3	NAG	B	1012	14/15	0.20	1.31	57,61,64,66	0
3	NAG	B	1011	14/15	0.20	0.91	59,67,75,76	0
3	NAG	A	1013	14/15	0.13	-0.54	17,20,24,26	0

6.5 Other polymers

There are no such residues in this entry.