



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:28 am 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 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

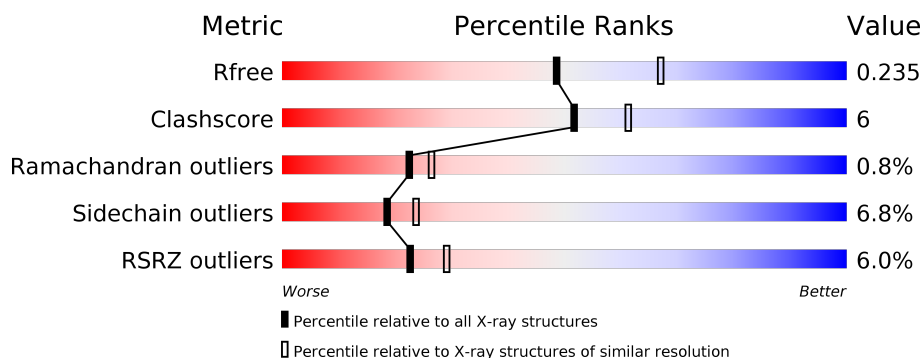
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (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. 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	811	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>•</div> <div>7%</div> </div> </div>
1	B	811	<div> <div>8%</div> <div> <div></div> <div>73%</div> <div>15%</div> <div>•</div> <div>8%</div> </div> </div>

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
3	NAG	A	1014	-	-	-	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 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 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			

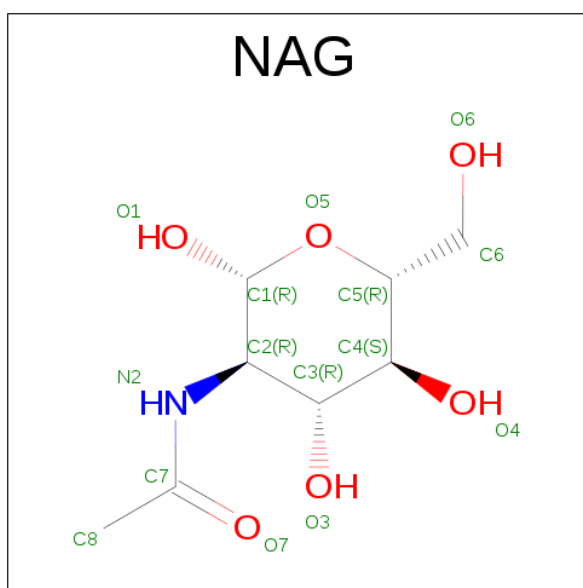
There are 20 discrepancies between the modelled and reference sequences:

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		

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



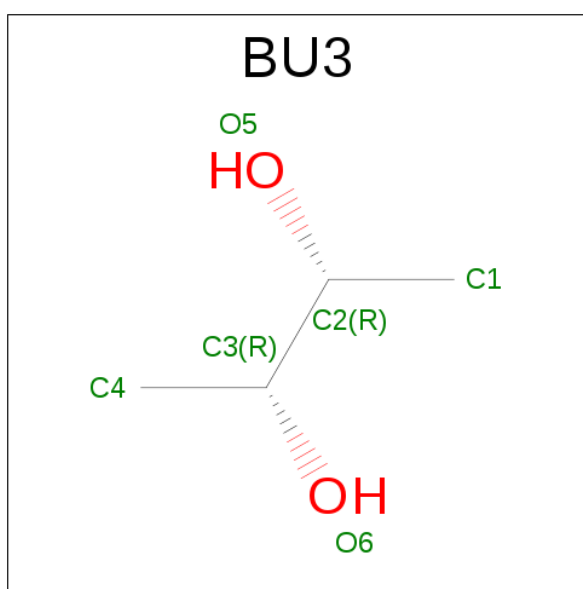
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
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		
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		

- Molecule 6 is water.

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

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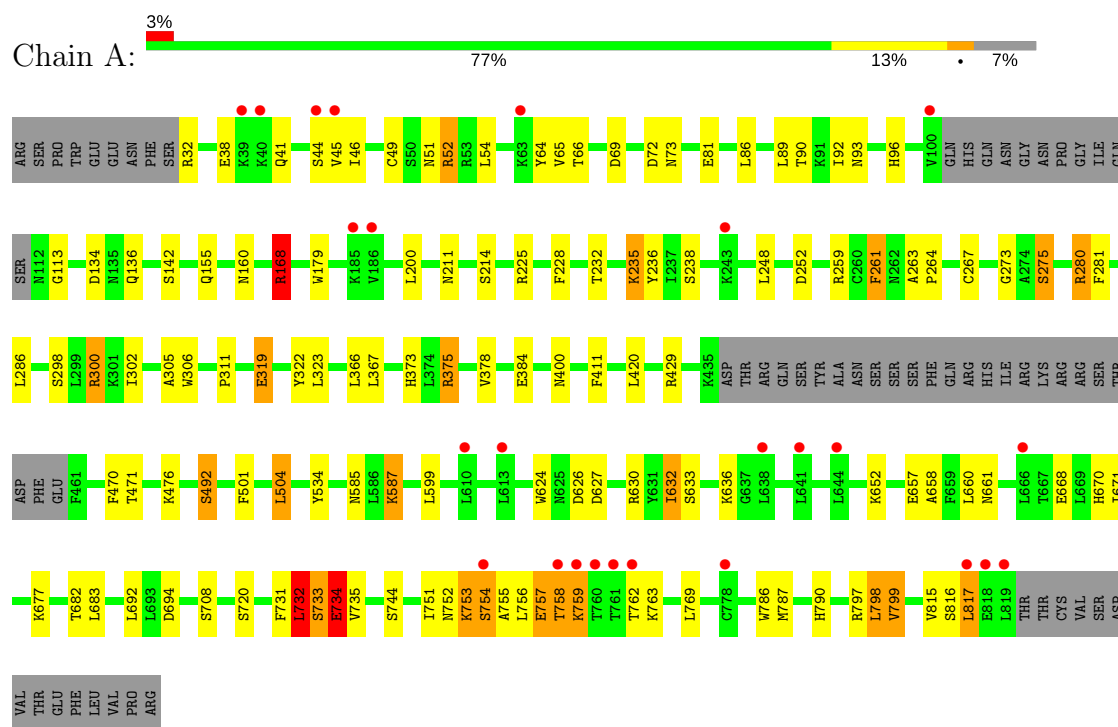
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	157	Total	O	0	0
			157	157		

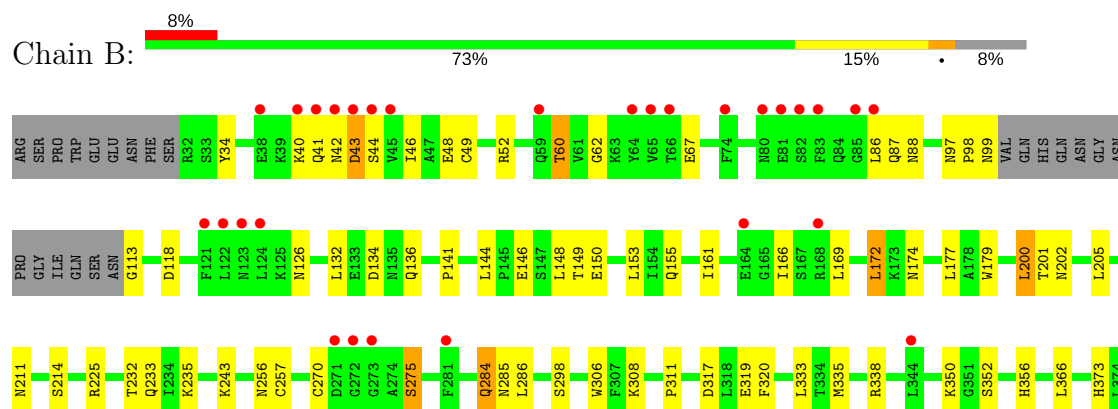
3 Residue-property plots [i](#)

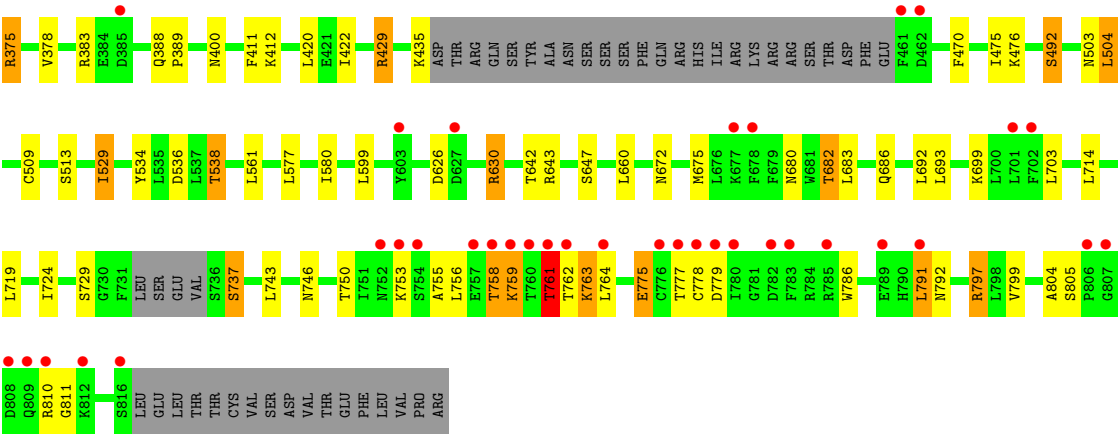
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Toll-like receptor 8



• Molecule 1: Toll-like receptor 8





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 0.181 , 0.235	Depositor DCC
R_{free} test set	4182 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)	0.33 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	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.

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: 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 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	6055	0	6054	72	0
1	B	5985	0	5981	86	0
2	A	117	0	102	0	0
2	B	78	0	68	0	0
3	A	84	0	78	0	0
3	B	56	0	52	1	0
4	A	6	0	10	2	0
5	B	28	0	25	0	0
6	A	299	0	0	13	0
6	B	157	0	0	7	0
All	All	12865	0	12370	158	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 6.

All (158) 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:172:LEU:HD21	1:B:200:LEU:HG	1.25	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:708:SER:HB3	1:A:734:GLU:O	1.45	1.11
1:B:630:ARG:HG3	1:B:630:ARG:HH11	1.26	0.99
1:A:375:ARG:HD2	6:A:1191:HOH:O	1.74	0.87
1:B:536:ASP:OD1	1:B:538:THR:HB	1.75	0.85
1:B:429:ARG:HD2	1:B:492:SER:OG	1.79	0.82
1:B:172:LEU:CD2	1:B:200:LEU:HG	2.09	0.80
1:A:731:PHE:C	1:A:733:SER:H	1.86	0.77
1:B:150:GLU:HG2	1:B:174:ASN:HB2	1.68	0.76
1:A:96:HIS:HD2	1:A:134:ASP:OD2	1.71	0.73
1:A:375:ARG:CD	6:A:1191:HOH:O	2.32	0.73
1:B:422:ILE:HG23	1:B:475:ILE:HD12	1.71	0.73
1:A:168:ARG:HH11	1:A:168:ARG:HG3	1.54	0.72
1:B:746:ASN:HA	6:B:1249:HOH:O	1.88	0.72
1:A:733:SER:HB3	1:A:734:GLU:HA	1.75	0.69
1:B:660:LEU:HD22	1:B:686:GLN:HG3	1.75	0.69
1:B:630:ARG:CG	1:B:630:ARG:HH11	2.03	0.69
1:A:708:SER:CB	1:A:734:GLU:O	2.32	0.68
1:B:319:GLU:HG2	6:B:1118:HOH:O	1.94	0.67
1:B:46:ILE:HG13	1:B:67:GLU:HB2	1.77	0.66
1:A:732:LEU:HB2	1:A:755:ALA:O	1.95	0.66
1:B:804:ALA:HA	1:B:810:ARG:HG3	1.78	0.66
1:B:577:LEU:HB3	1:B:580:ILE:HD12	1.77	0.65
1:A:168:ARG:HH11	1:A:168:ARG:CG	2.09	0.65
1:A:752:ASN:O	1:A:756:LEU:HG	1.98	0.63
1:B:52:ARG:HG3	1:B:799:VAL:HG21	1.80	0.63
1:A:319:GLU:HG2	6:A:1128:HOH:O	1.99	0.62
1:A:280:ARG:NH1	1:A:305:ALA:HB1	2.15	0.62
1:B:529:ILE:HD13	1:B:529:ILE:H	1.65	0.61
1:A:626:ASP:OD2	1:A:630:ARG:HD3	2.01	0.60
1:A:45:VAL:HG23	1:A:65:VAL:HA	1.83	0.60
1:A:501:PHE:HA	1:A:504:LEU:HD22	1.84	0.60
1:B:797:ARG:CG	1:B:797:ARG:HH11	2.14	0.59
1:A:384:GLU:HG3	6:A:1293:HOH:O	2.01	0.59
1:A:280:ARG:HD3	1:A:281:PHE:CE1	2.38	0.59
1:B:169:LEU:O	1:B:172:LEU:HD22	2.02	0.59
1:B:350:LYS:HE3	6:B:1221:HOH:O	2.02	0.58
1:B:113:GLY:HA3	1:B:136:GLN:HB3	1.85	0.58
1:B:411:PHE:HB3	1:B:504:LEU:HD13	1.85	0.57
1:B:714:LEU:O	1:B:737:SER:HB3	2.05	0.56
1:B:777:THR:HG22	1:B:778:CYS:H	1.70	0.56
1:B:797:ARG:HB3	1:B:797:ARG:HH11	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:585:ASN:O	1:A:587:LYS:HD2	2.06	0.56
1:B:626:ASP:OD2	1:B:630:ARG:NH1	2.39	0.56
1:A:302:ILE:HD11	1:A:323:LEU:HD13	1.89	0.55
1:B:284:GLN:HG2	1:B:285:ASN:N	2.20	0.55
1:B:52:ARG:CG	1:B:799:VAL:HG21	2.36	0.55
1:A:731:PHE:C	1:A:733:SER:N	2.59	0.55
1:B:172:LEU:HD21	1:B:200:LEU:CG	2.18	0.55
1:A:692:LEU:HD23	1:A:692:LEU:C	2.26	0.55
1:A:731:PHE:O	1:A:733:SER:N	2.38	0.54
1:A:657:GLU:CD	1:A:657:GLU:H	2.11	0.54
1:B:356:HIS:CD2	1:B:383:ARG:HD2	2.43	0.54
1:A:632:ILE:HD13	1:A:658:ALA:HB2	1.89	0.54
1:B:41:GLN:O	1:B:44:SER:HB2	2.07	0.54
1:A:757:GLU:HB2	1:A:759:LYS:NZ	2.24	0.53
1:A:275:SER:HB2	1:A:298:SER:O	2.08	0.53
1:A:168:ARG:NH1	1:A:168:ARG:HG3	2.20	0.53
1:A:96:HIS:CD2	1:A:134:ASP:OD2	2.57	0.53
4:A:1016:BU3:H42	6:A:1192:HOH:O	2.08	0.52
1:B:630:ARG:HG3	1:B:630:ARG:NH1	2.06	0.52
1:B:172:LEU:CB	6:B:1233:HOH:O	2.58	0.52
1:B:729:SER:HA	1:B:755:ALA:HA	1.92	0.52
1:B:34:TYR:O	1:B:60:THR:HB	2.11	0.51
1:B:88:ASN:HA	1:B:126:ASN:HD22	1.75	0.51
1:A:429:ARG:HB3	1:B:429:ARG:NH1	2.26	0.51
1:A:41:GLN:NE2	1:A:46:ILE:HD11	2.26	0.51
1:A:411:PHE:HB3	1:A:504:LEU:HD13	1.93	0.51
1:A:51:ASN:HA	1:A:72:ASP:O	2.10	0.51
1:B:388:GLN:HB2	1:B:389:PRO:HD3	1.91	0.51
1:B:319:GLU:HB3	1:B:320:PHE:CD2	2.46	0.51
1:B:797:ARG:CB	1:B:797:ARG:HH11	2.24	0.50
1:B:513:SER:OG	1:B:538:THR:HG22	2.10	0.50
1:B:797:ARG:HH11	1:B:797:ARG:HG2	1.75	0.50
1:B:172:LEU:HB3	6:B:1233:HOH:O	2.12	0.49
1:A:211:ASN:O	1:A:232:THR:HA	2.12	0.49
1:A:476:LYS:HD3	6:A:1266:HOH:O	2.13	0.49
1:B:758:THR:OG1	1:B:759:LYS:HA	2.12	0.48
1:B:132:LEU:HB2	1:B:153:LEU:HD23	1.96	0.48
1:B:87:GLN:HG2	1:B:88:ASN:OD1	2.14	0.48
1:B:214:SER:HA	1:B:233:GLN:O	2.14	0.47
1:B:529:ILE:HD13	1:B:529:ILE:N	2.29	0.47
1:A:113:GLY:HA2	1:A:136:GLN:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:660:LEU:HD21	1:A:683:LEU:HD22	1.97	0.47
1:B:412:LYS:HB3	1:B:503:ASN:HB3	1.96	0.47
1:B:797:ARG:HG2	1:B:797:ARG:NH1	2.29	0.47
1:A:134:ASP:HA	1:A:155:GLN:O	2.14	0.47
1:B:692:LEU:HD23	1:B:692:LEU:C	2.35	0.47
1:B:235:LYS:HD2	1:B:270:CYS:SG	2.54	0.47
1:A:720:SER:HA	1:A:744:SER:O	2.15	0.47
1:A:280:ARG:CZ	1:A:305:ALA:HB1	2.46	0.46
1:B:200:LEU:O	1:B:202:ASN:N	2.43	0.46
1:B:743:LEU:C	1:B:746:ASN:HD22	2.19	0.46
1:B:626:ASP:CG	1:B:630:ARG:HH12	2.18	0.46
1:B:161:ILE:HD12	1:B:177:LEU:HD13	1.96	0.46
1:B:375:ARG:HD2	6:B:1130:HOH:O	2.16	0.46
1:B:141:PRO:O	1:B:144:LEU:HG	2.15	0.46
1:B:692:LEU:HD23	1:B:693:LEU:N	2.31	0.46
1:B:205:LEU:HD23	1:B:205:LEU:C	2.37	0.45
1:B:308:LYS:HA	1:B:335:MET:CE	2.46	0.45
1:B:375:ARG:CD	6:B:1130:HOH:O	2.63	0.45
1:A:787:MET:HE3	1:A:798:LEU:HD11	1.98	0.45
1:B:211:ASN:O	1:B:232:THR:HA	2.17	0.45
1:B:626:ASP:CG	1:B:630:ARG:NH1	2.70	0.45
1:A:44:SER:HB2	1:A:66:THR:OG1	2.17	0.45
1:B:626:ASP:OD1	1:B:630:ARG:NH1	2.43	0.45
1:B:683:LEU:HD21	3:B:1011:NAG:O5	2.17	0.44
1:B:680:ASN:OD1	1:B:682:THR:HG23	2.17	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:HD1	2.20	0.44
1:A:261:PHE:CD1	1:A:261:PHE:C	2.91	0.44
1:B:675:MET:HB3	1:B:699:LYS:HE2	1.99	0.44
1:A:228:PHE:HA	1:A:252:ASP:HB3	2.00	0.44
1:B:275:SER:HB2	1:B:298:SER:O	2.17	0.44
1:B:373:HIS:HA	1:B:400:ASN:HB3	2.00	0.44
1:A:492:SER:HA	6:A:1274:HOH:O	2.17	0.44
1:B:333:LEU:HD22	1:B:366:LEU:HD11	1.99	0.44
1:A:753:LYS:O	1:A:754:SER:CB	2.66	0.43
1:B:41:GLN:N	1:B:44:SER:O	2.44	0.43
1:B:775:GLU:HA	1:B:805:SER:HB2	2.00	0.43
1:A:263:ALA:HA	1:A:264:PRO:HD3	1.85	0.43
1:B:166:ILE:HD12	1:B:200:LEU:HD21	2.00	0.43
1:B:529:ILE:CD1	1:B:529:ILE:N	2.82	0.43
1:B:763:LYS:HB3	1:B:764:LEU:H	1.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:HD3	1:A:798:LEU:HD21	2.00	0.43
1:A:373:HIS:HA	1:A:400:ASN:HB3	2.00	0.43
1:A:69:ASP:HA	1:A:93:ASN:HB3	2.01	0.43
1:A:236:TYR:CE2	1:A:238:SER:HB3	2.53	0.42
1:A:267:CYS:CB	6:A:1248:HOH:O	2.66	0.42
1:A:636:LYS:HE2	1:A:661:ASN:OD1	2.19	0.42
1:A:267:CYS:HB2	6:A:1248:HOH:O	2.18	0.42
1:A:751:ILE:HD11	1:A:769:LEU:HD22	2.00	0.42
1:A:52:ARG:HG2	1:A:799:VAL:HG21	2.01	0.42
1:A:89:LEU:HD13	1:A:92:ILE:HD11	2.01	0.42
1:B:308:LYS:HA	1:B:335:MET:HE2	2.01	0.42
1:B:703:LEU:HD21	1:B:719:LEU:HD13	2.02	0.42
1:A:38:GLU:OE1	1:A:64:TYR:OH	2.30	0.42
1:A:235:LYS:HG2	6:A:1282:HOH:O	2.19	0.42
1:B:810:ARG:HA	1:B:811:GLY:HA2	1.64	0.41
1:A:300:ARG:HG2	1:A:322:TYR:HB2	2.01	0.41
1:A:758:THR:OG1	1:A:758:THR:O	2.37	0.41
1:A:758:THR:HB	1:A:790:HIS:NE2	2.35	0.41
1:B:660:LEU:HD23	1:B:660:LEU:HA	1.92	0.41
1:B:97:ASN:HA	1:B:98:PRO:HA	1.85	0.41
1:B:134:ASP:HA	1:B:155:GLN:O	2.20	0.41
4:A:1016:BU3:C4	6:A:1204:HOH:O	2.67	0.41
1:A:54:LEU:HD12	1:A:73:ASN:ND2	2.36	0.41
1:A:763:LYS:HD2	1:A:763:LYS:HA	1.82	0.41
1:A:155:GLN:HA	1:A:179:TRP:O	2.21	0.41
1:A:86:LEU:HA	6:A:1211:HOH:O	2.21	0.41
1:B:311:PRO:O	1:B:338:ARG:HD2	2.21	0.41
1:A:429:ARG:HE	1:B:492:SER:HB3	1.86	0.41
1:A:816:SER:C	1:A:817:LEU:HD13	2.42	0.41
1:B:647:SER:HA	1:B:672:ASN:O	2.20	0.40
1:A:311:PRO:HD2	6:A:1183:HOH:O	2.20	0.40
1:A:733:SER:HA	1:A:735:VAL:H	1.85	0.40
1:A:670:HIS:HA	1:A:694:ASP:HB3	2.02	0.40
1:B:256:ASN:O	1:B:257:CYS:HB2	2.22	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	746/811 (92%)	691 (93%)	49 (7%)	6 (1%)	22	26
1	B	735/811 (91%)	677 (92%)	52 (7%)	6 (1%)	22	26
All	All	1481/1622 (91%)	1368 (92%)	101 (7%)	12 (1%)	22	26

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 [i](#)

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%)	20	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	690/755 (91%)	641 (93%)	49 (7%)	17	22
All	All	1389/1510 (92%)	1295 (93%)	94 (7%)	18	24

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

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Mol	Chain	Res	Type
1	A	753	LYS
1	A	757	GLU
1	A	758	THR
1	A	759	LYS
1	A	797	ARG
1	A	798	LEU
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

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Mol	Chain	Res	Type
1	B	642	THR
1	B	682	THR
1	B	724	ILE
1	B	737	SER
1	B	750	THR
1	B	753	LYS
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. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	77	HIS
1	A	96	HIS
1	A	604	ASN
1	A	752	ASN
1	B	126	ASN
1	B	157	ASN
1	B	233	GLN
1	B	285	ASN
1	B	792	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

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	14,14,15	0.89	0	15,19,21	1.74	2 (13%)
2	NAG	A	1002	2	14,14,15	0.86	0	15,19,21	1.74	4 (26%)
2	BMA	A	1003	2	11,11,12	0.27	0	13,15,17	0.53	0
2	NAG	A	1005	1,2	14,14,15	1.01	1 (7%)	15,19,21	1.39	2 (13%)
2	NAG	A	1006	2	14,14,15	0.79	1 (7%)	15,19,21	2.39	4 (26%)
2	BMA	A	1007	2	11,11,12	0.45	0	13,15,17	1.33	2 (15%)
2	NAG	A	1009	1,2	14,14,15	0.57	0	15,19,21	1.66	5 (33%)
2	NAG	A	1010	2	14,14,15	1.04	1 (7%)	15,19,21	2.15	5 (33%)
2	BMA	A	1011	2	11,11,12	0.77	0	13,15,17	1.56	2 (15%)
5	NAG	B	1001	1,5	14,14,15	0.75	0	15,19,21	1.92	6 (40%)
5	NAG	B	1002	5	14,14,15	0.50	0	15,19,21	1.11	1 (6%)
2	NAG	B	1004	1,2	14,14,15	0.59	0	15,19,21	1.46	3 (20%)
2	NAG	B	1005	2	14,14,15	0.66	0	15,19,21	1.94	2 (13%)
2	BMA	B	1006	2	11,11,12	0.58	0	13,15,17	0.92	1 (7%)
2	NAG	B	1008	1,2	14,14,15	0.82	0	15,19,21	1.74	4 (26%)
2	NAG	B	1009	2	14,14,15	0.80	0	15,19,21	1.94	2 (13%)
2	BMA	B	1010	2	11,11,12	0.25	0	13,15,17	0.54	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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1010	NAG	O5-C1	-2.43	1.39	1.43
2	A	1005	NAG	O5-C1	-2.34	1.39	1.43
2	A	1006	NAG	O5-C1	-2.01	1.40	1.43

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1010	NAG	O6-C6-C5	-4.61	95.84	111.34
2	A	1001	NAG	O5-C1-C2	-4.48	105.23	111.47
2	B	1004	NAG	C1-C2-N2	-4.03	103.60	110.49
2	A	1006	NAG	C6-C5-C4	-3.58	104.61	113.00
2	B	1008	NAG	O5-C1-C2	-3.54	106.54	111.47
2	A	1002	NAG	O5-C1-C2	-3.52	106.58	111.47
2	A	1005	NAG	C1-C2-N2	-3.42	104.65	110.49
2	A	1010	NAG	C6-C5-C4	-3.13	105.68	113.00
2	B	1005	NAG	C6-C5-C4	-3.00	105.99	113.00
5	B	1001	NAG	O5-C1-C2	-2.91	107.43	111.47
5	B	1001	NAG	O6-C6-C5	-2.90	101.58	111.34
2	B	1009	NAG	C6-C5-C4	-2.89	106.23	113.00
2	A	1002	NAG	C2-N2-C7	-2.82	118.84	122.94
2	A	1006	NAG	O3-C3-C4	-2.79	104.28	110.36
2	A	1010	NAG	O3-C3-C4	-2.52	104.87	110.36
5	B	1001	NAG	O3-C3-C2	-2.50	104.03	109.39
2	A	1009	NAG	O4-C4-C3	-2.50	104.92	110.36
2	A	1009	NAG	C3-C4-C5	-2.41	105.97	110.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1010	NAG	C2-N2-C7	-2.29	119.60	122.94
2	A	1009	NAG	O7-C7-N2	-2.21	117.66	121.92
5	B	1001	NAG	C2-N2-C7	-2.19	119.74	122.94
5	B	1002	NAG	C2-N2-C7	-2.15	119.81	122.94
2	A	1006	NAG	O6-C6-C5	-2.11	104.23	111.34
2	A	1001	NAG	C2-N2-C7	-2.07	119.92	122.94
2	A	1005	NAG	C4-C3-C2	-2.07	107.99	111.02
2	B	1004	NAG	C1-O5-C5	2.14	115.11	112.17
2	B	1008	NAG	C8-C7-N2	2.14	119.97	116.11
2	A	1002	NAG	C4-C3-C2	2.32	114.42	111.02
5	B	1001	NAG	C1-C2-N2	2.35	114.50	110.49
2	B	1004	NAG	O5-C1-C2	2.40	114.82	111.47
2	B	1006	BMA	C1-C2-C3	2.43	112.73	109.65
2	A	1007	BMA	C1-O5-C5	2.44	115.53	112.17
2	A	1007	BMA	C3-C4-C5	2.45	114.54	110.22
2	B	1008	NAG	C1-O5-C5	2.47	115.57	112.17
2	A	1009	NAG	C8-C7-N2	2.57	120.75	116.11
2	A	1011	BMA	O3-C3-C2	2.69	114.92	110.02
2	A	1002	NAG	C1-C2-N2	2.98	115.58	110.49
2	A	1009	NAG	C1-O5-C5	3.03	116.34	112.17
2	B	1008	NAG	C1-C2-N2	3.04	115.67	110.49
5	B	1001	NAG	C1-O5-C5	3.10	116.44	112.17
2	A	1011	BMA	C1-O5-C5	3.35	116.78	112.17
2	A	1010	NAG	C1-O5-C5	4.03	117.72	112.17
2	B	1009	NAG	C1-O5-C5	5.53	119.79	112.17
2	B	1005	NAG	C1-O5-C5	5.53	119.79	112.17
2	A	1006	NAG	C1-O5-C5	6.73	121.44	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	14,14,15	0.70	0	15,19,21	1.16	0
3	NAG	A	1008	1	14,14,15	0.79	1 (7%)	15,19,21	1.40	2 (13%)
3	NAG	A	1012	1	14,14,15	0.53	0	15,19,21	1.23	2 (13%)
3	NAG	A	1013	1	14,14,15	0.90	1 (7%)	15,19,21	2.06	5 (33%)
3	NAG	A	1014	1	14,14,15	0.65	0	15,19,21	0.92	1 (6%)
3	NAG	A	1015	1	14,14,15	0.62	0	15,19,21	1.13	1 (6%)
4	BU3	A	1016	-	4,5,5	0.45	0	6,6,6	0.80	0
3	NAG	B	1003	1	14,14,15	0.55	0	15,19,21	1.24	2 (13%)
3	NAG	B	1007	1	14,14,15	0.75	0	15,19,21	1.12	1 (6%)
3	NAG	B	1011	1	14,14,15	0.47	0	15,19,21	1.67	2 (13%)
3	NAG	B	1012	1	14,14,15	0.57	0	15,19,21	0.72	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1013	NAG	O3-C3	-2.35	1.37	1.43
3	A	1008	NAG	O5-C1	-2.04	1.40	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1011	NAG	O5-C1-C2	-3.17	107.06	111.47
3	A	1012	NAG	O5-C1-C2	-2.94	107.38	111.47
3	A	1013	NAG	C1-C2-N2	-2.92	105.49	110.49
3	A	1008	NAG	O5-C1-C2	-2.92	107.41	111.47
3	A	1013	NAG	C6-C5-C4	-2.80	106.46	113.00
3	A	1013	NAG	O4-C4-C3	-2.79	104.29	110.36
3	B	1003	NAG	O5-C1-C2	-2.34	108.22	111.47
3	A	1014	NAG	C3-C4-C5	-2.27	106.22	110.22
3	A	1013	NAG	O6-C6-C5	-2.22	103.89	111.34
3	B	1007	NAG	O5-C1-C2	-2.12	108.52	111.47
3	B	1003	NAG	C8-C7-N2	2.27	120.22	116.11
3	A	1012	NAG	C1-O5-C5	2.29	115.32	112.17
3	A	1008	NAG	C1-O5-C5	2.87	116.13	112.17
3	A	1015	NAG	C1-O5-C5	3.73	117.31	112.17
3	B	1011	NAG	C1-O5-C5	4.84	118.83	112.17
3	A	1013	NAG	C1-O5-C5	5.10	119.19	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1016	BU3	2	0
3	B	1011	NAG	1	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	752/811 (92%)	-0.13	25 (3%)	47 54	14, 27, 61, 139	0
1	B	743/811 (91%)	0.29	65 (8%)	11 15	17, 44, 102, 137	0
All	All	1495/1622 (92%)	0.08	90 (6%)	23 29	14, 33, 92, 139	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	ASN	6.8
1	B	273	GLY	5.9
1	B	778	CYS	5.7
1	A	762	THR	5.7
1	B	760	THR	5.4
1	B	41	GLN	5.3
1	A	819	LEU	5.1
1	B	780	ILE	5.1
1	B	806	PRO	5.0
1	A	760	THR	4.7
1	B	83	PHE	4.6
1	A	761	THR	4.5
1	B	785	ARG	4.4
1	B	812	LYS	4.2
1	B	783	PHE	3.9
1	A	641	LEU	3.9
1	B	81	GLU	3.8
1	A	185	LYS	3.6
1	A	817	LEU	3.6
1	B	808	ASP	3.5
1	B	816	SER	3.5
1	B	777	THR	3.5
1	B	753	LYS	3.5
1	B	461	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	43	ASP	3.4
1	B	74	PHE	3.4
1	B	757	GLU	3.4
1	B	810	ARG	3.4
1	B	701	LEU	3.4
1	B	791	LEU	3.4
1	B	123	ASN	3.4
1	B	779	ASP	3.3
1	B	281	PHE	3.3
1	B	782	ASP	3.3
1	B	40	LYS	3.3
1	B	759	LYS	3.2
1	B	776	CYS	3.2
1	B	124	LEU	3.1
1	B	761	THR	3.1
1	B	809	GLN	3.0
1	A	638	LEU	2.9
1	B	38	GLU	2.8
1	B	807	GLY	2.8
1	B	121	PHE	2.8
1	B	762	THR	2.7
1	B	86	LEU	2.7
1	B	764	LEU	2.7
1	A	644	LEU	2.6
1	B	66	THR	2.5
1	A	40	LYS	2.5
1	B	59	GLN	2.5
1	A	613	LEU	2.5
1	A	818	GLU	2.5
1	B	627	ASP	2.5
1	B	64	TYR	2.4
1	B	85	GLY	2.4
1	B	82	SER	2.4
1	A	100	VAL	2.3
1	A	39	LYS	2.3
1	B	603	TYR	2.3
1	B	344	LEU	2.3
1	B	752	ASN	2.3
1	B	385	ASP	2.2
1	A	754	SER	2.2
1	B	754	SER	2.2
1	B	677	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	44	SER	2.2
1	B	272	GLY	2.2
1	B	80	ASN	2.2
1	B	164	GLU	2.2
1	A	610	LEU	2.2
1	B	168	ARG	2.2
1	B	44	SER	2.2
1	A	778	CYS	2.2
1	A	759	LYS	2.1
1	A	186	VAL	2.1
1	B	65	VAL	2.1
1	A	758	THR	2.1
1	A	45	VAL	2.1
1	B	45	VAL	2.1
1	B	702	PHE	2.1
1	A	243	LYS	2.1
1	B	789	GLU	2.1
1	B	271	ASP	2.1
1	B	462	ASP	2.0
1	A	666	LEU	2.0
1	B	122	LEU	2.0
1	A	63	LYS	2.0
1	B	678	PHE	2.0
1	B	758	THR	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. 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
5	NAG	B	1001	14/15	0.97	0.14	0.05	26,30,34,39	0
2	NAG	A	1002	14/15	0.97	0.10	-0.14	16,20,28,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	A	1001	14/15	0.98	0.09	-0.56	14,16,18,19	0
5	NAG	B	1002	14/15	0.94	0.11	-0.73	34,37,48,49	0
2	NAG	A	1009	14/15	0.98	0.10	-1.13	15,18,19,22	0
2	NAG	B	1004	14/15	0.98	0.08	-1.17	22,24,26,30	0
2	NAG	A	1005	14/15	0.98	0.09	-1.21	17,21,24,26	0
2	NAG	B	1008	14/15	0.98	0.08	-1.68	19,22,23,25	0
2	NAG	A	1010	14/15	0.96	0.10	-	21,23,27,29	0
2	NAG	B	1005	14/15	0.95	0.15	-	35,44,63,63	0
2	BMA	A	1003	11/12	0.85	0.21	-	45,57,64,68	0
2	NAG	B	1009	14/15	0.97	0.09	-	27,29,35,42	0
2	BMA	B	1010	11/12	0.79	0.19	-	42,51,55,57	0
2	NAG	A	1006	14/15	0.95	0.15	-	31,36,45,52	0
2	BMA	A	1011	11/12	0.94	0.17	-	31,37,40,47	0
2	BMA	B	1006	11/12	0.84	0.29	-	66,70,75,80	0
2	BMA	A	1007	11/12	0.80	0.28	-	51,60,64,69	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
4	BU3	A	1016	6/6	0.85	0.33	2.52	49,55,58,69	0
3	NAG	A	1014	14/15	0.93	0.23	2.21	42,50,56,57	0
3	NAG	B	1011	14/15	0.90	0.18	0.70	59,67,75,76	0
3	NAG	A	1013	14/15	0.97	0.15	-0.15	17,20,24,26	0
3	NAG	B	1012	14/15	0.91	0.24	-	57,61,64,66	0
3	NAG	A	1008	14/15	0.94	0.29	-	40,47,55,56	0
3	NAG	B	1003	14/15	0.78	0.28	-	59,69,73,76	0
3	NAG	B	1007	14/15	0.91	0.25	-	51,63,70,71	0
3	NAG	A	1015	14/15	0.87	0.20	-	55,64,69,70	0
3	NAG	A	1012	14/15	0.94	0.25	-	44,47,49,49	0
3	NAG	A	1004	14/15	0.94	0.20	-	37,44,49,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.