



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2016 – 03:22 PM EDT

PDB ID : 5IJB
Title : The ligand-free structure of the mouse TLR4/MD-2 complex
Authors : Wang, Y.; Su, L.; Morin, M.D.; Jones, B.T.; Whitby, L.R.; Surakattula, M.; Huang, H.; Shi, H.; Choi, J.H.; Wang, K.; Moresco, E.M.; Berger, M.; Zhan, X.; Zhang, H.; Boger, D.L.; Beutler, B.
Deposited on : 2016-03-01
Resolution : 2.91 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027257
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) : rb-20027257

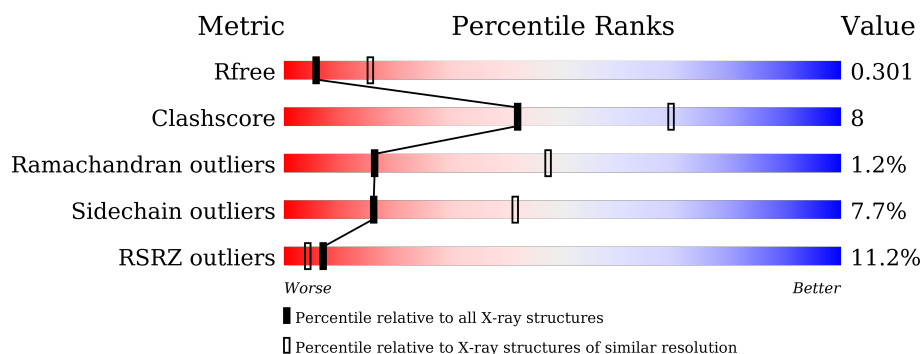
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	1643 (2.94-2.90)
Clashscore	102246	1871 (2.94-2.90)
Ramachandran outliers	100387	1824 (2.94-2.90)
Sidechain outliers	100360	1826 (2.94-2.90)
RSRZ outliers	91569	1650 (2.94-2.90)

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	594	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div>.</div> </div> </div>
1	B	594	<div> <div>15%</div> <div> <div></div> <div>72%</div> <div>25%</div> <div>.</div> </div> </div>
2	C	150	<div> <div>11%</div> <div> <div></div> <div>69%</div> <div>17%</div> <div>5%</div> <div>9%</div> </div> </div>
2	D	150	<div> <div>19%</div> <div> <div></div> <div>71%</div> <div>17%</div> <div>.</div> <div>11%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	702	X	-	-	-
3	NAG	A	703	X	-	-	-
3	NAG	B	703	X	-	-	-
3	NAG	B	707	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11873 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 4, Variable lymphocyte receptor B chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	593	Total	C	N	O	S	0	0	0
			4720	3018	784	893	25			
1	B	592	Total	C	N	O	S	0	0	0
			4713	3014	783	891	25			

- Molecule 2 is a protein called Lymphocyte antigen 96.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	136	Total	C	N	O	S	0	0	0
			1105	713	188	197	7			
2	D	134	Total	C	N	O	S	0	0	0
			1083	701	180	195	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	161	LYS	-	cloning artifact	UNP Q9JHF9
C	162	GLY	-	cloning artifact	UNP Q9JHF9
C	163	GLU	-	cloning artifact	UNP Q9JHF9
C	164	ASN	-	cloning artifact	UNP Q9JHF9
C	165	LEU	-	cloning artifact	UNP Q9JHF9
C	166	TYR	-	cloning artifact	UNP Q9JHF9
C	167	PHE	-	cloning artifact	UNP Q9JHF9
C	168	GLN	-	cloning artifact	UNP Q9JHF9
D	161	LYS	-	cloning artifact	UNP Q9JHF9
D	162	GLY	-	cloning artifact	UNP Q9JHF9
D	163	GLU	-	cloning artifact	UNP Q9JHF9
D	164	ASN	-	cloning artifact	UNP Q9JHF9
D	165	LEU	-	cloning artifact	UNP Q9JHF9
D	166	TYR	-	cloning artifact	UNP Q9JHF9
D	167	PHE	-	cloning artifact	UNP Q9JHF9
D	168	GLN	-	cloning artifact	UNP Q9JHF9

- Molecule 3 is 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	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	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		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

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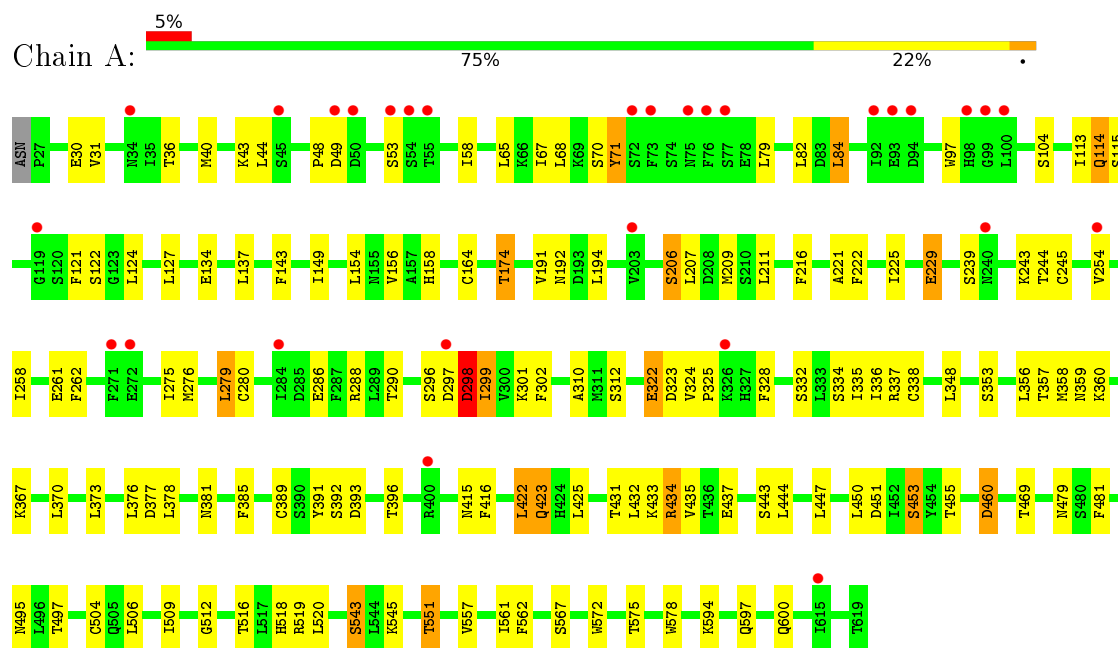
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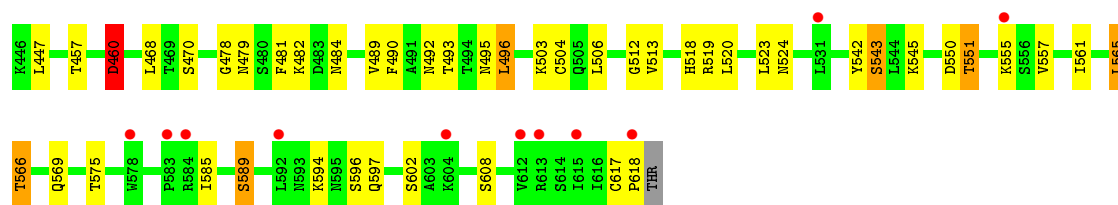
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots

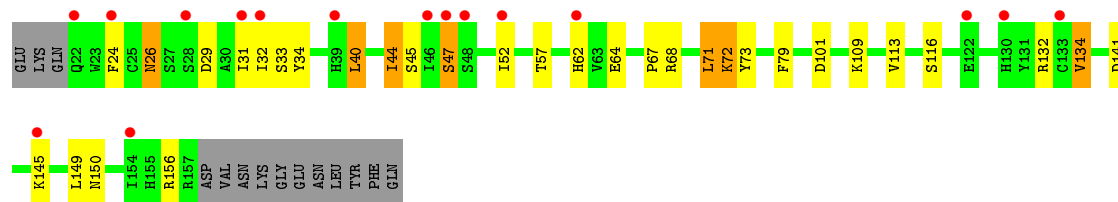
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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 4, Variable lymphocyte receptor B chimera

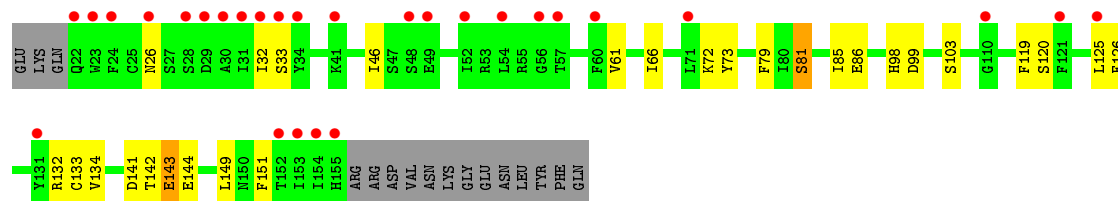
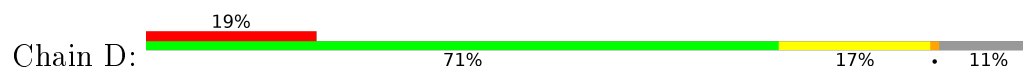




• Molecule 2: Lymphocyte antigen 96



• Molecule 2: Lymphocyte antigen 96



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.32Å 128.32Å 277.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.81 – 2.91 47.35 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.81-2.91) 99.6 (47.35-2.91)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.243 , 0.308 0.241 , 0.301	Depositor DCC
R_{free} test set	2639 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	80.5	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11873	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.60	0/4821	0.79	4/6534 (0.1%)
1	B	0.58	1/4814 (0.0%)	0.77	5/6524 (0.1%)
2	C	0.48	0/1136	0.69	0/1535
2	D	0.45	0/1114	0.60	0/1507
All	All	0.57	1/11885 (0.0%)	0.76	9/16100 (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	2
1	B	0	3
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	460	ASP	CB-CG	-5.45	1.40	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	380	ARG	NE-CZ-NH2	-7.03	116.78	120.30
1	A	460	ASP	CB-CA-C	-6.27	97.87	110.40
1	B	460	ASP	CB-CA-C	-6.23	97.94	110.40
1	A	377	ASP	CB-CG-OD1	5.61	123.35	118.30
1	B	422	LEU	CA-CB-CG	5.26	127.41	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	460	ASP	Peptide
1	A	512	GLY	Peptide
1	B	460	ASP	Peptide
1	B	512	GLY	Peptide
1	B	565	LEU	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	4720	0	4701	79	0
1	B	4713	0	4696	81	0
2	C	1105	0	1067	17	0
2	D	1083	0	1041	16	0
3	A	70	0	64	0	0
3	B	112	0	99	7	0
3	C	42	0	37	4	0
3	D	28	0	26	0	0
All	All	11873	0	11731	198	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 8.

The worst 5 of 198 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:518:HIS:O	1:B:543:SER:HB2	1.70	0.91
1:B:222:PHE:CD2	1:B:225:ILE:HD11	2.07	0.89
1:B:296:SER:O	1:B:299:ILE:HG22	1.76	0.86
1:B:585:ILE:O	1:B:589:SER:OG	1.98	0.80
3:B:703:NAG:H4	3:B:704:NAG:N2	2.03	0.74

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	591/594 (100%)	517 (88%)	70 (12%)	4 (1%)	26	62
1	B	590/594 (99%)	498 (84%)	83 (14%)	9 (2%)	13	41
2	C	134/150 (89%)	125 (93%)	7 (5%)	2 (2%)	13	41
2	D	132/150 (88%)	122 (92%)	8 (6%)	2 (2%)	13	41
All	All	1447/1488 (97%)	1262 (87%)	168 (12%)	17 (1%)	16	47

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	298	ASP
1	A	323	ASP
1	B	66	LYS
1	B	98	HIS
1	B	566	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	550/551 (100%)	510 (93%)	40 (7%)	17	45
1	B	549/551 (100%)	507 (92%)	42 (8%)	16	41
2	C	123/136 (90%)	108 (88%)	15 (12%)	6	18
2	D	121/136 (89%)	115 (95%)	6 (5%)	30	65
All	All	1343/1374 (98%)	1240 (92%)	103 (8%)	16	41

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	47	SER
1	B	59	ASP
1	B	602	SER
2	C	57	THR
2	C	134	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	101	HIS
2	D	98	HIS
1	B	423	GLN
1	A	484	ASN
1	B	111	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

18 non-standard protein/DNA/RNA residues 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	701	1	14,14,15	0.70	0	15,19,21	1.25	3 (20%)
3	NAG	A	702	1	14,14,15	0.43	0	15,19,21	2.43	3 (20%)
3	NAG	A	703	1	14,14,15	1.14	1 (7%)	15,19,21	1.87	3 (20%)
3	NAG	A	704	1,3	14,14,15	0.73	0	15,19,21	1.42	2 (13%)
3	NAG	A	705	3	14,14,15	0.71	0	15,19,21	1.76	4 (26%)
3	NAG	B	701	1,3	14,14,15	0.48	0	15,19,21	1.68	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	702	3	14,14,15	0.67	0	15,19,21	1.46	2 (13%)
3	NAG	B	703	1,3	14,14,15	1.25	2 (14%)	15,19,21	3.60	6 (40%)
3	NAG	B	704	3	14,14,15	0.95	1 (7%)	15,19,21	1.51	3 (20%)
3	NAG	B	705	1,3	14,14,15	1.15	1 (7%)	15,19,21	2.48	9 (60%)
3	NAG	B	706	3	14,14,15	0.71	0	15,19,21	1.46	2 (13%)
3	NAG	B	707	1,3	14,14,15	0.83	0	15,19,21	2.03	5 (33%)
3	NAG	B	708	3	14,14,15	0.60	0	15,19,21	1.38	3 (20%)
3	NAG	C	201	2	14,14,15	0.53	0	15,19,21	1.65	2 (13%)
3	NAG	C	202	3,2	14,14,15	1.21	1 (7%)	15,19,21	3.07	6 (40%)
3	NAG	C	203	3	14,14,15	0.79	1 (7%)	15,19,21	1.65	2 (13%)
3	NAG	D	201	2	14,14,15	0.56	0	15,19,21	1.50	1 (6%)
3	NAG	D	202	2	14,14,15	0.66	0	15,19,21	1.66	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
3	NAG	A	701	1	-	0/6/23/26	0/1/1/1
3	NAG	A	702	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	703	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	704	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	705	3	-	0/6/23/26	0/1/1/1
3	NAG	B	701	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	702	3	-	0/6/23/26	0/1/1/1
3	NAG	B	703	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	704	3	-	0/6/23/26	0/1/1/1
3	NAG	B	705	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	706	3	-	0/6/23/26	0/1/1/1
3	NAG	B	707	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	708	3	-	0/6/23/26	0/1/1/1
3	NAG	C	201	2	-	0/6/23/26	0/1/1/1
3	NAG	C	202	3,2	-	0/6/23/26	0/1/1/1
3	NAG	C	203	3	-	0/6/23/26	0/1/1/1
3	NAG	D	201	2	-	0/6/23/26	0/1/1/1
3	NAG	D	202	2	-	0/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	202	NAG	O4-C4	-3.77	1.34	1.43
3	B	705	NAG	O4-C4	-3.56	1.34	1.43
3	B	704	NAG	C1-C2	2.42	1.55	1.52
3	B	703	NAG	C2-N2	2.46	1.50	1.46
3	C	203	NAG	C1-C2	2.57	1.56	1.52

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	703	NAG	O5-C5-C4	-6.01	100.17	110.13
3	B	707	NAG	O5-C5-C4	-3.79	103.85	110.13
3	B	703	NAG	O7-C7-C8	-3.55	115.53	122.07
3	C	202	NAG	O4-C4-C3	-3.51	102.45	110.36
3	A	705	NAG	O5-C5-C4	-3.42	104.47	110.13

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	703	NAG	C1
3	B	707	NAG	C1
3	A	702	NAG	C1
3	B	703	NAG	C1

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	703	NAG	4	0
3	B	704	NAG	2	0
3	B	705	NAG	1	0
3	B	706	NAG	1	0
3	B	707	NAG	1	0
3	C	202	NAG	4	0
3	C	203	NAG	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

18 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	701	1	14,14,15	0.70	0	15,19,21	1.25	3 (20%)
3	NAG	A	702	1	14,14,15	0.43	0	15,19,21	2.43	3 (20%)
3	NAG	A	703	1	14,14,15	1.14	1 (7%)	15,19,21	1.87	3 (20%)
3	NAG	A	704	1,3	14,14,15	0.73	0	15,19,21	1.42	2 (13%)
3	NAG	A	705	3	14,14,15	0.71	0	15,19,21	1.76	4 (26%)
3	NAG	B	701	1,3	14,14,15	0.48	0	15,19,21	1.68	5 (33%)
3	NAG	B	702	3	14,14,15	0.67	0	15,19,21	1.46	2 (13%)
3	NAG	B	703	1,3	14,14,15	1.25	2 (14%)	15,19,21	3.60	6 (40%)
3	NAG	B	704	3	14,14,15	0.95	1 (7%)	15,19,21	1.51	3 (20%)
3	NAG	B	705	1,3	14,14,15	1.15	1 (7%)	15,19,21	2.48	9 (60%)
3	NAG	B	706	3	14,14,15	0.71	0	15,19,21	1.46	2 (13%)
3	NAG	B	707	1,3	14,14,15	0.83	0	15,19,21	2.03	5 (33%)
3	NAG	B	708	3	14,14,15	0.60	0	15,19,21	1.38	3 (20%)
3	NAG	C	201	2	14,14,15	0.53	0	15,19,21	1.65	2 (13%)
3	NAG	C	202	3,2	14,14,15	1.21	1 (7%)	15,19,21	3.07	6 (40%)
3	NAG	C	203	3	14,14,15	0.79	1 (7%)	15,19,21	1.65	2 (13%)
3	NAG	D	201	2	14,14,15	0.56	0	15,19,21	1.50	1 (6%)
3	NAG	D	202	2	14,14,15	0.66	0	15,19,21	1.66	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
3	NAG	A	701	1	-	0/6/23/26	0/1/1/1
3	NAG	A	702	1	1/1/5/7	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	703	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	704	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	705	3	-	0/6/23/26	0/1/1/1
3	NAG	B	701	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	702	3	-	0/6/23/26	0/1/1/1
3	NAG	B	703	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	704	3	-	0/6/23/26	0/1/1/1
3	NAG	B	705	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	706	3	-	0/6/23/26	0/1/1/1
3	NAG	B	707	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	708	3	-	0/6/23/26	0/1/1/1
3	NAG	C	201	2	-	0/6/23/26	0/1/1/1
3	NAG	C	202	3,2	-	0/6/23/26	0/1/1/1
3	NAG	C	203	3	-	0/6/23/26	0/1/1/1
3	NAG	D	201	2	-	0/6/23/26	0/1/1/1
3	NAG	D	202	2	-	0/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	202	NAG	O4-C4	-3.77	1.34	1.43
3	B	705	NAG	O4-C4	-3.56	1.34	1.43
3	B	704	NAG	C1-C2	2.42	1.55	1.52
3	B	703	NAG	C2-N2	2.46	1.50	1.46
3	C	203	NAG	C1-C2	2.57	1.56	1.52

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	703	NAG	O5-C5-C4	-6.01	100.17	110.13
3	B	707	NAG	O5-C5-C4	-3.79	103.85	110.13
3	B	703	NAG	O7-C7-C8	-3.55	115.53	122.07
3	C	202	NAG	O4-C4-C3	-3.51	102.45	110.36
3	A	705	NAG	O5-C5-C4	-3.42	104.47	110.13

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	703	NAG	C1
3	B	707	NAG	C1
3	A	702	NAG	C1
3	B	703	NAG	C1

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	703	NAG	4	0
3	B	704	NAG	2	0
3	B	705	NAG	1	0
3	B	706	NAG	1	0
3	B	707	NAG	1	0
3	C	202	NAG	4	0
3	C	203	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	593/594 (99%)	0.41	29 (4%) 33 28	47, 90, 140, 171	0
1	B	592/594 (99%)	0.90	90 (15%) 3 2	47, 97, 182, 240	0
2	C	136/150 (90%)	0.54	16 (11%) 6 4	74, 107, 166, 191	2 (1%)
2	D	134/150 (89%)	1.10	28 (20%) 1 1	80, 117, 158, 179	2 (1%)
All	All	1455/1488 (97%)	0.69	163 (11%) 7 4	47, 97, 165, 240	4 (0%)

The worst 5 of 163 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	100	LEU	13.8
1	A	76	PHE	10.3
1	B	73	PHE	8.8
2	D	22	GLN	8.2
1	B	76	PHE	8.2

6.2 Non-standard residues in protein, DNA, RNA chains [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	D	201	14/15	0.77	0.31	1.00	115,120,122,127	0
3	NAG	A	704	14/15	0.93	0.18	-0.59	66,71,76,76	0
3	NAG	B	705	14/15	0.88	0.17	-1.05	65,78,88,97	0
3	NAG	C	202	14/15	0.91	0.11	-1.38	116,122,129,138	0
3	NAG	B	704	14/15	0.64	0.31	-	107,131,137,139	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	C	201	14/15	0.86	0.13	-	138,147,150,156	0
3	NAG	B	707	14/15	0.88	0.12	-	119,134,139,149	0
3	NAG	A	702	14/15	0.90	0.24	-	126,130,133,134	0
3	NAG	A	705	14/15	0.89	0.21	-	70,81,91,95	0
3	NAG	A	703	14/15	0.76	0.25	-	96,105,115,117	0
3	NAG	A	701	14/15	0.84	0.21	-	99,111,132,134	0
3	NAG	B	701	14/15	0.89	0.19	-	117,124,127,127	0
3	NAG	B	706	14/15	0.87	0.22	-	90,100,104,107	0
3	NAG	C	203	14/15	0.76	0.33	-	123,142,156,158	0
3	NAG	B	702	14/15	0.83	0.22	-	105,119,127,129	0
3	NAG	D	202	14/15	0.79	0.20	-	134,143,146,149	0
3	NAG	B	708	14/15	0.82	0.22	-	155,164,170,171	0
3	NAG	B	703	14/15	0.73	0.21	-	98,120,136,138	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(\AA^2)	Q<0.9
3	NAG	D	201	14/15	0.77	0.31	1.00	115,120,122,127	0
3	NAG	A	704	14/15	0.93	0.18	-0.59	66,71,76,76	0
3	NAG	B	705	14/15	0.88	0.17	-1.05	65,78,88,97	0
3	NAG	C	202	14/15	0.91	0.11	-1.38	116,122,129,138	0
3	NAG	B	704	14/15	0.64	0.31	-	107,131,137,139	0
3	NAG	C	201	14/15	0.86	0.13	-	138,147,150,156	0
3	NAG	B	707	14/15	0.88	0.12	-	119,134,139,149	0
3	NAG	A	702	14/15	0.90	0.24	-	126,130,133,134	0
3	NAG	A	705	14/15	0.89	0.21	-	70,81,91,95	0
3	NAG	A	703	14/15	0.76	0.25	-	96,105,115,117	0
3	NAG	A	701	14/15	0.84	0.21	-	99,111,132,134	0
3	NAG	B	701	14/15	0.89	0.19	-	117,124,127,127	0
3	NAG	B	706	14/15	0.87	0.22	-	90,100,104,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	C	203	14/15	0.76	0.33	-	123,142,156,158	0
3	NAG	B	702	14/15	0.83	0.22	-	105,119,127,129	0
3	NAG	D	202	14/15	0.79	0.20	-	134,143,146,149	0
3	NAG	B	708	14/15	0.82	0.22	-	155,164,170,171	0
3	NAG	B	703	14/15	0.73	0.21	-	98,120,136,138	0

6.5 Other polymers [i](#)

There are no such residues in this entry.