



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 01:10 AM GMT

PDB ID : 3W3M  
Title : Crystal structure of human TLR8 in complex with Resiquimod (R848) crystal form 2  
Authors : Tanji, H.; Ohto, U.; Shimizu, T.  
Deposited on : 2012-12-22  
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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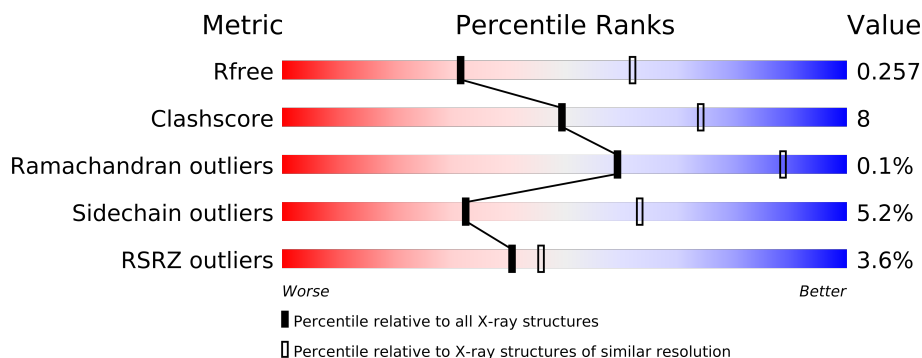
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	

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

Mol	Type	Chain	Res	Geometry	Electron density
6	SO4	A	919	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6348 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.

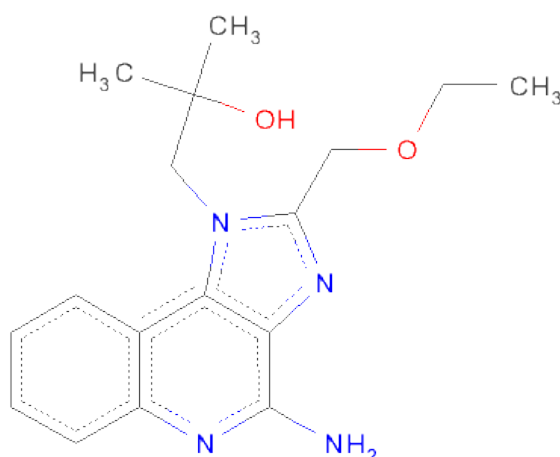
- Molecule 1 is a protein called Toll-like receptor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	751	Total	C	N	O	S	0	0	0
			6035	3859	1025	1132	19			

There are 10 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

- Molecule 2 is 1-[4-AMINO-2-(ETHOXYMETHYL)-1H-IMIDAZO[4,5-C]QUINOLIN-1-YL]-2-METHYLPROPAN-2-OL (three-letter code: RX8) (formula: C<sub>17</sub>H<sub>22</sub>N<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	17	4	2		

- Molecule 3 is a polymer of unknown type called SUGAR (5-MER).

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

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
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97

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Chain	Residue	Modelled	Actual	Comment	Reference
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

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

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

There are 10 discrepancies between the modelled and reference sequences:

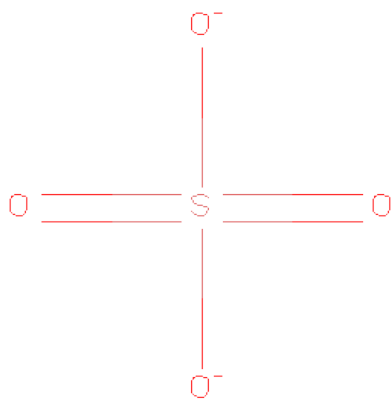
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ARG	-	EXPRESSION TAG	UNP Q9NR97
A	24	SER	-	EXPRESSION TAG	UNP Q9NR97
A	25	PRO	-	EXPRESSION TAG	UNP Q9NR97
A	26	TRP	-	EXPRESSION TAG	UNP Q9NR97
A	828	GLU	-	EXPRESSION TAG	UNP Q9NR97
A	829	PHE	-	EXPRESSION TAG	UNP Q9NR97
A	830	LEU	-	EXPRESSION TAG	UNP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

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		

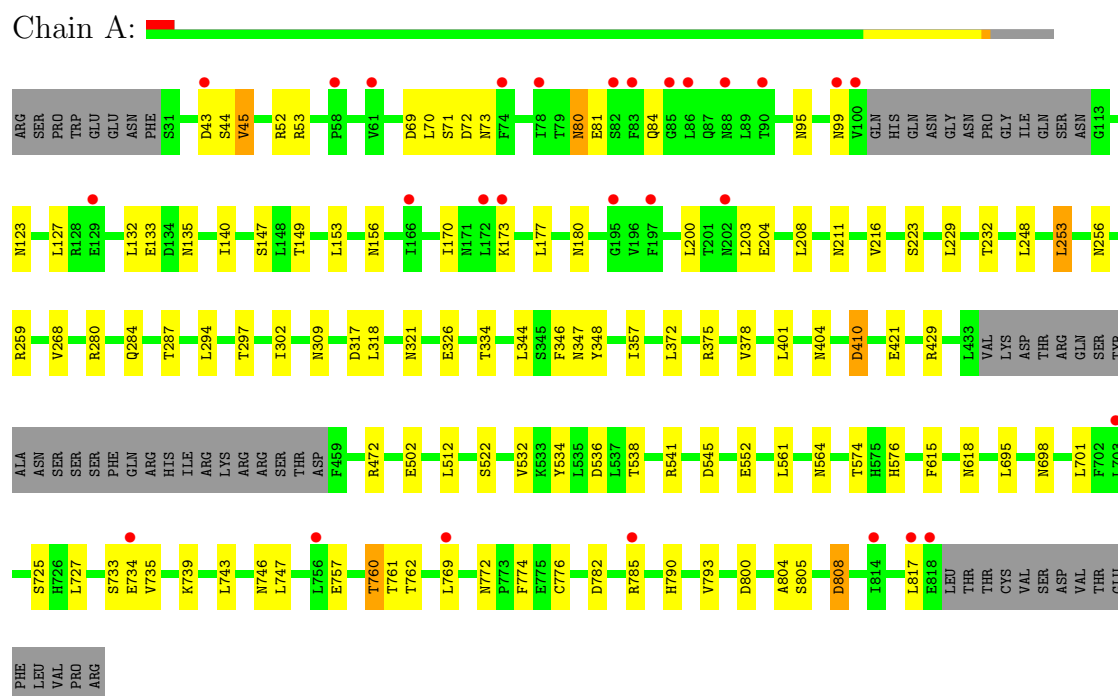
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	68	Total	O	0	0
			68	68		

### 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





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.77Å 106.00Å 72.32Å 90.00° 106.94° 90.00°	Depositor
Resolution (Å)	41.84 – 2.70 41.84 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.8 (41.84-2.70) 97.8 (41.84-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.220 , 0.255 0.223 , 0.257	Depositor DCC
$R_{free}$ test set	1340 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.4	Xtriage
Anisotropy	0.516	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 30.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 26593 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6348	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: MAN, RX8, BMA, NAG, SO4

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	0.28	0/6160	0.53	0/8356

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	6035	0	0	48	2
2	A	23	0	0	0	0
3	A	122	0	0	0	0
4	A	39	0	0	0	0
5	A	56	0	0	0	0
6	A	5	0	0	1	0
7	A	68	0	0	5	1
All	All	6348	0	0	48	2

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 8.

All (48) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:725:SER:N	7:A:1023:HOH:O	2.17	0.75
1:A:776:CYS:N	1:A:805:SER:O	2.21	0.73
1:A:344:LEU:O	1:A:347:ASN:ND2	2.23	0.72
1:A:375:ARG:NH2	6:A:919:SO4:O4	2.26	0.68
1:A:318:LEU:O	1:A:321:ASN:ND2	2.28	0.67
1:A:346:PHE:N	1:A:375:ARG:O	2.27	0.67
1:A:72:ASP:OD1	1:A:99:ASN:ND2	2.29	0.65
1:A:80:ASN:N	1:A:80:ASN:OD1	2.27	0.65
1:A:177:LEU:O	1:A:180:ASN:ND2	2.30	0.65
1:A:253:LEU:O	1:A:256:ASN:ND2	2.30	0.64
1:A:284:GLN:O	1:A:309:ASN:ND2	2.31	0.64
1:A:760:THR:OG1	1:A:761:THR:N	2.31	0.63
1:A:576:HIS:NE2	7:A:1040:HOH:O	2.31	0.62
1:A:153:LEU:O	1:A:156:ASN:ND2	2.34	0.61
1:A:733:SER:OG	1:A:757:GLU:O	2.18	0.60
1:A:302:ILE:N	1:A:326:GLU:OE2	2.36	0.59
1:A:44:SER:OG	1:A:45:VAL:N	2.36	0.58
1:A:774:PHE:O	1:A:804:ALA:N	2.36	0.58
1:A:782:ASP:OD1	1:A:785:ARG:NH2	2.37	0.58
1:A:410:ASP:OD1	1:A:410:ASP:N	2.37	0.57
1:A:259:ARG:NH2	1:A:348:TYR:O	2.37	0.57
1:A:208:LEU:O	1:A:211:ASN:ND2	2.38	0.57
1:A:357:ILE:N	7:A:1016:HOH:O	2.39	0.55
1:A:808:ASP:N	1:A:808:ASP:OD1	2.41	0.53
1:A:259:ARG:NH1	1:A:321:ASN:O	2.42	0.53
1:A:84:GLN:OE1	1:A:123:ASN:ND2	2.42	0.53
1:A:561:LEU:O	1:A:564:ASN:ND2	2.43	0.51
1:A:149:THR:O	1:A:173:LYS:N	2.44	0.51
1:A:739:LYS:NZ	7:A:1025:HOH:O	2.44	0.51
1:A:70:LEU:O	1:A:73:ASN:ND2	2.46	0.48
1:A:69:ASP:OD1	1:A:71:SER:OG	2.31	0.48
1:A:53:ARG:NH1	1:A:800:ASP:OD1	2.47	0.48
1:A:615:PHE:O	1:A:618:ASN:ND2	2.47	0.47
1:A:229:LEU:O	1:A:232:THR:OG1	2.34	0.46
1:A:695:LEU:O	1:A:698:ASN:ND2	2.49	0.46
1:A:769:LEU:O	1:A:772:ASN:ND2	2.49	0.46
1:A:401:LEU:O	1:A:404:ASN:ND2	2.50	0.45
1:A:132:LEU:O	1:A:135:ASN:ND2	2.50	0.45
1:A:81:GLU:N	1:A:81:GLU:OE1	2.50	0.44
1:A:216:VAL:N	7:A:1047:HOH:O	2.51	0.44
1:A:536:ASP:OD1	1:A:538:THR:OG1	2.36	0.42
1:A:294:LEU:O	1:A:297:THR:OG1	2.37	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:95:ASN:OD1	1:A:133:GLU:N	2.52	0.42
1:A:203:LEU:O	1:A:223:SER:OG	2.39	0.41
1:A:309:ASN:OD1	1:A:309:ASN:N	2.54	0.41
1:A:743:LEU:O	1:A:746:ASN:ND2	2.54	0.40
1:A:552:GLU:N	1:A:552:GLU:OE1	2.55	0.40
1:A:545:ASP:OD1	1:A:574:THR:OG1	2.39	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:280:ARG:NH2	1:A:734:GLU:OE2[3_455]	2.08	0.12
1:A:429:ARG:NH2	7:A:1060:HOH:O[2_555]	2.11	0.09

## 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	745/811 (92%)	714 (96%)	30 (4%)	1 (0%)	59 89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	VAL

### 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	693/755 (92%)	657 (95%)	36 (5%)	32 63

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

Mol	Chain	Res	Type
1	A	43	ASP
1	A	45	VAL
1	A	52	ARG
1	A	80	ASN
1	A	127	LEU
1	A	140	ILE
1	A	147	SER
1	A	170	ILE
1	A	200	LEU
1	A	204	GLU
1	A	248	LEU
1	A	253	LEU
1	A	268	VAL
1	A	287	THR
1	A	317	ASP
1	A	334	THR
1	A	372	LEU
1	A	410	ASP
1	A	421	GLU
1	A	472	ARG
1	A	502	GLU
1	A	512	LEU
1	A	522	SER
1	A	532	VAL
1	A	534	TYR
1	A	541	ARG
1	A	701	LEU
1	A	727	LEU
1	A	735	VAL
1	A	747	LEU
1	A	760	THR
1	A	762	THR
1	A	790	HIS
1	A	793	VAL
1	A	808	ASP
1	A	817	LEU

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 ⓘ

13 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	$\# Z  > 2$
3	NAG	A	902	1,3	12,14,15	0.68	0	15,19,21	0.83	1 (6%)
3	NAG	A	903	3	12,14,15	0.65	0	15,19,21	0.85	0
3	BMA	A	904	3	10,11,12	0.53	0	11,15,17	0.94	0
3	MAN	A	905	3	10,11,12	0.78	0	11,15,17	0.72	0
3	MAN	A	906	3	10,11,12	0.80	0	11,15,17	0.63	0
4	NAG	A	907	1,4	12,14,15	0.64	0	15,19,21	0.81	1 (6%)
4	NAG	A	908	4	12,14,15	0.71	1 (8%)	15,19,21	0.98	0
4	BMA	A	909	4	10,11,12	0.60	0	11,15,17	0.91	0
3	NAG	A	911	1,3	12,14,15	1.46	2 (16%)	15,19,21	1.30	2 (13%)
3	NAG	A	912	3	12,14,15	1.80	4 (33%)	15,19,21	1.91	5 (33%)
3	BMA	A	913	3	10,11,12	1.22	2 (20%)	11,15,17	1.60	5 (45%)
3	MAN	A	914	3	10,11,12	0.84	1 (10%)	11,15,17	0.84	1 (9%)
3	MAN	A	915	3	10,11,12	0.74	0	11,15,17	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	902	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	903	3	-	0/6/23/26	0/1/1/1
3	BMA	A	904	3	-	0/2/19/22	0/1/1/1
3	MAN	A	905	3	-	0/2/19/22	0/1/1/1
3	MAN	A	906	3	-	0/2/19/22	0/1/1/1
4	NAG	A	907	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	908	4	-	0/6/23/26	0/1/1/1
4	BMA	A	909	4	-	0/2/19/22	0/1/1/1
3	NAG	A	911	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	912	3	-	0/6/23/26	0/1/1/1
3	BMA	A	913	3	-	0/2/19/22	0/1/1/1
3	MAN	A	914	3	-	0/2/19/22	0/1/1/1
3	MAN	A	915	3	-	0/2/19/22	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	912	NAG	O5-C5	-2.92	1.40	1.45
3	A	911	NAG	C2-N2	-2.87	1.43	1.46
3	A	912	NAG	C2-N2	-2.57	1.43	1.46
3	A	912	NAG	O7-C7	-2.34	1.18	1.23
3	A	912	NAG	C8-C7	-2.28	1.45	1.50
3	A	911	NAG	O7-C7	-2.25	1.18	1.23
4	A	908	NAG	O5-C5	-2.21	1.41	1.45
3	A	913	BMA	O5-C5	-2.16	1.41	1.45
3	A	913	BMA	O2-C2	-2.15	1.39	1.43
3	A	914	MAN	O5-C5	-2.12	1.41	1.45

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	912	NAG	O3-C3-C4	-3.83	101.77	110.35
3	A	912	NAG	C6-C5-C4	-3.45	104.66	113.00
3	A	911	NAG	C3-C4-C5	-2.89	105.04	110.20
3	A	912	NAG	O4-C4-C3	-2.65	104.40	110.35
3	A	913	BMA	O2-C2-C3	-2.62	104.53	110.18
3	A	914	MAN	O5-C5-C6	2.28	109.37	106.98
3	A	912	NAG	O7-C7-C8	-2.28	117.60	122.04
3	A	913	BMA	O5-C5-C4	-2.21	107.85	110.65
3	A	902	NAG	O5-C5-C6	2.15	109.24	106.98
3	A	913	BMA	C6-C5-C4	-2.12	107.88	113.00
3	A	911	NAG	O5-C5-C4	-2.07	108.03	110.65
3	A	912	NAG	C8-C7-N2	2.05	120.11	116.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	913	BMA	C3-C4-C5	2.05	113.86	110.20
4	A	907	NAG	O5-C5-C6	2.03	109.11	106.98
3	A	913	BMA	O4-C4-C5	-2.03	103.94	109.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

6 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
2	RX8	A	901	-	25,25,25	1.58	4 (16%)	37,37,37	1.50	6 (16%)
5	NAG	A	910	1	12,14,15	0.71	1 (8%)	15,19,21	0.97	0
5	NAG	A	916	1	12,14,15	0.65	0	15,19,21	1.01	1 (6%)
5	NAG	A	917	1	12,14,15	0.64	0	15,19,21	0.86	1 (6%)
5	NAG	A	918	1	12,14,15	0.69	1 (8%)	15,19,21	0.89	1 (6%)
6	SO4	A	919	-	4,4,4	0.26	0	6,6,6	0.08	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	RX8	A	901	-	-	2/9/9/9	0/0/3/3
5	NAG	A	910	1	-	0/6/23/26	0/1/1/1
5	NAG	A	916	1	-	0/6/23/26	0/1/1/1
5	NAG	A	917	1	-	0/6/23/26	0/1/1/1
5	NAG	A	918	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SO4	A	919	-	-	0/0/0/0	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	RX8	C2-C3	4.73	1.49	1.40
2	A	901	RX8	C2-C1	-2.71	1.37	1.41
2	A	901	RX8	C-N	2.70	1.43	1.35
2	A	901	RX8	O1-C10	-2.26	1.38	1.44
5	A	910	NAG	O5-C5	-2.18	1.41	1.45
5	A	918	NAG	O5-C5	-2.10	1.41	1.45

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	RX8	C9-N3-C5	-5.29	124.20	127.34
2	A	901	RX8	C-N1-C1	4.04	121.90	118.42
2	A	901	RX8	C6-O-C7	3.33	119.69	112.57
5	A	916	NAG	O5-C5-C6	2.95	110.08	106.98
2	A	901	RX8	C2-C1-N1	-2.49	120.75	123.02
5	A	918	NAG	O5-C5-C6	2.49	109.59	106.98
5	A	917	NAG	O5-C5-C6	2.08	109.16	106.98
2	A	901	RX8	C2-C3-N3	2.05	134.76	130.42
2	A	901	RX8	O-C6-C5	2.02	117.16	111.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	RX8	O-C6-C5-N3
2	A	901	RX8	O-C6-C5-N2

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	751/811 (92%)	0.23	28 (3%)	39 44	21, 54, 99, 122	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	GLY	5.7
1	A	83	PHE	4.9
1	A	86	LEU	4.3
1	A	166	ILE	4.3
1	A	202	ASN	3.9
1	A	100	VAL	3.8
1	A	43	ASP	3.8
1	A	734	GLU	3.5
1	A	197	PHE	3.5
1	A	61	VAL	3.2
1	A	58	PRO	3.0
1	A	756	LEU	2.9
1	A	82	SER	2.9
1	A	88	ASN	2.9
1	A	769	LEU	2.8
1	A	78	ILE	2.7
1	A	90	THR	2.6
1	A	99	ASN	2.5
1	A	172	LEU	2.3
1	A	195	GLY	2.2
1	A	814	ILE	2.2
1	A	74	PHE	2.2
1	A	817	LEU	2.2
1	A	129	GLU	2.1
1	A	818	GLU	2.1
1	A	785	ARG	2.1
1	A	173	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	703	LEU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	NAG	A	908	14/15	0.19	1.65	54,64,70,71	0
3	MAN	A	905	11/12	0.14	1.02	50,54,56,57	0
3	NAG	A	903	14/15	0.19	0.29	34,41,48,50	0
3	NAG	A	902	14/15	0.18	0.14	37,47,50,50	0
4	NAG	A	907	14/15	0.14	-0.38	28,32,40,43	0
3	NAG	A	912	14/15	0.13	-1.32	21,33,44,47	0
3	NAG	A	911	14/15	0.10	-2.78	17,30,37,41	0
3	BMA	A	904	11/12	0.13	-	45,48,55,63	0
3	MAN	A	906	11/12	0.17	-	69,72,78,82	0
3	MAN	A	914	11/12	0.16	-	87,89,92,93	0
3	BMA	A	913	11/12	0.10	-	57,67,82,87	0
4	BMA	A	909	11/12	0.15	-	68,70,75,77	0
3	MAN	A	915	11/12	0.25	-	81,86,90,91	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	SO4	A	919	5/5	0.28	2.47	113,114,115,117	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	917	14/15	0.21	1.76	45,60,71,72	0
5	NAG	A	916	14/15	0.15	1.19	60,71,73,76	0
5	NAG	A	918	14/15	0.17	0.82	32,47,56,57	0
2	RX8	A	901	23/23	0.20	0.74	28,36,51,52	0
5	NAG	A	910	14/15	0.14	-0.73	54,59,75,79	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.