



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2016 – 02:18 PM EDT

PDB ID : 5GMG
Title : Crystal structure of monkey TLR7 in complex with loxoribine and polyU
Authors : Zhang, Z.; Ohto, U.; Shimizu, T.
Deposited on : 2016-07-14
Resolution : 2.60 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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-20027939

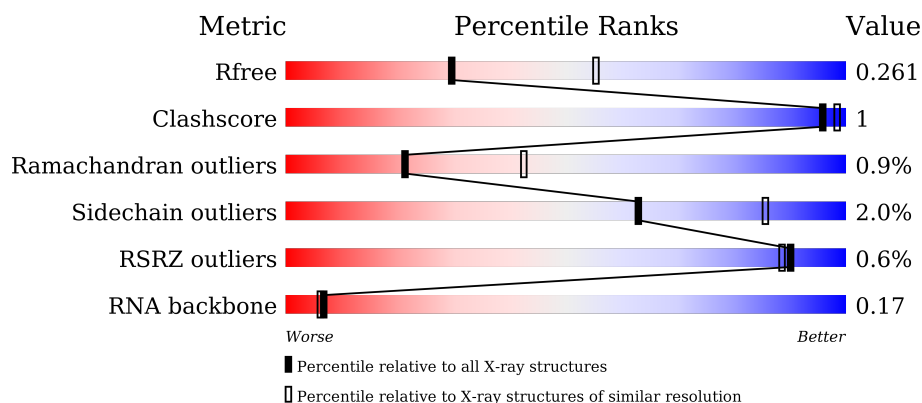
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)
RNA backbone	2183	1022 (3.00-2.20)

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	817	
1	B	817	
2	C	4	
2	D	4	

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	904	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12680 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 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	762	Total	C	N	O	S	0	0	0
			6166	3952	1050	1134	30			
1	B	762	Total	C	N	O	S	0	0	0
			6160	3949	1047	1134	30			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ARG	-	expression tag	UNP B3Y653
A	24	SER	-	expression tag	UNP B3Y653
A	25	PRO	-	expression tag	UNP B3Y653
A	26	TRP	-	expression tag	UNP B3Y653
A	167	GLN	ASN	engineered mutation	UNP B3Y653
A	389	GLN	ASN	engineered mutation	UNP B3Y653
A	488	GLN	ASN	engineered mutation	UNP B3Y653
A	799	GLN	ASN	engineered mutation	UNP B3Y653
B	23	ARG	-	expression tag	UNP B3Y653
B	24	SER	-	expression tag	UNP B3Y653
B	25	PRO	-	expression tag	UNP B3Y653
B	26	TRP	-	expression tag	UNP B3Y653
B	167	GLN	ASN	engineered mutation	UNP B3Y653
B	389	GLN	ASN	engineered mutation	UNP B3Y653
B	488	GLN	ASN	engineered mutation	UNP B3Y653
B	799	GLN	ASN	engineered mutation	UNP B3Y653

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*U)-3').

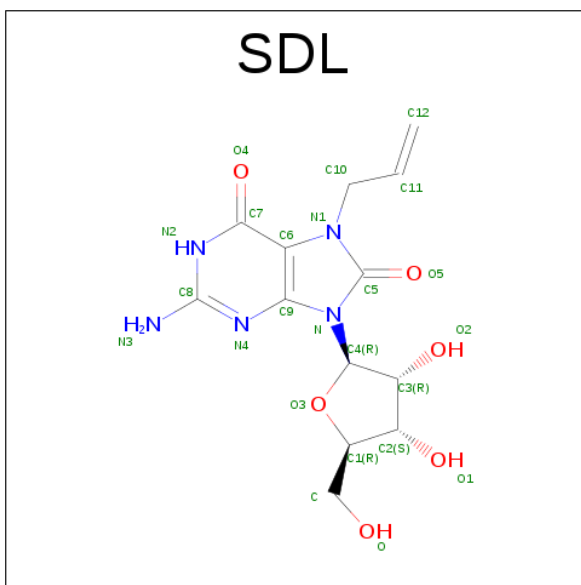
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	P	0	0	0
			64	27	6	27	4			
2	D	4	Total	C	N	O	P	0	0	0
			64	27	6	27	4			

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



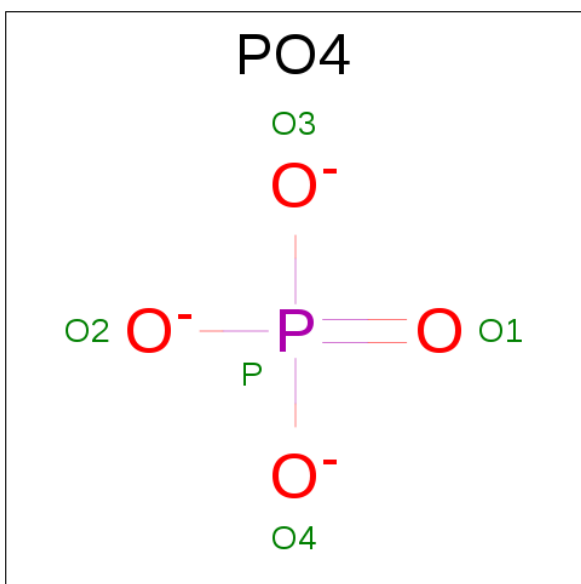
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	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 2-azanyl-9-[(2 {R},3 {R},4 {S},5 {R})-5-(hydroxymethyl)-3,4-bis(oxidan-yl)oxolan-2-yl]-7-prop-2-enyl-1 {H}-purine-6,8-dione (three-letter code: SDL) (formula: $C_{13}H_{17}N_5O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			24	13	5	6		
4	B	1	Total	C	N	O	0	0
			24	13	5	6		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		

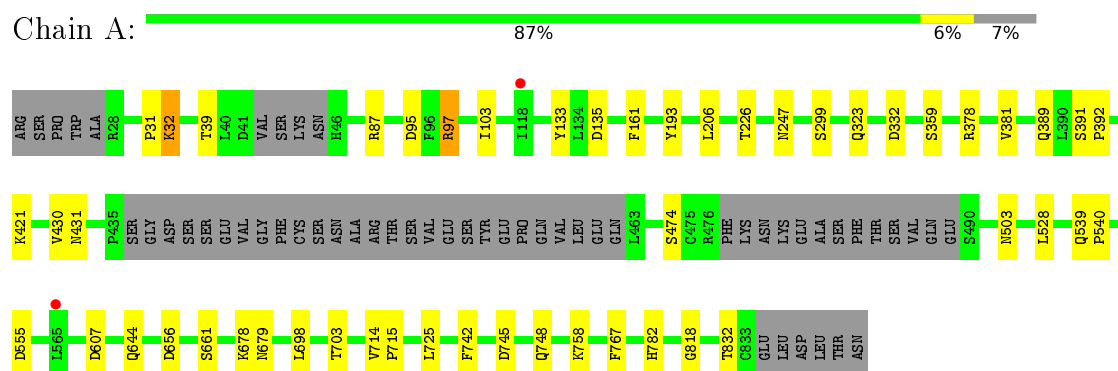
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	16	Total 16	O 16	0	0
6	B	17	Total 17	O 17	0	0

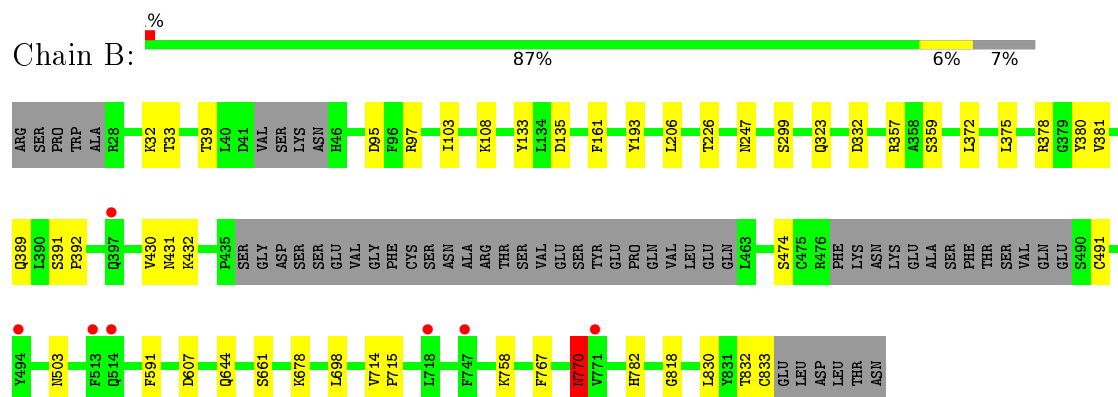
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

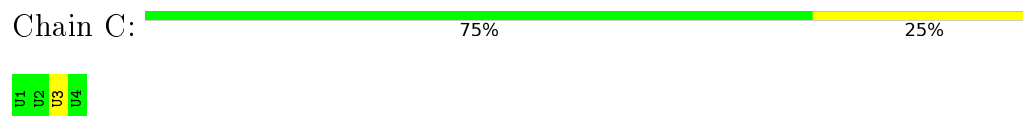
• Molecule 1: Toll-like receptor 7



• Molecule 1: Toll-like receptor 7



• Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



• Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.28 Å 99.41 Å 112.10 Å 90.00° 98.58° 90.00°	Depositor
Resolution (Å)	50.01 – 2.60 48.59 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.5 (50.01-2.60) 93.6 (48.59-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.61 Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.215 , 0.258 0.216 , 0.261	Depositor DCC
R_{free} test set	3088 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	64.0	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.3	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	0.94	EDS
Total number of atoms	12680	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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: SDL, PO4, 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	0.61	0/6295	0.80	4/8530 (0.0%)
1	B	0.61	0/6289	0.79	4/8523 (0.0%)
2	C	0.50	0/69	0.78	0/105
2	D	0.42	0/69	0.93	0/105
All	All	0.61	0/12722	0.80	8/17263 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	A	378	ARG	NE-CZ-NH2	-6.57	117.02	120.30
1	B	378	ARG	NE-CZ-NH1	6.33	123.47	120.30
1	B	378	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	B	833	CYS	CA-CB-SG	-5.64	103.85	114.00
1	B	770	ASN	CB-CA-C	-5.63	99.14	110.40
1	A	97	ARG	NE-CZ-NH1	5.09	122.85	120.30
1	A	87	ARG	NE-CZ-NH1	5.07	122.83	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6166	0	6206	21	0
1	B	6160	0	6195	17	0
2	C	64	0	30	0	0
2	D	64	0	30	0	0
3	A	70	0	64	1	0
3	B	70	0	64	1	0
4	B	48	0	0	0	0
5	B	5	0	0	0	0
6	A	16	0	0	2	0
6	B	17	0	0	0	0
All	All	12680	0	12589	37	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 1.

All (37) 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:A:679:ASN:HB2	1:A:703:THR:HB	1.59	0.85
1:A:679:ASN:CB	1:A:703:THR:HB	2.24	0.66
1:B:431:ASN:HB2	1:B:503:ASN:HD21	1.69	0.58
1:A:299:SER:HA	1:A:323:GLN:O	2.04	0.58
1:B:299:SER:HA	1:B:323:GLN:O	2.05	0.57
1:A:431:ASN:HB2	1:A:503:ASN:HD21	1.70	0.54
1:B:247:ASN:N	1:B:247:ASN:OD1	2.43	0.52
1:A:206:LEU:O	1:A:226:THR:HG23	2.10	0.52
1:A:555:ASP:OD2	1:B:432:LYS:NZ	2.43	0.52
1:A:247:ASN:N	1:A:247:ASN:OD1	2.44	0.50
1:B:206:LEU:O	1:B:226:THR:HG23	2.09	0.50
1:B:431:ASN:CB	1:B:503:ASN:HD21	2.24	0.50
1:B:770:ASN:H	1:B:770:ASN:HD22	1.58	0.50
1:A:656:ASP:HB2	3:A:904:NAG:H81	1.94	0.49
1:A:31:PRO:HA	1:A:32:LYS:CB	2.42	0.49
1:A:421:LYS:NZ	6:A:1004:HOH:O	2.45	0.49
1:B:714:VAL:HB	1:B:715:PRO:HD2	1.93	0.49
1:A:431:ASN:CB	1:A:503:ASN:HD21	2.26	0.49
1:B:95:ASP:OD1	1:B:97:ARG:HD3	2.14	0.48
1:A:714:VAL:HB	1:A:715:PRO:HD2	1.96	0.48
1:A:95:ASP:OD1	1:A:97:ARG:HD3	2.15	0.47
1:A:725:LEU:O	1:A:748:GLN:HG2	2.15	0.47
1:B:95:ASP:HA	1:B:133:TYR:HB2	1.99	0.45
1:A:528:LEU:HA	6:A:1003:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ASP:HA	1:A:133:TYR:HB2	1.99	0.44
1:B:359:SER:HB2	1:B:389:GLN:NE2	2.34	0.43
1:A:161:PHE:HA	1:A:193:TYR:CE1	2.54	0.43
1:B:372:LEU:HD21	1:B:375:LEU:HB2	2.00	0.43
1:A:359:SER:HB2	1:A:389:GLN:NE2	2.34	0.42
1:B:491:CYS:HB3	3:B:906:NAG:H81	2.02	0.42
1:B:161:PHE:HA	1:B:193:TYR:CE1	2.54	0.42
1:B:391:SER:N	1:B:392:PRO:CD	2.84	0.41
1:B:97:ARG:NH2	1:B:474:SER:O	2.54	0.41
1:A:391:SER:N	1:A:392:PRO:CD	2.84	0.41
1:A:97:ARG:NH2	1:A:474:SER:O	2.53	0.41
1:A:539:GLN:N	1:A:540:PRO:CD	2.84	0.41
1:B:357:ARG:HD2	1:B:380:TYR:CE1	2.57	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	754/817 (92%)	690 (92%)	58 (8%)	6 (1%)	24	46
1	B	754/817 (92%)	683 (91%)	64 (8%)	7 (1%)	21	42
All	All	1508/1634 (92%)	1373 (91%)	122 (8%)	13 (1%)	21	42

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	818	GLY
1	B	818	GLY
1	A	32	LYS
1	A	332	ASP
1	B	332	ASP

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Mol	Chain	Res	Type
1	B	32	LYS
1	B	832	THR
1	A	381	VAL
1	B	381	VAL
1	B	591	PHE
1	A	742	PHE
1	A	430	VAL
1	B	430	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	715/768 (93%)	702 (98%)	13 (2%)	66	87
1	B	714/768 (93%)	699 (98%)	15 (2%)	61	85
All	All	1429/1536 (93%)	1401 (98%)	28 (2%)	63	85

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	THR
1	A	103	ILE
1	A	135	ASP
1	A	607	ASP
1	A	644	GLN
1	A	661	SER
1	A	678	LYS
1	A	698	LEU
1	A	745	ASP
1	A	758	LYS
1	A	767	PHE
1	A	782	HIS
1	A	832	THR
1	B	33	THR
1	B	39	THR

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Mol	Chain	Res	Type
1	B	103	ILE
1	B	108	LYS
1	B	135	ASP
1	B	607	ASP
1	B	644	GLN
1	B	661	SER
1	B	678	LYS
1	B	698	LEU
1	B	758	LYS
1	B	767	PHE
1	B	770	ASN
1	B	782	HIS
1	B	830	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	HIS
1	A	503	ASN
1	A	581	GLN
1	A	800	HIS
1	A	820	HIS
1	B	90	HIS
1	B	503	ASN
1	B	581	GLN
1	B	734	GLN
1	B	770	ASN
1	B	800	HIS
1	B	820	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	2/4 (50%)	0	1 (50%)
2	D	2/4 (50%)	0	0
All	All	4/8 (50%)	0	1 (25%)

There are no RNA backbone outliers to report.

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	3	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

13 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	901	1	14,14,15	0.88	1 (7%)	15,19,21	1.66	4 (26%)
3	NAG	A	902	1,3	14,14,15	0.51	0	15,19,21	1.66	4 (26%)
3	NAG	A	903	3	14,14,15	0.56	0	15,19,21	1.71	4 (26%)
3	NAG	A	904	1	14,14,15	0.60	0	15,19,21	2.08	4 (26%)
3	NAG	A	905	1	14,14,15	0.44	0	15,19,21	1.89	4 (26%)
4	SDL	B	901	-	19,26,26	1.20	1 (5%)	20,39,39	2.50	4 (20%)
4	SDL	B	902	-	19,26,26	1.24	2 (10%)	20,39,39	2.56	6 (30%)
3	NAG	B	903	1	14,14,15	0.49	0	15,19,21	2.79	5 (33%)
3	NAG	B	904	1,3	14,14,15	0.48	0	15,19,21	1.30	2 (13%)
3	NAG	B	905	3	14,14,15	0.90	1 (7%)	15,19,21	1.66	3 (20%)
3	NAG	B	906	1	14,14,15	0.49	0	15,19,21	1.37	2 (13%)
3	NAG	B	907	1	14,14,15	0.74	1 (7%)	15,19,21	2.23	4 (26%)
5	PO4	B	908	-	4,4,4	0.45	0	6,6,6	0.27	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	901	1	-	0/6/23/26	0/1/1/1
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	NAG	A	904	1	-	0/6/23/26	0/1/1/1
3	NAG	A	905	1	-	0/6/23/26	0/1/1/1
4	SDL	B	901	-	-	0/4/25/25	0/3/3/3
4	SDL	B	902	-	-	0/4/25/25	0/3/3/3
3	NAG	B	903	1	-	0/6/23/26	0/1/1/1
3	NAG	B	904	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	905	3	-	0/6/23/26	0/1/1/1
3	NAG	B	906	1	-	0/6/23/26	0/1/1/1
3	NAG	B	907	1	-	0/6/23/26	0/1/1/1
5	PO4	B	908	-	-	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)
3	A	901	NAG	C1-C2	2.11	1.55	1.52
3	B	905	NAG	C1-C2	2.23	1.55	1.52
4	B	902	SDL	C10-C11	2.24	1.53	1.49
3	B	907	NAG	O4-C4	2.36	1.48	1.43
4	B	902	SDL	C7-C6	3.46	1.48	1.41
4	B	901	SDL	C7-C6	3.77	1.48	1.41

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	902	SDL	O3-C4-N	-6.19	101.08	108.30
4	B	901	SDL	C6-C7-N2	-5.95	115.74	123.52
4	B	902	SDL	C6-C7-N2	-4.82	117.22	123.52
3	B	907	NAG	C3-C4-C5	-4.49	102.22	110.23
4	B	901	SDL	O3-C4-N	-3.93	103.72	108.30
4	B	902	SDL	N4-C8-N2	-3.73	122.48	127.56
4	B	901	SDL	N4-C8-N2	-3.72	122.50	127.56
3	A	901	NAG	C3-C4-C5	-3.49	104.01	110.23
3	A	904	NAG	C4-C3-C2	-3.06	106.60	111.34
3	B	905	NAG	O3-C3-C2	-2.77	103.45	109.37
3	A	903	NAG	C3-C4-C5	-2.61	105.57	110.23
3	A	905	NAG	C6-C5-C4	-2.44	106.86	112.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	906	NAG	O4-C4-C3	-2.31	105.15	110.36
4	B	902	SDL	C7-C6-C9	-2.22	118.32	120.86
3	B	903	NAG	O7-C7-C8	-2.19	118.05	122.07
3	A	905	NAG	C8-C7-N2	-2.17	111.94	116.10
3	A	902	NAG	C3-C4-C5	-2.05	106.56	110.23
3	A	902	NAG	O5-C5-C6	-2.04	102.97	107.34
3	A	903	NAG	C2-N2-C7	2.01	125.73	123.11
3	A	902	NAG	O5-C5-C4	2.15	113.70	110.13
3	A	904	NAG	O3-C3-C2	2.16	114.00	109.37
3	A	902	NAG	O4-C4-C5	2.17	114.94	109.23
3	B	903	NAG	O5-C5-C4	2.20	113.78	110.13
3	A	901	NAG	C2-N2-C7	2.33	126.14	123.11
3	A	904	NAG	O7-C7-N2	2.39	126.71	121.84
3	B	904	NAG	O7-C7-N2	2.39	126.72	121.84
3	A	903	NAG	O4-C4-C5	2.45	115.68	109.23
3	B	903	NAG	O7-C7-N2	2.52	126.97	121.84
3	B	907	NAG	O5-C5-C4	2.58	114.41	110.13
3	A	901	NAG	O4-C4-C5	2.68	116.29	109.23
4	B	902	SDL	O2-C3-C4	2.69	120.04	111.61
3	B	905	NAG	C2-N2-C7	2.70	126.62	123.11
3	B	904	NAG	O5-C5-C6	2.71	113.14	107.34
3	A	901	NAG	C1-O5-C5	3.05	116.63	112.14
3	B	907	NAG	O4-C4-C5	3.28	117.87	109.23
3	B	906	NAG	C1-O5-C5	3.29	116.98	112.14
3	B	905	NAG	C4-C3-C2	3.46	116.71	111.34
3	A	905	NAG	O5-C5-C4	3.73	116.32	110.13
3	A	903	NAG	C1-O5-C5	4.06	118.11	112.14
3	A	905	NAG	C1-O5-C5	4.08	118.13	112.14
3	B	903	NAG	C2-N2-C7	4.67	129.19	123.11
3	B	907	NAG	C1-O5-C5	5.35	120.01	112.14
3	A	904	NAG	C1-O5-C5	5.71	120.54	112.14
4	B	902	SDL	C7-N2-C8	5.76	122.64	115.88
4	B	901	SDL	C7-N2-C8	6.70	123.73	115.88
3	B	903	NAG	C1-O5-C5	8.53	124.69	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	904	NAG	1	0
3	B	906	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	762/817 (93%)	-0.09	2 (0%) 94 93	37, 67, 97, 122	0
1	B	762/817 (93%)	-0.06	7 (0%) 85 83	40, 65, 94, 120	0
2	C	4/4 (100%)	-0.43	0 100 100	61, 72, 74, 82	0
2	D	4/4 (100%)	-0.44	0 100 100	54, 72, 73, 75	0
All	All	1532/1642 (93%)	-0.08	9 (0%) 90 88	37, 66, 96, 122	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	397	GLN	3.3
1	B	747	PHE	2.6
1	B	494	TYR	2.6
1	B	513	PHE	2.4
1	B	771	VAL	2.3
1	B	718	LEU	2.2
1	A	565	LEU	2.1
1	B	514	GLN	2.1
1	A	118	ILE	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](#)

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(Å ²)	Q<0.9
3	NAG	A	904	14/15	0.83	0.26	3.35	70,91,118,120	0
3	NAG	B	907	14/15	0.85	0.19	0.05	58,73,83,84	0
3	NAG	A	901	14/15	0.86	0.20	-0.11	77,85,97,99	0
3	NAG	A	905	14/15	0.94	0.14	-0.44	44,49,52,53	0
4	SDL	B	901	24/24	0.97	0.16	-0.88	56,67,80,80	0
3	NAG	A	902	14/15	0.97	0.12	-1.04	64,76,85,85	0
3	NAG	B	903	14/15	0.94	0.14	-1.19	80,84,91,94	0
3	NAG	B	906	14/15	0.97	0.14	-1.20	49,50,57,58	0
3	NAG	B	904	14/15	0.98	0.12	-1.41	46,57,61,64	0
4	SDL	B	902	24/24	0.97	0.14	-1.70	63,70,75,81	0
3	NAG	B	905	14/15	0.90	0.16	-	69,78,84,84	0
5	PO4	B	908	5/5	0.95	0.17	-	97,103,114,117	0
3	NAG	A	903	14/15	0.86	0.16	-	88,99,102,110	0

6.5 Other polymers [i](#)

There are no such residues in this entry.