



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:21 AM GMT

PDB ID : 2WT2  
Title : GALECTIN DOMAIN OF PORCINE ADENOVIRUS TYPE 4 NADC-1 ISOLATE FIBRE COMPLEXED WITH TRI(N-ACETYL-LACTOSAMINE)  
Authors : Guardado-Calvo, P.; Munoz, E.M.; Llamas-Saiz, A.L.; Fox, G.C.; Glasgow, J.N.; Van Raaij, M.J.  
Deposited on : 2009-09-10  
Resolution : 2.50 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](mailto: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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

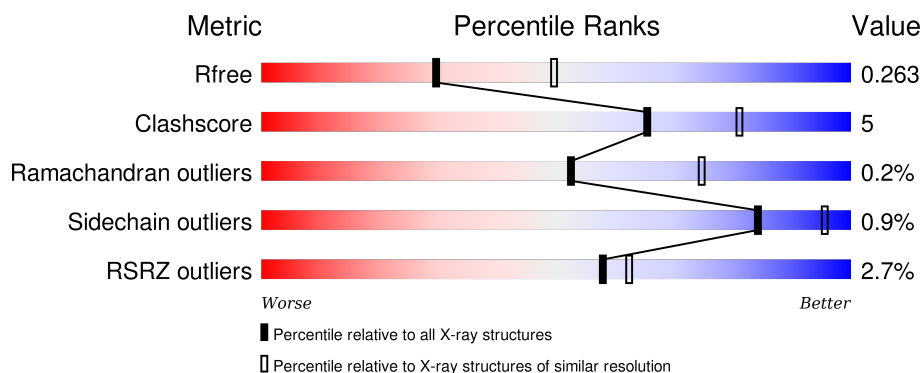
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	343	 3% 76% 11% 10%
1	B	343	 2% 77% 10% 11%

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
2	NO3	A	1686	-	X	-	X
2	NO3	A	1687	-	X	-	X
2	NO3	A	1688	-	X	-	-
2	NO3	B	1686	-	X	-	-
2	NO3	B	1687	-	X	-	X
2	NO3	B	1688	-	X	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5013 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 PUTATIVE FIBER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	0	0
			2354	1521	397	431	5			
1	B	300	Total	C	N	O	S	0	0	0
			2354	1521	397	431	5			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	361	MET	-	EXPRESSION TAG	UNP Q83467
A	362	GLY	-	EXPRESSION TAG	UNP Q83467
A	363	SER	-	EXPRESSION TAG	UNP Q83467
A	364	SER	-	EXPRESSION TAG	UNP Q83467
A	365	HIS	-	EXPRESSION TAG	UNP Q83467
A	366	HIS	-	EXPRESSION TAG	UNP Q83467
A	367	HIS	-	EXPRESSION TAG	UNP Q83467
A	368	HIS	-	EXPRESSION TAG	UNP Q83467
A	369	HIS	-	EXPRESSION TAG	UNP Q83467
A	370	HIS	-	EXPRESSION TAG	UNP Q83467
A	371	SER	-	EXPRESSION TAG	UNP Q83467
A	372	SER	-	EXPRESSION TAG	UNP Q83467
A	373	GLY	-	EXPRESSION TAG	UNP Q83467
A	374	LEU	-	EXPRESSION TAG	UNP Q83467
A	375	VAL	-	EXPRESSION TAG	UNP Q83467
A	376	PRO	-	EXPRESSION TAG	UNP Q83467
A	377	ARG	-	EXPRESSION TAG	UNP Q83467
A	378	GLY	-	EXPRESSION TAG	UNP Q83467
A	379	SER	-	EXPRESSION TAG	UNP Q83467
A	380	HIS	-	EXPRESSION TAG	UNP Q83467
A	381	MET	-	EXPRESSION TAG	UNP Q83467
A	382	ALA	-	EXPRESSION TAG	UNP Q83467
A	383	SER	-	EXPRESSION TAG	UNP Q83467
A	384	MET	-	EXPRESSION TAG	UNP Q83467
A	385	THR	-	EXPRESSION TAG	UNP Q83467

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Chain	Residue	Modelled	Actual	Comment	Reference
A	386	GLY	-	EXPRESSION TAG	UNP Q83467
A	387	GLY	-	EXPRESSION TAG	UNP Q83467
A	388	GLN	-	EXPRESSION TAG	UNP Q83467
A	389	GLN	-	EXPRESSION TAG	UNP Q83467
A	390	GLY	-	EXPRESSION TAG	UNP Q83467
A	391	ARG	-	EXPRESSION TAG	UNP Q83467
A	392	ILE	-	EXPRESSION TAG	UNP Q83467
B	361	MET	-	EXPRESSION TAG	UNP Q83467
B	362	GLY	-	EXPRESSION TAG	UNP Q83467
B	363	SER	-	EXPRESSION TAG	UNP Q83467
B	364	SER	-	EXPRESSION TAG	UNP Q83467
B	365	HIS	-	EXPRESSION TAG	UNP Q83467
B	366	HIS	-	EXPRESSION TAG	UNP Q83467
B	367	HIS	-	EXPRESSION TAG	UNP Q83467
B	368	HIS	-	EXPRESSION TAG	UNP Q83467
B	369	HIS	-	EXPRESSION TAG	UNP Q83467
B	370	HIS	-	EXPRESSION TAG	UNP Q83467
B	371	SER	-	EXPRESSION TAG	UNP Q83467
B	372	SER	-	EXPRESSION TAG	UNP Q83467
B	373	GLY	-	EXPRESSION TAG	UNP Q83467
B	374	LEU	-	EXPRESSION TAG	UNP Q83467
B	375	VAL	-	EXPRESSION TAG	UNP Q83467
B	376	PRO	-	EXPRESSION TAG	UNP Q83467
B	377	ARG	-	EXPRESSION TAG	UNP Q83467
B	378	GLY	-	EXPRESSION TAG	UNP Q83467
B	379	SER	-	EXPRESSION TAG	UNP Q83467
B	380	HIS	-	EXPRESSION TAG	UNP Q83467
B	381	MET	-	EXPRESSION TAG	UNP Q83467
B	382	ALA	-	EXPRESSION TAG	UNP Q83467
B	383	SER	-	EXPRESSION TAG	UNP Q83467
B	384	MET	-	EXPRESSION TAG	UNP Q83467
B	385	THR	-	EXPRESSION TAG	UNP Q83467
B	386	GLY	-	EXPRESSION TAG	UNP Q83467
B	387	GLY	-	EXPRESSION TAG	UNP Q83467
B	388	GLN	-	EXPRESSION TAG	UNP Q83467
B	389	GLN	-	EXPRESSION TAG	UNP Q83467
B	390	GLY	-	EXPRESSION TAG	UNP Q83467
B	391	ARG	-	EXPRESSION TAG	UNP Q83467
B	392	ILE	-	EXPRESSION TAG	UNP Q83467

- Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	N	O	0	0
			4	1	3		
2	A	1	Total	N	O	0	0
			4	1	3		
2	A	1	Total	N	O	0	0
			4	1	3		
2	B	1	Total	N	O	0	0
			4	1	3		
2	B	1	Total	N	O	0	0
			4	1	3		
2	B	1	Total	N	O	0	0
			4	1	3		

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	6	Total	C	N	O	0	0
			76	42	3	31		
3	B	6	Total	C	N	O	0	0
			76	42	3	31		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	61	Total	O	0	0
			61	61		

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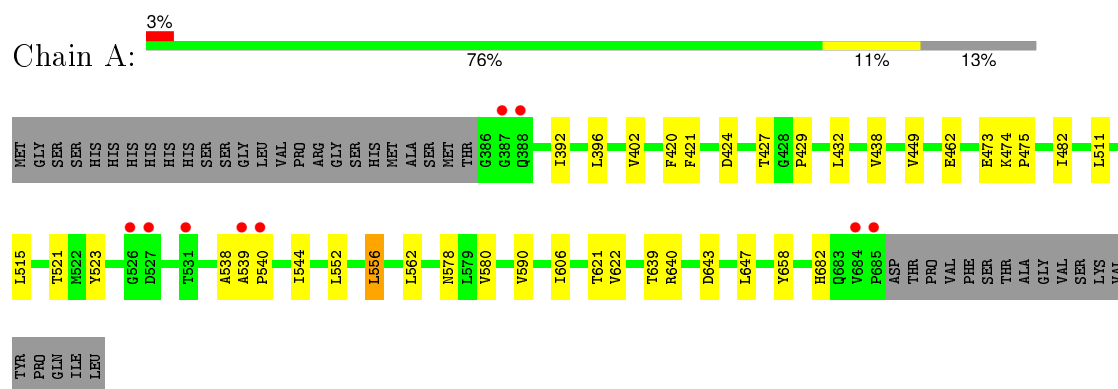
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	68	Total	O	0	0
			68	68		

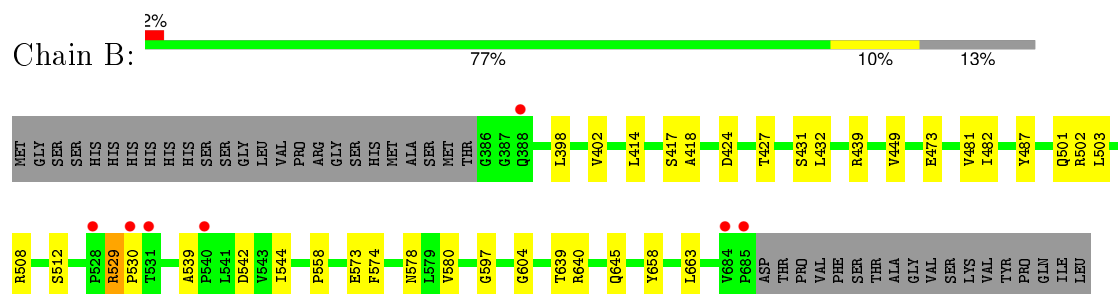
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: PUTATIVE FIBER PROTEIN



#### • Molecule 1: PUTATIVE FIBER PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	176.13Å 38.26Å 86.52Å 90.00° 92.12° 90.00°	Depositor
Resolution (Å)	35.00 – 2.50 39.82 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (35.00-2.50) 99.9 (39.82-2.50)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, $R_{free}$	0.200 , 0.268 0.198 , 0.263	Depositor DCC
$R_{free}$ test set	1123 reflections (5.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.0	Xtriage
Anisotropy	0.646	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 28.4	EDS
Estimated twinning fraction	0.020 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	4 of 20440 reflections (0.020%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5013	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.19 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0277e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, NAG, NO3

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	0.44	0/2421	0.60	0/3313
1	B	0.45	0/2421	0.62	0/3313
All	All	0.45	0/4842	0.61	0/6626

There are no bond length outliers.

There are no bond angle outliers.

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	2354	0	2350	24	0
1	B	2354	0	2350	24	0
2	A	12	0	0	1	0
2	B	12	0	0	0	0
3	A	76	0	66	0	0
3	B	76	0	66	1	0
4	A	61	0	0	1	0
4	B	68	0	0	2	0
All	All	5013	0	4832	49	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 5.

All (49) 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)
2:A:1687:NO3:O1	4:A:2059:HOH:O	2.08	0.72
1:B:508:ARG:HD2	4:B:2038:HOH:O	1.96	0.65
1:B:398:LEU:HD13	1:B:402:VAL:HG22	1.85	0.59
1:B:398:LEU:HD13	1:B:402:VAL:CG2	2.34	0.57
1:A:449:VAL:HG13	1:A:462:GLU:HG2	1.85	0.56
1:B:539:ALA:HB3	1:B:542:ASP:OD1	2.06	0.56
1:A:640:ARG:HD2	1:A:643:ASP:OD1	2.07	0.54
1:A:552:LEU:HD13	1:A:556:LEU:HD13	1.90	0.54
1:B:487:TYR:CZ	1:B:501:GLN:HG3	2.43	0.53
1:A:475:PRO:CD	1:A:538:ALA:HB2	2.39	0.53
1:B:414:LEU:HD22	1:B:418:ALA:HB1	1.91	0.52
1:A:475:PRO:HD2	1:A:538:ALA:HB2	1.90	0.52
1:B:414:LEU:HD22	1:B:418:ALA:CB	2.40	0.52
1:B:512:SER:HG	1:B:574:PHE:HZ	1.59	0.51
1:B:473:GLU:HA	1:B:544:ILE:HD13	1.92	0.51
1:B:558:PRO:HA	1:B:639:THR:HG22	1.94	0.49
1:A:552:LEU:HD13	1:A:556:LEU:CD1	2.43	0.49
1:B:439:ARG:CZ	1:B:449:VAL:HG21	2.43	0.49
1:B:402:VAL:CG1	1:B:482:ILE:HG13	2.44	0.48
1:A:562:LEU:HD23	1:A:682:HIS:HB2	1.95	0.48
1:A:511:LEU:HD11	1:A:515:LEU:HD12	1.95	0.48
1:A:578:ASN:HB3	1:A:580:VAL:HG13	1.96	0.48
1:A:473:GLU:HA	1:A:544:ILE:HD13	1.95	0.48
1:A:511:LEU:HD11	1:A:515:LEU:CD1	2.44	0.47
1:A:427:THR:O	1:A:427:THR:HG23	2.15	0.46
1:B:481:VAL:HG23	4:B:2019:HOH:O	2.17	0.45
1:B:578:ASN:HB3	1:B:580:VAL:HG13	1.98	0.45
1:B:639:THR:HG23	1:B:658:TYR:OH	2.17	0.45
1:B:402:VAL:HG11	1:B:482:ILE:HG13	1.99	0.44
1:B:658:TYR:CE2	1:B:663:LEU:HD11	2.52	0.44
1:B:424:ASP:OD1	1:B:432:LEU:HD13	2.18	0.44
1:A:580:VAL:HG12	1:A:590:VAL:HG13	2.00	0.44
1:B:573:GLU:HB3	3:B:1690:NAG:H5	1.99	0.43
1:A:647:LEU:N	1:A:647:LEU:HD12	2.32	0.43
1:A:639:THR:HG23	1:A:658:TYR:OH	2.18	0.43
1:A:562:LEU:HD23	1:A:682:HIS:CB	2.49	0.42
1:B:640:ARG:CZ	1:B:645:GLN:HB2	2.50	0.42
1:A:424:ASP:OD1	1:A:432:LEU:HD13	2.19	0.42
1:B:529:ARG:N	1:B:530:PRO:CD	2.82	0.42
1:B:597:GLY:O	1:B:604:GLY:HA3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:ILE:HD13	1:A:396:LEU:CD1	2.50	0.41
1:B:502:ARG:O	1:B:503:LEU:HD23	2.21	0.41
1:A:521:THR:HG21	1:A:523:TYR:CE2	2.55	0.41
1:A:606:ILE:HB	1:A:622:VAL:HB	2.03	0.41
1:A:474:LYS:HD2	1:A:538:ALA:HB3	2.03	0.41
1:B:427:THR:HG23	1:B:431:SER:HB2	2.03	0.41
1:A:539:ALA:HB1	1:A:540:PRO:HD2	2.02	0.40
1:A:402:VAL:HG11	1:A:482:ILE:HG13	2.02	0.40
1:A:421:PHE:CE2	1:A:438:VAL:HG21	2.57	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	298/343 (87%)	286 (96%)	11 (4%)	1 (0%)	46	68
1	B	298/343 (87%)	288 (97%)	10 (3%)	0	100	100
All	All	596/686 (87%)	574 (96%)	21 (4%)	1 (0%)	52	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	PRO

### 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	265/302 (88%)	262 (99%)	3 (1%)	80	94
1	B	265/302 (88%)	263 (99%)	2 (1%)	86	96
All	All	530/604 (88%)	525 (99%)	5 (1%)	84	95

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	420	PHE
1	A	556	LEU
1	A	621	THR
1	B	417	SER
1	B	529	ARG

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

### 5.3.3 RNA ⓘ

There are no RNA 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 ⓘ

12 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	GAL	A	1689	3	11,11,12	0.82	0	14,15,17	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	A	1690	3	14,14,15	0.57	0	15,19,21	0.89	1 (6%)
3	GAL	A	1691	3	11,11,12	0.70	0	14,15,17	1.23	2 (14%)
3	NAG	A	1692	3	14,14,15	0.56	0	15,19,21	0.87	0
3	GAL	A	1693	3	11,11,12	0.68	0	14,15,17	0.69	0
3	NAG	A	1694	3	15,15,15	0.46	0	17,21,21	0.94	0
3	GAL	B	1689	3	11,11,12	0.95	1 (9%)	14,15,17	1.16	0
3	NAG	B	1690	3	14,14,15	0.51	0	15,19,21	1.02	1 (6%)
3	GAL	B	1691	3	11,11,12	0.70	0	14,15,17	1.19	3 (21%)
3	NAG	B	1692	3	14,14,15	0.45	0	15,19,21	0.88	0
3	GAL	B	1693	3	11,11,12	0.73	0	14,15,17	0.73	0
3	NAG	B	1694	3	15,15,15	0.45	0	17,21,21	0.81	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	GAL	A	1689	3	-	0/2/19/22	0/1/1/1
3	NAG	A	1690	3	-	0/6/23/26	0/1/1/1
3	GAL	A	1691	3	-	0/2/19/22	0/1/1/1
3	NAG	A	1692	3	-	0/6/23/26	0/1/1/1
3	GAL	A	1693	3	-	0/2/19/22	0/1/1/1
3	NAG	A	1694	3	-	0/6/26/26	0/1/1/1
3	GAL	B	1689	3	-	0/2/19/22	0/1/1/1
3	NAG	B	1690	3	-	0/6/23/26	0/1/1/1
3	GAL	B	1691	3	-	0/2/19/22	0/1/1/1
3	NAG	B	1692	3	-	0/6/23/26	0/1/1/1
3	GAL	B	1693	3	-	0/2/19/22	0/1/1/1
3	NAG	B	1694	3	-	0/6/26/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1689	GAL	O5-C1	-2.27	1.39	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1691	GAL	O3-C3-C2	-2.03	106.33	110.00
3	B	1691	GAL	C1-O5-C5	2.07	114.87	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1691	GAL	C1-O5-C5	2.07	114.88	112.25
3	A	1690	NAG	C4-C3-C2	2.49	115.11	111.23
3	B	1690	NAG	C4-C3-C2	2.65	115.35	111.23
3	A	1691	GAL	C1-C2-C3	2.74	112.78	109.54
3	B	1691	GAL	C1-C2-C3	2.82	112.88	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1690	NAG	1	0

## 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	NO3	A	1686	-	3,3,3	3.10	3 (100%)	3,3,3	0.07	0
2	NO3	A	1687	-	3,3,3	3.03	3 (100%)	3,3,3	0.34	0
2	NO3	A	1688	-	3,3,3	3.32	3 (100%)	3,3,3	0.09	0
2	NO3	B	1686	-	3,3,3	3.08	3 (100%)	3,3,3	0.08	0
2	NO3	B	1687	-	3,3,3	3.11	3 (100%)	3,3,3	0.15	0
2	NO3	B	1688	-	3,3,3	3.51	3 (100%)	3,3,3	0.17	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	NO3	A	1686	-	-	0/0/0/0	0/0/0/0
2	NO3	A	1687	-	-	0/0/0/0	0/0/0/0
2	NO3	A	1688	-	-	0/0/0/0	0/0/0/0
2	NO3	B	1686	-	-	0/0/0/0	0/0/0/0
2	NO3	B	1687	-	-	0/0/0/0	0/0/0/0
2	NO3	B	1688	-	-	0/0/0/0	0/0/0/0

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1687	NO3	O2-N	2.67	1.39	1.25
2	B	1686	NO3	O2-N	2.68	1.39	1.25
2	B	1686	NO3	O3-N	2.69	1.39	1.25
2	A	1686	NO3	O3-N	2.70	1.39	1.25
2	B	1687	NO3	O3-N	2.73	1.39	1.25
2	A	1686	NO3	O2-N	2.78	1.39	1.25
2	A	1687	NO3	O3-N	2.79	1.39	1.25
2	A	1688	NO3	O2-N	2.79	1.39	1.25
2	B	1687	NO3	O2-N	2.87	1.40	1.25
2	B	1688	NO3	O2-N	2.93	1.40	1.25
2	A	1688	NO3	O3-N	2.94	1.40	1.25
2	B	1688	NO3	O3-N	2.98	1.40	1.25
2	A	1687	NO3	O1-N	3.56	1.39	1.24
2	B	1687	NO3	O1-N	3.66	1.39	1.24
2	A	1686	NO3	O1-N	3.70	1.39	1.24
2	B	1686	NO3	O1-N	3.75	1.39	1.24
2	A	1688	NO3	O1-N	4.07	1.41	1.24
2	B	1688	NO3	O1-N	4.41	1.42	1.24

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1687	NO3	1	0

## 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 [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, 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	300/343 (87%)	-0.23	9 (3%) 54 59	11, 26, 72, 160	0
1	B	300/343 (87%)	-0.23	7 (2%) 64 67	10, 26, 64, 115	0
All	All	600/686 (87%)	-0.23	16 (2%) 58 62	10, 26, 70, 160	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	685	PRO	6.3
1	A	540	PRO	4.4
1	A	685	PRO	4.3
1	A	684	VAL	3.5
1	B	684	VAL	3.3
1	A	531	THR	3.3
1	B	388	GLN	3.2
1	B	531	THR	2.5
1	A	526	GLY	2.5
1	B	530	PRO	2.5
1	A	387	GLY	2.4
1	A	539	ALA	2.4
1	A	388	GLN	2.4
1	B	528	PRO	2.3
1	B	540	PRO	2.1
1	A	527	ASP	2.1

### 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 ⓘ

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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	B	1690	14/15	0.90	0.17	1.44	31,36,40,43	0
3	NAG	A	1690	14/15	0.91	0.16	1.14	33,39,44,47	0
3	NAG	A	1694	15/15	0.94	0.18	1.01	31,37,42,46	0
3	GAL	A	1689	11/12	0.91	0.16	0.86	34,43,49,50	0
3	NAG	A	1692	14/15	0.96	0.10	-0.43	23,24,35,35	0
3	NAG	B	1692	14/15	0.95	0.10	-0.54	18,26,43,43	0
3	GAL	B	1689	11/12	0.94	0.14	-0.62	28,37,40,41	0
3	GAL	A	1693	11/12	0.96	0.11	-0.64	21,26,29,32	0
3	GAL	B	1691	11/12	0.94	0.10	-0.91	20,23,27,27	0
3	GAL	B	1693	11/12	0.93	0.10	-1.19	27,29,31,36	0
3	NAG	B	1694	15/15	0.93	0.17	-	27,34,41,41	0
3	GAL	A	1691	11/12	0.94	0.10	-	24,28,31,35	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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	NO3	A	1687	4/4	0.96	0.18	6.17	20,20,21,25	0
2	NO3	B	1687	4/4	0.97	0.17	5.26	24,25,26,31	0
2	NO3	A	1686	4/4	0.98	0.17	3.31	18,20,23,27	0
2	NO3	B	1688	4/4	0.88	0.17	2.74	31,35,38,40	0
2	NO3	B	1686	4/4	0.99	0.12	-0.45	18,19,23,28	0
2	NO3	A	1688	4/4	0.95	0.11	-0.88	32,36,37,39	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.