



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:37 PM GMT

PDB ID : 4FMK  
Title : Crystal structure of mouse nectin-2 extracellular fragment D1-D2  
Authors : Harrison, O.J.; Brasch, J.; Shapiro, L.  
Deposited on : 2012-06-17  
Resolution : 2.56 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

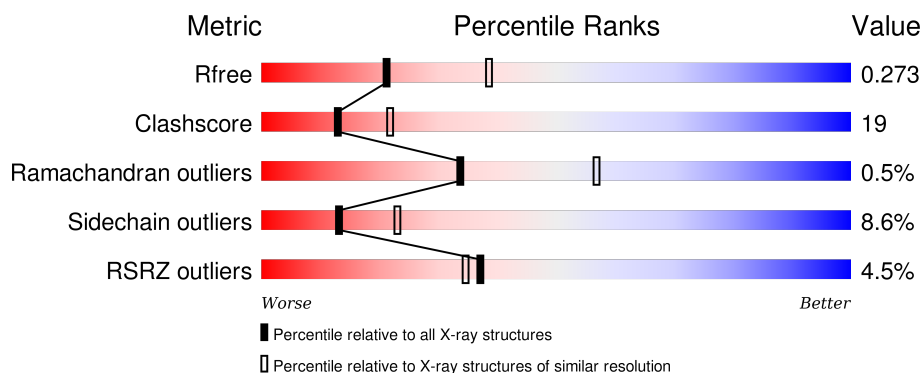
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.56 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	3324 (2.60-2.52)
Clashscore	102246	3729 (2.60-2.52)
Ramachandran outliers	100387	3673 (2.60-2.52)
Sidechain outliers	100360	3673 (2.60-2.52)
RSRZ outliers	91569	3333 (2.60-2.52)

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	225	<div> <div>4%</div> <div>67%</div> <div>26%</div> <div>5%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 1888 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 Poliovirus receptor-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1717	1074	320	319	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	HIS	-	EXPRESSION TAG	UNP P32507
A	252	HIS	-	EXPRESSION TAG	UNP P32507
A	253	HIS	-	EXPRESSION TAG	UNP P32507
A	254	HIS	-	EXPRESSION TAG	UNP P32507
A	255	HIS	-	EXPRESSION TAG	UNP P32507
A	256	HIS	-	EXPRESSION TAG	UNP P32507

- Molecule 2 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	6	Total	C	N	O	0	0
			71	40	2	29		

- 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
			60	34	2	24		

- Molecule 4 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Cd	0	0
			4	4		

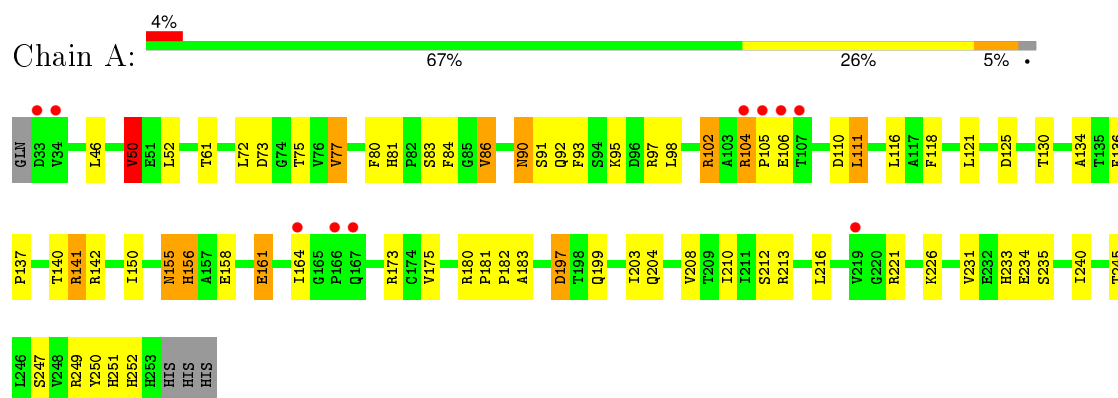
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		

### 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: Poliovirus receptor-related protein 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.67Å 68.67Å 159.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.56 29.73 – 2.56	Depositor EDS
% Data completeness (in resolution range)	99.5 (20.00-2.56) 99.6 (29.73-2.56)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.99 (at 2.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.221 , 0.268 0.223 , 0.273	Depositor DCC
$R_{free}$ test set	708 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.0	Xtriage
Anisotropy	0.739	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 58.2	EDS
Estimated twinning fraction	0.053 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 14122 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	1888	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, MAN, BMA, NAG, CD

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	0.87	2/1757 (0.1%)	0.79	2/2396 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	110	ASP	CB-CG	6.70	1.65	1.51
1	A	161	GLU	CD-OE1	-5.00	1.20	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	50	VAL	CB-CA-C	-5.73	100.51	111.40
1	A	110	ASP	CB-CG-OD1	5.47	123.23	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	1717	0	1693	63	1
2	A	71	0	61	5	0
3	A	60	0	52	2	0
4	A	4	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	36	0	0	5	0
All	All	1888	0	1806	70	1

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 19.

All (70) 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:301:NAG:C6	2:A:306:FUC:H5	1.64	1.22
2:A:301:NAG:C6	2:A:306:FUC:C5	2.32	1.06
2:A:301:NAG:H62	2:A:306:FUC:H5	1.08	1.05
1:A:111:LEU:O	1:A:111:LEU:HD22	1.75	0.86
1:A:50:VAL:HG22	1:A:121:LEU:HD11	1.56	0.86
1:A:140:THR:HG23	5:A:429:HOH:O	1.77	0.85
1:A:111:LEU:O	1:A:111:LEU:HD13	1.77	0.84
2:A:301:NAG:H62	2:A:306:FUC:C5	1.99	0.75
1:A:226:LYS:HD3	1:A:245:THR:HG22	1.67	0.75
1:A:81:HIS:HD2	1:A:83:SER:H	1.33	0.73
1:A:81:HIS:CD2	1:A:83:SER:H	2.09	0.70
1:A:226:LYS:HD3	1:A:245:THR:CG2	2.23	0.69
1:A:203:ILE:HD12	1:A:203:ILE:H	1.59	0.68
1:A:90:ASN:ND2	1:A:92:GLN:H	1.92	0.67
1:A:111:LEU:HD22	1:A:111:LEU:C	2.15	0.66
1:A:73:ASP:OD1	1:A:75:THR:HG23	1.96	0.65
1:A:111:LEU:CD2	1:A:111:LEU:O	2.45	0.64
1:A:90:ASN:HD22	1:A:92:GLN:H	1.46	0.64
2:A:301:NAG:H61	2:A:306:FUC:C5	2.22	0.64
1:A:111:LEU:O	1:A:111:LEU:CD1	2.45	0.62
1:A:141:ARG:HH11	1:A:141:ARG:HG3	1.65	0.61
1:A:97:ARG:HD3	5:A:428:HOH:O	2.00	0.61
1:A:97:ARG:NH2	1:A:125:ASP:OD2	2.33	0.61
1:A:158:GLU:OE1	1:A:173:ARG:NH1	2.34	0.61
1:A:233:HIS:CD2	1:A:235:SER:H	2.19	0.60
1:A:251:HIS:O	1:A:252:HIS:CG	2.55	0.59
1:A:199:GLN:HG2	1:A:210:ILE:HG12	1.84	0.59
1:A:183:ALA:O	1:A:210:ILE:HD12	2.00	0.59
1:A:80:PHE:HE2	1:A:111:LEU:HG	1.68	0.58
1:A:104:ARG:CZ	1:A:106:GLU:HA	2.33	0.58
1:A:142:ARG:NH1	5:A:432:HOH:O	2.36	0.58
1:A:104:ARG:HB2	1:A:105:PRO:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:HIS:CE1	1:A:175:VAL:HB	2.40	0.55
3:A:308:NAG:HN2	3:A:311:FUC:H61	1.72	0.55
1:A:90:ASN:HD22	1:A:92:GLN:N	2.05	0.55
1:A:46:LEU:HD21	1:A:204:GLN:NE2	2.22	0.55
1:A:111:LEU:O	1:A:111:LEU:CG	2.52	0.54
1:A:46:LEU:HD21	1:A:204:GLN:HE22	1.71	0.54
1:A:102:ARG:O	1:A:102:ARG:HD3	2.07	0.54
1:A:81:HIS:CD2	1:A:84:PHE:H	2.26	0.53
1:A:104:ARG:NH2	1:A:106:GLU:HA	2.23	0.53
1:A:233:HIS:HD2	1:A:235:SER:OG	1.91	0.53
1:A:249:ARG:HG3	1:A:250:TYR:N	2.26	0.51
1:A:98:LEU:HD21	1:A:118:PHE:CE1	2.47	0.50
1:A:81:HIS:HD2	1:A:84:PHE:H	1.61	0.49
1:A:150:ILE:HG23	1:A:180:ARG:O	2.13	0.49
1:A:155:ASN:ND2	1:A:231:VAL:HG21	2.28	0.48
1:A:52:LEU:N	1:A:52:LEU:HD12	2.28	0.48
1:A:197:ASP:HB3	1:A:212:SER:HA	1.95	0.48
1:A:72:LEU:HD11	5:A:401:HOH:O	2.13	0.48
1:A:77:VAL:HG22	1:A:93:PHE:CG	2.49	0.47
1:A:111:LEU:CD2	1:A:111:LEU:C	2.83	0.47
1:A:98:LEU:HD13	1:A:116:LEU:HD21	1.97	0.46
1:A:80:PHE:HD1	1:A:86:VAL:HG23	1.80	0.46
1:A:130:THR:HG21	1:A:142:ARG:HD3	1.96	0.46
1:A:231:VAL:HG13	1:A:240:ILE:HB	1.98	0.46
1:A:221:ARG:NH2	5:A:426:HOH:O	2.39	0.46
1:A:141:ARG:N	1:A:141:ARG:HD2	2.30	0.45
1:A:181:PRO:HB2	1:A:182:PRO:HD2	1.98	0.45
1:A:182:PRO:HG3	1:A:208:VAL:HG21	1.98	0.44
3:A:307:NAG:O5	3:A:311:FUC:C1	2.66	0.44
1:A:141:ARG:N	1:A:141:ARG:CD	2.82	0.43
1:A:233:HIS:CG	1:A:234:GLU:N	2.87	0.42
1:A:80:PHE:CE2	1:A:111:LEU:HG	2.52	0.41
1:A:158:GLU:OE1	1:A:173:ARG:CZ	2.68	0.41
1:A:141:ARG:NH1	1:A:141:ARG:HG3	2.32	0.41
1:A:181:PRO:HB2	1:A:182:PRO:CD	2.51	0.41
1:A:134:ALA:HA	1:A:140:THR:HG22	2.03	0.40
1:A:161:GLU:HA	1:A:247:SER:O	2.21	0.40
1:A:136:PHE:HA	1:A:137:PRO:HA	1.83	0.40

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:GLU:OE1	4:A:312:CD:CD[4_445]	2.18	0.02

## 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	219/225 (97%)	205 (94%)	13 (6%)	1 (0%)	34 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	ILE

### 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	187/191 (98%)	171 (91%)	16 (9%)	13 23

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	VAL
1	A	61	THR
1	A	77	VAL
1	A	86	VAL
1	A	90	ASN

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Mol	Chain	Res	Type
1	A	91	SER
1	A	95	LYS
1	A	102	ARG
1	A	104	ARG
1	A	111	LEU
1	A	141	ARG
1	A	155	ASN
1	A	156	HIS
1	A	197	ASP
1	A	213	ARG
1	A	216	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	81	HIS
1	A	90	ASN
1	A	155	ASN
1	A	199	GLN
1	A	204	GLN
1	A	233	HIS

### 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 ⓘ

11 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected

value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	A	301	1,2	14,14,15	0.84	0	15,19,21	2.54	5 (33%)
2	NAG	A	302	2	14,14,15	0.76	0	15,19,21	1.16	1 (6%)
2	BMA	A	303	2	11,11,12	0.65	0	14,15,17	1.31	1 (7%)
2	MAN	A	304	2	11,11,12	0.65	0	14,15,17	1.32	3 (21%)
2	MAN	A	305	2	11,11,12	0.43	0	14,15,17	1.41	3 (21%)
2	FUC	A	306	2	10,10,11	0.61	0	14,14,16	0.78	0
3	NAG	A	307	1,3	14,14,15	0.83	1 (7%)	15,19,21	0.84	1 (6%)
3	NAG	A	308	3	14,14,15	0.44	0	15,19,21	0.68	0
3	BMA	A	309	3	11,11,12	0.55	0	14,15,17	1.51	2 (14%)
3	MAN	A	310	3	11,11,12	0.46	0	14,15,17	1.56	2 (14%)
3	FUC	A	311	3	10,10,11	0.61	0	14,14,16	1.72	3 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	301	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	302	2	-	0/6/23/26	0/1/1/1
2	BMA	A	303	2	-	0/2/19/22	0/1/1/1
2	MAN	A	304	2	-	0/2/19/22	0/1/1/1
2	MAN	A	305	2	-	0/2/19/22	0/1/1/1
2	FUC	A	306	2	-	0/0/17/20	0/1/1/1
3	NAG	A	307	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	308	3	-	0/6/23/26	0/1/1/1
3	BMA	A	309	3	-	0/2/19/22	0/1/1/1
3	MAN	A	310	3	-	0/2/19/22	0/1/1/1
3	FUC	A	311	3	-	0/0/17/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	307	NAG	O5-C1	-2.69	1.39	1.43

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAG	C6-C5-C4	-5.26	100.03	113.02
3	A	310	MAN	C1-C2-C3	-3.15	105.81	109.54
2	A	301	NAG	O3-C3-C4	-2.70	104.25	110.34
3	A	311	FUC	O5-C5-C4	-2.68	104.88	109.53
2	A	305	MAN	O5-C1-C2	-2.62	106.61	110.86
2	A	302	NAG	C4-C3-C2	-2.41	107.48	111.23
2	A	304	MAN	C6-C5-C4	-2.25	107.45	113.02
3	A	307	NAG	C2-N2-C7	-2.24	120.16	123.04
2	A	305	MAN	C6-C5-C4	-2.13	107.75	113.02
3	A	309	BMA	O5-C5-C6	2.17	112.04	107.35
2	A	304	MAN	O5-C5-C6	2.34	112.41	107.35
2	A	301	NAG	O3-C3-C2	2.46	113.99	109.11
2	A	301	NAG	O6-C6-C5	2.53	119.70	111.33
2	A	305	MAN	C1-O5-C5	2.53	115.47	112.25
3	A	311	FUC	O5-C1-C2	2.88	115.53	110.86
2	A	304	MAN	C1-O5-C5	2.94	115.98	112.25
3	A	309	BMA	C3-C4-C5	3.09	115.58	110.20
3	A	311	FUC	O5-C5-C6	3.25	111.51	106.13
2	A	303	BMA	C1-O5-C5	3.63	116.85	112.25
3	A	310	MAN	C1-O5-C5	4.12	117.47	112.25
2	A	301	NAG	C1-O5-C5	6.73	120.79	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NAG	5	0
2	A	306	FUC	5	0
3	A	307	NAG	1	0
3	A	308	NAG	1	0
3	A	311	FUC	2	0

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	221/225 (98%)	0.33	10 (4%) 37 34	41, 80, 129, 212	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	105	PRO	7.7
1	A	107	THR	4.2
1	A	106	GLU	3.4
1	A	167	GLN	3.4
1	A	219	VAL	3.2
1	A	166	PRO	3.0
1	A	34	VAL	2.5
1	A	164	ILE	2.4
1	A	33	ASP	2.4
1	A	104	ARG	2.4

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

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

### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	NAG	A	301	14/15	0.94	0.10	-1.52	69,80,106,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	FUC	A	311	10/11	0.84	0.25	-	144,155,158,164	0
3	BMA	A	309	11/12	0.69	0.34	-	128,168,179,188	0
3	NAG	A	308	14/15	0.88	0.27	-	78,125,143,163	0
2	FUC	A	306	10/11	0.70	0.29	-	116,130,136,138	0
3	NAG	A	307	14/15	0.94	0.15	-	60,85,120,138	0
2	NAG	A	302	14/15	0.88	0.22	-	96,136,166,183	0
2	MAN	A	305	11/12	0.72	0.39	-	150,183,203,205	0
3	MAN	A	310	11/12	0.77	0.27	-	167,182,192,193	0
2	MAN	A	304	11/12	0.79	0.37	-	148,176,181,182	0
2	BMA	A	303	11/12	0.69	0.34	-	179,194,209,224	0

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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( $\text{\AA}^2$ )	Q<0.9
4	CD	A	313	1/1	0.99	0.13	-1.11	80,80,80,80	0
4	CD	A	312	1/1	0.97	0.15	-1.26	73,73,73,73	0
4	CD	A	315	1/1	0.83	0.09	-	121,121,121,121	0
4	CD	A	314	1/1	0.69	0.09	-	178,178,178,178	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.