



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2016 – 12:53 PM EDT

PDB ID : 4X9H  
Title : Crystal structure of Dscam1 isoform 8.4, N-terminal four Ig domains  
Authors : Chen, Q.  
Deposited on : 2014-12-11  
Resolution : 2.95 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 : 1.7.1 (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

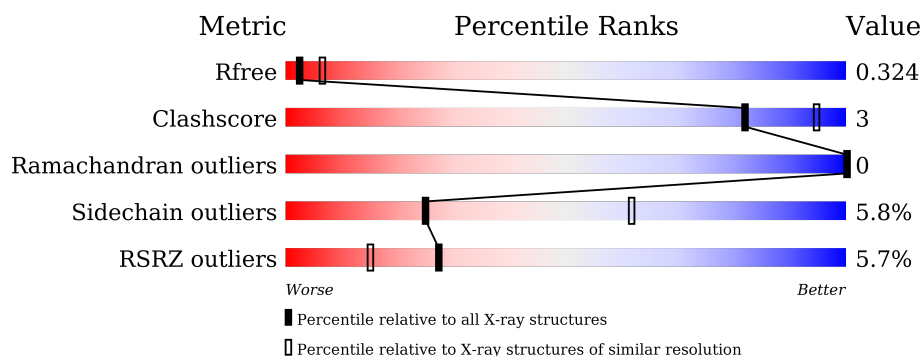
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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	400	<div> <div>4%</div> <div>87%</div> <div>10%</div> <div>..</div> </div>
1	B	400	<div> <div>7%</div> <div>85%</div> <div>12%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	B	404	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6231 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.

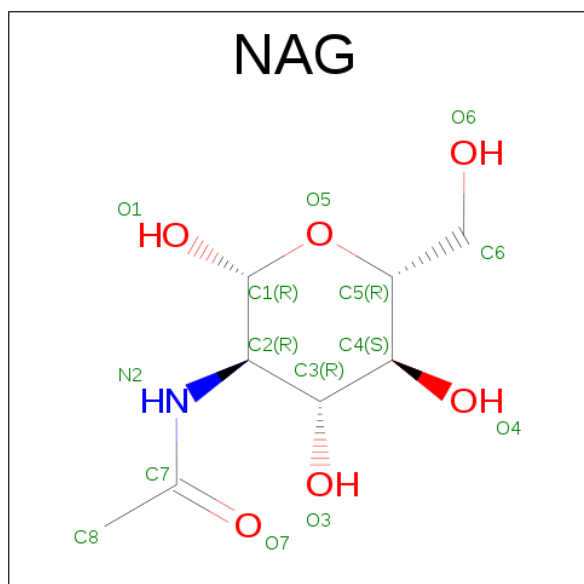
- Molecule 1 is a protein called Down syndrome cell adhesion molecule, isoform AP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	2	0
			3052	1925	530	583	14			
1	B	392	Total	C	N	O	S	0	1	0
			3048	1923	528	583	14			

There are 4 discrepancies between the modelled and reference sequences:

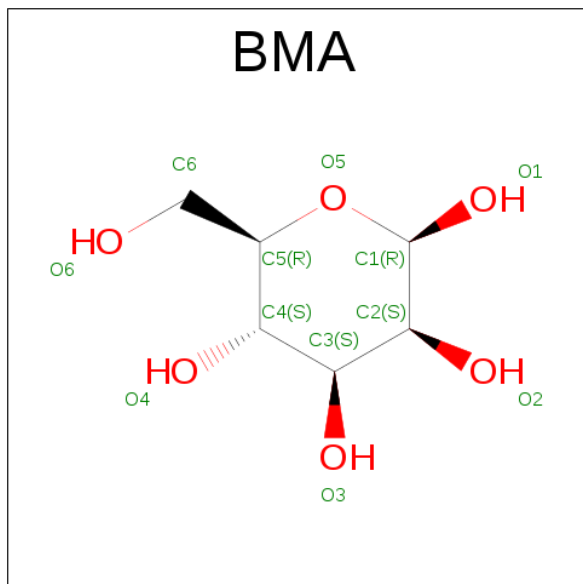
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q0E9L0
A	-2	GLY	-	expression tag	UNP Q0E9L0
B	-3	GLY	-	expression tag	UNP Q0E9L0
B	-2	GLY	-	expression tag	UNP Q0E9L0

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		

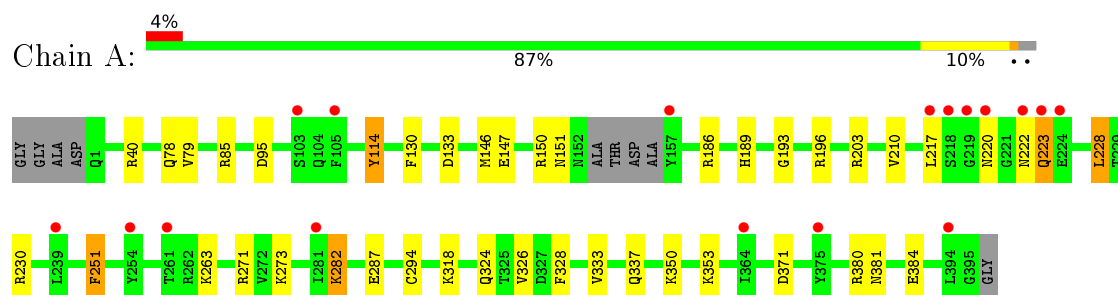
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	O	0	0
			1	1		
5	B	2	Total	O	0	0
			2	2		

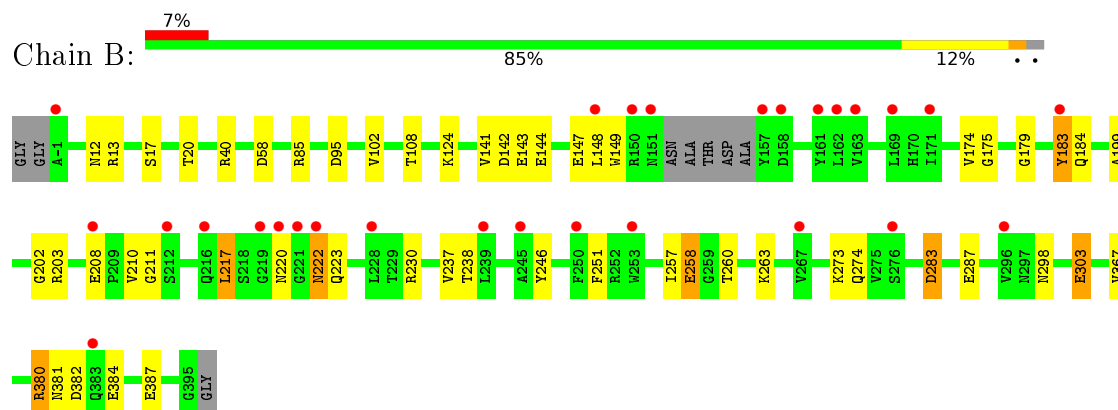
### 3 Residue-property plots

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: Down syndrome cell adhesion molecule, isoform AP



- Molecule 1: Down syndrome cell adhesion molecule, isoform AP



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.22Å 60.95Å 92.35Å 90.00° 93.56° 90.00°	Depositor
Resolution (Å)	47.52 – 2.95 47.52 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.52-2.95) 99.3 (47.52-2.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.272 , 0.324 0.273 , 0.324	Depositor DCC
$R_{free}$ test set	1149 reflections (5.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	80.4	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 10.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	6231	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: BMA, NAG, MAN

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	0.23	0/3119	0.46	0/4228
1	B	0.24	0/3115	0.46	0/4223
All	All	0.23	0/6234	0.46	0/8451

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	ASN	Peptide
1	A	223	GLN	Peptide

### 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	3052	0	3025	18	0
1	B	3048	0	3022	25	0
2	A	42	0	37	0	0
2	B	42	0	37	0	0
3	A	11	0	9	0	0
3	B	11	0	9	0	0
4	A	11	0	10	0	0
4	B	11	0	10	0	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
All	All	6231	0	6159	40	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 3.

All (40) 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:133:ASP:O	1:B:220:ASN:ND2	2.28	0.67
1:A:271:ARG:NH1	1:A:282:LYS:O	2.30	0.65
1:B:246:TYR:O	1:B:298:ASN:ND2	2.32	0.63
1:B:251:PHE:O	1:B:274:GLN:NE2	2.32	0.62
1:B:183:TYR:O	1:B:202:GLY:N	2.35	0.59
1:A:40:ARG:NH1	1:A:78:GLN:OE1	2.39	0.56
1:B:17:SER:OG	1:B:20:THR:OG1	2.24	0.55
1:B:381:ASN:OD1	1:B:382:ASP:N	2.40	0.54
1:A:350:LYS:NZ	1:A:371:ASP:O	2.41	0.53
1:B:95:ASP:OD2	1:B:380:ARG:NH1	2.43	0.52
1:A:287:GLU:OE2	1:A:287:GLU:N	2.41	0.51
1:A:150:ARG:O	1:A:151:ASN:ND2	2.44	0.50
1:A:318:LYS:N	1:A:337:GLN:O	2.45	0.50
1:B:179:GLY:O	1:B:203:ARG:NH1	2.45	0.50
1:B:12:ASN:OD1	1:B:13:ARG:NH2	2.45	0.49
1:B:258:GLU:N	1:B:258:GLU:OE1	2.45	0.49
1:A:114:TYR:N	1:A:114:TYR:CD2	2.79	0.48
1:A:381:ASN:OD1	1:A:384:GLU:N	2.46	0.48
1:B:183:TYR:CD1	1:B:183:TYR:N	2.81	0.47
1:A:222:ASN:OD1	1:A:223:GLN:N	2.40	0.47
1:A:251:PHE:CD1	1:A:251:PHE:N	2.82	0.47
1:A:189:HIS:O	1:A:193:GLY:N	2.47	0.47
1:A:146:MET:HG2	1:A:147:GLU:H	1.81	0.46
1:A:95:ASP:OD2	1:A:380:ARG:NE	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:GLN:NE2	1:A:333:VAL:O	2.48	0.45
1:B:257:ILE:O	1:B:260:THR:OG1	2.22	0.44
1:B:208:GLU:OE1	1:B:208:GLU:N	2.49	0.44
1:B:210:VAL:HG13	1:B:211:GLY:H	1.82	0.44
1:B:283:ASP:N	1:B:283:ASP:OD1	2.50	0.44
1:B:58:ASP:OD1	1:B:58:ASP:N	2.50	0.44
1:A:210:VAL:CG1	1:B:102:VAL:HG11	2.48	0.44
1:B:108:THR:O	1:B:199:ALA:N	2.35	0.42
1:B:141:VAL:HG12	1:B:142:ASP:N	2.35	0.42
1:B:149:TRP:CD1	1:B:149:TRP:N	2.88	0.41
1:A:228:LEU:O	1:B:223:GLN:HB2	2.21	0.41
1:B:174:VAL:HG13	1:B:175:GLY:N	2.35	0.41
1:B:217:LEU:HD23	1:B:303:GLU:HB2	2.02	0.41
1:A:78:GLN:CG	1:A:79:VAL:N	2.83	0.41
1:B:222:ASN:N	1:B:222:ASN:OD1	2.53	0.41
1:B:237:VAL:HG12	1:B:238:THR:H	1.85	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	389/400 (97%)	370 (95%)	19 (5%)	0	100	100
1	B	389/400 (97%)	366 (94%)	23 (6%)	0	100	100
All	All	778/800 (97%)	736 (95%)	42 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	337/338 (100%)	320 (95%)	17 (5%)	30	68
1	B	336/338 (99%)	314 (94%)	22 (6%)	21	56
All	All	673/676 (100%)	634 (94%)	39 (6%)	25	62

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ARG
1	A	114	TYR
1	A	130	PHE
1	A	186	ARG
1	A	196	ARG
1	A	203	ARG
1	A	217	LEU
1	A	228	LEU
1	A	230	ARG
1	A	251	PHE
1	A	263	LYS
1	A	273	LYS
1	A	282	LYS
1	A	294	CYS
1	A	326	VAL
1	A	328	PHE
1	A	353	LYS
1	B	40	ARG
1	B	85	ARG
1	B	124	LYS
1	B	143	GLU
1	B	144	GLU
1	B	147	GLU
1	B	148	LEU
1	B	183	TYR
1	B	184	GLN
1	B	217	LEU

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Mol	Chain	Res	Type
1	B	222	ASN
1	B	230	ARG
1	B	258	GLU
1	B	263	LYS
1	B	273	LYS
1	B	283	ASP
1	B	287	GLU
1	B	303	GLU
1	B	367	VAL
1	B	380	ARG
1	B	384	GLU
1	B	387	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	ASN
1	B	225	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

10 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	NAG	A	401	1,2	14,14,15	0.64	1 (7%)	15,19,21	0.49	0
2	NAG	A	402	3,2	14,14,15	0.59	1 (7%)	15,19,21	0.53	0
3	BMA	A	403	2,4	11,11,12	0.68	0	15,15,17	1.88	4 (26%)
4	MAN	A	404	3	11,11,12	0.67	1 (9%)	15,15,17	1.73	4 (26%)
2	NAG	A	405	1	14,14,15	0.27	0	15,19,21	0.27	0
2	NAG	B	401	1,2	14,14,15	0.31	0	15,19,21	0.38	0
2	NAG	B	402	3,2	14,14,15	0.25	0	15,19,21	0.33	0
3	BMA	B	403	2,4	11,11,12	0.80	0	15,15,17	1.24	2 (13%)
4	MAN	B	404	3	11,11,12	0.97	1 (9%)	15,15,17	1.80	3 (20%)
2	NAG	B	405	1	14,14,15	0.26	0	15,19,21	0.35	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	NAG	A	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	402	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	403	2,4	-	0/2/19/22	0/1/1/1
4	MAN	A	404	3	-	0/2/19/22	0/1/1/1
2	NAG	A	405	1	-	0/6/23/26	0/1/1/1
2	NAG	B	401	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	402	3,2	-	0/6/23/26	0/1/1/1
3	BMA	B	403	2,4	-	0/2/19/22	0/1/1/1
4	MAN	B	404	3	-	0/2/19/22	0/1/1/1
2	NAG	B	405	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	NAG	O5-C1	-2.30	1.40	1.43
2	A	402	NAG	O5-C1	-2.07	1.40	1.43
4	A	404	MAN	C1-C2	2.04	1.57	1.52
4	B	404	MAN	O5-C5	2.22	1.48	1.43

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	B	403	BMA	C1-C2-C3	-2.83	106.12	109.55
4	B	404	MAN	O2-C2-C3	-2.50	105.15	110.19
3	A	403	BMA	O2-C2-C3	-2.39	105.37	110.19
4	A	404	MAN	O2-C2-C3	-2.31	105.53	110.19
4	A	404	MAN	C1-C2-C3	2.46	112.53	109.55
3	B	403	BMA	C1-O5-C5	2.48	115.79	112.14
3	A	403	BMA	C1-C2-C3	2.74	112.87	109.55
4	B	404	MAN	O5-C1-C2	3.31	116.19	110.89
4	A	404	MAN	O5-C1-C2	3.57	116.60	110.89
3	A	403	BMA	O5-C1-C2	3.83	117.02	110.89
3	A	403	BMA	C1-O5-C5	3.91	117.89	112.14
4	A	404	MAN	C1-O5-C5	3.92	117.90	112.14
4	B	404	MAN	C1-O5-C5	4.42	118.65	112.14

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 [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 ⓘ

### 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	391/400 (97%)	0.30	17 (4%) 39 23	48, 71, 97, 118	0
1	B	392/400 (98%)	0.48	28 (7%) 19 10	52, 77, 111, 150	0
All	All	783/800 (97%)	0.39	45 (5%) 27 15	48, 73, 108, 150	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	220	ASN	8.6
1	B	161	TYR	5.8
1	B	216	GLN	5.0
1	B	150	ARG	4.8
1	B	250	PHE	4.8
1	B	219	GLY	4.5
1	A	394	LEU	4.5
1	B	162	LEU	4.4
1	A	219	GLY	4.2
1	A	364	ILE	3.9
1	B	253	TRP	3.9
1	A	222	ASN	3.8
1	A	218	SER	3.6
1	A	261	THR	3.6
1	B	163	VAL	3.6
1	A	105	PHE	3.4
1	B	151	ASN	3.4
1	A	157	TYR	3.2
1	A	217	LEU	3.2
1	A	223	GLN	3.1
1	A	281	ILE	2.9
1	A	375	TYR	2.9
1	B	183	TYR	2.8
1	B	267	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	224	GLU	2.7
1	B	158	ASP	2.5
1	B	245	ALA	2.5
1	B	221	GLY	2.5
1	B	157	TYR	2.5
1	B	-1	ALA	2.4
1	B	222	ASN	2.4
1	A	220	ASN	2.4
1	B	208	GLU	2.3
1	B	171	ILE	2.3
1	B	212	SER	2.2
1	B	148	LEU	2.2
1	B	276	SER	2.2
1	B	228	LEU	2.2
1	B	296	VAL	2.1
1	A	103	SER	2.1
1	B	239	LEU	2.1
1	B	383	GLN	2.1
1	A	254	TYR	2.0
1	B	169	LEU	2.0
1	A	239	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 ⓘ

There are no carbohydrates in this entry.

## 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
4	MAN	B	404	11/12	0.68	0.35	5.88	78,84,91,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	405	14/15	0.77	0.34	1.40	83,88,92,94	0
2	NAG	B	405	14/15	0.80	0.31	0.90	106,117,121,121	0
2	NAG	B	401	14/15	0.89	0.22	-0.27	63,72,77,83	0
2	NAG	A	401	14/15	0.90	0.18	-0.55	54,66,74,76	0
2	NAG	B	402	14/15	0.92	0.17	-	73,78,82,85	0
3	BMA	A	403	11/12	0.50	0.37	-	120,128,137,144	0
3	BMA	B	403	11/12	0.86	0.17	-	73,80,86,87	0
4	MAN	A	404	11/12	0.66	0.58	-	115,137,142,142	0
2	NAG	A	402	14/15	0.85	0.22	-	81,93,106,114	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.