



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:40 AM GMT

PDB ID : 2I6S
Title : Complement component C2a
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P.
Deposited on : 2006-08-29
Resolution : 2.70 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 (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

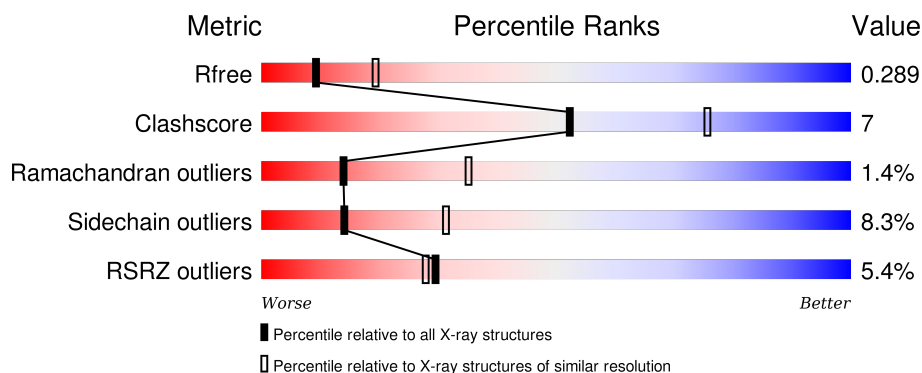
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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 ≥ 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	517	<div> <div>5%</div> <div>71%</div> <div>23%</div> <div>• •</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4110 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.

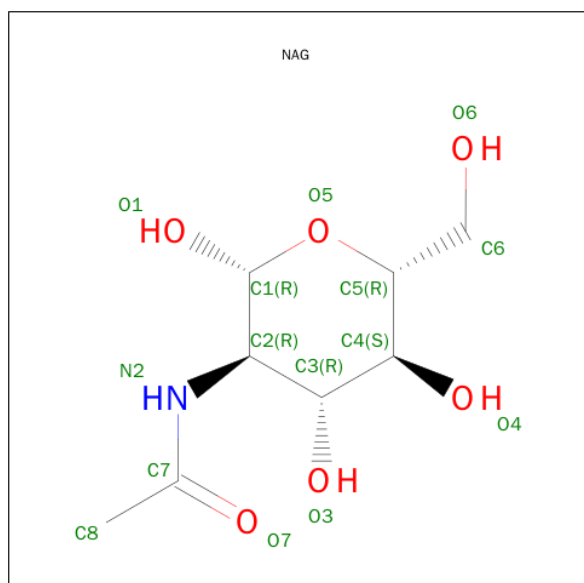
- Molecule 1 is a protein called Complement C2a fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	497	3928	2472	693	736	27	10	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	216	HIS	-	EXPRESSION TAG	UNP P06681
A	217	HIS	-	EXPRESSION TAG	UNP P06681
A	218	HIS	-	EXPRESSION TAG	UNP P06681
A	219	HIS	-	EXPRESSION TAG	UNP P06681
A	220	HIS	-	EXPRESSION TAG	UNP P06681
A	221	HIS	-	EXPRESSION TAG	UNP P06681
A	222	GLY	-	CLONING ARTIFACT	UNP P06681
A	223	SER	-	CLONING ARTIFACT	UNP P06681

- Molecule 2 is SUGAR (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		

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	4	Total	C	N	O	0	0
			49	28	2	19		

- 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		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		

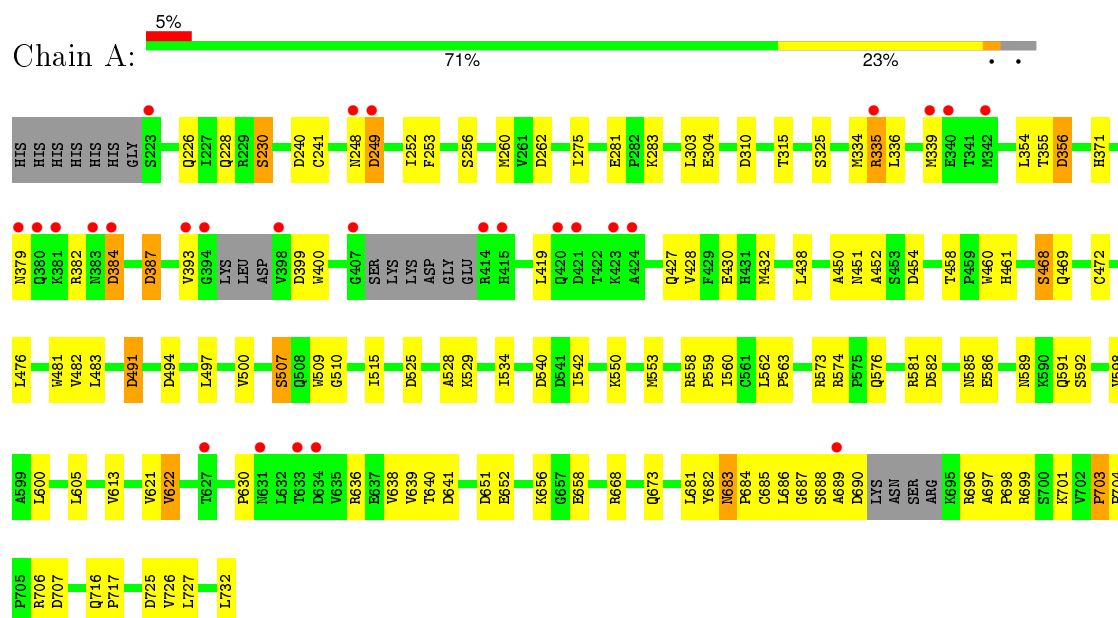
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	38	Total	O	0	0
			38	38		

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: Complement C2a fragment



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.16 Å 75.08 Å 71.56 Å 90.00° 110.32° 90.00°	Depositor
Resolution (Å)	37.50 – 2.70 37.54 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (37.50-2.70) 98.6 (37.54-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.69 Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.212 , 0.287 0.214 , 0.289	Depositor DCC
R_{free} test set	690 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.8	EDS
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 13867 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4110	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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, 0.375 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: FUL, BMA, 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	0.24	0/4006	0.60	17/5416 (0.3%)

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	1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	651	ASP	CB-CG-OD2	5.79	123.52	118.30
1	A	494	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	240	ASP	CB-CG-OD2	5.75	123.47	118.30
1	A	356	ASP	CB-CG-OD2	5.70	123.43	118.30
1	A	387	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	249	ASP	CB-CG-OD2	5.41	123.17	118.30
1	A	262	ASP	CB-CG-OD2	5.37	123.13	118.30
1	A	725	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	454	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	540	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	707	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	690	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	399	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	310	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	384	ASP	CB-CG-OD2	5.09	122.89	118.30
1	A	491	ASP	CB-CG-OD2	5.04	122.83	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	641	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	703	PRO	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	3928	0	3860	54	0
2	A	28	0	26	0	0
3	A	49	0	43	0	0
4	A	39	0	34	0	0
5	A	28	0	25	0	0
6	A	38	0	0	0	0
All	All	4110	0	3988	54	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 7.

All (54) 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:458:THR:HG22	1:A:461:HIS:HB2	1.59	0.84
1:A:334:MET:HE1	1:A:339:MET:HG3	1.66	0.77
1:A:226:GLN:HE22	1:A:384:ASP:HB3	1.57	0.69
1:A:458:THR:O	1:A:458:THR:HG22	1.93	0.68
1:A:468:SER:O	1:A:469:GLN:HB2	1.94	0.67
1:A:683:ASN:ND2	1:A:685:CYS:H	1.93	0.66
1:A:683:ASN:HD22	1:A:685:CYS:H	1.46	0.64
1:A:458:THR:HG21	1:A:598:VAL:HG21	1.79	0.64
1:A:638:VAL:HG23	1:A:639:VAL:HG23	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:605:LEU:HD22	1:A:652:GLU:HG3	1.83	0.61
1:A:458:THR:CG2	1:A:461:HIS:HB2	2.29	0.61
1:A:450:ALA:O	1:A:451:ASN:HB2	2.02	0.60
1:A:687:GLY:N	1:A:688:SER:HA	2.18	0.58
1:A:574:ARG:HH22	1:A:582:ASP:HB3	1.69	0.57
1:A:529:LYS:HB3	1:A:534:ILE:HB	1.86	0.57
1:A:683:ASN:HD22	1:A:683:ASN:C	2.08	0.57
1:A:393:VAL:HA	1:A:419:LEU:O	2.06	0.55
1:A:458:THR:HG23	1:A:460:TRP:CE2	2.43	0.54
1:A:525:ASP:HB3	1:A:528:ALA:HB2	1.91	0.52
1:A:622:VAL:HG23	1:A:681:LEU:HD21	1.91	0.52
1:A:335:ARG:HD3	1:A:335:ARG:O	2.10	0.52
1:A:428:VAL:HG12	1:A:432:MET:HE3	1.92	0.51
1:A:481:TRP:CD1	1:A:726:VAL:HG21	2.45	0.51
1:A:476:LEU:HD23	1:A:482:VAL:HG12	1.91	0.51
1:A:581:ARG:NH1	1:A:732:LEU:OXT	2.44	0.51
1:A:500:VAL:HG23	1:A:515:ILE:HD11	1.94	0.48
1:A:334:MET:CE	1:A:339:MET:HG3	2.41	0.47
1:A:574:ARG:NH2	1:A:582:ASP:HB3	2.30	0.46
1:A:581:ARG:HD3	1:A:732:LEU:O	2.15	0.46
1:A:427:GLN:O	1:A:430:GLU:HB2	2.17	0.45
1:A:553:MET:CE	1:A:559:PRO:HD3	2.46	0.45
1:A:379:ASN:H	1:A:382:ARG:HB2	1.82	0.45
1:A:334:MET:HE1	1:A:339:MET:CG	2.43	0.44
1:A:228:GLN:HE21	1:A:230:SER:HB2	1.83	0.44
1:A:683:ASN:HD22	1:A:685:CYS:N	2.14	0.44
1:A:683:ASN:HB3	1:A:686:LEU:HB2	1.99	0.44
1:A:253:PHE:CD1	1:A:354:LEU:HB3	2.53	0.44
1:A:716:GLN:N	1:A:717:PRO:CD	2.81	0.43
1:A:726:VAL:HG12	1:A:727:LEU:HG	2.00	0.43
1:A:275:ILE:HD12	1:A:303:LEU:HD13	2.01	0.43
1:A:560:ILE:HD13	1:A:673:GLN:HB2	2.01	0.42
1:A:562:LEU:HA	1:A:563:PRO:HD3	1.90	0.42
1:A:683:ASN:HA	1:A:684:PRO:HD3	1.92	0.42
1:A:249:ASP:O	1:A:252:ILE:HG12	2.20	0.42
1:A:682:TYR:HE2	1:A:697:ALA:O	2.03	0.41
1:A:600:LEU:HG	1:A:658:GLU:HG3	2.02	0.41
1:A:256:SER:O	1:A:260:MET:HG3	2.21	0.41
1:A:355:THR:OG1	1:A:356:ASP:N	2.54	0.41
1:A:683:ASN:HD22	1:A:684:PRO:N	2.19	0.41
1:A:483:LEU:HD11	1:A:542:ILE:HD11	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:ALA:C	1:A:452:ALA:H	2.24	0.40
1:A:438:LEU:O	1:A:558:ARG:NH2	2.54	0.40
1:A:589:ASN:N	1:A:589:ASN:OD1	2.55	0.40
1:A:507:SER:HB3	1:A:510:GLY:H	1.87	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	489/517 (95%)	452 (92%)	30 (6%)	7 (1%)	14	35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	698	PRO
1	A	689	ALA
1	A	704	PRO
1	A	468	SER
1	A	630	PRO
1	A	699	ARG
1	A	703	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	436/455 (96%)	400 (92%)	36 (8%)	14	31

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

Mol	Chain	Res	Type
1	A	230	SER
1	A	241	CYS
1	A	248	ASN
1	A	281	GLU
1	A	283	LYS
1	A	304	GLU
1	A	315	THR
1	A	325	SER
1	A	335	ARG
1	A	336	LEU
1	A	371	HIS
1	A	387	ASP
1	A	400	TRP
1	A	472	CYS
1	A	491	ASP
1	A	497	LEU
1	A	507	SER
1	A	509	TRP
1	A	550	LYS
1	A	573	ARG
1	A	576	GLN
1	A	585	ASN
1	A	586	GLU
1	A	591	GLN
1	A	592	SER
1	A	613	VAL
1	A	621	VAL
1	A	622	VAL
1	A	636	ARG
1	A	640	THR
1	A	656	LYS
1	A	668	ARG
1	A	683	ASN
1	A	696	ARG
1	A	701	LYS
1	A	706	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	GLN
1	A	228	GLN
1	A	549	GLN
1	A	683	ASN

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 ⓘ

9 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	1313	1,3	14,14,15	0.51	0	15,19,21	0.85	0
3	NAG	A	1314	3	14,14,15	0.52	0	15,19,21	0.87	0
3	FUL	A	1315	3	10,10,11	0.37	0	14,14,16	1.08	2 (14%)
3	BMA	A	1316	3	11,11,12	0.60	0	14,15,17	0.69	0
4	NAG	A	1447	1,4	14,14,15	0.48	0	15,19,21	0.94	1 (6%)
4	NAG	A	1448	4	14,14,15	0.50	0	15,19,21	0.82	0
4	BMA	A	1449	4	11,11,12	0.59	0	14,15,17	0.70	0
5	NAG	A	1601	1,5	14,14,15	0.45	0	15,19,21	0.72	0
5	NAG	A	1602	5	14,14,15	0.47	0	15,19,21	0.70	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	1313	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1314	3	-	0/6/23/26	0/1/1/1
3	FUL	A	1315	3	-	0/0/17/20	0/1/1/1
3	BMA	A	1316	3	-	0/2/19/22	0/1/1/1
4	NAG	A	1447	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1448	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1449	4	-	0/2/19/22	0/1/1/1
5	NAG	A	1601	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1602	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1315	FUL	O5-C5-C6	2.40	110.09	106.13
3	A	1315	FUL	C1-C2-C3	2.62	112.64	109.54
4	A	1447	NAG	C1-O5-C5	2.81	115.82	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry ⓘ

2 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	1270	1	14,14,15	0.60	0	15,19,21	0.84	1 (6%)
2	NAG	A	1451	1	14,14,15	0.58	0	15,19,21	0.83	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	1270	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1451	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1270	NAG	C4-C3-C2	2.24	114.71	111.23

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1451	NAG	O7-C7-N2-C2

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, 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	497/517 (96%)	0.22	27 (5%)	29 28	23, 30, 39, 55	1 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	420	GLN	5.4
1	A	342	MET	5.3
1	A	423	LYS	5.3
1	A	633	THR	5.1
1	A	340	GLU	4.4
1	A	394	GLY	4.4
1	A	381	LYS	4.2
1	A	380	GLN	3.9
1	A	421	ASP	3.6
1	A	379	ASN	3.4
1	A	393	VAL	3.2
1	A	424	ALA	3.1
1	A	407	GLY	2.8
1	A	249	ASP	2.7
1	A	689	ALA	2.7
1	A	383	ASN	2.5
1	A	339	MET	2.4
1	A	398	VAL	2.4
1	A	223	SER	2.3
1	A	414	ARG	2.3
1	A	335	ARG	2.3
1	A	627	THR	2.2
1	A	634	ASP	2.1
1	A	415	HIS	2.1
1	A	248	ASN	2.1
1	A	384	ASP	2.0
1	A	631	ASN	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](#)

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(\AA^2)	Q<0.9
3	NAG	A	1313	14/15	0.85	0.25	0.44	46,49,57,58	0
4	NAG	A	1447	14/15	0.91	0.13	-1.48	40,44,47,51	0
4	NAG	A	1448	14/15	0.88	0.20	-	55,58,59,62	0
3	NAG	A	1314	14/15	0.87	0.29	-	62,65,66,68	0
3	BMA	A	1316	11/12	0.74	0.38	-	70,71,72,72	0
5	NAG	A	1602	14/15	0.81	0.45	-	58,61,62,62	0
3	FUL	A	1315	10/11	0.89	0.34	-	59,61,62,62	0
5	NAG	A	1601	14/15	0.90	0.38	-	45,49,50,54	0
4	BMA	A	1449	11/12	0.83	0.26	-	64,65,66,66	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, 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(\AA^2)	Q<0.9
2	NAG	A	1270	14/15	0.81	0.48	-	34,36,37,37	0
2	NAG	A	1451	14/15	0.88	0.40	-	52,55,57,59	3

6.5 Other polymers [i](#)

There are no such residues in this entry.