



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 06:21 AM BST

PDB ID : 5VVX
Title : Structural Investigations of the Substrate Specificity of Human O-GlcNAcase
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Deposited on : 2017-05-21
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

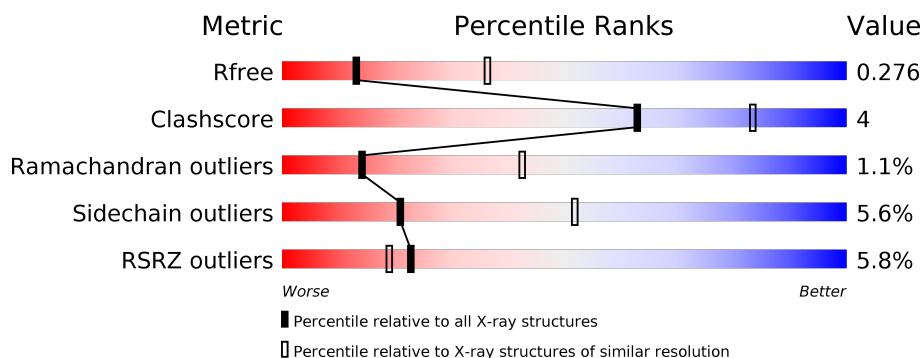
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 respectively. 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	504	<div> <div>4%</div> <div> <div></div> <div>73%</div> <div>11%</div> <div>16%</div> </div> </div>
1	C	504	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>12%</div> <div>14%</div> </div> </div>
2	B	13	<div> <div>15%</div> <div>15%</div> <div>8%</div> <div>62%</div> </div>
2	D	13	<div> <div>23%</div> <div> <div>8%</div> <div>8%</div> <div>8%</div> <div>8%</div> <div>69%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	D	101	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7104 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 Protein O-GlcNAcase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3457	2243	569	623	22			
1	C	431	Total	C	N	O	S	0	0	0
			3538	2290	584	640	24			

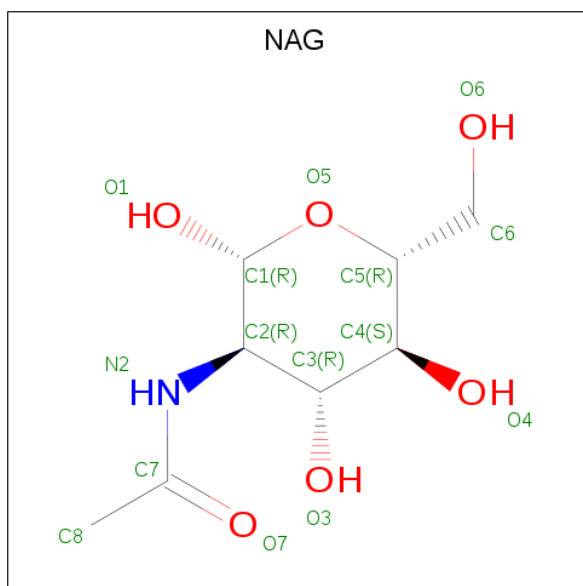
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	HIS	-	expression tag	UNP O60502
A	175	ASN	ASP	engineered mutation	UNP O60502
A	543	GLY	-	linker	UNP O60502
A	544	GLY	-	linker	UNP O60502
A	545	GLY	-	linker	UNP O60502
A	546	GLY	-	linker	UNP O60502
A	547	SER	-	linker	UNP O60502
A	548	GLY	-	linker	UNP O60502
A	549	GLY	-	linker	UNP O60502
A	550	GLY	-	linker	UNP O60502
A	551	GLY	-	linker	UNP O60502
A	552	SER	-	linker	UNP O60502
C	59	HIS	-	expression tag	UNP O60502
C	175	ASN	ASP	engineered mutation	UNP O60502
C	543	GLY	-	linker	UNP O60502
C	544	GLY	-	linker	UNP O60502
C	545	GLY	-	linker	UNP O60502
C	546	GLY	-	linker	UNP O60502
C	547	SER	-	linker	UNP O60502
C	548	GLY	-	linker	UNP O60502
C	549	GLY	-	linker	UNP O60502
C	550	GLY	-	linker	UNP O60502
C	551	GLY	-	linker	UNP O60502
C	552	SER	-	linker	UNP O60502

- Molecule 2 is a protein called Lamin B1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	0	0	0
			37	21	8	8			
2	D	4	Total	C	N	O	0	0	0
			31	18	7	6			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

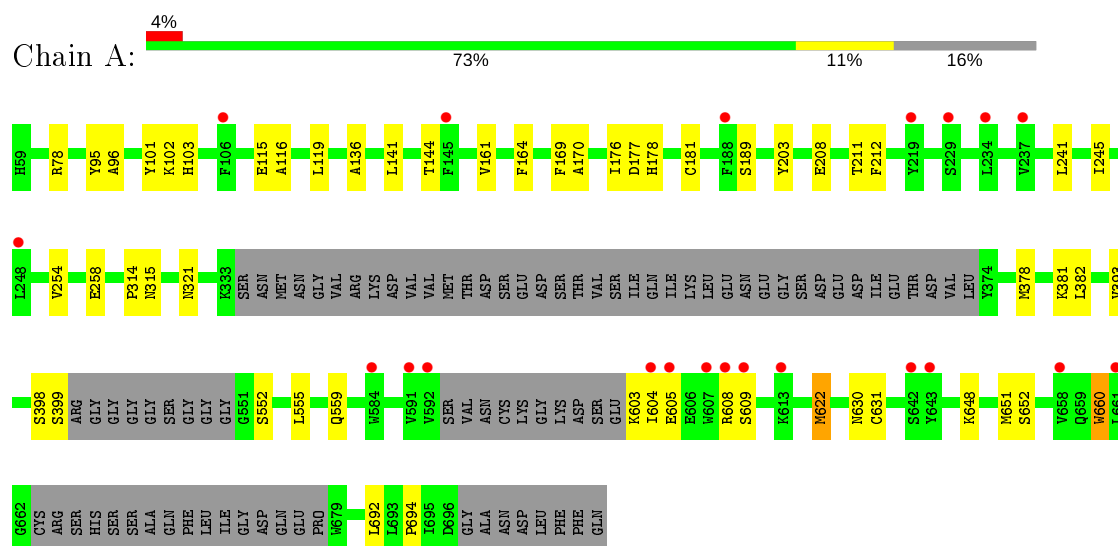
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total	O	0	0
			9	9		
4	C	4	Total	O	0	0
			4	4		

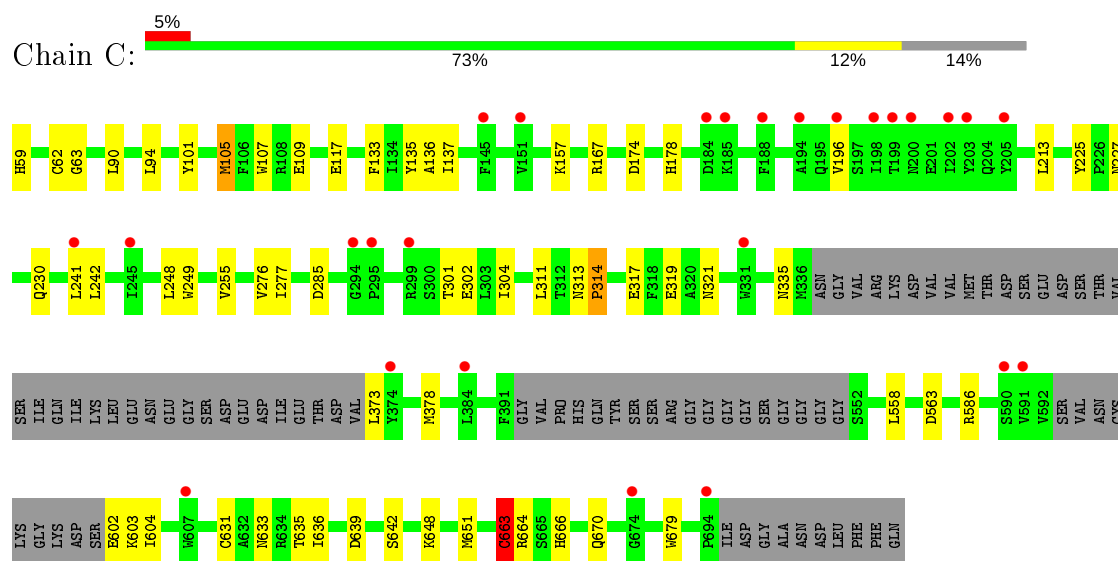
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Protein O-GlcNAcase



• Molecule 1: Protein O-GlcNAcase



• Molecule 2: Lamin B1



LYS	LEU	SER	PRO	SER	PRO	SER	S-4	S-3	R-2	V-1	TO	VAL	SER
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● Molecule 2: Lamin B1



LYS	LEU	SER	PRO	SER	PRO	SER	S-3	R-2	V-1	TO	VAL	SER
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.92Å 96.22Å 89.65Å 90.00° 114.56° 90.00°	Depositor
Resolution (Å)	50.00 – 2.90 48.11 – 2.89	Depositor EDS
% Data completeness (in resolution range)	96.4 (50.00-2.90) 96.4 (48.11-2.89)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.200 , 0.282 0.203 , 0.276	Depositor DCC
R_{free} test set	1341 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	83.6	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7104	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0/3551	0.76	0/4806
1	C	0.59	1/3633 (0.0%)	0.74	1/4916 (0.0%)
2	B	0.77	0/36	0.97	0/47
2	D	1.43	1/30 (3.3%)	0.84	0/39
All	All	0.61	2/7250 (0.0%)	0.75	1/9808 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	663	CYS	CB-SG	6.25	1.92	1.82
2	D	-1	VAL	C-N	5.70	1.47	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	563	ASP	CB-CG-OD1	5.45	123.21	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	3457	0	3386	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3538	0	3465	30	0
2	B	37	0	40	4	0
2	D	31	0	35	4	0
3	B	14	0	13	2	0
3	D	14	0	13	7	0
4	A	9	0	0	0	0
4	C	4	0	0	1	0
All	All	7104	0	6952	61	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 4.

All (61) 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:C:663:CYS:SG	4:C:803:HOH:O	2.25	0.94
1:A:241:LEU:HD11	1:A:245:ILE:HD11	1.61	0.83
1:A:315:ASN:HD22	1:A:321:ASN:ND2	1.87	0.73
1:C:663:CYS:SG	1:C:666:HIS:NE2	2.35	0.72
1:A:241:LEU:CD1	1:A:245:ILE:HD11	2.24	0.66
1:C:663:CYS:HG	1:C:666:HIS:CE1	2.13	0.64
1:A:254:VAL:HG11	2:B:0:THR:HG23	1.81	0.61
1:A:161:VAL:HA	1:A:164:PHE:CD2	2.39	0.58
1:C:227:ASN:HD21	1:C:230:GLN:CD	2.07	0.57
1:C:663:CYS:HA	1:C:666:HIS:CE1	2.41	0.56
1:C:319:GLU:HG3	1:C:635:THR:HG22	1.88	0.56
1:A:315:ASN:H	1:A:321:ASN:HD21	1.55	0.55
1:C:174:ASP:OD2	3:D:101:NAG:H82	2.07	0.55
1:C:94:LEU:HD11	1:C:136:ALA:HB2	1.88	0.55
1:C:663:CYS:HG	1:C:666:HIS:HE2	0.59	0.54
1:A:241:LEU:CG	1:A:245:ILE:HD11	2.37	0.53
2:B:0:THR:HG21	3:B:101:NAG:O5	2.09	0.52
1:A:604:ILE:O	1:A:604:ILE:HG23	2.09	0.52
1:A:96:ALA:HA	1:A:103:HIS:CE1	2.45	0.52
1:A:660:TRP:O	1:A:660:TRP:CD1	2.64	0.51
1:C:604:ILE:HG23	1:C:604:ILE:O	2.12	0.50
1:C:304:ILE:HD12	1:C:335:ASN:HB3	1.93	0.49
1:A:78:ARG:NH1	1:A:95:TYR:HE2	2.11	0.49
1:C:249:TRP:O	1:C:277:ILE:HA	2.14	0.48
1:A:315:ASN:HD22	1:A:321:ASN:HD22	1.60	0.48
1:A:136:ALA:HB2	1:A:170:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:174:ASP:OD2	3:D:101:NAG:C8	2.62	0.47
1:C:317:GLU:HG2	1:C:639:ASP:O	2.15	0.46
2:D:0:THR:HA	3:D:101:NAG:O5	2.15	0.46
1:C:319:GLU:HB3	1:C:636:ILE:HG12	1.99	0.45
2:D:0:THR:CA	3:D:101:NAG:O5	2.65	0.45
1:A:254:VAL:HG11	2:B:0:THR:CG2	2.46	0.45
1:A:144:THR:HG23	1:A:181:CYS:SG	2.57	0.45
1:C:633:ASN:ND2	1:C:636:ILE:HD12	2.31	0.45
1:A:398:SER:OG	1:A:399:SER:N	2.50	0.44
1:A:102:LYS:NZ	1:A:115:GLU:OE1	2.45	0.44
1:A:203:TYR:CE1	1:A:208:GLU:HA	2.53	0.44
1:C:314:PRO:HB2	1:C:321:ASN:OD1	2.18	0.44
1:C:196:VAL:HG12	1:C:241:LEU:HD13	1.99	0.44
1:A:315:ASN:N	1:A:321:ASN:HD21	2.15	0.44
1:C:319:GLU:CG	1:C:635:THR:HG22	2.47	0.44
1:C:63:GLY:O	1:C:311:LEU:HA	2.18	0.43
1:C:285:ASP:OD1	3:D:101:NAG:H61	2.19	0.43
1:A:630:ASN:OD1	1:C:105:MET:HG2	2.19	0.42
1:C:107:TRP:HB2	1:C:137:ILE:HD11	2.01	0.42
1:C:313:ASN:ND2	3:D:101:NAG:O4	2.51	0.42
1:C:62:CYS:SG	1:C:90:LEU:CD2	3.07	0.42
1:C:602:GLU:O	1:C:603:LYS:HG2	2.19	0.42
1:A:116:ALA:HB1	1:A:164:PHE:CE1	2.55	0.42
2:B:0:THR:CG2	3:B:101:NAG:O5	2.67	0.42
2:D:-2:ARG:O	2:D:-1:VAL:HG13	2.20	0.42
1:A:555:LEU:HG	1:A:559:GLN:NE2	2.35	0.41
1:A:692:LEU:O	1:C:586:ARG:NH1	2.52	0.41
2:D:0:THR:C	3:D:101:NAG:O6	2.57	0.41
1:A:141:LEU:HD12	1:A:176:ILE:HG22	2.02	0.41
1:A:622:MET:HE1	1:A:652:SER:HA	2.03	0.41
1:C:133:PHE:HE1	1:C:135:TYR:HB2	1.85	0.41
1:A:169:PHE:O	1:A:212:PHE:HA	2.21	0.41
1:C:109:GLU:O	1:C:157:LYS:NZ	2.38	0.40
1:A:241:LEU:HG	1:A:245:ILE:HD11	2.02	0.40
1:C:248:LEU:HA	1:C:276:VAL:O	2.21	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	411/504 (82%)	376 (92%)	30 (7%)	5 (1%)	13	40
1	C	423/504 (84%)	388 (92%)	32 (8%)	3 (1%)	22	54
2	B	3/13 (23%)	2 (67%)	0	1 (33%)	0	0
2	D	2/13 (15%)	0	2 (100%)	0	100	100
All	All	839/1034 (81%)	766 (91%)	64 (8%)	9 (1%)	14	42

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	TYR
2	B	-3	SER
1	C	302	GLU
1	A	552	SER
1	A	694	PRO
1	C	314	PRO
1	A	314	PRO
1	A	660	TRP
1	C	679	TRP

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	373/442 (84%)	355 (95%)	18 (5%)	25	58
1	C	383/442 (87%)	362 (94%)	21 (6%)	21	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	5/13 (38%)	3 (60%)	2 (40%)	0	0
2	D	4/13 (31%)	2 (50%)	2 (50%)	0	0
All	All	765/910 (84%)	722 (94%)	43 (6%)	21	52

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	LEU
1	A	177	ASP
1	A	178	HIS
1	A	189	SER
1	A	211	THR
1	A	258	GLU
1	A	378	MET
1	A	381	LYS
1	A	382	LEU
1	A	393	VAL
1	A	603	LYS
1	A	605	GLU
1	A	608	ARG
1	A	609	SER
1	A	622	MET
1	A	631	CYS
1	A	648	LYS
1	A	651	MET
1	C	59	HIS
1	C	101	TYR
1	C	105	MET
1	C	117	GLU
1	C	167	ARG
1	C	178	HIS
1	C	213	LEU
1	C	225	TYR
1	C	242	LEU
1	C	255	VAL
1	C	301	THR
1	C	373	LEU
1	C	378	MET
1	C	558	LEU
1	C	631	CYS
1	C	642	SER

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Mol	Chain	Res	Type
1	C	648	LYS
1	C	651	MET
1	C	663	CYS
1	C	664	ARG
1	C	670	GLN
2	B	-2	ARG
2	B	0	THR
2	D	-2	ARG
2	D	-1	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	ASN
1	A	284	ASN
1	A	321	ASN
1	C	227	ASN
1	C	676	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
3	NAG	B	101	2	14,14,15	2.06	2 (14%)	17,19,21	3.05	11 (64%)
3	NAG	D	101	2	14,14,15	1.93	3 (21%)	17,19,21	2.75	8 (47%)

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	B	101	2	-	3/6/23/26	0/1/1/1
3	NAG	D	101	2	-	4/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	101	NAG	C1-C2	6.14	1.61	1.52
3	D	101	NAG	C1-C2	5.48	1.60	1.52
3	D	101	NAG	C3-C2	2.99	1.58	1.52
3	B	101	NAG	C3-C2	2.54	1.57	1.52
3	D	101	NAG	O5-C1	-2.11	1.40	1.43

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	101	NAG	C8-C7-N2	5.79	125.91	116.10
3	D	101	NAG	C8-C7-N2	5.49	125.40	116.10
3	B	101	NAG	C3-C4-C5	-4.96	101.39	110.24
3	D	101	NAG	C3-C4-C5	-4.73	101.81	110.24
3	B	101	NAG	O4-C4-C3	-4.15	100.76	110.35
3	B	101	NAG	C6-C5-C4	-3.75	104.21	113.00
3	B	101	NAG	O3-C3-C4	-3.72	101.75	110.35
3	D	101	NAG	C6-C5-C4	-3.68	104.38	113.00
3	D	101	NAG	O3-C3-C4	-3.66	101.88	110.35
3	D	101	NAG	O4-C4-C3	-3.43	102.42	110.35
3	D	101	NAG	O7-C7-C8	-3.41	115.72	122.06
3	B	101	NAG	O7-C7-C8	-3.29	115.95	122.06
3	B	101	NAG	O5-C5-C4	-3.17	103.12	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	101	NAG	C1-O5-C5	2.87	116.08	112.19
3	D	101	NAG	O5-C5-C4	-2.81	103.99	110.83
3	B	101	NAG	O3-C3-C2	-2.64	104.00	109.47
3	B	101	NAG	O5-C1-C2	2.44	115.14	111.29
3	D	101	NAG	O3-C3-C2	-2.15	105.01	109.47
3	B	101	NAG	O7-C7-N2	-2.07	118.15	121.95

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	101	NAG	O5-C5-C6-O6
3	D	101	NAG	C4-C5-C6-O6
3	B	101	NAG	O5-C5-C6-O6
3	B	101	NAG	C1-C2-N2-C7
3	D	101	NAG	C3-C2-N2-C7
3	D	101	NAG	C1-C2-N2-C7
3	B	101	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	101	NAG	2	0
3	D	101	NAG	7	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 ⓘ

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	421/504 (83%)	0.26	21 (4%)	28	25	50, 79, 121, 148	0
1	C	431/504 (85%)	0.39	26 (6%)	21	18	59, 94, 129, 155	0
2	B	5/13 (38%)	1.12	0	100	100	114, 137, 146, 165	0
2	D	4/13 (30%)	2.67	3 (75%)	0	0	130, 148, 159, 175	0
All	All	861/1034 (83%)	0.34	50 (5%)	23	19	50, 88, 127, 175	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	-3	SER	5.0
1	C	196	VAL	4.9
1	C	590	SER	4.7
1	A	607	TRP	4.6
1	A	605	GLU	4.5
1	C	203	TYR	4.3
1	C	151	VAL	3.9
1	A	642	SER	3.8
1	C	202	ILE	3.7
1	C	607	TRP	3.7
1	A	145	PHE	3.7
1	A	609	SER	3.6
1	A	584	TRP	3.5
1	C	591	VAL	3.5
1	C	184	ASP	3.5
1	C	674	GLY	3.5
1	C	205	TYR	3.4
1	A	658	VAL	3.3
1	A	592	VAL	3.2
1	C	374	TYR	3.1
1	C	198	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	295	PRO	3.0
1	C	299	ARG	2.8
1	C	200	ASN	2.7
1	A	661	LEU	2.7
1	C	145	PHE	2.7
1	A	608	ARG	2.7
1	C	185	LYS	2.6
1	A	237	VAL	2.6
2	D	0	THR	2.6
1	C	384	LEU	2.6
1	C	199	THR	2.5
1	A	229	SER	2.4
1	A	248	LEU	2.4
1	A	604	ILE	2.4
1	A	188	PHE	2.4
1	A	591	VAL	2.4
1	C	694	PRO	2.3
1	A	219	TYR	2.3
1	C	194	ALA	2.3
1	A	613	LYS	2.3
1	A	106	PHE	2.2
1	C	331	TRP	2.2
1	C	241	LEU	2.1
1	A	234	LEU	2.1
1	A	643	TYR	2.1
1	C	294	GLY	2.1
2	D	-1	VAL	2.0
1	C	245	ILE	2.0
1	C	188	PHE	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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	NAG	D	101	14/15	0.94	0.18	60,69,88,88	0
3	NAG	B	101	14/15	0.95	0.17	52,69,78,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.