



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:25 AM EDT

PDB ID : 2A39 / pdb_00002a39
Title : HUMICOLA INSOLENS ENDOCELLULASE EGI NATIVE STRUCTURE
Authors : Davies, G.J.; Sulzenbacher, G.; Mackenzie, L.; Withers, S.G.; Divne, C.; Jones, T.A.; Woldike, H.F.; Schulein, M.
Deposited on : 1998-01-30
Resolution : 2.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

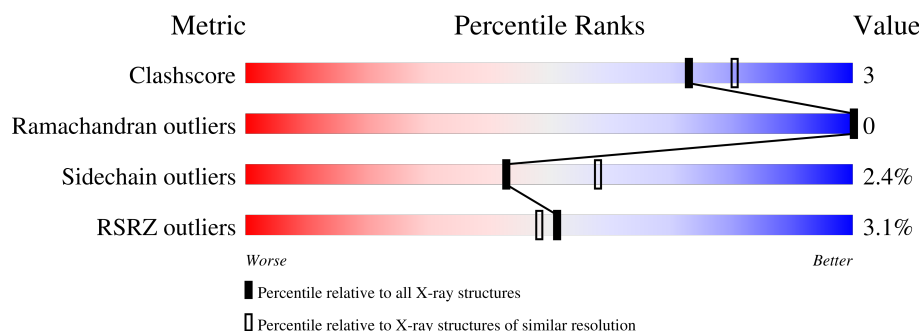
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 of 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	398	3% 83% 14% .
1	B	398	3% 85% 13% .

2 Entry composition [i](#)

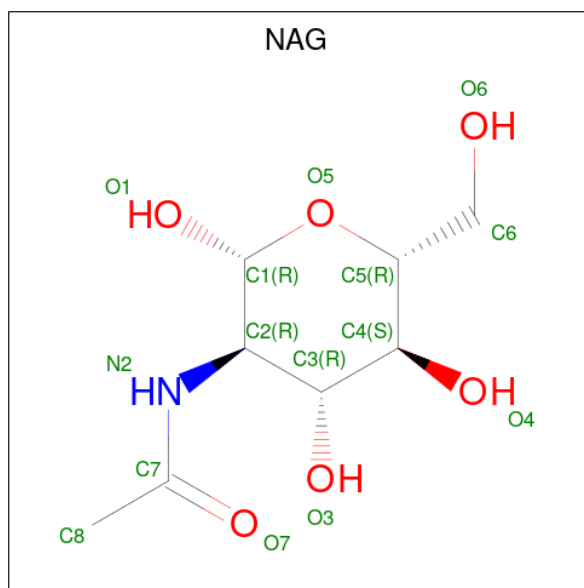
There are 3 unique types of molecules in this entry. The entry contains 6652 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDOGLUCANASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	0	0
			3088	1938	530	591	29			
1	B	398	Total	C	N	O	S	0	0	0
			3088	1938	530	591	29			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: 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	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		

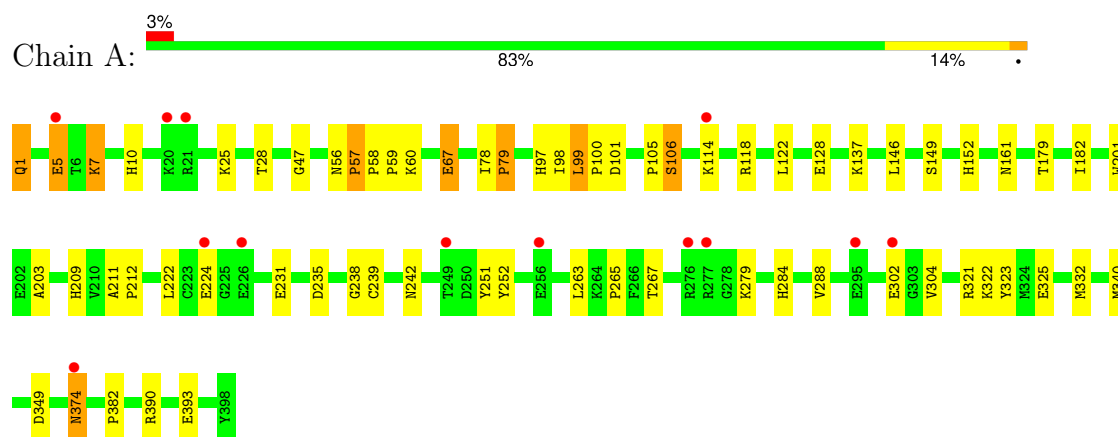
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	207	Total 207	O 207	0	0
3	B	213	Total 213	O 213	0	0

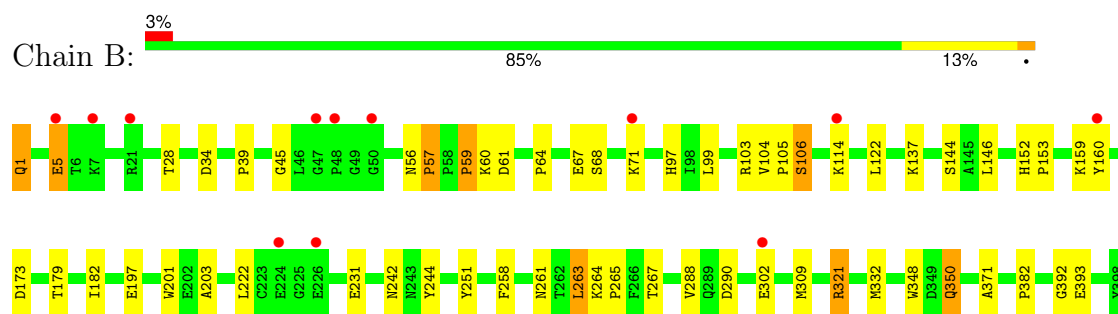
3 Residue-property plots

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: ENDOGLUCANASE I



• Molecule 1: ENDOGLUCANASE I



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.90Å 102.90Å 282.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.6 (30.00-2.20) 96.6 (30.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.66 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.180 , 0.230 0.172 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6652	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PCA, 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	0.78	0/3162	1.62	47/4284 (1.1%)
1	B	0.78	0/3162	1.65	35/4284 (0.8%)
All	All	0.78	0/6324	1.64	82/8568 (1.0%)

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1	PCA	CA-C-N	10.32	140.28	121.70
1	B	1	PCA	C-N-CA	10.32	140.28	121.70
1	A	1	PCA	O-C-N	-10.00	106.99	123.00
1	A	1	PCA	CA-C-N	8.95	137.81	121.70
1	A	1	PCA	C-N-CA	8.95	137.81	121.70
1	B	1	PCA	O-C-N	-8.60	109.24	123.00
1	A	304	VAL	CA-C-O	7.27	124.02	119.51
1	A	390	ARG	CD-NE-CZ	7.16	134.42	124.40
1	B	392	GLY	CA-C-O	6.93	125.69	120.91
1	B	106	SER	N-CA-CB	-6.63	104.31	111.66
1	A	152	HIS	CA-C-N	6.62	126.56	119.28
1	A	152	HIS	C-N-CA	6.62	126.56	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	332	MET	CA-C-O	6.58	127.52	120.55
1	A	10	HIS	CA-CB-CG	6.56	120.36	113.80
1	A	179	THR	CA-C-N	6.42	126.34	119.28
1	A	179	THR	C-N-CA	6.42	126.34	119.28
1	B	242	ASN	CA-CB-CG	6.40	119.00	112.60
1	A	374	ASN	CA-CB-CG	-6.35	106.25	112.60
1	A	349	ASP	CA-CB-CG	6.28	118.88	112.60
1	B	265	PRO	N-CA-CB	6.25	108.79	103.35
1	B	103	ARG	NE-CZ-NH2	6.22	124.80	119.20
1	B	321	ARG	NE-CZ-NH2	-6.07	113.74	119.20
1	B	106	SER	CB-CA-C	-6.04	106.91	111.20
1	A	209	HIS	CA-CB-CG	5.94	119.74	113.80
1	B	45	GLY	N-CA-C	-5.93	107.64	114.69
1	A	25	LYS	CA-C-N	5.92	125.68	119.76
1	A	25	LYS	C-N-CA	5.92	125.68	119.76
1	B	152	HIS	CA-C-N	5.91	125.78	119.28
1	B	152	HIS	C-N-CA	5.91	125.78	119.28
1	A	79	PRO	N-CA-CB	5.88	108.93	103.46
1	A	224	GLU	CB-CG-CD	5.83	122.52	112.60
1	B	382	PRO	N-CA-CB	5.77	108.37	103.35
1	B	152	HIS	CA-CB-CG	-5.70	108.10	113.80
1	A	252	TYR	N-CA-CB	-5.66	101.55	110.77
1	A	265	PRO	N-CA-CB	5.63	108.25	103.35
1	B	59	PRO	N-CA-CB	5.62	108.33	103.27
1	A	106	SER	N-CA-CB	-5.61	105.43	111.66
1	A	78	ILE	CA-C-N	5.57	125.27	119.64
1	A	78	ILE	C-N-CA	5.57	125.27	119.64
1	A	118	ARG	NE-CZ-NH2	-5.52	114.23	119.20
1	A	98	ILE	CA-C-O	-5.52	114.51	120.36
1	A	128	GLU	CA-CB-CG	5.50	125.11	114.10
1	A	47	GLY	CA-C-N	5.50	125.45	119.78
1	A	47	GLY	C-N-CA	5.50	125.45	119.78
1	A	58	PRO	CA-C-N	5.50	125.26	119.76
1	A	58	PRO	C-N-CA	5.50	125.26	119.76
1	B	179	THR	CA-C-N	5.50	125.33	119.28
1	B	179	THR	C-N-CA	5.50	125.33	119.28
1	A	97	HIS	CA-CB-CG	-5.49	108.31	113.80
1	B	244	TYR	CA-C-O	-5.47	114.75	120.55
1	B	258	PHE	CA-C-O	-5.46	114.83	121.28
1	B	309	MET	CA-C-O	-5.46	115.43	121.33
1	B	251	TYR	N-CA-C	5.41	118.35	111.69
1	A	101	ASP	CA-CB-CG	5.41	118.01	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	TYR	N-CA-C	5.37	118.29	111.69
1	B	99	LEU	CA-C-N	5.33	125.14	119.28
1	B	99	LEU	C-N-CA	5.33	125.14	119.28
1	B	57	PRO	N-CA-CB	5.26	108.18	103.08
1	A	211	ALA	CA-C-N	5.24	125.64	119.99
1	A	211	ALA	C-N-CA	5.24	125.64	119.99
1	A	340	MET	CG-SD-CE	5.20	112.33	100.90
1	B	104	VAL	CA-C-N	5.19	124.69	119.19
1	B	104	VAL	C-N-CA	5.19	124.69	119.19
1	B	371	ALA	CA-C-N	5.18	125.22	119.32
1	B	371	ALA	C-N-CA	5.18	125.22	119.32
1	B	39	PRO	N-CA-CB	5.15	107.75	103.17
1	B	144	SER	N-CA-CB	5.15	118.81	110.42
1	A	99	LEU	CA-C-N	5.13	124.79	119.56
1	A	99	LEU	C-N-CA	5.13	124.79	119.56
1	A	393	GLU	CA-C-O	-5.12	115.56	121.19
1	A	161	ASN	CA-C-N	5.09	124.58	119.19
1	A	161	ASN	C-N-CA	5.09	124.58	119.19
1	B	153	PRO	N-CA-CB	5.08	108.88	103.39
1	A	284	HIS	N-CA-CB	-5.08	102.15	110.68
1	A	57	PRO	CA-C-N	5.06	125.59	120.38
1	A	57	PRO	C-N-CA	5.06	125.59	120.38
1	A	59	PRO	N-CA-CB	5.05	108.04	103.34
1	A	242	ASN	CA-CB-CG	5.04	117.64	112.60
1	B	34	ASP	CA-CB-CG	-5.04	107.56	112.60
1	A	382	PRO	N-CA-CB	5.01	107.77	103.31
1	B	393	GLU	N-CA-C	5.01	117.49	110.23
1	A	149	SER	CA-C-O	-5.00	115.46	121.11

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PCA	Mainchain
1	B	1	PCA	Mainchain

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	3088	0	2923	19	0
1	B	3088	0	2923	20	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
3	A	207	0	0	1	0
3	B	213	0	0	1	0
All	All	6652	0	5898	39	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 (39) 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:182:ILE:HG21	1:A:222:LEU:HD21	1.70	0.71
1:A:5:GLU:H	1:A:5:GLU:CD	2.07	0.62
1:B:28:THR:HB	1:B:114:LYS:HG3	1.83	0.61
1:B:5:GLU:H	1:B:5:GLU:CD	2.10	0.60
1:B:56:ASN:HB3	1:B:57:PRO:HD2	1.84	0.59
1:B:350:GLN:HG2	3:B:984:HOH:O	2.02	0.58
1:B:182:ILE:HG21	1:B:222:LEU:HD21	1.87	0.56
1:B:64:PRO:HD2	1:B:68:SER:HB2	1.90	0.54
1:B:231:GLU:CD	1:B:321:ARG:HH22	2.17	0.52
1:A:231:GLU:CD	1:A:321:ARG:HH22	2.18	0.51
1:A:7:LYS:HZ3	1:A:79:PRO:HB3	1.77	0.49
1:A:28:THR:HB	1:A:114:LYS:HG3	1.95	0.49
1:A:67:GLU:H	1:A:67:GLU:CD	2.22	0.47
1:A:332:MET:HE3	1:A:332:MET:HA	1.98	0.46
1:B:267:THR:HB	1:B:288:VAL:HB	1.98	0.46
1:B:67:GLU:H	1:B:67:GLU:CD	2.24	0.46
1:B:264:LYS:NZ	1:B:290:ASP:OD2	2.49	0.45
1:B:97:HIS:HE1	1:B:348:TRP:CD2	2.34	0.45
1:B:261:ASN:OD1	1:B:263:LEU:HB2	2.16	0.44
1:A:99:LEU:HB3	1:A:100:PRO:HD2	1.99	0.43
1:A:267:THR:HB	1:A:288:VAL:HB	2.01	0.43
1:A:374:ASN:ND2	3:A:981:HOH:O	2.51	0.42
1:B:159:LYS:HD3	1:B:160:TYR:CE2	2.54	0.42
1:B:201:TRP:CZ2	1:B:203:ALA:HB3	2.55	0.42
1:A:212:PRO:HD2	1:A:239:CYS:O	2.19	0.42
1:A:146:LEU:C	1:A:146:LEU:HD23	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:LEU:C	1:B:146:LEU:HD23	2.45	0.41
1:A:105:PRO:O	1:A:106:SER:C	2.63	0.41
1:B:201:TRP:CE2	1:B:203:ALA:HB3	2.55	0.41
1:B:56:ASN:HB3	1:B:57:PRO:CD	2.51	0.41
1:A:322:LYS:O	1:A:323:TYR:C	2.63	0.41
1:B:105:PRO:O	1:B:106:SER:C	2.64	0.41
1:A:279:LYS:HA	1:A:279:LYS:HD2	1.84	0.40
1:A:321:ARG:O	1:A:325:GLU:HG3	2.21	0.40
1:B:59:PRO:HB2	1:B:61:ASP:OD1	2.20	0.40
1:A:201:TRP:CZ2	1:A:203:ALA:HB3	2.56	0.40
1:A:235:ASP:OD2	1:A:238:GLY:HA2	2.21	0.40
1:A:56:ASN:HB3	1:A:57:PRO:HD2	2.04	0.40
1:B:173:ASP:HB2	1:B:197:GLU:OE1	2.22	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	396/398 (100%)	388 (98%)	8 (2%)	0	100	100
1	B	396/398 (100%)	388 (98%)	8 (2%)	0	100	100
All	All	792/796 (100%)	776 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	330/330 (100%)	322 (98%)	8 (2%)	43	58
1	B	330/330 (100%)	322 (98%)	8 (2%)	43	58
All	All	660/660 (100%)	644 (98%)	16 (2%)	43	58

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

Mol	Chain	Res	Type
1	A	5	GLU
1	A	7	LYS
1	A	60	LYS
1	A	67	GLU
1	A	122	LEU
1	A	137	LYS
1	A	263	LEU
1	A	302	GLU
1	B	5	GLU
1	B	60	LYS
1	B	71	LYS
1	B	122	LEU
1	B	137	LYS
1	B	263	LEU
1	B	302	GLU
1	B	350	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	HIS
1	B	97	HIS
1	B	353	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	PCA	B	1	1	7,8,9	1.23	1 (14%)	9,10,12	1.58	1 (11%)
1	PCA	A	1	1	7,8,9	1.23	1 (14%)	9,10,12	1.42	1 (11%)

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
1	PCA	B	1	1	-	0/0/11/13	0/1/1/1
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	O-C	2.43	1.29	1.20
1	B	1	PCA	O-C	2.23	1.28	1.20

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1	PCA	CB-CA-C	-2.99	108.55	112.66
1	A	1	PCA	CB-CA-N	2.70	110.66	103.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	B	800	1	14,14,15	1.18	1 (7%)	17,19,21	0.93	0
2	NAG	B	801	1	14,14,15	1.27	1 (7%)	17,19,21	1.51	4 (23%)
2	NAG	A	801	1	14,14,15	1.25	1 (7%)	17,19,21	1.90	4 (23%)
2	NAG	A	800	1	14,14,15	1.31	1 (7%)	17,19,21	1.05	1 (5%)

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	B	800	1	-	0/6/23/26	0/1/1/1
2	NAG	B	801	1	-	0/6/23/26	0/1/1/1
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
2	NAG	A	800	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	B	801	NAG	O7-C7	-3.99	1.14	1.23
2	B	800	NAG	O7-C7	-3.73	1.14	1.23
2	A	800	NAG	O7-C7	-3.70	1.15	1.23
2	A	801	NAG	O7-C7	-3.48	1.15	1.23

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAG	O5-C1-C2	-4.45	104.40	111.29
2	B	801	NAG	C1-O5-C5	3.21	116.49	112.19
2	A	801	NAG	O7-C7-C8	2.97	127.35	122.05
2	A	801	NAG	C8-C7-N2	-2.82	111.44	116.12
2	B	801	NAG	C8-C7-N2	-2.60	111.80	116.12
2	B	801	NAG	O7-C7-C8	2.51	126.53	122.05
2	A	800	NAG	C6-C5-C4	-2.48	106.92	113.02
2	B	801	NAG	C4-C3-C2	-2.20	107.80	111.02
2	A	801	NAG	C2-N2-C7	-2.19	119.97	122.90

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, 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	397/398 (99%)	-0.08	13 (3%) 49 46	16, 27, 46, 68	0
1	B	397/398 (99%)	-0.19	12 (3%) 52 49	15, 27, 47, 69	0
All	All	794/796 (99%)	-0.13	25 (3%) 51 48	15, 27, 47, 69	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	276	ARG	4.6
1	B	47	GLY	4.3
1	A	224	GLU	4.2
1	A	21	ARG	4.0
1	B	224	GLU	3.8
1	A	277	ARG	3.7
1	A	114	LYS	3.6
1	B	5	GLU	3.4
1	A	302	GLU	3.3
1	A	256	GLU	3.2
1	A	5	GLU	2.9
1	B	7	LYS	2.8
1	A	226	GLU	2.7
1	B	71	LYS	2.6
1	B	50	GLY	2.5
1	B	160	TYR	2.4
1	B	48	PRO	2.2
1	B	302	GLU	2.2
1	A	374	ASN	2.2
1	A	295	GLU	2.2
1	B	226	GLU	2.2
1	B	21	ARG	2.1
1	A	249	THR	2.1
1	A	20	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	114	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PCA	B	1	8/9	0.92	0.10	33,36,36,36	0
1	PCA	A	1	8/9	0.96	0.07	21,22,23,24	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
2	NAG	A	800	14/15	0.75	0.15	49,55,60,61	0
2	NAG	A	801	14/15	0.75	0.16	46,52,58,58	0
2	NAG	B	801	14/15	0.81	0.15	47,49,57,57	0
2	NAG	B	800	14/15	0.88	0.12	38,45,52,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.