



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:25 AM UTC

PDB ID : 1E6Z / pdb_00001e6z
Title : CHITINASE B FROM SERRATIA MARCESCENS WILDTYPE IN COM-
PLEX WITH CATALYTIC INTERMEDIATE
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Deposited on : 2000-08-23
Resolution : 1.99 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

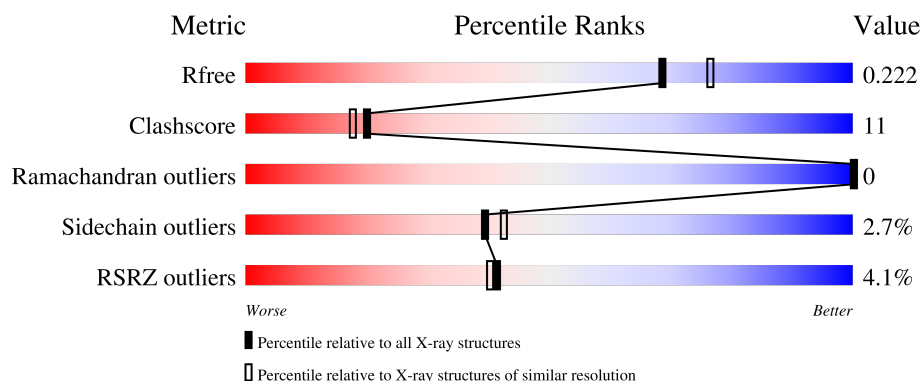
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	498	6% 83% 16% .
1	B	498	2% 81% 17% ..
2	C	2	50% 50%

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	NGO	A	502	-	-	X	-
4	NGO	B	504	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8889 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 CHITINASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	498	Total	C	N	O	S	6	4	1
			3924	2508	663	739	14			
1	B	498	Total	C	N	O	S	0	8	0
			3940	2517	666	743	14			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



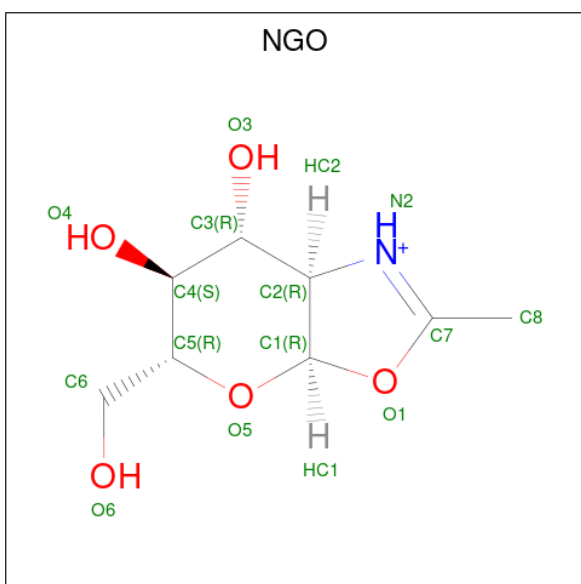
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			29	16	2	11			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



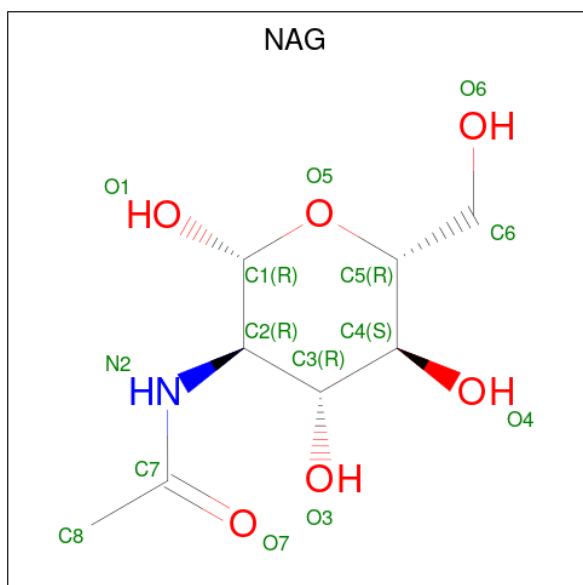
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-METHYL-4,5-DIHYDRO-(1,2-DIDEOXY-ALPHA-D-GLUCOPYRANOSO)[2,1-D]-1,3-OXAZOLE (CCD ID: NGO) (formula: $C_8H_{14}NO_5$).



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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			15	8	1	6		

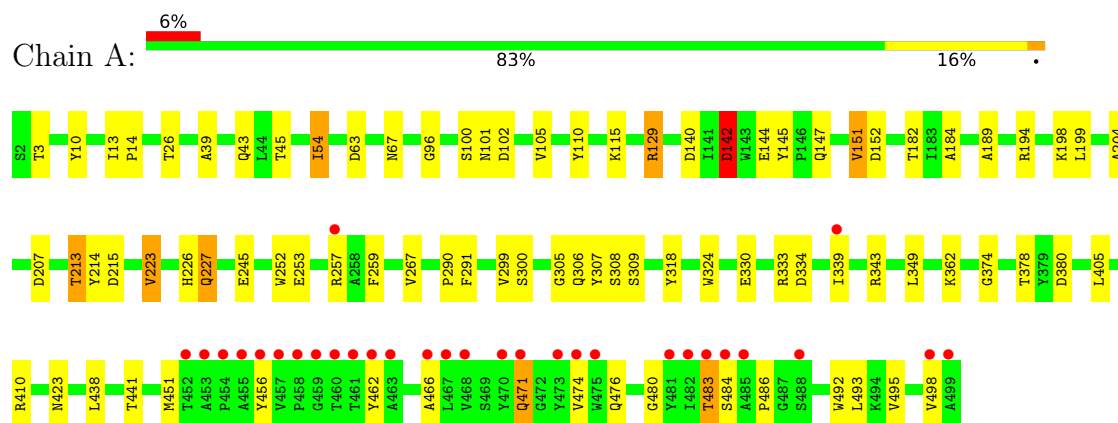
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	474	Total	O	0	0
			474	474		
6	B	459	Total	O	0	0
			459	459		

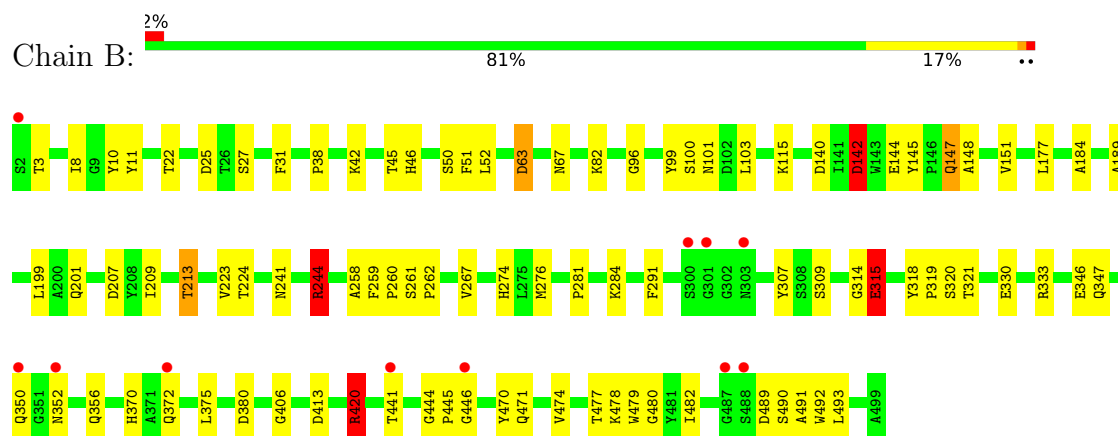
3 Residue-property plots

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: CHITINASE B



• Molecule 1: CHITINASE B



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.80Å 103.81Å 186.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.87 – 1.99 47.87 – 1.99	Depositor EDS
% Data completeness (in resolution range)	93.3 (47.87-1.99) 93.4 (47.87-1.99)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.98Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.187 , 0.225 0.182 , 0.222	Depositor DCC
R_{free} test set	1444 reflections (2.05%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8889	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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, 0.333 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: SO4, NAG, NGO

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	2.31	7/4053 (0.2%)	1.56	35/5525 (0.6%)
1	B	9.50	18/4090 (0.4%)	3.58	48/5572 (0.9%)
All	All	6.93	25/8143 (0.3%)	2.77	83/11097 (0.7%)

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	2	2
1	B	0	8
All	All	2	10

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	244[A]	ARG	CZ-NH2	265.18	4.78	1.33
1	B	244[B]	ARG	CZ-NH2	265.18	4.78	1.33
1	B	420[A]	ARG	CZ-NH1	229.22	4.53	1.32
1	B	420[B]	ARG	CZ-NH1	229.22	4.53	1.32
1	B	244[A]	ARG	NE-CZ	195.18	3.47	1.33
1	B	244[B]	ARG	NE-CZ	195.18	3.47	1.33
1	B	244[A]	ARG	CZ-NH1	92.03	2.61	1.32
1	B	244[B]	ARG	CZ-NH1	92.03	2.61	1.32
1	A	142[A]	ASP	CG-OD1	84.57	2.86	1.25
1	A	142[B]	ASP	CG-OD1	84.57	2.86	1.25
1	B	315[A]	GLU	CD-OE2	78.86	2.75	1.25
1	B	315[B]	GLU	CD-OE2	78.86	2.75	1.25
1	B	142[A]	ASP	CG-OD2	69.03	2.56	1.25
1	B	142[B]	ASP	CG-OD2	69.03	2.56	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	315[A]	GLU	CD-OE1	57.49	2.34	1.25
1	B	315[B]	GLU	CD-OE1	57.49	2.34	1.25
1	A	129[A]	ARG	CZ-NH2	38.70	1.83	1.33
1	A	129[B]	ARG	CZ-NH2	38.70	1.83	1.33
1	A	142[A]	ASP	CG-OD2	38.23	1.98	1.25
1	A	142[B]	ASP	CG-OD2	38.23	1.98	1.25
1	B	420[A]	ARG	CG-CD	6.59	1.72	1.52
1	B	420[B]	ARG	CG-CD	6.59	1.72	1.52
1	B	42[A]	LYS	CE-NZ	5.51	1.65	1.49
1	B	42[B]	LYS	CE-NZ	5.51	1.65	1.49
1	A	498	VAL	C-N	-5.28	1.25	1.33

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	244[A]	ARG	NE-CZ-NH2	-101.84	27.54	119.20
1	B	244[B]	ARG	NE-CZ-NH2	-101.84	27.54	119.20
1	B	244[A]	ARG	NE-CZ-NH1	-79.89	41.62	121.50
1	B	244[B]	ARG	NE-CZ-NH1	-79.89	41.62	121.50
1	B	244[A]	ARG	NH1-CZ-NH2	-79.80	15.56	119.30
1	B	244[B]	ARG	NH1-CZ-NH2	-79.80	15.56	119.30
1	B	420[A]	ARG	NE-CZ-NH1	-59.41	62.09	121.50
1	B	420[B]	ARG	NE-CZ-NH1	-59.41	62.09	121.50
1	B	244[A]	ARG	CD-NE-CZ	-54.36	48.30	124.40
1	B	244[B]	ARG	CD-NE-CZ	-54.36	48.30	124.40
1	A	129[A]	ARG	NE-CZ-NH2	-36.15	86.67	119.20
1	A	129[B]	ARG	NE-CZ-NH2	-36.15	86.67	119.20
1	B	315[A]	GLU	OE1-CD-OE2	-34.88	39.20	122.90
1	B	315[B]	GLU	OE1-CD-OE2	-34.88	39.20	122.90
1	A	142[A]	ASP	OD1-CG-OD2	-31.37	47.60	122.90
1	A	142[B]	ASP	OD1-CG-OD2	-31.37	47.60	122.90
1	A	142[A]	ASP	CB-CG-OD1	-26.70	56.99	118.40
1	A	142[B]	ASP	CB-CG-OD1	-26.70	56.99	118.40
1	B	315[A]	GLU	CG-CD-OE2	-25.19	60.47	118.40
1	B	315[B]	GLU	CG-CD-OE2	-25.19	60.47	118.40
1	A	129[A]	ARG	NH1-CZ-NH2	25.01	151.81	119.30
1	A	129[B]	ARG	NH1-CZ-NH2	25.01	151.81	119.30
1	B	142[A]	ASP	CB-CG-OD2	-24.25	62.64	118.40
1	B	142[B]	ASP	CB-CG-OD2	-24.25	62.64	118.40
1	B	315[A]	GLU	CG-CD-OE1	-22.20	67.33	118.40
1	B	315[B]	GLU	CG-CD-OE1	-22.20	67.33	118.40
1	A	142[A]	ASP	CB-CG-OD2	-15.93	81.76	118.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142[B]	ASP	CB-CG-OD2	-15.93	81.76	118.40
1	B	420[A]	ARG	NH1-CZ-NH2	15.90	139.97	119.30
1	B	420[B]	ARG	NH1-CZ-NH2	15.90	139.97	119.30
1	A	100	SER	N-CA-C	9.07	125.46	113.30
1	B	115	LYS	N-CA-C	8.41	120.07	111.07
1	B	142[A]	ASP	OD1-CG-OD2	8.16	142.50	122.90
1	B	142[B]	ASP	OD1-CG-OD2	8.16	142.50	122.90
1	A	115	LYS	N-CA-C	7.86	119.48	111.07
1	A	45	THR	N-CA-C	-7.66	104.46	113.88
1	B	100	SER	N-CA-C	7.42	123.37	113.72
1	B	189	ALA	N-CA-C	7.39	119.34	111.28
1	B	309	SER	N-CA-C	-7.18	101.05	110.53
1	B	207	ASP	N-CA-C	-7.09	102.97	111.69
1	A	151	VAL	N-CA-C	6.93	117.07	110.42
1	A	309	SER	N-CA-C	-6.79	101.57	110.53
1	B	45	THR	N-CA-C	-6.73	105.60	113.88
1	A	105	VAL	N-CA-C	6.35	119.02	111.09
1	B	151	VAL	N-CA-C	6.35	117.09	110.62
1	B	63	ASP	N-CA-C	-6.29	101.83	109.57
1	A	184	ALA	N-CA-C	-6.16	99.17	108.96
1	B	177	LEU	CA-C-N	6.13	126.15	119.90
1	B	177	LEU	C-N-CA	6.13	126.15	119.90
1	B	318	TYR	CA-C-N	6.08	125.78	119.64
1	B	318	TYR	C-N-CA	6.08	125.78	119.64
1	B	413	ASP	N-CA-C	6.08	117.91	111.28
1	A	423	ASN	N-CA-C	6.06	122.55	114.12
1	B	96	GLY	N-CA-C	-6.01	105.56	112.29
1	B	480	GLY	N-CA-C	5.94	121.69	112.60
1	B	291	PHE	N-CA-C	-5.94	105.95	112.72
1	A	405	LEU	N-CA-C	5.92	118.49	111.33
1	A	441	THR	N-CA-C	5.82	120.01	113.02
1	A	362	LYS	N-CA-C	-5.74	103.77	112.04
1	B	319	PRO	N-CA-C	5.67	122.06	114.18
1	B	441	THR	N-CA-C	5.66	120.18	112.88
1	B	321	THR	N-CA-C	-5.61	105.03	112.94
1	B	67	ASN	N-CA-C	-5.58	100.01	108.67
1	A	207	ASP	N-CA-C	-5.54	104.87	111.69
1	B	52	LEU	N-CA-C	-5.52	101.84	110.17
1	A	291	PHE	N-CA-C	-5.50	106.35	112.57
1	A	96	GLY	N-CA-C	-5.50	105.75	112.68
1	A	189	ALA	N-CA-C	5.50	117.98	111.33
1	B	11	TYR	N-CA-C	-5.40	98.57	108.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	TYR	N-CA-C	5.36	117.21	111.36
1	B	184	ALA	N-CA-C	-5.32	100.62	109.46
1	A	480	GLY	N-CA-C	5.27	120.67	112.60
1	A	318	TYR	CA-C-N	5.26	126.41	119.84
1	A	318	TYR	C-N-CA	5.26	126.41	119.84
1	A	67	ASN	N-CA-C	-5.23	101.62	109.15
1	A	324	TRP	N-CA-C	5.13	119.52	113.16
1	B	209	ILE	N-CA-C	-5.10	100.31	107.75
1	A	54	ILE	N-CA-C	-5.10	100.31	107.75
1	A	63	ASP	N-CA-C	-5.07	102.18	109.48
1	A	204	ALA	CA-C-N	-5.05	114.84	120.45
1	A	204	ALA	C-N-CA	-5.05	114.84	120.45
1	A	259	PHE	N-CA-C	5.05	117.82	108.94
1	B	474	VAL	N-CA-C	-5.02	101.14	108.17

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	79[A]	THR	CB
1	A	79[B]	THR	CB

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	142[A]	ASP	Sidechain
1	A	142[B]	ASP	Sidechain
1	B	142[A]	ASP	Sidechain
1	B	142[B]	ASP	Sidechain
1	B	244[A]	ARG	Sidechain
1	B	244[B]	ARG	Sidechain
1	B	315[A]	GLU	Sidechain
1	B	315[B]	GLU	Sidechain
1	B	420[A]	ARG	Sidechain
1	B	420[B]	ARG	Sidechain

5.2 Too-close contacts ⓘ

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	3924	0	3754	78	0
1	B	3940	0	3763	97	0
2	C	29	0	27	4	0
3	A	5	0	0	0	0
3	B	15	0	0	0	0
4	A	14	0	14	12	0
4	B	14	0	14	7	0
5	B	15	0	15	0	0
6	A	474	0	0	8	0
6	B	459	0	0	7	0
All	All	8889	0	7587	178	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 11.

All (178) 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:B:315[B]:GLU:CD	1:B:315[B]:GLU:CG	1.90	1.44
1:A:129[B]:ARG:CZ	1:A:129[B]:ARG:NH2	1.83	1.38
1:A:129[A]:ARG:NH2	1:A:129[A]:ARG:CZ	1.88	1.35
1:B:315[B]:GLU:OE2	1:B:315[B]:GLU:HG3	1.44	1.14
4:A:502:NGO:HC4	6:A:650:HOH:O	1.46	1.13
1:A:142[B]:ASP:HB3	1:A:142[B]:ASP:OD1	1.51	1.10
1:A:142[B]:ASP:OD2	1:A:142[B]:ASP:CG	1.98	1.07
1:B:315[A]:GLU:OE2	1:B:315[A]:GLU:HG2	1.54	1.06
1:A:10:TYR:CZ	4:A:502:NGO:HC81	1.91	1.05
1:B:244[A]:ARG:NH2	1:B:244[A]:ARG:HH11	1.56	1.01
1:B:244[B]:ARG:HH11	1:B:244[B]:ARG:NE	1.57	1.00
1:B:142[A]:ASP:OD2	1:B:142[A]:ASP:HB3	1.64	0.98
1:B:142[B]:ASP:OD2	1:B:142[B]:ASP:HB2	1.64	0.97
1:B:315[A]:GLU:HG2	1:B:315[A]:GLU:OE1	1.65	0.96
1:B:244[B]:ARG:HH11	1:B:244[B]:ARG:NH2	1.65	0.93
1:A:483:THR:HG21	1:B:103:LEU:HD11	1.50	0.93
1:B:10:TYR:CZ	4:B:504:NGO:HC82	2.03	0.93
1:A:142[A]:ASP:OD2	1:A:142[A]:ASP:HB2	1.69	0.92
1:B:244[A]:ARG:HH11	1:B:244[A]:ARG:NE	1.67	0.92
1:A:142[B]:ASP:OD2	4:A:502:NGO:HC83	1.70	0.91
1:A:129[B]:ARG:NH2	1:A:129[B]:ARG:NE	2.19	0.90
1:A:142[A]:ASP:HB2	1:A:142[A]:ASP:OD1	1.73	0.89
1:A:10:TYR:CZ	4:A:502:NGO:C8	2.55	0.88
4:A:502:NGO:HC2	6:A:697:HOH:O	1.72	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:GLU:O	1:A:257:ARG:HG2	1.76	0.86
4:B:504:NGO:HC2	6:B:872:HOH:O	1.75	0.86
1:A:129[A]:ARG:NH2	1:A:129[A]:ARG:NE	2.24	0.85
6:A:997:HOH:O	2:C:2:NAG:H81	1.76	0.84
1:B:244[A]:ARG:CZ	1:B:244[A]:ARG:HD2	2.08	0.82
1:B:244[A]:ARG:NH2	1:B:244[A]:ARG:NH1	2.27	0.82
1:B:244[B]:ARG:NH2	1:B:244[B]:ARG:NH1	2.29	0.81
1:B:244[B]:ARG:NE	1:B:244[B]:ARG:NH2	2.30	0.79
1:B:244[B]:ARG:NE	1:B:244[B]:ARG:NH1	2.30	0.79
1:B:350:GLN:NE2	6:B:601:HOH:O	2.16	0.79
1:B:244[A]:ARG:NH2	1:B:244[A]:ARG:NE	2.31	0.79
1:B:142[A]:ASP:OD2	1:B:142[A]:ASP:CB	2.29	0.79
1:B:142[B]:ASP:OD2	1:B:142[B]:ASP:CB	2.30	0.79
1:B:244[A]:ARG:CZ	1:B:244[A]:ARG:CD	2.61	0.78
1:B:244[A]:ARG:NE	1:B:244[A]:ARG:NH1	2.31	0.77
1:B:241:ASN:O	1:B:244[A]:ARG:HG2	1.85	0.77
1:A:142[B]:ASP:OD2	1:A:142[B]:ASP:CB	2.33	0.76
1:B:244[A]:ARG:NH2	1:B:244[A]:ARG:HE	1.84	0.75
1:A:483:THR:CG2	1:B:103:LEU:HD11	2.18	0.74
1:B:315[A]:GLU:OE1	1:B:315[A]:GLU:CG	2.37	0.72
1:B:244[B]:ARG:NH2	1:B:244[B]:ARG:HE	1.86	0.72
1:A:483:THR:HG21	1:B:103:LEU:CD1	2.21	0.71
1:A:451:MET:HB2	1:A:474:VAL:HG21	1.72	0.71
1:A:142[B]:ASP:HB3	1:A:142[B]:ASP:OD2	1.91	0.71
1:B:315[B]:GLU:CG	1:B:315[B]:GLU:OE1	2.38	0.71
1:B:315[B]:GLU:CD	1:B:315[B]:GLU:OE1	2.34	0.70
1:A:142[A]:ASP:OD2	1:A:142[A]:ASP:CB	2.38	0.69
1:A:142[A]:ASP:OD1	1:A:142[A]:ASP:CB	2.40	0.69
1:A:299[B]:VAL:HG23	1:A:308:SER:HB3	1.74	0.68
1:B:315[B]:GLU:HG3	1:B:315[B]:GLU:OE1	1.94	0.67
1:B:244[B]:ARG:CZ	1:B:244[B]:ARG:HD2	2.24	0.67
1:A:330:GLU:HG2	6:A:796:HOH:O	1.96	0.65
1:B:315[A]:GLU:OE2	1:B:315[A]:GLU:CG	2.39	0.64
1:B:199:LEU:HD21	1:B:274:HIS:CD2	2.33	0.64
1:B:244[B]:ARG:NH1	1:B:244[B]:ARG:CZ	2.61	0.63
1:A:129[B]:ARG:NH2	1:A:129[B]:ARG:HE	1.94	0.62
1:B:10:TYR:OH	4:B:504:NGO:C8	2.45	0.62
1:A:142[B]:ASP:OD1	1:A:142[B]:ASP:CB	2.37	0.62
1:B:10:TYR:OH	4:B:504:NGO:HC82	1.98	0.62
1:A:299[B]:VAL:HG12	1:A:374:GLY:C	2.25	0.62
1:B:420[A]:ARG:HD3	1:B:420[A]:ARG:NH1	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:2:NAG:H3	2:C:2:NAG:H83	1.82	0.62
1:A:129[A]:ARG:NH2	1:A:129[A]:ARG:HE	1.97	0.61
1:A:142[A]:ASP:OD2	1:A:142[A]:ASP:OD1	2.19	0.61
1:B:315[A]:GLU:OE2	1:B:315[A]:GLU:OE1	2.18	0.61
1:A:10:TYR:CE1	4:A:502:NGO:HC81	2.34	0.61
1:B:315[B]:GLU:OE2	1:B:315[B]:GLU:OE1	2.19	0.61
1:B:489:ASP:OD2	1:B:491:ALA:HB3	2.01	0.60
1:B:147:GLN:HE21	1:B:148:ALA:H	1.48	0.60
1:A:299[B]:VAL:HG12	1:A:374:GLY:O	2.02	0.60
1:B:244[A]:ARG:CZ	1:B:244[A]:ARG:HD3	2.29	0.60
1:A:142[B]:ASP:OD1	1:A:142[B]:ASP:OD2	2.19	0.59
1:A:299[B]:VAL:HG23	1:A:308:SER:CB	2.31	0.59
1:A:10:TYR:OH	4:A:502:NGO:C8	2.50	0.58
1:B:489:ASP:HB3	6:B:621:HOH:O	2.04	0.57
1:B:244[B]:ARG:HE	1:B:244[B]:ARG:HH21	1.51	0.57
1:A:10:TYR:CE2	4:A:502:NGO:C8	2.87	0.56
1:A:471:GLN:O	1:A:471:GLN:HG3	2.05	0.56
1:A:226:HIS:HD2	6:A:666:HOH:O	1.89	0.56
1:B:244[B]:ARG:CZ	1:B:244[B]:ARG:CD	2.85	0.55
1:A:486:PRO:HA	1:A:492:TRP:CD1	2.42	0.55
1:A:142[B]:ASP:OD1	1:A:144:GLU:OE2	2.26	0.54
1:B:244[A]:ARG:HE	1:B:244[A]:ARG:HH21	1.56	0.54
1:A:142[A]:ASP:OD2	1:A:142[A]:ASP:CG	2.51	0.53
1:A:343:ARG:HH11	1:A:410:ARG:NH1	2.07	0.53
1:B:201:GLN:HG3	6:B:933:HOH:O	2.08	0.53
1:A:101:ASN:HA	1:A:144:GLU:O	2.09	0.53
1:B:10:TYR:CZ	4:B:504:NGO:C8	2.86	0.52
1:A:226:HIS:HE1	1:A:306:GLN:OE1	1.93	0.52
1:A:471:GLN:O	1:A:471:GLN:CG	2.59	0.51
1:A:215:ASP:H	1:A:227:GLN:NE2	2.09	0.51
1:B:346:GLU:O	1:B:350:GLN:HG2	2.10	0.51
1:A:10:TYR:CE2	4:A:502:NGO:HC82	2.45	0.51
1:B:244[A]:ARG:CZ	1:B:244[A]:ARG:NH1	2.75	0.50
1:A:456:TYR:CE1	1:A:462:TYR:HE2	2.30	0.49
1:B:482:ILE:HD12	1:B:491:ALA:HB1	1.94	0.49
1:B:8:ILE:HG12	1:B:46:HIS:HB2	1.94	0.49
1:A:307:TYR:CD1	1:A:307:TYR:N	2.81	0.49
1:A:486:PRO:HG3	1:A:492:TRP:CZ2	2.48	0.49
1:B:101:ASN:HA	1:B:144:GLU:O	2.12	0.48
1:B:478:LYS:HE3	1:B:490:SER:O	2.13	0.48
1:B:142[B]:ASP:OD2	1:B:142[B]:ASP:CG	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:THR:HG23	1:A:483:THR:O	2.14	0.48
1:B:224:THR:O	1:B:307:TYR:HA	2.13	0.48
1:B:330:GLU:HG3	1:B:333:ARG:NH2	2.29	0.48
1:A:252:TRP:HB2	1:B:244[A]:ARG:HB2	1.95	0.47
1:B:470:TYR:CD2	1:B:471:GLN:HG3	2.50	0.47
1:A:257:ARG:CZ	1:A:493:LEU:HD21	2.44	0.47
1:B:223:VAL:HG12	1:B:307:TYR:HA	1.98	0.46
1:B:356:GLN:HG3	6:B:881:HOH:O	2.15	0.46
1:B:370:HIS:CE1	1:B:372:GLN:HB2	2.51	0.46
1:A:471:GLN:O	1:A:471:GLN:NE2	2.48	0.45
1:A:245:GLU:HG3	1:B:478:LYS:HD2	1.98	0.45
1:A:299[B]:VAL:HG21	1:A:305:GLY:HA2	1.98	0.45
1:A:466:ALA:O	1:A:476:GLN:HA	2.16	0.45
1:A:144:GLU:HA	1:A:145:TYR:CG	2.53	0.44
1:A:299[B]:VAL:HG22	1:A:300:SER:N	2.32	0.44
1:B:31:PHE:CG	1:B:406:GLY:HA2	2.52	0.44
1:B:261:SER:HA	1:B:262:PRO:C	2.42	0.44
1:A:483:THR:CG2	1:A:483:THR:O	2.64	0.44
1:B:259:PHE:O	1:B:260:PRO:C	2.60	0.44
1:A:227:GLN:HE21	1:A:227:GLN:HB2	1.67	0.44
1:A:215:ASP:H	1:A:227:GLN:HE21	1.64	0.44
1:B:477:THR:HG23	1:B:492:TRP:CZ3	2.53	0.44
1:A:451:MET:CB	1:A:474:VAL:HG21	2.44	0.44
1:A:102:ASP:OD2	1:A:194:ARG:NH2	2.42	0.44
1:A:147:GLN:O	1:A:151:VAL:HG23	2.18	0.43
1:B:63:ASP:OD1	1:B:63:ASP:C	2.61	0.43
1:A:152:ASP:OD1	1:A:198:LYS:NZ	2.52	0.43
1:B:142[A]:ASP:OD2	4:B:504:NGO:HC83	2.18	0.43
1:A:142[B]:ASP:OD2	4:A:502:NGO:C8	2.54	0.43
2:C:2:NAG:C1	2:C:2:NAG:H82	2.49	0.43
1:B:444:GLY:C	1:B:446:GLY:H	2.27	0.43
1:B:370:HIS:HE1	1:B:372:GLN:HB2	1.83	0.43
4:A:502:NGO:C2	6:A:697:HOH:O	2.47	0.43
2:C:2:NAG:H3	2:C:2:NAG:C8	2.47	0.43
1:B:479:TRP:CD1	1:B:482:ILE:HD11	2.54	0.42
1:B:314:GLY:N	1:B:315[A]:GLU:OE1	2.52	0.42
1:B:445:PRO:HB3	6:B:781:HOH:O	2.19	0.42
1:A:39:ALA:O	1:A:43:GLN:HG3	2.19	0.42
1:B:50:SER:HA	1:B:51:PHE:HA	1.75	0.42
1:B:478:LYS:HE2	1:B:493:LEU:HB2	2.00	0.42
1:A:330:GLU:O	1:A:333:ARG:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:LYS:NZ	6:B:619:HOH:O	2.53	0.42
1:B:25:ASP:OD1	1:B:27:SER:OG	2.33	0.42
1:B:244[B]:ARG:NH1	1:B:244[B]:ARG:CD	2.82	0.42
1:A:54:ILE:HD12	1:A:110:TYR:CD2	2.55	0.42
1:B:244[A]:ARG:NH1	1:B:244[A]:ARG:CD	2.83	0.42
1:B:281:PRO:HG2	1:B:284:LYS:HG3	2.02	0.42
1:B:444:GLY:C	1:B:446:GLY:N	2.78	0.41
1:A:10:TYR:OH	4:A:502:NGO:HC83	2.18	0.41
1:A:484:SER:HA	6:A:966:HOH:O	2.19	0.41
1:B:50:SER:HB2	1:B:51:PHE:CG	2.55	0.41
1:B:258:ALA:O	1:B:276:MET:HE1	2.20	0.41
1:A:299[A]:VAL:HG22	1:A:374:GLY:C	2.44	0.41
1:B:140:ASP:OD2	1:B:142[A]:ASP:OD1	2.38	0.41
1:B:142[B]:ASP:OD1	1:B:144:GLU:OE2	2.39	0.41
1:B:347:GLN:HE21	1:B:347:GLN:HB3	1.64	0.41
1:B:144:GLU:HA	1:B:145:TYR:CG	2.56	0.41
1:A:333:ARG:HG3	1:A:334:ASP:N	2.34	0.41
1:B:142[B]:ASP:OD2	4:B:504:NGO:HC83	2.21	0.41
1:A:13:ILE:HA	1:A:14:PRO:HD3	1.88	0.41
1:A:213:THR:HB	1:A:267:VAL:HG22	2.02	0.41
1:A:493:LEU:O	1:A:495:VAL:HG13	2.21	0.41
1:A:140:ASP:HA	1:A:182:THR:O	2.21	0.41
1:B:244[A]:ARG:NH2	1:B:259:PHE:O	2.54	0.41
1:B:213:THR:HB	1:B:267:VAL:HG22	2.04	0.40
1:A:129[B]:ARG:HE	1:A:129[B]:ARG:HH21	1.68	0.40
1:A:223:VAL:HG13	6:A:962:HOH:O	2.21	0.40
1:B:470:TYR:CE2	1:B:471:GLN:HG3	2.55	0.40
1:A:214:TYR:O	1:A:215:ASP:HB2	2.21	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	500/498 (100%)	486 (97%)	14 (3%)	0	100	100
1	B	504/498 (101%)	494 (98%)	10 (2%)	0	100	100
All	All	1004/996 (101%)	980 (98%)	24 (2%)	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	408/404 (101%)	394 (97%)	14 (3%)	32	33
1	B	411/404 (102%)	403 (98%)	8 (2%)	50	56
All	All	819/808 (101%)	797 (97%)	22 (3%)	39	42

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	26	THR
1	A	199	LEU
1	A	213	THR
1	A	223	VAL
1	A	227	GLN
1	A	290	PRO
1	A	339	ILE
1	A	349	LEU
1	A	378	THR
1	A	380	ASP
1	A	438	LEU
1	A	471	GLN
1	A	483	THR
1	B	3	THR
1	B	22	THR
1	B	147	GLN
1	B	213	THR

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Mol	Chain	Res	Type
1	B	320	SER
1	B	352	ASN
1	B	375	LEU
1	B	380	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	76	ASN
1	A	112	ASN
1	A	147	GLN
1	A	226	HIS
1	A	227	GLN
1	A	394	GLN
1	B	43	GLN
1	B	57	ASN
1	B	84	HIS
1	B	147	GLN
1	B	273	GLN
1	B	347	GLN
1	B	350	GLN
1	B	352	ASN
1	B	394	GLN
1	B	431	GLN

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 ⓘ

2 monosaccharides 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	C	1	2	15,15,15	0.60	0	21,21,21	0.77	0
2	NAG	C	2	2	14,14,15	0.53	0	17,19,21	1.18	2 (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
2	NAG	C	1	2	-	0/6/26/26	0/1/1/1
2	NAG	C	2	2	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C8-C7-N2	2.28	119.90	116.12
2	C	2	NAG	C4-C3-C2	-2.13	107.90	111.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

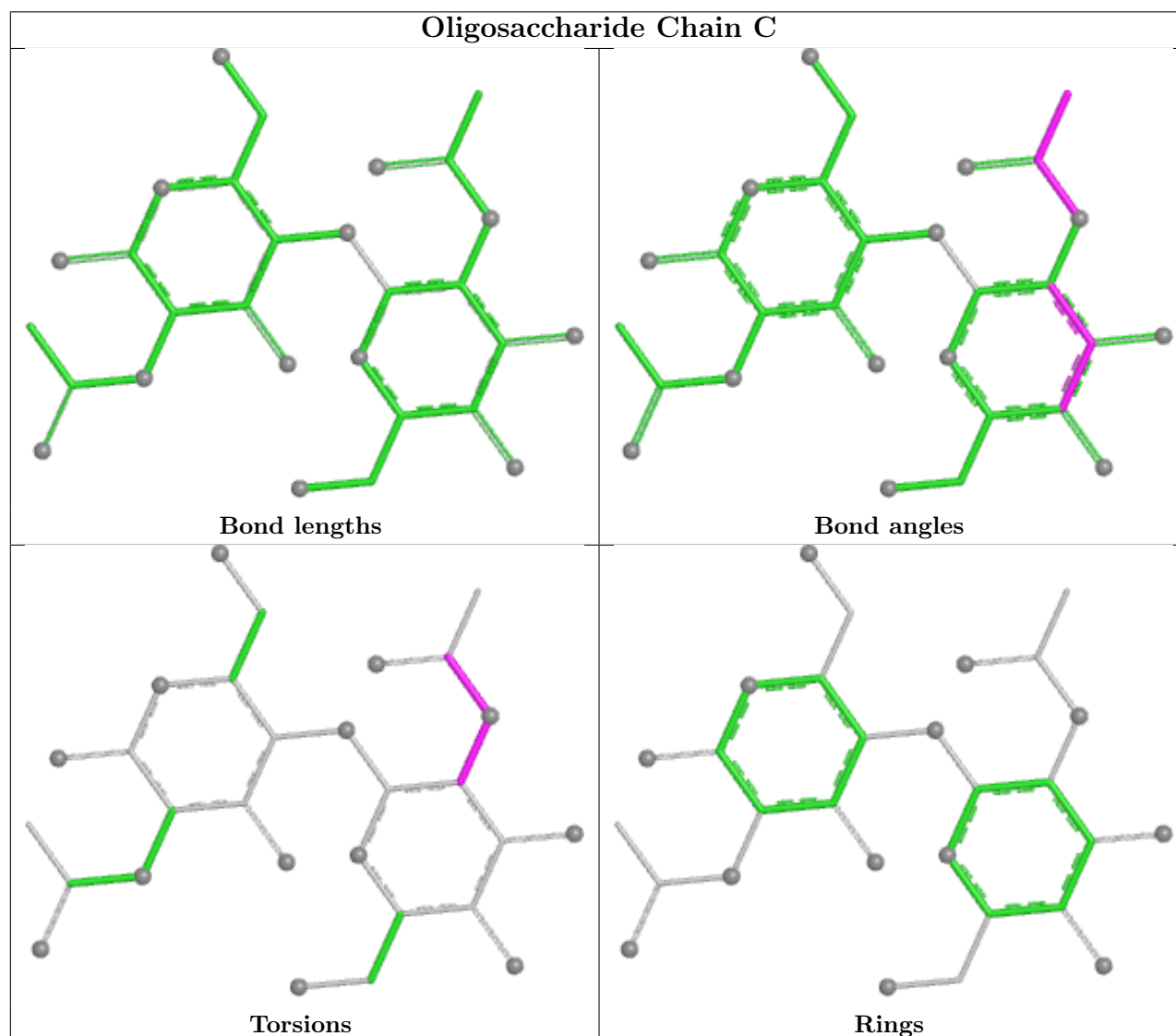
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	C	2	NAG	C1-C2-N2-C7
2	C	2	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

7 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
5	NAG	B	505	-	15,15,15	0.57	0	21,21,21	0.64	0
3	SO4	B	503	-	4,4,4	0.39	0	6,6,6	0.10	0
4	NGO	A	502	-	14,15,15	3.32	3 (21%)	15,22,22	2.37	4 (26%)
4	NGO	B	504	-	14,15,15	2.45	4 (28%)	15,22,22	1.14	1 (6%)
3	SO4	B	501	-	4,4,4	0.40	0	6,6,6	0.09	0
3	SO4	B	502	-	4,4,4	0.39	0	6,6,6	0.18	0
3	SO4	A	501	-	4,4,4	0.39	0	6,6,6	0.13	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
5	NAG	B	505	-	-	3/6/26/26	0/1/1/1
4	NGO	B	504	-	-	2/2/30/30	0/2/2/2
4	NGO	A	502	-	-	0/2/30/30	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	NGO	C2-N2	-11.05	1.36	1.47
4	B	504	NGO	C2-N2	-7.60	1.39	1.47
4	A	502	NGO	C1-C2	4.17	1.60	1.52
4	B	504	NGO	C1-C2	2.80	1.58	1.52
4	B	504	NGO	O1-C1	-2.73	1.40	1.45
4	A	502	NGO	O1-C1	-2.43	1.41	1.45
4	B	504	NGO	C7-N2	2.18	1.35	1.27

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	502	NGO	C8-C7-N2	-5.98	118.43	127.05
4	A	502	NGO	O5-C1-O1	5.16	118.32	109.25
4	B	504	NGO	C8-C7-N2	-3.42	122.12	127.05
4	A	502	NGO	C3-C2-N2	-3.22	106.05	110.56
4	A	502	NGO	C1-O1-C7	-2.13	103.93	106.88

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	505	NAG	C1-C2-N2-C7
5	B	505	NAG	C8-C7-N2-C2
5	B	505	NAG	O7-C7-N2-C2
4	B	504	NGO	O5-C5-C6-O6
4	B	504	NGO	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	NGO	12	0
4	B	504	NGO	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	498/498 (100%)	-0.10	30 (6%) 27 26	9, 19, 44, 52	6 (1%)
1	B	498/498 (100%)	-0.16	11 (2%) 62 61	9, 20, 36, 48	8 (1%)
All	All	996/996 (100%)	-0.13	41 (4%) 41 40	9, 19, 40, 52	14 (1%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	456	TYR	5.4
1	A	457	VAL	4.6
1	A	485	ALA	3.9
1	A	499	ALA	3.8
1	A	458	PRO	3.7
1	A	484	SER	3.7
1	A	466	ALA	3.1
1	B	441	THR	3.1
1	A	483	THR	3.0
1	A	460	THR	3.0
1	A	470	TYR	3.0
1	A	461	THR	3.0
1	B	2	SER	2.9
1	A	459	GLY	2.9
1	A	467	LEU	2.9
1	A	474	VAL	2.8
1	A	453	ALA	2.7
1	A	452	THR	2.7
1	A	488	SER	2.7
1	A	463	ALA	2.6
1	A	339	ILE	2.6
1	B	300	SER	2.5
1	A	482	ILE	2.5
1	B	372	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	498	VAL	2.4
1	A	462	TYR	2.4
1	B	446	GLY	2.4
1	A	455	ALA	2.3
1	B	488	SER	2.3
1	B	350	GLN	2.3
1	A	468	VAL	2.3
1	B	352	ASN	2.3
1	A	471	GLN	2.2
1	B	301	GLY	2.2
1	A	454	PRO	2.2
1	A	481	TYR	2.1
1	B	487	GLY	2.1
1	B	303	ASN	2.1
1	A	473	TYR	2.1
1	A	257	ARG	2.1
1	A	475	TRP	2.0

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

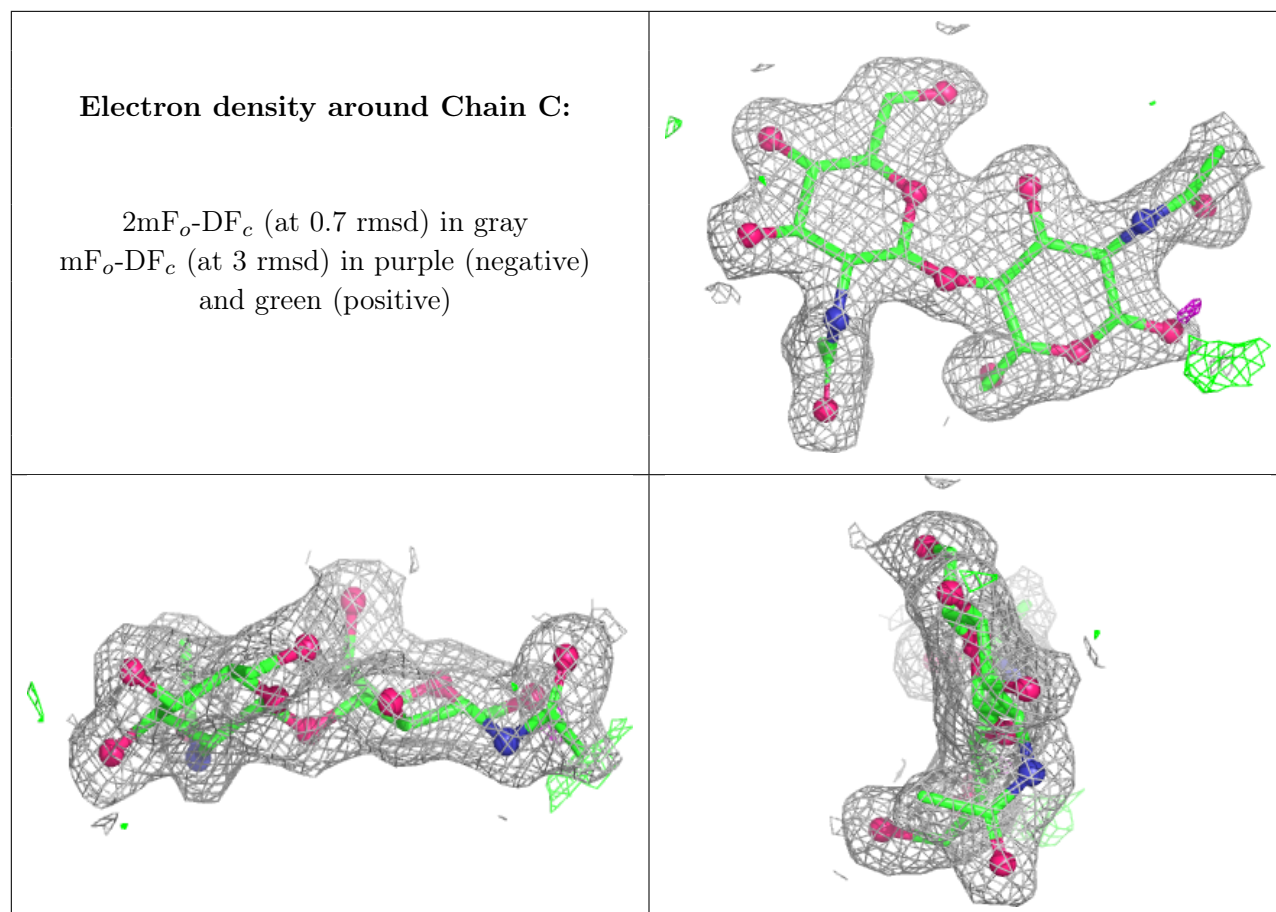
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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	C	2	14/15	0.93	0.07	19,23,26,31	0
2	NAG	C	1	15/15	0.95	0.07	19,22,25,29	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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($\text{\AA}^2$)	Q<0.9
4	NGO	A	502	14/14	0.71	0.26	21,27,30,32	14
4	NGO	B	504	14/14	0.73	0.21	23,28,32,34	14
5	NAG	B	505	15/15	0.78	0.16	47,49,54,56	0
3	SO4	B	502	5/5	0.87	0.12	57,58,59,60	0
3	SO4	B	503	5/5	0.93	0.09	51,52,53,54	0
3	SO4	B	501	5/5	0.93	0.08	50,51,52,53	0
3	SO4	A	501	5/5	0.96	0.07	37,38,41,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.