



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:28 PM UTC

PDB ID : 5A7E / pdb_00005a7e
Title : Crystallographic Structural Determination of a Trigonal Laccase from *Coriopsis Gallica* (CgL) to 1.5 Å resolution
Authors : Ruiz-Arellano, R.R.; Diaz, A.; Ayala, M.; De la Mora, E.; Rudino-Pinera, E.
Deposited on : 2015-07-03
Resolution : 1.50 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

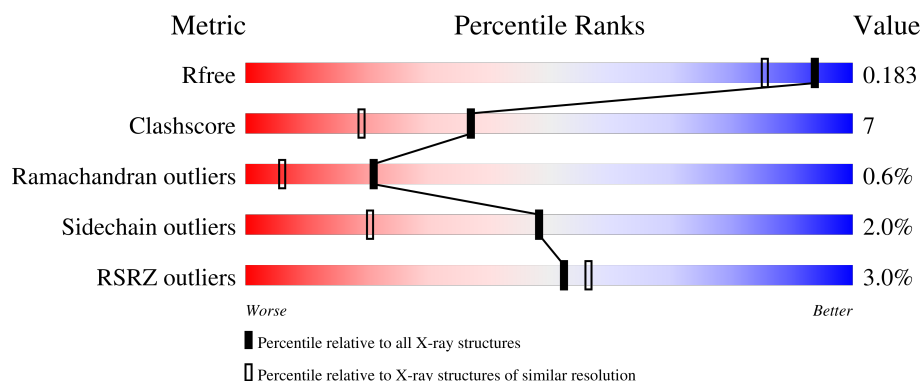
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	496	3% 52% 44% .
2	B	3	67% 33%
3	C	5	60% 40%
4	D	2	100%

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
2	BMA	B	3	X	-	-	-
3	BMA	C	3	X	-	X	-
3	MAN	C	4	X	-	-	-
3	MAN	C	5	X	-	-	-
4	BGC	D	2	X	-	-	-
6	ACT	A	505	-	X	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4646 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 CORIOLOPSIS GALLICA LACCASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	496	3935	2485	666	771	13	0	25	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ASP	TYR	conflict	UNP Q1W6B1
A	129	ASN	GLN	conflict	UNP Q1W6B1
A	156	LYS	ARG	conflict	UNP Q1W6B1
A	159	ALA	PRO	conflict	UNP Q1W6B1
A	160	PRO	ALA	conflict	UNP Q1W6B1
A	161	VAL	ILE	conflict	UNP Q1W6B1
A	176	SER	ILE	conflict	UNP Q1W6B1
A	177	SER	ASN	conflict	UNP Q1W6B1
A	180	ALA	ASN	conflict	UNP Q1W6B1
A	207	TYR	HIS	conflict	UNP Q1W6B1
A	234	LEU	ILE	conflict	UNP Q1W6B1
A	265	THR	ASN	conflict	UNP Q1W6B1
A	266	GLN	THR	conflict	UNP Q1W6B1
A	269	ALA	ASP	conflict	UNP Q1W6B1
A	272	THR	VAL	conflict	UNP Q1W6B1
A	292	THR	ALA	conflict	UNP Q1W6B1
A	334	ASN	ARG	conflict	UNP Q1W6B1
A	336	THR	SER	conflict	UNP Q1W6B1
A	361	ALA	GLN	conflict	UNP Q1W6B1
A	366	ALA	THR	conflict	UNP Q1W6B1
A	386	ALA	THR	conflict	UNP Q1W6B1
A	401	ILE	ALA	conflict	UNP Q1W6B1
A	416	ALA	GLU	conflict	UNP Q1W6B1
A	428	ALA	SER	conflict	UNP Q1W6B1

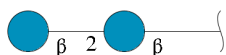
- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(4-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(3-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	D	2	Total	C	O	0	0	0
			22	12	10			

- Molecule 5 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	Cu	0	0
			4	4		

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

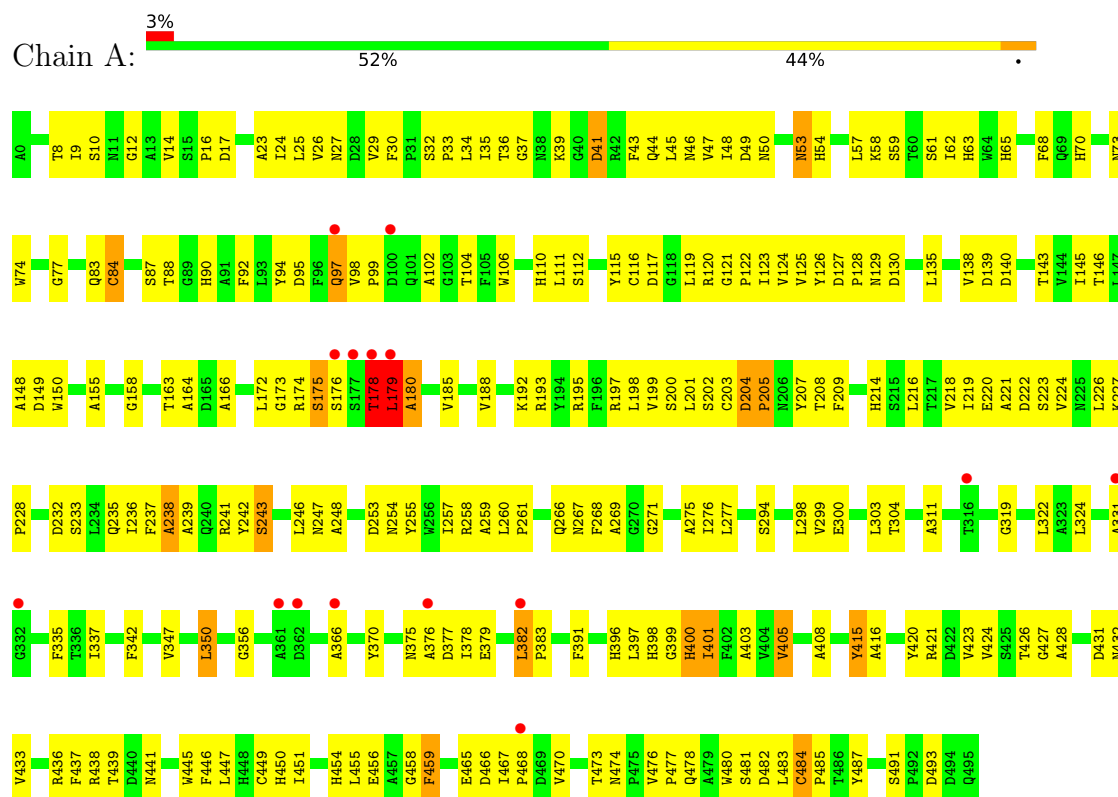
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	581	Total	O	0	0
			581	581		

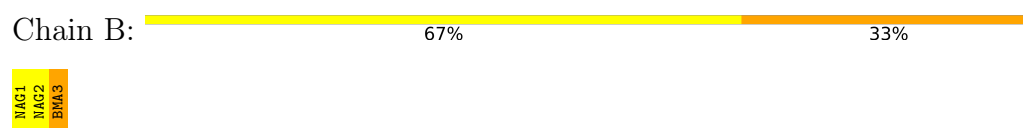
3 Residue-property plots

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: CORIOLOPSIS GALLICA LACCASE



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



• Molecule 3: alpha-D-mannopyranose-(3-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 4: beta-D-glucopyranose-(1-2)-beta-D-glucopyranose

Chain D:

100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.74Å 56.41Å 59.17Å 75.67° 73.03° 76.49°	Depositor
Resolution (Å)	43.08 – 1.50 43.08 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.4 (43.08-1.50) 94.4 (43.08-1.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 1.50Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.163 , 0.183 0.165 , 0.183	Depositor DCC
R_{free} test set	4051 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	15.0	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.9	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	0.97	EDS
Total number of atoms	4646	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.69% 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, BMA, CU, ACT, MAN, BGC

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	2.11	215/4051 (5.3%)	1.11	25/5570 (0.4%)

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	4

All (215) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	266[A]	GLN	CD-OE1	-9.45	1.05	1.23
1	A	266[B]	GLN	CD-OE1	-9.45	1.05	1.23
1	A	127	ASP	C-O	-9.26	1.16	1.25
1	A	65	HIS	C-O	-9.05	1.13	1.24
1	A	400	HIS	C-O	-8.03	1.14	1.23
1	A	258	ARG	C-O	-8.02	1.13	1.24
1	A	209	PHE	C-O	-7.99	1.14	1.24
1	A	23	ALA	C-O	-7.83	1.16	1.24
1	A	428	ALA	C-O	-7.74	1.16	1.24
1	A	121	GLY	C-O	-7.68	1.13	1.24
1	A	43	PHE	C-O	-7.62	1.15	1.23
1	A	145	ILE	C-O	-7.62	1.15	1.24
1	A	173	GLY	C-O	-7.58	1.15	1.24
1	A	421	ARG	C-O	-7.47	1.17	1.24
1	A	484	CYS	C-O	-7.47	1.17	1.24
1	A	242	TYR	C-O	-7.43	1.15	1.23
1	A	26	VAL	C-O	-7.41	1.16	1.24
1	A	33	PRO	C-O	-7.41	1.15	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	299	VAL	C-O	-7.40	1.16	1.24
1	A	433	VAL	C-O	-7.33	1.16	1.24
1	A	124	VAL	C-O	-7.27	1.16	1.24
1	A	255	TYR	C-O	-7.27	1.14	1.24
1	A	94	TYR	C-O	-7.24	1.15	1.24
1	A	166	ALA	C-O	-7.05	1.15	1.23
1	A	45	LEU	C-O	-7.04	1.15	1.24
1	A	49	ASP	C-O	-7.04	1.15	1.24
1	A	257	ILE	C-O	-6.99	1.16	1.24
1	A	9	ILE	C-O	-6.95	1.16	1.24
1	A	158	GLY	C-O	-6.95	1.17	1.23
1	A	259	ALA	C-O	-6.93	1.15	1.23
1	A	36	THR	C-O	-6.89	1.15	1.23
1	A	150	TRP	C-O	-6.89	1.15	1.23
1	A	197	ARG	C-O	-6.84	1.16	1.24
1	A	396	HIS	C-O	-6.83	1.16	1.24
1	A	441	ASN	C-O	-6.82	1.16	1.24
1	A	87	SER	C-O	-6.81	1.15	1.23
1	A	24	ILE	C-O	-6.80	1.16	1.24
1	A	122	PRO	C-O	-6.74	1.16	1.23
1	A	95	ASP	C-O	-6.74	1.16	1.24
1	A	125	VAL	C-O	-6.73	1.17	1.24
1	A	130[A]	ASP	C-O	-6.71	1.15	1.24
1	A	130[B]	ASP	C-O	-6.71	1.15	1.24
1	A	253	ASP	C-O	-6.66	1.18	1.24
1	A	269	ALA	C-O	-6.65	1.16	1.23
1	A	174	ARG	C-O	-6.64	1.16	1.23
1	A	449	CYS	C-O	-6.64	1.16	1.23
1	A	175[A]	SER	C-O	-6.60	1.15	1.23
1	A	175[B]	SER	C-O	-6.60	1.15	1.23
1	A	423	VAL	C-O	-6.60	1.17	1.24
1	A	208	THR	C-O	-6.56	1.16	1.24
1	A	104	THR	C-O	-6.56	1.16	1.24
1	A	451	ILE	C-O	-6.56	1.16	1.23
1	A	163	THR	C-O	-6.56	1.16	1.24
1	A	424	VAL	C-O	-6.55	1.17	1.24
1	A	260	LEU	C-O	-6.50	1.16	1.24
1	A	304	THR	C-O	-6.47	1.15	1.23
1	A	436	ARG	C-O	-6.47	1.16	1.23
1	A	58	LYS	C-O	-6.46	1.15	1.24
1	A	202	SER	C-O	-6.46	1.16	1.23
1	A	347	VAL	C-O	-6.44	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	THR	C-O	-6.42	1.16	1.23
1	A	111	LEU	C-O	-6.40	1.16	1.24
1	A	192	LYS	C-O	-6.40	1.16	1.23
1	A	30	PHE	C-O	-6.39	1.15	1.25
1	A	416	ALA	C-O	-6.38	1.16	1.24
1	A	445	TRP	C-O	-6.36	1.16	1.24
1	A	35	ILE	C-O	-6.35	1.17	1.24
1	A	129	ASN	C-O	-6.33	1.15	1.24
1	A	437	PHE	C-O	-6.32	1.16	1.23
1	A	88	THR	C-O	-6.29	1.16	1.23
1	A	236	ILE	C-O	-6.22	1.17	1.24
1	A	29	VAL	C-O	-6.22	1.17	1.23
1	A	276	ILE	C-O	-6.22	1.17	1.24
1	A	200	SER	C-O	-6.21	1.16	1.24
1	A	267[A]	ASN	C-O	-6.18	1.17	1.24
1	A	267[B]	ASN	C-O	-6.18	1.17	1.24
1	A	143	THR	C-O	-6.16	1.15	1.24
1	A	102	ALA	C-O	-6.16	1.16	1.23
1	A	221	ALA	C-O	-6.15	1.17	1.24
1	A	199	VAL	C-O	-6.13	1.17	1.24
1	A	233	SER	C-O	-6.13	1.16	1.23
1	A	427	GLY	C-O	-6.11	1.15	1.23
1	A	70	HIS	C-O	-6.10	1.16	1.24
1	A	207	TYR	C-O	-6.10	1.16	1.24
1	A	179	LEU	C-O	-6.09	1.16	1.24
1	A	126	TYR	C-O	-6.08	1.15	1.23
1	A	198	LEU	C-O	-6.07	1.16	1.24
1	A	214	HIS	C-O	-6.06	1.16	1.23
1	A	63	HIS	C-O	-6.06	1.16	1.23
1	A	224	VAL	C-O	-6.04	1.17	1.24
1	A	228	PRO	C-O	-6.03	1.16	1.23
1	A	37	GLY	C-O	-6.01	1.17	1.23
1	A	370	TYR	C-O	-6.00	1.16	1.24
1	A	62[A]	ILE	C-O	-6.00	1.17	1.24
1	A	62[B]	ILE	C-O	-6.00	1.17	1.24
1	A	106	TRP	C-O	-5.99	1.16	1.23
1	A	50	ASN	C-O	-5.99	1.16	1.23
1	A	117	ASP	C-O	-5.99	1.16	1.24
1	A	254	ASN	C-O	-5.98	1.16	1.24
1	A	188	VAL	C-O	-5.97	1.17	1.23
1	A	92	PHE	C-O	-5.96	1.17	1.23
1	A	110	HIS	C-O	-5.95	1.14	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	473	THR	C-O	-5.91	1.16	1.24
1	A	68	PHE	C-O	-5.91	1.16	1.24
1	A	112	SER	C-O	-5.90	1.16	1.24
1	A	44	GLN	C-O	-5.89	1.16	1.23
1	A	8	THR	C-O	-5.89	1.16	1.24
1	A	401[A]	ILE	C-O	-5.89	1.17	1.24
1	A	401[C]	ILE	C-O	-5.89	1.17	1.24
1	A	53	ASN	C-O	-5.86	1.16	1.24
1	A	420	TYR	C-O	-5.84	1.16	1.23
1	A	216	LEU	C-O	-5.82	1.17	1.24
1	A	482	ASP	C-O	-5.82	1.16	1.24
1	A	246	LEU	C-O	-5.81	1.17	1.24
1	A	235	GLN	C-O	-5.81	1.17	1.24
1	A	466	ASP	C-O	-5.79	1.15	1.23
1	A	487	TYR	C-O	-5.78	1.17	1.24
1	A	39	LYS	C-O	-5.76	1.17	1.23
1	A	483	LEU	C-O	-5.76	1.17	1.24
1	A	123	ILE	C-O	-5.74	1.18	1.24
1	A	149	ASP	C-O	-5.74	1.16	1.23
1	A	25	LEU	C-O	-5.72	1.17	1.23
1	A	164	ALA	C-O	-5.72	1.16	1.23
1	A	450	HIS	C-O	-5.68	1.16	1.24
1	A	155	ALA	C-O	-5.67	1.17	1.24
1	A	195	ARG	C-O	-5.65	1.17	1.24
1	A	10	SER	C-O	-5.65	1.17	1.23
1	A	311	ALA	C-O	-5.64	1.16	1.23
1	A	397	LEU	C-O	-5.63	1.17	1.24
1	A	415	TYR	C-O	-5.62	1.16	1.24
1	A	47	VAL	C-O	-5.62	1.17	1.23
1	A	48	ILE	C-O	-5.61	1.18	1.24
1	A	232	ASP	C-O	-5.59	1.16	1.24
1	A	135	LEU	C-O	-5.57	1.16	1.24
1	A	84[B]	CYS	C-O	-5.55	1.16	1.23
1	A	84[C]	CYS	C-O	-5.55	1.16	1.23
1	A	480	TRP	C-O	-5.55	1.17	1.24
1	A	46	ASN	C-O	-5.53	1.17	1.24
1	A	178	THR	CB-CG2	-5.53	1.34	1.52
1	A	16	PRO	C-O	-5.52	1.17	1.24
1	A	61[A]	SER	C-O	-5.50	1.17	1.23
1	A	61[B]	SER	C-O	-5.50	1.17	1.23
1	A	474	ASN	C-O	-5.49	1.18	1.24
1	A	138	VAL	C-O	-5.49	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	271	GLY	C-O	-5.48	1.17	1.24
1	A	476	VAL	C-O	-5.48	1.17	1.24
1	A	238	ALA	C-O	-5.47	1.17	1.23
1	A	218	VAL	C-O	-5.46	1.18	1.24
1	A	185	VAL	C-O	-5.46	1.18	1.24
1	A	227[A]	LYS	C-O	-5.45	1.16	1.24
1	A	227[B]	LYS	C-O	-5.45	1.16	1.24
1	A	431	ASP	C-O	-5.45	1.16	1.23
1	A	300	GLU	C-O	-5.45	1.17	1.24
1	A	481	SER	C-O	-5.44	1.17	1.24
1	A	115	TYR	C-O	-5.43	1.17	1.24
1	A	478	GLN	C-O	-5.43	1.17	1.24
1	A	350	LEU	C-O	-5.42	1.17	1.24
1	A	83	GLN	C-O	-5.42	1.17	1.23
1	A	335	PHE	C-O	-5.41	1.17	1.23
1	A	454	HIS	C-O	-5.41	1.17	1.24
1	A	426	THR	C-O	-5.40	1.16	1.24
1	A	241	ARG	C-O	-5.38	1.17	1.23
1	A	275	ALA	C-O	-5.37	1.17	1.24
1	A	447	LEU	C-O	-5.37	1.18	1.24
1	A	12	GLY	C-O	-5.34	1.18	1.23
1	A	14	VAL	C-O	-5.34	1.18	1.23
1	A	139	ASP	C-O	-5.34	1.17	1.23
1	A	243	SER	C-O	-5.33	1.17	1.24
1	A	172	LEU	C-O	-5.31	1.17	1.23
1	A	128	PRO	C-O	-5.30	1.17	1.24
1	A	391	PHE	C-O	-5.29	1.17	1.23
1	A	193	ARG	C-O	-5.29	1.17	1.24
1	A	455	LEU	C-O	-5.28	1.18	1.24
1	A	59	SER	C-O	-5.27	1.17	1.23
1	A	41	ASP	C-O	-5.26	1.17	1.23
1	A	148	ALA	C-O	-5.26	1.17	1.23
1	A	53	ASN	CG-OD1	-5.26	1.13	1.23
1	A	226	LEU	C-O	-5.25	1.17	1.23
1	A	34	LEU	C-O	-5.24	1.17	1.23
1	A	222	ASP	C-O	-5.24	1.17	1.23
1	A	180[A]	ALA	C-O	-5.23	1.16	1.24
1	A	180[B]	ALA	C-O	-5.23	1.16	1.24
1	A	140	ASP	C-O	-5.22	1.18	1.23
1	A	477	PRO	C-O	-5.20	1.18	1.23
1	A	399	GLY	C-O	-5.20	1.17	1.24
1	A	379	GLU	C-O	-5.19	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	319	GLY	C-O	-5.19	1.17	1.23
1	A	237	PHE	C-O	-5.17	1.17	1.23
1	A	485	PRO	C-O	-5.17	1.18	1.24
1	A	261	PRO	C-O	-5.17	1.17	1.23
1	A	303	LEU	C-O	-5.17	1.17	1.23
1	A	408	ALA	C-O	-5.16	1.17	1.23
1	A	470	VAL	C-O	-5.15	1.18	1.24
1	A	465	GLU	C-O	-5.15	1.17	1.24
1	A	201	LEU	C-O	-5.14	1.17	1.24
1	A	456	GLU	C-O	-5.14	1.17	1.24
1	A	366	ALA	C-O	-5.13	1.17	1.23
1	A	403	ALA	C-O	-5.12	1.17	1.23
1	A	277	LEU	C-O	-5.12	1.17	1.24
1	A	337	ILE	C-O	-5.11	1.18	1.24
1	A	120	ARG	C-O	-5.10	1.17	1.24
1	A	459	PHE	C-O	-5.09	1.18	1.23
1	A	74	TRP	C-O	-5.08	1.17	1.24
1	A	342	PHE	C-O	-5.08	1.17	1.23
1	A	32	SER	C-O	-5.07	1.17	1.23
1	A	247	ASN	C-O	-5.07	1.18	1.24
1	A	324	LEU	C-O	-5.07	1.17	1.23
1	A	405[A]	VAL	C-O	-5.07	1.17	1.24
1	A	405[B]	VAL	C-O	-5.07	1.17	1.24
1	A	398	HIS	C-O	-5.07	1.17	1.23
1	A	219	ILE	C-O	-5.07	1.18	1.24
1	A	294	SER	C-O	-5.07	1.18	1.24
1	A	268	PHE	C-O	-5.06	1.16	1.24
1	A	27	ASN	C-O	-5.05	1.17	1.23
1	A	248	ALA	C-O	-5.03	1.18	1.23

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	THR	CB-CA-C	8.27	124.79	110.23
1	A	178	THR	N-CA-C	7.61	123.31	113.18
1	A	356	GLY	N-CA-C	7.30	123.17	114.48
1	A	458	GLY	N-CA-C	6.47	124.56	115.43
1	A	178	THR	OG1-CB-CG2	6.11	121.52	109.30
1	A	77	GLY	N-CA-C	6.09	124.77	112.34
1	A	427	GLY	N-CA-C	5.85	122.90	112.02
1	A	451	ILE	N-CA-C	-5.48	99.70	107.98
1	A	205	PRO	N-CA-C	5.48	119.92	111.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331[A]	ALA	CA-C-N	-5.35	110.20	120.80
1	A	331[A]	ALA	C-N-CA	-5.35	110.20	120.80
1	A	331[B]	ALA	CA-C-N	-5.35	110.20	120.80
1	A	331[B]	ALA	C-N-CA	-5.35	110.20	120.80
1	A	331[C]	ALA	CA-C-N	-5.35	110.20	120.80
1	A	331[C]	ALA	C-N-CA	-5.35	110.20	120.80
1	A	331[D]	ALA	CA-C-N	-5.35	110.20	120.80
1	A	331[D]	ALA	C-N-CA	-5.35	110.20	120.80
1	A	178	THR	N-CA-CB	-5.34	98.22	110.83
1	A	276	ILE	N-CA-C	5.26	115.48	108.11
1	A	416	ALA	N-CA-C	5.24	118.13	111.69
1	A	115	TYR	CA-CB-CG	5.19	123.25	113.90
1	A	130[A]	ASP	CA-C-N	-5.10	114.57	119.87
1	A	130[A]	ASP	C-N-CA	-5.10	114.57	119.87
1	A	130[B]	ASP	CA-C-N	-5.10	114.57	119.87
1	A	130[B]	ASP	C-N-CA	-5.10	114.57	119.87

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	176[A]	SER	Mainchain
1	A	176[B]	SER	Mainchain
1	A	400	HIS	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	3935	0	3716	47	0
2	B	39	0	34	1	0
3	C	61	0	51	9	0
4	D	22	0	17	0	0
5	A	4	0	0	0	0
6	A	4	0	3	4	0
7	A	581	0	0	17	3
All	All	4646	0	3821	56	3

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 (56) 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:178:THR:C	7:A:602:HOH:O	1.77	1.26
1:A:179:LEU:N	7:A:602:HOH:O	1.73	1.22
3:C:3:BMA:O2	3:C:4:MAN:H4	1.33	1.21
1:A:178:THR:O	7:A:601:HOH:O	1.72	1.07
1:A:375:ASN:C	1:A:376[B]:ALA:CA	2.28	1.05
1:A:41:ASP:OD1	7:A:603:HOH:O	1.86	0.94
1:A:17:ASP:O	1:A:178:THR:HG21	1.69	0.91
1:A:175[A]:SER:H	1:A:178:THR:HG22	1.37	0.90
7:A:1014:HOH:O	3:C:1:NAG:H81	1.73	0.88
3:C:3:BMA:HO2	3:C:4:MAN:H4	1.35	0.88
1:A:491:SER:OG	7:A:604:HOH:O	1.92	0.87
1:A:175[B]:SER:H	1:A:178:THR:HG22	1.39	0.87
1:A:377:ASP:O	7:A:605:HOH:O	1.94	0.85
3:C:3:BMA:O2	3:C:4:MAN:C4	2.24	0.82
1:A:97[B]:GLN:HG3	1:A:99:PRO:HD3	1.61	0.80
1:A:178:THR:O	1:A:180[B]:ALA:N	2.16	0.77
1:A:376[B]:ALA:CA	1:A:377:ASP:N	2.49	0.76
7:A:1176:HOH:O	2:B:3:BMA:H2	1.88	0.73
1:A:54:HIS:H	6:A:505:ACT:H2	1.54	0.72
1:A:376[C]:ALA:O	1:A:438:ARG:HG3	1.91	0.71
1:A:178:THR:HG23	7:A:602:HOH:O	1.91	0.71
1:A:378:ILE:HA	7:A:605:HOH:O	1.91	0.71
6:A:505:ACT:H1	7:A:997:HOH:O	1.94	0.67
1:A:90:HIS:HD2	7:A:1046:HOH:O	1.80	0.65
1:A:17:ASP:O	1:A:178:THR:CG2	2.48	0.60
1:A:220:GLU:HB3	1:A:243:SER:HB2	1.85	0.58
1:A:73:ASN:HD22	1:A:350:LEU:HD22	1.70	0.56
3:C:3:BMA:C2	3:C:4:MAN:H4	2.23	0.55
1:A:84[B]:CYS:HG	1:A:484:CYS:HG	1.54	0.54
1:A:84[C]:CYS:HG	1:A:484:CYS:HG	1.54	0.54
1:A:178:THR:CG2	7:A:602:HOH:O	2.52	0.53
1:A:204:ASP:HB3	1:A:205:PRO:CD	2.38	0.53
1:A:375:ASN:O	1:A:376[B]:ALA:CA	2.59	0.50
3:C:2:NAG:H62	3:C:3:BMA:C1	2.43	0.49
1:A:432:ASN:HD22	3:C:1:NAG:H83	1.78	0.48
1:A:116[A]:CYS:HB2	1:A:203[A]:CYS:SG	2.54	0.48
1:A:53:ASN:HA	6:A:505:ACT:H2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:LEU:O	7:A:605:HOH:O	2.20	0.47
1:A:54:HIS:N	6:A:505:ACT:H2	2.26	0.46
1:A:493:ASP:CG	7:A:604:HOH:O	2.58	0.46
1:A:376[C]:ALA:C	1:A:376[C]:ALA:N	2.73	0.46
1:A:376[C]:ALA:N	1:A:439:THR:OG1	2.50	0.45
1:A:432:ASN:ND2	3:C:1:NAG:H83	2.32	0.45
1:A:98:VAL:O	7:A:606:HOH:O	2.20	0.45
1:A:238:ALA:O	1:A:239:ALA:HB3	2.16	0.45
1:A:84[C]:CYS:SG	1:A:484:CYS:SG	3.09	0.45
1:A:84[B]:CYS:SG	1:A:484:CYS:SG	3.09	0.44
1:A:204:ASP:HB3	1:A:205:PRO:HD3	1.99	0.44
1:A:405[B]:VAL:HG11	1:A:415:TYR:CE1	2.53	0.43
1:A:382[B]:LEU:N	1:A:383:PRO:CD	2.82	0.43
3:C:3:BMA:H61	3:C:5:MAN:H2	1.29	0.43
1:A:179:LEU:HB3	7:A:625:HOH:O	2.19	0.43
1:A:178:THR:O	1:A:180[A]:ALA:N	2.16	0.42
1:A:467:ILE:HB	1:A:468:PRO:HD3	2.00	0.42
1:A:298:LEU:HD23	1:A:298:LEU:C	2.45	0.41

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:603:HOH:O	7:A:691:HOH:O[1_655]	2.00	0.20
7:A:1140:HOH:O	7:A:1154:HOH:O[1_455]	2.02	0.18
7:A:1086:HOH:O	7:A:1171:HOH:O[1_655]	2.13	0.07

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	524/496 (106%)	501 (96%)	20 (4%)	3 (1%)	21 6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	LEU
1	A	204	ASP
1	A	57	LEU

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	428/404 (106%)	416 (97%)	12 (3%)	38	11

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97[A]	GLN
1	A	97[B]	GLN
1	A	119	LEU
1	A	178	THR
1	A	223[A]	SER
1	A	223[B]	SER
1	A	382[A]	LEU
1	A	382[B]	LEU
1	A	401[A]	ILE
1	A	401[C]	ILE
1	A	446	PHE
1	A	459	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	ASN
1	A	83	GLN
1	A	90	HIS
1	A	132	HIS
1	A	273	ASN

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Mol	Chain	Res	Type
1	A	325	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 ⓘ

10 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	B	1	2,1	14,14,15	1.01	1 (7%)	17,19,21	1.30	2 (11%)
2	NAG	B	2	2	14,14,15	0.98	1 (7%)	17,19,21	1.13	1 (5%)
2	BMA	B	3	2	11,11,12	0.60	0	15,15,17	0.97	0
3	NAG	C	1	1,3	14,14,15	1.70	4 (28%)	17,19,21	1.30	2 (11%)
3	NAG	C	2	3	14,14,15	2.52	3 (21%)	17,19,21	2.22	10 (58%)
3	BMA	C	3	3	11,11,12	1.94	5 (45%)	15,15,17	2.09	3 (20%)
3	MAN	C	4	3	11,11,12	2.85	5 (45%)	14,15,17	3.03	5 (35%)
3	MAN	C	5	3	11,11,12	2.96	6 (54%)	15,15,17	3.28	7 (46%)
4	BGC	D	1	4	11,11,12	2.24	2 (18%)	15,15,17	4.34	8 (53%)
4	BGC	D	2	4	11,11,12	2.53	4 (36%)	15,15,17	2.95	6 (40%)

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	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	2/2/4/5	0/2/18/22	0/1/1/1
3	NAG	C	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	0/1/1/1
3	BMA	C	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	C	4	3	2/2/4/5	1/2/18/22	1/1/1/1
3	MAN	C	5	3	2/2/4/5	2/2/19/22	0/1/1/1
4	BGC	D	1	4	-	0/2/19/22	0/1/1/1
4	BGC	D	2	4	1/1/4/5	0/2/19/22	0/1/1/1

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	NAG	O4-C4	-7.88	1.23	1.43
3	C	5	MAN	O5-C1	7.09	1.55	1.43
4	D	1	BGC	O5-C1	5.92	1.53	1.43
4	D	2	BGC	O5-C1	5.84	1.53	1.43
3	C	4	MAN	C1-C2	4.88	1.56	1.52
3	C	4	MAN	C4-C5	-4.39	1.44	1.52
3	C	4	MAN	O5-C1	4.16	1.53	1.42
3	C	5	MAN	C2-C3	-4.02	1.46	1.52
3	C	1	NAG	O5-C1	-3.80	1.37	1.43
3	C	4	MAN	O1-C1	-3.58	1.28	1.39
4	D	2	BGC	O2-C2	-3.53	1.35	1.43
3	C	4	MAN	C3-C4	-3.34	1.46	1.52
4	D	1	BGC	C2-C3	-3.25	1.47	1.52
3	C	5	MAN	C4-C3	-3.02	1.44	1.52
3	C	3	BMA	O5-C1	2.99	1.48	1.43
4	D	2	BGC	C4-C3	-2.96	1.44	1.52
3	C	1	NAG	O7-C7	-2.90	1.16	1.23
3	C	5	MAN	O5-C5	2.87	1.49	1.43
4	D	2	BGC	C2-C3	-2.77	1.48	1.52
3	C	2	NAG	C8-C7	-2.74	1.44	1.50
3	C	1	NAG	C8-C7	-2.64	1.45	1.50
2	B	2	NAG	O7-C7	-2.62	1.17	1.23
3	C	3	BMA	O2-C2	-2.50	1.38	1.43
2	B	1	NAG	O7-C7	-2.48	1.17	1.23
3	C	3	BMA	C4-C5	-2.43	1.47	1.53
3	C	3	BMA	C4-C3	-2.40	1.46	1.52
3	C	1	NAG	C2-N2	-2.38	1.42	1.46
3	C	5	MAN	C4-C5	-2.26	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	NAG	C2-N2	-2.23	1.42	1.46
3	C	5	MAN	O2-C2	-2.12	1.38	1.43
3	C	3	BMA	O3-C3	2.05	1.48	1.43

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	BGC	O2-C2-C3	9.71	130.25	110.15
3	C	4	MAN	C3-C4-C5	7.37	120.17	110.76
3	C	5	MAN	O5-C5-C6	6.63	120.56	107.66
3	C	5	MAN	C1-C2-C3	6.50	119.11	109.64
3	C	3	BMA	O5-C1-C2	-6.41	95.51	110.79
4	D	1	BGC	O5-C1-C2	-6.32	95.72	110.79
4	D	1	BGC	O2-C2-C1	6.01	122.99	109.22
4	D	1	BGC	C2-C3-C4	-5.92	100.46	110.86
4	D	1	BGC	C1-C2-C3	-5.75	101.27	109.64
3	C	5	MAN	C1-O5-C5	5.45	119.50	112.19
4	D	2	BGC	C1-C2-C3	-5.44	101.73	109.64
4	D	2	BGC	O2-C2-C1	5.28	121.32	109.22
4	D	2	BGC	O5-C1-C2	-5.28	98.19	110.79
4	D	1	BGC	C1-O5-C5	4.80	118.62	112.19
3	C	4	MAN	O4-C4-C5	-4.78	100.16	110.08
3	C	4	MAN	O5-C5-C6	4.38	117.30	106.44
4	D	2	BGC	C2-C3-C4	-4.21	103.46	110.86
3	C	4	MAN	C6-C5-C4	-3.85	108.27	113.53
3	C	5	MAN	O6-C6-C5	3.80	124.28	111.33
3	C	2	NAG	O4-C4-C3	3.74	119.19	110.38
3	C	2	NAG	O6-C6-C5	-3.44	99.60	111.33
3	C	3	BMA	C1-C2-C3	-3.39	104.70	109.64
4	D	2	BGC	C1-O5-C5	3.25	116.54	112.19
3	C	5	MAN	O3-C3-C4	3.15	117.79	110.38
2	B	1	NAG	O7-C7-N2	3.06	127.39	121.98
3	C	2	NAG	C1-C2-N2	3.05	115.24	110.43
3	C	5	MAN	O3-C3-C2	-2.89	104.16	110.05
4	D	2	BGC	O2-C2-C3	2.74	115.83	110.15
2	B	2	NAG	C1-O5-C5	2.69	115.79	112.19
3	C	5	MAN	C3-C4-C5	-2.64	105.45	110.23
3	C	2	NAG	C4-C3-C2	2.60	114.82	111.02
3	C	1	NAG	C3-C4-C5	-2.55	105.60	110.23
4	D	1	BGC	O5-C5-C6	-2.53	102.74	107.66
3	C	2	NAG	O5-C1-C2	-2.50	107.42	111.29
3	C	2	NAG	C8-C7-N2	2.48	120.23	116.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	NAG	C1-O5-C5	2.36	115.35	112.19
3	C	1	NAG	C2-N2-C7	2.32	126.00	122.90
3	C	2	NAG	C2-N2-C7	2.28	125.96	122.90
2	B	1	NAG	C2-N2-C7	-2.20	119.95	122.90
3	C	2	NAG	C6-C5-C4	-2.13	107.78	113.02
3	C	3	BMA	O3-C3-C2	2.09	114.32	110.05
3	C	4	MAN	C1-O5-C5	-2.06	109.67	113.65
4	D	1	BGC	O3-C3-C4	2.04	115.19	110.38
3	C	2	NAG	O7-C7-C8	-2.03	118.44	122.05

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3	BMA	C2
2	B	3	BMA	C4
3	C	3	BMA	C2
3	C	4	MAN	C1
3	C	4	MAN	C2
3	C	5	MAN	C1
3	C	5	MAN	C2
4	D	2	BGC	C1

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	5	MAN	O5-C5-C6-O6
3	C	5	MAN	C4-C5-C6-O6
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	C	4	MAN	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6

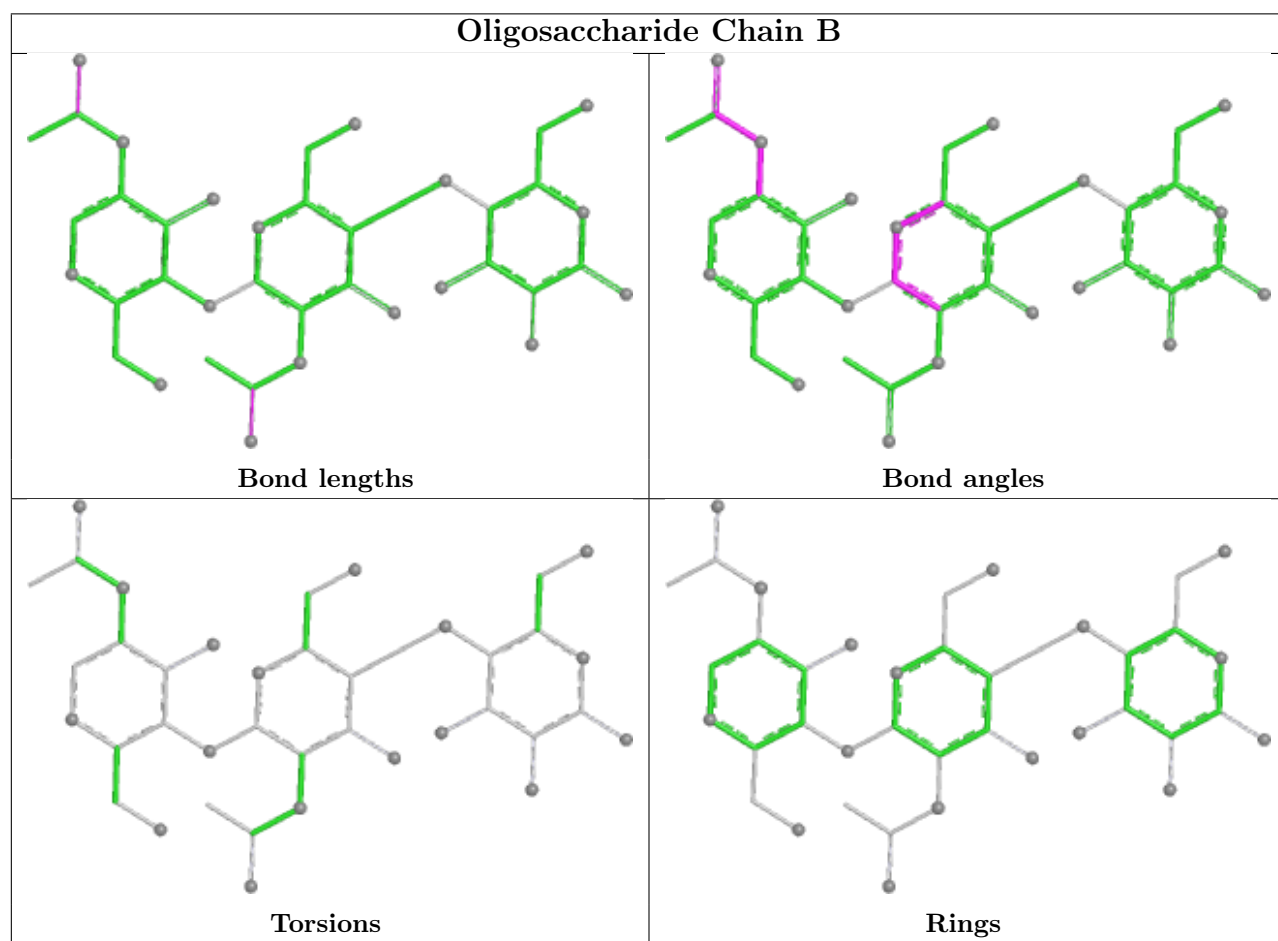
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	4	MAN	C1-C2-C3-C4-C5-O5

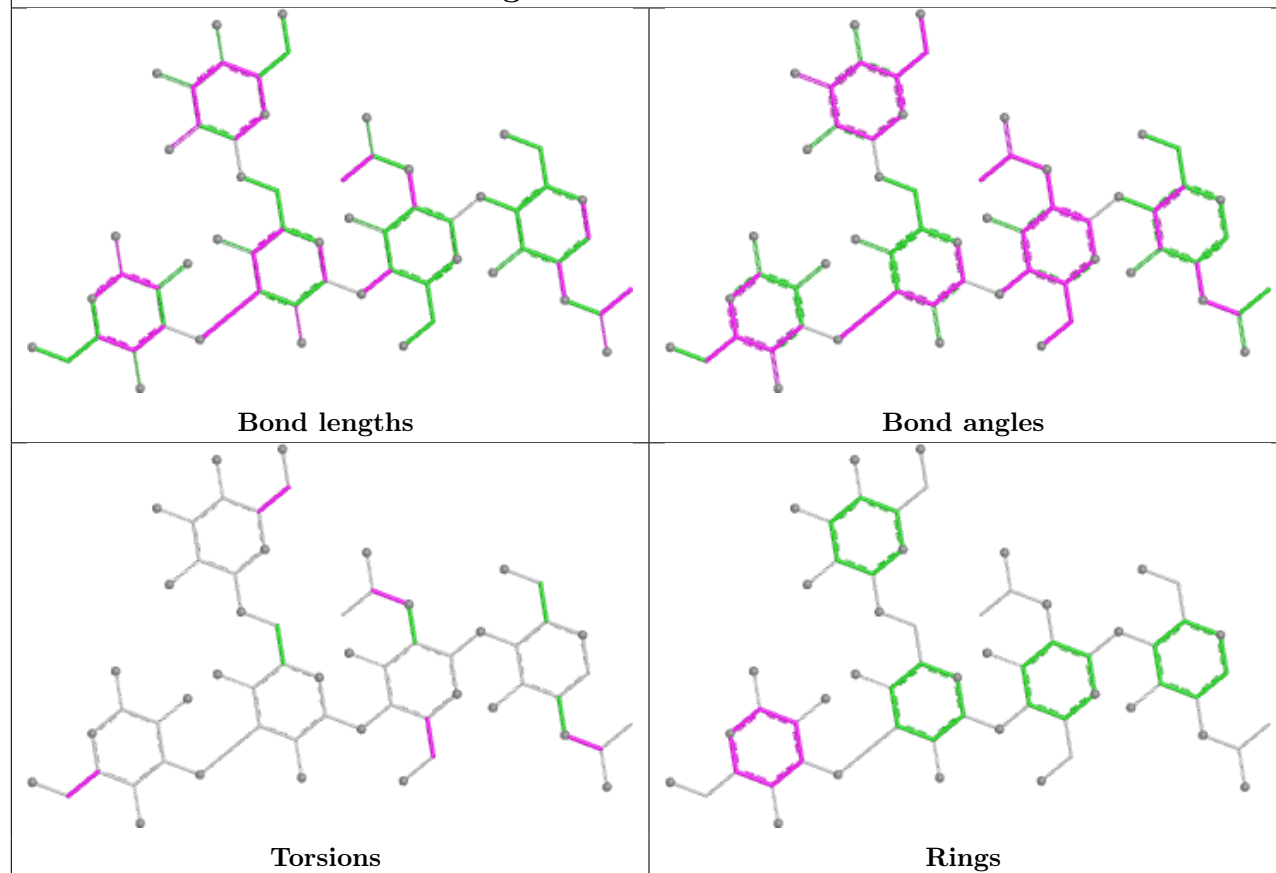
6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	NAG	1	0
3	C	1	NAG	3	0
3	C	5	MAN	1	0
3	C	3	BMA	6	0
2	B	3	BMA	1	0
3	C	4	MAN	4	0

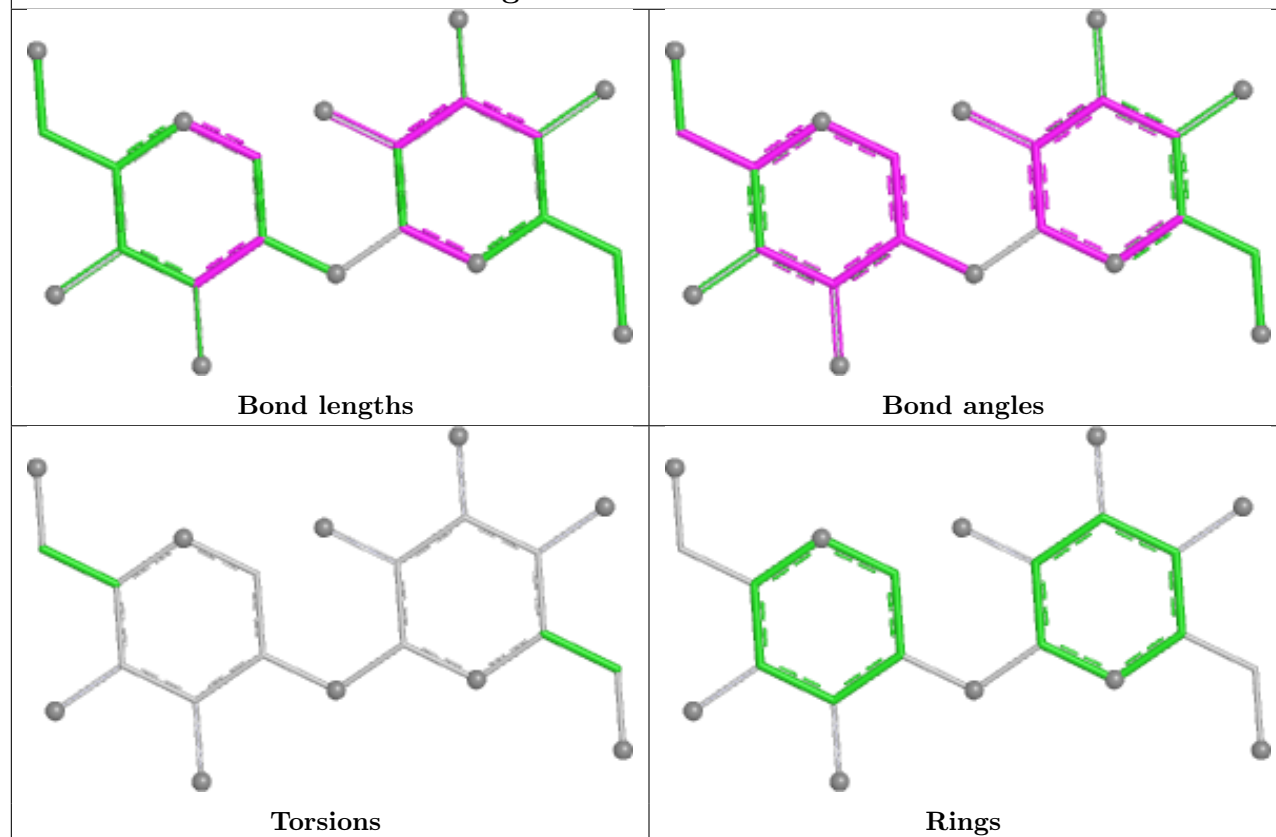
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



Oligosaccharide Chain C



Oligosaccharide Chain D



5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
6	ACT	A	505	-	3,3,3	1.67	1 (33%)	3,3,3	2.23	2 (66%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	505	ACT	OXT-C	-2.12	1.21	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	505	ACT	OXT-C-CH3	2.88	127.15	115.05
6	A	505	ACT	O-C-CH3	-2.51	112.22	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	505	ACT	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	496/496 (100%)	0.20	15 (3%) 52 56	4, 17, 32, 57	25 (5%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	178	THR	4.7
1	A	177	SER	3.8
1	A	376[A]	ALA	3.7
1	A	331[A]	ALA	3.7
1	A	361	ALA	2.6
1	A	332	GLY	2.5
1	A	362	ASP	2.4
1	A	100	ASP	2.3
1	A	316	THR	2.2
1	A	176[A]	SER	2.1
1	A	97[A]	GLN	2.1
1	A	366	ALA	2.0
1	A	468	PRO	2.0
1	A	179	LEU	2.0
1	A	382[A]	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

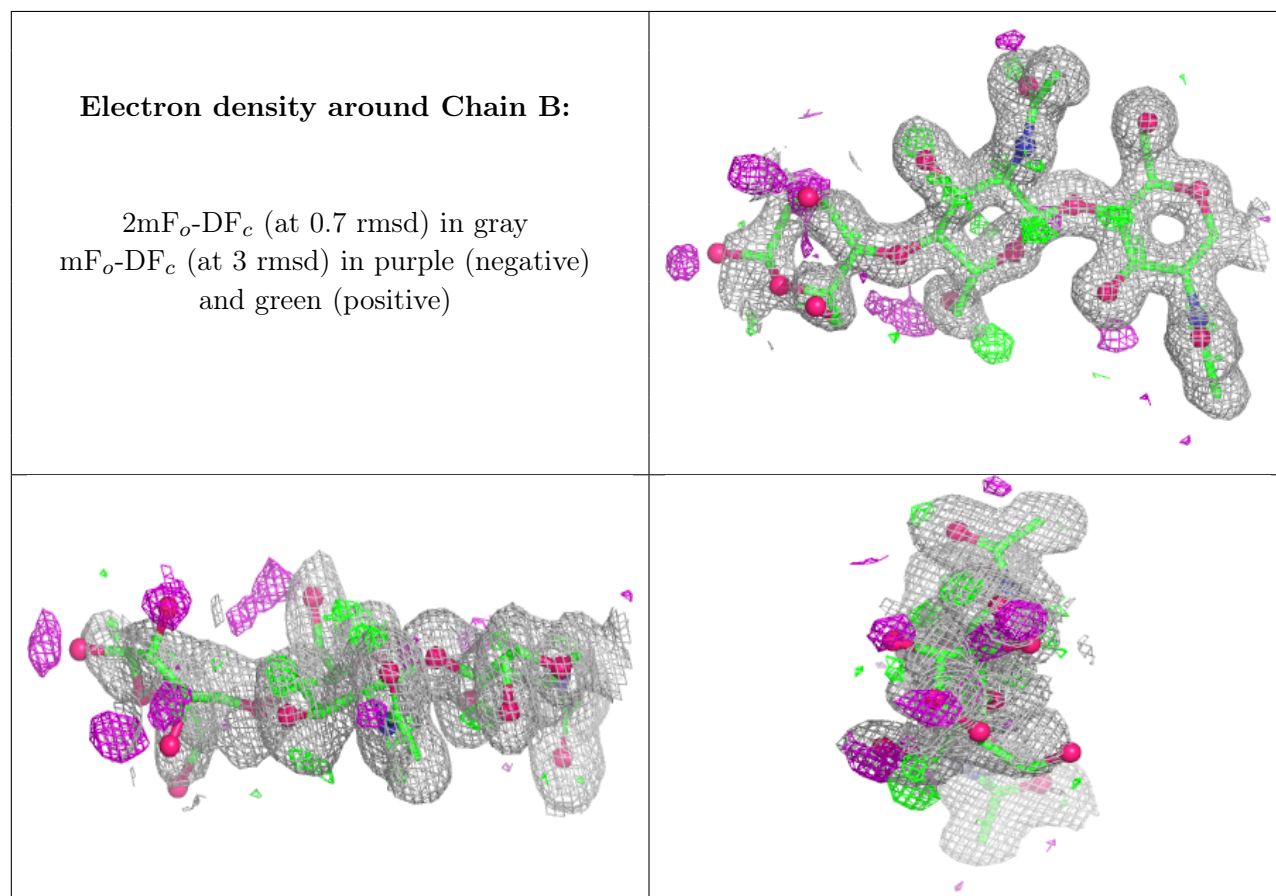
There are no non-standard protein/DNA/RNA residues in this entry.

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. 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.

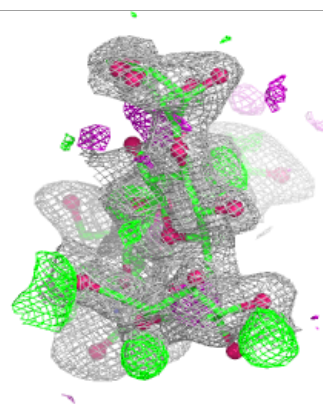
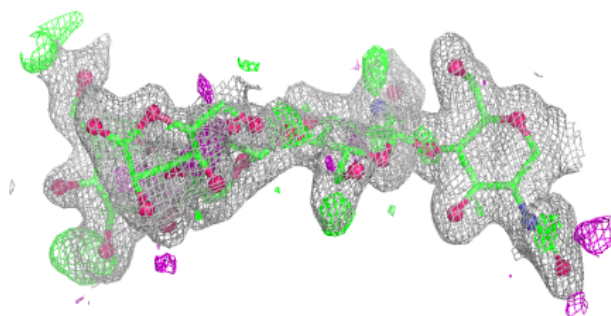
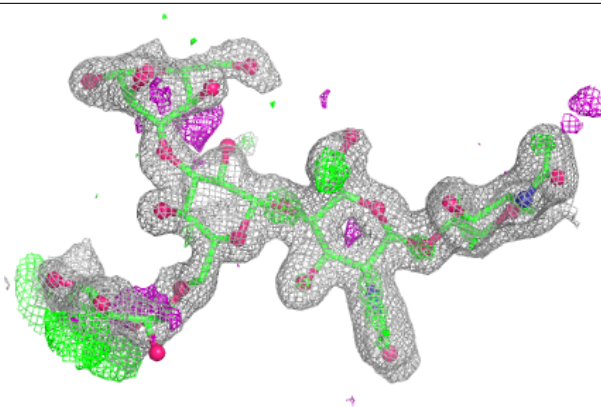
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BMA	B	3	11/12	0.64	0.19	31,52,64,67	0
3	MAN	C	5	11/12	0.64	0.20	34,45,52,67	0
3	MAN	C	4	11/12	0.78	0.13	37,50,59,62	0
3	NAG	C	2	14/15	0.85	0.15	22,39,59,60	0
3	BMA	C	3	11/12	0.85	0.15	29,45,63,71	0
4	BGC	D	1	11/12	0.88	0.11	22,26,39,55	0
4	BGC	D	2	11/12	0.91	0.10	21,25,48,51	0
3	NAG	C	1	14/15	0.92	0.12	22,29,43,52	0
2	NAG	B	2	14/15	0.93	0.10	12,19,23,30	0
2	NAG	B	1	14/15	0.95	0.08	14,17,20,21	0

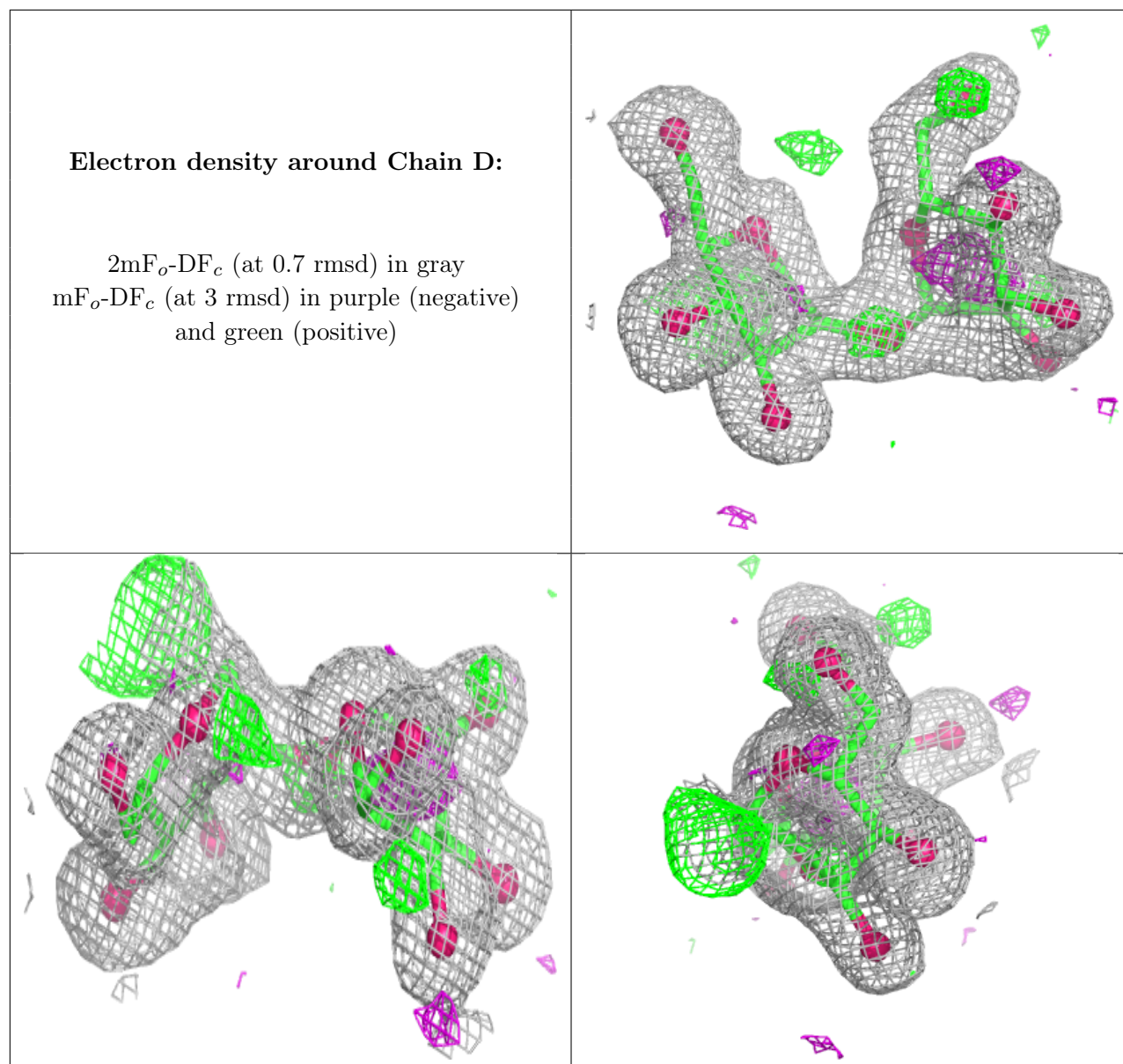
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
6	ACT	A	505	4/4	0.91	0.12	15,23,28,39	0
5	CU	A	502	1/1	1.00	0.03	12,12,12,12	1
5	CU	A	503	1/1	1.00	0.04	15,15,15,15	1
5	CU	A	504	1/1	1.00	0.01	15,15,15,15	0
5	CU	A	501	1/1	1.00	0.01	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.