



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:10 PM UTC

PDB ID : 5KOE / pdb_00005koe
Title : The structure of Arabidopsis thaliana FUT1 in complex with XXLG
Authors : Alahuhta, P.M.; Lunin, V.V.
Deposited on : 2016-06-30
Resolution : 1.79 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

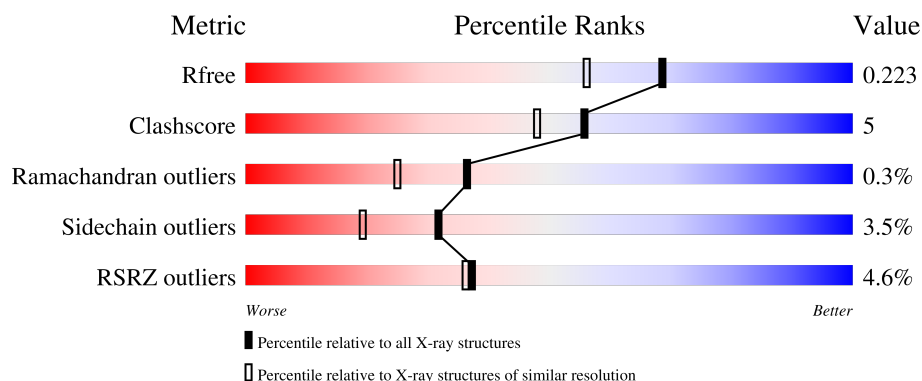
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	476	3% 81% 11% • 6%
1	B	476	5% 78% 15% • 5%
1	C	476	5% 84% 12% •
1	D	476	5% 82% 12% • 5%
2	E	8	100%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 17403 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.

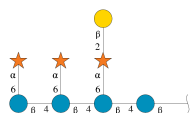
- Molecule 1 is a protein called Galactoside 2-alpha-L-fucosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	17	0
			3700	2379	616	683	22			
1	B	452	Total	C	N	O	S	0	19	0
			3772	2420	625	705	22			
1	C	458	Total	C	N	O	S	0	17	0
			3819	2443	647	707	22			
1	D	454	Total	C	N	O	S	0	19	0
			3768	2416	632	696	24			

There are 4 discrepancies between the modelled and reference sequences:

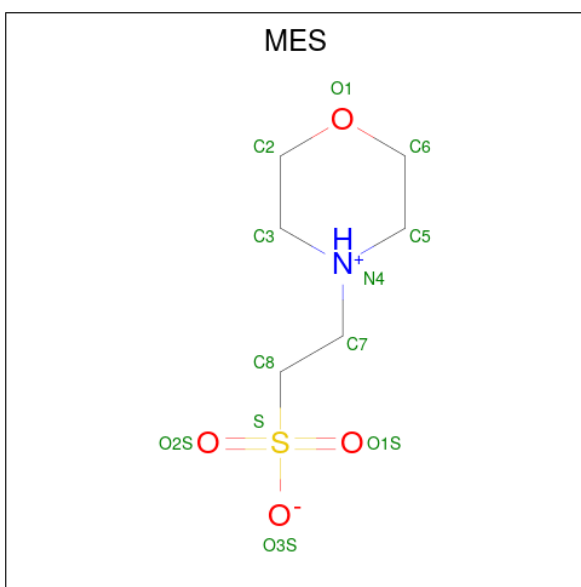
Chain	Residue	Modelled	Actual	Comment	Reference
A	83	GLY	-	expression tag	UNP Q9SWH5
B	83	GLY	-	expression tag	UNP Q9SWH5
C	83	GLY	-	expression tag	UNP Q9SWH5
D	83	GLY	-	expression tag	UNP Q9SWH5

- Molecule 2 is an oligosaccharide called alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose-(1-4)-[alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	8	Total	C	O	0	0	0
			83	45	38			

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

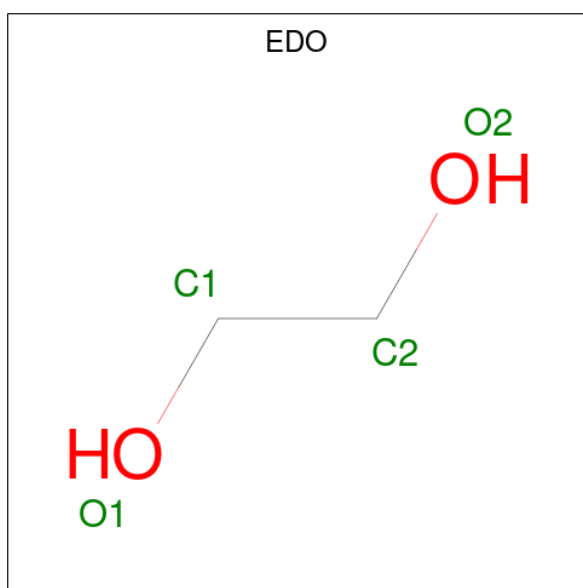
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	Cl	0	0
			8	8		
4	B	4	Total	Cl	0	0
			4	4		
4	C	4	Total	Cl	0	0
			4	4		
4	D	3	Total	Cl	0	0
			3	3		

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

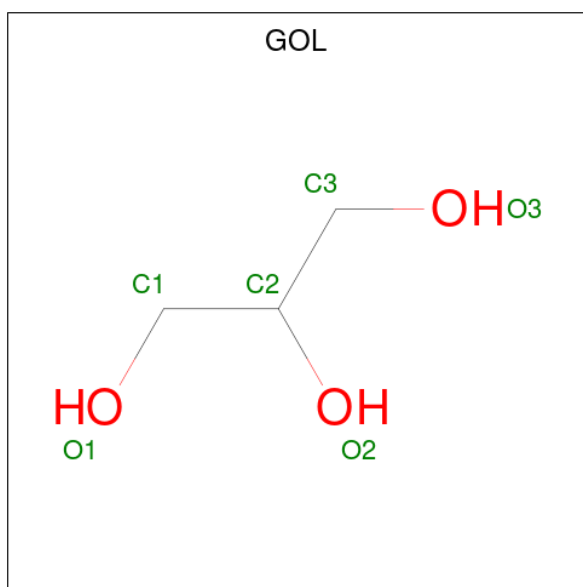
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total K 2 2	0	0
5	B	2	Total K 2 2	0	0
5	C	3	Total K 3 3	0	0
5	D	1	Total K 1 1	0	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	D	1	Total C O 8 4 4	0	1

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		

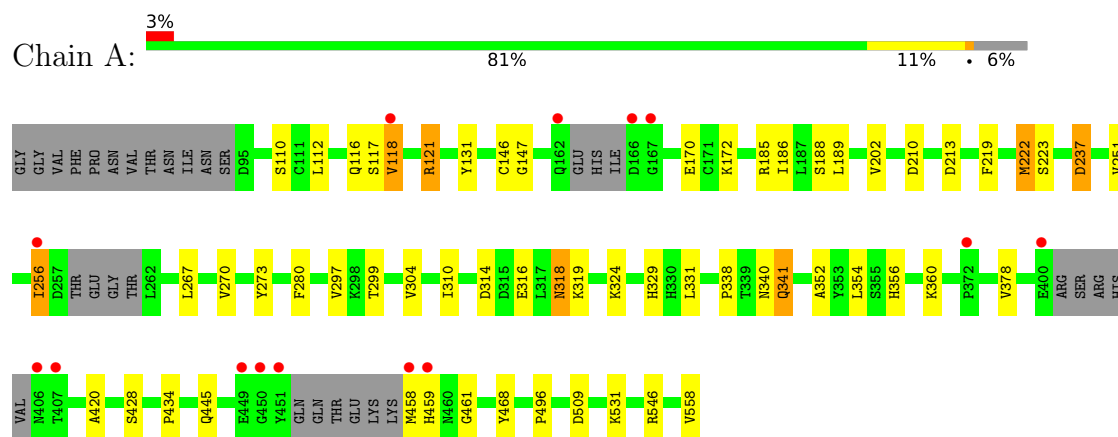
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	544	Total	O	0	24
			568	568		
8	B	492	Total	O	0	14
			506	506		
8	C	546	Total	O	0	18
			564	564		
8	D	495	Total	O	0	13
			508	508		

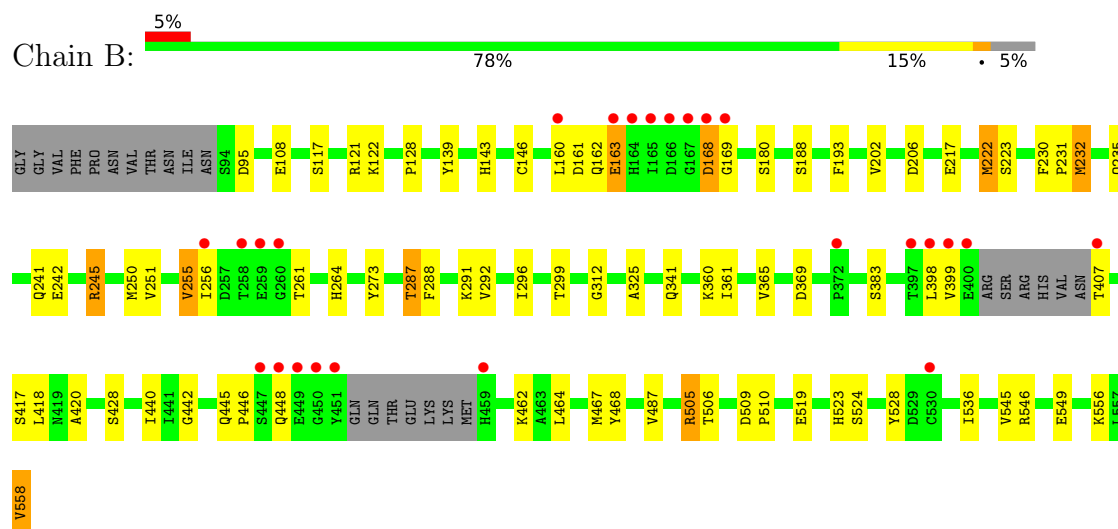
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

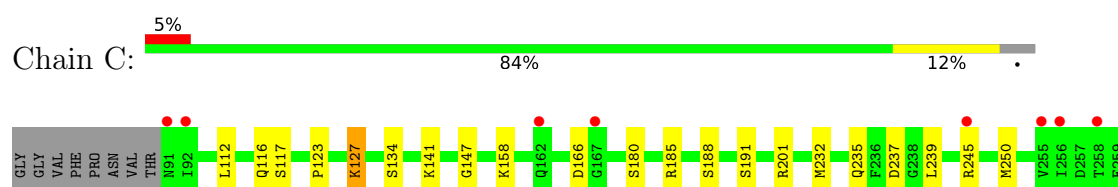
- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase

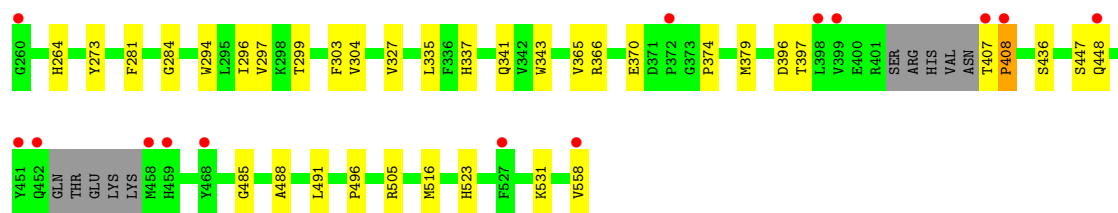


- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase

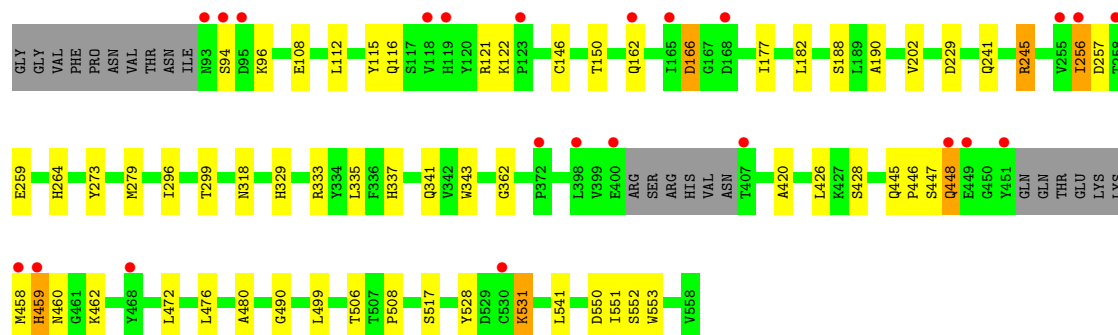
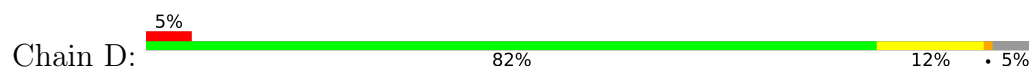


- Molecule 1: Galactoside 2-alpha-L-fucosyltransferase





● Molecule 1: Galactoside 2-alpha-L-fucosyltransferase



● Molecule 2: alpha-D-xylopyranose-(1-6)-beta-D-glucopyranose-(1-4)-[alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-[beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.75Å 80.15Å 157.62Å 90.00° 91.91° 90.00°	Depositor
Resolution (Å)	157.53 – 1.79 157.53 – 1.79	Depositor EDS
% Data completeness (in resolution range)	99.5 (157.53-1.79) 99.7 (157.53-1.79)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.166 , 0.217 0.174 , 0.223	Depositor DCC
R_{free} test set	9306 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.011 for k,h,-l 0.010 for -k,-h,-l 0.024 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17403	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.1476e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: K, EDO, BGC, GAL, MES, XYS, GOL, CL

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	1.49	16/3801 (0.4%)	1.26	14/5147 (0.3%)
1	B	1.49	18/3876 (0.5%)	1.26	9/5253 (0.2%)
1	C	1.48	19/3925 (0.5%)	1.20	4/5321 (0.1%)
1	D	1.43	12/3876 (0.3%)	1.21	6/5258 (0.1%)
All	All	1.47	65/15478 (0.4%)	1.23	33/20979 (0.2%)

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	B	0	1

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	459	HIS	C-O	7.61	1.32	1.24
1	C	496	PRO	N-CA	-7.26	1.39	1.47
1	A	189	LEU	N-CA	-7.09	1.37	1.46
1	C	365	VAL	N-CA	-7.08	1.37	1.46
1	B	549	GLU	C-O	-6.95	1.15	1.24
1	B	445	GLN	CA-C	6.79	1.59	1.52
1	B	487	VAL	N-CA	-6.75	1.38	1.46
1	A	434	PRO	CA-C	6.55	1.60	1.52
1	C	337	HIS	C-O	-6.40	1.17	1.24
1	B	169	GLY	N-CA	6.36	1.50	1.44
1	D	517	SER	C-O	-6.31	1.16	1.23
1	A	297	VAL	C-O	6.30	1.31	1.24
1	C	505	ARG	C-O	-6.25	1.15	1.23
1	C	327	VAL	CA-CB	-6.22	1.47	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	297	VAL	CA-C	-6.18	1.45	1.52
1	D	190	ALA	CA-C	6.13	1.60	1.52
1	B	122	LYS	CA-C	6.02	1.59	1.53
1	C	485	GLY	N-CA	-5.85	1.38	1.45
1	B	442	GLY	C-O	5.85	1.31	1.23
1	D	256	ILE	CA-CB	5.85	1.61	1.53
1	B	117	SER	N-CA	-5.84	1.38	1.46
1	C	191	SER	C-O	-5.84	1.17	1.24
1	C	488	ALA	CA-C	-5.79	1.45	1.52
1	C	436	SER	N-CA	-5.75	1.38	1.46
1	B	255	VAL	CA-C	5.72	1.60	1.52
1	D	490	GLY	N-CA	-5.71	1.38	1.45
1	C	284	GLY	C-O	5.66	1.30	1.23
1	A	314	ASP	C-O	5.65	1.30	1.24
1	A	121	ARG	CA-C	-5.65	1.45	1.52
1	C	491	LEU	N-CA	-5.64	1.39	1.46
1	D	508	PRO	N-CA	-5.60	1.40	1.47
1	C	201	ARG	CZ-NH1	5.57	1.40	1.32
1	A	378	VAL	C-O	-5.49	1.17	1.24
1	B	428	SER	CA-C	5.47	1.59	1.52
1	D	362	GLY	CA-C	-5.45	1.48	1.52
1	A	316	GLU	C-O	5.42	1.30	1.24
1	D	337	HIS	C-O	-5.41	1.18	1.25
1	C	185	ARG	CA-C	-5.40	1.46	1.52
1	D	553	TRP	CA-C	5.39	1.60	1.52
1	C	408	PRO	N-CA	5.34	1.54	1.47
1	A	270	VAL	CA-C	5.30	1.59	1.53
1	B	361	ILE	CA-C	-5.29	1.46	1.52
1	A	329	HIS	C-O	5.26	1.30	1.24
1	B	193	PHE	C-O	-5.24	1.18	1.24
1	A	509	ASP	C-O	-5.23	1.20	1.25
1	C	366	ARG	C-O	5.23	1.29	1.23
1	B	128	PRO	C-O	-5.22	1.17	1.23
1	C	127	LYS	C-O	-5.22	1.17	1.24
1	B	440	ILE	N-CA	5.16	1.52	1.46
1	C	304	VAL	CA-C	5.15	1.58	1.52
1	B	312	GLY	C-O	5.14	1.30	1.23
1	D	499	LEU	C-O	-5.13	1.17	1.24
1	C	303	PHE	CA-C	-5.12	1.44	1.52
1	D	506	THR	CA-C	5.12	1.58	1.52
1	A	110	SER	CA-C	5.11	1.59	1.52
1	A	186	ILE	N-CA	-5.11	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	250	MET	C-O	-5.10	1.18	1.24
1	A	219	PHE	CA-C	-5.09	1.46	1.52
1	B	206	ASP	C-O	-5.08	1.17	1.24
1	B	545	VAL	C-O	5.06	1.29	1.24
1	B	292	VAL	CA-C	5.05	1.56	1.53
1	D	476	LEU	N-CA	-5.04	1.39	1.46
1	A	251	VAL	C-O	5.03	1.29	1.24
1	A	340	ASN	C-O	-5.03	1.18	1.24
1	D	241	GLN	CA-C	-5.01	1.45	1.52

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	232	MET	N-CA-C	7.71	122.72	113.16
1	A	459	HIS	N-CA-C	-7.71	102.83	111.07
1	B	255	VAL	N-CA-CB	-7.17	102.75	112.28
1	A	118	VAL	N-CA-C	6.79	119.53	111.05
1	B	95	ASP	N-CA-CB	6.66	119.91	110.46
1	A	352	ALA	N-CA-C	6.63	118.58	111.36
1	C	396	ASP	N-CA-CB	-6.57	99.24	111.13
1	D	241	GLN	N-CA-C	6.34	119.00	111.71
1	C	147	GLY	N-CA-C	6.25	119.50	112.00
1	A	304	VAL	CA-C-N	-6.22	112.44	119.28
1	A	304	VAL	C-N-CA	-6.22	112.44	119.28
1	B	325	ALA	N-CA-C	6.18	119.52	112.97
1	D	428	SER	N-CA-C	6.18	117.68	111.07
1	A	118	VAL	CB-CA-C	-6.16	102.61	112.16
1	B	523	HIS	N-CA-C	5.87	118.63	111.82
1	C	335	LEU	N-CA-C	5.79	118.81	111.69
1	D	490	GLY	N-CA-C	5.70	119.12	112.50
1	B	245	ARG	NE-CZ-NH1	-5.67	115.83	121.50
1	D	257	ASP	N-CA-C	5.63	118.42	109.24
1	A	459	HIS	O-C-N	5.55	127.79	122.07
1	A	237	ASP	N-CA-CB	5.50	118.81	110.28
1	B	467	MET	CG-SD-CE	5.49	112.97	100.90
1	A	147	GLY	CA-C-N	5.49	125.80	119.93
1	A	147	GLY	C-N-CA	5.49	125.80	119.93
1	C	523	HIS	N-CA-C	5.37	118.05	111.82
1	D	552	SER	CA-CB-OG	-5.32	100.46	111.10
1	A	310	ILE	CA-C-O	5.30	122.28	119.15
1	B	163	GLU	N-CA-C	-5.25	107.01	113.41
1	D	335	LEU	N-CA-C	5.21	117.04	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331	LEU	CA-C-N	5.18	125.69	120.00
1	A	331	LEU	C-N-CA	5.18	125.69	120.00
1	B	383	SER	CA-CB-OG	-5.10	100.90	111.10
1	A	213	ASP	N-CA-C	5.00	117.62	111.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	161	ASP	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3700	0	3573	34	0
1	B	3772	0	3622	43	0
1	C	3819	0	3663	28	0
1	D	3768	0	3608	32	0
2	E	83	0	69	0	0
3	A	24	0	26	0	0
3	C	24	0	26	1	0
3	D	12	0	13	0	0
4	A	8	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	3	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	3	0	0	0	0
5	D	1	0	0	0	0
6	A	4	0	6	0	0
6	C	4	0	6	2	0
6	D	8	0	12	0	0
7	C	6	0	8	0	0
7	D	6	0	8	1	0
8	A	568	0	0	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	506	0	0	11	1
8	C	564	0	0	4	1
8	D	508	0	0	6	0
All	All	17403	0	14640	138	1

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 5.

All (138) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:516[A]:MET:CE	1:C:558[A]:VAL:HG11	1.49	1.41
1:C:516[A]:MET:HE3	1:C:558[A]:VAL:HG11	1.20	1.19
1:B:222[A]:MET:HE2	1:B:223[A]:SER:N	1.65	1.09
1:B:546[B]:ARG:HD3	1:B:558[B]:VAL:HG11	1.34	1.08
1:C:516[A]:MET:CE	1:C:558[A]:VAL:CG1	2.32	1.07
1:B:222[A]:MET:HE2	1:B:223[A]:SER:H	0.91	1.06
1:D:121[A]:ARG:NH2	8:D:707[A]:HOH:O	1.89	1.05
1:C:516[A]:MET:HE1	1:C:558[A]:VAL:HG11	1.49	0.95
1:D:182:LEU:HD22	1:D:460[B]:ASN:OD1	1.67	0.94
1:A:121:ARG:HD2	8:A:853:HOH:O	1.72	0.88
1:B:222[A]:MET:CE	1:B:223[A]:SER:H	1.84	0.87
1:A:172[A]:LYS:NZ	8:A:705[A]:HOH:O	2.09	0.86
8:A:1151[B]:HOH:O	1:C:516[B]:MET:HE3	1.79	0.81
1:B:546[B]:ARG:HD3	1:B:558[B]:VAL:CG1	2.12	0.80
1:A:222[A]:MET:HE2	1:A:223[A]:SER:N	1.98	0.79
1:D:341[A]:GLN:OE1	1:D:458[A]:MET:SD	2.45	0.75
1:A:172[A]:LYS:CE	8:A:705[A]:HOH:O	2.35	0.75
1:D:448[B]:GLN:HA	1:D:448[B]:GLN:OE1	1.86	0.74
1:A:172[A]:LYS:HE2	8:A:705[A]:HOH:O	1.87	0.74
1:B:261:THR:HG23	1:B:291[A]:LYS:HG3	1.70	0.73
1:B:546[B]:ARG:CD	1:B:558[B]:VAL:HG11	2.16	0.73
1:B:121[A]:ARG:HG3	1:B:121[A]:ARG:NH1	2.04	0.72
1:A:222[B]:MET:HA	1:A:222[B]:MET:HE2	1.71	0.72
1:C:516[A]:MET:HE3	1:C:558[A]:VAL:CG1	2.09	0.72
1:B:121[A]:ARG:HG3	1:B:121[A]:ARG:HH11	1.56	0.71
1:B:369:ASP:OD2	1:B:505:ARG:NH1	2.22	0.71
1:B:288:PHE:CE1	1:B:291[A]:LYS:HE2	2.26	0.71
1:B:139:TYR:OH	1:B:143:HIS:HD2	1.74	0.70
1:D:121[A]:ARG:CZ	8:D:707[A]:HOH:O	2.35	0.67
1:D:458[B]:MET:O	1:D:459[B]:HIS:C	2.36	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222[A]:MET:CE	1:A:223[A]:SER:H	2.08	0.67
3:C:602:MES:O1	8:C:1004[B]:HOH:O	2.14	0.66
1:B:188:SER:HB2	1:B:299:THR:HG23	1.76	0.66
1:C:447:SER:HB2	8:C:917:HOH:O	1.96	0.65
1:A:131:TYR:CD1	1:A:319[B]:LYS:HE2	2.32	0.65
1:D:420:ALA:HB2	1:D:448[A]:GLN:HE22	1.61	0.65
1:A:546:ARG:NH1	8:A:710:HOH:O	2.29	0.64
1:D:188:SER:HB2	1:D:299:THR:HG23	1.80	0.64
1:B:232:MET:HE1	1:B:296:ILE:HG13	1.80	0.64
1:B:287:THR:HG21	8:B:1125:HOH:O	1.98	0.64
1:C:516[A]:MET:HE2	1:C:558[A]:VAL:CG1	2.27	0.64
1:B:160[A]:LEU:O	1:B:162:GLN:O	2.16	0.63
1:A:222[A]:MET:HE2	1:A:222[A]:MET:C	2.24	0.62
1:B:241:GLN:HG2	8:B:795:HOH:O	1.97	0.62
1:A:558[A]:VAL:OXT	1:A:558[A]:VAL:HG12	2.00	0.62
1:A:318:ASN:HD21	1:A:324:LYS:HE3	1.64	0.61
1:A:222[A]:MET:HE3	8:A:1133:HOH:O	1.98	0.61
1:D:279[A]:MET:HE1	1:D:528:TYR:CZ	2.37	0.60
1:A:118:VAL:HG12	8:A:1198:HOH:O	2.02	0.60
1:C:188:SER:HB2	1:C:299:THR:HG23	1.83	0.59
1:A:222[A]:MET:CE	1:A:223[A]:SER:N	2.65	0.59
1:C:232:MET:HE1	1:C:296:ILE:CD1	2.33	0.58
1:B:505:ARG:HH11	1:B:505:ARG:CG	2.18	0.57
1:D:245:ARG:HG2	1:D:264[B]:HIS:NE2	2.19	0.57
1:C:232:MET:HE1	1:C:296:ILE:HD13	1.85	0.56
1:B:251:VAL:HG22	1:B:256:ILE:HD11	1.88	0.55
1:B:365:VAL:HB	1:B:417[B]:SER:HB2	1.90	0.54
1:A:112:LEU:HD22	1:A:116[A]:GLN:NE2	2.23	0.53
1:D:279[A]:MET:HE1	1:D:528:TYR:CE2	2.43	0.53
1:D:112:LEU:O	1:D:116[A]:GLN:HB3	2.07	0.53
1:B:287:THR:HG22	8:B:933:HOH:O	2.08	0.53
1:A:188:SER:HB2	1:A:299:THR:HG23	1.90	0.52
1:D:96:LYS:HG2	1:D:115:TYR:HB3	1.91	0.52
1:B:217:GLU:OE1	1:B:223[B]:SER:HA	2.10	0.52
1:B:360:LYS:HE2	8:B:816:HOH:O	2.10	0.51
1:B:288:PHE:CD1	1:B:291[A]:LYS:HE2	2.46	0.51
1:B:464:LEU:HD11	1:B:468[B]:TYR:HE2	1.77	0.50
1:B:287:THR:CG2	8:B:1125:HOH:O	2.58	0.50
1:D:121[A]:ARG:HG2	1:D:472:LEU:CD2	2.42	0.50
1:A:185:ARG:NH1	8:A:706:HOH:O	2.45	0.50
1:D:116[A]:GLN:NE2	1:D:343:TRP:HE1	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:TYR:OH	1:B:143:HIS:CD2	2.62	0.49
1:B:121[B]:ARG:HD2	8:B:1098:HOH:O	2.12	0.49
1:A:338:PRO:HD3	1:A:468:TYR:CZ	2.48	0.48
1:B:462:LYS:NZ	8:B:732:HOH:O	2.46	0.48
1:A:222[B]:MET:HA	1:A:222[B]:MET:CE	2.41	0.48
1:C:516[B]:MET:HE2	1:C:558[B]:VAL:HG21	1.93	0.48
1:A:360:LYS:HE2	8:A:953:HOH:O	2.13	0.48
1:D:426[B]:LEU:HA	1:D:426[B]:LEU:HD23	1.63	0.48
1:C:516[A]:MET:HE1	1:C:558[A]:VAL:CG1	2.24	0.48
1:A:267[A]:LEU:HD13	1:A:280:PHE:CE1	2.50	0.47
1:B:230:PHE:CD1	1:B:231:PRO:HD2	2.49	0.47
1:B:235:GLN:NE2	8:B:716:HOH:O	2.37	0.47
1:A:222[A]:MET:HE2	1:A:222[A]:MET:CA	2.45	0.47
1:C:112:LEU:O	1:C:116[A]:GLN:HB3	2.14	0.47
1:A:210:ASP:OD1	8:A:706:HOH:O	2.21	0.47
1:C:235:GLN:OE1	1:C:245[C]:ARG:NH2	2.48	0.47
1:B:242:GLU:HB3	8:B:765:HOH:O	2.15	0.47
1:D:245:ARG:HG2	1:D:264[B]:HIS:CE1	2.49	0.47
1:D:480:ALA:HB1	1:D:550:ASP:HB2	1.96	0.47
1:B:143:HIS:CD2	1:B:202:VAL:HG13	2.50	0.46
1:C:281:PHE:HB2	6:C:610:EDO:C2	2.46	0.46
1:D:177:ILE:HD11	1:D:296:ILE:HG22	1.97	0.46
1:C:245[B]:ARG:HA	1:C:250:MET:HE3	1.98	0.46
1:D:229:ASP:OD2	8:D:712[A]:HOH:O	2.21	0.46
1:B:121[A]:ARG:NH1	8:B:731:HOH:O	2.46	0.46
1:D:447:SER:HB2	8:D:736:HOH:O	2.16	0.45
1:B:505:ARG:HH11	1:B:505:ARG:HG2	1.80	0.45
1:A:420:ALA:HA	1:A:445:GLN:HE22	1.82	0.45
1:B:509:ASP:HA	1:B:510:PRO:C	2.42	0.45
1:A:256:ILE:HA	8:A:788:HOH:O	2.16	0.45
1:A:445:GLN:NE2	8:A:746:HOH:O	2.48	0.45
1:C:407:THR:N	1:C:408:PRO:HD3	2.32	0.44
1:D:150:THR:HA	7:D:607:GOL:H2	1.99	0.44
1:C:374:PRO:HB2	1:C:379:MET:HE3	1.98	0.44
1:B:121[A]:ARG:HH11	1:B:121[A]:ARG:CG	2.26	0.44
1:C:239:LEU:HD21	1:C:245[C]:ARG:HE	1.83	0.44
1:B:519:GLU:O	1:B:556:LYS:HE2	2.17	0.44
1:A:558[A]:VAL:OXT	1:A:558[A]:VAL:CG1	2.64	0.43
1:C:235:GLN:OE1	1:C:245[C]:ARG:CZ	2.66	0.43
1:A:222[A]:MET:CE	1:A:222[A]:MET:CA	2.96	0.43
1:D:341[A]:GLN:HE22	1:D:458[A]:MET:N	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:LYS:HD2	8:C:1186:HOH:O	2.18	0.43
1:C:516[A]:MET:HE2	1:C:516[A]:MET:HB2	1.44	0.43
1:A:458:MET:HA	1:A:461:GLY:H	1.83	0.43
1:D:108:GLU:OE2	1:D:116[B]:GLN:NE2	2.48	0.43
1:D:166:ASP:N	1:D:166:ASP:OD1	2.51	0.43
1:D:420:ALA:HB2	1:D:448[A]:GLN:NE2	2.31	0.43
1:B:420:ALA:HB2	1:B:448[B]:GLN:NE2	2.33	0.43
1:D:146:CYS:HB2	1:D:202:VAL:HG21	2.00	0.43
1:C:281:PHE:HB2	6:C:610:EDO:H22	2.00	0.43
1:D:531[B]:LYS:HG2	8:D:733:HOH:O	2.18	0.42
1:D:462:LYS:NZ	8:D:736:HOH:O	2.51	0.42
1:A:222[A]:MET:CE	1:A:222[A]:MET:HA	2.50	0.42
1:C:116[A]:GLN:NE2	1:C:343:TRP:HE1	2.18	0.42
1:B:146:CYS:HB2	1:B:202:VAL:HG21	2.01	0.41
1:B:139:TYR:CD2	1:B:139:TYR:C	2.98	0.41
1:C:123:PRO:HA	8:C:1089[B]:HOH:O	2.20	0.41
1:A:341[A]:GLN:NE2	8:A:759:HOH:O	2.53	0.41
1:D:531[A]:LYS:HZ2	1:D:531[A]:LYS:HG2	1.75	0.41
1:B:160[B]:LEU:HD21	1:B:264:HIS:HB3	2.03	0.41
1:A:267[B]:LEU:HD13	1:A:267[B]:LEU:HA	1.78	0.41
1:C:264:HIS:HA	1:C:294:TRP:O	2.21	0.41
1:B:528:TYR:OH	8:B:706:HOH:O	2.21	0.40
1:C:141:LYS:HE2	1:C:141:LYS:HB2	1.78	0.40
1:D:329:HIS:O	1:D:333:ARG:HG3	2.21	0.40
1:D:445[B]:GLN:HA	1:D:446:PRO:HD3	1.90	0.40
1:A:146:CYS:HB2	1:A:202:VAL:HG21	2.03	0.40

All (1) 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)
8:B:918:HOH:O	8:C:1143:HOH:O[1_655]	2.15	0.05

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	452/476 (95%)	441 (98%)	11 (2%)	0	100	100
1	B	464/476 (98%)	444 (96%)	17 (4%)	3 (1%)	21	11
1	C	469/476 (98%)	457 (97%)	11 (2%)	1 (0%)	43	31
1	D	466/476 (98%)	449 (96%)	14 (3%)	3 (1%)	21	11
All	All	1851/1904 (97%)	1791 (97%)	53 (3%)	7 (0%)	36	19

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	459[A]	HIS
1	D	459[B]	HIS
1	C	180	SER
1	D	94	SER
1	B	168[A]	ASP
1	B	168[B]	ASP
1	B	180	SER

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	407/423 (96%)	391 (96%)	16 (4%)	28	16
1	B	416/423 (98%)	393 (94%)	23 (6%)	19	8
1	C	419/423 (99%)	408 (97%)	11 (3%)	40	28
1	D	411/423 (97%)	396 (96%)	15 (4%)	31	18
All	All	1653/1692 (98%)	1588 (96%)	65 (4%)	32	16

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	117	SER

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Mol	Chain	Res	Type
1	A	170	GLU
1	A	222[A]	MET
1	A	222[B]	MET
1	A	237	ASP
1	A	256	ILE
1	A	273	TYR
1	A	318	ASN
1	A	341[A]	GLN
1	A	341[B]	GLN
1	A	354	LEU
1	A	356[A]	HIS
1	A	356[B]	HIS
1	A	428	SER
1	A	496	PRO
1	A	531	LYS
1	B	108	GLU
1	B	163	GLU
1	B	168[A]	ASP
1	B	168[B]	ASP
1	B	222[A]	MET
1	B	222[B]	MET
1	B	245	ARG
1	B	255	VAL
1	B	273	TYR
1	B	287	THR
1	B	341[A]	GLN
1	B	341[B]	GLN
1	B	398	LEU
1	B	399	VAL
1	B	407	THR
1	B	418	LEU
1	B	446	PRO
1	B	505	ARG
1	B	506	THR
1	B	524	SER
1	B	536	ILE
1	B	558[A]	VAL
1	B	558[B]	VAL
1	C	117	SER
1	C	134	SER
1	C	158	LYS
1	C	166	ASP

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Mol	Chain	Res	Type
1	C	237	ASP
1	C	273	TYR
1	C	341	GLN
1	C	370	GLU
1	C	397	THR
1	C	448	GLN
1	C	531	LYS
1	D	122	LYS
1	D	162[A]	GLN
1	D	162[B]	GLN
1	D	166	ASP
1	D	245	ARG
1	D	256	ILE
1	D	259	GLU
1	D	273	TYR
1	D	318	ASN
1	D	448[A]	GLN
1	D	448[B]	GLN
1	D	531[A]	LYS
1	D	531[B]	LYS
1	D	541	LEU
1	D	551	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	A	364	GLN
1	A	445	GLN
1	B	143	HIS
1	B	159	GLN
1	B	253	ASN
1	B	425	ASN
1	C	93	ASN
1	C	138	ASN
1	C	241	GLN
1	C	253	ASN
1	C	276	HIS
1	C	323	GLN
1	C	448	GLN
1	D	301	ASN
1	D	504	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 ⓘ

8 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	BGC	E	1	2	12,12,12	0.81	0	17,17,17	1.27	1 (5%)
2	BGC	E	2	2	11,11,12	0.88	0	15,15,17	1.21	1 (6%)
2	BGC	E	3	2	11,11,12	1.06	1 (9%)	15,15,17	1.29	1 (6%)
2	BGC	E	4	2	11,11,12	1.04	1 (9%)	15,15,17	0.96	1 (6%)
2	XYS	E	5	2	9,9,10	1.03	1 (11%)	10,12,14	1.13	1 (10%)
2	XYS	E	6	2	9,9,10	1.62	2 (22%)	10,12,14	1.92	3 (30%)
2	XYS	E	7	2	9,9,10	1.67	2 (22%)	10,12,14	1.24	2 (20%)
2	GAL	E	8	2	11,11,12	1.91	2 (18%)	15,15,17	1.06	1 (6%)

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	BGC	E	1	2	-	0/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	0/2/19/22	0/1/1/1
2	BGC	E	4	2	-	0/2/19/22	0/1/1/1
2	XYS	E	5	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYS	E	6	2	-	-	1/1/1/1
2	XYS	E	7	2	-	-	0/1/1/1
2	GAL	E	8	2	-	2/2/19/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	8	GAL	O5-C1	5.23	1.52	1.43
2	E	6	XYS	O5-C1	3.69	1.50	1.43
2	E	7	XYS	O5-C5	3.53	1.49	1.43
2	E	8	GAL	C2-C3	2.86	1.56	1.52
2	E	4	BGC	C2-C3	2.59	1.56	1.52
2	E	6	XYS	C5-C4	2.57	1.58	1.52
2	E	3	BGC	C2-C3	-2.28	1.49	1.52
2	E	7	XYS	C4-C3	-2.21	1.49	1.52
2	E	5	XYS	O4-C4	2.12	1.47	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	6	XYS	C5-O5-C1	3.71	117.40	111.42
2	E	6	XYS	C4-C3-C2	-3.10	107.25	110.92
2	E	3	BGC	C6-C5-C4	-2.89	105.92	113.02
2	E	7	XYS	O4-C4-C3	-2.85	104.26	110.15
2	E	5	XYS	C5-O5-C1	2.83	115.98	111.42
2	E	6	XYS	C1-C2-C3	-2.58	105.89	109.64
2	E	1	BGC	C1-O5-C5	-2.56	108.69	113.65
2	E	8	GAL	O6-C6-C5	-2.55	102.66	111.33
2	E	4	BGC	C1-O5-C5	-2.53	108.80	112.19
2	E	2	BGC	O5-C5-C6	2.23	112.00	107.66
2	E	7	XYS	O2-C2-C3	-2.01	105.99	110.15

There are no chirality outliers.

All (2) torsion outliers are listed below:

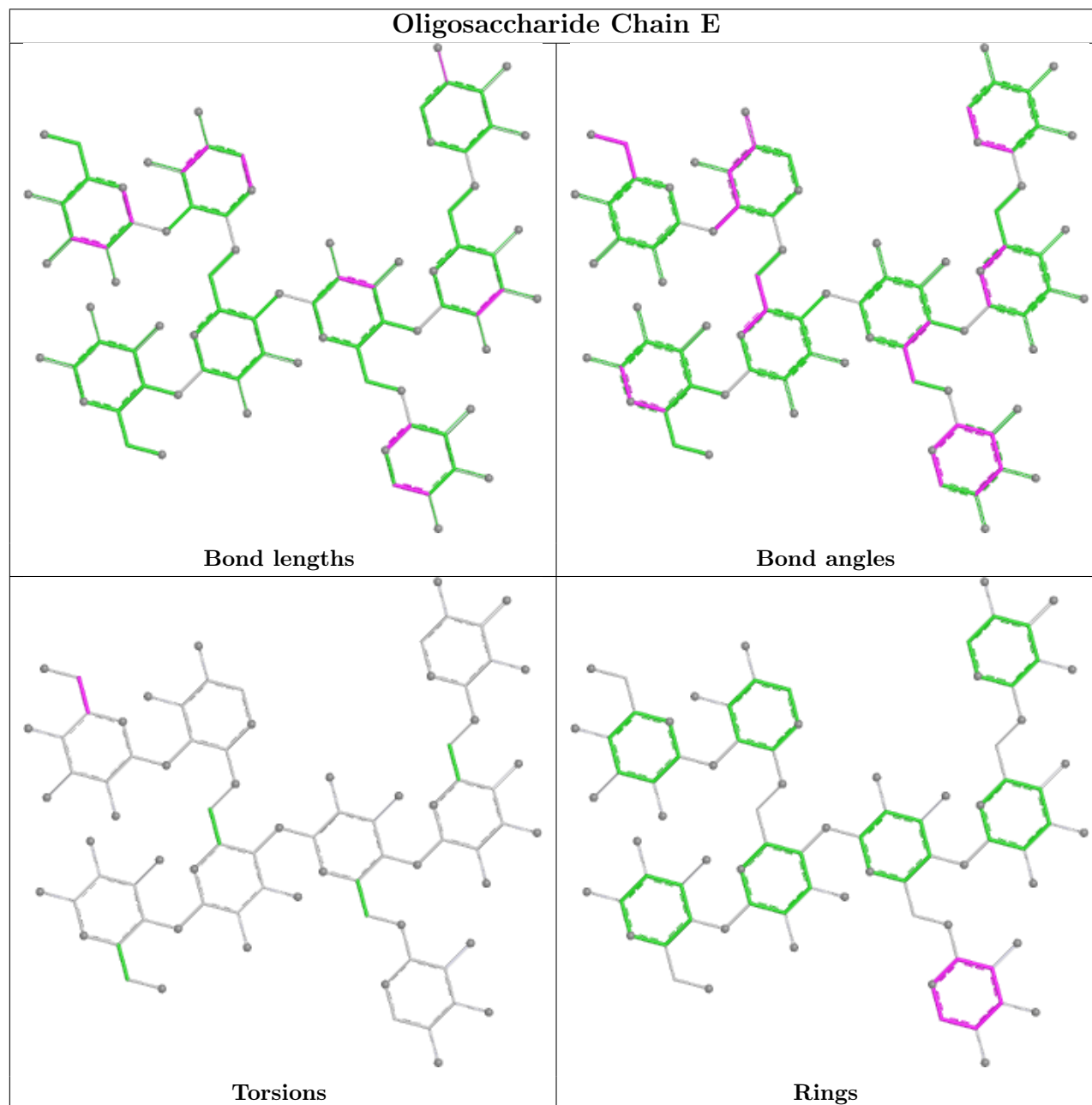
Mol	Chain	Res	Type	Atoms
2	E	8	GAL	O5-C5-C6-O6
2	E	8	GAL	C4-C5-C6-O6

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	6	XYS	C1-C2-C3-C4-C5-O5

No monomer is involved in short contacts.

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](#)

Of 38 ligands modelled in this entry, 27 are monoatomic - leaving 11 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$
7	GOL	C	611	-	5,5,5	0.37	0	5,5,5	0.61	0
6	EDO	C	610	-	3,3,3	0.46	0	2,2,2	0.68	0
6	EDO	D	606[B]	-	3,3,3	0.47	0	2,2,2	0.28	0
3	MES	D	601	-	12,12,12	2.24	1 (8%)	15,16,16	1.14	2 (13%)
6	EDO	A	613	-	3,3,3	0.37	0	2,2,2	0.70	0
3	MES	A	602	-	12,12,12	1.87	1 (8%)	15,16,16	1.38	2 (13%)
6	EDO	D	606[A]	-	3,3,3	0.58	0	2,2,2	0.11	0
3	MES	C	601	-	12,12,12	1.83	1 (8%)	15,16,16	1.77	3 (20%)
3	MES	A	601	-	12,12,12	1.65	1 (8%)	15,16,16	1.21	1 (6%)
7	GOL	D	607	-	5,5,5	0.27	0	5,5,5	0.58	0
3	MES	C	602	-	12,12,12	2.17	1 (8%)	15,16,16	1.67	4 (26%)

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
7	GOL	C	611	-	-	3/4/4/4	-
6	EDO	C	610	-	-	1/1/1/1	-
6	EDO	D	606[B]	-	-	1/1/1/1	-
3	MES	D	601	-	-	0/6/14/14	0/1/1/1
6	EDO	A	613	-	-	1/1/1/1	-
3	MES	A	602	-	-	5/6/14/14	0/1/1/1
6	EDO	D	606[A]	-	-	0/1/1/1	-
3	MES	C	601	-	-	3/6/14/14	0/1/1/1
3	MES	A	601	-	-	0/6/14/14	0/1/1/1
7	GOL	D	607	-	-	0/4/4/4	-
3	MES	C	602	-	-	3/6/14/14	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	601	MES	C8-S	-7.29	1.67	1.77
3	C	602	MES	C8-S	-7.11	1.67	1.77
3	A	602	MES	C8-S	-5.91	1.69	1.77
3	C	601	MES	C8-S	-5.55	1.69	1.77
3	A	601	MES	C8-S	-5.13	1.70	1.77

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601	MES	C2-C3-N4	3.97	116.16	110.12
3	A	602	MES	O3S-S-C8	3.82	113.47	106.00
3	A	601	MES	O3S-S-O1S	-3.14	103.56	111.40
3	C	601	MES	O2S-S-C8	2.66	110.74	106.73
3	C	602	MES	O1S-S-C8	2.55	110.58	106.73
3	C	602	MES	C2-C3-N4	2.51	113.93	110.12
3	D	601	MES	O1S-S-C8	2.48	110.47	106.73
3	C	601	MES	O3S-S-C8	2.47	110.83	106.00
3	C	602	MES	O3S-S-C8	2.34	110.58	106.00
3	A	602	MES	O2S-S-O1S	-2.31	106.31	113.82
3	C	602	MES	O2S-S-C8	2.23	110.10	106.73
3	D	601	MES	O3S-S-C8	2.02	109.95	106.00

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	MES	C8-C7-N4-C3
3	A	602	MES	C8-C7-N4-C5
3	A	602	MES	C7-C8-S-O1S
3	A	602	MES	C7-C8-S-O2S
3	C	602	MES	C7-C8-S-O1S
3	C	602	MES	C7-C8-S-O3S
7	C	611	GOL	O1-C1-C2-C3
3	A	602	MES	C7-C8-S-O3S
7	C	611	GOL	O1-C1-C2-O2
3	C	601	MES	C7-C8-S-O1S
3	C	602	MES	C7-C8-S-O2S
3	C	601	MES	C8-C7-N4-C5
3	C	601	MES	C7-C8-S-O3S
7	C	611	GOL	O2-C2-C3-O3
6	C	610	EDO	O1-C1-C2-O2
6	D	606[B]	EDO	O1-C1-C2-O2
6	A	613	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	610	EDO	2	0
7	D	607	GOL	1	0
3	C	602	MES	1	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	446/476 (93%)	-0.14	14 (3%) 51 51	6, 19, 45, 82	20 (4%)
1	B	452/476 (94%)	-0.06	25 (5%) 30 29	7, 19, 57, 94	19 (4%)
1	C	458/476 (96%)	-0.04	22 (4%) 35 34	8, 21, 54, 87	18 (3%)
1	D	454/476 (95%)	-0.02	23 (5%) 33 32	7, 21, 50, 90	19 (4%)
All	All	1810/1904 (95%)	-0.06	84 (4%) 37 36	6, 20, 53, 94	76 (4%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	451	TYR	7.9
1	A	450	GLY	5.6
1	C	91	ASN	5.4
1	A	449	GLU	4.8
1	B	165	ILE	4.8
1	B	399	VAL	4.4
1	B	451	TYR	4.4
1	C	407	THR	4.3
1	B	400	GLU	4.2
1	C	459	HIS	4.2
1	A	162	GLN	4.2
1	A	406	ASN	4.2
1	C	245[A]	ARG	4.0
1	B	397	THR	4.0
1	D	458[A]	MET	4.0
1	B	258	THR	4.0
1	C	458	MET	3.8
1	D	256	ILE	3.7
1	C	258	THR	3.7
1	A	459	HIS	3.5
1	B	450	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	407	THR	3.5
1	D	451	TYR	3.5
1	D	162[A]	GLN	3.4
1	D	459[A]	HIS	3.3
1	B	164	HIS	3.3
1	D	123	PRO	3.2
1	D	119	HIS	3.2
1	B	163	GLU	3.1
1	A	458	MET	3.1
1	D	407	THR	3.1
1	B	448[A]	GLN	3.0
1	C	162[A]	GLN	2.9
1	B	256	ILE	2.9
1	C	92	ILE	2.9
1	D	94	SER	2.9
1	B	407	THR	2.9
1	C	451	TYR	2.9
1	B	398	LEU	2.8
1	A	166	ASP	2.8
1	B	167	GLY	2.8
1	B	260	GLY	2.7
1	D	258	THR	2.7
1	D	165	ILE	2.6
1	C	256	ILE	2.6
1	D	168	ASP	2.5
1	C	452	GLN	2.5
1	D	400	GLU	2.5
1	A	118	VAL	2.5
1	D	448[A]	GLN	2.5
1	C	399	VAL	2.5
1	B	168[A]	ASP	2.4
1	B	259	GLU	2.4
1	A	372	PRO	2.4
1	B	372	PRO	2.4
1	D	95	ASP	2.4
1	C	260	GLY	2.4
1	B	449	GLU	2.4
1	B	459	HIS	2.4
1	A	256	ILE	2.3
1	C	448	GLN	2.3
1	D	255	VAL	2.3
1	C	398	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	400	GLU	2.3
1	D	118	VAL	2.3
1	D	93	ASN	2.2
1	B	160[A]	LEU	2.2
1	D	398	LEU	2.2
1	C	558[A]	VAL	2.2
1	B	447	SER	2.2
1	A	167	GLY	2.2
1	C	468	TYR	2.2
1	C	372	PRO	2.2
1	D	530	CYS	2.1
1	B	530	CYS	2.1
1	D	449	GLU	2.1
1	C	408	PRO	2.1
1	C	527	PHE	2.1
1	D	468	TYR	2.1
1	B	169	GLY	2.0
1	C	167	GLY	2.0
1	B	166	ASP	2.0
1	C	255	VAL	2.0
1	D	372	PRO	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.

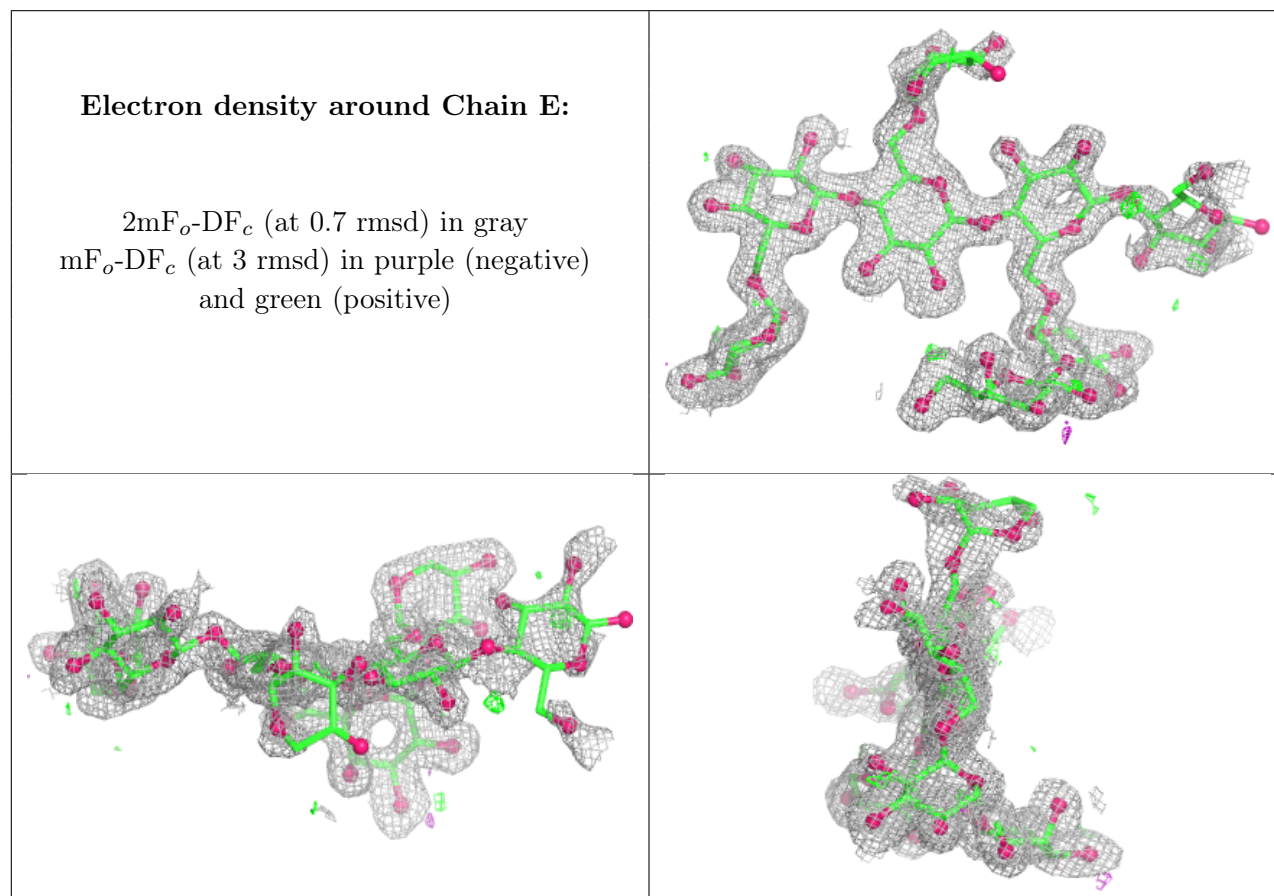
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BGC	E	1	12/12	0.63	0.18	46,57,61,63	12
2	XYS	E	6	9/10	0.71	0.17	48,51,55,56	9
2	XYS	E	5	9/10	0.86	0.11	22,24,26,29	9
2	BGC	E	2	11/12	0.87	0.11	25,31,37,39	11
2	BGC	E	4	11/12	0.89	0.10	24,27,31,32	11
2	BGC	E	3	11/12	0.91	0.10	23,27,34,39	11
2	GAL	E	8	11/12	0.91	0.09	15,17,19,19	11

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	XYS	E	7	9/10	0.92	0.09	19,24,25,25	9

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 ⓘ

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
7	GOL	C	611	6/6	0.74	0.20	35,36,37,39	6
7	GOL	D	607	6/6	0.77	0.16	24,28,28,29	6
6	EDO	A	613	4/4	0.78	0.33	33,34,34,36	4
3	MES	C	602	12/12	0.82	0.19	38,44,48,50	12
6	EDO	C	610	4/4	0.87	0.12	7,7,7,7	4
6	EDO	D	606[A]	4/4	0.89	0.11	37,41,45,46	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	D	606[B]	4/4	0.89	0.11	15,16,16,16	4
3	MES	D	601	12/12	0.90	0.11	49,50,52,53	0
4	CL	A	610	1/1	0.90	0.16	41,41,41,41	1
3	MES	A	602	12/12	0.91	0.13	26,33,39,41	12
3	MES	A	601	12/12	0.91	0.12	25,32,35,36	12
5	K	C	609	1/1	0.92	0.12	40,40,40,40	1
3	MES	C	601	12/12	0.93	0.10	39,43,50,50	0
4	CL	D	604	1/1	0.94	0.14	40,40,40,40	0
4	CL	B	603	1/1	0.95	0.14	48,48,48,48	0
4	CL	C	606	1/1	0.95	0.13	39,39,39,39	0
4	CL	A	607	1/1	0.96	0.12	44,44,44,44	0
4	CL	A	609	1/1	0.96	0.12	42,42,42,42	0
4	CL	C	603	1/1	0.96	0.08	32,32,32,32	0
4	CL	A	604	1/1	0.97	0.07	32,32,32,32	0
4	CL	C	605	1/1	0.97	0.09	36,36,36,36	0
4	CL	B	601	1/1	0.97	0.09	28,28,28,28	0
4	CL	A	606	1/1	0.97	0.12	37,37,37,37	0
5	K	A	612	1/1	0.97	0.17	38,38,38,38	0
5	K	B	606	1/1	0.97	0.19	40,40,40,40	0
5	K	C	608	1/1	0.97	0.21	43,43,43,43	0
4	CL	D	602	1/1	0.98	0.07	33,33,33,33	0
5	K	D	605	1/1	0.98	0.07	25,25,25,25	0
4	CL	B	604	1/1	0.98	0.09	28,28,28,28	0
5	K	A	611	1/1	0.98	0.05	20,20,20,20	0
4	CL	C	604	1/1	0.99	0.05	21,21,21,21	1
4	CL	B	602	1/1	0.99	0.04	29,29,29,29	0
5	K	B	605	1/1	0.99	0.04	23,23,23,23	0
4	CL	A	603	1/1	0.99	0.04	18,18,18,18	0
5	K	C	607	1/1	0.99	0.06	26,26,26,26	0
4	CL	A	605	1/1	0.99	0.08	29,29,29,29	0
4	CL	A	608	1/1	0.99	0.08	27,27,27,27	0
4	CL	D	603	1/1	1.00	0.10	26,26,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.