



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:10 PM UTC

PDB ID : 4XR8 / pdb_00004xr8
Title : Crystal structure of the HPV16 E6/E6AP/p53 ternary complex at 2.25 Å resolution
Authors : Martinez-Zapien, D.; Ruiz, F.X.; Mitschler, A.; Podjarny, A.; Trave, G.; Zanier, K.
Deposited on : 2015-01-20
Resolution : 2.25 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:

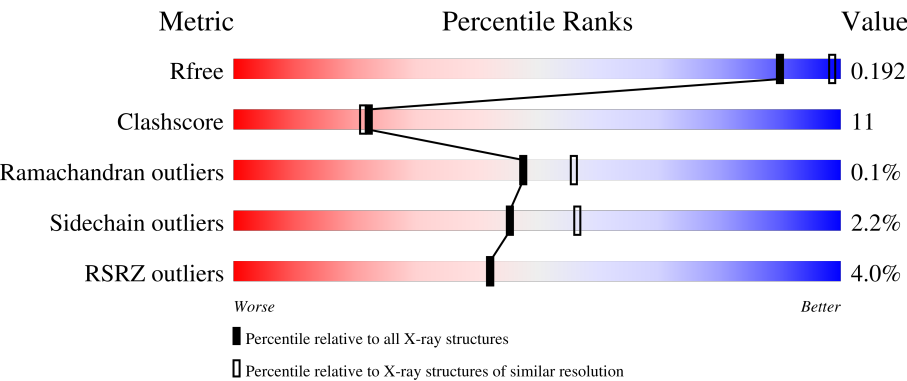
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	383	5% 76% 22% .
1	B	383	4% 73% 25% ..
2	C	199	2% 83% 16% .
2	D	199	2% 87% 13% .
3	F	151	3% 75% 19% . 5%

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Mol	Chain	Length	Quality of chain
3	H	151	7% 78% 19%
4	E	2	50% 50%
4	G	2	100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12034 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 Maltose-binding periplasmic protein, ubiquitin ligase E6AP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	6	0
			2990	1921	489	573	7			
1	B	381	Total	C	N	O	S	0	5	0
			2965	1906	480	573	6			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	83	ALA	ASP	engineered mutation	UNP P0AEX9
A	84	ALA	LYS	engineered mutation	UNP P0AEX9
A	240	ALA	LYS	engineered mutation	UNP P0AEX9
A	360	ALA	GLU	engineered mutation	UNP P0AEX9
A	363	ALA	LYS	engineered mutation	UNP P0AEX9
A	364	ALA	ASP	engineered mutation	UNP P0AEX9
A	368	ASN	ARG	linker	UNP P0AEX9
A	369	ALA	-	linker	UNP P0AEX9
A	370	ALA	-	linker	UNP P0AEX9
A	371	ALA	-	linker	UNP P0AEX9
B	1	MET	-	initiating methionine	UNP P0AEX9
B	83	ALA	ASP	engineered mutation	UNP P0AEX9
B	84	ALA	LYS	engineered mutation	UNP P0AEX9
B	240	ALA	LYS	engineered mutation	UNP P0AEX9
B	360	ALA	GLU	engineered mutation	UNP P0AEX9
B	363	ALA	LYS	engineered mutation	UNP P0AEX9
B	364	ALA	ASP	engineered mutation	UNP P0AEX9
B	368	ASN	ARG	linker	UNP P0AEX9
B	369	ALA	-	linker	UNP P0AEX9
B	370	ALA	-	linker	UNP P0AEX9
B	371	ALA	-	linker	UNP P0AEX9

- Molecule 2 is a protein called Cellular tumor antigen p53.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	199	Total	C	N	O	S	0	0	0
			1564	963	291	294	16			
2	D	199	Total	C	N	O	S	0	0	0
			1564	963	291	294	16			

- Molecule 3 is a protein called Protein E6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	143	Total	C	N	O	S	0	2	0
			1218	767	222	216	13			
3	H	151	Total	C	N	O	S	0	1	0
			1287	805	240	230	12			

There are 8 discrepancies between the modelled and reference sequences:

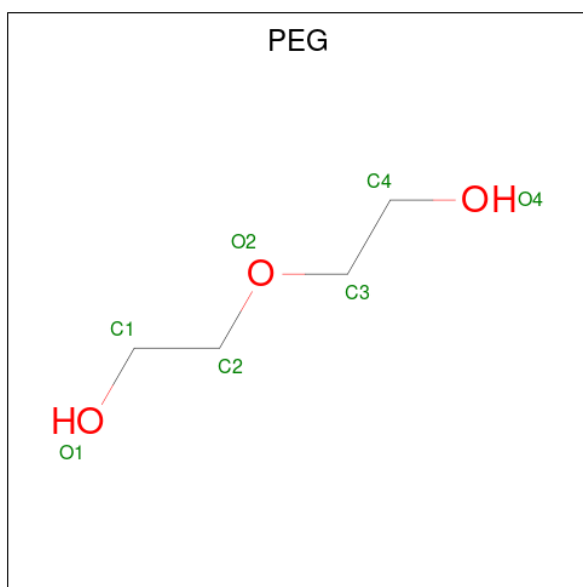
Chain	Residue	Modelled	Actual	Comment	Reference
F	80	SER	CYS	engineered mutation	UNP P03126
F	97	SER	CYS	engineered mutation	UNP P03126
F	111	SER	CYS	engineered mutation	UNP P03126
F	140	SER	CYS	engineered mutation	UNP P03126
H	80	SER	CYS	engineered mutation	UNP P03126
H	97	SER	CYS	engineered mutation	UNP P03126
H	111	SER	CYS	engineered mutation	UNP P03126
H	140	SER	CYS	engineered mutation	UNP P03126

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	E	2	Total	C	O	0	0	0
			23	12	11			
4	G	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).

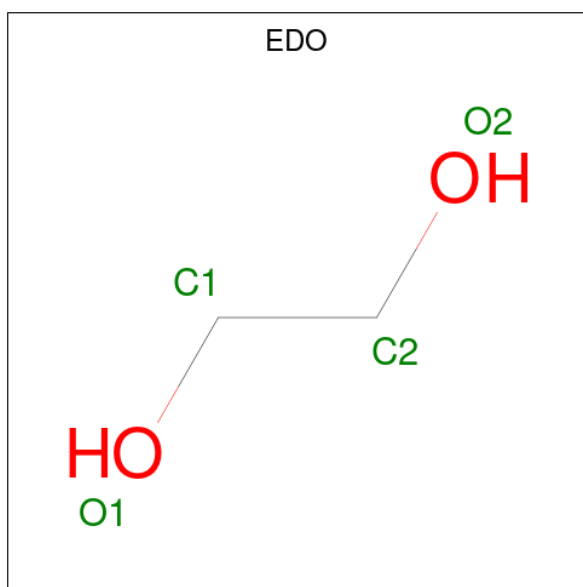


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	1	Total	Zn	0	0
			1	1		
6	D	1	Total	Zn	0	0
			1	1		
6	F	2	Total	Zn	0	0
			2	2		
6	H	2	Total	Zn	0	0
			2	2		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	F	1	Total	C	O	0	0
			4	2	2		

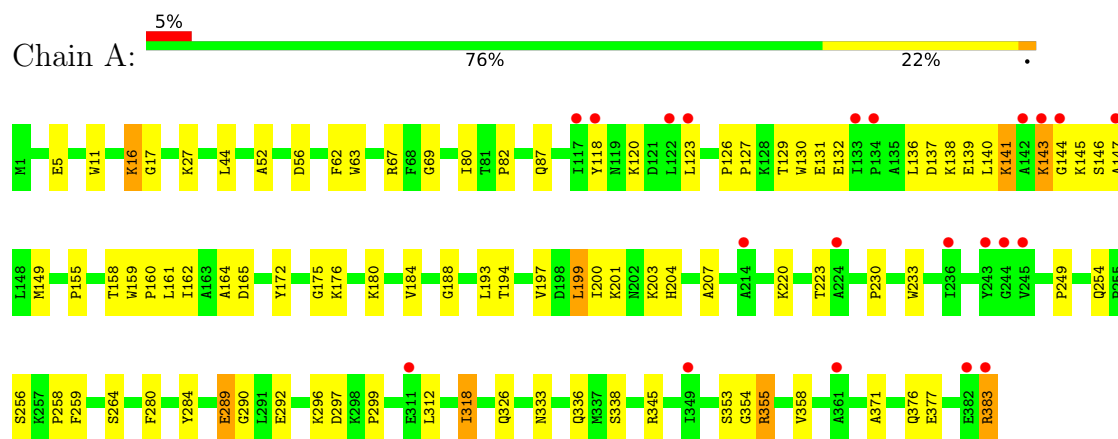
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	91	Total	O	0	2
			94	94		
8	B	62	Total	O	0	1
			62	62		
8	C	83	Total	O	0	2
			85	85		
8	D	56	Total	O	0	2
			58	58		
8	F	35	Total	O	0	0
			35	35		
8	H	27	Total	O	0	1
			28	28		

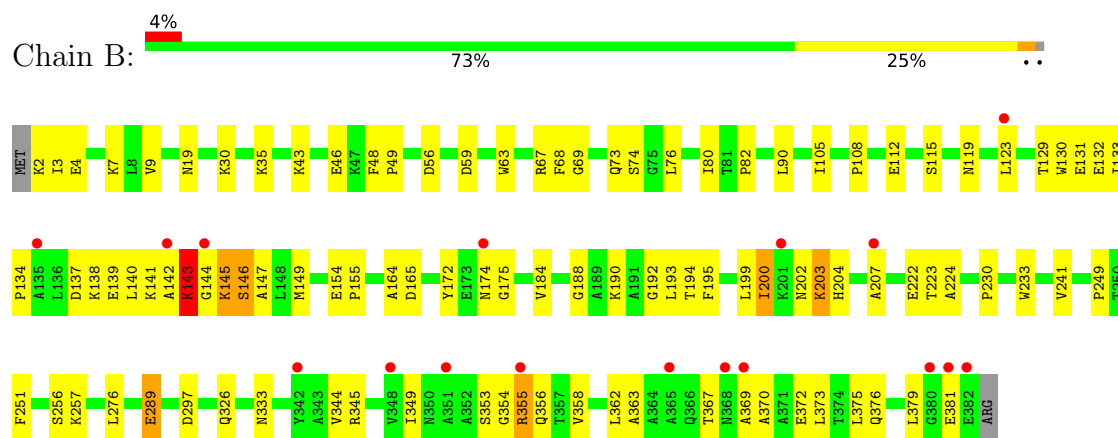
3 Residue-property plots

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.

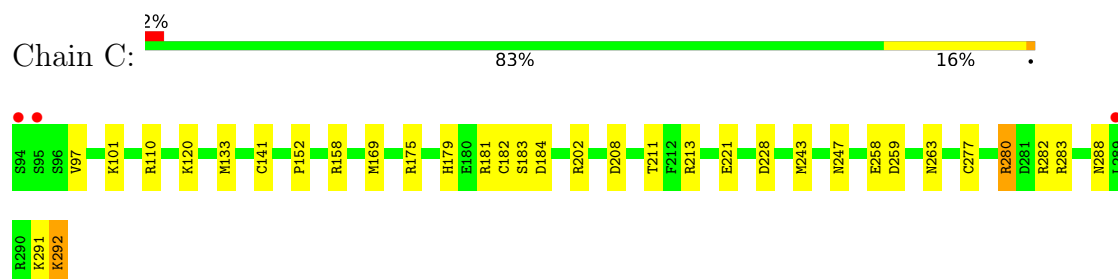
- Molecule 1: Maltose-binding periplasmic protein, ubiquitin ligase E6AP



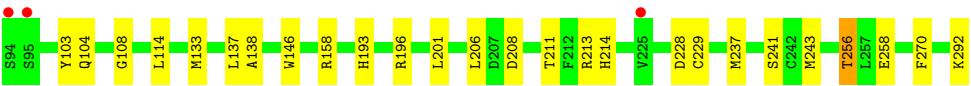
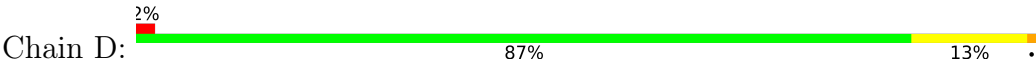
- Molecule 1: Maltose-binding periplasmic protein, ubiquitin ligase E6AP



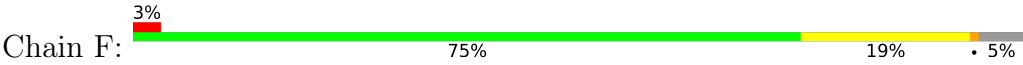
- Molecule 2: Cellular tumor antigen p53



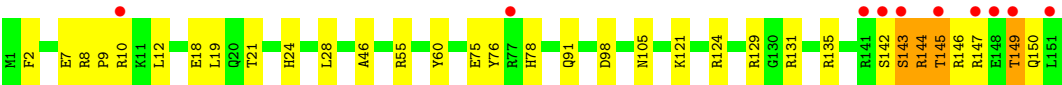
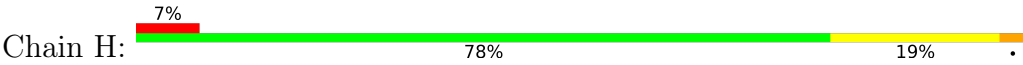
• Molecule 2: Cellular tumor antigen p53



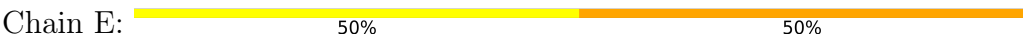
• Molecule 3: Protein E6



• Molecule 3: Protein E6



• Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



• Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-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	77.84Å 128.94Å 81.56Å 90.00° 92.33° 90.00°	Depositor
Resolution (Å)	49.63 – 2.25 49.63 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.63-2.25) 99.5 (49.63-2.25)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.194 , 0.246 0.202 , 0.192	Depositor DCC
R_{free} test set	3883 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.004 for l,k,-h 0.029 for h,-k,-l 0.019 for l,-k,h	Xtriage
F_o , F_c correlation	0.95	EDS
Total number of atoms	12034	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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: EDO, GLC, PEG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.63	0/3068	0.95	7/4161 (0.2%)
1	B	0.58	0/3039	0.99	11/4128 (0.3%)
2	C	0.62	0/1599	0.88	1/2165 (0.0%)
2	D	0.59	0/1599	0.92	0/2165
3	F	0.57	0/1251	0.91	3/1681 (0.2%)
3	H	0.58	0/1317	0.93	2/1768 (0.1%)
All	All	0.60	0/11873	0.94	24/16068 (0.1%)

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
3	F	0	1
3	H	0	2
All	All	0	4

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	48	PHE	CA-C-N	-9.45	109.18	119.19
1	B	48	PHE	C-N-CA	-9.45	109.18	119.19
1	A	143	LYS	N-CA-C	9.19	124.29	112.89
3	H	144	ARG	N-CA-C	8.59	122.83	109.52
1	B	139	GLU	N-CA-C	-7.69	103.16	112.54
1	B	142	ALA	N-CA-C	-7.08	100.91	111.81
1	B	56	ASP	N-CA-C	-6.67	100.35	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	370	ALA	N-CA-C	-6.16	105.59	113.23
1	B	145	LYS	N-CA-C	6.13	119.70	109.95
2	C	152	PRO	O-C-N	5.76	123.96	121.31
1	A	199	LEU	N-CA-C	-5.73	106.08	114.39
1	A	139	GLU	N-CA-C	-5.72	105.19	111.82
3	F	142	SER	N-CA-C	5.65	118.64	110.28
1	A	159	TRP	CA-C-N	-5.48	113.54	119.24
1	A	159	TRP	C-N-CA	-5.48	113.54	119.24
1	A	16	LYS	N-CA-C	5.40	120.15	113.50
1	A	254	GLN	N-CA-C	5.37	117.36	110.39
1	B	146	SER	N-CA-C	5.37	117.45	110.53
1	B	200	ILE	N-CA-C	-5.20	107.76	112.96
3	F	94	LYS	CA-C-N	-5.07	114.73	119.85
3	F	94	LYS	C-N-CA	-5.07	114.73	119.85
1	B	257	LYS	N-CA-C	5.03	120.92	109.81
3	H	145	THR	N-CA-C	5.02	119.65	111.37
1	B	143	LYS	N-CA-C	5.01	121.48	110.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	143	LYS	Peptide
3	F	141	ARG	Peptide
3	H	143	SER	Peptide
3	H	149	THR	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	2990	0	2969	74	0
1	B	2965	0	2927	87	0
2	C	1564	0	1529	25	0
2	D	1564	0	1529	21	0
3	F	1218	0	1213	21	0
3	H	1287	0	1282	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	23	0	21	3	0
4	G	23	0	21	0	0
5	A	7	0	10	0	0
5	B	7	0	10	2	0
5	D	7	0	10	2	0
5	F	7	0	10	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	F	2	0	0	0	0
6	H	2	0	0	0	0
7	F	4	0	6	3	0
8	A	94	0	0	2	0
8	B	62	0	0	4	0
8	C	85	0	0	3	0
8	D	58	0	0	1	0
8	F	35	0	0	0	0
8	H	28	0	0	0	0
All	All	12034	0	11537	245	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 (245) 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)
3:H:105:ASN:HB2	3:H:144:ARG:HH12	1.23	0.97
3:H:105:ASN:CB	3:H:144:ARG:HH12	1.79	0.94
1:B:376:GLN:CD	3:H:129:ARG:HH12	1.78	0.92
1:B:143:LYS:HB2	1:B:145:LYS:H	1.34	0.92
1:B:141:LYS:HA	1:B:143:LYS:HD3	1.53	0.91
1:A:355:ARG:HG2	1:A:355:ARG:HH11	1.35	0.90
3:H:105:ASN:HB2	3:H:144:ARG:NH1	1.94	0.82
1:A:193:LEU:HD23	1:A:358:VAL:HG13	1.63	0.81
1:A:140:LEU:HB3	1:A:145:LYS:HB2	1.64	0.78
1:B:143:LYS:HB2	1:B:145:LYS:N	1.98	0.77
1:A:137:ASP:HA	1:A:147:ALA:HB2	1.65	0.76
1:A:123:LEU:HD21	1:A:136:LEU:HD21	1.68	0.76
1:A:27:LYS:HD3	1:A:289:GLU:OE2	1.85	0.75
1:A:289:GLU:HG2	1:A:290:GLY:N	2.02	0.75
2:D:193:HIS:CE1	2:D:214:HIS:HB3	2.23	0.74
1:B:145:LYS:HE3	1:B:145:LYS:HA	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:LEU:HD23	1:B:358:VAL:HG13	1.71	0.73
1:A:312:LEU:HB3	1:A:318:ILE:HD12	1.71	0.72
1:A:220:LYS:NZ	8:A:570:HOH:O	2.22	0.72
2:D:211:THR:HG23	2:D:213:ARG:H	1.55	0.71
1:B:145:LYS:HE2	1:B:222:GLU:HA	1.71	0.71
1:A:355:ARG:HG2	1:A:355:ARG:NH1	2.06	0.71
1:B:143:LYS:HG3	1:B:144:GLY:N	2.06	0.70
1:B:369:ALA:HB1	1:B:372:GLU:HB3	1.74	0.70
2:C:282:ARG:HH22	7:F:203:EDO:H12	1.57	0.69
1:B:129:THR:HG22	1:B:131:GLU:H	1.58	0.69
3:H:75:GLU:OE1	3:H:144:ARG:HD2	1.92	0.69
3:H:135:ARG:HG3	3:H:135:ARG:HH11	1.57	0.68
1:B:2:LYS:O	1:B:7:LYS:NZ	2.22	0.68
1:B:73[B]:GLN:NE2	2:D:228:ASP:OD2	2.28	0.66
2:D:158:ARG:HB3	2:D:256:THR:HG22	1.77	0.66
1:A:82:PRO:HG2	1:A:87:GLN:HE21	1.61	0.66
2:C:110:ARG:HD2	3:F:10:ARG:CZ	2.27	0.65
2:C:211:THR:HG23	2:C:213:ARG:H	1.60	0.65
1:B:143:LYS:HG3	1:B:144:GLY:H	1.59	0.65
1:B:376:GLN:CD	3:H:129:ARG:NH1	2.53	0.65
1:B:376:GLN:NE2	3:H:129:ARG:NH1	2.45	0.64
1:B:289:GLU:HG3	5:B:402:PEG:H11	1.80	0.63
1:B:376:GLN:NE2	3:H:129:ARG:HH12	1.97	0.63
2:D:243:MET:HE2	5:D:902:PEG:H12	1.80	0.63
1:A:67[B]:ARG:NH1	1:A:338:SER:HB2	2.14	0.62
2:C:158:ARG:NH1	2:C:258:GLU:OE1	2.31	0.62
2:D:104:GLN:HE21	3:H:10[B]:ARG:HE	1.48	0.62
1:A:67[B]:ARG:NH2	4:E:2:GLC:O4	2.30	0.62
1:B:80:ILE:HG22	1:B:82:PRO:HD3	1.82	0.62
1:B:4:GLU:HB2	1:B:7:LYS:HZ2	1.65	0.61
1:B:372:GLU:OE2	3:H:129:ARG:HD3	2.00	0.61
1:A:138:LYS:HA	1:A:141:LYS:HB2	1.82	0.61
1:A:383[B]:ARG:HH21	1:A:383[B]:ARG:HB2	1.65	0.61
2:C:292:LYS:HB2	3:F:24:HIS:CE1	2.36	0.60
1:B:4:GLU:H	1:B:7:LYS:NZ	2.00	0.60
1:A:16:LYS:NZ	4:E:1:GLC:O2	2.36	0.59
1:A:118:TYR:CE2	1:A:120:LYS:HG2	2.37	0.59
1:B:289:GLU:CD	1:B:289:GLU:H	2.08	0.59
2:D:206:LEU:HB2	8:D:1047:HOH:O	2.01	0.59
1:A:140:LEU:HA	1:A:143:LYS:HB2	1.85	0.59
2:D:158:ARG:NH1	2:D:258:GLU:OE1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:GLY:HA3	1:B:333:ASN:O	2.03	0.59
1:B:119:ASN:HD22	1:B:241:VAL:HG13	1.66	0.58
1:B:141:LYS:HA	1:B:143:LYS:CD	2.31	0.58
3:H:55:ARG:HB2	3:H:60:TYR:HE2	1.69	0.57
1:B:145:LYS:HE3	1:B:145:LYS:CA	2.34	0.57
3:H:145:THR:HG22	3:H:146:ARG:HB3	1.85	0.57
1:B:129:THR:HG22	1:B:131:GLU:N	2.19	0.57
1:B:73[B]:GLN:OE1	1:B:73[B]:GLN:HA	2.05	0.57
3:H:143:SER:OG	3:H:144:ARG:N	2.37	0.57
3:F:19:LEU:HB2	3:F:21:THR:HG22	1.86	0.56
1:A:149:MET:HG3	1:A:223:THR:HG21	1.88	0.56
1:A:143:LYS:N	1:A:144:GLY:HA2	2.21	0.56
2:C:221:GLU:HG2	8:C:1026:HOH:O	2.04	0.56
2:D:241:SER:O	5:D:902:PEG:H11	2.05	0.56
1:A:63:TRP:CD1	1:A:67[B]:ARG:HG3	2.41	0.55
1:B:154:GLU:OE2	1:B:345:ARG:NH2	2.38	0.55
3:H:76:TYR:O	3:H:146:ARG:NH1	2.39	0.55
1:B:145:LYS:CE	1:B:222:GLU:HA	2.36	0.55
1:B:149:MET:HB2	1:B:223:THR:HG21	1.89	0.55
1:A:140:LEU:O	1:A:145:LYS:N	2.35	0.55
2:C:288:ASN:HA	2:C:291:LYS:HD2	1.89	0.55
1:A:118:TYR:CD2	1:A:126:PRO:HG3	2.42	0.54
1:B:137:ASP:OD2	1:B:204:HIS:CD2	2.61	0.54
1:A:67[B]:ARG:HH12	1:A:338:SER:HB2	1.72	0.54
1:B:7:LYS:HB2	1:B:35:LYS:HG2	1.90	0.54
1:B:137:ASP:HA	1:B:147:ALA:HB2	1.88	0.53
3:H:12:LEU:HD23	3:H:46:ALA:HB2	1.89	0.53
1:A:69:GLY:HA3	1:A:333:ASN:O	2.09	0.53
2:C:277:CYS:SG	2:C:280:ARG:HB2	2.49	0.52
3:H:145:THR:HG22	3:H:146:ARG:CB	2.39	0.52
3:H:76:TYR:HB2	3:H:145:THR:CG2	2.39	0.52
1:A:11:TRP:HB3	1:A:44:LEU:HD11	1.92	0.52
1:B:4:GLU:H	1:B:7:LYS:HZ2	1.57	0.52
2:C:208:ASP:OD1	2:C:211:THR:HG22	2.10	0.52
1:A:353:SER:OG	1:A:354:GLY:N	2.42	0.52
1:A:130:TRP:CD1	1:A:249:PRO:HB2	2.45	0.52
1:B:195:PHE:O	1:B:199:LEU:HD13	2.09	0.52
1:A:220:LYS:NZ	1:A:220:LYS:HB2	2.25	0.51
3:H:19:LEU:HB2	3:H:21:THR:HG22	1.91	0.51
1:A:194:THR:HG23	1:A:358:VAL:HG11	1.92	0.51
2:D:193:HIS:CD2	2:D:214:HIS:CD2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:208:ASP:CG	2:C:211:THR:HG22	2.36	0.51
1:A:129:THR:HB	1:A:132:GLU:OE1	2.12	0.50
1:A:230:PRO:HA	1:A:233:TRP:CE2	2.47	0.50
1:A:80:ILE:HG22	1:A:82:PRO:HD3	1.93	0.50
1:B:2:LYS:HB3	8:B:524:HOH:O	2.10	0.50
3:H:2:PHE:O	3:H:8:ARG:NH1	2.40	0.50
1:A:129:THR:HG22	1:A:131:GLU:H	1.76	0.50
1:B:174:ASN:ND2	8:B:502:HOH:O	2.45	0.50
1:A:200:ILE:HG21	1:A:207:ALA:HB2	1.93	0.49
2:C:120:LYS:HZ2	2:C:283:ARG:HH22	1.60	0.49
1:B:4:GLU:CB	1:B:7:LYS:HZ2	2.25	0.49
3:F:114:GLU:HG2	3:F:137[A]:MET:HG2	1.94	0.49
2:C:202:ARG:HD2	8:C:1072:HOH:O	2.13	0.49
1:B:63:TRP:CD1	1:B:67:ARG:HG3	2.48	0.49
1:A:383[B]:ARG:NH1	2:C:228:ASP:OD2	2.46	0.48
1:A:137:ASP:OD2	1:A:204:HIS:CD2	2.66	0.48
1:B:372:GLU:HG3	1:B:376:GLN:HE21	1.78	0.48
3:F:23:ILE:O	3:F:39:ARG:NH1	2.47	0.48
1:A:172:TYR:OH	1:A:175:GLY:HA2	2.12	0.48
1:B:363:ALA:O	1:B:367:THR:HG22	2.13	0.48
2:C:120:LYS:NZ	2:C:283:ARG:HH22	2.11	0.48
1:B:90:LEU:HD23	1:B:108:PRO:HG2	1.95	0.48
2:C:282:ARG:NH2	7:F:203:EDO:H12	2.25	0.48
3:H:78:HIS:CG	3:H:129:ARG:HD2	2.49	0.48
1:B:137:ASP:OD2	1:B:204:HIS:CG	2.67	0.47
1:B:165:ASP:O	1:B:188:GLY:HA3	2.13	0.47
2:C:133:MET:SD	2:C:141:CYS:HB3	2.54	0.47
3:F:114:GLU:HG2	3:F:137[B]:MET:HG2	1.94	0.47
1:B:140:LEU:C	1:B:143:LYS:HB3	2.39	0.47
1:B:3:ILE:HG23	1:B:3:ILE:O	2.15	0.47
1:A:164:ALA:HB2	1:A:256:SER:HA	1.97	0.47
2:D:103:TYR:HD1	3:H:7:GLU:HG3	1.78	0.47
1:B:115:SER:HB2	8:B:539:HOH:O	2.13	0.47
1:B:133:ILE:H	1:B:134:PRO:HD2	1.79	0.47
1:B:381[B]:GLU:HG2	3:H:131:ARG:HG2	1.96	0.47
3:H:105:ASN:HA	3:H:144:ARG:HH22	1.80	0.47
1:A:155:PRO:HG3	1:A:345:ARG:HB2	1.96	0.47
1:B:74:SER:O	3:H:91:GLN:NE2	2.44	0.47
1:B:137:ASP:OD1	1:B:141:LYS:NZ	2.37	0.47
1:B:230:PRO:HA	1:B:233:TRP:CE2	2.49	0.47
1:A:194:THR:HA	1:A:358:VAL:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:LYS:HD2	1:B:145:LYS:C	2.40	0.47
3:H:76:TYR:HB2	3:H:145:THR:HG21	1.96	0.47
1:A:144:GLY:C	1:A:145:LYS:HD3	2.40	0.47
2:C:101:LYS:HE3	3:F:7:GLU:OE2	2.15	0.47
3:F:12:LEU:HD23	3:F:46:ALA:HB2	1.96	0.47
1:B:4:GLU:HB2	1:B:7:LYS:HG2	1.97	0.46
1:B:19:ASN:HB2	1:B:297:ASP:OD2	2.14	0.46
1:A:336:GLN:OE1	1:A:336:GLN:N	2.48	0.46
1:B:355:ARG:O	1:B:356:GLN:HG3	2.16	0.46
1:B:68:PHE:HB3	1:B:105:ILE:HD13	1.98	0.46
2:C:259:ASP:OD2	2:C:263:ASN:HB2	2.15	0.46
1:B:143:LYS:HD2	1:B:145:LYS:O	2.16	0.46
1:B:345:ARG:NH1	8:B:555:HOH:O	2.49	0.46
3:F:12:LEU:HB3	3:F:13:PRO:HD3	1.97	0.46
1:B:74:SER:HB2	1:B:76:LEU:HG	1.96	0.45
1:B:194:THR:HA	1:B:358:VAL:HG21	1.98	0.45
1:B:353:SER:OG	1:B:354:GLY:N	2.49	0.45
1:B:200:ILE:HG21	1:B:207:ALA:HB2	1.99	0.45
2:D:114:LEU:HD22	3:H:98:ASP:HA	1.97	0.45
2:D:193:HIS:NE2	2:D:214:HIS:CD2	2.85	0.45
3:F:109:PRO:O	7:F:203:EDO:H22	2.15	0.45
1:A:326:GLN:OE1	1:A:326:GLN:HA	2.17	0.45
3:H:135:ARG:HG3	3:H:135:ARG:NH1	2.26	0.45
1:A:127:PRO:HB3	1:A:132:GLU:HG3	1.99	0.45
1:A:137:ASP:O	1:A:140:LEU:N	2.45	0.45
1:A:280:PHE:O	1:A:284:TYR:HB2	2.16	0.45
1:B:130:TRP:CD1	1:B:249:PRO:HB2	2.52	0.45
1:B:172:TYR:OH	1:B:175:GLY:HA2	2.16	0.45
3:F:114:GLU:CG	3:F:137[A]:MET:HG2	2.47	0.45
3:H:105:ASN:CA	3:H:144:ARG:HH12	2.29	0.45
1:A:233:TRP:HB2	1:A:299:PRO:HG2	1.97	0.45
1:A:118:TYR:HE2	1:A:120:LYS:HG2	1.79	0.45
1:A:146:SER:HB3	1:A:223:THR:CG2	2.47	0.45
1:A:158:THR:O	1:A:162:ILE:HG13	2.17	0.45
1:A:371:ALA:HB1	1:A:376:GLN:NE2	2.32	0.45
3:H:144:ARG:HG2	3:H:149:THR:HG21	1.99	0.45
3:H:55:ARG:HB2	3:H:60:TYR:CE2	2.49	0.44
1:A:146:SER:HB3	1:A:223:THR:HG22	1.99	0.44
1:B:143:LYS:CG	1:B:144:GLY:N	2.75	0.44
3:F:55:ARG:HB2	3:F:60:TYR:CE2	2.53	0.44
3:H:147:ARG:HA	3:H:149:THR:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:LEU:HD13	1:B:224:ALA:CB	2.48	0.44
1:A:180:LYS:HE2	1:A:180:LYS:HB2	1.85	0.44
2:D:292:LYS:HB2	3:H:24:HIS:CE1	2.53	0.44
1:B:289:GLU:HG3	5:B:402:PEG:C1	2.48	0.43
2:D:104:GLN:HB3	2:D:108:GLY:HA2	2.00	0.43
2:D:137:LEU:HD23	2:D:138:ALA:N	2.33	0.43
1:A:200:ILE:HD13	1:A:207:ALA:HA	2.00	0.43
2:C:97:VAL:HG11	2:C:169:MET:HB3	2.00	0.43
3:H:9:PRO:HD3	3:H:18:GLU:OE2	2.17	0.43
1:A:160:PRO:O	1:A:256:SER:O	2.36	0.43
2:C:243:MET:HA	2:C:247:ASN:OD1	2.18	0.43
3:F:48:ARG:HG2	3:F:108:LYS:HB2	2.00	0.43
1:A:160:PRO:HG3	1:A:258:PRO:HB3	2.00	0.43
2:C:280:ARG:HG3	2:C:283:ARG:NH2	2.34	0.43
3:H:12:LEU:HD11	3:H:28:LEU:HD11	1.99	0.43
1:B:203:LYS:HA	1:B:203:LYS:HD3	1.81	0.43
1:A:130:TRP:CE2	1:A:161:LEU:HD13	2.54	0.43
1:B:9:VAL:O	1:B:59:ASP:N	2.51	0.42
2:C:175:ARG:NH2	2:C:179:HIS:HB3	2.34	0.42
1:B:119:ASN:ND2	1:B:241:VAL:HG13	2.33	0.42
1:B:202:ASN:O	1:B:204:HIS:CD2	2.72	0.42
1:A:292:GLU:O	1:A:296:LYS:HG3	2.19	0.42
1:B:138:LYS:HE3	1:B:204:HIS:NE2	2.35	0.42
2:D:201:LEU:HD23	2:D:201:LEU:HA	1.90	0.42
1:B:119:ASN:HD22	1:B:241:VAL:CG1	2.33	0.42
1:A:67[B]:ARG:HH21	4:E:2:GLC:HO4	1.63	0.42
1:A:165:ASP:O	1:A:188:GLY:HA3	2.20	0.42
1:A:197:VAL:HG12	1:A:201:LYS:HD2	2.01	0.42
1:A:383[B]:ARG:HD3	3:F:130:GLY:C	2.44	0.42
3:F:11:LYS:HB2	3:F:14:GLN:OE1	2.19	0.42
1:A:197:VAL:C	1:A:199:LEU:H	2.28	0.41
1:B:190:LYS:HG2	1:B:362:LEU:HD12	2.01	0.41
1:B:155:PRO:HB3	1:B:344:VAL:HG12	2.02	0.41
1:A:138:LYS:O	1:A:138:LYS:HG2	2.19	0.41
1:B:202:ASN:O	1:B:202:ASN:OD1	2.38	0.41
1:A:136:LEU:O	1:A:140:LEU:HD12	2.20	0.41
1:A:383[B]:ARG:HB2	1:A:383[B]:ARG:NH2	2.35	0.41
1:B:192:GLY:HA2	1:B:251:PHE:CE2	2.54	0.41
2:D:133:MET:HE2	2:D:270:PHE:CE2	2.55	0.41
2:D:208:ASP:CG	2:D:211:THR:HG22	2.46	0.41
1:A:17:GLY:HA2	1:A:297:ASP:OD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:PHE:HA	1:A:264:SER:O	2.21	0.41
1:B:164:ALA:HB2	1:B:256:SER:HA	2.02	0.41
1:B:146:SER:O	1:B:223:THR:HA	2.20	0.41
2:D:146:TRP:CE2	2:D:229:CYS:HB3	2.56	0.41
3:F:127:ASN:HB2	3:F:132:TRP:CZ3	2.55	0.41
1:B:375:LEU:O	1:B:379:LEU:HG	2.21	0.41
3:F:55:ARG:HB2	3:F:60:TYR:HE2	1.85	0.41
1:A:149:MET:HG2	8:A:552:HOH:O	2.21	0.41
1:B:129:THR:HB	1:B:132:GLU:OE1	2.21	0.41
1:B:276:LEU:HD23	1:B:276:LEU:HA	1.94	0.41
1:B:326:GLN:HA	1:B:326:GLN:OE1	2.21	0.41
1:B:345:ARG:O	1:B:349:ILE:HG12	2.20	0.41
2:C:182:CYS:O	2:C:184:ASP:N	2.54	0.41
8:C:1081:HOH:O	3:F:10:ARG:HD2	2.21	0.41
1:A:377:GLU:OE1	3:F:53:VAL:HG13	2.21	0.41
1:A:5:GLU:OE2	3:H:121:LYS:NZ	2.52	0.41
2:D:196:ARG:NH1	2:D:237:MET:HE2	2.36	0.41
3:F:88:LEU:HD23	3:F:88:LEU:HA	1.78	0.41
1:A:52:ALA:HA	1:A:56:ASP:O	2.21	0.40
1:B:46:GLU:O	1:B:49:PRO:HD2	2.22	0.40
3:F:40:ARG:HD2	3:F:44:ASP:OD2	2.22	0.40
1:A:118:TYR:CE2	1:A:126:PRO:HG3	2.57	0.40
2:C:158:ARG:HH11	2:C:258:GLU:CD	2.30	0.40
2:C:288:ASN:O	2:C:292:LYS:HD3	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	385/383 (100%)	366 (95%)	19 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	383/383 (100%)	366 (96%)	17 (4%)	0	100	100
2	C	197/199 (99%)	195 (99%)	1 (0%)	1 (0%)	24	24
2	D	197/199 (99%)	195 (99%)	2 (1%)	0	100	100
3	F	143/151 (95%)	137 (96%)	6 (4%)	0	100	100
3	H	150/151 (99%)	137 (91%)	13 (9%)	0	100	100
All	All	1455/1466 (99%)	1396 (96%)	58 (4%)	1 (0%)	48	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	183	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	305/300 (102%)	295 (97%)	10 (3%)	33	42
1	B	302/300 (101%)	294 (97%)	8 (3%)	40	50
2	C	179/179 (100%)	176 (98%)	3 (2%)	53	65
2	D	179/179 (100%)	178 (99%)	1 (1%)	78	84
3	F	139/145 (96%)	136 (98%)	3 (2%)	45	56
3	H	146/145 (101%)	143 (98%)	3 (2%)	47	58
All	All	1250/1248 (100%)	1222 (98%)	28 (2%)	45	56

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	LYS
1	A	176	LYS
1	A	184	VAL
1	A	203	LYS
1	A	259	PHE

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Mol	Chain	Res	Type
1	A	289	GLU
1	A	318	ILE
1	A	355	ARG
1	A	383[A]	ARG
1	A	383[B]	ARG
1	B	30	LYS
1	B	43	LYS
1	B	112	GLU
1	B	184	VAL
1	B	203	LYS
1	B	289	GLU
1	B	355	ARG
1	B	373	LEU
2	C	181	ARG
2	C	280	ARG
2	C	292	LYS
2	D	256	THR
3	F	3	GLN
3	F	40	ARG
3	F	142	SER
3	H	124	ARG
3	H	142	SER
3	H	150	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	87	GLN
1	A	174	ASN
1	A	204	HIS
1	A	254	GLN
1	B	125	ASN
1	B	376	GLN
2	C	239	ASN
2	C	263	ASN
2	D	100	GLN
2	D	214	HIS

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 ⓘ

4 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
4	GLC	E	1	4	12,12,12	0.59	0	17,17,17	0.84	0
4	GLC	E	2	4	11,11,12	0.68	0	15,15,17	1.37	2 (13%)
4	GLC	G	1	4	12,12,12	0.66	0	17,17,17	0.93	1 (5%)
4	GLC	G	2	4	11,11,12	0.59	0	15,15,17	1.16	2 (13%)

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
4	GLC	E	1	4	-	0/2/22/22	0/1/1/1
4	GLC	E	2	4	-	0/2/19/22	0/1/1/1
4	GLC	G	1	4	-	0/2/22/22	0/1/1/1
4	GLC	G	2	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	2	GLC	C1-O5-C5	2.74	115.86	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	2	GLC	C1-O5-C5	2.72	115.83	112.19
4	E	2	GLC	O2-C2-C3	2.34	114.99	110.15
4	G	1	GLC	O2-C2-C3	-2.01	105.64	110.38
4	G	2	GLC	C6-C5-C4	-2.01	108.09	113.02

There are no chirality outliers.

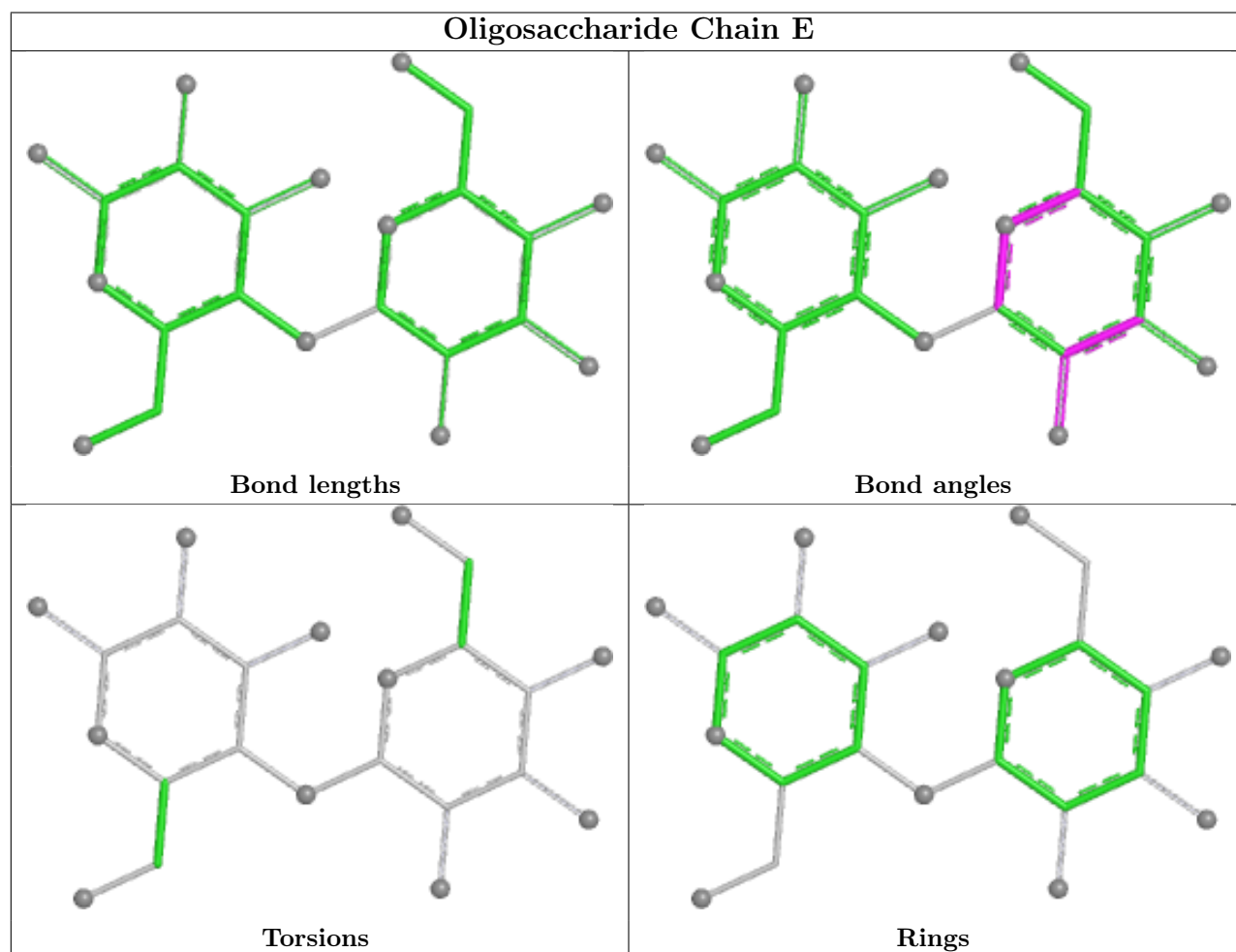
There are no torsion outliers.

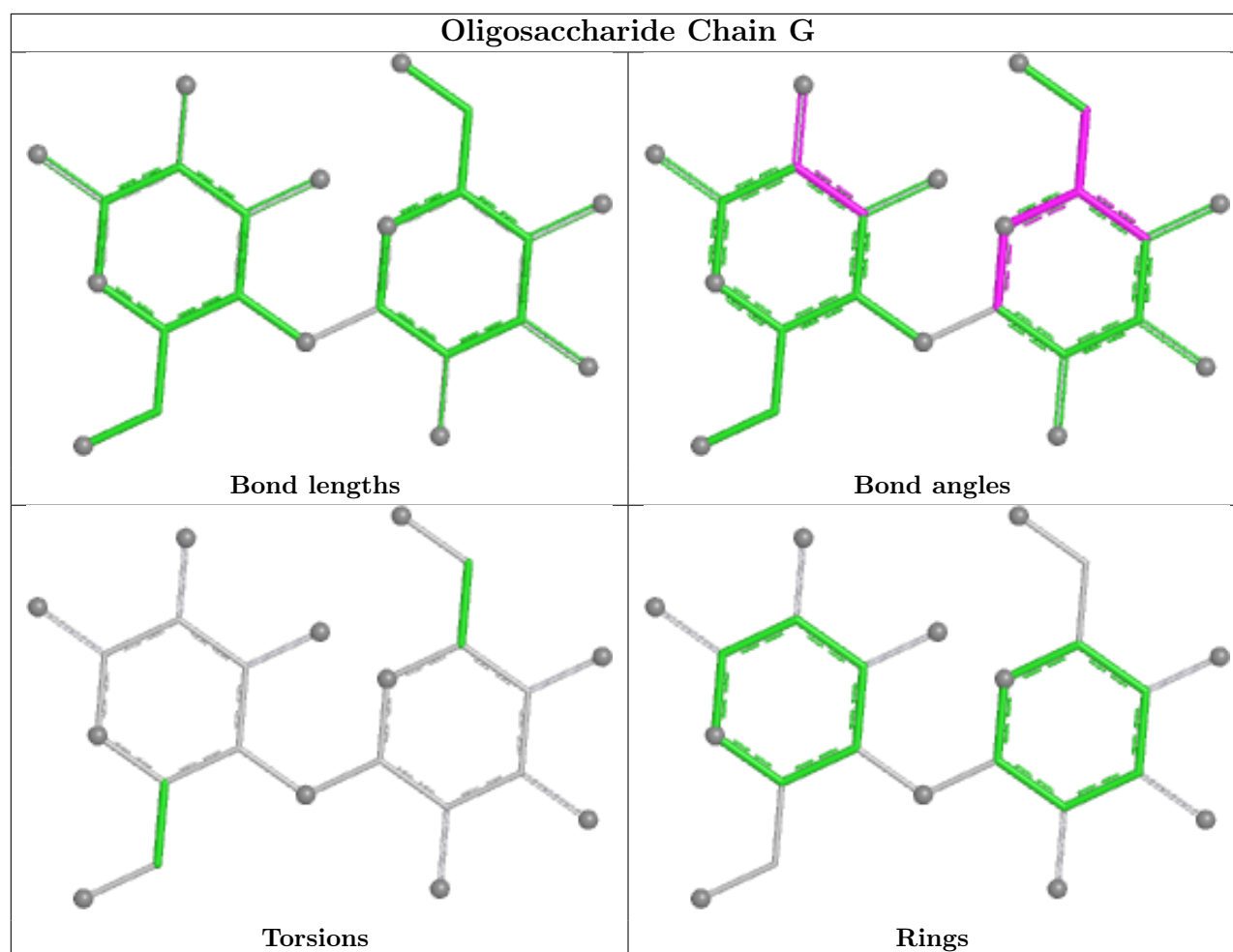
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	2	GLC	2	0
4	E	1	GLC	1	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](#)

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 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	EDO	F	203	-	3,3,3	0.39	0	2,2,2	0.45	0
5	PEG	F	204	-	6,6,6	0.95	0	5,5,5	0.55	0
5	PEG	A	402	-	6,6,6	0.99	0	5,5,5	0.71	0
5	PEG	D	902	-	6,6,6	1.12	0	5,5,5	0.75	0
5	PEG	B	402	-	6,6,6	0.88	0	5,5,5	0.41	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
7	EDO	F	203	-	-	0/1/1/1	-
5	PEG	F	204	-	-	0/4/4/4	-
5	PEG	A	402	-	-	0/4/4/4	-
5	PEG	D	902	-	-	3/4/4/4	-
5	PEG	B	402	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	402	PEG	O1-C1-C2-O2
5	D	902	PEG	O1-C1-C2-O2
5	D	902	PEG	C1-C2-O2-C3
5	B	402	PEG	O2-C3-C4-O4
5	D	902	PEG	C4-C3-O2-C2

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	203	EDO	3	0
5	D	902	PEG	2	0
5	B	402	PEG	2	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	383/383 (100%)	0.35	21 (5%) 30 29	16, 50, 89, 101	5 (1%)
1	B	381/383 (99%)	0.46	17 (4%) 38 37	29, 57, 89, 103	5 (1%)
2	C	199/199 (100%)	-0.16	3 (1%) 72 73	29, 43, 69, 98	0
2	D	199/199 (100%)	-0.02	3 (1%) 72 73	31, 45, 72, 111	0
3	F	143/151 (94%)	0.14	4 (2%) 55 55	24, 49, 73, 104	2 (1%)
3	H	151/151 (100%)	0.33	10 (6%) 24 23	32, 55, 85, 93	1 (0%)
All	All	1456/1466 (99%)	0.24	58 (3%) 42 42	16, 50, 85, 111	13 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	381[A]	GLU	8.4
3	H	151	LEU	5.3
1	B	369	ALA	4.6
3	H	145	THR	4.5
1	B	380[A]	GLY	3.6
2	D	94	SER	3.4
3	F	142	SER	3.4
1	A	383[A]	ARG	3.2
3	F	143	SER	3.2
1	B	174	ASN	3.2
1	A	244	GLY	3.1
3	H	147	ARG	3.1
3	H	77	ARG	2.9
1	B	348	VAL	2.9
1	B	342	TYR	2.8
3	F	141	ARG	2.8
2	D	225	VAL	2.8
1	A	118	TYR	2.8
1	A	144	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	351	ALA	2.6
1	A	142	ALA	2.6
1	B	201	LYS	2.6
1	B	365	ALA	2.5
1	B	368	ASN	2.5
1	B	382[A]	GLU	2.5
1	A	147	ALA	2.5
3	H	148	GLU	2.5
1	B	142	ALA	2.5
1	A	214	ALA	2.4
2	D	95	SER	2.4
1	B	355	ARG	2.4
1	A	382[A]	GLU	2.4
3	H	142	SER	2.4
3	H	141	ARG	2.4
1	A	224	ALA	2.4
1	B	135	ALA	2.4
2	C	94	SER	2.4
1	A	245	VAL	2.4
1	A	243	TYR	2.3
1	A	117	ILE	2.3
1	A	236	ILE	2.3
3	F	1	MET	2.2
3	H	149	THR	2.2
3	H	143	SER	2.2
1	A	349	ILE	2.1
1	B	144	GLY	2.1
1	B	207	ALA	2.1
2	C	289	LEU	2.1
1	A	134	PRO	2.1
1	A	361	ALA	2.1
3	H	10[A]	ARG	2.1
1	A	311	GLU	2.0
1	A	123	LEU	2.0
1	B	123	LEU	2.0
1	A	143	LYS	2.0
2	C	95	SER	2.0
1	A	122	LEU	2.0
1	A	133	ILE	2.0

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

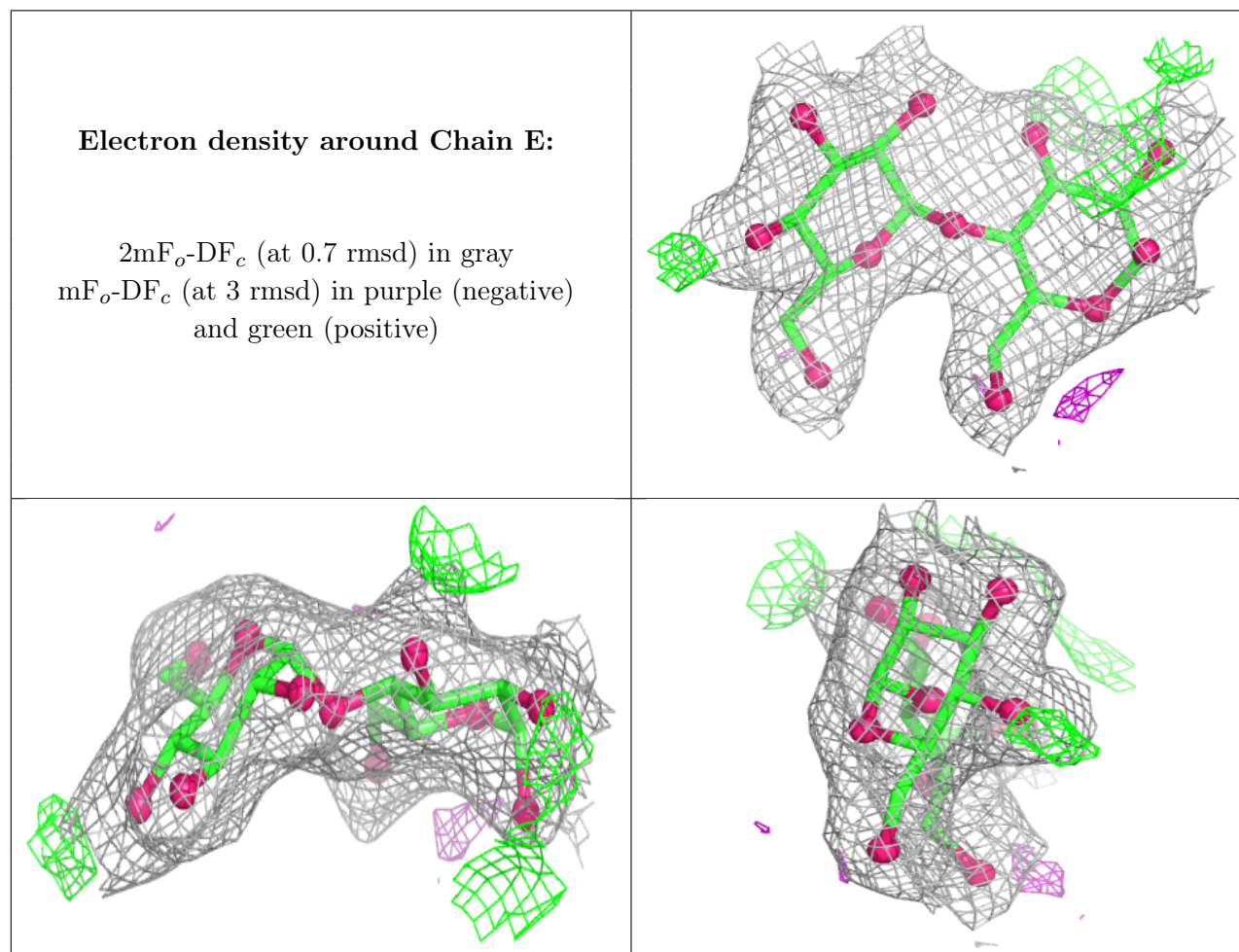
There are no non-standard protein/DNA/RNA residues in this entry.

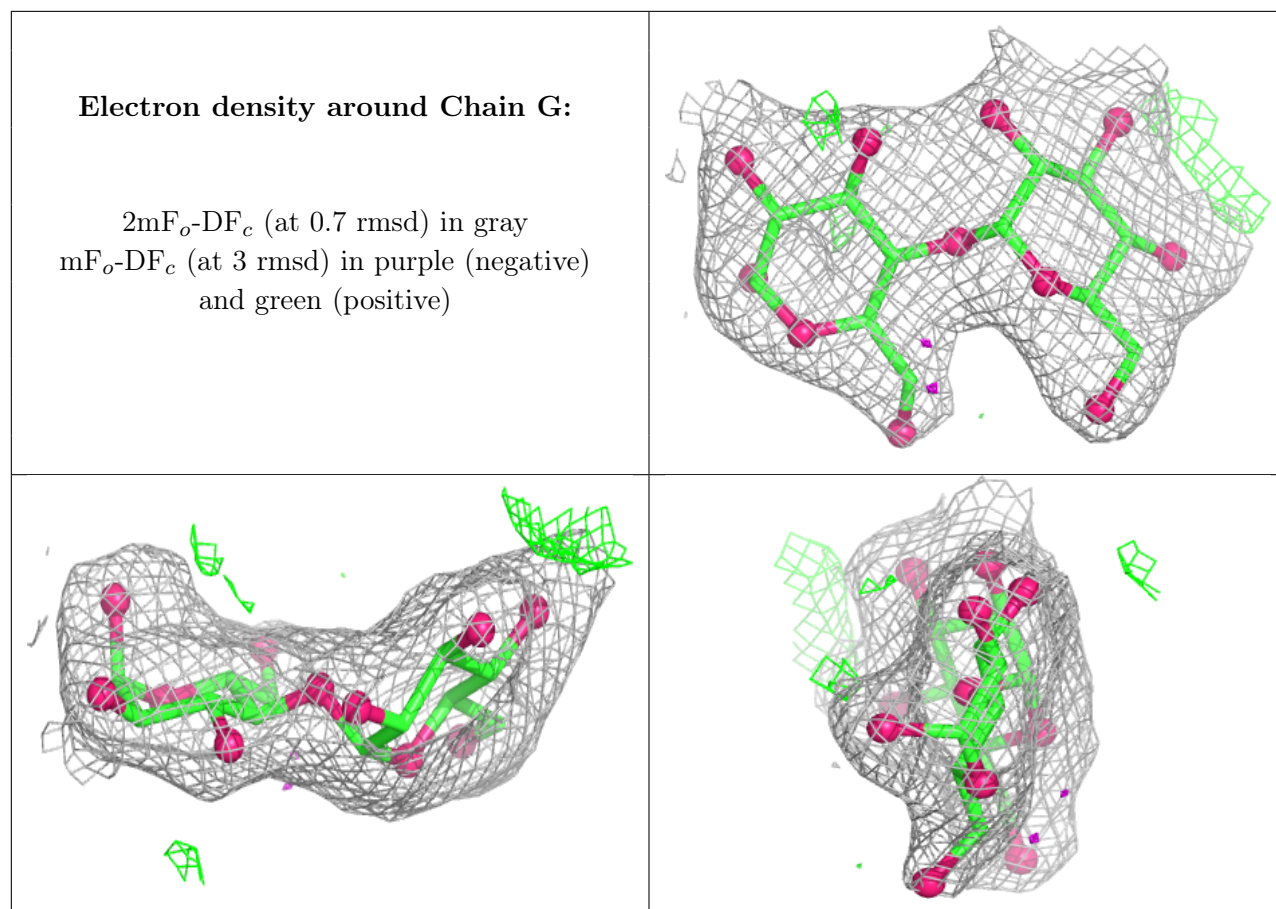
6.3 Carbohydrates [i](#)

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
4	GLC	E	1	12/12	-	-	33,40,47,48	0
4	GLC	E	2	11/12	-	-	32,36,41,43	0
4	GLC	G	1	12/12	0.94	0.09	44,51,54,63	0
4	GLC	G	2	11/12	0.97	0.06	44,47,50,53	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 ⓘ

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
5	PEG	B	402	7/7	0.80	0.13	56,57,62,64	0
5	PEG	D	902	7/7	0.86	0.15	41,45,54,60	0
5	PEG	A	402	7/7	0.87	0.14	32,48,55,56	0
5	PEG	F	204	7/7	0.92	0.12	43,49,52,61	0
6	ZN	H	202	1/1	0.93	0.07	58,58,58,58	0
7	EDO	F	203	4/4	0.94	0.13	50,54,54,55	0
6	ZN	F	202	1/1	0.96	0.05	49,49,49,49	0
6	ZN	H	201	1/1	0.99	0.02	42,42,42,42	0
6	ZN	F	201	1/1	0.99	0.02	47,47,47,47	0
6	ZN	C	900	1/1	0.99	0.04	42,42,42,42	0
6	ZN	D	901	1/1	1.00	0.02	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.