wwPDB X-ray Structure Validation Summary Report (i)

Nov 13, 2023 – 07:03 PM JST

PDB ID	:	5XQG
Title	:	Crystal structure of a PL 26 exo-rhamnogalacturonan lyase from Penicillium chrysogenum complexed with unsaturated galacturonosyl rhamnose
Authors	:	Kunishige, Y.; Iwai, M.; Tada, T.; Nishimura, S.; Sakamoto, T.
Deposited on	:	2017-06-07
Resolution	:	2.74 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

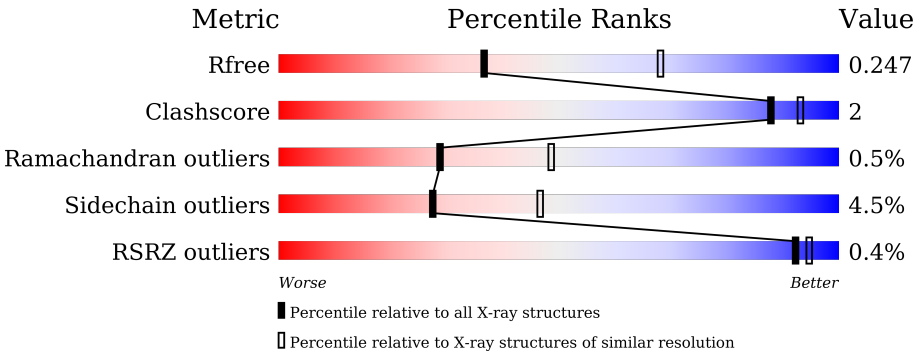
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.74 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}	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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 <=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	906	89% 9% ••
1	B	906	90% 8% ••
1	C	906	89% 8% ••
1	D	906	89% 8% ••
1	E	906	90% 8% ••
1	F	906	92% 7% ••

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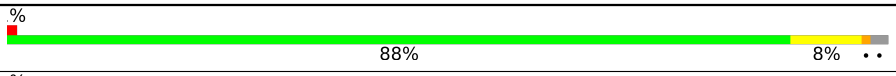
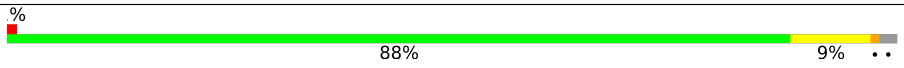
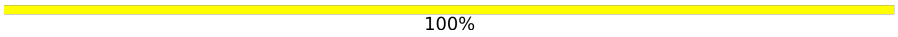
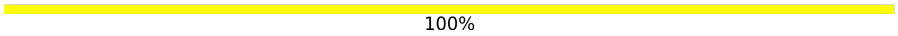
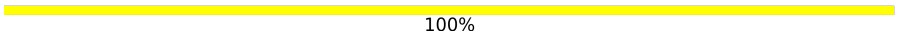
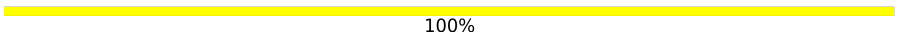
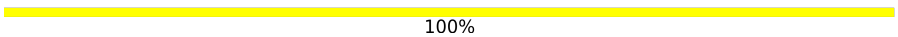
Mol	Chain	Length	Quality of chain
1	G	906	
1	H	906	
2	I	2	
2	J	2	
2	K	2	
2	L	2	
2	M	2	
2	N	2	
2	O	2	
2	P	2	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 57208 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 Pcrglx protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	896	Total	C	N	O	S	0	1	0
			7025	4479	1178	1362	6			
1	B	896	Total	C	N	O	S	0	2	0
			7052	4492	1182	1372	6			
1	C	885	Total	C	N	O	S	0	5	0
			7007	4473	1176	1352	6			
1	D	884	Total	C	N	O	S	0	6	0
			6994	4464	1174	1350	6			
1	E	899	Total	C	N	O	S	0	1	0
			7054	4493	1183	1372	6			
1	F	900	Total	C	N	O	S	0	0	0
			7040	4487	1183	1364	6			
1	G	888	Total	C	N	O	S	0	1	0
			6989	4460	1170	1353	6			
1	H	888	Total	C	N	O	S	0	1	0
			6997	4462	1174	1355	6			

- Molecule 2 is an oligosaccharide called 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	2	Total	C	O		0	0	0
			22	12	10				
2	J	2	Total	C	O		0	0	0
			22	12	10				
2	K	2	Total	C	O		0	0	0
			22	12	10				
2	L	2	Total	C	O		0	0	0
			22	12	10				

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	M	2	Total C O 22 12 10	0	0	0
2	N	2	Total C O 22 12 10	0	0	0
2	O	2	Total C O 22 12 10	0	0	0
2	P	2	Total C O 22 12 10	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	D	1	Total Ca 1 1	0	0
3	E	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0
3	G	1	Total Ca 1 1	0	0
3	H	1	Total Ca 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	122	Total O 122 122	0	0
4	B	128	Total O 128 128	0	0
4	C	122	Total O 122 122	0	0
4	D	95	Total O 95 95	0	0
4	E	122	Total O 122 122	0	0

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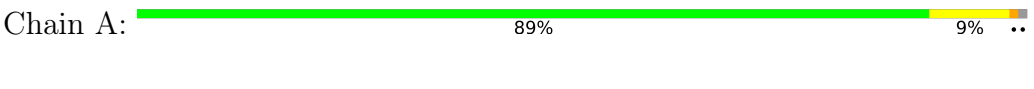
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	116	Total O 116 116	0	0
4	G	72	Total O 72 72	0	0
4	H	89	Total O 89 89	0	0

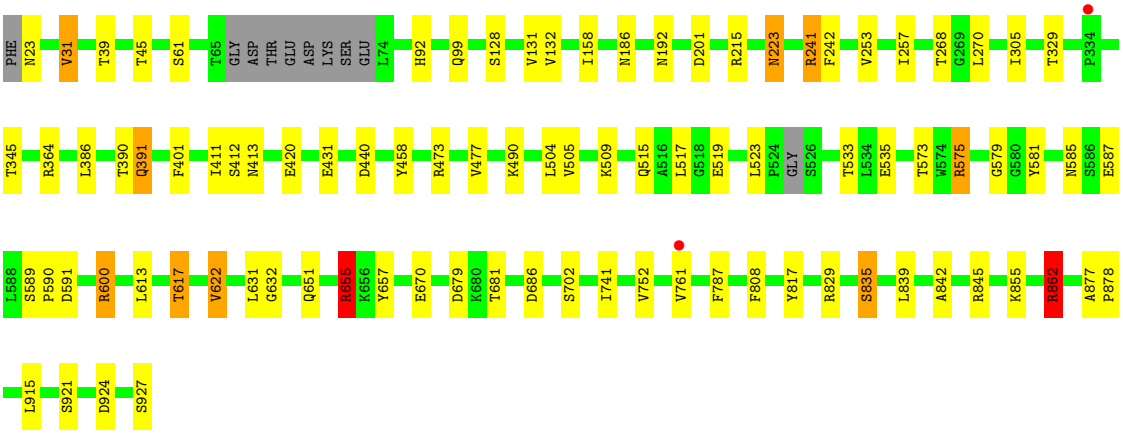
3 Residue-property plots (i)

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: Pcrglx protein

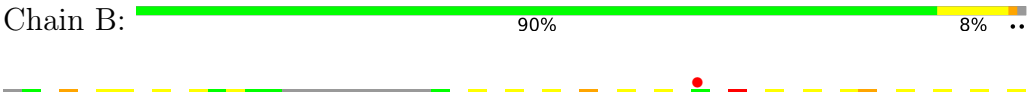
Chain A:

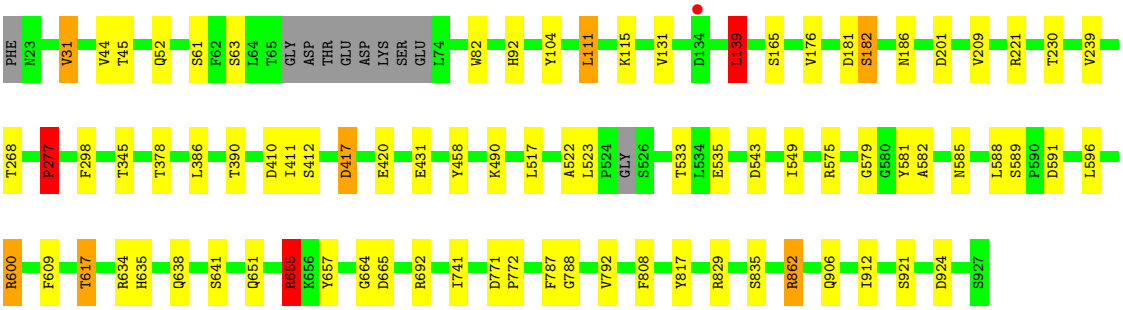




• Molecule 1: Pcrglx protein

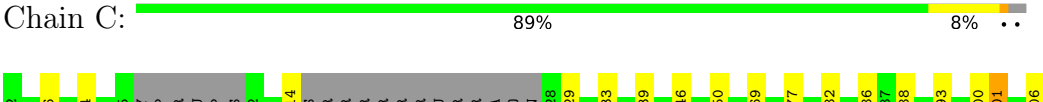
Chain B:

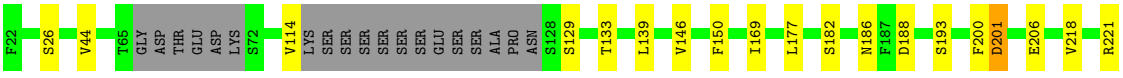


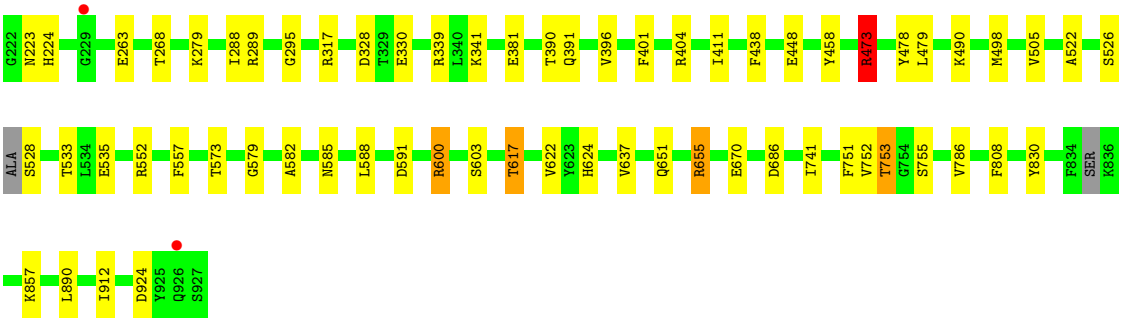


• Molecule 1: Pcrglx protein

Chain C:

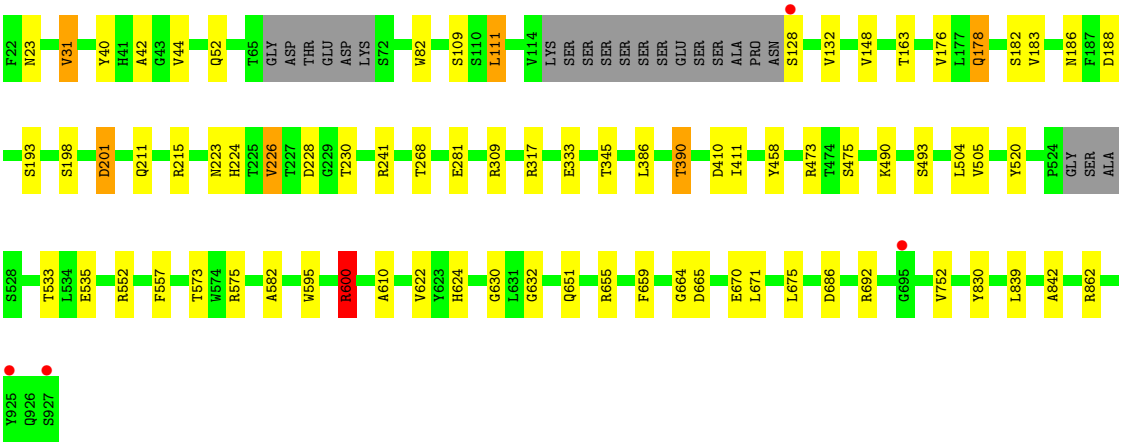






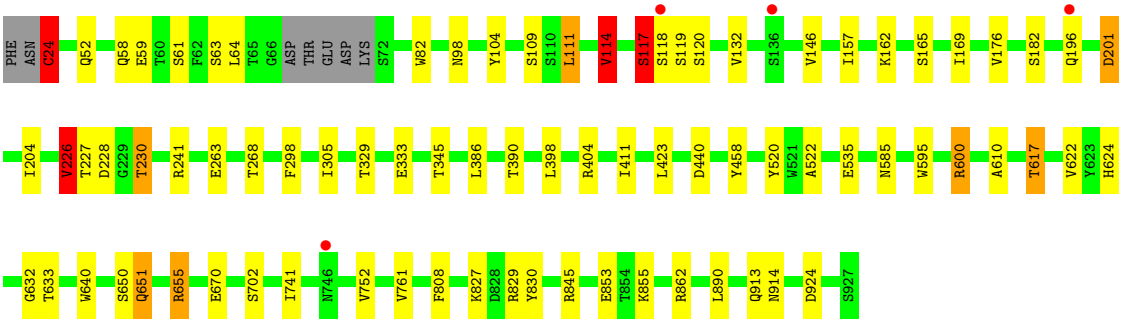
• Molecule 1: Pcrglx protein

Chain D:



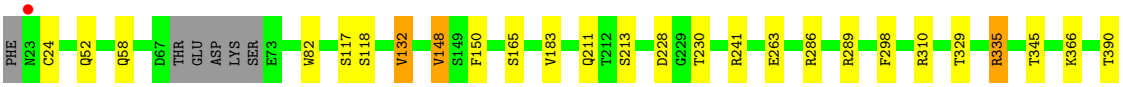
• Molecule 1: Pcrglx protein

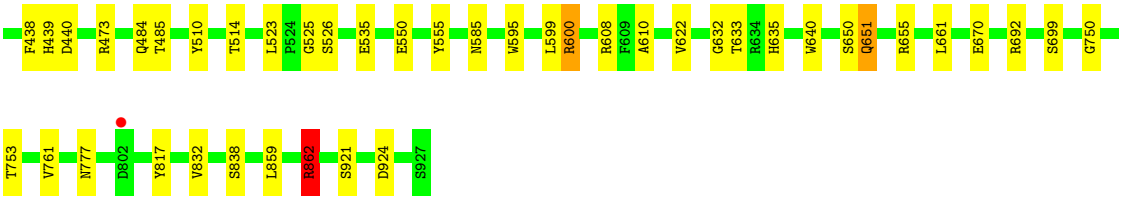
Chain E:



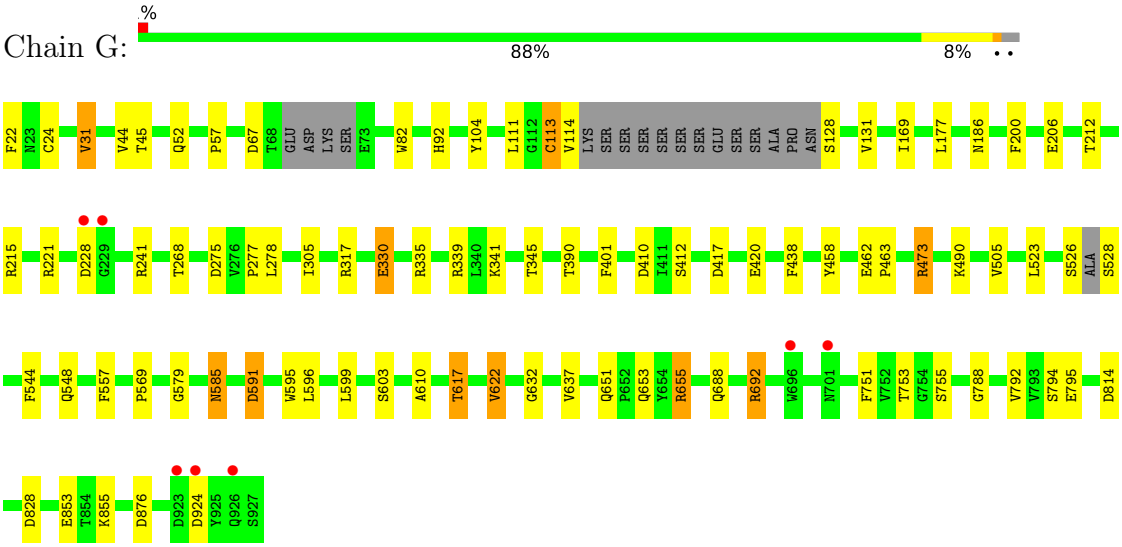
• Molecule 1: Pcrglx protein

Chain F:

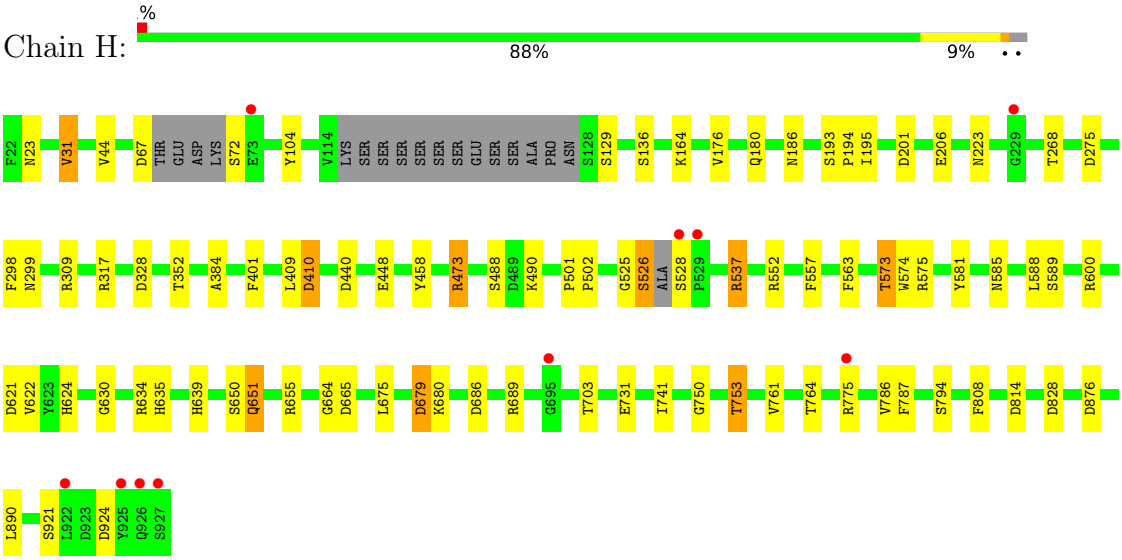




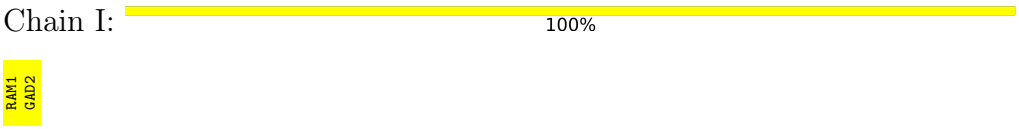
• Molecule 1: Pcrglx protein



• Molecule 1: Pcrglx protein

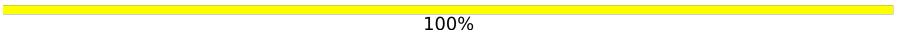


• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose



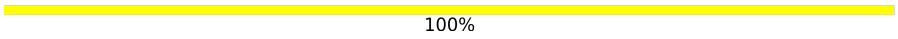
• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain J:



• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain K:

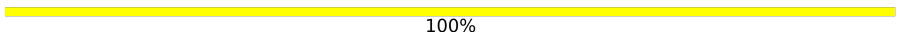


• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain L:

• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain M:



• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

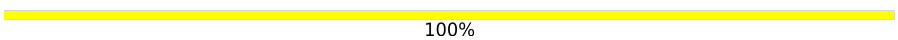
Chain N:

• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain O:

• Molecule 2: 2,6-anhydro-3-deoxy-L-threo-hex-2-enonic acid-(1-2)-alpha-L-rhamnopyranose

Chain P:



RAM1
GAD2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	167.88Å 171.94Å 342.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	171.19 – 2.74 49.16 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.7 (171.19-2.74) 99.7 (49.16-2.74)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.08 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.188 , 0.247 0.192 , 0.247	Depositor DCC
R_{free} test set	12767 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 25.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	57208	wwPDB-VP
Average B, all atoms (Å^2)	30.0	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 46.86 % 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 1.0780e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, RAM, GAD

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	0.73	1/7232 (0.0%)	0.89	17/9878 (0.2%)
1	B	0.76	4/7256 (0.1%)	0.88	16/9907 (0.2%)
1	C	0.72	0/7223	0.86	8/9857 (0.1%)
1	D	0.71	0/7218	0.87	13/9854 (0.1%)
1	E	0.74	1/7262 (0.0%)	0.89	11/9914 (0.1%)
1	F	0.72	0/7245	0.89	9/9892 (0.1%)
1	G	0.70	0/7196	0.88	12/9822 (0.1%)
1	H	0.73	0/7204	0.89	17/9833 (0.2%)
All	All	0.73	6/57836 (0.0%)	0.88	103/78957 (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	E	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	24	CYS	C-N	10.18	1.57	1.34
1	B	201[A]	ASP	CB-CG	6.94	1.66	1.51
1	B	201[B]	ASP	CB-CG	6.94	1.66	1.51
1	B	431	GLU	CG-CD	5.55	1.60	1.51
1	B	431	GLU	CD-OE2	5.49	1.31	1.25

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	24	CYS	O-C-N	-21.61	88.12	122.70
1	A	600	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	E	600	ARG	NE-CZ-NH1	8.72	124.66	120.30
1	A	655	ARG	NE-CZ-NH2	8.25	124.42	120.30
1	F	600	ARG	NE-CZ-NH1	7.79	124.20	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	24	CYS	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	7025	0	6584	31	0
1	B	7052	0	6618	30	0
1	C	7007	0	6587	27	0
1	D	6994	0	6572	21	1
1	E	7054	0	6633	34	1
1	F	7040	0	6601	21	0
1	G	6989	0	6553	31	0
1	H	6997	0	6567	26	0
2	I	22	0	17	0	0
2	J	22	0	17	0	0
2	K	22	0	16	0	0
2	L	22	0	17	0	0
2	M	22	0	17	0	0
2	N	22	0	17	0	0
2	O	22	0	17	2	0
2	P	22	0	17	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	122	0	0	2	0
4	B	128	0	0	1	0
4	C	122	0	0	1	0
4	D	95	0	0	0	0
4	E	122	0	0	2	0
4	F	116	0	0	0	0
4	G	72	0	0	1	0
4	H	89	0	0	1	0
All	All	57208	0	52850	217	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 2.

The worst 5 of 217 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:G:24:CYS:CB	1:G:113:CYS:SG	2.14	1.34
1:G:526:SER:HG	1:G:528:SER:N	1.56	1.04
1:E:201:ASP:OD2	1:E:227:THR:HG21	1.73	0.88
1:G:24:CYS:HG	1:G:113:CYS:CB	1.95	0.78
1:E:119:SER:O	1:E:120:SER:C	2.23	0.76

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)
1:D:211:GLN:O	1:E:117:SER:CB[3_644]	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	891/906 (98%)	850 (95%)	37 (4%)	4 (0%)	34	55
1	B	892/906 (98%)	856 (96%)	31 (4%)	5 (1%)	25	44
1	C	880/906 (97%)	842 (96%)	34 (4%)	4 (0%)	29	48
1	D	882/906 (97%)	830 (94%)	50 (6%)	2 (0%)	47	69
1	E	896/906 (99%)	851 (95%)	41 (5%)	4 (0%)	34	55
1	F	896/906 (99%)	849 (95%)	39 (4%)	8 (1%)	17	32
1	G	881/906 (97%)	839 (95%)	35 (4%)	7 (1%)	19	36
1	H	881/906 (97%)	841 (96%)	37 (4%)	3 (0%)	41	61
All	All	7099/7248 (98%)	6758 (95%)	304 (4%)	37 (0%)	29	48

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	117	SER
1	E	263	GLU
1	F	526	SER
1	A	401	PHE
1	F	24	CYS

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	724/745 (97%)	687 (95%)	37 (5%)	24	41
1	B	731/745 (98%)	704 (96%)	27 (4%)	34	54
1	C	726/745 (97%)	692 (95%)	34 (5%)	26	45
1	D	724/745 (97%)	689 (95%)	35 (5%)	25	44
1	E	732/745 (98%)	700 (96%)	32 (4%)	28	47
1	F	724/745 (97%)	700 (97%)	24 (3%)	38	59
1	G	721/745 (97%)	686 (95%)	35 (5%)	25	43
1	H	724/745 (97%)	686 (95%)	38 (5%)	23	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5806/5960 (97%)	5544 (96%)	262 (4%)	27 47

5 of 262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	164	LYS
1	H	223	ASN
1	H	921	SER
1	C	755	SER
1	C	617	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	98	ASN
1	H	324	GLN
1	F	32	HIS
1	H	186	ASN
1	G	515	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

16 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	RAM	I	1	2	11,11,11	0.53	0	15,16,16	1.41	2 (13%)
2	GAD	I	2	2	10,11,11	2.00	3 (30%)	13,15,15	1.88	3 (23%)
2	RAM	J	1	2	11,11,11	0.42	0	15,16,16	1.18	2 (13%)
2	GAD	J	2	2	10,11,11	2.06	3 (30%)	13,15,15	1.94	3 (23%)
2	RAM	K	1	2	11,11,11	0.55	0	15,16,16	1.26	2 (13%)
2	GAD	K	2	2	10,11,11	2.19	2 (20%)	13,15,15	2.47	5 (38%)
2	RAM	L	1	2	11,11,11	0.54	0	15,16,16	0.87	0
2	GAD	L	2	2	10,11,11	2.03	3 (30%)	13,15,15	2.10	5 (38%)
2	RAM	M	1	2	11,11,11	0.51	0	15,16,16	1.19	2 (13%)
2	GAD	M	2	2	10,11,11	2.20	1 (10%)	13,15,15	2.00	3 (23%)
2	RAM	N	1	2	11,11,11	0.84	0	15,16,16	1.28	0
2	GAD	N	2	2	10,11,11	2.20	1 (10%)	13,15,15	2.63	5 (38%)
2	RAM	O	1	2	11,11,11	0.70	0	15,16,16	1.72	5 (33%)
2	GAD	O	2	2	10,11,11	2.14	1 (10%)	13,15,15	1.57	5 (38%)
2	RAM	P	1	2	11,11,11	0.43	0	15,16,16	1.32	3 (20%)
2	GAD	P	2	2	10,11,11	2.01	1 (10%)	13,15,15	2.25	3 (23%)

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	RAM	I	1	2	-	-	0/1/1/1
2	GAD	I	2	2	-	0/4/17/17	0/1/1/1
2	RAM	J	1	2	-	-	0/1/1/1
2	GAD	J	2	2	-	0/4/17/17	0/1/1/1
2	RAM	K	1	2	-	-	0/1/1/1
2	GAD	K	2	2	-	2/4/17/17	0/1/1/1
2	RAM	L	1	2	-	-	0/1/1/1
2	GAD	L	2	2	-	0/4/17/17	0/1/1/1
2	RAM	M	1	2	-	-	0/1/1/1
2	GAD	M	2	2	-	0/4/17/17	0/1/1/1
2	RAM	N	1	2	-	-	0/1/1/1
2	GAD	N	2	2	-	0/4/17/17	0/1/1/1
2	RAM	O	1	2	-	-	0/1/1/1
2	GAD	O	2	2	-	0/4/17/17	0/1/1/1
2	RAM	P	1	2	-	-	0/1/1/1
2	GAD	P	2	2	-	0/4/17/17	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	2	GAD	O5-C5	5.93	1.45	1.37
2	N	2	GAD	O5-C5	5.89	1.45	1.37
2	K	2	GAD	O5-C5	5.89	1.45	1.37
2	O	2	GAD	O5-C5	5.67	1.45	1.37
2	P	2	GAD	O5-C5	5.10	1.44	1.37

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	K	2	GAD	O5-C5-C4	-6.18	119.59	124.81
2	P	2	GAD	O5-C5-C4	-5.89	119.84	124.81
2	N	2	GAD	O5-C5-C4	-5.77	119.94	124.81
2	J	2	GAD	O5-C5-C4	-5.22	120.40	124.81
2	N	2	GAD	O5-C5-C6	5.09	119.17	111.52

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	2	GAD	O5-C5-C6-O6A
2	K	2	GAD	C4-C5-C6-O6A

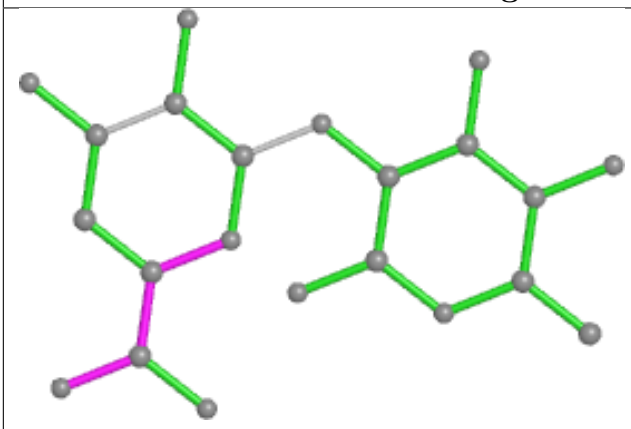
There are no ring outliers.

1 monomer is involved in 2 short contacts:

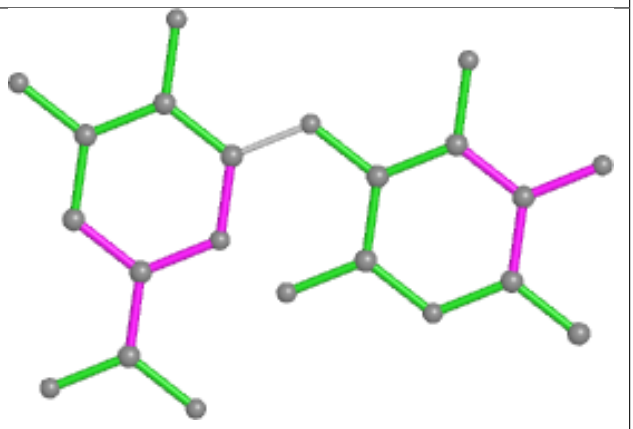
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	1	RAM	2	0

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

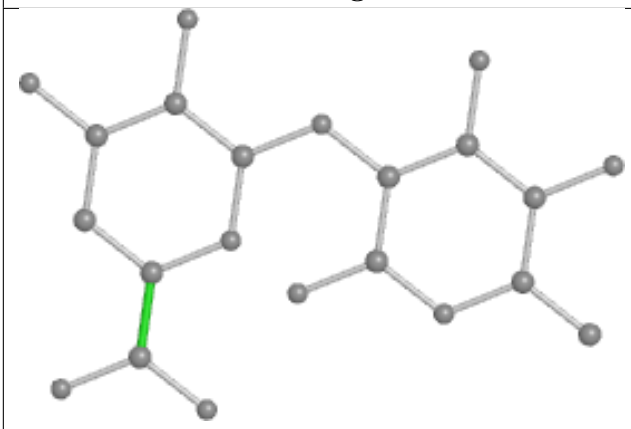
Oligosaccharide Chain I



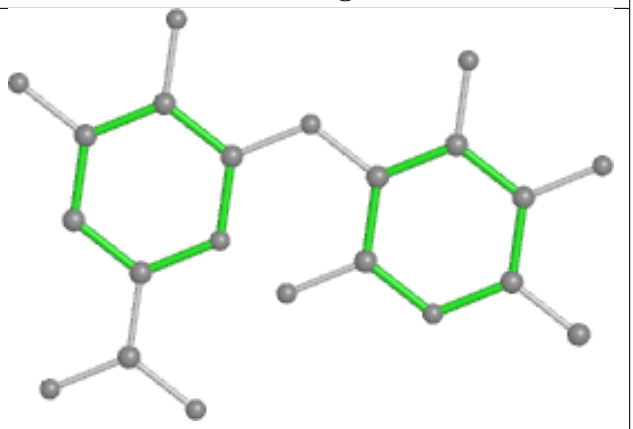
Bond lengths



Bond angles

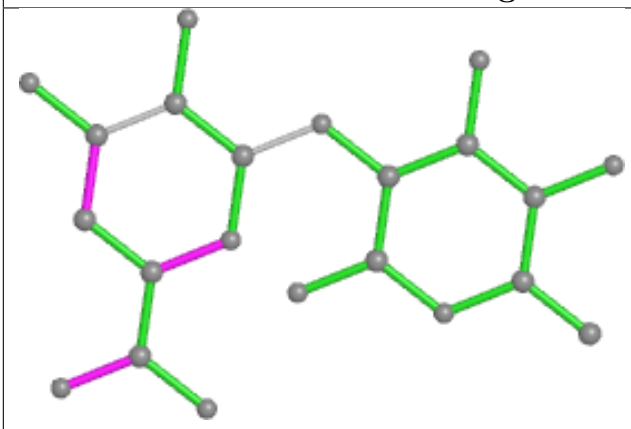


Torsions

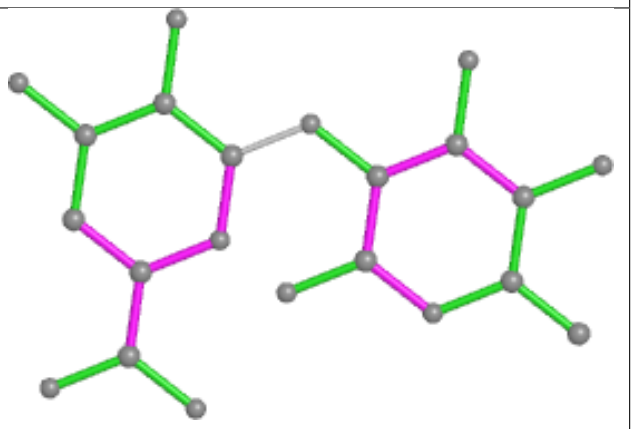


Rings

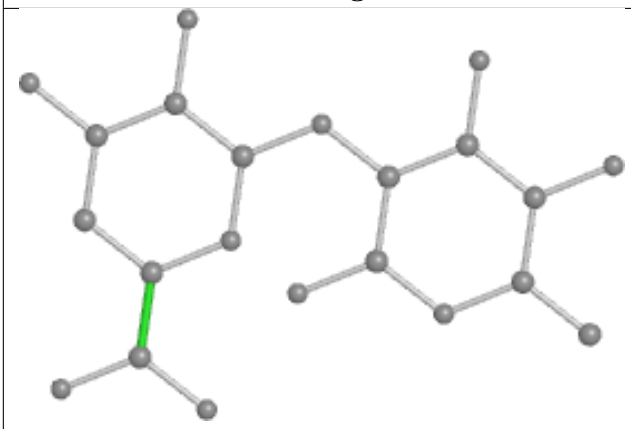
Oligosaccharide Chain J



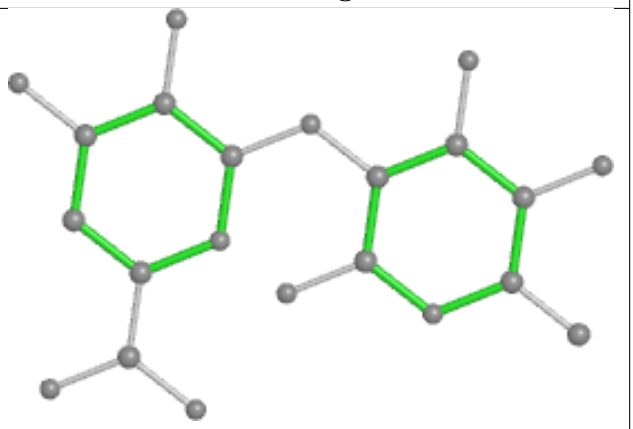
Bond lengths



Bond angles

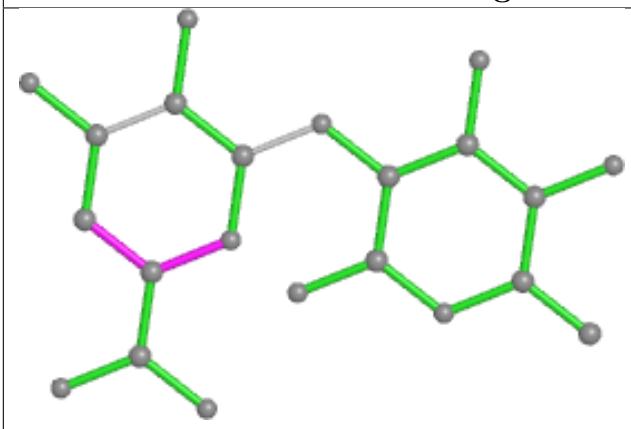


Torsions

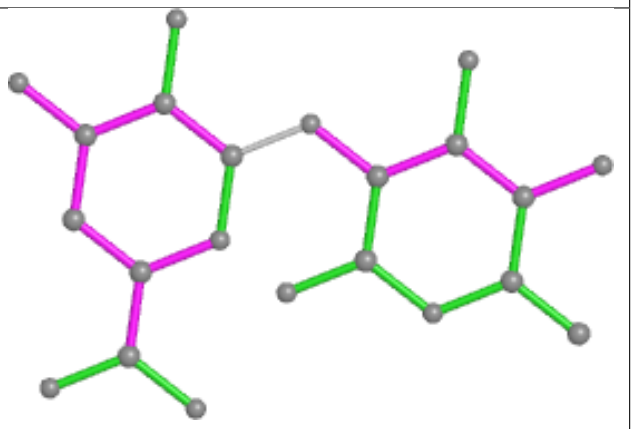


Rings

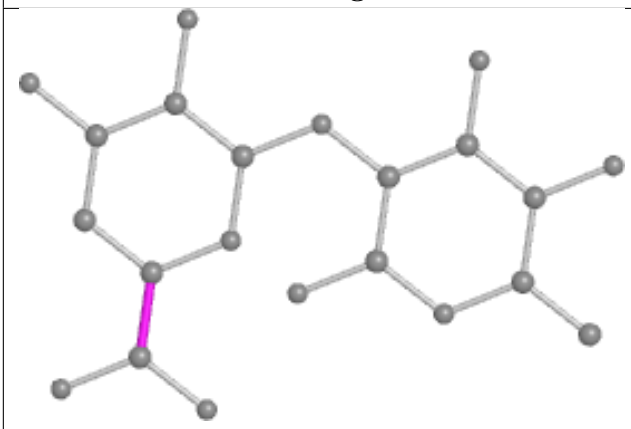
Oligosaccharide Chain K



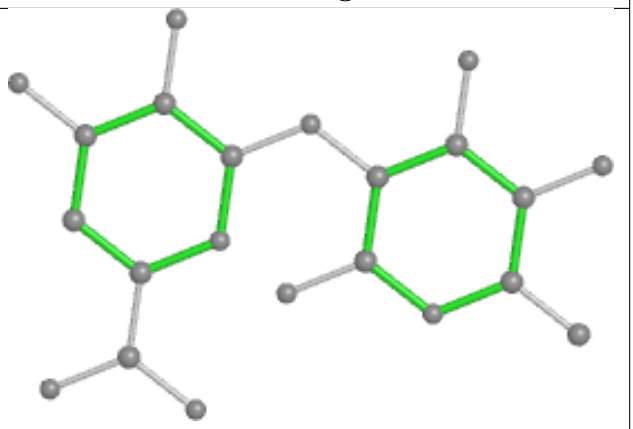
Bond lengths



Bond angles

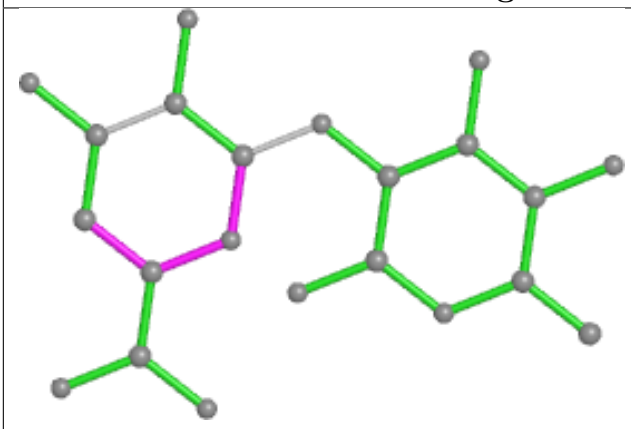


Torsions

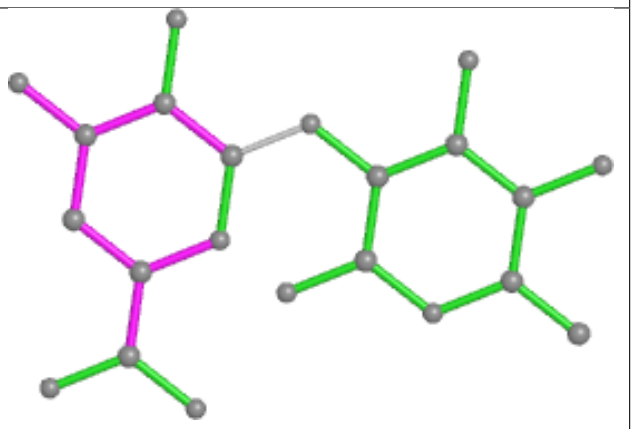


Rings

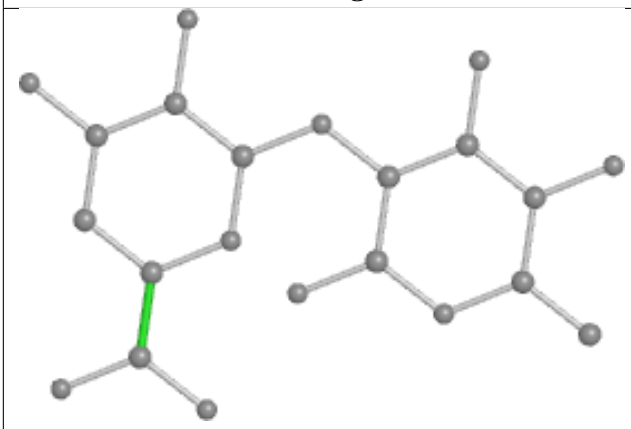
Oligosaccharide Chain L



Bond lengths



Bond angles



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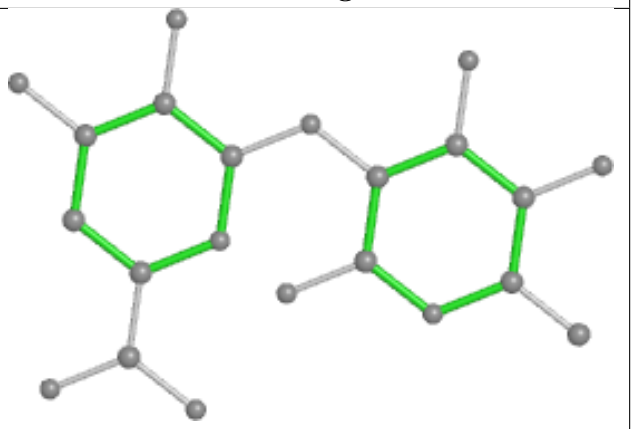
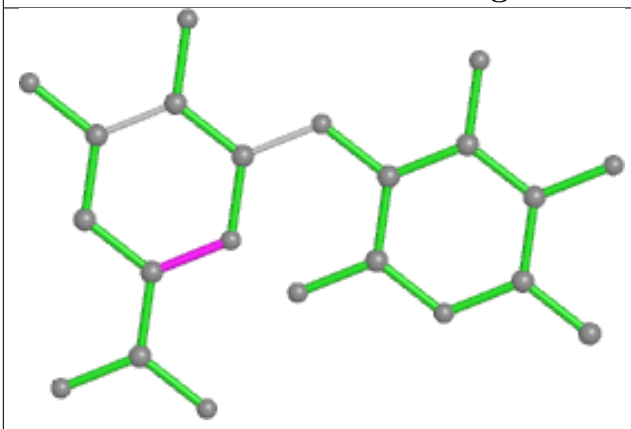
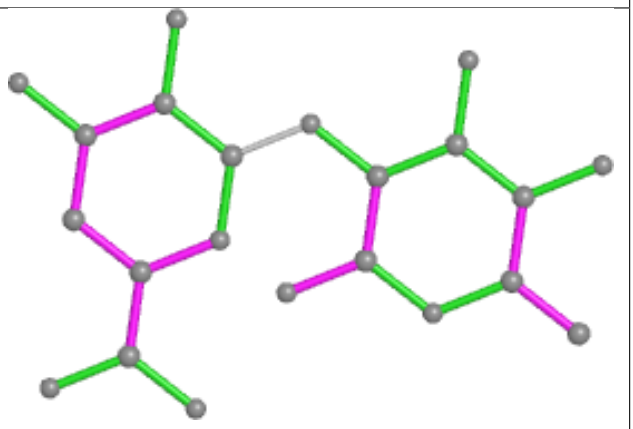


Rings

Oligosaccharide Chain M



Bond lengths



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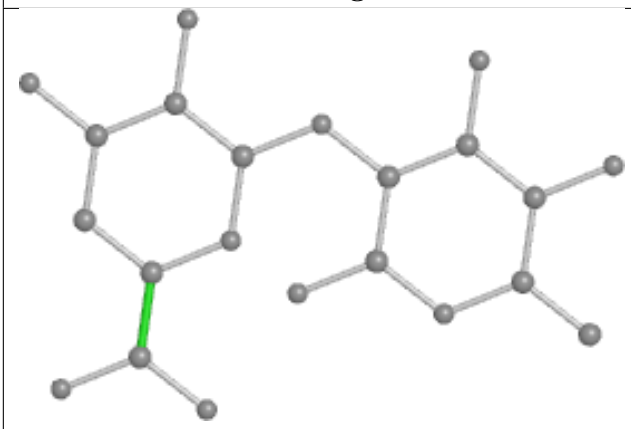

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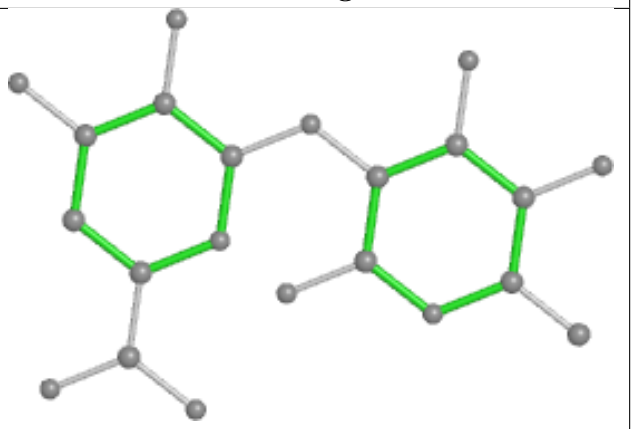
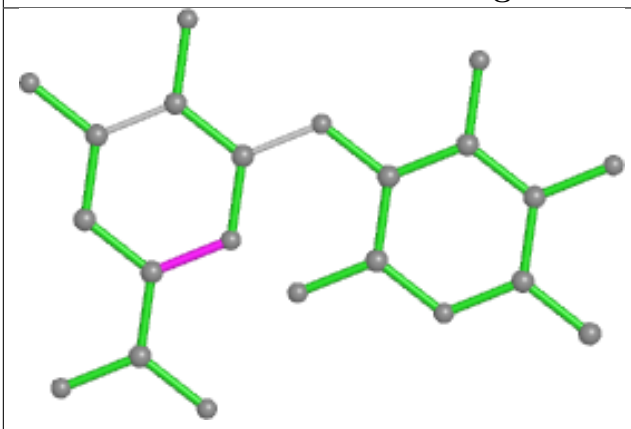


Rings

Oligosaccharide Chain N



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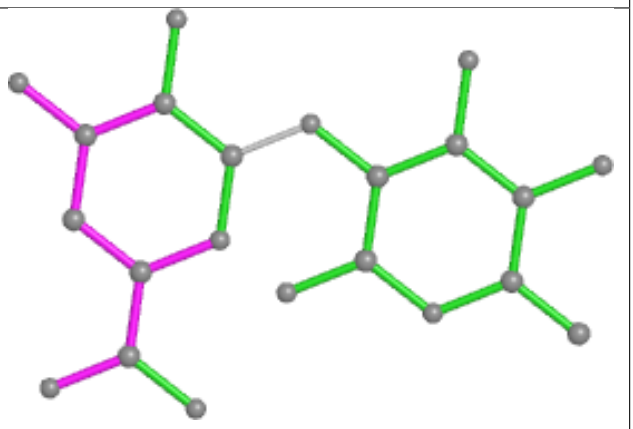
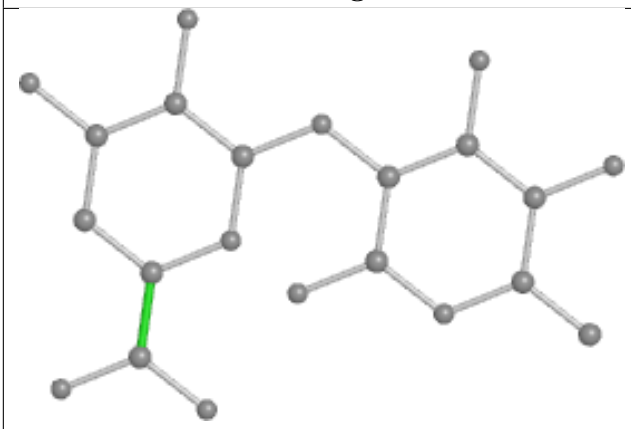


Bond angles



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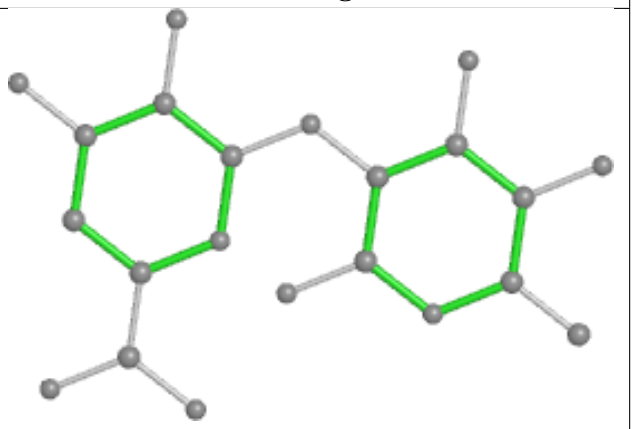
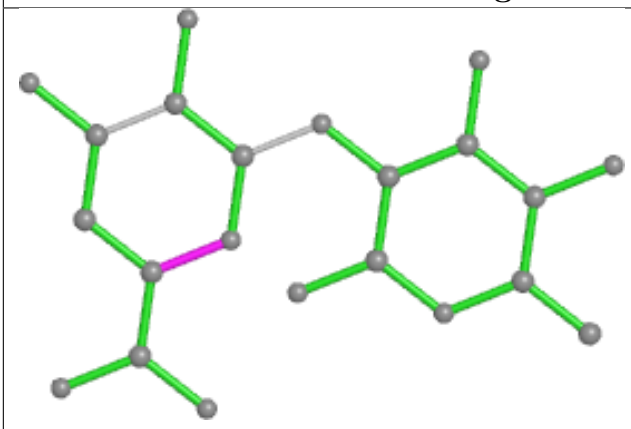


Rings

Oligosaccharide Chain O



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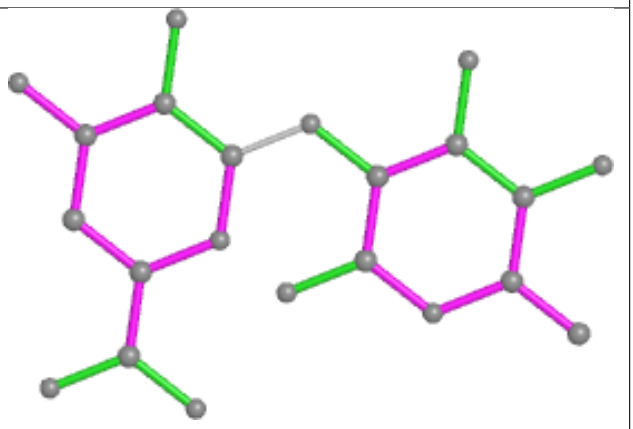
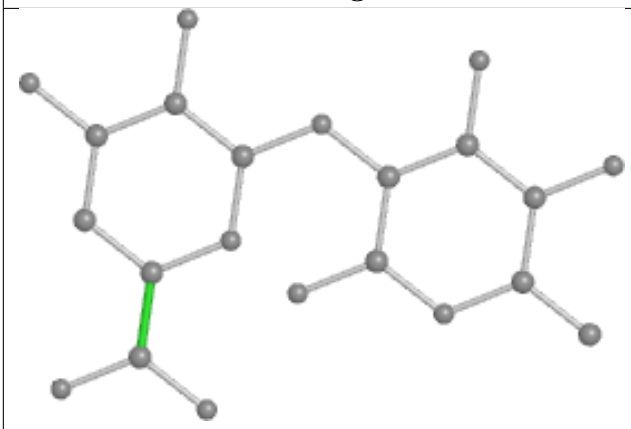
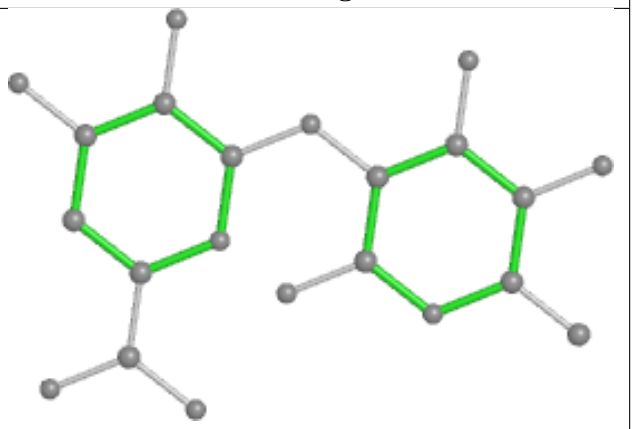


Bond angles

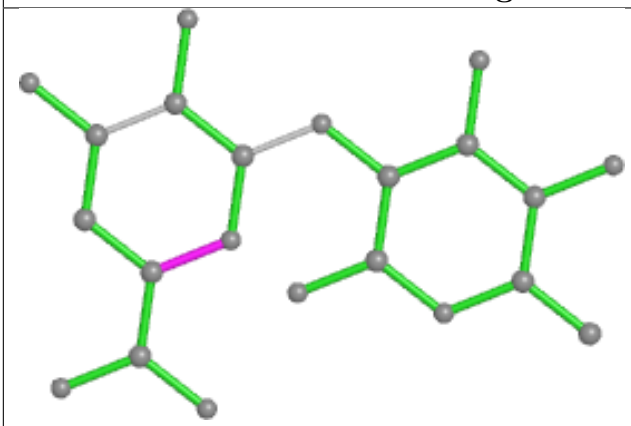


Torsions

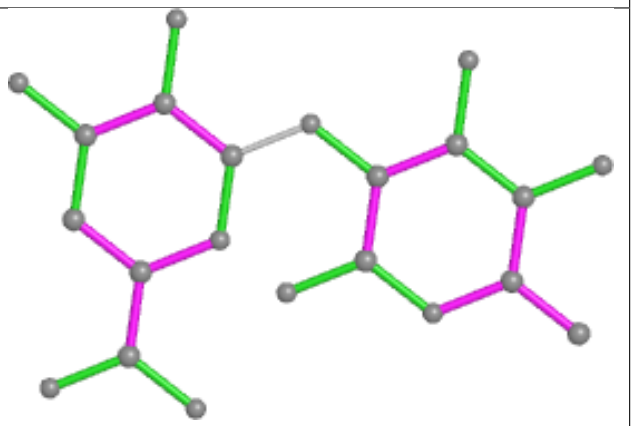


Rings

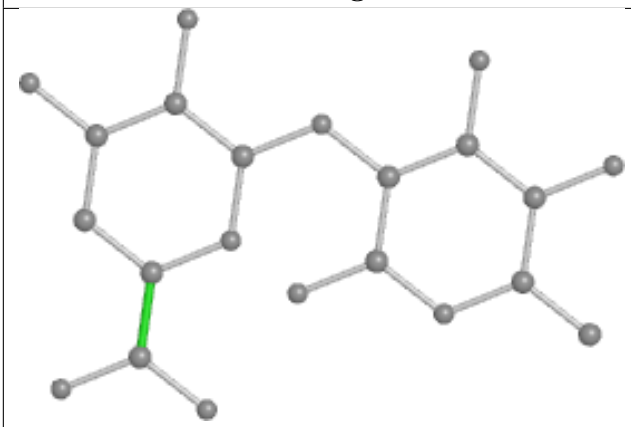
Oligosaccharide Chain P



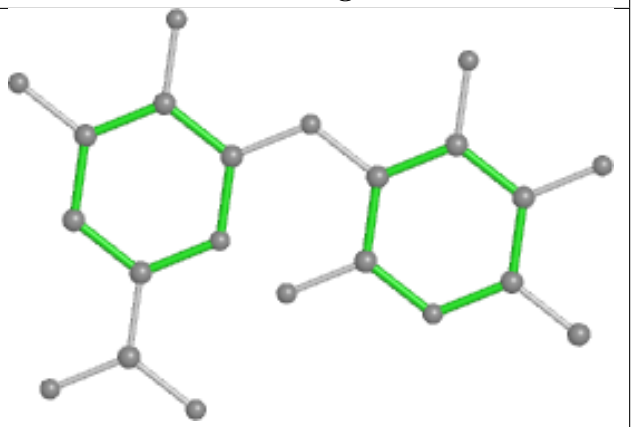
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	896/906 (98%)	-0.47	2 (0%)	95	97	16, 26, 45, 71	0
1	B	896/906 (98%)	-0.47	1 (0%)	95	97	14, 26, 45, 68	0
1	C	885/906 (97%)	-0.44	2 (0%)	95	97	15, 28, 47, 74	0
1	D	884/906 (97%)	-0.42	4 (0%)	91	93	17, 30, 49, 71	0
1	E	899/906 (99%)	-0.38	4 (0%)	92	95	16, 28, 49, 72	0
1	F	900/906 (99%)	-0.42	2 (0%)	95	97	16, 28, 49, 75	0
1	G	888/906 (98%)	-0.30	7 (0%)	86	89	16, 32, 56, 84	0
1	H	888/906 (98%)	-0.30	10 (1%)	80	85	16, 32, 55, 79	0
All	All	7136/7248 (98%)	-0.40	32 (0%)	92	95	14, 29, 50, 84	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	923	ASP	4.4
1	G	926	GLN	3.4
1	H	528	SER	3.2
1	F	23	ASN	3.0
1	E	118	SER	3.0

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

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

6.3 Carbohydrates

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

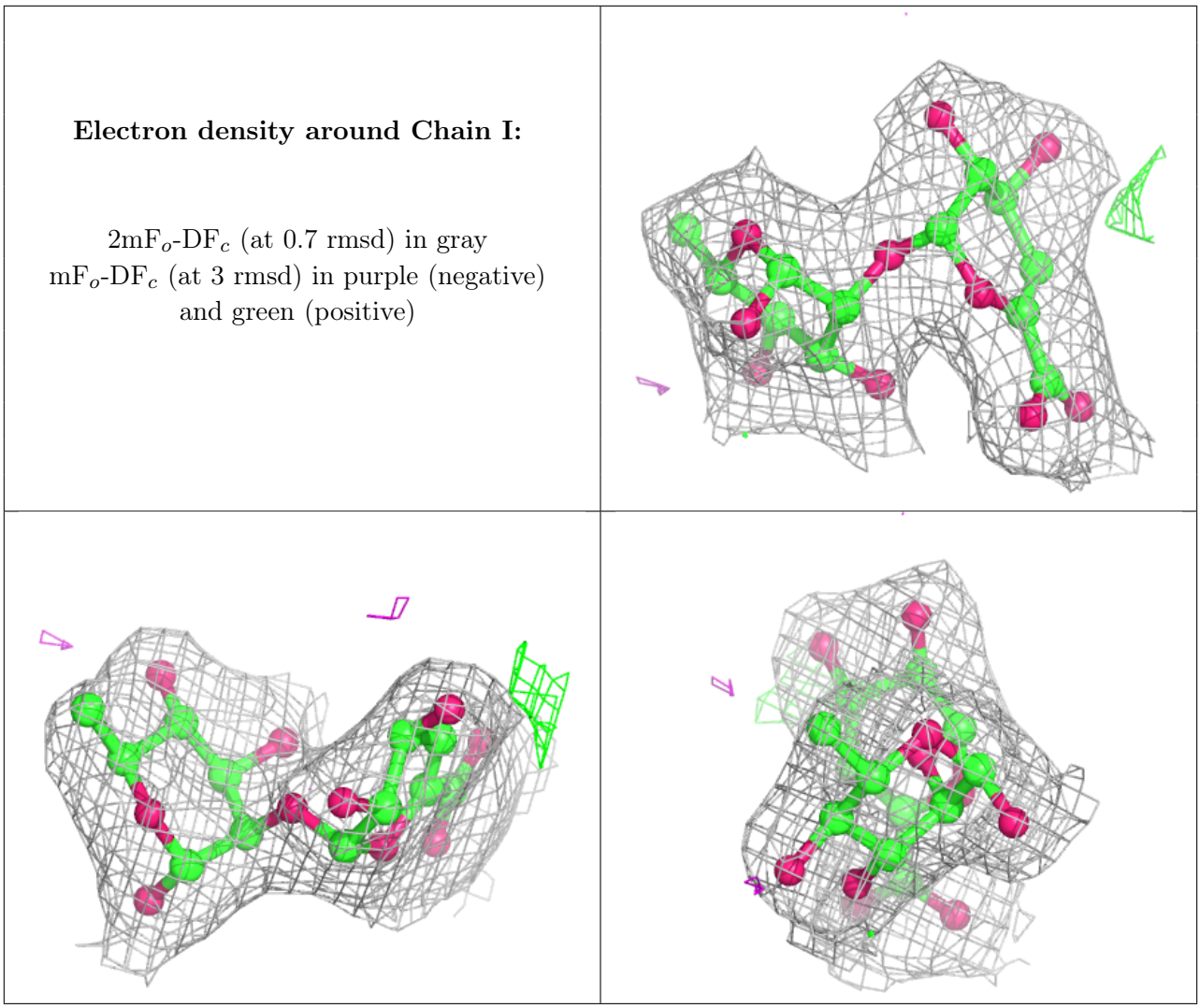
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GAD	K	2	11/11	0.96	0.10	29,32,34,36	0
2	GAD	L	2	11/11	0.96	0.12	27,30,32,34	0
2	GAD	M	2	11/11	0.96	0.12	29,31,33,33	0
2	GAD	N	2	11/11	0.96	0.11	25,29,30,30	0
2	RAM	O	1	11/11	0.96	0.11	40,44,46,50	0
2	GAD	O	2	11/11	0.96	0.12	30,38,42,45	0
2	RAM	K	1	11/11	0.97	0.12	31,34,36,41	0
2	RAM	M	1	11/11	0.97	0.14	26,27,30,34	0
2	RAM	P	1	11/11	0.97	0.12	31,34,36,38	0
2	GAD	P	2	11/11	0.97	0.11	30,35,38,39	0
2	RAM	N	1	11/11	0.98	0.12	23,24,26,29	0
2	GAD	I	2	11/11	0.98	0.12	19,23,24,26	0
2	RAM	L	1	11/11	0.98	0.11	28,32,34,37	0
2	RAM	J	1	11/11	0.98	0.12	21,23,24,25	0
2	GAD	J	2	11/11	0.98	0.10	22,25,26,29	0
2	RAM	I	1	11/11	0.98	0.11	21,23,24,24	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.

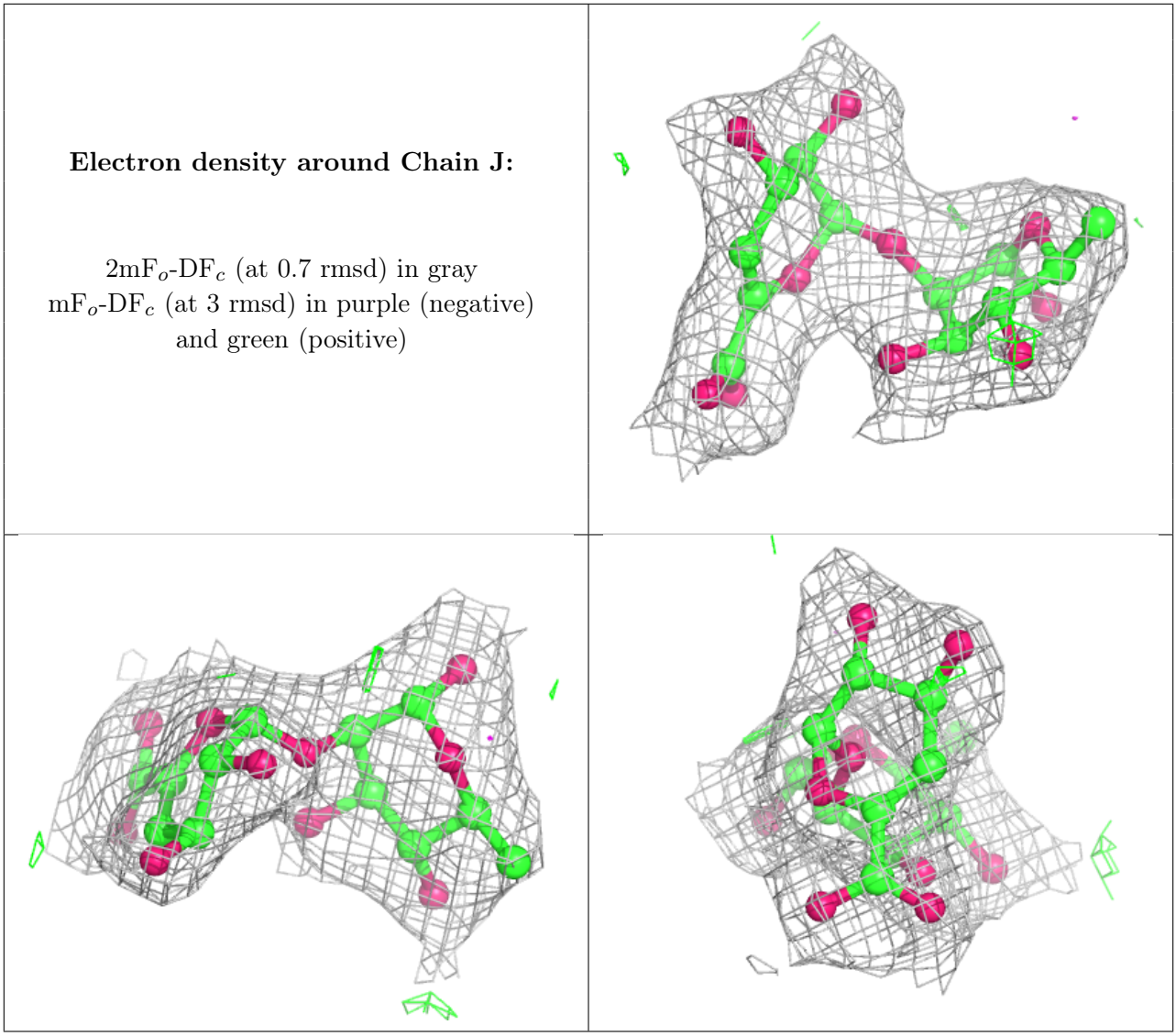
Electron density around Chain I:

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



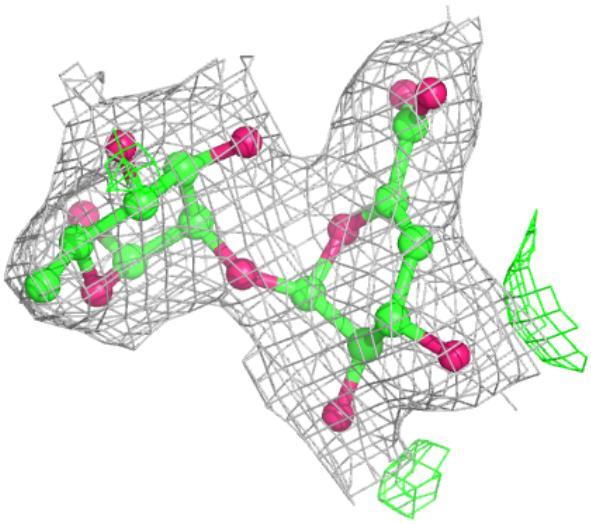
Electron density around Chain J:

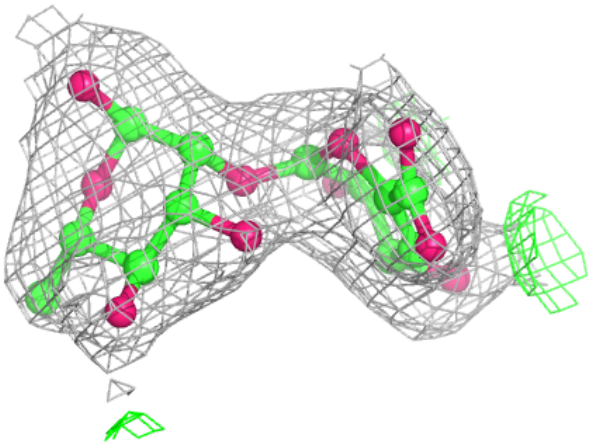
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

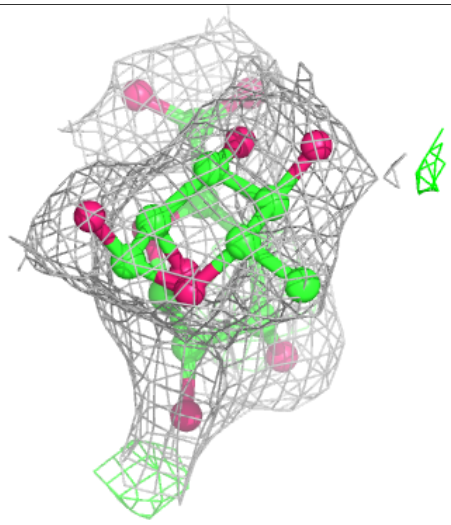


Electron density around Chain K:

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

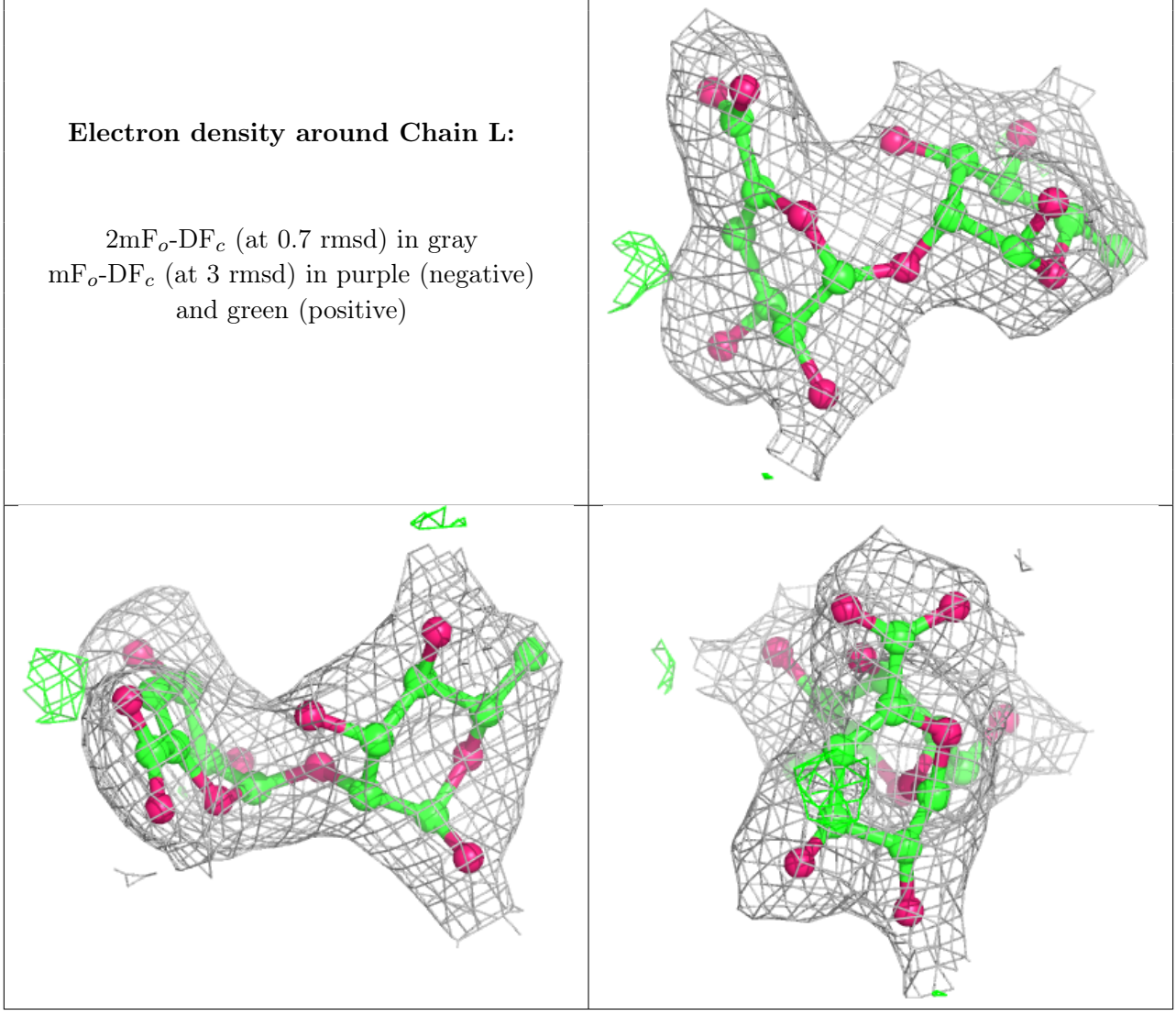






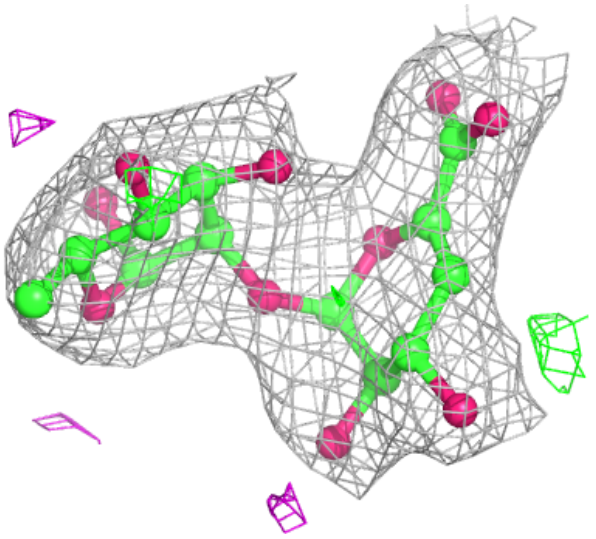
Electron density around Chain L:

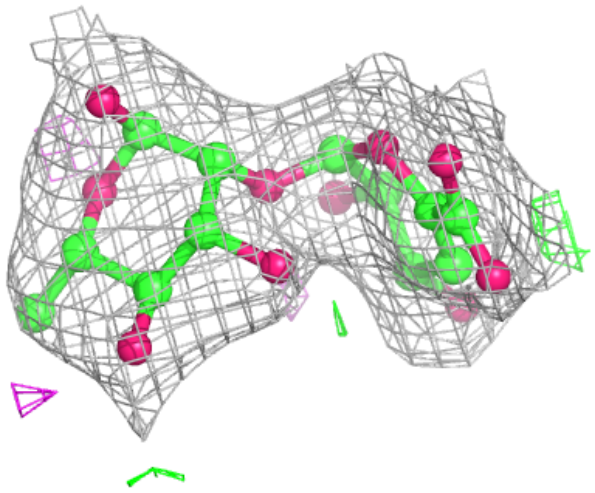
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

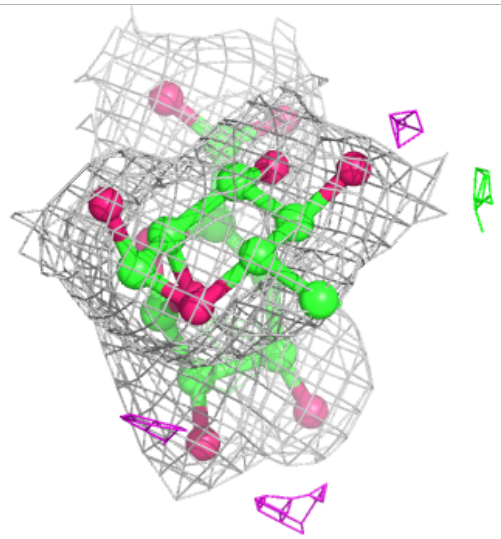


Electron density around Chain M:

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

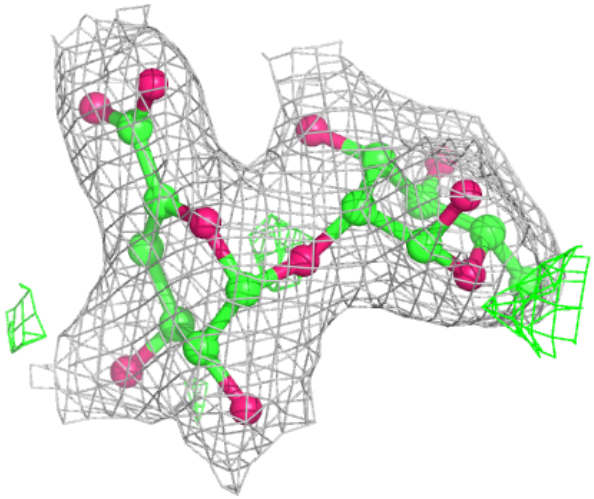


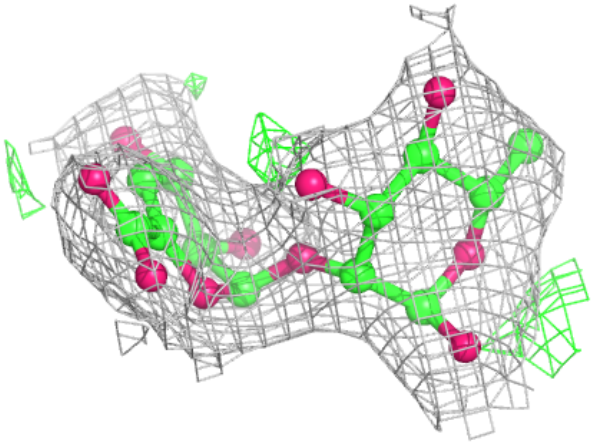


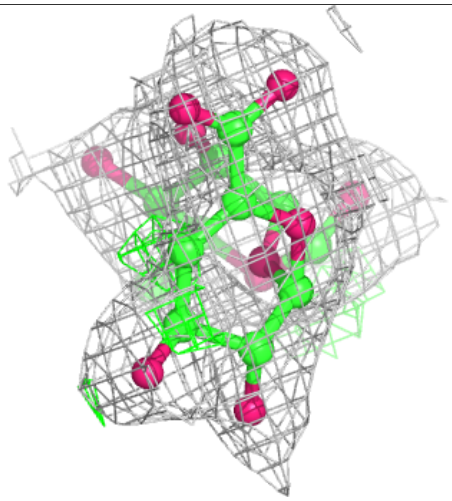


Electron density around Chain N:

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

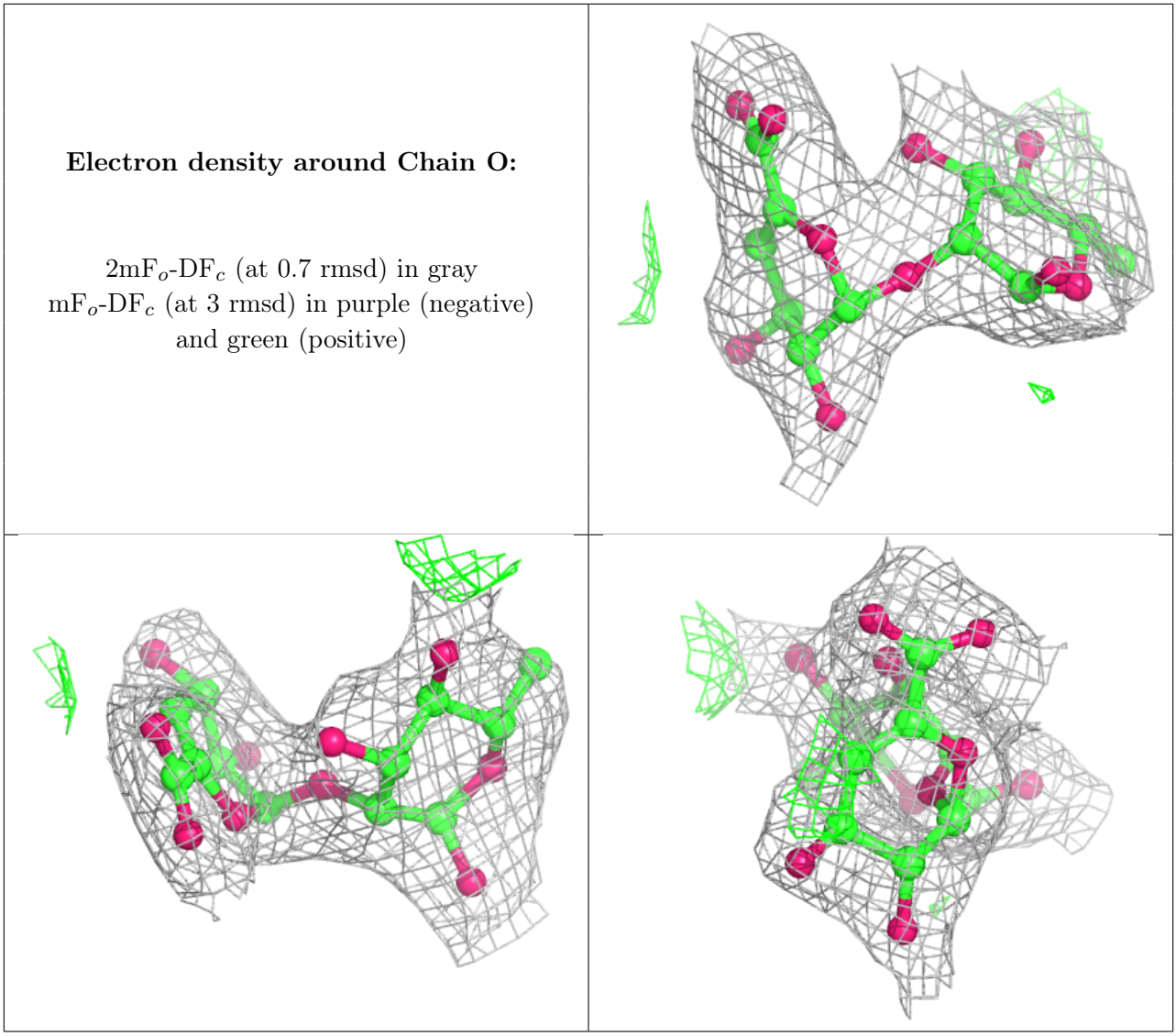






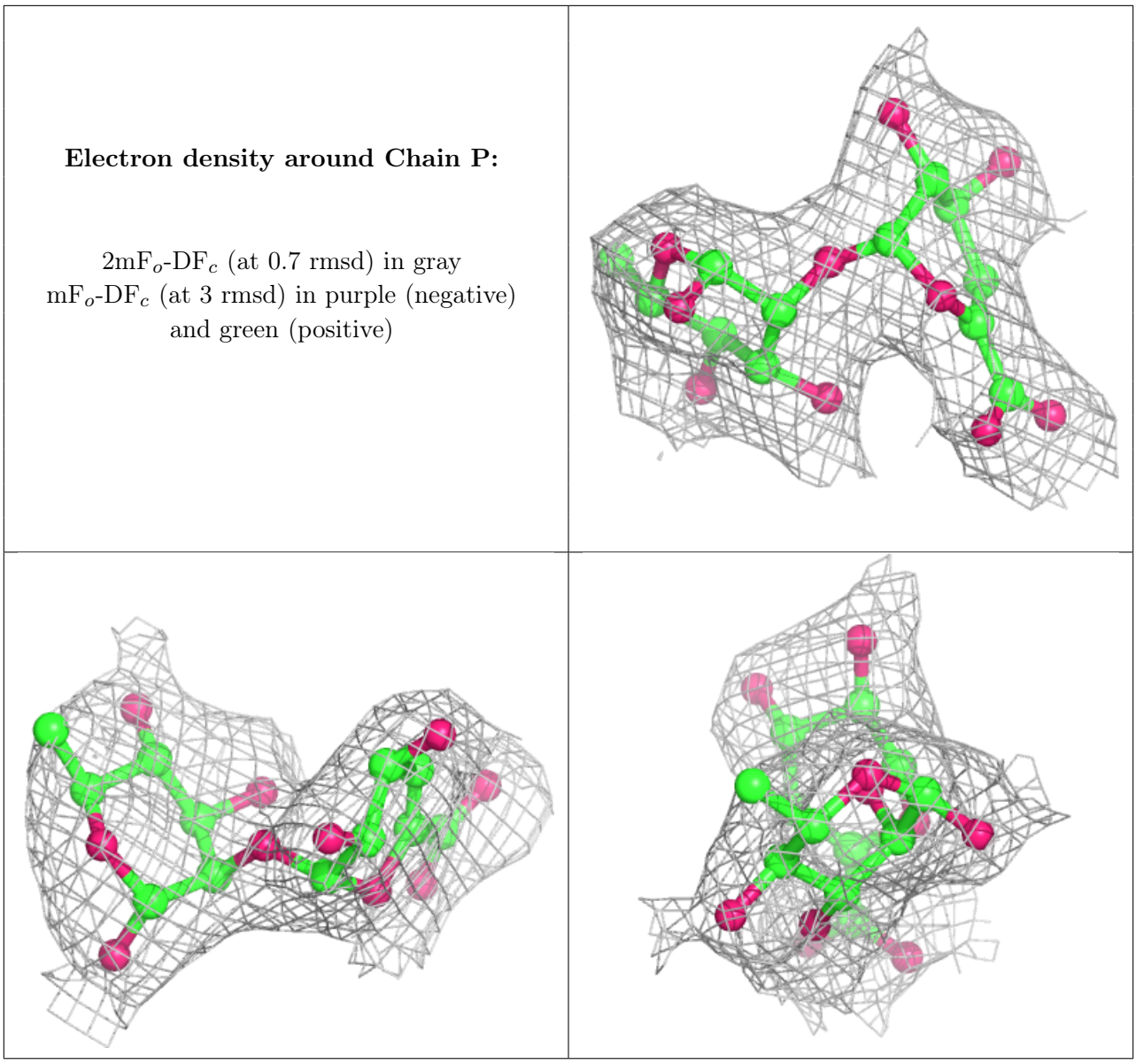
Electron density around Chain O:

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



Electron density around Chain P:

$2mF_o$-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, 95^{th} 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
3	CA	H	1003	1/1	0.96	0.17	19,19,19,19	0
3	CA	B	1003	1/1	0.98	0.15	11,11,11,11	0
3	CA	C	1003	1/1	0.99	0.15	9,9,9,9	0
3	CA	E	1003	1/1	0.99	0.15	12,12,12,12	0
3	CA	F	1003	1/1	0.99	0.13	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	CA	G	1003	1/1	0.99	0.17	18,18,18,18	0
3	CA	A	1003	1/1	0.99	0.16	11,11,11,11	0
3	CA	D	1003	1/1	1.00	0.17	12,12,12,12	0

6.5 Other polymers (i)

There are no such residues in this entry.