



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 03:17 AM BST

PDB ID : 5Y32
Title : Crystal structure of PTP delta Ig1-Ig2 in complex with IL1RAPL1
Authors : Yamagata, A.; Fukai, S.
Deposited on : 2017-07-27
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

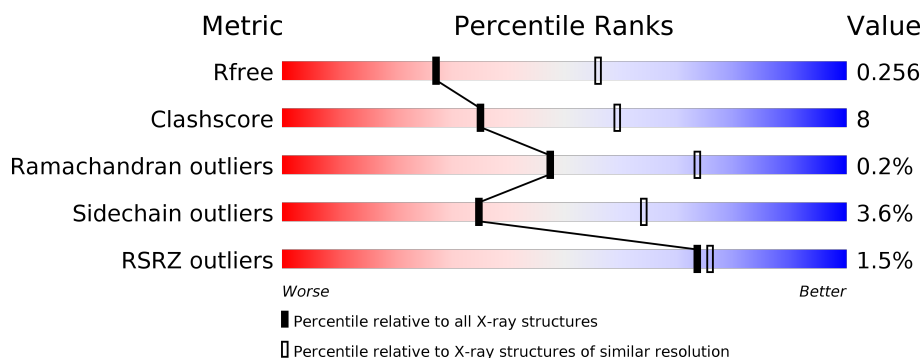
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	B	346	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 1%, grey 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 73% 19% • 7% </div> </div>
2	A	305	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 1%, grey 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 55% 12% • 31% </div> </div>
3	C	3	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 33%, orange 67%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 33% 67% </div> </div>
4	D	2	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 50%, orange 50%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 50% 50% </div> </div>
5	E	4	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 25%, yellow 25%, orange 50%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 25% 25% 50% </div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4428 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 Interleukin-1 receptor accessory protein-like 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	322	Total	C	N	O	S	0	0	0
			2591	1649	429	497	16			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	14	PRO	-	expression tag	UNP P59823
B	15	ALA	-	expression tag	UNP P59823
B	16	ALA	-	expression tag	UNP P59823
B	17	ARG	-	expression tag	UNP P59823
B	18	ASP	-	expression tag	UNP P59823
B	353	LYS	-	expression tag	UNP P59823
B	354	HIS	-	expression tag	UNP P59823
B	355	HIS	-	expression tag	UNP P59823
B	356	HIS	-	expression tag	UNP P59823
B	357	HIS	-	expression tag	UNP P59823
B	358	HIS	-	expression tag	UNP P59823
B	359	HIS	-	expression tag	UNP P59823

- Molecule 2 is a protein called Receptor-type tyrosine-protein phosphatase delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	209	Total	C	N	O	S	0	0	0
			1617	999	294	318	6			

There are 7 discrepancies between the modelled and reference sequences:

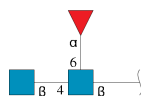
Chain	Residue	Modelled	Actual	Comment	Reference
A	326	LYS	-	expression tag	UNP Q64487
A	327	HIS	-	expression tag	UNP Q64487
A	328	HIS	-	expression tag	UNP Q64487
A	329	HIS	-	expression tag	UNP Q64487

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Chain	Residue	Modelled	Actual	Comment	Reference
A	330	HIS	-	expression tag	UNP Q64487
A	331	HIS	-	expression tag	UNP Q64487
A	332	HIS	-	expression tag	UNP Q64487

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



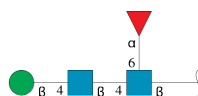
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			38	22	2	14			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

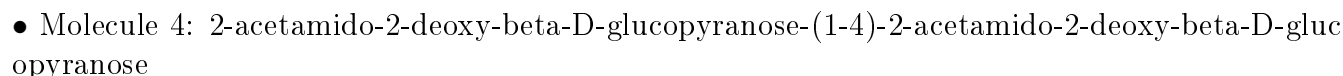
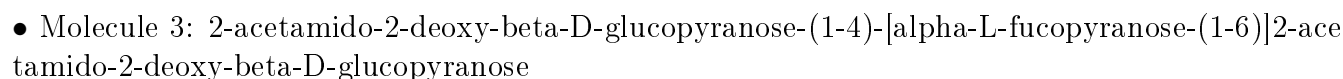
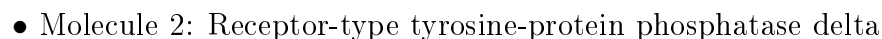


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	39	Total	O	0	0
			39	39		
7	A	38	Total	O	0	0
			38	38		


- Molecule 1: Interleukin-1 receptor accessory protein-like 1



Chain D:  50% 50%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  25% 25% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.97Å 81.17Å 91.48Å 90.00° 91.27° 90.00°	Depositor
Resolution (Å)	45.73 – 2.70 45.73 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.9 (45.73-2.70) 97.9 (45.73-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.214 , 0.257 0.219 , 0.256	Depositor DCC
R_{free} test set	1639 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.550	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4428	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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: BMA, NAG, FUC

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	B	0.36	0/2647	0.57	2/3576 (0.1%)
2	A	0.35	0/1646	0.54	0/2232
All	All	0.35	0/4293	0.56	2/5808 (0.0%)

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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	310	LEU	CA-CB-CG	5.40	127.72	115.30
1	B	311	GLY	N-CA-C	-5.08	100.41	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	85	PHE	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2591	0	2546	43	0
2	A	1617	0	1600	25	0
3	C	38	0	34	1	0
4	D	28	0	25	1	0
5	E	49	0	43	3	0
6	B	28	0	26	1	0
7	A	38	0	0	2	0
7	B	39	0	0	3	0
All	All	4428	0	4274	71	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 8.

All (71) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:LEU:O	1:B:198:ARG:NH2	2.15	0.79
1:B:122:ASN:HB2	1:B:125:TYR:HB3	1.69	0.75
1:B:306:LEU:HD11	1:B:316:SER:HB2	1.67	0.74
1:B:144:TYR:HB3	1:B:228:THR:HG21	1.69	0.73
2:A:236:ARG:HG3	2:A:236:ARG:HH11	1.54	0.72
5:E:1:NAG:H3	5:E:1:NAG:H83	1.75	0.69
1:B:122:ASN:HB3	1:B:124:THR:H	1.57	0.69
2:A:83:ASP:OD1	2:A:83:ASP:N	2.26	0.68
2:A:108:SER:HB3	2:A:113:GLU:HG3	1.78	0.66
1:B:174:THR:O	7:B:501:HOH:O	2.14	0.65
1:B:191:ARG:NE	1:B:193:SER:OG	2.30	0.60
1:B:150:TYR:HB2	1:B:229:THR:HG22	1.83	0.60
1:B:297:ARG:NH2	1:B:328:ASP:OD1	2.34	0.59
2:A:65:ASN:HB2	2:A:104:GLU:HG3	1.87	0.57
2:A:43:VAL:HG21	2:A:128:ILE:HD11	1.86	0.57
3:C:1:NAG:H61	3:C:3:FUC:O2	2.06	0.56
1:B:242:PRO:HG3	1:B:338:ASN:HB2	1.88	0.54
1:B:215:THR:HG23	1:B:228:THR:HG22	1.90	0.53
1:B:54:ALA:HB3	1:B:129:VAL:HG11	1.91	0.52
1:B:221:GLY:N	1:B:222:GLY:HA2	2.24	0.52
1:B:139:ASP:OD2	1:B:146:SER:OG	2.18	0.52
1:B:149:LYS:NZ	4:D:1:NAG:O6	2.39	0.52
2:A:126:ASP:OD2	2:A:126:ASP:N	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:CYS:N	1:B:185:CYS:SG	2.79	0.51
2:A:168:LYS:HD3	2:A:212:TYR:CZ	2.47	0.50
1:B:78:LYS:HB2	1:B:89:ILE:HD11	1.94	0.50
1:B:160:LYS:HD2	1:B:161:GLU:H	1.77	0.49
1:B:138:ASN:N	1:B:138:ASN:OD1	2.31	0.49
1:B:78:LYS:NZ	7:B:506:HOH:O	2.36	0.49
2:A:161:ASP:HB3	2:A:195:ILE:HD11	1.95	0.48
1:B:79:SER:OG	1:B:86:GLU:HG2	2.14	0.48
1:B:261:GLY:O	1:B:324:VAL:HG23	2.14	0.48
1:B:82:PRO:HA	1:B:83:GLY:HA2	1.47	0.48
1:B:297:ARG:HH22	1:B:328:ASP:CG	2.16	0.48
5:E:1:NAG:H3	5:E:1:NAG:C8	2.42	0.48
2:A:125:GLU:HA	2:A:128:ILE:HG13	1.95	0.47
1:B:292:ASP:CG	2:A:98:ARG:HH21	2.17	0.47
1:B:52:LYS:HB3	1:B:57:TYR:HE2	1.79	0.47
1:B:156:LEU:O	1:B:157:SER:HB3	2.15	0.47
2:A:69:LYS:NZ	7:A:408:HOH:O	2.48	0.46
2:A:98:ARG:NH1	7:A:407:HOH:O	2.47	0.46
2:A:181:ARG:NH1	2:A:208:ASP:OD2	2.29	0.46
1:B:307:LYS:HB2	1:B:314:GLU:HB2	1.97	0.46
2:A:148:ARG:O	2:A:204:SER:OG	2.27	0.46
1:B:110:LEU:HD23	1:B:110:LEU:HA	1.79	0.46
1:B:242:PRO:CG	1:B:338:ASN:HB2	2.46	0.46
1:B:92:ASP:OD1	1:B:94:SER:N	2.37	0.45
2:A:100:GLU:HG3	2:A:121:THR:HA	1.99	0.45
1:B:61:ARG:NH2	2:A:189:SER:O	2.49	0.44
2:A:144:VAL:HG11	2:A:150:ALA:HB2	1.99	0.44
1:B:297:ARG:NH1	7:B:507:HOH:O	2.51	0.44
2:A:181:ARG:HG2	2:A:202:GLU:O	2.18	0.44
1:B:78:LYS:HB2	1:B:89:ILE:CD1	2.47	0.44
2:A:146:ARG:HG2	2:A:147:THR:HG23	2.01	0.43
2:A:173:VAL:HG11	2:A:199:LEU:HD21	2.01	0.43
1:B:106:ARG:HA	1:B:107:PRO:HA	1.83	0.43
1:B:50:ARG:HB2	1:B:104:TRP:CE2	2.54	0.42
2:A:128:ILE:HA	2:A:129:PRO:HD3	1.89	0.42
2:A:168:LYS:HE3	2:A:209:GLN:O	2.20	0.42
2:A:186:ARG:NH1	2:A:195:ILE:HD13	2.35	0.42
5:E:1:NAG:H62	5:E:4:FUC:O2	2.19	0.42
2:A:28:GLU:HB3	2:A:111:VAL:HG21	2.01	0.42
1:B:73:SER:O	1:B:120:ILE:HA	2.20	0.41
1:B:122:ASN:HB2	1:B:125:TYR:CB	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:39:ASP:OD1	2:A:119:ARG:N	2.43	0.41
1:B:297:ARG:NH1	1:B:323:SER:O	2.51	0.41
1:B:220:TYR:C	1:B:223:PHE:H	2.23	0.41
6:B:410:NAG:O7	6:B:410:NAG:O3	2.33	0.41
1:B:181:TRP:CZ3	1:B:216:CYS:HB3	2.55	0.41
1:B:268:ARG:NH1	1:B:306:LEU:HD13	2.36	0.41
1:B:48:PRO:HG2	1:B:170:PHE:CE1	2.56	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	B	320/346 (92%)	293 (92%)	26 (8%)	1 (0%)	41	66
2	A	207/305 (68%)	204 (99%)	3 (1%)	0	100	100
All	All	527/651 (81%)	497 (94%)	29 (6%)	1 (0%)	47	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	82	PRO

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	B	289/308 (94%)	280 (97%)	9 (3%)	40	69
2	A	180/264 (68%)	172 (96%)	8 (4%)	28	56
All	All	469/572 (82%)	452 (96%)	17 (4%)	35	64

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	86	GLU
1	B	125	TYR
1	B	138	ASN
1	B	139	ASP
1	B	166	ASP
1	B	176	GLU
1	B	179	ILE
1	B	185	CYS
1	B	187	THR
2	A	38	VAL
2	A	83	ASP
2	A	126	ASP
2	A	168	LYS
2	A	188	GLU
2	A	196	ARG
2	A	214	CYS
2	A	236	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	68	GLN
1	B	258	GLN
2	A	74	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

9 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$
3	NAG	C	1	1,3	14,14,15	1.35	2 (14%)	17,19,21	0.93	1 (5%)
3	NAG	C	2	3	14,14,15	0.26	0	17,19,21	0.35	0
3	FUC	C	3	3	10,10,11	2.07	2 (20%)	14,14,16	1.51	1 (7%)
4	NAG	D	1	1,4	14,14,15	0.60	1 (7%)	17,19,21	0.56	0
4	NAG	D	2	4	14,14,15	0.20	0	17,19,21	0.48	0
5	NAG	E	1	1,5	14,14,15	0.85	1 (7%)	17,19,21	1.55	2 (11%)
5	NAG	E	2	5	14,14,15	0.40	0	17,19,21	0.75	0
5	BMA	E	3	5	11,11,12	1.17	1 (9%)	15,15,17	1.16	2 (13%)
5	FUC	E	4	5	10,10,11	2.17	3 (30%)	14,14,16	1.47	3 (21%)

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
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	1/6/23/26	0/1/1/1
3	FUC	C	3	3	-	-	0/1/1/1
4	NAG	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	1/6/23/26	0/1/1/1
5	NAG	E	1	1,5	-	5/6/23/26	0/1/1/1
5	NAG	E	2	5	-	1/6/23/26	0/1/1/1
5	BMA	E	3	5	-	2/2/19/22	0/1/1/1
5	FUC	E	4	5	-	-	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	FUC	C1-C2	5.64	1.65	1.52
3	C	1	NAG	O5-C1	-4.21	1.37	1.43
5	E	4	FUC	C1-C2	4.09	1.61	1.52
5	E	4	FUC	C2-C3	3.78	1.58	1.52
5	E	1	NAG	O5-C1	-2.98	1.38	1.43
5	E	4	FUC	O5-C5	2.58	1.49	1.43
5	E	3	BMA	C1-C2	2.41	1.57	1.52
3	C	1	NAG	C1-C2	-2.39	1.48	1.52
3	C	3	FUC	O3-C3	-2.30	1.37	1.43
4	D	1	NAG	O5-C1	-2.15	1.40	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1	NAG	C2-N2-C7	4.47	129.27	122.90
3	C	3	FUC	O2-C2-C1	4.21	117.76	109.15
5	E	1	NAG	C1-O5-C5	3.05	116.33	112.19
5	E	4	FUC	O2-C2-C1	2.90	115.09	109.15
3	C	1	NAG	C3-C4-C5	2.81	115.25	110.24
5	E	4	FUC	C1-O5-C5	2.67	118.83	112.78
5	E	3	BMA	O2-C2-C3	-2.52	105.08	110.14
5	E	4	FUC	O5-C5-C4	2.23	113.52	109.52
5	E	3	BMA	C1-C2-C3	-2.21	106.95	109.67

There are no chirality outliers.

All (10) torsion outliers are listed below:

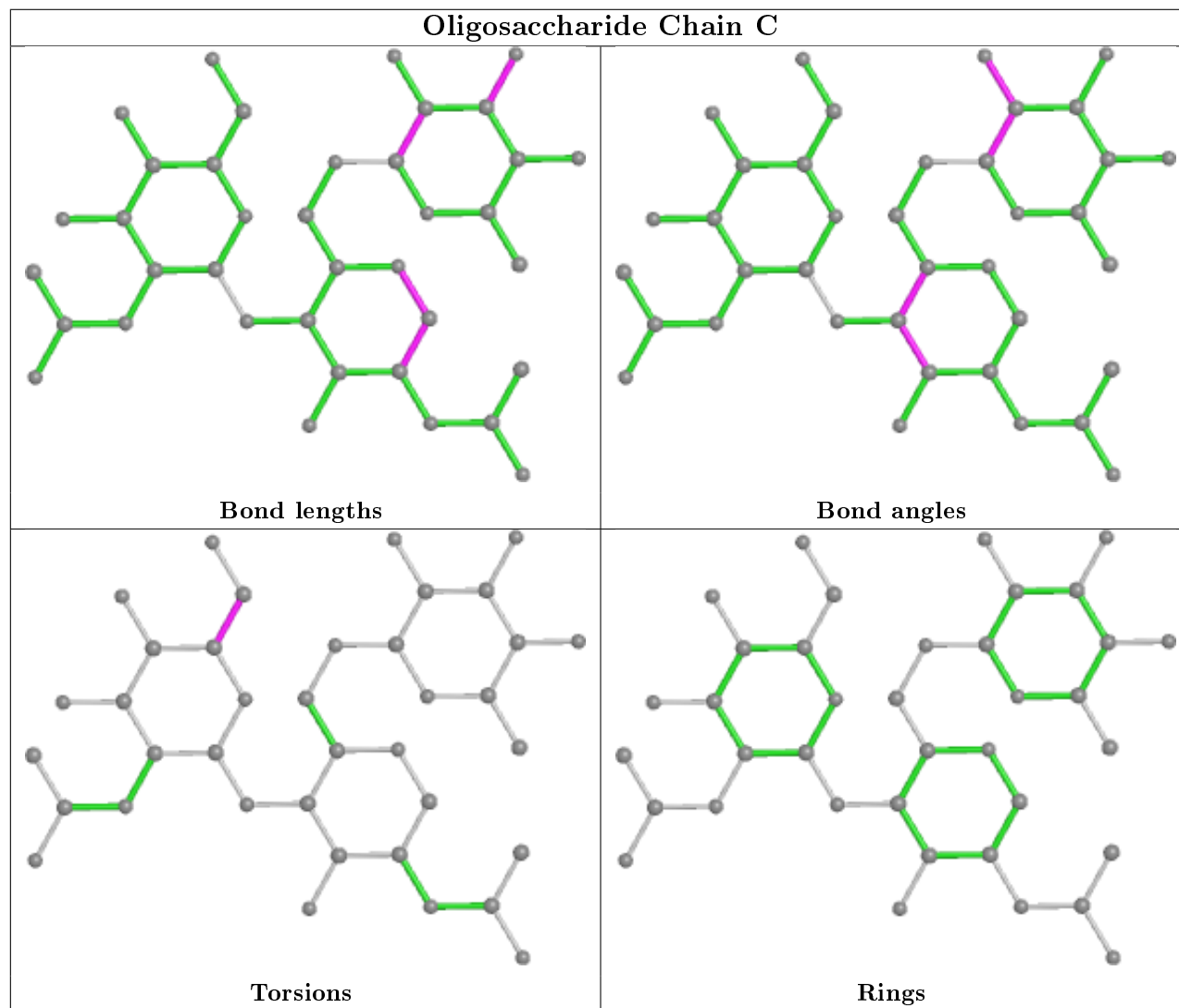
Mol	Chain	Res	Type	Atoms
5	E	1	NAG	C4-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
5	E	1	NAG	C8-C7-N2-C2
5	E	1	NAG	O7-C7-N2-C2
5	E	3	BMA	C4-C5-C6-O6
5	E	3	BMA	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
5	E	1	NAG	C3-C2-N2-C7

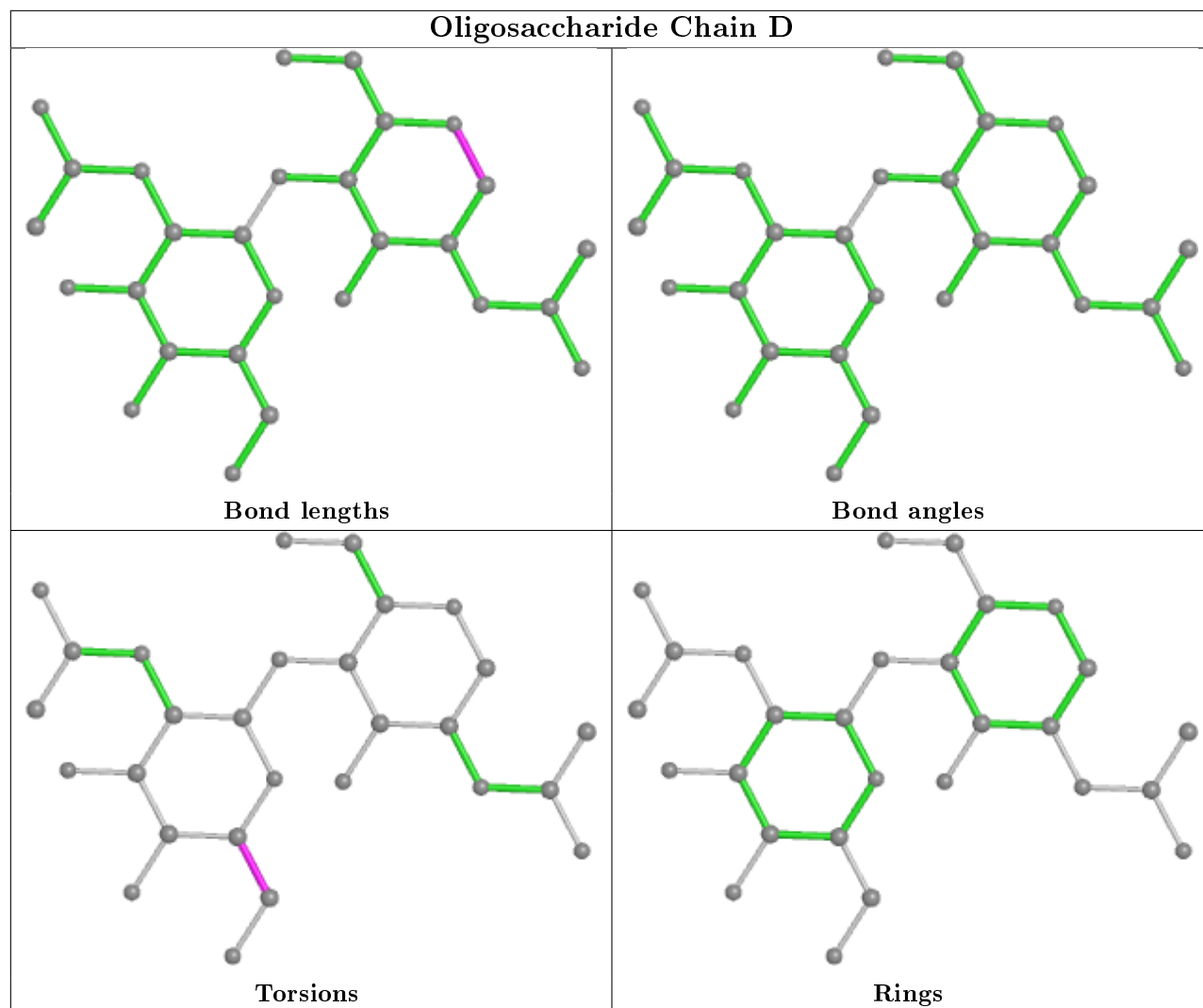
There are no ring outliers.

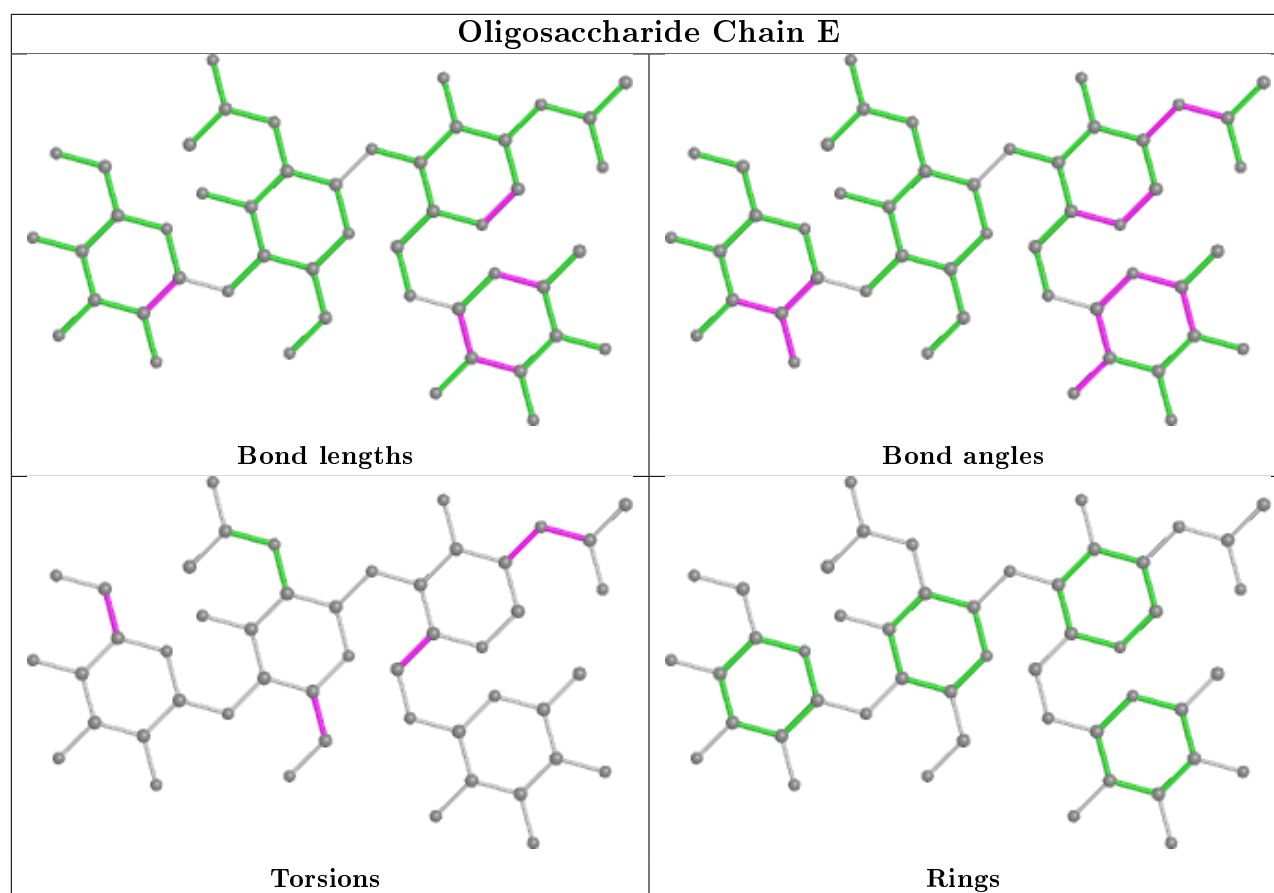
5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1	NAG	3	0
4	D	1	NAG	1	0
3	C	3	FUC	1	0
3	C	1	NAG	1	0
5	E	4	FUC	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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	B	409	1	14,14,15	0.28	0	17,19,21	0.36	0
6	NAG	B	410	1	14,14,15	0.87	2 (14%)	17,19,21	0.75	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
6	NAG	B	409	1	-	2/6/23/26	0/1/1/1
6	NAG	B	410	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	410	NAG	O5-C1	-2.25	1.40	1.43
6	B	410	NAG	C1-C2	2.02	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	410	NAG	C1-C2-N2-C7
6	B	409	NAG	C4-C5-C6-O6
6	B	409	NAG	O5-C5-C6-O6
6	B	410	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	410	NAG	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	322/346 (93%)	-0.07	5 (1%) 72 74	32, 54, 88, 130	0
2	A	209/305 (68%)	-0.16	3 (1%) 75 77	20, 38, 85, 169	0
All	All	531/651 (81%)	-0.11	8 (1%) 73 76	20, 48, 88, 169	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	179	ASN	5.3
1	B	82	PRO	4.2
2	A	178	ASN	3.9
1	B	85	PHE	3.6
1	B	81	GLY	3.5
1	B	351	LYS	2.9
1	B	83	GLY	2.3
2	A	235	LEU	2.1

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
5	BMA	E	3	11/12	0.80	0.24	111,120,132,133	0

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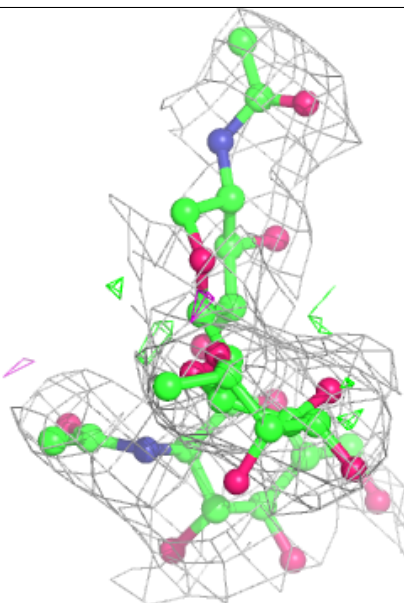
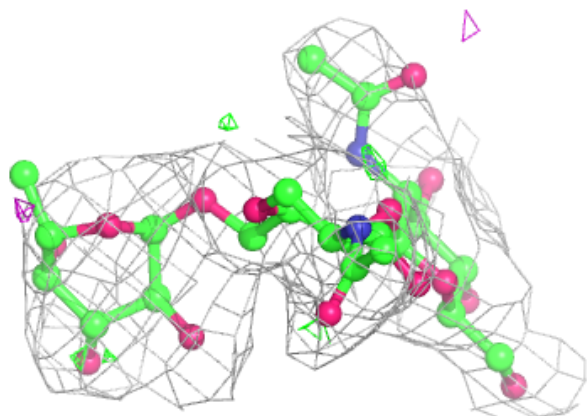
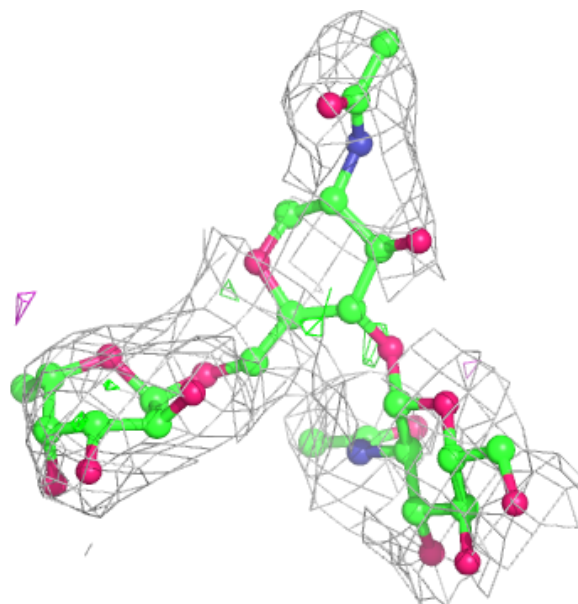
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	FUC	C	3	10/11	0.89	0.24	66,81,92,106	0
3	NAG	C	2	14/15	0.89	0.18	57,98,109,110	0
4	NAG	D	2	14/15	0.90	0.24	92,112,120,120	0
5	FUC	E	4	10/11	0.90	0.21	74,94,127,132	0
5	NAG	E	2	14/15	0.91	0.19	42,79,100,110	0
4	NAG	D	1	14/15	0.93	0.16	56,64,84,97	0
3	NAG	C	1	14/15	0.94	0.11	52,63,75,82	0
5	NAG	E	1	14/15	0.94	0.14	51,63,68,72	0

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

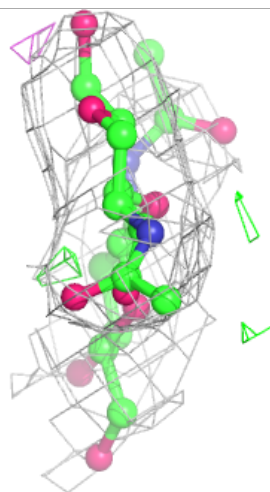
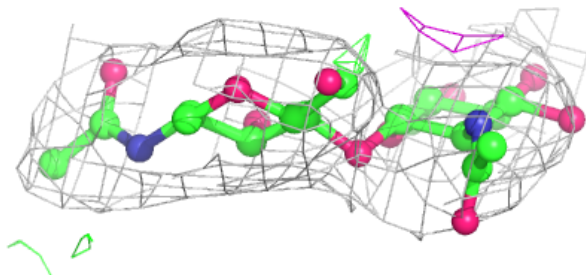
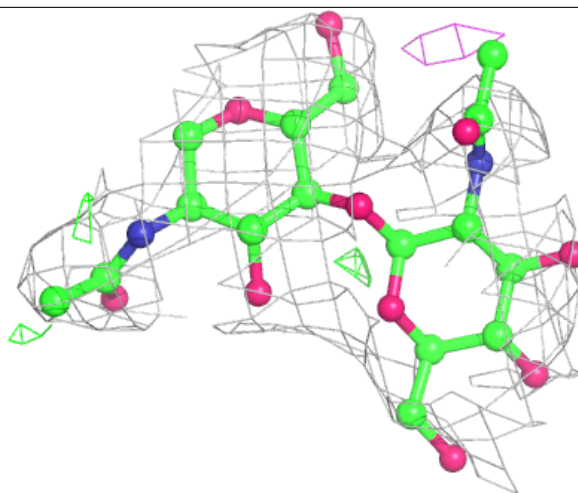
Electron density around Chain C:

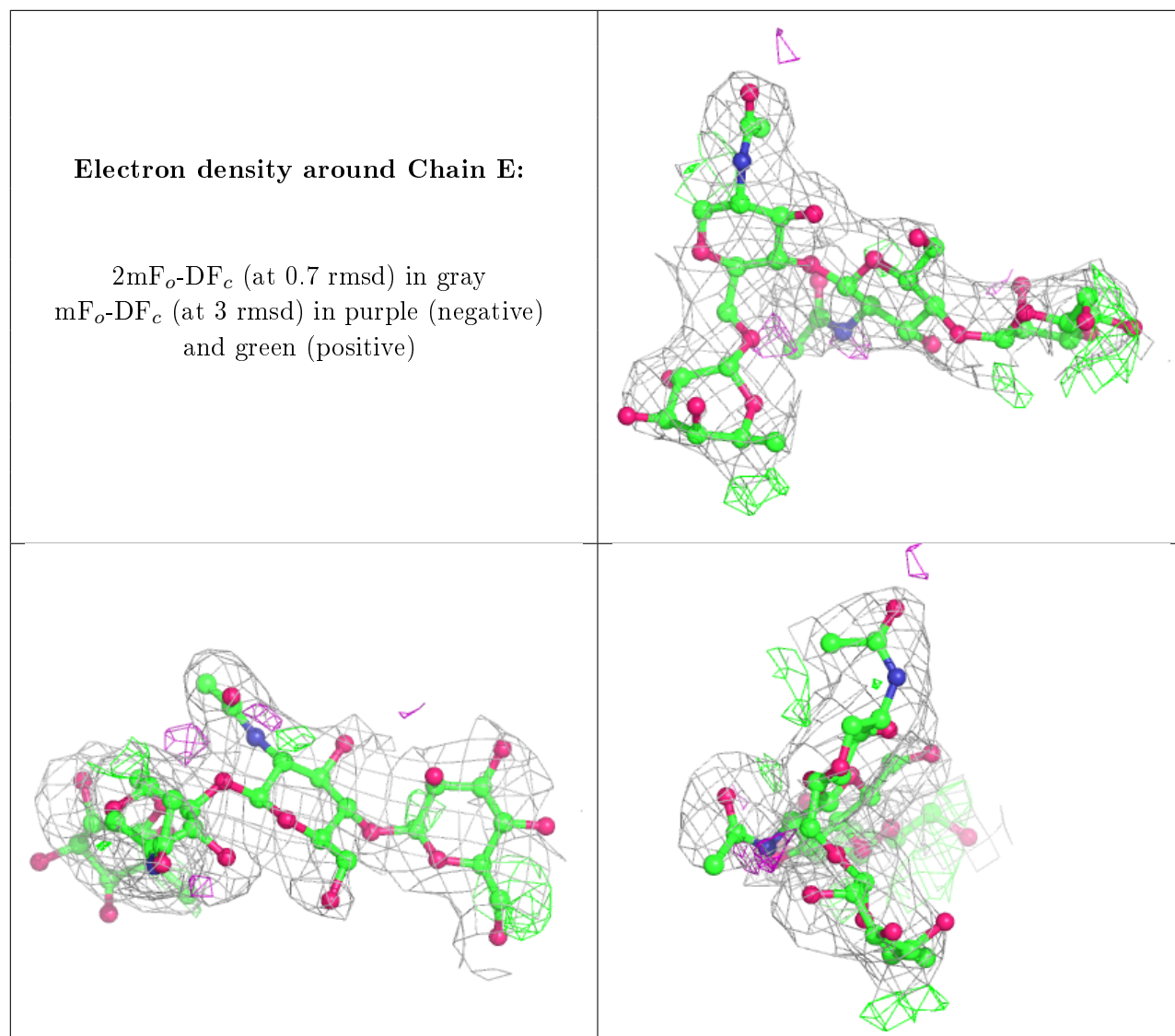
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
 and green (positive)



Electron density around Chain D:

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





6.4 Ligands [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
6	NAG	B	409	14/15	0.56	0.24	119,140,143,145	0
6	NAG	B	410	14/15	0.85	0.14	81,95,108,110	0

6.5 Other polymers [i](#)

There are no such residues in this entry.