



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 12:38 AM EDT

PDB ID : 7LSK
Title : Structure of HIV-1 Reverse Transcriptase in complex with DNA, L-dTTP, and CA(2+) ion
Authors : Hoang, A.; Ruiz, F.X.; Arnold, E.
Deposited on : 2021-02-18
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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
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) : 2.35.1

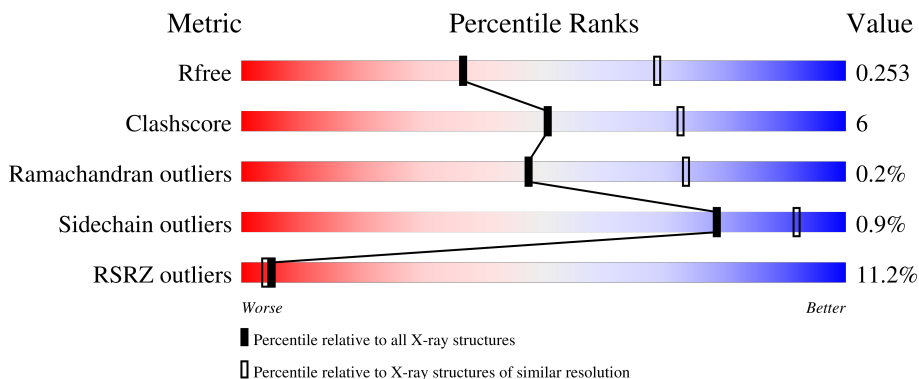
1 Overall quality at a glance

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.



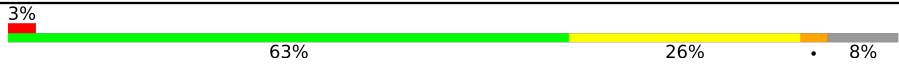

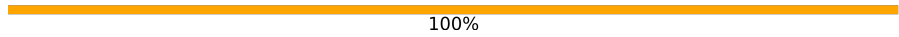
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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	555	
1	C	555	
2	B	429	
2	D	429	
3	E	38	

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Mol	Chain	Length	Quality of chain
3	F	38	 3% 63% 26% 8%
4	N	2	 50% 50%
4	O	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GLC	O	1	-	-	X	-
4	FRU	O	2	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 17642 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 Reverse transcriptase p66.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	554	4509	2919	751	832	7	0	0	0
1	C	554	4509	2919	751	832	7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	280	SER	CYS	engineered mutation	UNP P03366
A	498	ASN	ASP	engineered mutation	UNP P03366
C	280	SER	CYS	engineered mutation	UNP P03366
C	498	ASN	ASP	engineered mutation	UNP P03366

- Molecule 2 is a protein called Reverse transcriptase p51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	412	3400	2212	563	619	6	0	0	0
2	D	412	3400	2212	563	619	6	0	0	0

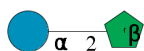
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P03366
B	280	SER	CYS	engineered mutation	UNP P03366
D	0	GLY	-	expression tag	UNP P03366
D	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is a DNA chain called DNA/RNA (38-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	35	Total	C	N	O	P	0	0	0
			720	340	130	215	35			
3	E	35	Total	C	N	O	P	0	0	0
			720	340	130	215	35			

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

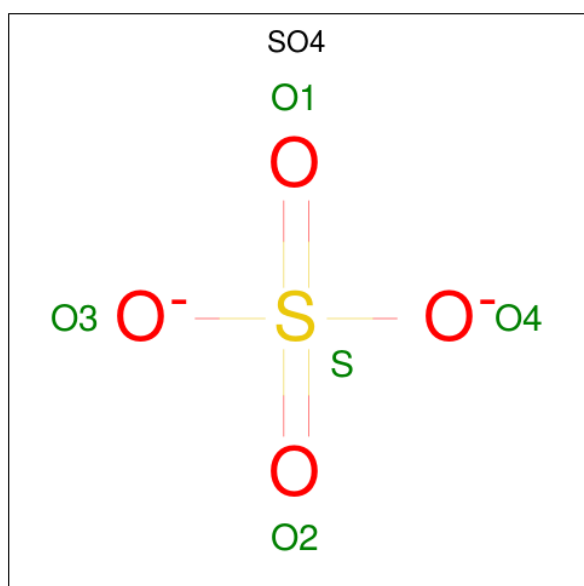


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	N	2	Total	C	O	0	0	0
			23	12	11			
4	O	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

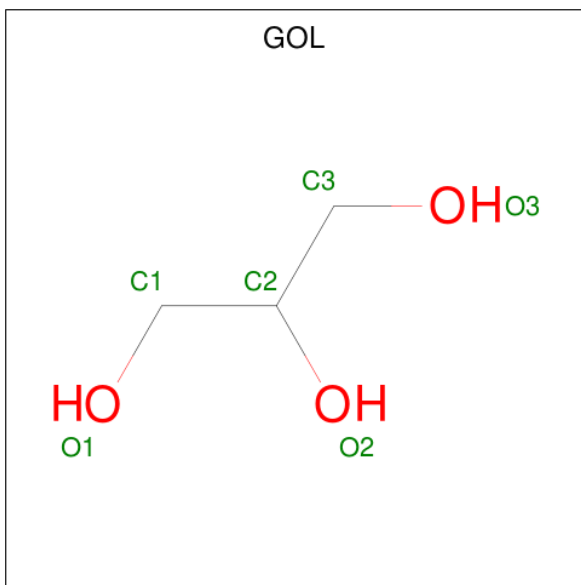
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



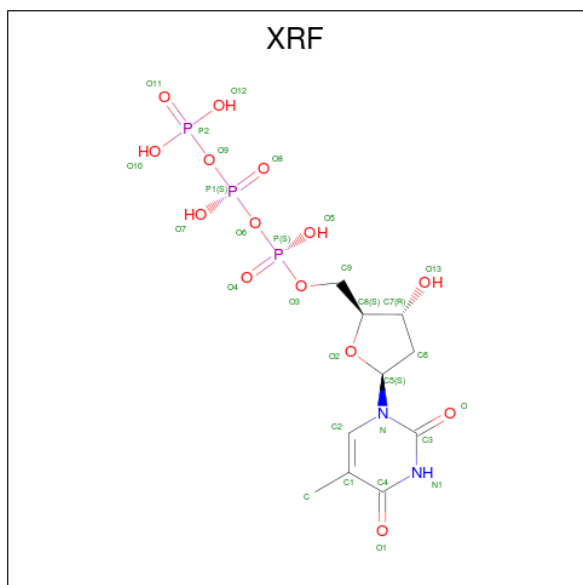
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



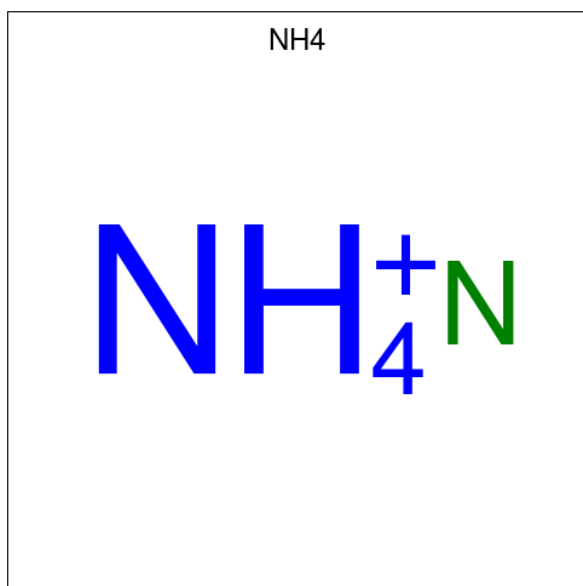
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 6 3 3	0	0
7	A	1	Total C O 6 3 3	0	0
7	D	1	Total C O 6 3 3	0	0

- Molecule 8 is 1-{2-deoxy-5-O-[(S)-hydroxy{[(S)-hydroxy(phosphonoxy)phosphoryl]oxy}phosphoryl]-beta-L-erythro-pentofuranosyl}-5-methylpyrimidine-2,4(1H,3H)-dione (three-letter code: XRF) (formula: C₁₀H₁₇N₂O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
8	A	1	29	10	2	14	3	0	0
8	C	1	29	10	2	14	3	0	0

- Molecule 9 is AMMONIUM ION (three-letter code: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	N		
9	A	1	1	1	0	0
9	C	1	1	1	0	0

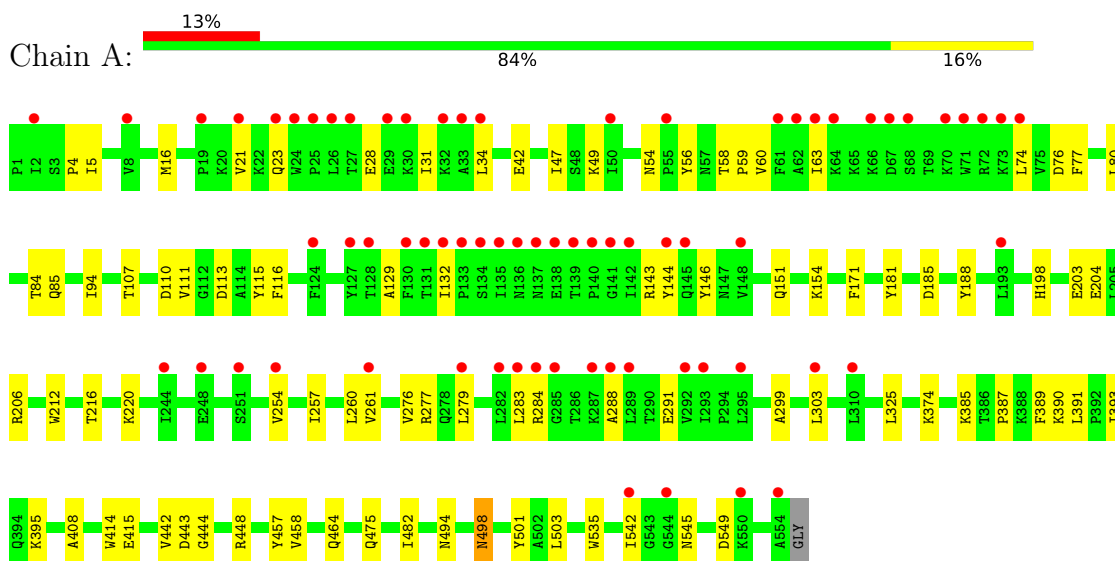
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	49	Total O 49 49	0	0
10	B	57	Total O 57 57	0	0
10	C	72	Total O 72 72	0	0
10	D	51	Total O 51 51	0	0
10	F	8	Total O 8 8	0	0
10	E	11	Total O 11 11	0	0

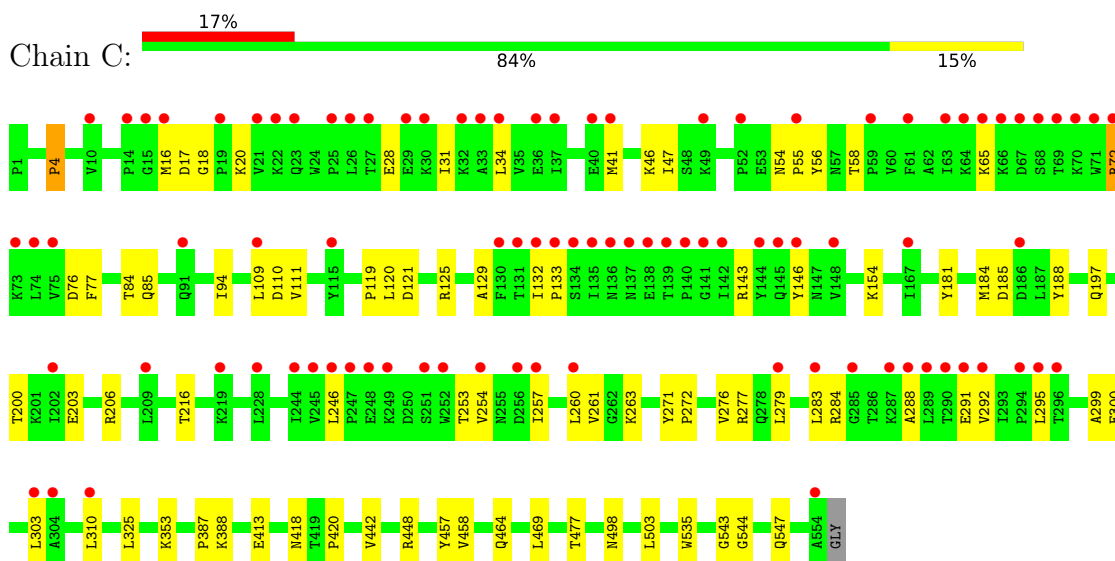
3 Residue-property plots [i](#)

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.

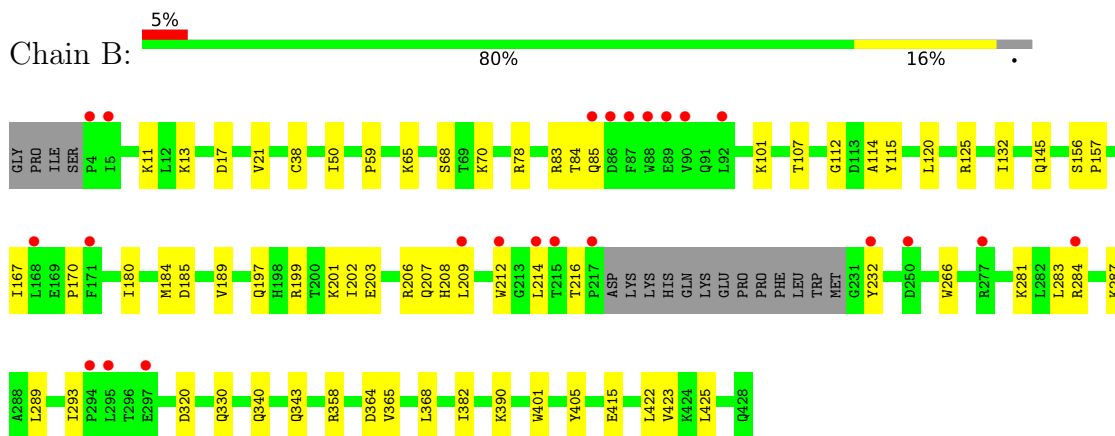
- Molecule 1: Reverse transcriptase p66



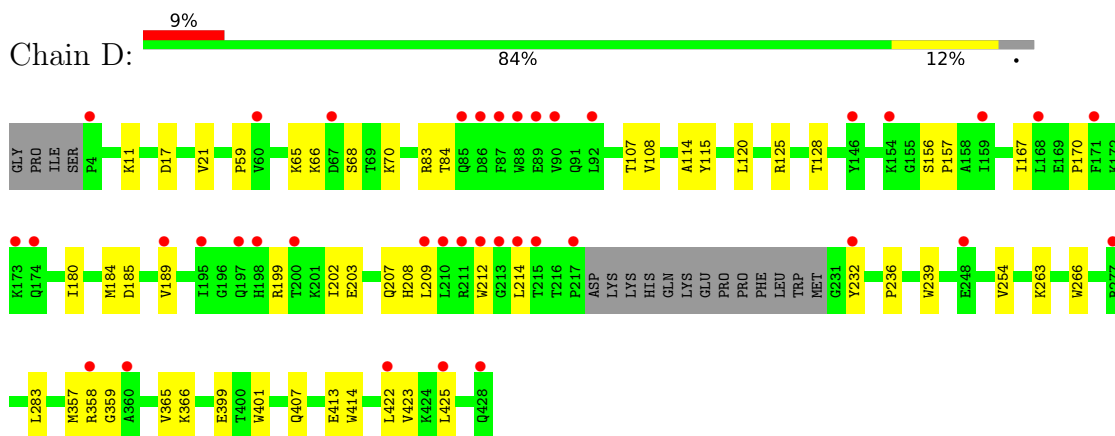
- Molecule 1: Reverse transcriptase p66



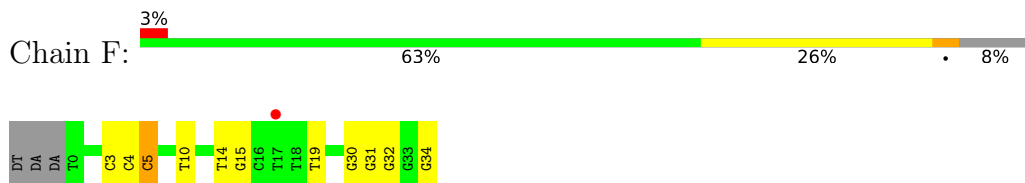
- Molecule 2: Reverse transcriptase p51



- Molecule 2: Reverse transcriptase p51



- Molecule 3: DNA/RNA (38-MER)



- Molecule 3: DNA/RNA (38-MER)



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



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

Chain O:  100%

6L61
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.94Å 132.47Å 139.34Å 90.00° 97.60° 90.00°	Depositor
Resolution (Å)	70.76 – 2.70 70.76 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (70.76-2.70) 100.0 (70.76-2.70)	Depositor EDS
R_{merge}	0.34	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 2.69Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.215 , 0.253 0.215 , 0.253	Depositor DCC
R_{free} test set	1999 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å ²)	63.6	Xtrriage
Anisotropy	0.302	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17642	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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: GLC, CA, OMC, SO4, FRU, GOL, NH4, XRF

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	0.25	0/4627	0.42	0/6286
1	C	0.25	0/4627	0.42	0/6286
2	B	0.24	0/3497	0.41	0/4751
2	D	0.24	0/3497	0.42	0/4751
3	E	0.48	0/759	0.90	0/1170
3	F	0.50	0/759	0.89	0/1170
All	All	0.28	0/17766	0.49	0/24414

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	4509	0	4572	53	0
1	C	4509	0	4572	49	0
2	B	3400	0	3433	40	0
2	D	3400	0	3433	36	0
3	E	720	0	397	9	0
3	F	720	0	397	10	0
4	N	23	0	21	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	O	23	0	21	12	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	5	0	0	0	0
6	C	5	0	0	0	0
7	A	12	0	16	0	0
7	D	6	0	8	0	0
8	A	29	0	0	0	0
8	C	29	0	0	0	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
10	A	49	0	0	1	0
10	B	57	0	0	2	0
10	C	72	0	0	0	0
10	D	51	0	0	2	0
10	E	11	0	0	0	0
10	F	8	0	0	0	0
All	All	17642	0	16870	195	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 6.

All (195) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ASP:HB3	1:A:220:LYS:HB3	1.48	0.95
4:O:1:GLC:O5	4:O:2:FRU:H61	1.73	0.88
2:D:399:GLU:OE2	4:N:2:FRU:H12	1.78	0.83
4:O:1:GLC:C5	4:O:2:FRU:H61	2.13	0.79
2:D:413:GLU:OE1	4:N:1:GLC:H3	1.83	0.78
1:C:34:LEU:HD21	1:C:132:ILE:HD12	1.65	0.77
1:A:34:LEU:HD21	1:A:132:ILE:HD12	1.70	0.74
4:N:1:GLC:O5	4:N:2:FRU:O6	2.05	0.73
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.74	0.69
1:A:448:ARG:HH21	3:E:19:DT:H5''	1.58	0.69
3:F:14:DT:H4'	3:F:15:DG:OP1	1.95	0.67
1:C:203:GLU:OE2	1:C:206:ARG:NH1	2.28	0.66
2:D:414:TRP:HE1	4:N:2:FRU:HO1	1.43	0.64
1:C:254:VAL:HG13	1:C:283:LEU:HD22	1.78	0.64
1:C:448:ARG:HH21	3:F:19:DT:H5''	1.63	0.64
4:O:1:GLC:O2	4:O:2:FRU:H12	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:199:ARG:HA	2:B:202:ILE:HD12	1.81	0.63
2:B:78:ARG:NH2	4:O:2:FRU:O1	2.33	0.62
1:A:84:THR:HB	1:A:154:LYS:HE2	1.81	0.61
1:A:203:GLU:OE2	1:A:206:ARG:NH1	2.33	0.61
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.82	0.60
1:C:279:LEU:HD23	1:C:299:ALA:HB1	1.83	0.60
1:A:391:LEU:HB3	1:A:393:ILE:HG22	1.84	0.59
1:A:482:ILE:HA	10:A:749:HOH:O	2.01	0.59
1:A:54:ASN:O	1:A:143:ARG:NH2	2.36	0.59
1:A:408:ALA:HB1	2:B:364:ASP:HB3	1.84	0.59
1:A:257:ILE:HB	1:A:283:LEU:HD21	1.84	0.59
1:C:56:TYR:HB2	1:C:129:ALA:HB3	1.83	0.59
2:D:199:ARG:HA	2:D:202:ILE:HD12	1.86	0.58
1:A:171:PHE:HE2	1:A:204:GLU:HG2	1.68	0.58
2:D:422:LEU:HG	2:D:423:VAL:HG12	1.85	0.57
4:O:1:GLC:C1	4:O:2:FRU:H61	2.33	0.57
1:A:442:VAL:HG12	1:A:457:TYR:HB3	1.86	0.57
2:B:50:ILE:HD13	2:B:145:GLN:HG3	1.87	0.57
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.88	0.56
1:A:56:TYR:HB2	1:A:129:ALA:HB3	1.87	0.56
4:O:1:GLC:H5	4:O:2:FRU:H61	1.85	0.56
1:C:41:MET:HB3	1:C:46:LYS:HB2	1.87	0.55
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.88	0.55
2:B:157:PRO:HG3	2:B:184:MET:HA	1.88	0.55
1:A:389:PHE:HB3	1:A:391:LEU:HD13	1.89	0.55
1:C:54:ASN:O	1:C:143:ARG:NH2	2.39	0.55
1:C:288:ALA:HB3	1:C:291:GLU:HB2	1.88	0.55
1:A:110:ASP:HB3	1:A:220:LYS:CB	2.31	0.55
1:A:47:ILE:HD12	1:A:146:TYR:HA	1.90	0.54
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.90	0.54
2:B:422:LEU:HG	2:B:423:VAL:HG12	1.88	0.54
1:A:63:ILE:HG12	1:A:74:LEU:HD11	1.89	0.54
3:F:30:DG:H2'	3:F:31:DG:H8	1.73	0.54
1:C:58:THR:OG1	1:C:76:ASP:O	2.27	0.53
3:E:24:DC:H2''	3:E:25:DG:C8	2.44	0.53
1:A:181:TYR:HB2	1:A:188:TYR:HB3	1.91	0.53
1:C:260:LEU:HD21	1:C:303:LEU:HD13	1.89	0.53
1:A:58:THR:HG21	1:A:77:PHE:HE1	1.74	0.53
2:D:70:LYS:NZ	10:D:601:HOH:O	2.38	0.53
2:B:13:LYS:HD2	2:B:85:GLN:HB3	1.90	0.52
1:C:84:THR:HB	1:C:154:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:ARG:NH2	1:C:216:THR:O	2.43	0.52
2:B:120:LEU:HD23	2:B:125:ARG:HG2	1.90	0.52
1:A:21:VAL:HG23	1:A:59:PRO:HD3	1.90	0.52
3:E:30:DG:H2'	3:E:31:DG:C8	2.46	0.51
2:B:206:ARG:NH2	2:B:216:THR:O	2.44	0.51
1:C:263:LYS:HD2	3:F:31:DG:H4'	1.93	0.51
2:D:115:TYR:CD2	2:D:156:SER:HB3	2.45	0.51
1:A:395:LYS:NZ	1:A:414:TRP:O	2.44	0.51
1:C:261:VAL:HG13	1:C:276:VAL:HG11	1.92	0.51
1:A:542:ILE:HG23	2:B:283:LEU:HD13	1.92	0.51
2:B:197:GLN:O	2:B:201:LYS:HG2	2.11	0.51
3:F:30:DG:H2'	3:F:31:DG:C8	2.46	0.51
1:C:197:GLN:O	1:C:200:THR:OG1	2.20	0.51
2:D:413:GLU:CD	4:N:1:GLC:H3	2.31	0.51
2:B:203:GLU:O	2:B:207:GLN:HG2	2.12	0.50
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.92	0.50
2:B:209:LEU:HD22	2:B:214:LEU:HD23	1.94	0.50
1:C:257:ILE:HB	1:C:283:LEU:HD21	1.93	0.50
1:A:58:THR:OG1	1:A:76:ASP:O	2.30	0.49
1:A:458:VAL:HG22	1:A:464:GLN:HG3	1.94	0.49
2:D:413:GLU:OE2	4:N:1:GLC:H4	2.12	0.49
3:E:11:DC:H2''	3:E:12:DG:C8	2.48	0.49
1:C:58:THR:HG21	1:C:77:PHE:HE1	1.77	0.49
1:C:253:THR:HA	1:C:292:VAL:HA	1.93	0.49
4:O:1:GLC:H5	4:O:2:FRU:C6	2.42	0.49
2:D:209:LEU:HD13	2:D:214:LEU:HD23	1.94	0.49
1:A:94:ILE:HD11	3:E:32:DG:H21	1.78	0.49
1:C:47:ILE:HD12	1:C:146:TYR:HA	1.95	0.49
1:C:458:VAL:HG22	1:C:464:GLN:HG3	1.95	0.48
2:D:266:TRP:CD1	2:D:425:LEU:HD22	2.48	0.48
1:C:325:LEU:HB3	1:C:387:PRO:HB3	1.96	0.48
1:A:325:LEU:HD12	1:A:385:LYS:HG3	1.95	0.48
2:B:114:ALA:HB2	2:B:214:LEU:HD22	1.95	0.48
1:C:94:ILE:HD11	3:F:32:DG:H21	1.79	0.48
2:B:368:LEU:HD22	10:B:501:HOH:O	2.14	0.48
1:C:111:VAL:HB	1:C:185:ASP:HB2	1.97	0.47
1:A:42:GLU:OE2	1:A:144:TYR:HE1	1.98	0.47
2:B:330:GLN:NE2	2:B:340:GLN:OE1	2.44	0.47
1:A:390:LYS:HE2	1:A:415:GLU:OE2	2.14	0.47
1:C:469:LEU:HD12	1:C:477:THR:HG22	1.96	0.47
2:B:180:ILE:HG12	2:B:189:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:503:LEU:HD22	1:C:535:TRP:HB2	1.95	0.47
2:D:21:VAL:HB	2:D:59:PRO:HD3	1.96	0.47
1:C:276:VAL:HG23	1:C:353:LYS:HE2	1.97	0.47
2:D:359:GLY:HA3	2:D:366:LYS:HD2	1.95	0.47
1:A:288:ALA:HB3	1:A:291:GLU:HB2	1.96	0.46
2:D:120:LEU:HD23	2:D:125:ARG:HG2	1.96	0.46
2:D:157:PRO:HG3	2:D:184:MET:HA	1.98	0.46
1:C:120:LEU:HD23	1:C:125:ARG:HG2	1.97	0.46
2:D:65:LYS:HB2	2:D:68:SER:HB2	1.97	0.46
1:C:4:PRO:HG2	1:C:119:PRO:HD3	1.96	0.46
2:D:108:VAL:HB	2:D:232:TYR:HB2	1.98	0.46
2:B:114:ALA:HB2	2:B:214:LEU:HD13	1.97	0.46
1:C:284:ARG:HB2	3:F:10:DT:OP1	2.16	0.45
4:O:1:GLC:C2	4:O:2:FRU:C1	2.93	0.45
1:A:58:THR:HG21	1:A:77:PHE:CE1	2.52	0.45
1:C:121:ASP:O	1:C:125:ARG:HG3	2.16	0.45
2:B:167:ILE:HG12	2:B:212:TRP:CD2	2.51	0.45
1:A:129:ALA:HA	1:A:144:TYR:O	2.16	0.45
1:C:31:ILE:HD13	1:C:133:PRO:HB2	1.99	0.45
2:D:180:ILE:HG12	2:D:189:VAL:HG22	1.98	0.45
2:D:17:ASP:O	2:D:83:ARG:HD3	2.17	0.44
2:D:185:ASP:N	2:D:185:ASP:OD1	2.50	0.44
1:A:5:ILE:HG22	1:A:212:TRP:HE3	1.83	0.44
2:B:390:LYS:NZ	2:B:415:GLU:OE2	2.43	0.44
1:C:94:ILE:HD12	3:F:5:OMC:HM23	1.99	0.44
2:B:266:TRP:CD1	2:B:425:LEU:HD22	2.53	0.44
2:B:68:SER:C	2:B:70:LYS:H	2.21	0.44
1:A:42:GLU:OE2	1:A:49:LYS:HG3	2.18	0.44
2:D:203:GLU:O	2:D:207:GLN:HG2	2.18	0.44
2:D:357:MET:HG2	2:D:358:ARG:H	1.82	0.44
2:B:17:ASP:O	2:B:83:ARG:HD3	2.18	0.44
2:D:114:ALA:HB2	2:D:214:LEU:HD22	2.00	0.44
3:E:30:DG:H2'	3:E:31:DG:H8	1.82	0.44
1:C:65:LYS:HE2	1:C:72:ARG:HB2	1.98	0.43
1:A:28:GLU:HA	1:A:31:ILE:HD12	1.99	0.43
1:A:498:ASN:O	1:A:535:TRP:NE1	2.51	0.43
2:B:78:ARG:NH2	4:O:2:FRU:C1	2.81	0.43
1:A:23:GLN:HE22	1:A:60:VAL:HB	1.83	0.43
2:D:107:THR:HA	2:D:232:TYR:O	2.19	0.43
2:D:167:ILE:HG23	2:D:212:TRP:CD1	2.53	0.43
4:O:2:FRU:H61	4:O:2:FRU:O2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:VAL:HG13	1:A:283:LEU:HD22	2.01	0.43
1:A:260:LEU:HD21	1:A:303:LEU:HD13	1.99	0.43
2:B:101:LYS:HD3	2:B:382:ILE:HG23	2.00	0.43
1:C:442:VAL:HG12	1:C:457:TYR:HB3	2.00	0.43
1:A:443:ASP:OD1	1:A:444:GLY:N	2.50	0.43
3:E:2:DC:H2'	3:E:3:OMC:C6	2.54	0.43
1:A:545:ASN:O	1:A:549:ASP:HB2	2.19	0.43
2:D:413:GLU:OE2	4:N:1:GLC:C4	2.67	0.43
2:B:107:THR:HA	2:B:232:TYR:O	2.19	0.42
2:B:358:ARG:NH2	2:B:405:TYR:O	2.43	0.42
3:E:4:DC:H2'	3:E:5:OMC:C6	2.54	0.42
2:B:85:GLN:NE2	10:B:504:HOH:O	2.52	0.42
2:B:170:PRO:HB2	2:B:208:HIS:NE2	2.34	0.42
1:C:544:GLY:HA2	1:C:547:GLN:HG2	2.01	0.42
2:D:68:SER:C	2:D:70:LYS:H	2.22	0.42
2:D:263:LYS:HA	2:D:423:VAL:HG21	2.02	0.42
2:B:65:LYS:HB2	2:B:68:SER:HB2	2.00	0.42
2:B:185:ASP:OD1	2:B:185:ASP:N	2.52	0.42
1:C:388:LYS:HE2	1:C:413:GLU:HG2	2.02	0.42
2:D:114:ALA:HB2	2:D:214:LEU:HD13	2.01	0.42
2:D:128:THR:HB	10:D:648:HOH:O	2.18	0.42
2:D:365:VAL:HG11	2:D:401:TRP:HB2	2.01	0.42
1:C:184:MET:HG2	3:F:34:DG:H1'	2.01	0.42
1:C:58:THR:HG21	1:C:77:PHE:CE1	2.54	0.42
2:D:236:PRO:HA	2:D:239:TRP:CD2	2.55	0.42
1:C:295:LEU:HB3	1:C:300:GLU:HG2	2.02	0.42
1:A:80:LEU:O	1:A:84:THR:OG1	2.29	0.42
1:A:107:THR:OG1	1:A:198:HIS:NE2	2.44	0.41
1:A:494:ASN:HB3	2:B:289:LEU:HD12	2.00	0.41
1:C:28:GLU:HA	1:C:31:ILE:HD12	2.02	0.41
1:C:184:MET:HB3	1:C:185:ASP:H	1.62	0.41
1:C:543:GLY:HA2	2:D:283:LEU:O	2.20	0.41
2:D:170:PRO:HB2	2:D:208:HIS:CE1	2.55	0.41
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.61	0.41
1:A:206:ARG:NH2	1:A:216:THR:O	2.53	0.41
1:A:284:ARG:HB2	3:E:10:DT:OP1	2.20	0.41
1:C:17:ASP:CG	1:C:18:GLY:H	2.22	0.41
1:A:279:LEU:HD23	1:A:299:ALA:HB1	2.01	0.41
1:C:418:ASN:O	1:C:420:PRO:HD3	2.20	0.41
2:D:66:LYS:HG2	2:D:407:GLN:OE1	2.19	0.41
1:A:113:ASP:HB3	1:A:116:PHE:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:4:DC:H2'	3:F:5:OMC:C6	2.56	0.41
2:B:287:LYS:HD3	2:B:293:ILE:HD11	2.01	0.41
1:C:17:ASP:OD2	1:C:20:LYS:HE3	2.21	0.41
2:B:115:TYR:CD2	2:B:156:SER:HB3	2.56	0.41
2:B:112:GLY:HA2	2:B:115:TYR:CD1	2.56	0.41
2:D:254:VAL:HG13	2:D:283:LEU:HD22	2.02	0.41
4:O:2:FRU:C6	4:O:2:FRU:O2	2.68	0.41
1:C:246:LEU:HD11	1:C:310:LEU:HD22	2.03	0.40
1:A:325:LEU:HB3	1:A:387:PRO:HB3	2.02	0.40
2:B:320:ASP:O	2:B:343:GLN:NE2	2.47	0.40
1:C:271:TYR:HA	1:C:272:PRO:HD3	1.95	0.40
4:O:1:GLC:C2	4:O:2:FRU:O1	2.69	0.40
1:A:115:TYR:CD2	1:A:151:GLN:HG2	2.56	0.40
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.56	0.40
2:B:281:LYS:HA	2:B:284:ARG:HD3	2.02	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	552/555 (100%)	533 (97%)	18 (3%)	1 (0%)	47 73
1	C	552/555 (100%)	534 (97%)	16 (3%)	2 (0%)	34 60
2	B	408/429 (95%)	391 (96%)	17 (4%)	0	100 100
2	D	408/429 (95%)	390 (96%)	18 (4%)	0	100 100
All	All	1920/1968 (98%)	1848 (96%)	69 (4%)	3 (0%)	47 73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	PRO
1	C	4	PRO
1	C	55	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	A	495/495 (100%)	490 (99%)	5 (1%)	76	91
1	C	495/495 (100%)	488 (99%)	7 (1%)	67	86
2	B	374/390 (96%)	372 (100%)	2 (0%)	88	96
2	D	374/390 (96%)	372 (100%)	2 (0%)	88	96
All	All	1738/1770 (98%)	1722 (99%)	16 (1%)	78	92

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	MET
1	A	85	GLN
1	A	277	ARG
1	A	374	LYS
1	A	498	ASN
2	B	11	LYS
2	B	84	THR
1	C	16	MET
1	C	72	ARG
1	C	85	GLN
1	C	109	LEU
1	C	110	ASP
1	C	277	ARG
1	C	498	ASN
2	D	11	LYS
2	D	84	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	373	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](#)

4 non-standard protein/DNA/RNA residues 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	OMC	E	3	3	19,22,23	3.04	7 (36%)	26,31,34	0.72	0
3	OMC	E	5	3	19,22,23	3.07	7 (36%)	26,31,34	0.74	0
3	OMC	F	5	3	19,22,23	3.05	7 (36%)	26,31,34	0.72	0
3	OMC	F	3	3	19,22,23	3.04	7 (36%)	26,31,34	0.77	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
3	OMC	E	3	3	-	0/9/27/28	0/2/2/2
3	OMC	E	5	3	-	0/9/27/28	0/2/2/2
3	OMC	F	5	3	-	0/9/27/28	0/2/2/2
3	OMC	F	3	3	-	0/9/27/28	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	5	OMC	C6-C5	6.48	1.50	1.35
3	F	5	OMC	C2-N3	6.47	1.49	1.36
3	E	5	OMC	C2-N3	6.44	1.49	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	3	OMC	C6-C5	6.44	1.50	1.35
3	F	5	OMC	C6-C5	6.42	1.50	1.35
3	E	3	OMC	C6-C5	6.40	1.49	1.35
3	E	3	OMC	C2-N3	6.36	1.49	1.36
3	F	3	OMC	C2-N3	6.34	1.49	1.36
3	E	5	OMC	C4-N3	6.16	1.46	1.34
3	F	5	OMC	C4-N3	6.10	1.46	1.34
3	E	3	OMC	C4-N3	6.05	1.46	1.34
3	F	3	OMC	C4-N3	6.02	1.46	1.34
3	E	5	OMC	C4-N4	4.03	1.43	1.33
3	E	3	OMC	C4-N4	4.03	1.43	1.33
3	F	5	OMC	C4-N4	4.02	1.43	1.33
3	F	3	OMC	C4-N4	3.99	1.43	1.33
3	E	5	OMC	C2-N1	3.99	1.48	1.40
3	E	3	OMC	C2-N1	3.94	1.48	1.40
3	F	3	OMC	C2-N1	3.93	1.48	1.40
3	F	5	OMC	C2-N1	3.91	1.48	1.40
3	F	3	OMC	C6-N1	3.81	1.47	1.38
3	E	3	OMC	C6-N1	3.78	1.47	1.38
3	F	5	OMC	C6-N1	3.73	1.47	1.38
3	E	5	OMC	C6-N1	3.72	1.47	1.38
3	E	3	OMC	O2-C2	-2.76	1.18	1.23
3	F	3	OMC	O2-C2	-2.73	1.18	1.23
3	F	5	OMC	O2-C2	-2.72	1.18	1.23
3	E	5	OMC	O2-C2	-2.69	1.18	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	3	OMC	1	0
3	E	5	OMC	1	0
3	F	5	OMC	2	0

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	N	1	4	11,11,12	0.38	0	15,15,17	0.94	1 (6%)
4	FRU	N	2	4	11,12,12	0.68	0	10,18,18	1.04	0
4	GLC	O	1	4	11,11,12	1.13	2 (18%)	15,15,17	2.32	5 (33%)
4	FRU	O	2	4	11,12,12	0.70	0	10,18,18	2.34	4 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GLC	N	1	4	-	0/2/19/22	0/1/1/1
4	FRU	N	2	4	-	1/5/24/24	0/1/1/1
4	GLC	O	1	4	-	1/2/19/22	0/1/1/1
4	FRU	O	2	4	-	5/5/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	1	GLC	O5-C1	-2.54	1.39	1.43
4	O	1	GLC	C2-C3	-2.52	1.48	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	1	GLC	O3-C3-C2	-5.47	99.52	109.99
4	O	1	GLC	C2-C3-C4	-4.13	103.75	110.89
4	O	2	FRU	O6-C6-C5	3.68	123.93	111.29
4	O	1	GLC	C1-O5-C5	-3.46	107.50	112.19
4	O	2	FRU	O1-C1-C2	3.43	119.16	111.86
4	O	2	FRU	O3-C3-C4	3.06	123.89	113.32
4	O	2	FRU	O2-C2-O5	-2.93	103.85	109.50
4	O	1	GLC	O2-C2-C1	2.60	114.47	109.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	1	GLC	O5-C1-C2	2.55	114.71	110.77
4	N	1	GLC	C1-C2-C3	2.26	112.45	109.67

There are no chirality outliers.

All (7) torsion outliers are listed below:

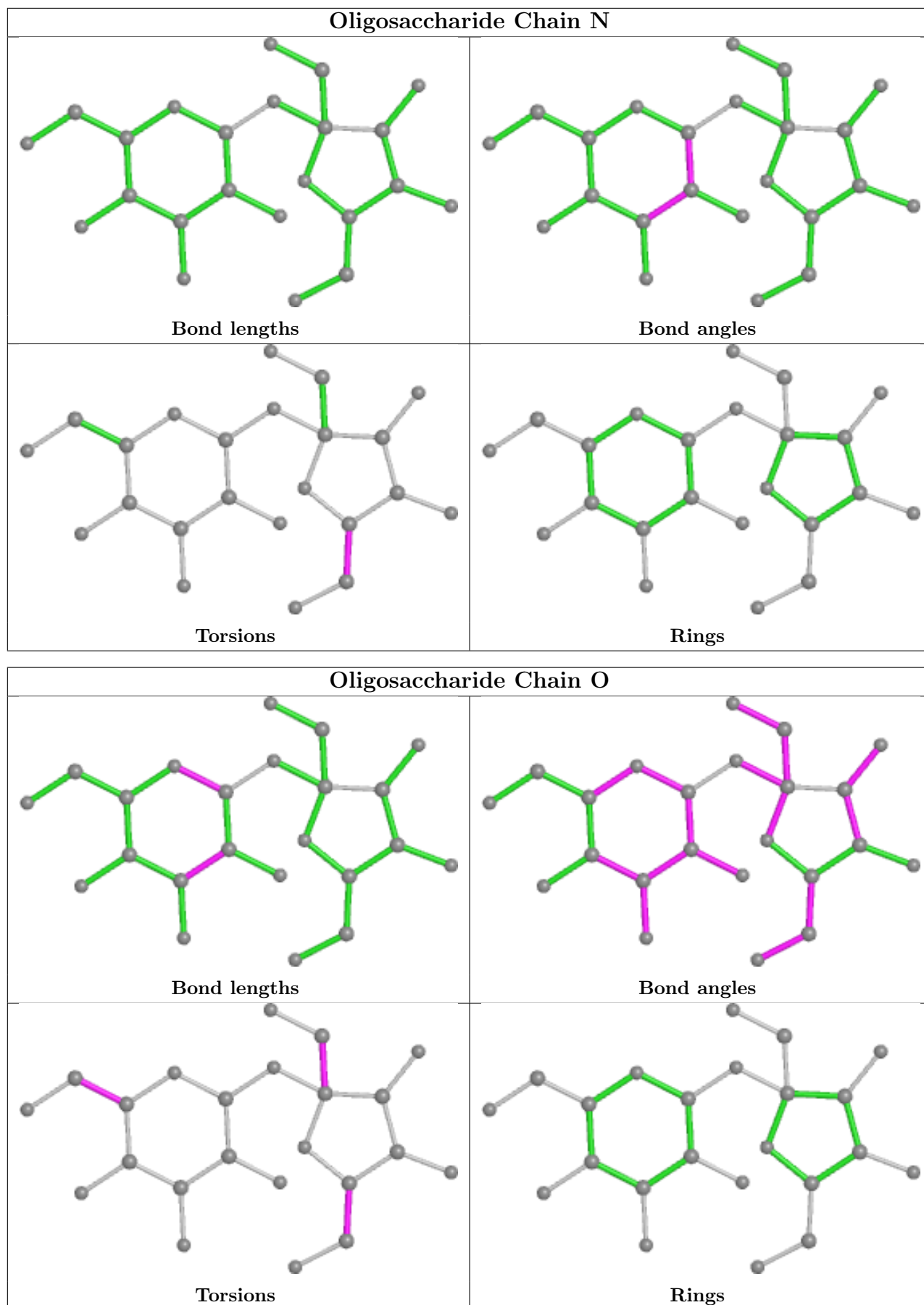
Mol	Chain	Res	Type	Atoms
4	O	2	FRU	O5-C5-C6-O6
4	O	2	FRU	C4-C5-C6-O6
4	O	2	FRU	O1-C1-C2-C3
4	O	1	GLC	O5-C5-C6-O6
4	O	2	FRU	O1-C1-C2-O5
4	N	2	FRU	O5-C5-C6-O6
4	O	2	FRU	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	N	1	GLC	5	0
4	O	1	GLC	8	0
4	O	2	FRU	12	0
4	N	2	FRU	3	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, 2 are monoatomic and 2 are modelled with single atom - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	A	604	-	5,5,5	0.93	0	5,5,5	1.00	0
6	SO4	A	602	-	4,4,4	0.14	0	6,6,6	0.06	0
7	GOL	A	603	-	5,5,5	0.94	0	5,5,5	0.95	0
8	XRF	C	603	5	26,30,30	0.51	0	39,47,47	0.75	2 (5%)
6	SO4	C	602	-	4,4,4	0.14	0	6,6,6	0.05	0
7	GOL	D	501	-	5,5,5	0.91	0	5,5,5	0.99	0
8	XRF	A	605	5	26,30,30	1.02	1 (3%)	39,47,47	0.88	2 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	A	604	-	-	0/4/4/4	-
8	XRF	C	603	5	-	4/22/34/34	0/2/2/2
7	GOL	A	603	-	-	1/4/4/4	-
7	GOL	D	501	-	-	0/4/4/4	-
8	XRF	A	605	5	-	10/22/34/34	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	605	XRF	P2-O10	-3.61	1.40	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	605	XRF	O10-P2-O9	2.95	114.52	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	603	XRF	P1-O9-P2	-2.23	125.17	132.83
8	C	603	XRF	O10-P2-O9	2.14	111.80	104.64
8	A	605	XRF	O3-P-O4	2.12	117.35	109.07

There are no chirality outliers.

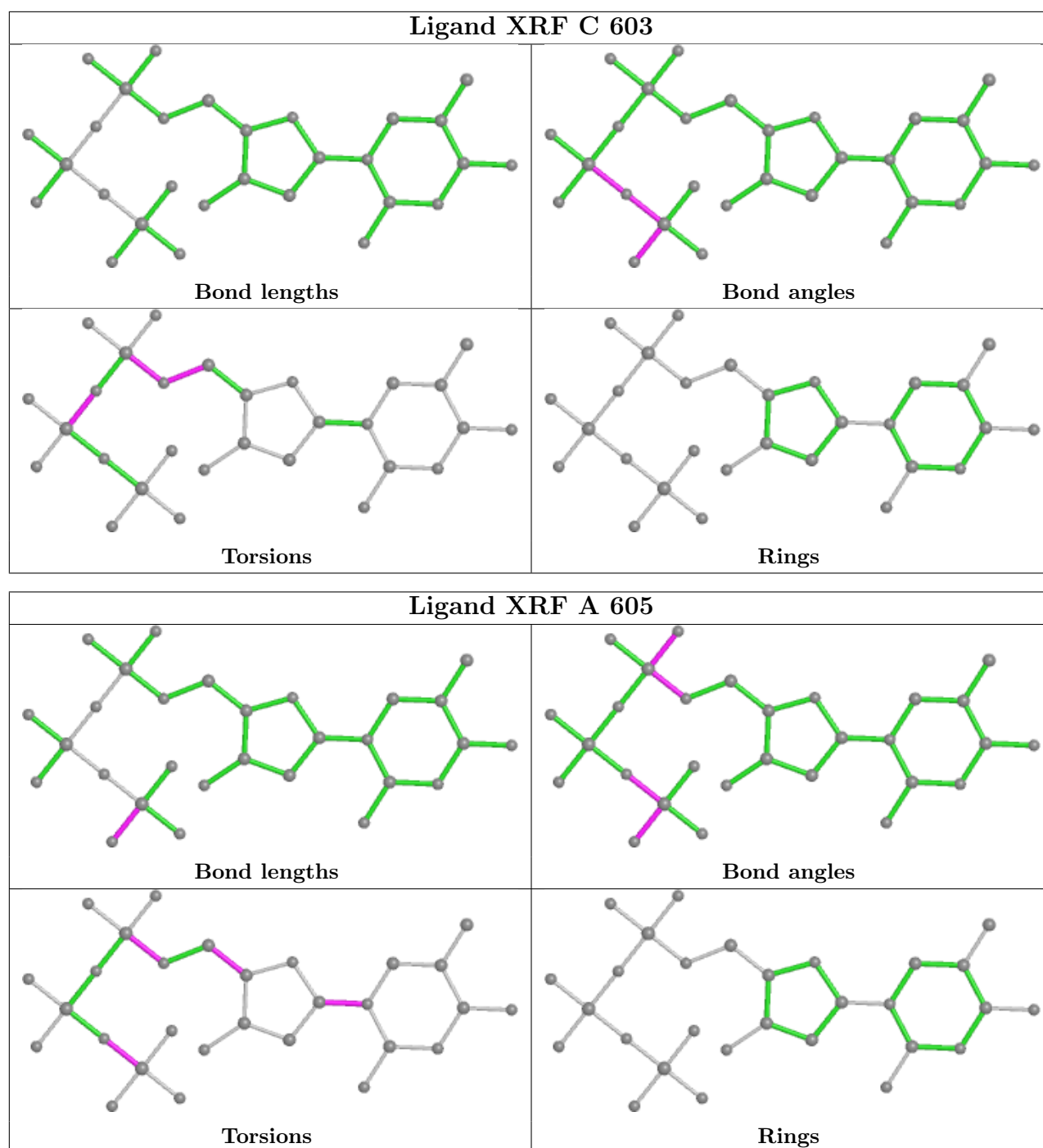
All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	605	XRF	C9-O3-P-O4
8	C	603	XRF	C9-O3-P-O6
8	A	605	XRF	C6-C5-N-C2
8	A	605	XRF	C6-C5-N-C3
8	A	605	XRF	O2-C5-N-C2
8	C	603	XRF	C8-C9-O3-P
8	A	605	XRF	O2-C5-N-C3
8	A	605	XRF	P1-O9-P2-O11
8	A	605	XRF	P1-O9-P2-O10
7	A	603	GOL	O1-C1-C2-C3
8	A	605	XRF	C9-O3-P-O5
8	C	603	XRF	C9-O3-P-O4
8	C	603	XRF	P-O6-P1-O7
8	A	605	XRF	O2-C8-C9-O3
8	A	605	XRF	C9-O3-P-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	554/555 (99%)	0.84	70 (12%) 3 3	40, 92, 183, 256	0
1	C	554/555 (99%)	1.01	92 (16%) 1 1	38, 95, 197, 296	0
2	B	412/429 (96%)	0.49	23 (5%) 24 23	40, 81, 151, 233	0
2	D	412/429 (96%)	0.75	38 (9%) 9 7	47, 92, 165, 246	0
3	E	33/38 (86%)	-0.42	0 100 100	69, 104, 151, 183	0
3	F	33/38 (86%)	-0.34	1 (3%) 50 51	71, 106, 156, 199	0
All	All	1998/2044 (97%)	0.76	224 (11%) 5 4	38, 90, 180, 296	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	133	PRO	18.9
1	A	135	ILE	18.7
1	C	26	LEU	14.3
2	B	214	LEU	13.1
2	D	214	LEU	12.8
1	C	25	PRO	12.5
1	A	26	LEU	12.1
1	A	133	PRO	11.7
1	A	134	SER	11.2
1	C	134	SER	11.1
1	A	132	ILE	10.8
1	A	30	LYS	10.7
1	C	63	ILE	10.5
1	C	74	LEU	10.5
1	C	132	ILE	9.8
1	C	135	ILE	9.8
1	C	33	ALA	9.5
2	D	215	THR	9.2
1	C	34	LEU	9.2

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Mol	Chain	Res	Type	RSRZ
1	C	67	ASP	9.1
2	D	4	PRO	9.0
1	C	142	ILE	9.0
1	C	136	ASN	8.2
2	D	89	GLU	8.2
1	A	136	ASN	8.1
1	A	67	ASP	7.4
1	C	61	PHE	7.2
1	A	25	PRO	7.0
1	C	69	THR	6.7
1	C	27	THR	6.6
1	C	66	LYS	6.5
1	C	289	LEU	6.2
2	D	358	ARG	6.2
1	C	37	ILE	6.2
1	C	29	GLU	6.1
1	C	32	LYS	6.1
2	B	88	TRP	5.9
1	C	30	LYS	5.9
1	A	142	ILE	5.9
2	D	88	TRP	5.7
1	A	73	LYS	5.5
1	A	27	THR	5.5
1	A	63	ILE	5.4
2	D	209	LEU	5.4
2	B	4	PRO	5.3
1	C	21	VAL	5.3
1	A	61	PHE	5.2
1	C	290	THR	5.1
1	C	137	ASN	5.0
1	A	139	THR	5.0
1	A	66	LYS	4.9
1	C	144	TYR	4.9
1	C	64	LYS	4.8
1	C	288	ALA	4.7
1	C	138	GLU	4.7
1	A	33	ALA	4.7
2	D	210	LEU	4.6
1	A	131	THR	4.6
1	C	248	GLU	4.5
2	D	211	ARG	4.5
1	A	254	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	141	GLY	4.5
1	A	74	LEU	4.5
2	B	215	THR	4.5
1	A	148	VAL	4.5
2	B	5	ILE	4.4
2	D	360	ALA	4.4
1	C	75	VAL	4.4
2	B	212	TRP	4.4
1	A	29	GLU	4.4
1	A	289	LEU	4.4
2	B	232	TYR	4.3
1	C	303	LEU	4.3
2	D	232	TYR	4.3
2	B	92	LEU	4.3
1	C	139	THR	4.2
1	C	246	LEU	4.2
1	A	70	LYS	4.1
2	D	173	LYS	4.1
2	D	90	VAL	4.1
1	C	73	LYS	4.0
2	D	212	TRP	4.0
2	D	213	GLY	4.0
2	D	87	PHE	4.0
1	C	295	LEU	4.0
1	C	287	LYS	4.0
1	C	72	ARG	3.9
1	C	68	SER	3.9
1	C	141	GLY	3.9
1	A	554	ALA	3.9
2	D	168	LEU	3.9
1	C	310	LEU	3.8
2	B	295	LEU	3.8
2	B	90	VAL	3.8
1	A	138	GLU	3.7
2	D	92	LEU	3.7
1	C	554	ALA	3.7
1	A	285	GLY	3.7
2	D	85	GLN	3.7
1	A	288	ALA	3.7
1	A	34	LEU	3.6
1	C	70	LYS	3.6
1	C	130	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	140	PRO	3.6
1	A	71	TRP	3.6
1	A	130	PHE	3.6
1	C	19	PRO	3.5
2	D	154	LYS	3.5
1	C	247	PRO	3.5
2	B	89	GLU	3.5
1	C	59	PRO	3.4
1	C	186	ASP	3.4
1	C	22	LYS	3.4
2	D	67	ASP	3.4
1	A	193	LEU	3.4
2	B	209	LEU	3.4
2	B	284	ARG	3.4
1	C	209	LEU	3.4
1	A	21	VAL	3.3
1	A	282	LEU	3.3
2	D	217	PRO	3.3
1	A	68	SER	3.2
1	A	295	LEU	3.2
1	C	254	VAL	3.2
1	A	284	ARG	3.1
2	B	168	LEU	3.1
1	A	128	THR	3.1
1	C	292	VAL	3.1
2	B	87	PHE	3.1
1	A	261	VAL	3.1
1	A	287	LYS	3.1
1	C	167	ILE	3.1
2	D	198	HIS	3.0
1	A	303	LEU	3.0
1	C	71	TRP	3.0
1	A	32	LYS	3.0
2	B	86	ASP	3.0
1	C	202	ILE	3.0
1	C	146	TYR	2.9
2	B	85	GLN	2.9
1	A	8	VAL	2.9
1	C	16	MET	2.9
2	D	195	ILE	2.9
1	C	52	PRO	2.9
2	B	277	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	148	VAL	2.8
1	C	285	GLY	2.8
1	C	251	SER	2.8
1	A	283	LEU	2.8
2	D	189	VAL	2.7
2	D	428	GLN	2.7
1	C	65	LYS	2.7
2	D	197	GLN	2.7
1	C	131	THR	2.6
1	A	62	ALA	2.6
1	A	2	ILE	2.6
2	B	297	GLU	2.6
2	D	60	VAL	2.6
1	C	283	LEU	2.6
1	A	50	ILE	2.6
1	C	40	GLU	2.6
1	A	251	SER	2.6
1	A	137	ASN	2.5
1	C	257	ILE	2.5
2	D	86	ASP	2.5
1	C	36	GLU	2.5
1	A	72	ARG	2.5
1	C	55	PRO	2.5
1	A	23	GLN	2.5
1	A	248	GLU	2.5
2	D	174	GLN	2.5
1	C	252	TRP	2.4
2	B	217	PRO	2.4
1	C	304	ALA	2.4
1	C	10	VAL	2.4
1	C	291	GLU	2.4
1	A	144	TYR	2.4
1	C	228	LEU	2.4
1	C	260	LEU	2.4
1	A	124	PHE	2.4
1	A	127	TYR	2.4
1	A	55	PRO	2.3
1	C	41	MET	2.3
2	D	146	TYR	2.3
1	A	310	LEU	2.3
1	C	115	TYR	2.3
2	D	422	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	244	ILE	2.3
1	C	249	LYS	2.3
1	A	544	GLY	2.3
1	C	109	LEU	2.3
1	C	15	GLY	2.3
1	C	23	GLN	2.3
1	C	279	LEU	2.3
1	C	296	THR	2.3
2	D	200	THR	2.2
1	C	49	LYS	2.2
1	C	256	ASP	2.2
1	A	550	LYS	2.2
1	C	245	VAL	2.2
2	D	171	PHE	2.2
1	A	279	LEU	2.2
2	B	250	ASP	2.2
1	A	293	ILE	2.2
1	C	14	PRO	2.2
1	A	244	ILE	2.2
2	D	159	ILE	2.2
2	D	248	GLU	2.1
1	C	145	GLN	2.1
3	F	17	DT	2.1
1	A	145	GLN	2.1
2	D	425	LEU	2.1
2	D	277	ARG	2.1
2	B	171	PHE	2.1
1	A	24	TRP	2.1
1	C	91	GLN	2.1
1	C	219	LYS	2.1
1	C	140	PRO	2.1
2	B	294	PRO	2.1
1	A	292	VAL	2.0
1	A	542	ILE	2.0
1	A	64	LYS	2.0
1	A	19	PRO	2.0
1	C	294	PRO	2.0

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

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
3	OMC	E	3	21/22	0.96	0.16	87,96,112,123	0
3	OMC	F	3	21/22	0.97	0.15	84,95,114,121	0
3	OMC	F	5	21/22	0.97	0.16	63,72,83,88	0
3	OMC	E	5	21/22	0.97	0.18	63,69,79,82	0

6.3 Carbohydrates [i](#)

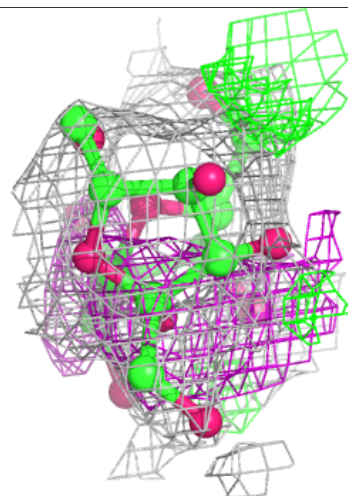
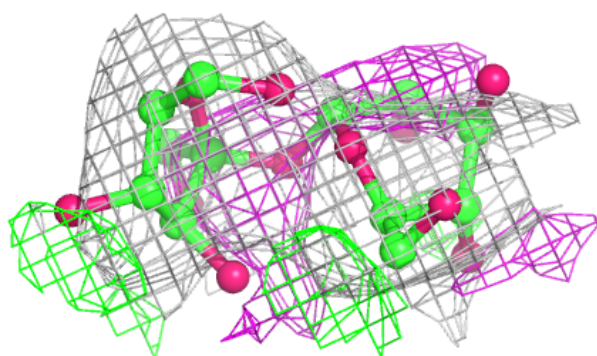
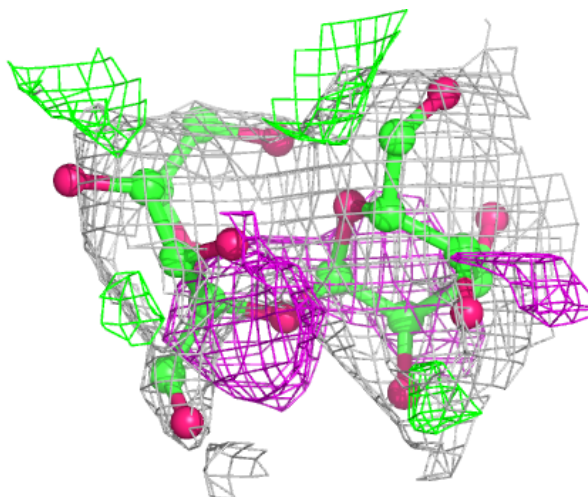
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

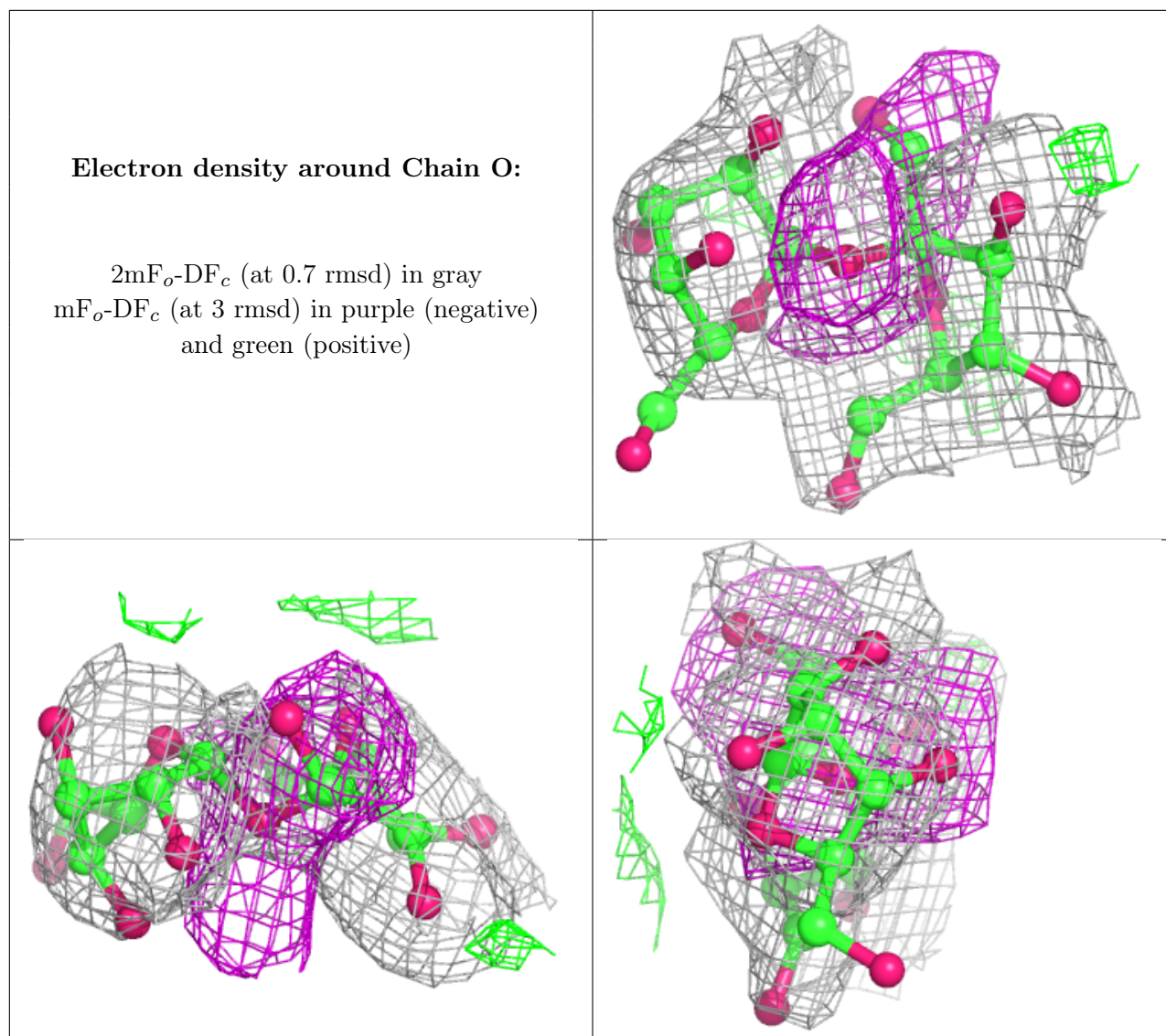
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	FRU	O	2	12/12	0.71	0.31	77,107,120,127	0
4	FRU	N	2	12/12	0.76	0.30	95,116,132,137	0
4	GLC	N	1	11/12	0.76	0.27	99,114,135,135	0
4	GLC	O	1	11/12	0.87	0.27	116,126,131,132	0

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 N:

$2mF_o-DF_c$ (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.

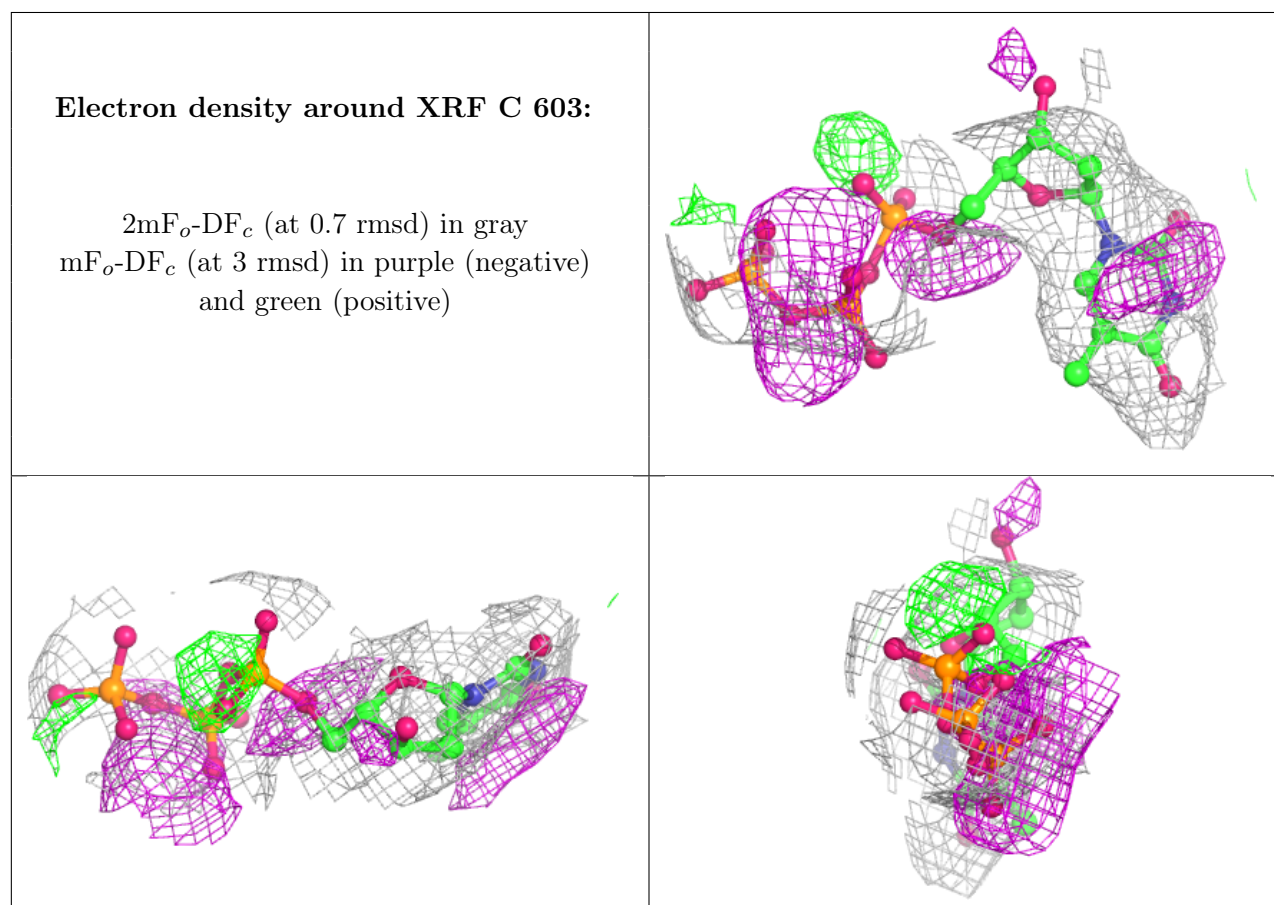
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CA	C	601	1/1	0.46	0.12	149,149,149,149	0
5	CA	A	601	1/1	0.63	0.18	115,115,115,115	0
7	GOL	D	501	6/6	0.79	0.31	71,85,106,116	0
8	XRF	C	603	29/29	0.84	0.21	105,116,169,184	0
6	SO4	A	602	5/5	0.85	0.23	98,114,127,138	0
8	XRF	A	605	29/29	0.89	0.19	99,124,159,173	0
7	GOL	A	604	6/6	0.93	0.34	89,89,92,93	0

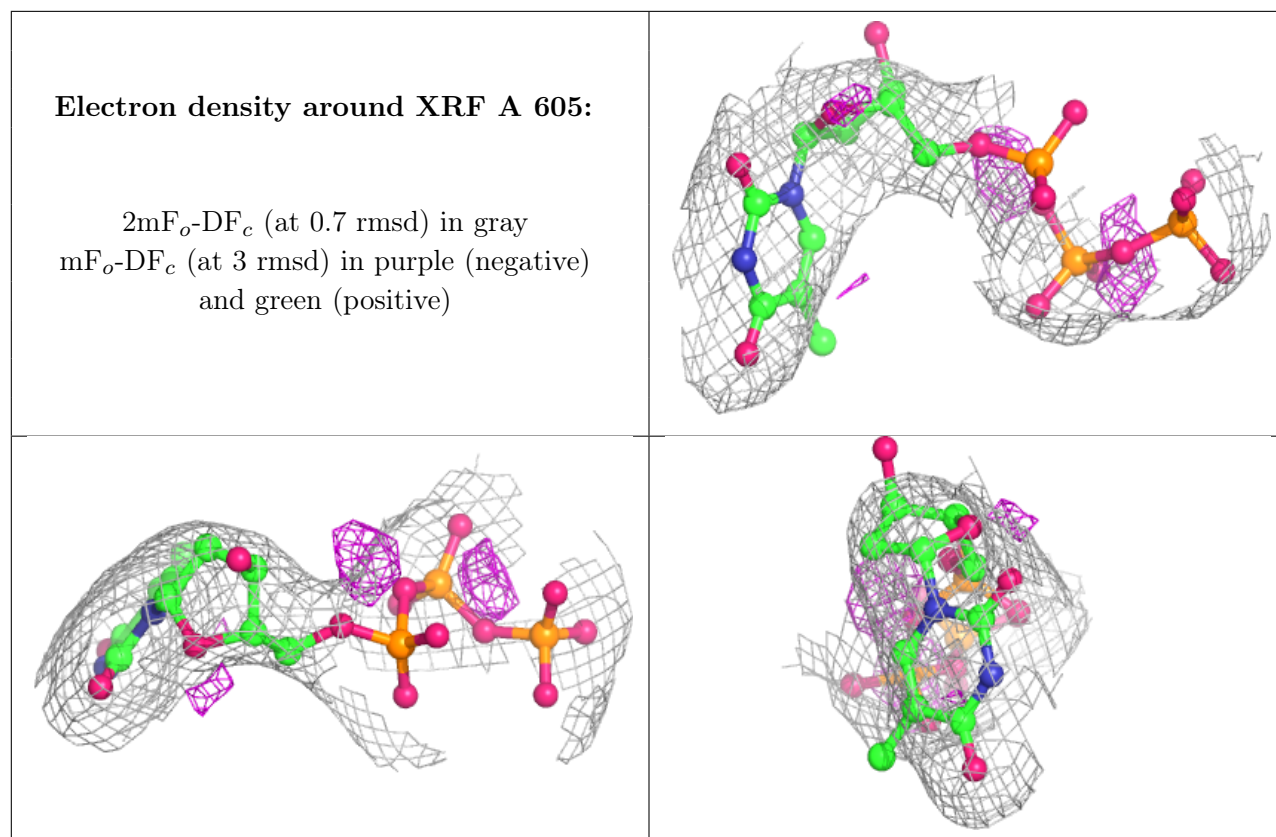
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GOL	A	603	6/6	0.93	0.31	60,68,72,93	0
6	SO4	C	602	5/5	0.95	0.14	99,105,124,126	0
9	NH4	A	606	1/1	0.97	0.38	48,48,48,48	0
9	NH4	C	604	1/1	0.98	0.54	39,39,39,39	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.