



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 03:10 AM BST

PDB ID : 5XN1
Title : HIV-1 reverse transcriptase Q151M:DNA:entecavir-triphosphate ternary complex
Authors : Yasutake, Y.; Tamura, N.; Hayashi, H.; Maeda, K.
Deposited on : 2017-05-17
Resolution : 2.45 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
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) : 2.13.1

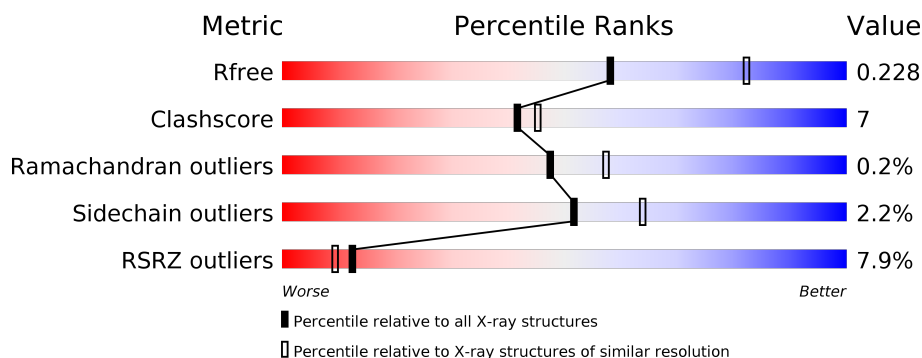
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	A	557	<div> <div>6%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>..</div> </div> </div>
1	C	557	<div> <div>10%</div> <div> <div></div> <div>82%</div> <div>15%</div> <div>..</div> </div> </div>
2	B	444	<div> <div>12%</div> <div> <div></div> <div>75%</div> <div>16%</div> <div>•</div> <div>8%</div> </div> </div>
2	D	444	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>9%</div> <div>•</div> <div>8%</div> </div> </div>
3	E	38	<div> <div></div> <div> <div></div> <div>74%</div> <div>11%</div> <div>8%</div> <div>8%</div> </div> </div>
3	F	38	<div> <div>3%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	G	2	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17562 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 Pol protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	1	0
			4488	2903	748	829	8			
1	C	551	Total	C	N	O	S	0	0	0
			4483	2900	748	827	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP D3XFN7
A	0	VAL	-	expression tag	UNP D3XFN7
A	151	MET	GLN	engineered mutation	UNP D3XFN7
A	162	SER	CYS	engineered mutation	UNP D3XFN7
A	280	SER	CYS	engineered mutation	UNP D3XFN7
C	-1	MET	-	expression tag	UNP D3XFN7
C	0	VAL	-	expression tag	UNP D3XFN7
C	151	MET	GLN	engineered mutation	UNP D3XFN7
C	162	SER	CYS	engineered mutation	UNP D3XFN7
C	280	SER	CYS	engineered mutation	UNP D3XFN7

- Molecule 2 is a protein called Pol protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	407	Total	C	N	O	S	0	0	0
			3354	2183	558	607	6			
2	D	407	Total	C	N	O	S	0	0	0
			3354	2183	558	607	6			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	expression tag	UNP D3XFN7
B	-14	ALA	-	expression tag	UNP D3XFN7

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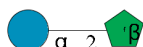
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	HIS	-	expression tag	UNP D3XFN7
B	-12	HIS	-	expression tag	UNP D3XFN7
B	-11	HIS	-	expression tag	UNP D3XFN7
B	-10	HIS	-	expression tag	UNP D3XFN7
B	-9	HIS	-	expression tag	UNP D3XFN7
B	-8	HIS	-	expression tag	UNP D3XFN7
B	-7	ALA	-	expression tag	UNP D3XFN7
B	-6	LEU	-	expression tag	UNP D3XFN7
B	-5	GLU	-	expression tag	UNP D3XFN7
B	-4	VAL	-	expression tag	UNP D3XFN7
B	-3	LEU	-	expression tag	UNP D3XFN7
B	-2	PHE	-	expression tag	UNP D3XFN7
B	-1	GLN	-	expression tag	UNP D3XFN7
B	0	GLY	-	expression tag	UNP D3XFN7
B	162	SER	CYS	engineered mutation	UNP D3XFN7
B	280	SER	CYS	engineered mutation	UNP D3XFN7
D	-15	MET	-	expression tag	UNP D3XFN7
D	-14	ALA	-	expression tag	UNP D3XFN7
D	-13	HIS	-	expression tag	UNP D3XFN7
D	-12	HIS	-	expression tag	UNP D3XFN7
D	-11	HIS	-	expression tag	UNP D3XFN7
D	-10	HIS	-	expression tag	UNP D3XFN7
D	-9	HIS	-	expression tag	UNP D3XFN7
D	-8	HIS	-	expression tag	UNP D3XFN7
D	-7	ALA	-	expression tag	UNP D3XFN7
D	-6	LEU	-	expression tag	UNP D3XFN7
D	-5	GLU	-	expression tag	UNP D3XFN7
D	-4	VAL	-	expression tag	UNP D3XFN7
D	-3	LEU	-	expression tag	UNP D3XFN7
D	-2	PHE	-	expression tag	UNP D3XFN7
D	-1	GLN	-	expression tag	UNP D3XFN7
D	0	GLY	-	expression tag	UNP D3XFN7
D	162	SER	CYS	engineered mutation	UNP D3XFN7
D	280	SER	CYS	engineered mutation	UNP D3XFN7

- Molecule 3 is a DNA chain called 38-MER DNA aptamer.

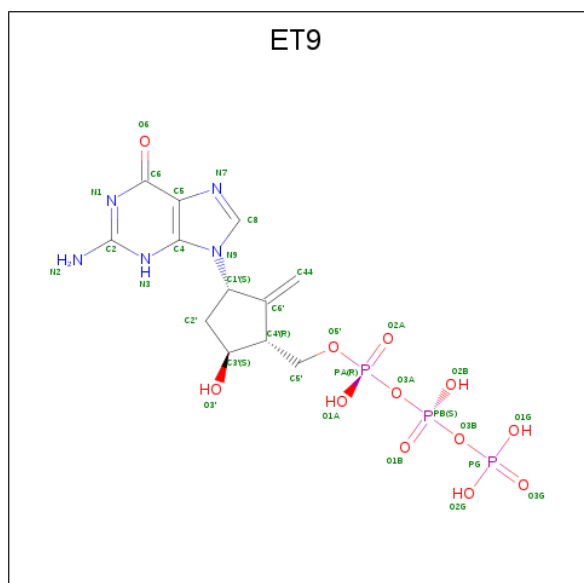
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	35	Total	C	N	O	P	0	0	0
			718	339	128	216	35			
3	F	38	Total	C	N	O	P	0	0	0
			777	369	140	231	37			

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



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

- Molecule 5 is [[(1R,3S,5S)-3-(2-azanyl-6-oxidanylidene-3H-purin-9-yl)-2-methylidene-5-oxida nyl-cyclopentyl]methoxy-oxidanyl-phosphory l] phosphono hydrogen phosphate (three-letter code: ET9) (formula: C₁₂H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			32	12	5	12	3		
5	C	1	Total	C	N	O	P	0	0
			32	12	5	12	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

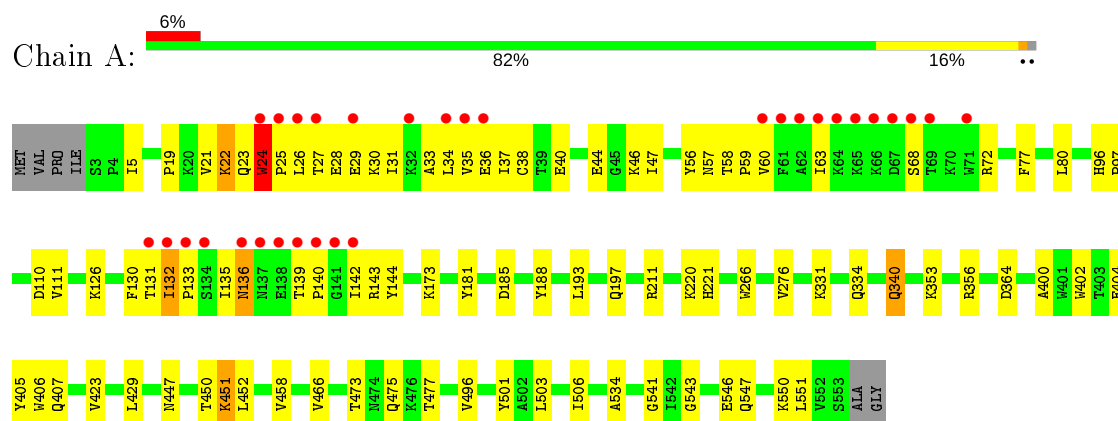
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	78	Total	O	0	0
			78	78		
8	B	28	Total	O	0	0
			28	28		
8	E	34	Total	O	0	0
			34	34		
8	C	56	Total	O	0	0
			56	56		
8	D	54	Total	O	0	0
			54	54		
8	F	19	Total	O	0	0
			19	19		

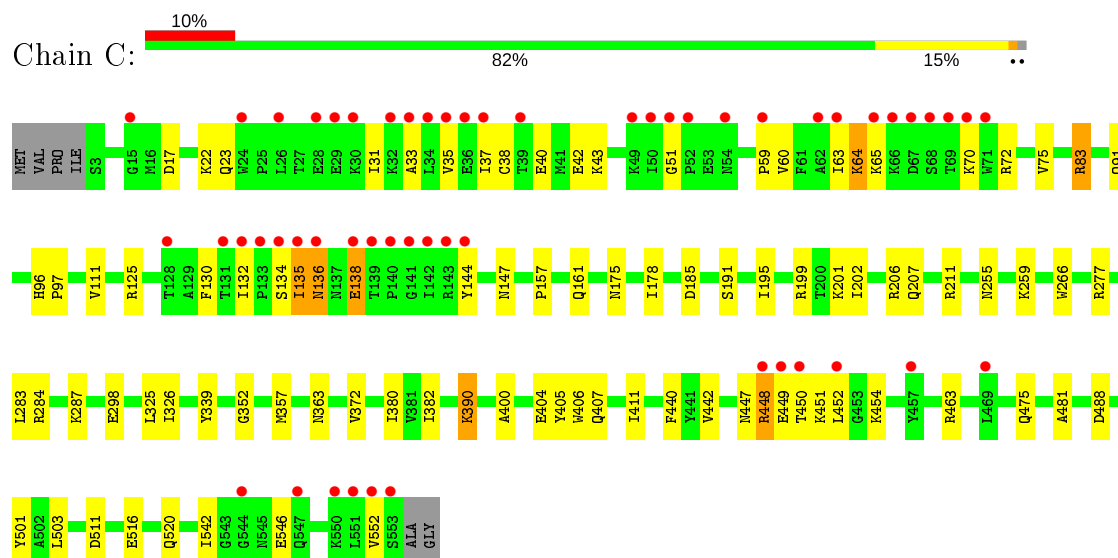
3 Residue-property plots [i](#)

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.

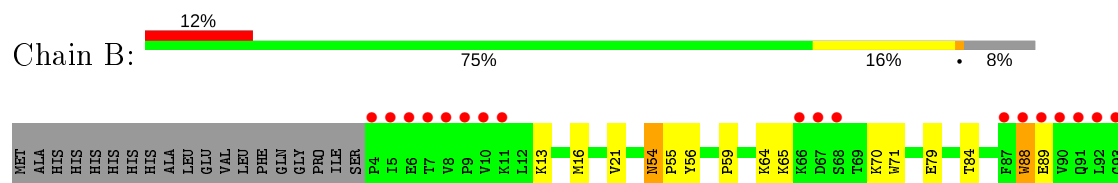
• Molecule 1: Pol protein

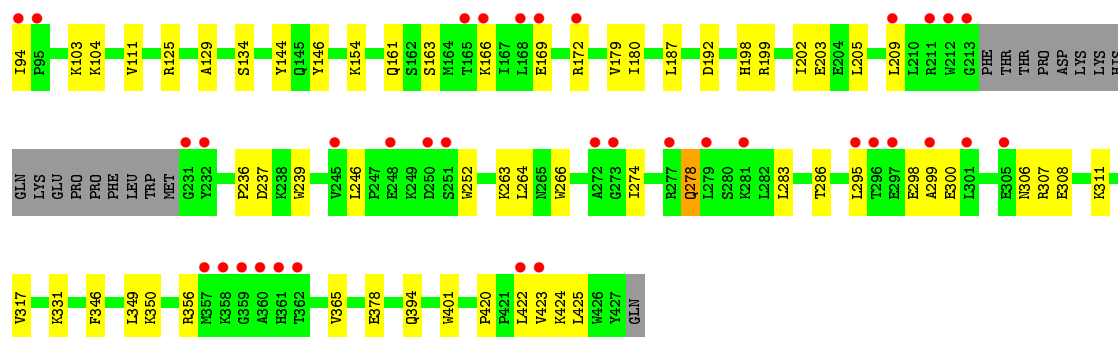


• Molecule 1: Pol protein

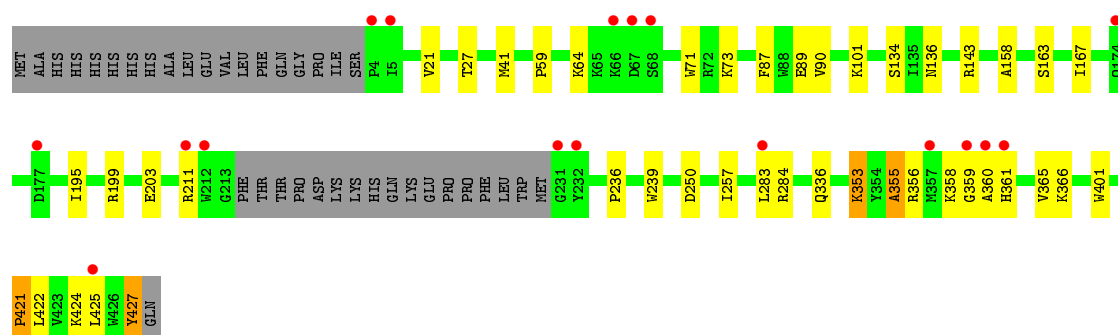
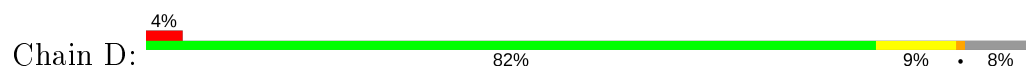


• Molecule 2: Pol protein





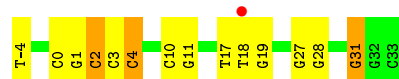
• Molecule 2: Pol protein



• Molecule 3: 38-MER DNA aptamer



• Molecule 3: 38-MER DNA aptamer



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



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	284.71 Å 284.71 Å 95.79 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.02 – 2.45 47.02 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.02-2.45) 99.9 (47.02-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.45 Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575)	Depositor
R, R_{free}	0.188 , 0.227 0.188 , 0.228	Depositor DCC
R_{free} test set	5440 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	45.8	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17562	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, GOL, MG, GLC, ET9, FRU

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	0.38	0/4608	0.54	0/6257
1	C	0.35	0/4600	0.52	1/6246 (0.0%)
2	B	0.37	0/3449	0.54	0/4684
2	D	0.34	0/3449	0.52	0/4684
3	E	0.77	0/756	0.96	1/1165 (0.1%)
3	F	0.77	1/823 (0.1%)	0.88	2/1269 (0.2%)
All	All	0.41	1/17685 (0.0%)	0.58	4/24305 (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	A	0	2
1	C	0	3
2	D	0	2
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	-4	DT	O3'-P	-6.56	1.53	1.61

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	31	DG	O4'-C4'-C3'	-5.95	102.12	104.50
1	C	51	GLY	C-N-CD	5.45	139.84	128.40
3	F	31	DG	O4'-C4'-C3'	-5.26	102.40	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	31	DG	C4'-C3'-C2'	-5.01	98.59	103.10

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	24	TRP	Peptide
1	A	68	SER	Peptide
1	C	135	ILE	Peptide
1	C	138	GLU	Peptide
1	C	448	ARG	Sidechain
2	D	355	ALA	Peptide
2	D	421	PRO	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	A	4488	0	4536	87	0
1	C	4483	0	4532	58	0
2	B	3354	0	3387	50	0
2	D	3354	0	3387	35	0
3	E	718	0	397	5	0
3	F	777	0	432	12	0
4	G	23	0	21	1	0
5	A	32	0	0	0	0
5	C	32	0	0	2	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	B	12	0	16	2	0
7	D	12	0	16	0	0
7	F	6	0	8	0	0
8	A	78	0	0	0	0
8	B	28	0	0	0	0
8	C	56	0	0	0	0
8	D	54	0	0	1	0
8	E	34	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	F	19	0	0	0	0
All	All	17562	0	16732	237	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 7.

All (237) 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:31:ILE:HB	1:A:132:ILE:HD11	1.18	1.09
1:A:24:TRP:CD1	1:A:25:PRO:HD3	2.11	0.86
1:C:450:THR:HG23	1:C:452:LEU:H	1.42	0.85
3:F:1:DG:H2'	3:F:2:OMC:C6	2.12	0.84
3:F:0:DC:H2''	3:F:1:DG:H5'	1.61	0.82
2:B:308:GLU:HA	2:B:311:LYS:HB2	1.61	0.81
2:B:394:GLN:HG2	7:B:501:GOL:H12	1.61	0.81
1:C:40:GLU:O	1:C:43:LYS:N	2.17	0.78
2:B:423:VAL:HB	2:B:425:LEU:CD1	2.15	0.77
1:C:195:ILE:O	1:C:199:ARG:HG3	1.86	0.76
1:C:136:ASN:O	1:C:138:GLU:N	2.19	0.74
1:A:31:ILE:HB	1:A:132:ILE:CD1	2.09	0.74
1:A:24:TRP:HD1	1:A:25:PRO:HD3	1.54	0.73
1:A:400:ALA:O	1:A:404:GLU:HG2	1.88	0.72
3:F:0:DC:C2'	3:F:1:DG:H5'	2.20	0.71
1:A:31:ILE:HD11	1:A:135:ILE:HA	1.72	0.71
1:A:31:ILE:CB	1:A:132:ILE:HD11	2.10	0.69
1:A:547:GLN:O	1:A:550:LYS:HB2	1.91	0.69
2:B:88:TRP:CD1	2:B:89:GLU:HG3	2.28	0.69
5:C:601:ET9:N2	3:F:0:DC:O2	2.25	0.69
1:A:34:LEU:HB3	1:A:132:ILE:HG13	1.75	0.69
2:B:423:VAL:HB	2:B:425:LEU:HD12	1.76	0.68
3:F:17:DT:H5''	3:F:17:DT:H6	1.58	0.67
2:D:422:LEU:N	2:D:422:LEU:HD22	2.09	0.67
1:C:372:VAL:HG11	1:C:411:ILE:HG23	1.77	0.66
2:D:90:VAL:HG11	2:D:158:ALA:HA	1.76	0.66
2:B:205:LEU:O	2:B:209:LEU:HD22	1.96	0.65
1:A:132:ILE:C	1:A:132:ILE:HD13	2.16	0.65
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.76	0.65
1:A:132:ILE:CG2	1:A:142:ILE:HB	2.28	0.64
1:C:134:SER:OG	1:C:135:ILE:N	2.30	0.64
2:B:350:LYS:NZ	2:B:378:GLU:OE2	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:496:VAL:HG22	1:A:534:ALA:HB3	1.81	0.62
1:A:543:GLY:HA2	2:B:283:LEU:O	1.99	0.62
3:F:3:DC:H2'	3:F:4:OMC:C6	2.35	0.62
1:A:131:THR:HG22	1:A:143:ARG:NE	2.14	0.62
1:A:193:LEU:HD13	1:A:197:GLN:HG3	1.80	0.61
1:A:132:ILE:HG23	1:A:142:ILE:HB	1.83	0.61
1:A:31:ILE:HA	1:A:34:LEU:HB2	1.83	0.61
1:A:131:THR:HG22	1:A:143:ARG:HE	1.64	0.61
2:B:394:GLN:CG	7:B:501:GOL:H12	2.32	0.60
2:B:163:SER:O	2:B:166:LYS:HG2	2.03	0.59
2:B:103:LYS:HE3	2:B:179:VAL:HG23	1.85	0.59
2:D:422:LEU:O	2:D:425:LEU:HD23	2.02	0.59
2:D:21:VAL:HB	2:D:59:PRO:HD3	1.85	0.58
3:E:3:DC:H2'	3:E:4:OMC:C6	2.37	0.58
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.85	0.58
1:A:450:THR:HG22	1:A:452:LEU:HG	1.84	0.58
1:C:454:LYS:HB2	1:C:552:VAL:HG13	1.85	0.58
1:C:38:CYS:SG	1:C:132:ILE:HD11	2.44	0.58
1:C:284:ARG:HH12	1:C:357:MET:HE1	1.70	0.57
3:F:18:DT:H4'	3:F:19:DG:C8	2.39	0.57
2:B:252:TRP:CD1	2:B:295:LEU:HD21	2.40	0.57
1:C:60:VAL:HG12	1:C:75:VAL:HG22	1.87	0.56
1:A:24:TRP:HD1	1:A:25:PRO:CD	2.18	0.56
2:D:356:ARG:HA	2:D:361:HIS:CE1	2.41	0.56
2:B:172:ARG:HH11	2:B:180:ILE:HB	1.70	0.56
1:C:255:ASN:O	1:C:259:LYS:HG3	2.06	0.56
1:A:402:TRP:O	2:B:331:LYS:NZ	2.37	0.56
1:A:5:ILE:H	1:A:5:ILE:HD12	1.70	0.56
1:C:17:ASP:O	1:C:83:ARG:NH1	2.39	0.55
1:C:405:TYR:CE2	1:C:407:GLN:HB2	2.42	0.55
1:A:23:GLN:OE1	1:A:60:VAL:HG12	2.05	0.55
1:C:400:ALA:O	1:C:404:GLU:HG2	2.07	0.55
1:A:450:THR:O	1:A:451:LYS:HG2	2.06	0.55
2:D:365:VAL:HG11	2:D:401:TRP:HB2	1.87	0.55
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.87	0.55
2:D:421:PRO:C	2:D:422:LEU:HD22	2.27	0.55
1:A:276:VAL:HG22	1:A:353:LYS:HE2	1.89	0.55
5:C:601:ET9:N1	3:F:0:DC:N3	2.54	0.55
1:C:339:TYR:CZ	1:C:352:GLY:HA3	2.42	0.54
1:A:26:LEU:HD22	1:A:133:PRO:HG2	1.89	0.54
2:B:54:ASN:C	2:B:54:ASN:HD22	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:ILE:HG22	1:C:64:LYS:H	1.72	0.54
2:D:421:PRO:HB3	2:D:424:LYS:HG3	1.88	0.53
1:A:21:VAL:CG2	1:A:59:PRO:HD3	2.38	0.53
1:A:450:THR:HG21	1:A:452:LEU:HB2	1.91	0.53
1:A:27:THR:HG22	1:A:29:GLU:N	2.24	0.53
1:C:125:ARG:HD3	1:C:147:ASN:HA	1.89	0.53
2:D:358:LYS:HB3	2:D:361:HIS:HB3	1.91	0.53
1:A:21:VAL:HG21	1:A:59:PRO:HD3	1.91	0.53
1:C:542:ILE:O	1:C:546:GLU:N	2.34	0.53
1:A:139:THR:HB	1:A:140:PRO:CD	2.38	0.53
2:B:199:ARG:O	2:B:203:GLU:HG2	2.10	0.52
1:C:447:ASN:OD1	1:C:449:GLU:N	2.38	0.52
2:B:278:GLN:HG2	2:B:299:ALA:N	2.25	0.52
1:A:447:ASN:HB3	1:A:450:THR:HB	1.90	0.52
1:C:111:VAL:HB	1:C:185:ASP:HB2	1.90	0.52
1:C:440:PHE:HZ	1:C:463:ARG:HH21	1.58	0.52
2:D:421:PRO:HB3	2:D:424:LYS:HE2	1.92	0.52
1:A:458:VAL:HG12	2:B:286:THR:HG21	1.90	0.52
2:B:266:TRP:CZ2	2:B:346:PHE:HE2	2.28	0.52
1:C:475:GLN:HB3	1:C:501:TYR:CE2	2.44	0.52
2:D:358:LYS:HE2	2:D:366:LYS:NZ	2.25	0.51
2:B:94:ILE:HG12	2:B:161:GLN:NE2	2.26	0.51
2:D:101:LYS:O	2:D:236:PRO:HB2	2.11	0.51
1:A:450:THR:HG22	1:A:452:LEU:CG	2.41	0.51
2:B:274:ILE:HG23	2:B:306:ASN:OD1	2.10	0.51
1:C:31:ILE:O	1:C:35:VAL:HG23	2.11	0.51
2:B:263:LYS:HB2	2:B:423:VAL:HG11	1.93	0.51
1:C:298:GLU:OE2	1:C:298:GLU:N	2.29	0.51
1:A:38:CYS:HB3	1:A:47:ILE:HD11	1.93	0.51
1:A:331:LYS:NZ	1:A:364:ASP:OD2	2.38	0.50
2:B:317:VAL:HG12	2:B:349:LEU:HD23	1.92	0.50
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.46	0.50
1:C:157:PRO:O	1:C:161:GLN:HG3	2.11	0.50
1:A:110[A]:ASP:HB2	1:A:220:LYS:HB3	1.93	0.50
1:A:181:TYR:HB2	1:A:188:TYR:HB3	1.93	0.50
1:A:23:GLN:HA	1:A:59:PRO:HB3	1.93	0.50
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.94	0.50
1:A:466:VAL:CG2	1:A:551:LEU:HG	2.42	0.49
1:A:450:THR:CG2	1:A:452:LEU:HB2	2.42	0.49
2:B:266:TRP:CE2	2:B:425:LEU:HD21	2.46	0.49
2:B:88:TRP:HD1	2:B:89:GLU:N	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ALA:O	1:C:37:ILE:HG22	2.12	0.49
1:A:135:ILE:HG13	1:A:136:ASN:OD1	2.12	0.48
2:B:125:ARG:HB3	2:B:146:TYR:O	2.13	0.48
2:B:54:ASN:HD22	2:B:55:PRO:N	2.12	0.48
1:A:26:LEU:HD22	1:A:133:PRO:CG	2.44	0.48
1:A:24:TRP:CD1	1:A:25:PRO:CD	2.91	0.48
1:A:31:ILE:O	1:A:35:VAL:HG23	2.14	0.48
1:A:541:GLY:HA2	1:A:546:GLU:HG3	1.96	0.48
1:C:130:PHE:CZ	1:C:144:TYR:HB2	2.49	0.48
3:F:1:DG:H2'	3:F:2:OMC:H6	1.75	0.48
1:A:23:GLN:OE1	1:A:59:PRO:HA	2.14	0.47
1:A:466:VAL:HG21	1:A:551:LEU:HG	1.95	0.47
2:D:64:LYS:HE3	2:D:71:TRP:CE2	2.48	0.47
2:D:336:GLN:HG3	2:D:427:TYR:OH	2.14	0.47
2:D:358:LYS:O	2:D:360:ALA:N	2.47	0.47
2:D:87:PHE:HB3	2:D:89:GLU:OE2	2.15	0.47
1:A:132:ILE:O	1:A:132:ILE:HG23	2.15	0.47
1:C:91:GLN:HB2	1:C:161:GLN:HE22	1.80	0.47
1:C:406:TRP:HB3	2:D:421:PRO:HG3	1.96	0.47
1:A:57:ASN:OD1	1:A:131:THR:HG23	2.14	0.46
1:A:132:ILE:N	1:A:142:ILE:O	2.42	0.46
2:B:88:TRP:NE1	2:B:89:GLU:HG3	2.29	0.46
1:C:450:THR:CG2	1:C:452:LEU:HB2	2.45	0.46
3:F:10:DC:H2''	3:F:11:DG:C8	2.50	0.46
1:A:266:TRP:CE2	3:E:31:DG:H4'	2.51	0.46
1:A:27:THR:HB	1:A:30:LYS:HG3	1.98	0.46
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.51	0.46
1:A:23:GLN:HG3	1:A:24:TRP:N	2.30	0.46
1:A:33:ALA:O	1:A:37:ILE:HG13	2.16	0.46
2:B:198:HIS:O	2:B:202:ILE:HG12	2.16	0.46
1:A:473:THR:O	1:A:477:THR:HG23	2.16	0.46
2:D:257:ILE:HG22	2:D:283:LEU:HD11	1.98	0.46
1:C:325:LEU:HD23	1:C:325:LEU:HA	1.77	0.46
1:C:380:ILE:HD12	2:D:27:THR:HG22	1.97	0.46
1:A:28:GLU:HG2	1:A:135:ILE:HD11	1.98	0.46
2:D:421:PRO:O	2:D:422:LEU:HD13	2.16	0.46
1:C:65:LYS:HG3	1:C:70:LYS:O	2.16	0.45
2:B:179:VAL:O	2:B:180:ILE:HD13	2.17	0.45
2:B:88:TRP:CD1	2:B:89:GLU:N	2.84	0.45
1:A:34:LEU:CB	1:A:132:ILE:HG13	2.44	0.45
1:A:40:GLU:O	1:A:44:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:266:TRP:NE1	2:B:425:LEU:HD21	2.31	0.45
1:C:451:LYS:N	1:C:451:LYS:HD3	2.32	0.45
1:A:34:LEU:HD11	1:A:60:VAL:HG11	1.99	0.45
2:B:111:VAL:HG11	2:B:187:LEU:HD12	1.98	0.45
1:C:516:GLU:O	1:C:520:GLN:HG3	2.17	0.45
2:B:278:GLN:CD	2:B:298:GLU:HB3	2.37	0.44
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.52	0.44
2:B:64:LYS:HD2	2:B:71:TRP:CZ2	2.53	0.44
1:C:448:ARG:O	1:C:451:LYS:NZ	2.31	0.44
1:C:22:LYS:HA	1:C:22:LYS:HD2	1.76	0.44
1:C:136:ASN:N	1:C:136:ASN:OD1	2.50	0.44
1:C:475:GLN:N	1:C:475:GLN:OE1	2.42	0.44
2:D:211:ARG:HG3	2:D:211:ARG:O	2.18	0.44
1:A:57:ASN:OD1	1:A:131:THR:N	2.48	0.44
1:A:56:TYR:O	1:A:143:ARG:NH2	2.50	0.44
3:E:1:DG:H2'	3:E:2:OMC:C6	2.52	0.44
1:C:266:TRP:CE2	3:F:31:DG:H4'	2.53	0.44
1:A:132:ILE:HD13	1:A:133:PRO:N	2.32	0.44
1:C:175:ASN:HB3	1:C:178:ILE:HG13	2.00	0.44
1:C:207:GLN:O	1:C:211:ARG:HG3	2.17	0.44
1:A:44:GLU:HB2	1:A:46:LYS:HG2	1.99	0.44
2:B:104:LYS:HB2	2:B:192:ASP:HA	2.00	0.44
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.99	0.44
1:A:406:TRP:CZ2	2:B:420:PRO:HG3	2.53	0.44
1:A:22:LYS:HZ2	1:A:23:GLN:H	1.64	0.43
1:C:442:VAL:HB	1:C:481:ALA:HB1	2.00	0.43
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.53	0.43
1:C:136:ASN:C	1:C:138:GLU:N	2.72	0.43
1:C:406:TRP:CE3	2:D:421:PRO:HD3	2.53	0.43
1:A:22:LYS:NZ	1:A:23:GLN:H	2.16	0.43
1:A:173:LYS:HE2	1:A:173:LYS:HB2	1.62	0.43
2:B:103:LYS:HE3	2:B:179:VAL:CG2	2.48	0.43
1:C:202:ILE:O	1:C:206:ARG:HG3	2.19	0.43
2:D:163:SER:O	2:D:167:ILE:HG12	2.19	0.43
1:C:463:ARG:NH2	1:C:488:ASP:O	2.52	0.43
2:B:84:THR:HB	2:B:154:LYS:HE2	2.01	0.42
1:C:195:ILE:HD12	1:C:195:ILE:HA	1.85	0.42
2:D:195:ILE:O	2:D:199:ARG:HG3	2.19	0.42
2:D:355:ALA:HB1	2:D:356:ARG:HG3	2.01	0.42
1:C:326:ILE:CG2	1:C:390:LYS:HD2	2.49	0.42
2:D:64:LYS:HE3	2:D:71:TRP:CZ2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:ASN:OD1	1:A:130:PHE:HA	2.19	0.42
1:A:58:THR:HG21	1:A:77:PHE:CD1	2.55	0.42
1:A:63:ILE:O	1:A:72:ARG:N	2.40	0.42
1:C:96:HIS:CG	1:C:97:PRO:HD2	2.54	0.42
2:D:358:LYS:HE3	2:D:358:LYS:HB3	1.81	0.42
2:D:361:HIS:HB2	8:D:643:HOH:O	2.20	0.42
3:E:13:DT:H2''	3:E:14:DG:C8	2.55	0.42
1:C:23:GLN:OE1	1:C:59:PRO:HA	2.20	0.42
2:D:422:LEU:N	2:D:422:LEU:CD2	2.80	0.42
2:B:103:LYS:HD3	2:B:103:LYS:HA	1.77	0.42
3:F:27:DG:H2'	3:F:28:DG:C8	2.55	0.42
1:A:33:ALA:O	1:A:36:GLU:HG2	2.20	0.42
2:D:353:LYS:HE2	2:D:427:TYR:CD1	2.55	0.42
1:A:429:LEU:HD11	1:A:506:ILE:HG22	2.02	0.41
2:B:172:ARG:NH1	2:B:180:ILE:HB	2.35	0.41
1:C:201:LYS:HA	1:C:201:LYS:HD3	1.76	0.41
2:D:143:ARG:HH11	2:D:143:ARG:HG2	1.84	0.41
1:A:404:GLU:H	1:A:404:GLU:HG2	1.71	0.41
2:B:129:ALA:HA	2:B:144:TYR:O	2.20	0.41
1:C:382:ILE:O	2:D:136:ASN:HB2	2.20	0.41
1:A:340:GLN:HE21	1:A:340:GLN:HB3	1.66	0.41
1:C:450:THR:HG23	1:C:452:LEU:HB2	2.02	0.41
1:A:447:ASN:HB3	1:A:450:THR:CB	2.51	0.41
2:B:278:GLN:HG2	2:B:298:GLU:C	2.41	0.41
1:A:19:PRO:HG3	1:A:80:LEU:HB2	2.03	0.41
3:E:4:OMC:H1'	3:E:4:OMC:HM23	1.93	0.41
2:D:236:PRO:HA	2:D:239:TRP:CD2	2.56	0.41
1:C:63:ILE:O	1:C:72:ARG:N	2.40	0.41
2:D:358:LYS:HE2	2:D:366:LYS:HZ2	1.86	0.41
1:A:130:PHE:CZ	1:A:144:TYR:HB2	2.56	0.40
2:B:54:ASN:ND2	2:B:56:TYR:H	2.20	0.40
2:B:79:GLU:OE1	4:G:1:GLC:O3	2.23	0.40
1:A:139:THR:HB	1:A:140:PRO:HD3	2.01	0.40
2:D:41:MET:SD	2:D:73:LYS:HE2	2.61	0.40
1:A:38:CYS:HB3	1:A:47:ILE:CD1	2.51	0.40
1:A:450:THR:O	1:A:451:LYS:CB	2.69	0.40
1:C:132:ILE:HD12	1:C:144:TYR:HE2	1.86	0.40
1:A:211:ARG:O	1:A:211:ARG:HD2	2.21	0.40
2:B:13:LYS:HB2	2:B:16:MET:HE3	2.04	0.40
1:C:136:ASN:C	1:C:138:GLU:H	2.16	0.40
1:C:363:ASN:HA	1:C:511:ASP:OD1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	550/557 (99%)	531 (96%)	18 (3%)	1 (0%)	47	57
1	C	549/557 (99%)	524 (95%)	25 (5%)	0	100	100
2	B	403/444 (91%)	391 (97%)	11 (3%)	1 (0%)	47	57
2	D	403/444 (91%)	388 (96%)	14 (4%)	1 (0%)	47	57
All	All	1905/2002 (95%)	1834 (96%)	68 (4%)	3 (0%)	47	57

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	359	GLY
1	A	24	TRP
2	B	237	ASP

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	491/494 (99%)	481 (98%)	10 (2%)	55	67
1	C	490/494 (99%)	480 (98%)	10 (2%)	55	67
2	B	366/400 (92%)	354 (97%)	12 (3%)	38	49
2	D	366/400 (92%)	360 (98%)	6 (2%)	62	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1713/1788 (96%)	1675 (98%)	38 (2%)	52 64

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	126	LYS
1	A	132	ILE
1	A	136	ASN
1	A	221	HIS
1	A	334	GLN
1	A	340	GLN
1	A	356	ARG
1	A	451	LYS
1	A	503	LEU
2	B	54	ASN
2	B	65	LYS
2	B	70	LYS
2	B	88	TRP
2	B	134	SER
2	B	169	GLU
2	B	278	GLN
2	B	300	GLU
2	B	307	ARG
2	B	356	ARG
2	B	422	LEU
2	B	424	LYS
1	C	42	GLU
1	C	64	LYS
1	C	83	ARG
1	C	136	ASN
1	C	191	SER
1	C	277	ARG
1	C	283	LEU
1	C	287	LYS
1	C	390	LYS
1	C	503	LEU
2	D	134	SER
2	D	203	GLU
2	D	250	ASP
2	D	284	ARG
2	D	353	LYS

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Mol	Chain	Res	Type
2	D	427	TYR

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

Mol	Chain	Res	Type
1	A	334	GLN
1	A	464	GLN
2	B	54	ASN
2	B	137	ASN
2	B	161	GLN
1	C	161	GLN
1	C	221	HIS
1	C	265	ASN
2	D	182	GLN
2	D	336	GLN
2	D	361	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	F	2	3	15,22,23	4.49	10 (66%)	17,31,34	1.07	1 (5%)
3	OMC	E	2	3	15,22,23	4.57	10 (66%)	17,31,34	1.37	2 (11%)
3	OMC	E	4	3	15,22,23	3.14	6 (40%)	17,31,34	1.37	1 (5%)
3	OMC	F	4	3	15,22,23	3.15	5 (33%)	17,31,34	1.30	2 (11%)

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	F	2	3	-	0/7/27/28	0/2/2/2
3	OMC	E	2	3	-	1/7/27/28	0/2/2/2
3	OMC	E	4	3	-	0/7/27/28	0/2/2/2
3	OMC	F	4	3	-	0/7/27/28	0/2/2/2

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	OMC	O4'-C1'	-8.83	1.28	1.41
3	F	2	OMC	O4'-C1'	-8.56	1.29	1.41
3	F	2	OMC	C3'-C4'	-8.18	1.32	1.53
3	E	2	OMC	C3'-C4'	-7.97	1.32	1.53
3	E	4	OMC	C6-N1	7.70	1.45	1.35
3	F	4	OMC	C6-N1	7.42	1.45	1.35
3	E	2	OMC	C6-N1	6.80	1.44	1.35
3	F	2	OMC	C6-N1	6.52	1.43	1.35
3	E	2	OMC	O4'-C4'	6.47	1.59	1.45
3	F	2	OMC	O4'-C4'	6.36	1.59	1.45
3	F	4	OMC	C4-N3	5.36	1.44	1.35
3	F	4	OMC	C2-N3	5.01	1.48	1.38
3	F	4	OMC	C6-C5	4.96	1.49	1.38
3	E	4	OMC	C4-N3	4.95	1.43	1.35
3	E	4	OMC	C2-N3	4.93	1.47	1.38
3	E	4	OMC	C6-C5	4.75	1.48	1.38
3	E	2	OMC	C4-N3	4.24	1.42	1.35
3	E	2	OMC	C6-C5	4.01	1.46	1.38
3	F	2	OMC	C4-N3	3.93	1.41	1.35
3	F	2	OMC	C6-C5	3.87	1.46	1.38
3	E	2	OMC	C2-N3	3.80	1.45	1.38
3	F	2	OMC	C2-N3	3.70	1.45	1.38
3	F	2	OMC	O5'-C5'	-3.56	1.36	1.44
3	F	2	OMC	O2'-C2'	-3.43	1.33	1.42
3	E	2	OMC	O2'-C2'	-3.34	1.34	1.42
3	E	4	OMC	C5-C4	3.27	1.49	1.41
3	E	2	OMC	O5'-C5'	-3.27	1.36	1.44
3	F	4	OMC	C5-C4	3.11	1.48	1.41
3	E	2	OMC	C5-C4	2.53	1.47	1.41
3	F	2	OMC	C5-C4	2.26	1.46	1.41
3	E	4	OMC	C4-N4	2.02	1.41	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4	OMC	C2-N3-C4	4.83	121.23	116.34
3	E	2	OMC	C2-N3-C4	4.14	120.54	116.34
3	F	4	OMC	C2-N3-C4	4.05	120.44	116.34
3	F	2	OMC	C2-N3-C4	3.21	119.60	116.34
3	E	2	OMC	N4-C4-N3	2.18	119.94	116.49
3	F	4	OMC	N4-C4-N3	2.12	119.84	116.49

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	2	OMC	2	0
3	E	2	OMC	1	0
3	E	4	OMC	2	0
3	F	4	OMC	1	0

5.5 Carbohydrates [i](#)

2 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	G	1	4	11,11,12	0.50	0	15,15,17	0.96	1 (6%)
4	FRU	G	2	4	11,12,12	0.56	0	10,18,18	0.46	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
4	GLC	G	1	4	-	1/2/19/22	0/1/1/1
4	FRU	G	2	4	-	0/5/24/24	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	G	1	GLC	C1-O5-C5	2.87	116.08	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

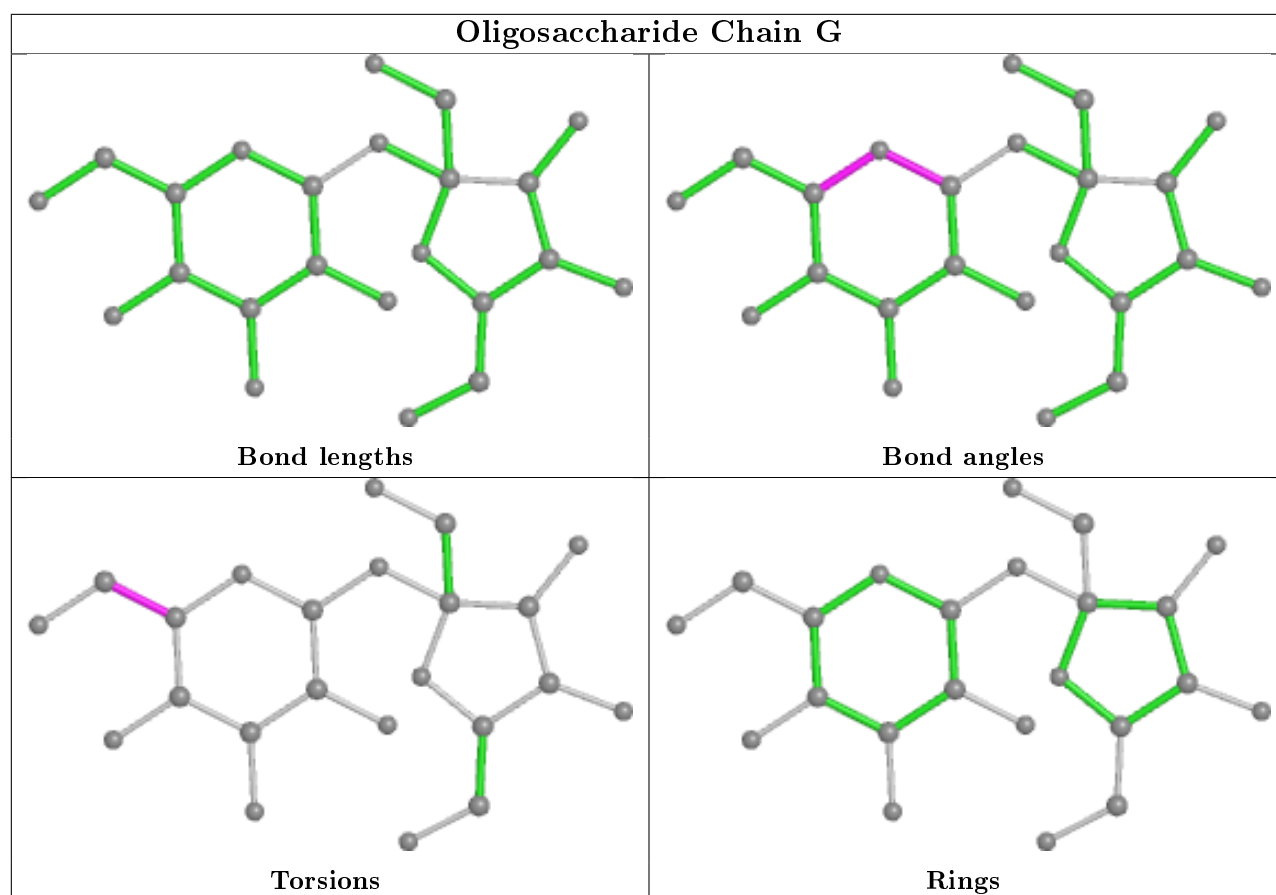
Mol	Chain	Res	Type	Atoms
4	G	1	GLC	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1	GLC	1	0

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



5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 2 are monoatomic - 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	B	501	-	5,5,5	0.38	0	5,5,5	0.69	0
7	GOL	F	101	-	5,5,5	0.31	0	5,5,5	0.33	0
7	GOL	D	501	-	5,5,5	0.35	0	5,5,5	0.53	0
7	GOL	B	502	-	5,5,5	0.44	0	5,5,5	0.31	0
7	GOL	D	502	-	5,5,5	0.47	0	5,5,5	0.50	0
5	ET9	A	601	6	26,34,34	1.36	1 (3%)	28,54,54	2.40	12 (42%)
5	ET9	C	601	6	26,34,34	1.24	2 (7%)	28,54,54	2.51	12 (42%)

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	B	501	-	-	2/4/4/4	-
7	GOL	F	101	-	-	2/4/4/4	-
7	GOL	D	501	-	-	2/4/4/4	-
7	GOL	B	502	-	-	2/4/4/4	-
7	GOL	D	502	-	-	2/4/4/4	-
5	ET9	A	601	6	-	4/18/38/38	0/3/3/3
5	ET9	C	601	6	-	7/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	ET9	C6-C5	3.57	1.47	1.41
5	C	601	ET9	C6-C5	3.17	1.46	1.41
5	C	601	ET9	C2'-C1'	-2.36	1.51	1.54

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	601	ET9	C2'-C1'-N9	-6.69	103.40	114.73
5	A	601	ET9	C2'-C1'-N9	-5.46	105.50	114.73
5	A	601	ET9	C2-N3-C4	5.03	121.10	115.36
5	C	601	ET9	C2-N3-C4	4.85	120.89	115.36
5	A	601	ET9	C6-C5-C4	-3.93	117.05	120.80
5	C	601	ET9	C5-C6-N1	-3.88	118.12	123.43
5	A	601	ET9	C4-C5-N7	-3.83	105.41	109.40
5	A	601	ET9	C5-C6-N1	-3.78	118.26	123.43
5	C	601	ET9	C6-N1-C2	3.64	121.70	115.93
5	A	601	ET9	C6-N1-C2	3.61	121.66	115.93
5	C	601	ET9	C4'-C6'-C44	-3.43	121.77	127.72
5	C	601	ET9	C6-C5-C4	-3.18	117.76	120.80
5	C	601	ET9	C4'-C6'-C1'	3.17	114.53	105.76
5	A	601	ET9	PB-O3A-PA	-3.05	122.37	132.83
5	A	601	ET9	C4'-C6'-C1'	3.04	114.18	105.76
5	C	601	ET9	PB-O3B-PG	-3.03	122.41	132.83
5	C	601	ET9	C4-C5-N7	-2.98	106.29	109.40
5	C	601	ET9	PB-O3A-PA	-2.87	122.97	132.83
5	C	601	ET9	N3-C2-N1	-2.75	123.55	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	601	ET9	PB-O3B-PG	-2.70	123.58	132.83
5	A	601	ET9	N3-C2-N1	-2.61	123.74	127.22
5	A	601	ET9	C4'-C6'-C44	-2.59	123.23	127.72
5	C	601	ET9	O2G-PG-O3B	2.15	111.83	104.64
5	A	601	ET9	C1'-C6'-C44	-2.03	122.58	125.68

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	501	GOL	C1-C2-C3-O3
7	F	101	GOL	O1-C1-C2-O2
7	F	101	GOL	O1-C1-C2-C3
7	D	501	GOL	C1-C2-C3-O3
7	D	502	GOL	O1-C1-C2-C3
5	C	601	ET9	PB-O3B-PG-O2G
7	B	502	GOL	O1-C1-C2-C3
7	D	501	GOL	O2-C2-C3-O3
7	D	502	GOL	O1-C1-C2-O2
5	C	601	ET9	PB-O3A-PA-O2A
7	B	501	GOL	O1-C1-C2-O2
5	C	601	ET9	PA-O3A-PB-O2B
5	A	601	ET9	PB-O3A-PA-O2A
5	A	601	ET9	PA-O3A-PB-O1B
5	C	601	ET9	PG-O3B-PB-O1B
5	A	601	ET9	PB-O3B-PG-O3G
5	A	601	ET9	PB-O3B-PG-O1G
5	C	601	ET9	PB-O3B-PG-O1G
7	B	502	GOL	O1-C1-C2-O2
5	C	601	ET9	PB-O3A-PA-O1A
5	C	601	ET9	PA-O3A-PB-O1B

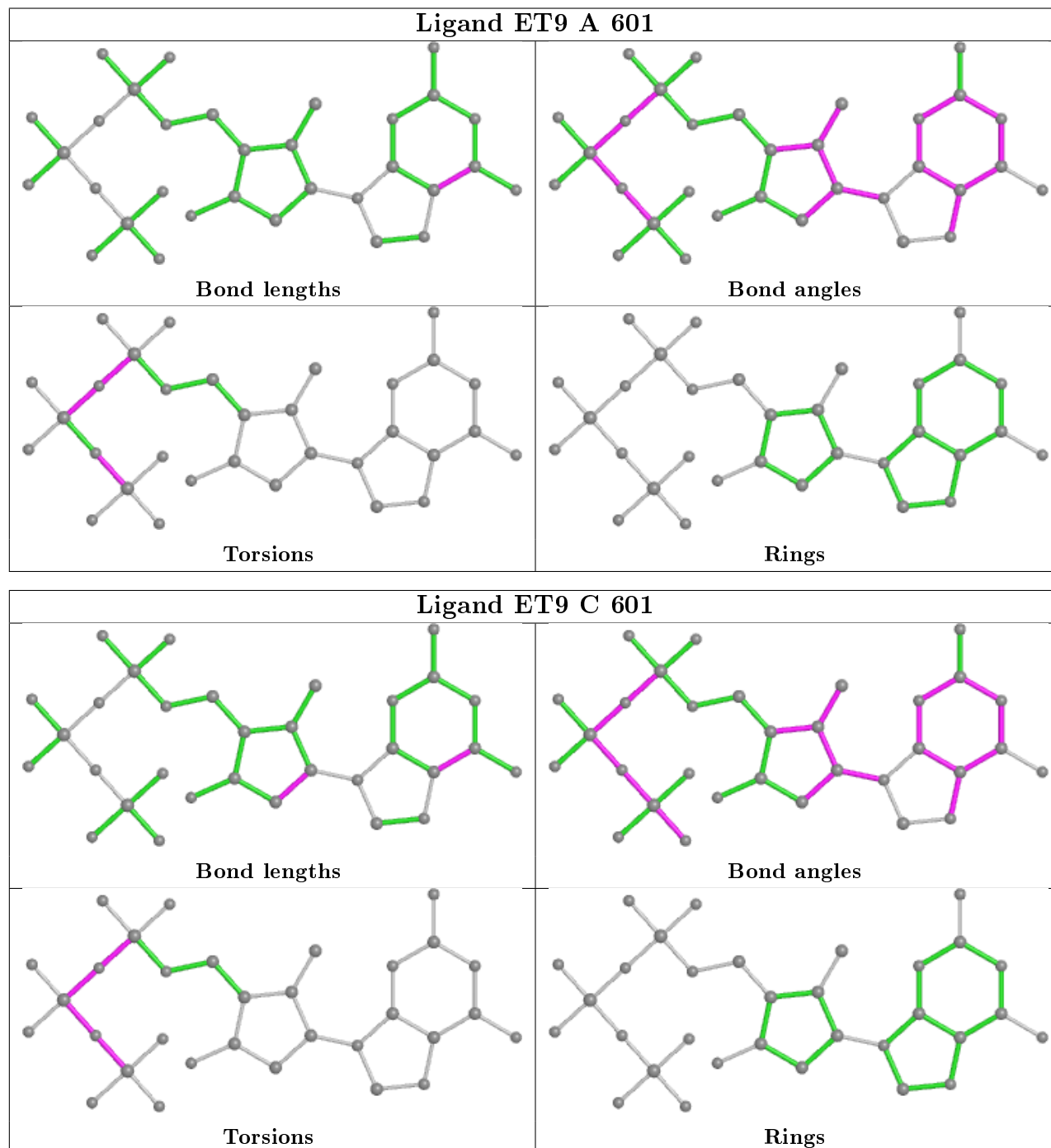
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	501	GOL	2	0
5	C	601	ET9	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 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	551/557 (98%)	0.16	31 (5%) 24 20	26, 48, 92, 175	0
1	C	551/557 (98%)	0.35	54 (9%) 7 5	29, 56, 111, 166	0
2	B	407/444 (91%)	0.75	54 (13%) 3 2	30, 65, 118, 164	0
2	D	407/444 (91%)	0.10	17 (4%) 36 33	29, 53, 94, 150	0
3	E	33/38 (86%)	-0.37	0 100 100	27, 43, 78, 117	0
3	F	36/38 (94%)	-0.28	1 (2%) 53 49	33, 57, 113, 148	0
All	All	1985/2078 (95%)	0.30	157 (7%) 12 9	26, 54, 110, 175	0

All (157) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	4	PRO	12.3
2	D	67	ASP	9.8
2	B	301	LEU	9.7
2	B	88	TRP	8.7
2	B	92	LEU	8.6
1	C	138	GLU	8.0
1	A	69	THR	7.9
1	C	133	PRO	7.7
1	C	34	LEU	7.5
1	A	34	LEU	7.2
2	B	94	ILE	6.6
2	D	360	ALA	6.6
1	A	137	ASN	6.5
2	B	212	TRP	6.5
2	D	4	PRO	6.4
2	B	360	ALA	6.3
1	C	132	ILE	6.3
1	A	136	ASN	6.3
2	B	5	ILE	6.2

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Mol	Chain	Res	Type	RSRZ
1	C	135	ILE	6.2
2	B	93	GLY	6.2
1	A	139	THR	6.1
2	B	209	LEU	6.1
1	A	66	LYS	5.9
1	A	68	SER	5.9
2	B	359	GLY	5.8
2	B	91	GLN	5.7
1	C	67	ASP	5.6
2	B	90	VAL	5.6
2	B	361	HIS	5.6
1	C	141	GLY	5.5
1	C	50	ILE	5.5
1	C	62	ALA	5.5
1	C	142	ILE	5.3
1	A	141	GLY	5.1
2	B	232	TYR	5.1
1	C	69	THR	5.0
1	C	28	GLU	4.9
1	A	140	PRO	4.9
2	B	213	GLY	4.8
2	D	231	GLY	4.7
1	A	67	ASP	4.6
1	C	35	VAL	4.4
1	A	25	PRO	4.4
1	C	140	PRO	4.4
2	D	232	TYR	4.3
1	A	62	ALA	4.3
2	B	89	GLU	4.3
1	A	61	PHE	4.2
1	C	452	LEU	4.2
1	C	51	GLY	4.2
1	C	68	SER	4.1
1	A	32	LYS	4.1
1	C	32	LYS	4.1
2	B	168	LEU	4.0
2	B	231	GLY	4.0
2	B	95	PRO	4.0
1	C	139	THR	4.0
1	C	551	LEU	4.0
2	B	295	LEU	3.9
2	B	7	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	37	ILE	3.8
2	D	212	TRP	3.8
1	C	71	TRP	3.7
1	A	63	ILE	3.7
1	C	553	SER	3.7
2	B	68	SER	3.7
2	B	357	MET	3.6
1	C	52	PRO	3.6
1	A	64	LYS	3.6
2	B	305	GLU	3.6
1	C	144	TYR	3.6
2	D	5	ILE	3.5
2	D	66	LYS	3.5
2	B	67	ASP	3.4
2	D	359	GLY	3.4
2	B	423	VAL	3.4
1	A	26	LEU	3.3
1	C	70	LYS	3.3
2	B	297	GLU	3.3
2	B	250	ASP	3.3
1	C	26	LEU	3.3
1	A	60	VAL	3.3
1	A	132	ILE	3.3
1	C	33	ALA	3.2
2	D	361	HIS	3.2
1	C	39	THR	3.2
2	D	68	SER	3.2
1	A	134	SER	3.1
2	B	245	VAL	3.1
2	B	172	ARG	3.1
2	B	6	GLU	3.1
2	D	283	LEU	3.1
1	A	27	THR	3.1
1	C	49	LYS	3.0
1	A	71	TRP	2.9
2	B	87	PHE	2.9
1	A	35	VAL	2.9
1	C	66	LYS	2.8
1	A	131	THR	2.8
1	C	552	VAL	2.7
2	B	272	ALA	2.7
1	C	65	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	136	ASN	2.7
1	C	24	TRP	2.7
2	D	357	MET	2.7
2	B	281	LYS	2.7
2	B	277	ARG	2.6
1	A	24	TRP	2.6
2	B	299	ALA	2.6
1	C	15	GLY	2.5
1	C	550	LYS	2.5
1	C	544	GLY	2.5
1	C	134	SER	2.5
1	C	469	LEU	2.5
1	C	36	GLU	2.5
2	B	8	VAL	2.4
1	A	142	ILE	2.4
2	B	362	THR	2.4
3	F	18	DT	2.4
1	C	29	GLU	2.4
2	B	422	LEU	2.4
2	D	177	ASP	2.4
2	B	166	LYS	2.4
1	A	29	GLU	2.4
1	A	133	PRO	2.4
1	C	450	THR	2.4
1	C	59	PRO	2.3
2	D	174	GLN	2.3
2	B	251	SER	2.3
1	C	448	ARG	2.3
1	A	65	LYS	2.3
2	B	211	ARG	2.3
1	C	54	ASN	2.3
2	B	169	GLU	2.3
1	C	547	GLN	2.3
2	D	211	ARG	2.3
2	B	296	THR	2.3
1	C	143	ARG	2.2
2	B	9	PRO	2.2
2	B	10	VAL	2.2
2	B	248	GLU	2.2
2	B	66	LYS	2.2
1	C	457	TYR	2.2
1	C	30	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	131	THR	2.1
2	B	165	THR	2.1
1	C	128	THR	2.1
1	A	138	GLU	2.1
2	B	358	LYS	2.1
2	B	273	GLY	2.1
1	C	449	GLU	2.1
1	A	36	GLU	2.1
1	C	63	ILE	2.0
2	B	11	LYS	2.0
2	B	279	LEU	2.0
2	D	425	LEU	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.

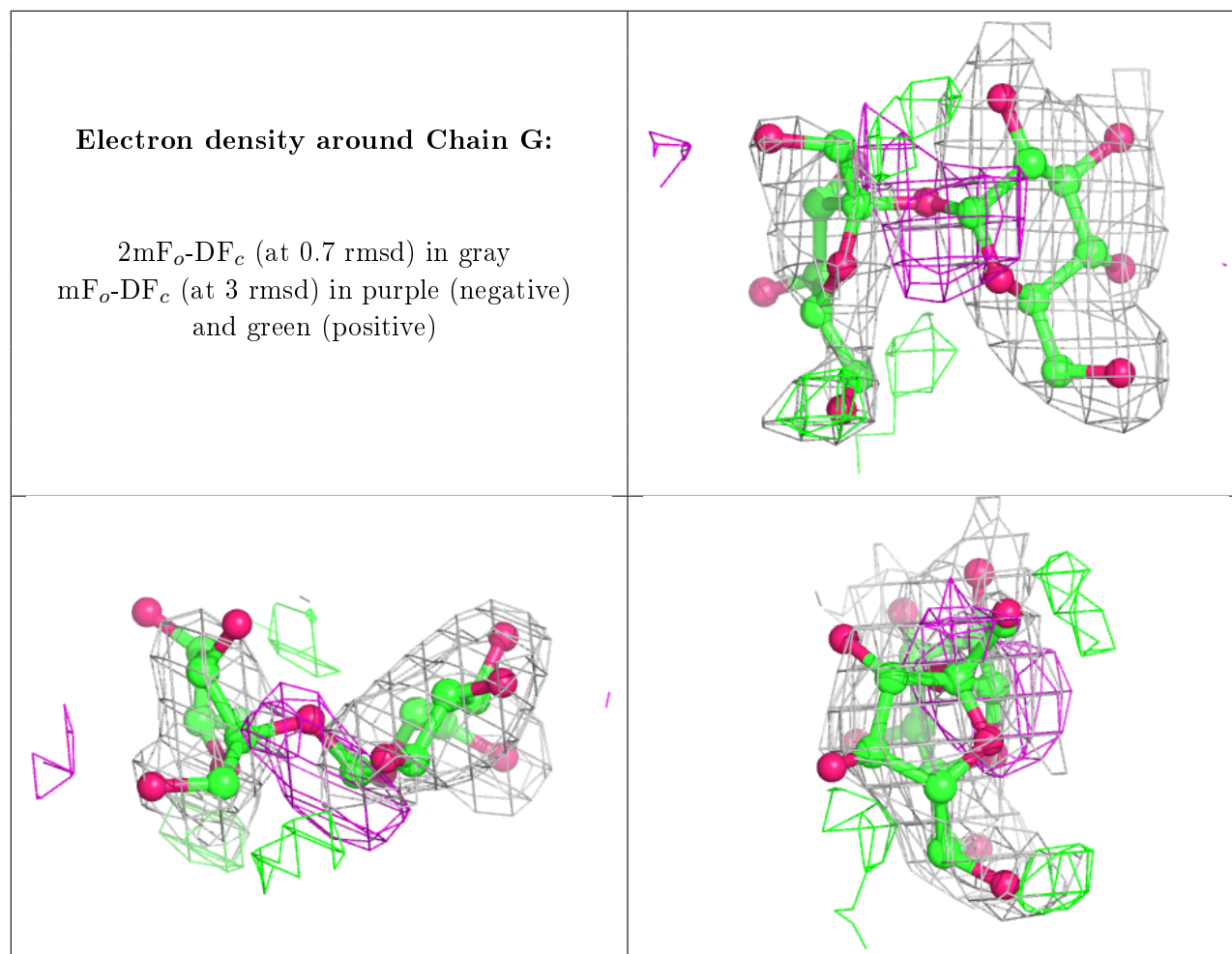
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	OMC	F	2	21/22	0.97	0.16	45,49,56,59	0
3	OMC	E	2	21/22	0.97	0.17	27,33,40,44	0
3	OMC	F	4	21/22	0.98	0.19	30,35,40,41	0
3	OMC	E	4	21/22	0.99	0.18	26,29,33,34	0

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, 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	G	2	12/12	0.74	0.30	93,102,104,105	0
4	GLC	G	1	11/12	0.87	0.20	47,67,78,84	0

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



6.4 Ligands [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.

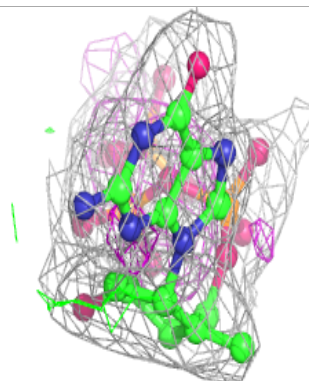
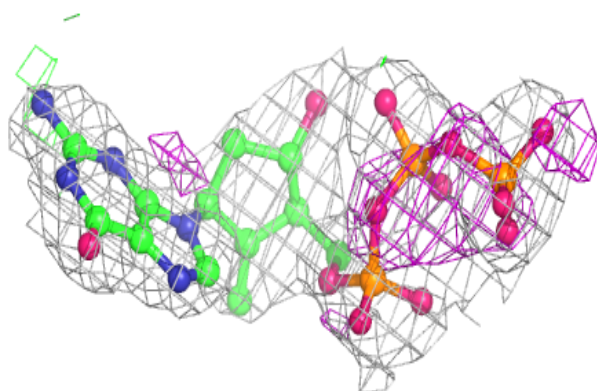
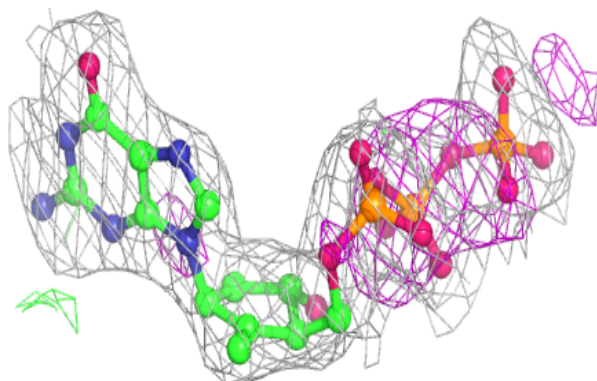
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	A	602	1/1	0.82	0.11	32,32,32,32	1
7	GOL	B	501	6/6	0.86	0.24	41,47,51,58	0
7	GOL	F	101	6/6	0.88	0.23	54,60,62,67	0
6	MG	C	602	1/1	0.89	0.11	54,54,54,54	0
5	ET9	A	601	32/32	0.90	0.18	47,56,72,73	0
5	ET9	C	601	32/32	0.91	0.14	62,67,84,86	0
7	GOL	D	502	6/6	0.92	0.20	40,44,53,55	0
7	GOL	D	501	6/6	0.93	0.18	40,44,44,46	0
7	GOL	B	502	6/6	0.95	0.23	40,46,48,51	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.

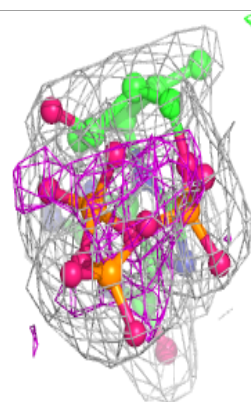
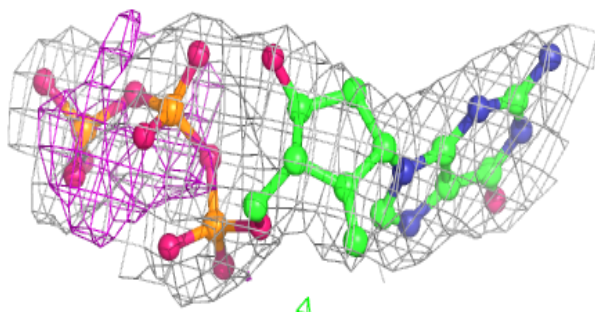
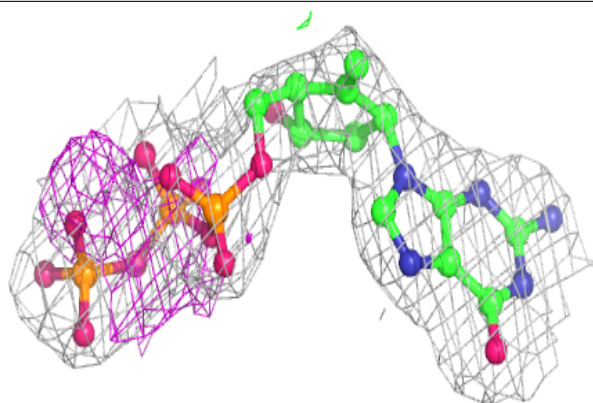
Electron density around ET9 A 601:

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



Electron density around ET9 C 601:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.