



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 02:53 PM UTC

PDB ID : 5TXO / pdb_00005txo
Title : STRUCTURE OF Q151M complex (A62V, V75I, F77L, F116Y, Q151M)
mutant HIV-1 REVERSE TRANSCRIPTASE (RT) TERNARY COMPLEX
WITH A DOUBLE STRANDED DNA AND AN INCOMING DATP
Authors : Das, K.; Martinez, S.M.; Arnold, E.
Deposited on : 2016-11-17
Resolution : 2.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

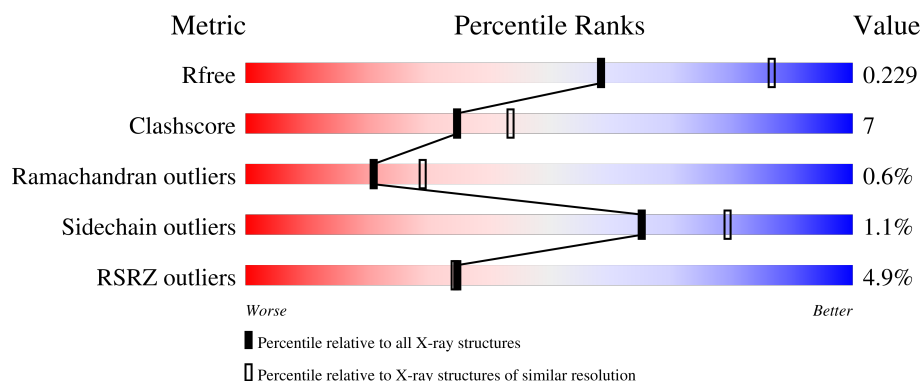
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



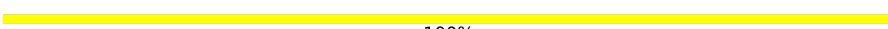
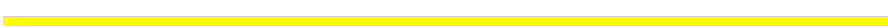
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	556	4% 80% 19% .
1	C	556	5% 75% 24% .
2	B	428	5% 84% 12% .
2	D	428	6% 79% 17% .

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Mol	Chain	Length	Quality of chain
3	E	27	 44% 44% 11%
3	T	27	 67% 22% 11%
4	F	21	 5% 43% 48% 5% 5%
4	P	21	 5% 43% 48% 5% 5%
5	G	2	 100%
5	H	2	 100%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 17928 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 HIV-1 REVERSE TRANSCRIPTASE P66 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4516	2923	751	833	9			
1	C	556	Total	C	N	O	S	0	0	0
			4516	2923	751	833	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	62	VAL	ALA	engineered mutation	UNP P03366
A	75	ILE	VAL	engineered mutation	UNP P03366
A	77	LEU	PHE	engineered mutation	UNP P03366
A	116	TYR	PHE	engineered mutation	UNP P03366
A	151	MET	GLN	engineered mutation	UNP P03366
A	258	CYS	GLN	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366
A	498	ASN	ASP	engineered mutation	UNP P03366
C	-1	MET	-	initiating methionine	UNP P03366
C	0	VAL	-	expression tag	UNP P03366
C	62	VAL	ALA	engineered mutation	UNP P03366
C	75	ILE	VAL	engineered mutation	UNP P03366
C	77	LEU	PHE	engineered mutation	UNP P03366
C	116	TYR	PHE	engineered mutation	UNP P03366
C	151	MET	GLN	engineered mutation	UNP P03366
C	258	CYS	GLN	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 HIV-1 REVERSE TRANSCRIPTASE P51 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3400	2212	563	619	6			
2	D	412	Total	C	N	O	S	0	0	0
			3397	2210	563	619	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366
D	280	SER	CYS	engineered mutation	UNP P03366

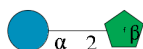
- Molecule 3 is a DNA chain called DNA (5'-D(*TP*GP*GP*TP*CP*GP*GP*CP*GP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	24	Total	C	N	O	P	0	0	0
			494	233	97	141	23			
3	E	24	Total	C	N	O	P	0	0	0
			494	233	97	141	23			

- Molecule 4 is a DNA chain called DNA (5'-D(*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	20	Total	C	N	O	P	S	0	0
			407	195	72	120	19	1		
4	F	20	Total	C	N	O	P	S	0	0
			407	195	72	120	19	1		

- Molecule 5 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.

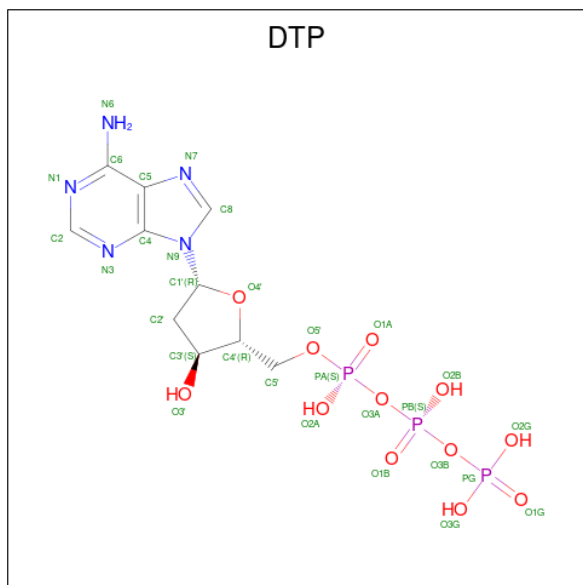


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
5	G	2	Total	C O	0	0	0
			23	12 11			
5	H	2	Total	C O	0	0	0
			23	12 11			

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		
6	C	2	Total	Mg	0	0
			2	2		

- Molecule 7 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (CCD ID: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$)



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
7	C	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is SULFATE ION (CCD ID: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		

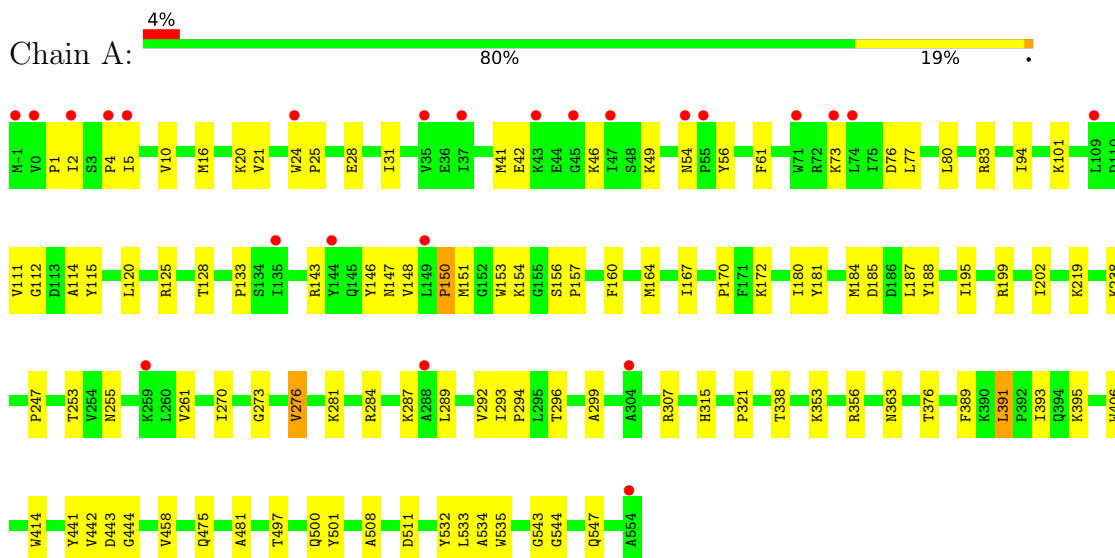
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	45	Total 45	O 45	0	0
10	B	37	Total 37	O 37	0	0
10	T	3	Total 3	O 3	0	0
10	P	1	Total 1	O 1	0	0
10	C	51	Total 51	O 51	0	0
10	D	27	Total 27	O 27	0	0
10	E	2	Total 2	O 2	0	0
10	F	3	Total 3	O 3	0	0

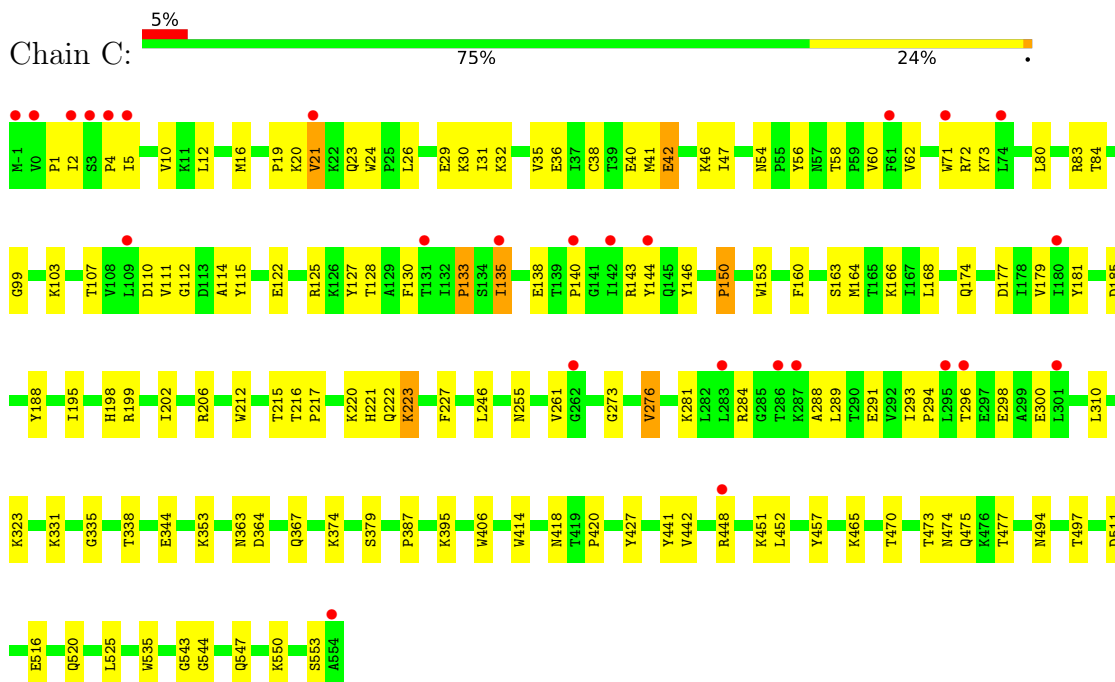
3 Residue-property plots [i](#)

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.

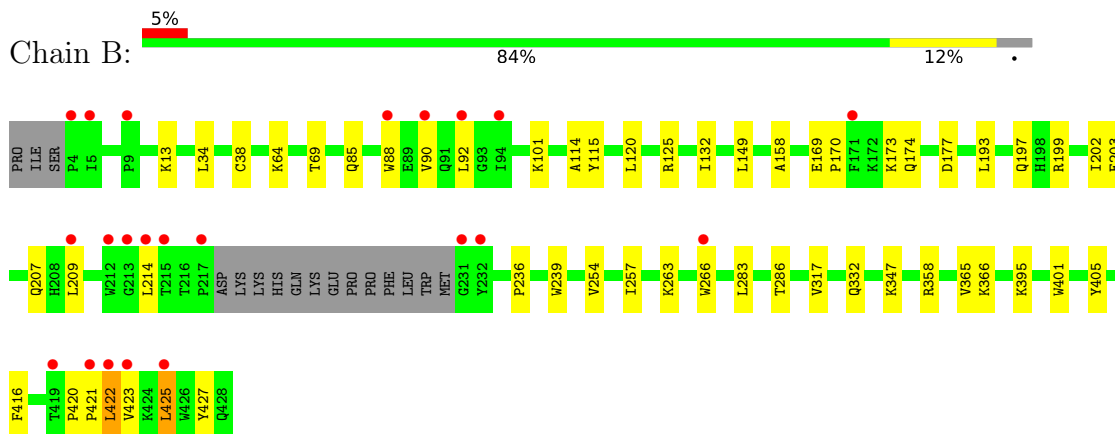
• Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 SUBUNIT



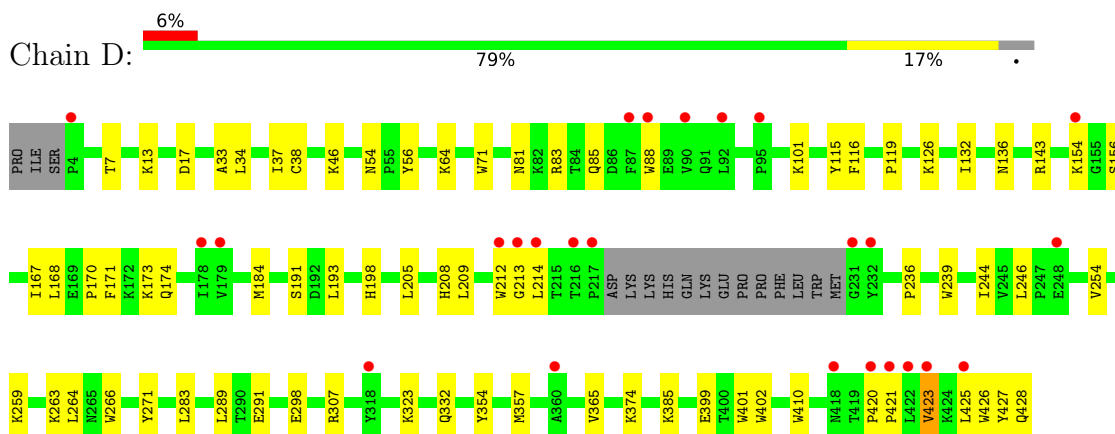
• Molecule 1: HIV-1 REVERSE TRANSCRIPTASE P66 SUBUNIT



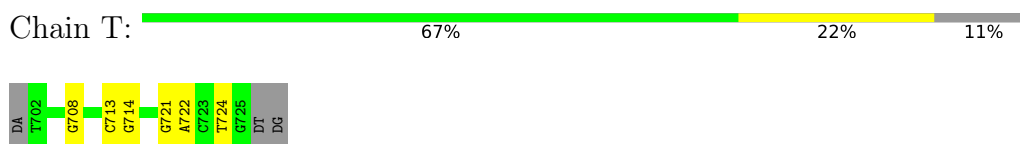
• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 SUBUNIT



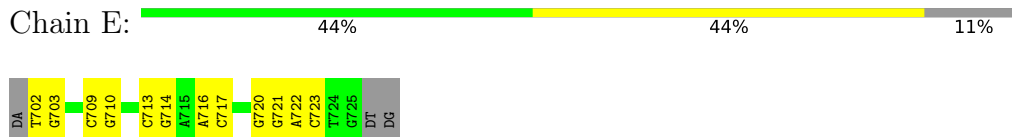
• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE P51 SUBUNIT



• Molecule 3: DNA (5'-D(*TP*GP*GP*TP*CP*GP*GP*CP*GP*CP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*G)-3')

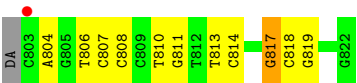


• Molecule 3: DNA (5'-D(*TP*GP*GP*TP*CP*GP*GP*CP*GP*CP*CP*CP*GP*AP*AP*CP*AP*GP*GP*GP*AP*CP*TP*G)-3')

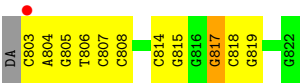


• Molecule 4: DNA (5'-D(*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*G)-3')

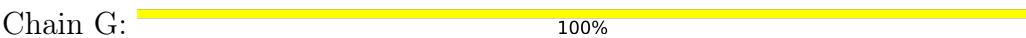




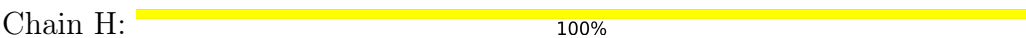
● Molecule 4: DNA (5'-D(*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(MRG)P*CP*GP*CP*CP*G)-3')



● Molecule 5: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



● Molecule 5: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.99Å 132.93Å 139.12Å 90.00° 97.38° 90.00°	Depositor
Resolution (Å)	45.99 – 2.55 45.99 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.8 (45.99-2.55) 98.7 (45.99-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.54Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.191 , 0.228 0.195 , 0.229	Depositor DCC
R_{free} test set	3140 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å ²)	58.6	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 86.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17928	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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: MRG, DTP, GLC, MG, EDO, FRU, SO4

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	0.19	0/4633	0.42	0/6296
1	C	0.26	0/4633	0.65	2/6296 (0.0%)
2	B	0.21	0/3497	0.48	0/4751
2	D	0.19	0/3494	0.45	0/4748
3	E	0.24	0/555	0.42	0/856
3	T	0.21	0/555	0.38	0/856
4	F	0.30	0/424	0.49	0/649
4	P	0.32	0/424	0.50	0/649
All	All	0.22	0/18215	0.50	2/25101 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	223	LYS	CA-CB-CG	-6.00	102.11	114.10
1	C	140	PRO	N-CA-C	-5.43	105.98	113.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4516	0	4581	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4516	0	4581	85	0
2	B	3400	0	3433	32	0
2	D	3397	0	3426	50	0
3	E	494	0	269	9	0
3	T	494	0	269	7	0
4	F	407	0	229	11	0
4	P	407	0	229	8	0
5	G	23	0	21	0	0
5	H	23	0	21	0	0
6	A	2	0	0	0	0
6	C	2	0	0	0	0
7	A	30	0	12	2	0
7	C	30	0	12	2	0
8	B	4	0	6	0	0
8	D	4	0	6	2	0
9	B	5	0	0	0	0
9	D	5	0	0	0	0
10	A	45	0	0	1	0
10	B	37	0	0	0	0
10	C	51	0	0	1	0
10	D	27	0	0	3	0
10	E	2	0	0	0	0
10	F	3	0	0	0	0
10	P	1	0	0	0	0
10	T	3	0	0	0	0
All	All	17928	0	17095	259	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 (259) 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:296:THR:HG23	1:A:299:ALA:H	1.51	0.76
2:B:13:LYS:HD2	2:B:85:GLN:HB3	1.69	0.74
1:C:163:SER:HA	1:C:166:LYS:HE2	1.70	0.73
1:A:128:THR:HG21	1:A:146:TYR:HB2	1.71	0.73
2:D:263:LYS:HE3	2:D:425:LEU:HA	1.71	0.71
1:C:261:VAL:HG13	1:C:276:VAL:HG11	1.73	0.70
1:C:323:LYS:NZ	1:C:344:GLU:OE2	2.24	0.69
1:C:54:ASN:HB3	1:C:143:ARG:HH12	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:722:DA:H2''	3:E:723:DC:H5''	1.74	0.69
2:D:298:GLU:OE1	10:D:601:HOH:O	2.10	0.68
1:C:164:MET:HE2	1:C:168:LEU:HG	1.76	0.68
1:A:253:THR:HA	1:A:292:VAL:HA	1.78	0.65
1:A:261:VAL:HG13	1:A:276:VAL:HG11	1.77	0.65
2:D:56:TYR:HE2	2:D:126:LYS:HE2	1.63	0.64
2:B:114:ALA:HB2	2:B:214:LEU:HD22	1.79	0.64
3:T:713:DC:H2''	3:T:714:DG:H5'	1.81	0.62
2:D:246:LEU:HD11	2:D:264:LEU:HD21	1.81	0.62
1:C:16:MET:HE2	1:C:83:ARG:HH11	1.64	0.62
2:D:254:VAL:HG13	2:D:283:LEU:HD22	1.81	0.62
2:B:209:LEU:HD22	2:B:214:LEU:HD23	1.82	0.61
1:C:114:ALA:HB1	1:C:160:PHE:CZ	2.35	0.61
2:D:332:GLN:CD	2:D:427:TYR:HB2	2.24	0.61
1:A:543:GLY:O	1:A:547:GLN:NE2	2.34	0.61
2:D:354:TYR:CE1	2:D:374:LYS:HD2	2.35	0.61
1:C:222:GLN:O	1:C:227:PHE:HE1	1.84	0.61
1:C:38:CYS:HA	1:C:41:MET:HE3	1.82	0.60
2:D:266:TRP:CE3	2:D:425:LEU:HG	2.36	0.60
1:A:164:MET:HE2	1:A:187:LEU:HD11	1.83	0.60
1:C:19:PRO:HG3	1:C:80:LEU:HB2	1.84	0.60
1:C:122:GLU:HA	1:C:125:ARG:HD2	1.84	0.60
2:D:259:LYS:NZ	10:D:604:HOH:O	2.29	0.59
2:B:120:LEU:HD23	2:B:125:ARG:HG2	1.83	0.59
2:B:199:ARG:HA	2:B:202:ILE:HD12	1.83	0.59
1:C:276:VAL:HG23	1:C:353:LYS:HE2	1.83	0.59
2:B:358:ARG:NH2	2:B:405:TYR:O	2.36	0.59
1:C:62:VAL:HG12	1:C:71:TRP:HE3	1.67	0.58
1:C:246:LEU:HD11	1:C:310:LEU:HD22	1.85	0.58
2:D:184:MET:HE2	2:D:410:TRP:HB3	1.85	0.58
1:A:41:MET:HE1	1:A:73:LYS:HD3	1.85	0.58
1:C:47:ILE:HD12	1:C:146:TYR:HA	1.83	0.58
1:A:56:TYR:O	1:A:143:ARG:NH2	2.38	0.57
2:B:203:GLU:O	2:B:207:GLN:HG2	2.04	0.57
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.40	0.57
1:C:107:THR:OG1	1:C:198:HIS:NE2	2.33	0.57
2:D:307:ARG:HH22	8:D:503:EDO:H12	1.69	0.57
4:F:804:DA:H2'	4:F:805:DG:C8	2.39	0.57
1:A:120:LEU:H	1:A:148:VAL:HA	1.69	0.57
1:A:389:PHE:HB3	1:A:391:LEU:HD13	1.87	0.57
1:C:543:GLY:O	1:C:547:GLN:NE2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:806:DT:H2'	4:P:807:DC:C6	2.39	0.57
1:C:448:ARG:O	1:C:451:LYS:NZ	2.38	0.57
1:A:112:GLY:HA2	7:A:603:DTP:O2G	2.06	0.56
2:D:213:GLY:O	2:D:214:LEU:HD23	2.05	0.56
2:D:323:LYS:O	2:D:385:LYS:NZ	2.39	0.56
2:D:64:LYS:HE3	2:D:71:TRP:CE2	2.41	0.56
3:E:720:DG:H2''	3:E:721:DG:C8	2.41	0.55
1:C:29:GLU:HG3	1:C:30:LYS:N	2.21	0.55
1:C:36:GLU:O	1:C:40:GLU:HG2	2.06	0.55
1:C:273:GLY:HA2	1:C:338:THR:HG21	1.89	0.55
2:B:365:VAL:HG11	2:B:401:TRP:HB2	1.88	0.55
1:C:110:ASP:HB3	1:C:220:LYS:HB3	1.88	0.55
1:C:195:ILE:HD11	1:C:199:ARG:HH21	1.72	0.55
2:B:266:TRP:CD1	2:B:425:LEU:HD22	2.41	0.55
1:A:16:MET:HG2	1:A:83:ARG:HD3	1.89	0.54
2:D:13:LYS:HD2	2:D:85:GLN:HB3	1.89	0.54
1:C:199:ARG:NH1	1:C:223:LYS:HD2	2.23	0.53
4:F:814:DC:H2''	4:F:815:DG:C8	2.43	0.53
2:B:92:LEU:HB3	2:B:158:ALA:HB1	1.90	0.53
1:C:32:LYS:HD2	1:C:135:ILE:HD12	1.90	0.53
1:C:111:VAL:HB	1:C:185:ASP:HB2	1.90	0.53
2:D:421:PRO:HB2	2:D:423:VAL:HG23	1.91	0.53
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.89	0.53
3:E:702:DT:H3'	3:E:703:DG:H8	1.74	0.53
2:D:209:LEU:HD22	2:D:214:LEU:HD12	1.89	0.53
1:A:167:ILE:O	1:A:170:PRO:HD2	2.08	0.52
1:A:195:ILE:HD11	1:A:199:ARG:HE	1.74	0.52
3:T:713:DC:H2'	3:T:714:DG:C8	2.44	0.52
1:C:353:LYS:O	1:C:374:LYS:NZ	2.42	0.52
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.50	0.52
1:A:406:TRP:CE2	2:B:420:PRO:HB3	2.44	0.52
4:F:818:DC:H2'	4:F:819:DG:C8	2.45	0.52
3:E:716:DA:H2''	3:E:717:DC:OP2	2.09	0.51
1:A:391:LEU:HB3	1:A:393:ILE:HG22	1.93	0.51
3:T:724:DT:H3	4:P:804:DA:H61	1.57	0.51
1:C:473:THR:O	1:C:477:THR:HG23	2.10	0.51
2:B:169:GLU:O	2:B:173:LYS:HG2	2.11	0.51
1:C:199:ARG:HH11	1:C:223:LYS:HD2	1.74	0.51
1:C:418:ASN:O	1:C:420:PRO:HD3	2.11	0.51
4:F:817:MRG:H2'	4:F:818:DC:C6	2.46	0.51
4:F:806:DT:H2'	4:F:807:DC:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ALA:HB1	1:C:160:PHE:CE1	2.46	0.50
1:A:458:VAL:HG12	2:B:286:THR:HG21	1.93	0.50
4:P:810:DT:H2''	4:P:811:DG:H5'	1.92	0.50
1:C:56:TYR:O	1:C:143:ARG:NH2	2.45	0.50
2:D:167:ILE:HD13	2:D:214:LEU:HD11	1.94	0.50
2:D:54:ASN:HB3	2:D:143:ARG:HH21	1.76	0.50
1:A:20:LYS:O	1:A:21:VAL:HG23	2.12	0.50
1:A:238:LYS:HD2	1:A:315:HIS:CG	2.47	0.50
2:D:85:GLN:HA	2:D:88:TRP:CE2	2.46	0.50
2:D:170:PRO:HB2	2:D:208:HIS:CE1	2.47	0.50
1:A:24:TRP:HE3	1:A:25:PRO:HD2	1.76	0.50
1:A:77:LEU:HD13	1:A:80:LEU:HD23	1.93	0.50
2:B:101:LYS:O	2:B:236:PRO:HB2	2.12	0.50
1:C:221:HIS:CE1	1:C:223:LYS:HG3	2.47	0.50
2:D:17:ASP:O	2:D:83:ARG:HD3	2.11	0.50
2:D:81:ASN:HB3	2:D:154:LYS:HD2	1.93	0.49
2:D:168:LEU:O	2:D:171:PHE:N	2.41	0.49
4:F:818:DC:H2'	4:F:819:DG:H8	1.78	0.49
1:C:181:TYR:HB2	1:C:188:TYR:HB3	1.92	0.49
2:B:170:PRO:O	2:B:174:GLN:HG3	2.12	0.49
1:A:281:LYS:O	1:A:284:ARG:HG2	2.13	0.49
1:C:31:ILE:HD13	1:C:133:PRO:HB2	1.95	0.49
1:C:5:ILE:HG21	1:C:212:TRP:HD1	1.77	0.49
1:A:125:ARG:O	1:A:128:THR:OG1	2.25	0.48
1:A:247:PRO:O	1:A:307:ARG:NH2	2.46	0.48
2:B:64:LYS:HD3	2:B:69:THR:HA	1.96	0.48
1:C:12:LEU:HD11	1:C:127:TYR:CZ	2.48	0.48
1:A:443:ASP:OD1	1:A:444:GLY:N	2.43	0.48
1:A:181:TYR:HB2	1:A:188:TYR:HB3	1.94	0.48
1:A:114:ALA:HB1	1:A:160:PHE:CE2	2.47	0.48
4:F:805:DG:H4'	4:F:806:DT:OP1	2.14	0.48
1:A:172:LYS:HE2	1:A:180:ILE:HB	1.96	0.48
3:E:702:DT:H3'	3:E:703:DG:C8	2.49	0.48
3:T:721:DG:H5'	3:T:721:DG:C8	2.49	0.48
2:D:236:PRO:HA	2:D:239:TRP:CE2	2.49	0.48
1:C:62:VAL:HG13	1:C:72:ARG:O	2.14	0.47
1:C:288:ALA:HB3	1:C:291:GLU:HB2	1.97	0.47
2:D:33:ALA:O	2:D:37:ILE:HG12	2.13	0.47
2:D:167:ILE:HG23	2:D:212:TRP:CG	2.49	0.47
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.95	0.47
2:D:307:ARG:HH12	8:D:503:EDO:H12	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:VAL:HG21	1:C:130:PHE:CD1	2.49	0.47
2:B:257:ILE:HB	2:B:283:LEU:HD21	1.97	0.47
3:T:721:DG:H2''	3:T:722:DA:C8	2.50	0.47
1:C:406:TRP:CZ2	2:D:420:PRO:HG3	2.50	0.47
2:B:193:LEU:HD13	2:B:197:GLN:HB3	1.97	0.47
4:P:807:DC:H4'	4:P:808:DC:OP1	2.15	0.47
1:C:47:ILE:HG12	1:C:144:TYR:HB3	1.95	0.47
1:C:103:LYS:HE3	1:C:179:VAL:HG21	1.97	0.47
1:C:216:THR:O	1:C:216:THR:OG1	2.29	0.47
2:B:254:VAL:HG13	2:B:283:LEU:HD22	1.97	0.46
1:C:128:THR:HG21	1:C:146:TYR:HB2	1.96	0.46
4:F:803:DC:H2'	4:F:804:DA:C8	2.50	0.46
4:F:807:DC:H2''	4:F:808:DC:H5''	1.97	0.46
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.50	0.46
1:C:125:ARG:O	1:C:128:THR:OG1	2.32	0.46
3:E:709:DC:H2'	3:E:710:DG:H8	1.81	0.46
1:C:20:LYS:O	1:C:21:VAL:HG23	2.16	0.46
2:D:38:CYS:SG	2:D:132:ILE:HD11	2.56	0.46
3:T:721:DG:H5'	3:T:721:DG:H8	1.80	0.46
1:C:10:VAL:HG21	1:C:153:TRP:HH2	1.80	0.46
1:A:276:VAL:HG23	1:A:353:LYS:HE2	1.98	0.46
1:C:441:TYR:CG	1:C:544:GLY:HA3	2.51	0.46
1:A:10:VAL:HG11	1:A:153:TRP:CZ2	2.51	0.46
1:A:61:PHE:HE2	1:A:76:ASP:HB2	1.81	0.46
2:D:173:LYS:HD2	2:D:173:LYS:HA	1.74	0.46
1:A:157:PRO:HA	1:A:184:MET:HE1	1.98	0.45
1:C:73:LYS:HZ1	1:C:130:PHE:HZ	1.62	0.45
1:C:80:LEU:O	1:C:84:THR:OG1	2.34	0.45
4:F:807:DC:H4'	4:F:808:DC:OP1	2.15	0.45
1:A:376:THR:HG21	2:B:401:TRP:CH2	2.52	0.45
1:C:31:ILE:O	1:C:35:VAL:HG23	2.17	0.45
1:C:335:GLY:HA2	1:C:367:GLN:HE22	1.81	0.45
1:C:24:TRP:HB2	1:C:26:LEU:HG	1.98	0.45
1:A:153:TRP:CD1	1:A:154:LYS:H	2.35	0.45
1:C:281:LYS:O	1:C:284:ARG:HG2	2.17	0.45
2:B:263:LYS:HA	2:B:423:VAL:HG21	1.99	0.45
2:B:317:VAL:HG12	2:B:347:LYS:HB3	1.99	0.45
2:B:358:ARG:HG3	2:B:366:LYS:HD3	1.98	0.45
4:P:817:MRG:H2'	4:P:818:DC:C6	2.52	0.45
1:C:293:ILE:HG13	1:C:294:PRO:HD2	2.00	0.44
2:D:191:SER:HB2	2:D:193:LEU:HG	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:GLY:HA2	7:C:601:DTP:O2G	2.16	0.44
1:C:255:ASN:HB2	1:C:289:LEU:HG	2.00	0.44
1:A:287:LYS:H	1:A:287:LYS:HG2	1.55	0.44
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.18	0.44
1:C:42:GLU:OE2	1:C:144:TYR:OH	2.30	0.44
1:C:12:LEU:HD11	1:C:127:TYR:CE2	2.53	0.43
1:C:395:LYS:HD2	1:C:414:TRP:CH2	2.53	0.43
2:D:115:TYR:CD2	2:D:156:SER:HB3	2.52	0.43
1:A:255:ASN:HB2	1:A:289:LEU:HG	2.01	0.43
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.54	0.43
1:C:146:TYR:CD1	1:C:150:PRO:HB3	2.53	0.43
1:A:441:TYR:CG	1:A:544:GLY:HA3	2.53	0.43
1:C:442:VAL:HG12	1:C:457:TYR:HB3	2.01	0.43
4:P:807:DC:H2''	4:P:808:DC:H5''	1.99	0.43
1:A:94:ILE:HD11	3:T:708:DG:H21	1.83	0.43
1:C:99:GLY:HA3	2:D:136:ASN:ND2	2.33	0.43
1:C:379:SER:CB	1:C:387:PRO:HD3	2.48	0.43
1:A:54:ASN:HB3	1:A:143:ARG:HH12	1.84	0.43
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.52	0.43
1:C:452:LEU:HD23	1:C:470:THR:HA	2.01	0.43
1:A:156:SER:HB2	1:A:157:PRO:HD3	2.01	0.43
2:B:115:TYR:O	2:B:149:LEU:HB2	2.18	0.43
1:A:219:LYS:H	1:A:219:LYS:HG3	1.48	0.43
2:D:170:PRO:O	2:D:174:GLN:HG3	2.18	0.43
2:D:365:VAL:HG11	2:D:401:TRP:HB2	2.00	0.43
4:F:805:DG:H2''	4:F:806:DT:O5'	2.18	0.43
1:C:406:TRP:CD2	2:D:420:PRO:HB3	2.54	0.43
2:B:395:LYS:HG3	2:B:416:PHE:CE2	2.54	0.42
2:D:399:GLU:HA	2:D:402:TRP:HD1	1.84	0.42
2:D:423:VAL:HG11	2:D:426:TRP:CD1	2.53	0.42
1:C:296:THR:HG22	1:C:298:GLU:H	1.83	0.42
2:D:101:LYS:O	2:D:236:PRO:HB2	2.19	0.42
1:C:395:LYS:NZ	1:C:414:TRP:O	2.52	0.42
3:E:713:DC:H2'	3:E:714:DG:C8	2.55	0.42
1:C:363:ASN:HA	1:C:511:ASP:OD1	2.19	0.42
2:D:427:TYR:O	2:D:428:GLN:HB2	2.19	0.42
1:C:202:ILE:O	1:C:206:ARG:HG3	2.19	0.42
1:A:273:GLY:HA2	1:A:338:THR:HG21	2.02	0.42
1:A:356:ARG:HD3	10:A:715:HOH:O	2.19	0.42
2:B:332:GLN:CD	2:B:427:TYR:HB2	2.44	0.42
1:A:46:LYS:O	1:A:147:ASN:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:MET:HG2	1:C:46:LYS:HB2	2.01	0.42
2:D:34:LEU:HD23	2:D:34:LEU:HA	1.83	0.42
2:D:291:GLU:OE1	10:D:602:HOH:O	2.21	0.42
1:A:42:GLU:OE1	1:A:49:LYS:HE3	2.20	0.42
1:A:202:ILE:HA	1:A:202:ILE:HD13	1.84	0.42
1:A:293:ILE:HG13	1:A:294:PRO:HD2	2.00	0.41
1:C:331:LYS:HE3	1:C:364:ASP:OD2	2.20	0.41
1:C:475:GLN:CD	1:C:475:GLN:H	2.28	0.41
1:C:550:LYS:HE2	1:C:550:LYS:HB3	1.92	0.41
3:E:709:DC:H2'	3:E:710:DG:C8	2.54	0.41
1:A:146:TYR:CD1	1:A:150:PRO:HB3	2.55	0.41
4:P:813:DT:H2''	4:P:814:DC:C6	2.56	0.41
4:P:818:DC:H2'	4:P:819:DG:C8	2.55	0.41
1:C:516:GLU:O	1:C:520:GLN:HG3	2.20	0.41
1:A:115:TYR:CD2	1:A:151:MET:HG2	2.56	0.41
1:C:465:LYS:NZ	10:C:707:HOH:O	2.49	0.41
1:C:115:TYR:CD2	7:C:601:DTP:H2'1	2.55	0.41
2:D:64:LYS:HE3	2:D:71:TRP:CZ2	2.56	0.41
1:A:270:ILE:HD12	1:A:270:ILE:HA	1.93	0.41
1:A:497:THR:O	1:A:535:TRP:HA	2.20	0.41
1:C:221:HIS:HE1	1:C:223:LYS:HG3	1.86	0.41
2:D:191:SER:OG	2:D:198:HIS:ND1	2.33	0.41
2:B:85:GLN:HA	2:B:88:TRP:CE2	2.56	0.41
2:B:177:ASP:OD1	2:B:177:ASP:N	2.37	0.41
1:C:174:GLN:OE1	1:C:174:GLN:HA	2.21	0.41
1:C:497:THR:O	1:C:535:TRP:HA	2.20	0.41
1:A:16:MET:HE2	1:A:83:ARG:HG2	2.02	0.41
1:A:115:TYR:CD2	7:A:603:DTP:H2'1	2.55	0.41
1:A:120:LEU:N	1:A:148:VAL:HA	2.34	0.41
2:B:34:LEU:HD23	2:B:34:LEU:HA	1.85	0.41
2:D:7:THR:HG22	2:D:119:PRO:HG2	2.02	0.41
3:E:721:DG:H2''	3:E:722:DA:C8	2.56	0.41
1:A:28:GLU:HA	1:A:31:ILE:HD12	2.03	0.40
1:A:500:GLN:HB3	2:B:422:LEU:HD21	2.03	0.40
1:C:494:ASN:HB3	2:D:289:LEU:HD12	2.03	0.40
2:D:46:LYS:HE2	2:D:116:PHE:HB3	2.03	0.40
2:D:244:ILE:HD12	2:D:271:TYR:HE2	1.86	0.40
1:A:395:LYS:HD2	1:A:414:TRP:CH2	2.57	0.40
1:A:101:LYS:HE2	1:A:321:PRO:HG3	2.03	0.40
1:A:406:TRP:HH2	1:A:508:ALA:HB2	1.86	0.40
1:A:533:LEU:HD23	1:A:533:LEU:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:222:GLN:O	1:C:227:PHE:CE1	2.70	0.40
2:D:171:PHE:CZ	2:D:205:LEU:HB2	2.56	0.40
1:A:406:TRP:CH2	1:A:508:ALA:HB2	2.55	0.40
1:C:215:THR:O	1:C:217:PRO:HD3	2.21	0.40
1:C:427:TYR:CE1	1:C:525:LEU:HD13	2.57	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	554/556 (100%)	535 (97%)	15 (3%)	4 (1%)	18	25
1	C	554/556 (100%)	536 (97%)	14 (2%)	4 (1%)	18	25
2	B	408/428 (95%)	396 (97%)	11 (3%)	1 (0%)	43	56
2	D	408/428 (95%)	391 (96%)	15 (4%)	2 (0%)	24	34
All	All	1924/1968 (98%)	1858 (97%)	55 (3%)	11 (1%)	21	29

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	PRO
1	C	4	PRO
2	D	357	MET
1	A	1	PRO
2	D	423	VAL
1	A	150	PRO
1	C	1	PRO
1	C	150	PRO
1	A	133	PRO
2	B	421	PRO

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Mol	Chain	Res	Type
1	C	133	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	496/498 (100%)	492 (99%)	4 (1%)	73	84
1	C	496/498 (100%)	484 (98%)	12 (2%)	43	61
2	B	374/390 (96%)	371 (99%)	3 (1%)	73	84
2	D	373/390 (96%)	373 (100%)	0	100	100
All	All	1739/1776 (98%)	1720 (99%)	19 (1%)	65	79

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	5	ILE
1	A	276	VAL
1	A	391	LEU
2	B	90	VAL
2	B	422	LEU
2	B	425	LEU
1	C	2	ILE
1	C	21	VAL
1	C	23	GLN
1	C	42	GLU
1	C	58	THR
1	C	135	ILE
1	C	138	GLU
1	C	177	ASP
1	C	276	VAL
1	C	300	GLU
1	C	474	ASN
1	C	553	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	367	GLN
1	A	547	GLN
2	B	96	HIS
2	B	147	ASN
2	B	255	ASN
2	B	258	GLN
2	B	278	GLN
1	C	498	ASN
1	C	545	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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$
4	MRG	P	817	4,3	25,28,29	2.71	7 (28%)	32,39,42	2.25	12 (37%)
4	MRG	F	817	4,1,3	25,28,29	2.64	7 (28%)	32,39,42	2.22	13 (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	MRG	P	817	4,3	-	3/12/26/27	0/3/3/3
4	MRG	F	817	4,1,3	-	1/12/26/27	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	817	MRG	C2-N2	7.08	1.49	1.34
4	F	817	MRG	C2-N2	6.73	1.48	1.34
4	P	817	MRG	C2-N3	6.69	1.44	1.32
4	F	817	MRG	C2-N3	6.57	1.44	1.32
4	P	817	MRG	C4-N3	4.84	1.45	1.34
4	F	817	MRG	C4-N3	4.77	1.45	1.34
4	F	817	MRG	C2-N1	4.24	1.43	1.36
4	P	817	MRG	C2-N1	4.23	1.43	1.36
4	P	817	MRG	C2'-C3'	-3.45	1.44	1.52
4	F	817	MRG	C2'-C3'	-3.42	1.44	1.52
4	P	817	MRG	O3'-C3'	-2.84	1.37	1.43
4	F	817	MRG	O4'-C4'	-2.65	1.39	1.45
4	P	817	MRG	O4'-C4'	-2.63	1.39	1.45
4	F	817	MRG	O3'-C3'	-2.63	1.37	1.43

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	817	MRG	C2-N3-C4	6.99	120.74	112.00
4	F	817	MRG	C2-N3-C4	6.77	120.47	112.00
4	F	817	MRG	C5-C4-N3	-5.18	120.14	128.39
4	P	817	MRG	C5-C4-N3	-5.15	120.19	128.39
4	F	817	MRG	C2-N1-C6	-3.82	119.93	124.55
4	P	817	MRG	C2-N1-C6	-3.23	120.64	124.55
4	P	817	MRG	N9-C4-N3	3.15	132.26	125.95
4	F	817	MRG	O4'-C1'-N9	3.05	113.27	107.86
4	P	817	MRG	C22-C21-N2	3.04	120.73	112.20
4	P	817	MRG	O4'-C1'-N9	2.96	113.12	107.86
4	F	817	MRG	N9-C4-N3	2.93	131.82	125.95
4	P	817	MRG	N1-C2-N3	-2.82	118.93	123.68
4	F	817	MRG	C5-C6-N1	2.65	120.01	113.25
4	P	817	MRG	C5-C6-N1	2.62	119.91	113.25
4	P	817	MRG	O6-C6-C5	-2.45	120.06	126.53
4	F	817	MRG	O6-C6-C5	-2.42	120.15	126.53
4	F	817	MRG	C4-C5-N7	-2.40	106.87	110.67
4	F	817	MRG	N1-C2-N3	-2.30	119.80	123.68
4	F	817	MRG	N9-C8-N7	-2.27	109.19	113.40
4	P	817	MRG	N9-C8-N7	-2.26	109.21	113.40
4	F	817	MRG	C8-N7-C5	2.18	108.14	104.26
4	P	817	MRG	C4-C5-N7	-2.06	107.41	110.67
4	F	817	MRG	C21-N2-C2	-2.04	119.53	123.36
4	F	817	MRG	C22-C21-N2	2.04	117.91	112.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	817	MRG	C8-N7-C5	2.02	107.86	104.26

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	P	817	MRG	C22-C21-N2-C2
4	P	817	MRG	C21-C22-C23-S24
4	F	817	MRG	N2-C21-C22-C23
4	P	817	MRG	N2-C21-C22-C23

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	817	MRG	1	0
4	F	817	MRG	1	0

5.5 Carbohydrates [i](#)

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	$\# Z > 2$
5	GLC	G	1	5	11,11,12	1.19	2 (18%)	15,15,17	1.30	1 (6%)
5	FRU	G	2	5	11,12,12	2.55	4 (36%)	10,18,18	5.22	5 (50%)
5	GLC	H	1	5	11,11,12	0.90	0	15,15,17	1.45	2 (13%)
5	FRU	H	2	5	11,12,12	2.27	4 (36%)	10,18,18	5.25	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
5	GLC	G	1	5	-	0/2/19/22	0/1/1/1
5	FRU	G	2	5	-	4/5/24/24	0/1/1/1
5	GLC	H	1	5	-	1/2/19/22	0/1/1/1
5	FRU	H	2	5	-	3/5/24/24	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	2	FRU	O5-C2	5.68	1.52	1.43
5	H	2	FRU	O3-C3	4.58	1.51	1.42
5	H	2	FRU	O5-C2	4.23	1.50	1.43
5	G	2	FRU	O3-C3	3.94	1.50	1.42
5	G	2	FRU	O2-C2	3.36	1.46	1.40
5	G	1	GLC	O5-C5	2.77	1.48	1.43
5	H	2	FRU	O5-C5	-2.43	1.38	1.43
5	H	2	FRU	C4-C5	2.34	1.58	1.53
5	G	2	FRU	C4-C5	2.34	1.58	1.53
5	G	1	GLC	O5-C1	2.32	1.47	1.43

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	2	FRU	O2-C2-O5	-14.34	81.80	109.33
5	G	2	FRU	O2-C2-O5	-13.84	82.75	109.33
5	G	2	FRU	O5-C5-C4	-7.51	86.48	105.42
5	H	2	FRU	O5-C5-C4	-7.00	87.77	105.42
5	G	1	GLC	O5-C5-C6	3.54	114.56	107.66
5	H	2	FRU	O3-C3-C4	3.48	125.55	113.25
5	G	2	FRU	O3-C3-C4	3.44	125.39	113.25
5	H	1	GLC	O5-C5-C6	-3.33	101.18	107.66
5	H	1	GLC	C6-C5-C4	-2.57	106.70	113.02
5	G	2	FRU	O1-C1-C2	2.38	116.94	111.67
5	G	2	FRU	C6-C5-C4	-2.23	109.82	115.10
5	H	2	FRU	C6-C5-C4	-2.17	109.98	115.10

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	1	GLC	O5-C5-C6-O6
5	G	2	FRU	O5-C5-C6-O6
5	G	2	FRU	O1-C1-C2-O2

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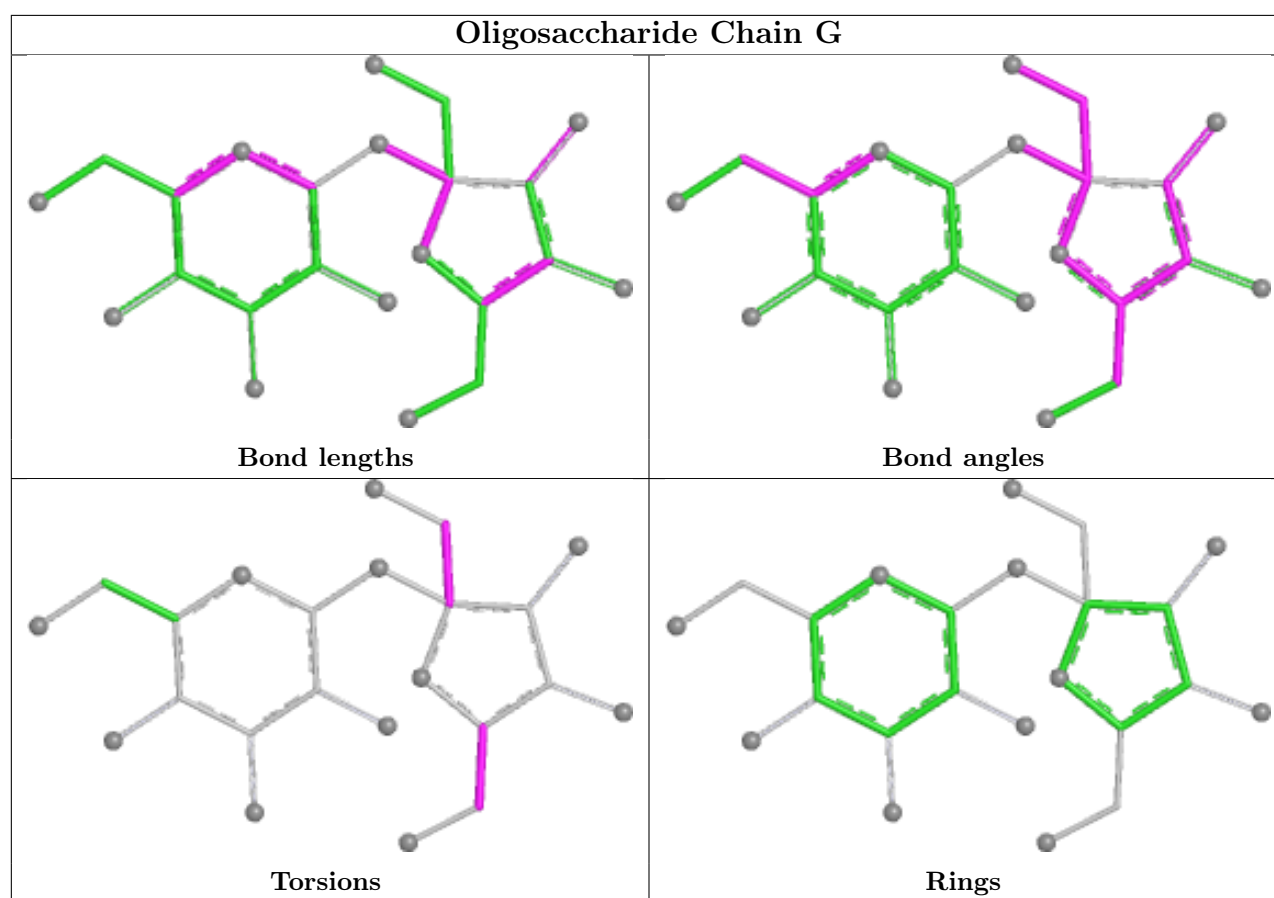
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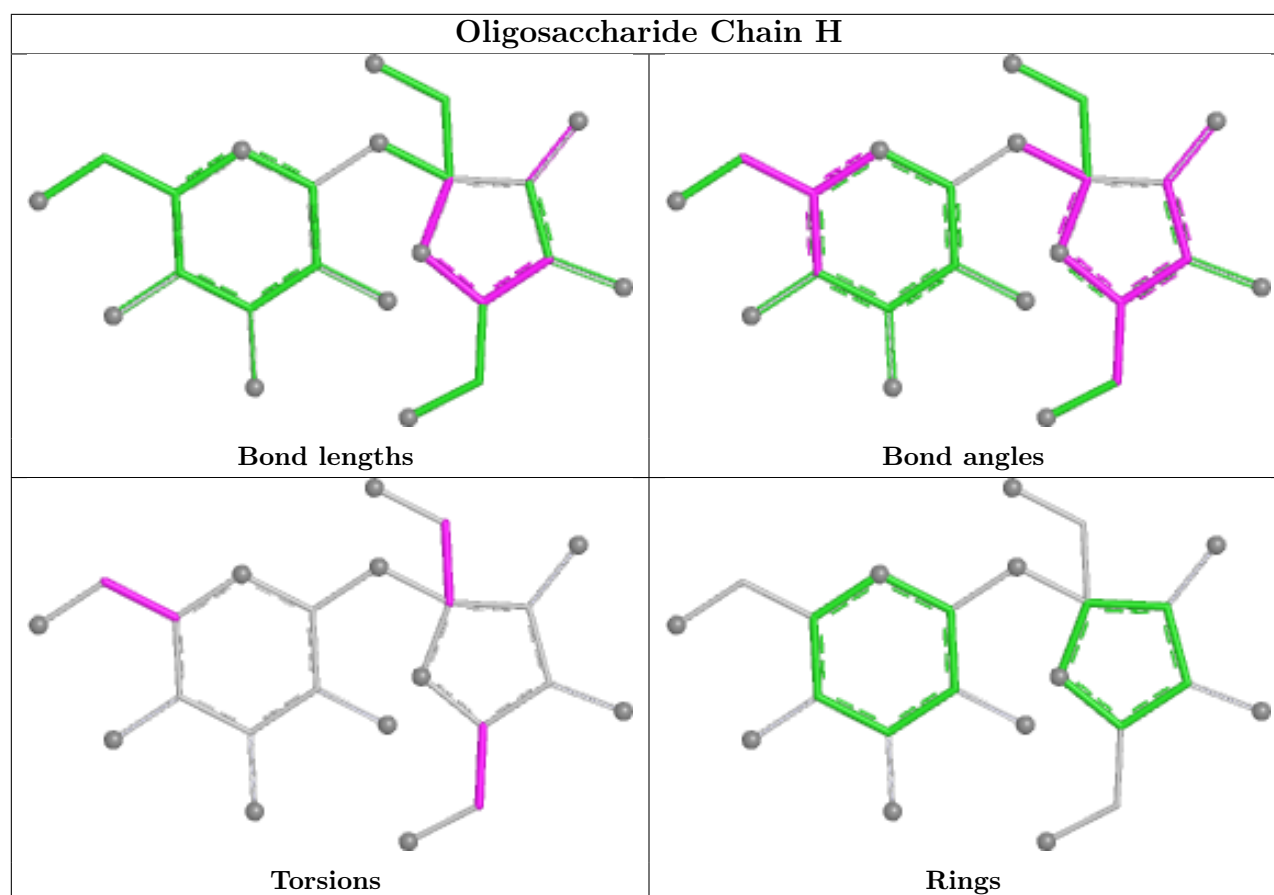
Mol	Chain	Res	Type	Atoms
5	H	2	FRU	O1-C1-C2-O2
5	H	2	FRU	O5-C5-C6-O6
5	G	2	FRU	O1-C1-C2-C3
5	H	2	FRU	O1-C1-C2-C3
5	G	2	FRU	O1-C1-C2-O5

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 oligosaccharide.





5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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$
9	SO4	D	502	-	4,4,4	0.24	0	6,6,6	0.06	0
7	DTP	C	601	6	31,32,32	1.77	7 (22%)	46,50,50	1.89	10 (21%)
7	DTP	A	603	6	31,32,32	1.76	7 (22%)	46,50,50	1.99	10 (21%)
8	EDO	B	502	-	3,3,3	0.47	0	2,2,2	0.37	0
9	SO4	B	503	-	4,4,4	0.23	0	6,6,6	0.06	0
8	EDO	D	503	-	3,3,3	0.40	0	2,2,2	0.30	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
8	EDO	B	502	-	-	0/1/1/1	-
7	DTP	C	601	6	-	2/22/34/34	0/3/3/3
8	EDO	D	503	-	-	1/1/1/1	-
7	DTP	A	603	6	-	2/22/34/34	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	601	DTP	C6-N6	5.09	1.47	1.34
7	A	603	DTP	C6-N6	4.94	1.46	1.34
7	A	603	DTP	PB-O3A	-4.47	1.54	1.59
7	C	601	DTP	PB-O3A	-4.45	1.54	1.59
7	A	603	DTP	C5'-C4'	-3.09	1.42	1.51
7	C	601	DTP	C5'-C4'	-3.05	1.42	1.51
7	A	603	DTP	C2'-C3'	-2.60	1.46	1.52
7	C	601	DTP	C2'-C3'	-2.57	1.46	1.52
7	A	603	DTP	O5'-C5'	-2.47	1.35	1.44
7	C	601	DTP	O5'-C5'	-2.45	1.35	1.44
7	C	601	DTP	O3'-C3'	-2.29	1.38	1.43
7	A	603	DTP	O3'-C3'	-2.26	1.38	1.43
7	C	601	DTP	C3'-C4'	-2.23	1.47	1.53
7	A	603	DTP	C3'-C4'	-2.19	1.47	1.53

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	603	DTP	C5-C4-N3	-5.71	118.85	126.72
7	C	601	DTP	C5-C4-N3	-5.49	119.15	126.72
7	A	603	DTP	N3-C2-N1	-4.46	121.83	128.58
7	C	601	DTP	N3-C2-N1	-4.45	121.85	128.58
7	A	603	DTP	N3-C4-N9	4.35	134.56	127.17
7	C	601	DTP	N3-C4-N9	4.28	134.44	127.17
7	A	603	DTP	N9-C8-N7	-4.17	108.03	113.94
7	C	601	DTP	N9-C8-N7	-3.90	108.40	113.94
7	A	603	DTP	C2-N3-C4	3.77	121.03	111.83
7	C	601	DTP	C2-N3-C4	3.65	120.74	111.83
7	A	603	DTP	C4-N9-C8	3.53	109.45	105.74
7	A	603	DTP	C5-N7-C8	3.46	108.89	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	603	DTP	O4'-C1'-N9	3.44	114.14	107.96
7	C	601	DTP	C4-N9-C8	3.44	109.34	105.74
7	C	601	DTP	C5-N7-C8	3.24	108.55	103.45
7	A	603	DTP	C4-C5-N7	-3.09	107.05	110.58
7	C	601	DTP	O4'-C1'-N9	3.00	113.35	107.96
7	C	601	DTP	C4-C5-N7	-2.87	107.30	110.58
7	C	601	DTP	O5'-C5'-C4'	2.74	118.31	108.99
7	A	603	DTP	O5'-C5'-C4'	2.62	117.91	108.99

There are no chirality outliers.

All (5) torsion outliers are listed below:

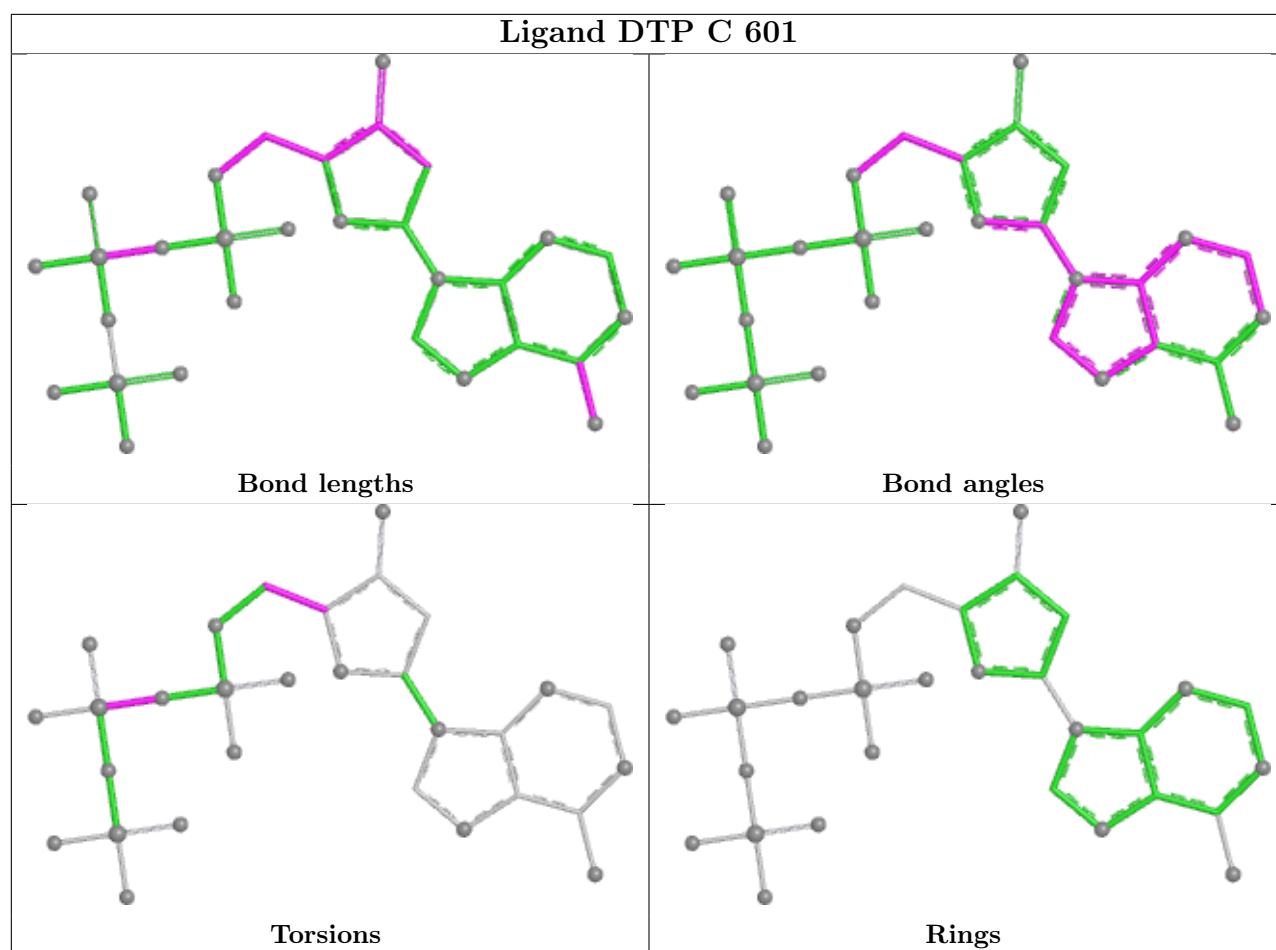
Mol	Chain	Res	Type	Atoms
7	C	601	DTP	PA-O3A-PB-O2B
7	A	603	DTP	PA-O3A-PB-O2B
7	C	601	DTP	O4'-C4'-C5'-O5'
8	D	503	EDO	O1-C1-C2-O2
7	A	603	DTP	PA-O3A-PB-O1B

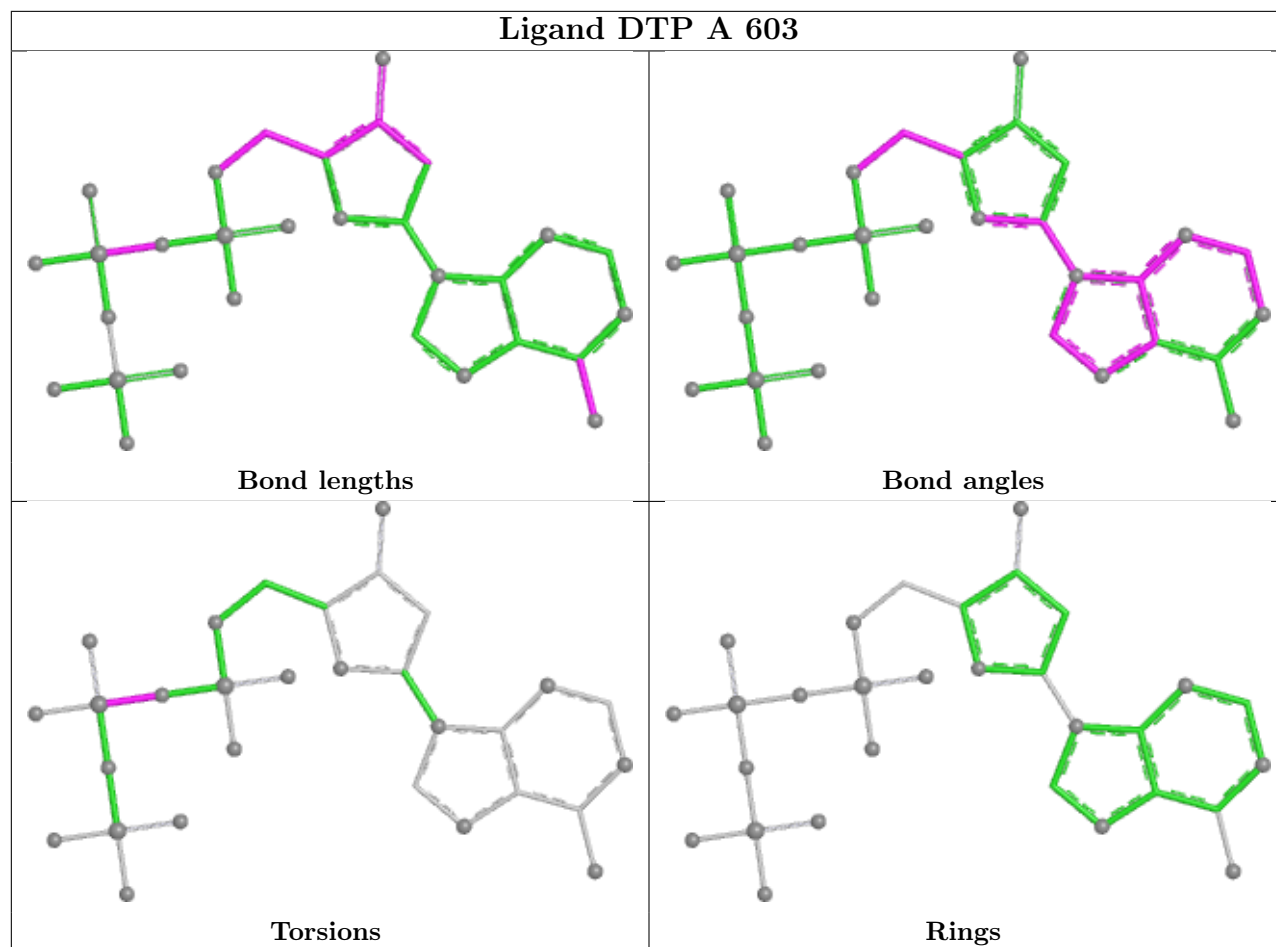
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	601	DTP	2	0
7	A	603	DTP	2	0
8	D	503	EDO	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	556/556 (100%)	0.23	24 (4%) 40 40	38, 89, 181, 228	0
1	C	556/556 (100%)	0.35	26 (4%) 36 36	40, 96, 172, 244	0
2	B	412/428 (96%)	0.16	22 (5%) 32 31	37, 74, 137, 215	0
2	D	412/428 (96%)	0.34	25 (6%) 27 26	45, 87, 162, 206	0
3	E	24/27 (88%)	0.29	0 100 100	84, 121, 230, 245	0
3	T	24/27 (88%)	0.24	0 100 100	80, 110, 232, 267	0
4	F	19/21 (90%)	0.23	1 (5%) 32 31	65, 100, 194, 217	0
4	P	19/21 (90%)	-0.05	1 (5%) 32 31	72, 99, 170, 215	0
All	All	2022/2064 (97%)	0.27	99 (4%) 35 34	37, 86, 171, 267	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	74	LEU	5.4
2	B	232	TYR	5.3
1	C	-1	MET	5.1
2	B	423	VAL	5.0
2	B	214	LEU	4.6
2	B	90	VAL	4.4
2	D	420	PRO	4.4
1	A	37	ILE	4.1
2	D	423	VAL	4.0
2	D	360	ALA	4.0
1	C	554	ALA	3.9
1	A	35	VAL	3.9
2	D	88	TRP	3.9
2	B	5	ILE	3.7
1	C	4	PRO	3.6
2	D	217	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
2	D	212	TRP	3.4
2	D	214	LEU	3.4
2	B	215	THR	3.2
1	A	109	LEU	3.2
1	C	142	ILE	3.2
2	B	425	LEU	3.2
2	D	421	PRO	3.1
1	C	448	ARG	3.1
1	A	47	ILE	3.1
2	B	231	GLY	2.9
1	A	5	ILE	2.9
1	A	4	PRO	2.9
2	D	216	THR	2.9
2	B	212	TRP	2.9
2	D	232	TYR	2.9
2	D	418	ASN	2.9
2	B	217	PRO	2.9
1	C	109	LEU	2.9
1	C	61	PHE	2.9
2	D	95	PRO	2.8
1	A	135	ILE	2.8
2	D	422	LEU	2.8
1	C	5	ILE	2.7
1	C	3	SER	2.7
2	B	88	TRP	2.7
2	B	422	LEU	2.7
1	C	144	TYR	2.7
1	A	554	ALA	2.7
1	A	0	VAL	2.6
2	B	213	GLY	2.6
2	B	4	PRO	2.6
1	C	286	THR	2.6
2	B	266	TRP	2.5
2	B	421	PRO	2.5
2	D	213	GLY	2.5
1	A	2	ILE	2.5
1	C	0	VAL	2.5
1	A	74	LEU	2.5
2	B	92	LEU	2.5
2	D	90	VAL	2.5
2	D	248	GLU	2.4
1	A	71	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	54	ASN	2.4
1	C	262	GLY	2.4
1	C	2	ILE	2.4
1	A	73	LYS	2.4
2	B	9	PRO	2.3
2	D	231	GLY	2.3
2	B	94	ILE	2.3
1	C	287	LYS	2.3
1	A	304	ALA	2.3
1	C	140	PRO	2.3
1	C	296	THR	2.3
1	A	-1	MET	2.3
2	D	318	TYR	2.3
1	C	301	LEU	2.3
1	A	149	LEU	2.2
1	C	180	ILE	2.2
4	P	803	DC	2.2
2	D	179	VAL	2.2
1	C	131	THR	2.2
1	A	43	LYS	2.2
1	A	259	LYS	2.2
1	A	144	TYR	2.2
2	B	209	LEU	2.2
1	C	135	ILE	2.2
1	A	24	TRP	2.2
1	C	21	VAL	2.1
2	D	87	PHE	2.1
1	A	288	ALA	2.1
1	C	283	LEU	2.1
1	A	55	PRO	2.1
2	D	154	LYS	2.1
2	D	4	PRO	2.1
1	C	295	LEU	2.1
2	D	425	LEU	2.1
2	B	419	THR	2.1
2	D	178	ILE	2.1
2	B	171	PHE	2.0
4	F	803	DC	2.0
2	D	92	LEU	2.0
1	A	45	GLY	2.0
1	C	71	TRP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	MRG	F	817	26/27	0.90	0.10	117,133,165,172	0
4	MRG	P	817	26/27	0.91	0.11	92,114,144,154	0

6.3 Carbohydrates [i](#)

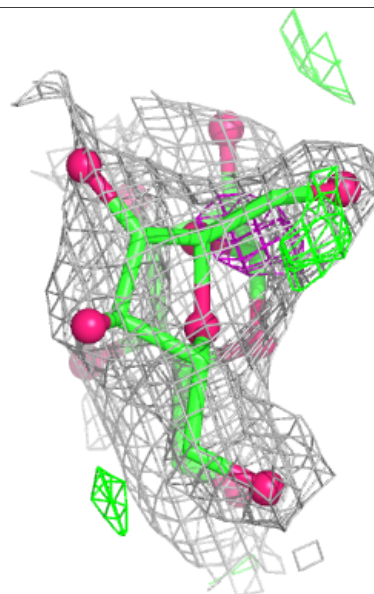
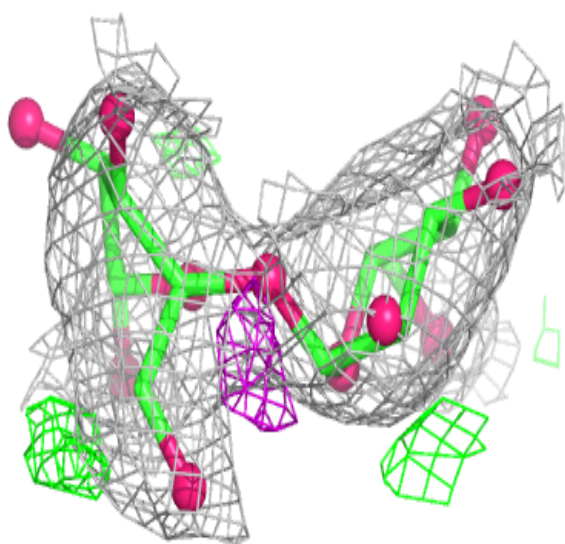
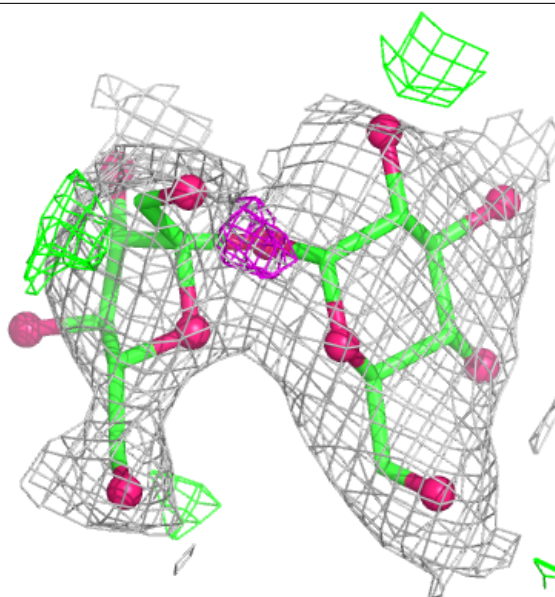
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

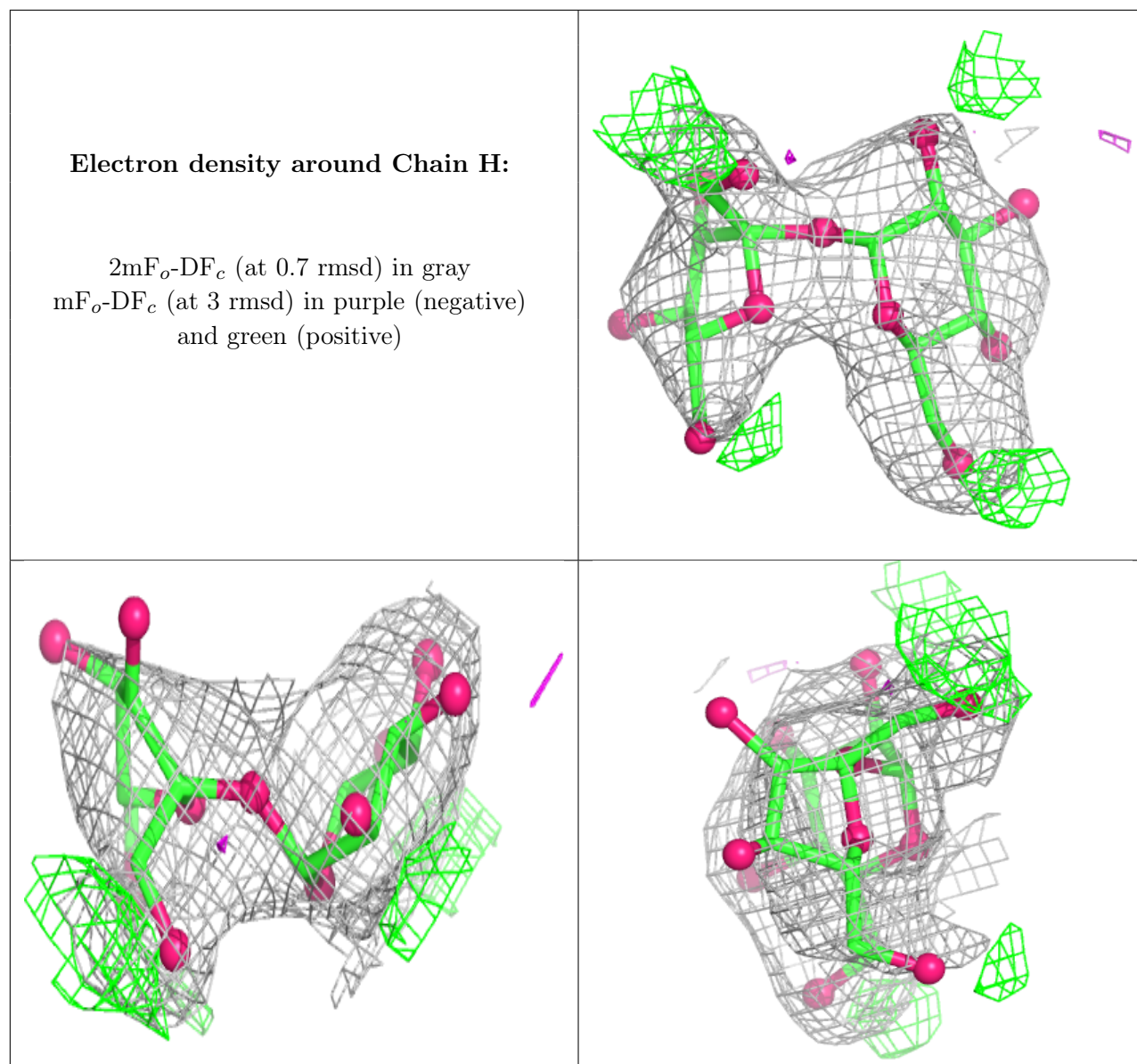
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GLC	G	1	11/12	-	-	66,101,110,117	0
5	FRU	G	2	12/12	-	-	81,123,127,130	0
5	GLC	H	1	11/12	-	-	84,115,131,134	0
5	FRU	H	2	12/12	-	-	108,130,142,150	0

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 G:

$2mF_o-DF_c$ (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.

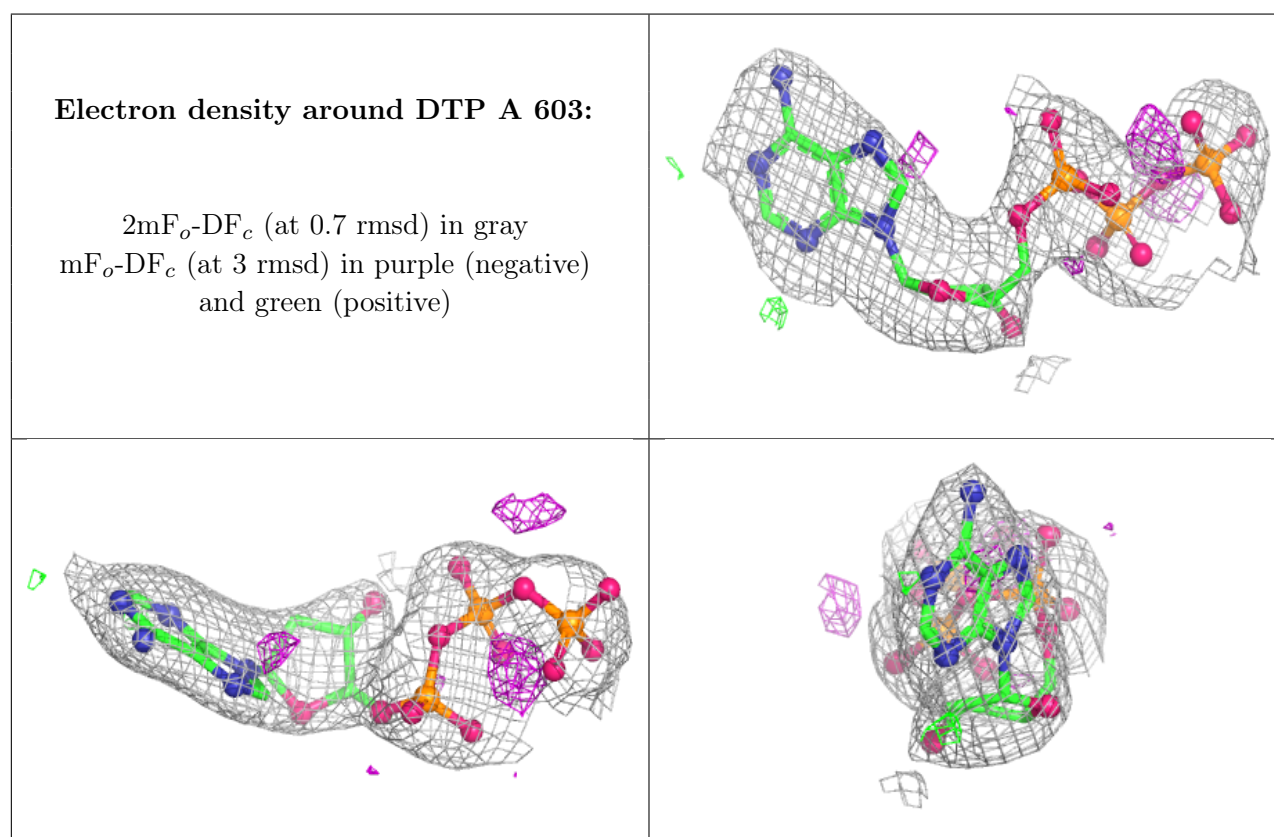
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	DTP	A	603	30/30	0.89	0.11	66,111,146,146	0
8	EDO	B	502	4/4	0.89	0.14	60,68,70,77	0
7	DTP	C	601	30/30	0.90	0.10	83,98,143,148	0
6	MG	C	603	1/1	0.91	0.12	105,105,105,105	0
8	EDO	D	503	4/4	0.91	0.19	68,75,80,80	0

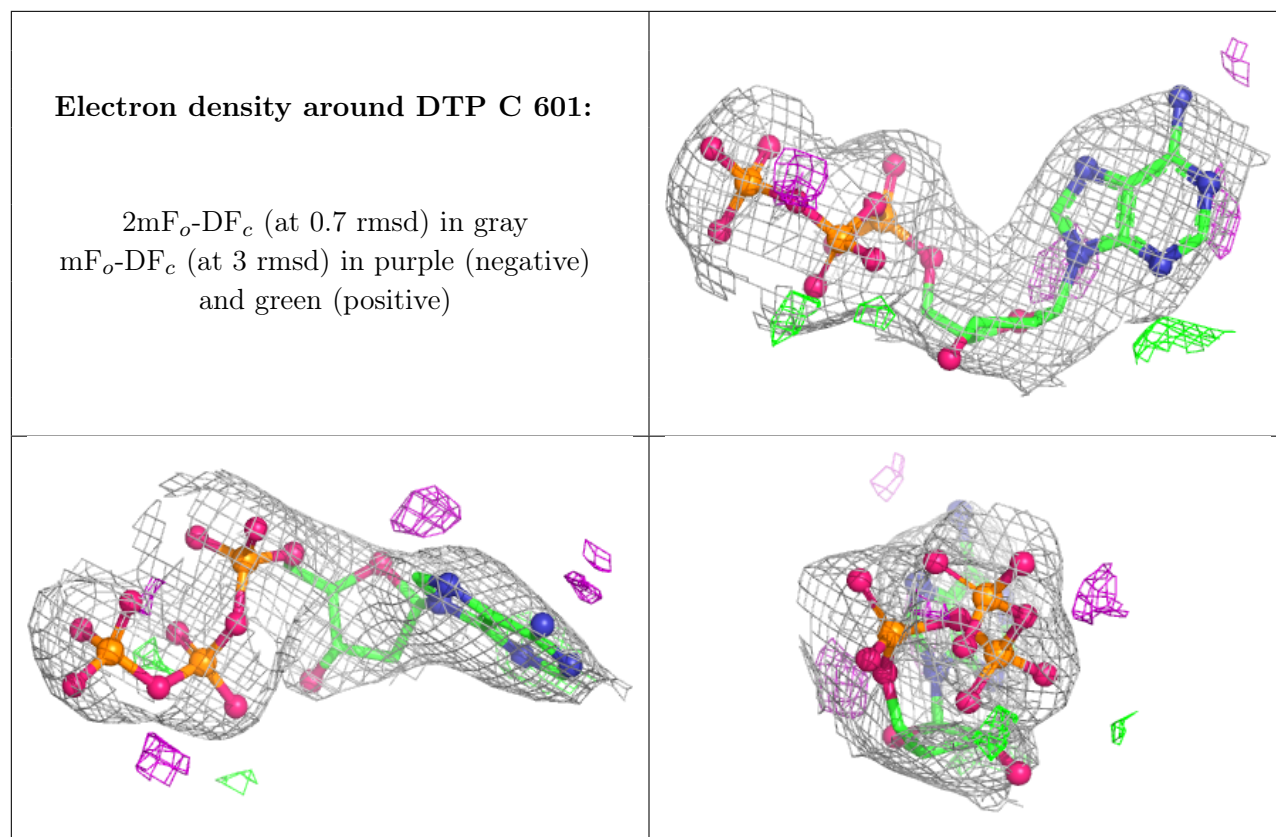
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	SO4	B	503	5/5	0.91	0.29	263,263,267,280	0
9	SO4	D	502	5/5	0.92	0.14	145,146,150,153	0
6	MG	C	602	1/1	0.94	0.07	116,116,116,116	0
6	MG	A	602	1/1	0.94	0.09	143,143,143,143	0
6	MG	A	601	1/1	0.95	0.08	129,129,129,129	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.