



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:19 PM UTC

PDB ID : 4U8O / pdb_00004u8o
Title : Structure of Aspergillus fumigatus UDP-Galactopyranose mutase mutant N207A complexed with UDP
Authors : Qureshi, I.A.; Chaudhary, R.; Tanner, J.J.
Deposited on : 2014-08-03
Resolution : 2.30 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

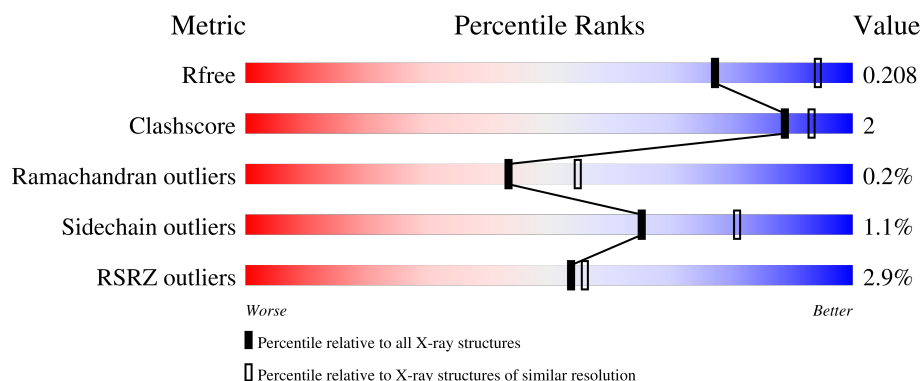
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	513	5% 91% 7% ..
1	B	513	3% 94% ..
1	C	513	2% 93% 5% .
1	D	513	2% 95% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16652 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 UDP-galactopyranose mutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	505	Total	C	N	O	S	0	0	0
			3882	2467	662	732	21			
1	B	505	Total	C	N	O	S	0	0	0
			3875	2460	660	734	21			
1	C	504	Total	C	N	O	S	0	0	0
			3871	2461	659	730	21			
1	D	505	Total	C	N	O	S	0	0	0
			3872	2460	658	733	21			

There are 28 discrepancies between the modelled and reference sequences:

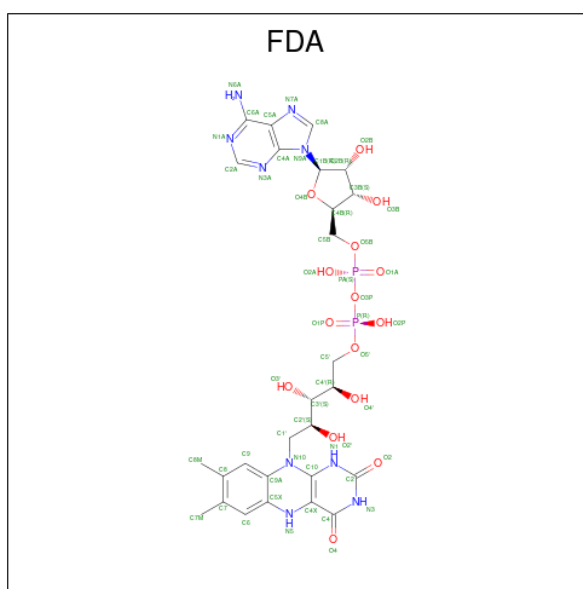
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	expression tag	UNP Q4W1X2
A	-1	ILE	-	expression tag	UNP Q4W1X2
A	0	ALA	-	expression tag	UNP Q4W1X2
A	207	ALA	ASN	engineered mutation	UNP Q4W1X2
A	344	ALA	LYS	engineered mutation	UNP Q4W1X2
A	345	ALA	LYS	engineered mutation	UNP Q4W1X2
A	429	THR	ALA	engineered mutation	UNP Q4W1X2
B	-2	ALA	-	expression tag	UNP Q4W1X2
B	-1	ILE	-	expression tag	UNP Q4W1X2
B	0	ALA	-	expression tag	UNP Q4W1X2
B	207	ALA	ASN	engineered mutation	UNP Q4W1X2
B	344	ALA	LYS	engineered mutation	UNP Q4W1X2
B	345	ALA	LYS	engineered mutation	UNP Q4W1X2
B	429	THR	ALA	engineered mutation	UNP Q4W1X2
C	-2	ALA	-	expression tag	UNP Q4W1X2
C	-1	ILE	-	expression tag	UNP Q4W1X2
C	0	ALA	-	expression tag	UNP Q4W1X2
C	207	ALA	ASN	engineered mutation	UNP Q4W1X2
C	344	ALA	LYS	engineered mutation	UNP Q4W1X2
C	345	ALA	LYS	engineered mutation	UNP Q4W1X2
C	429	THR	ALA	engineered mutation	UNP Q4W1X2

Continued on next page...

Continued from previous page...

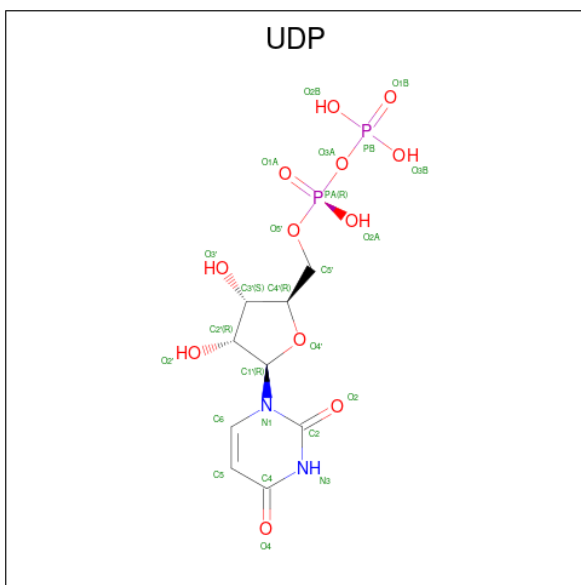
Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	ALA	-	expression tag	UNP Q4W1X2
D	-1	ILE	-	expression tag	UNP Q4W1X2
D	0	ALA	-	expression tag	UNP Q4W1X2
D	207	ALA	ASN	engineered mutation	UNP Q4W1X2
D	344	ALA	LYS	engineered mutation	UNP Q4W1X2
D	345	ALA	LYS	engineered mutation	UNP Q4W1X2
D	429	THR	ALA	engineered mutation	UNP Q4W1X2

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (CCD ID: UDP) (formula: $C_9H_{14}N_2O_{12}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	B	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	B	1	Total 21	C 9	N 2	O 9	P 1	0	0
3	C	1	Total 15	C 8	N 2	O 5		0	0
3	D	1	Total 15	C 8	N 2	O 5		0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



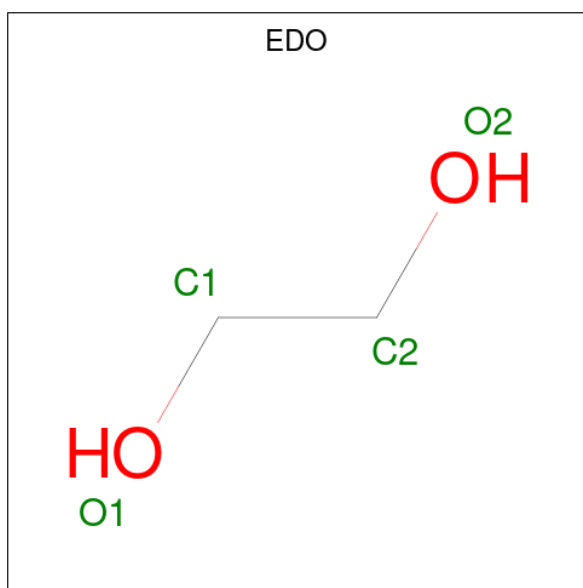
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total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

Continued on next page...

Continued from previous page...

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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

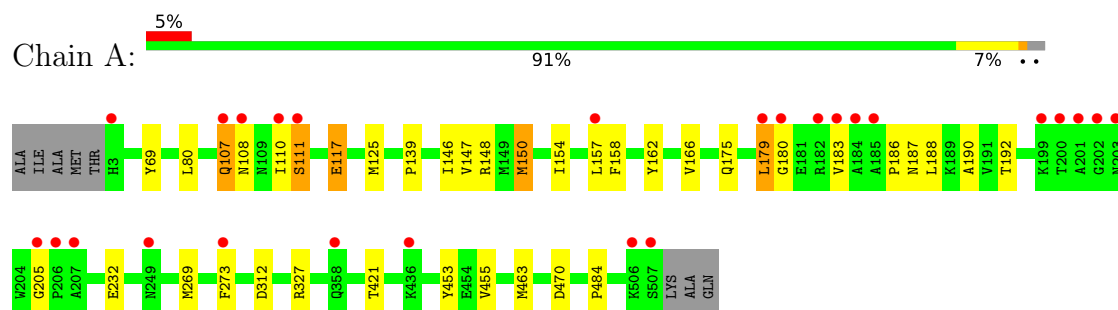
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	141	Total O 141 141	0	0
6	B	173	Total O 173 173	0	0
6	C	155	Total O 155 155	0	0
6	D	171	Total O 171 171	0	0

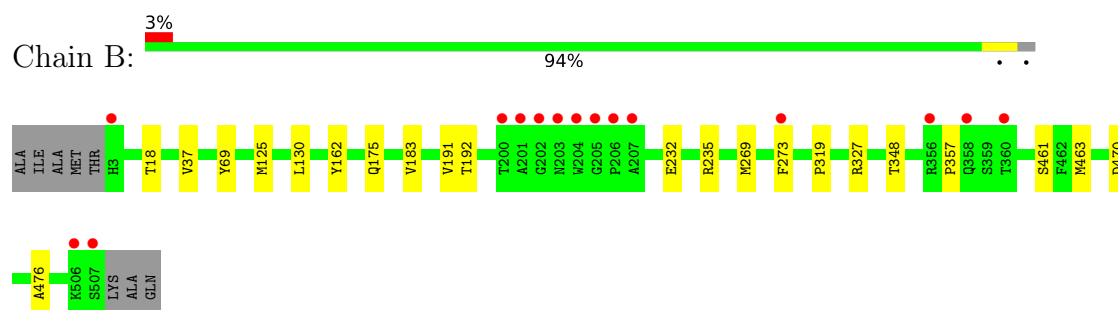
3 Residue-property plots [i](#)

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.

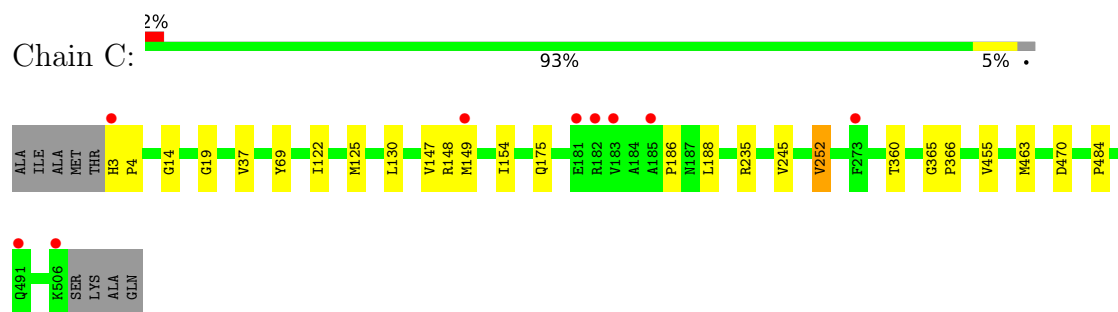
- Molecule 1: UDP-galactopyranose mutase



- Molecule 1: UDP-galactopyranose mutase

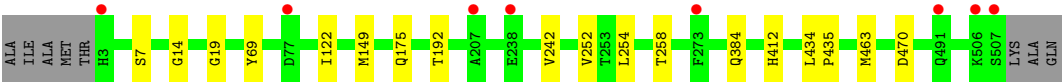


- Molecule 1: UDP-galactopyranose mutase



- Molecule 1: UDP-galactopyranose mutase





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	218.39Å 218.39Å 321.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	63.00 – 2.30 63.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (63.00-2.30) 100.0 (63.00-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.173 , 0.203 0.182 , 0.208	Depositor DCC
R_{free} test set	9980 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.502	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16652	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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: FDA, UDP, EDO, 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	0.48	0/3980	0.80	5/5427 (0.1%)
1	B	0.47	0/3973	0.78	0/5421
1	C	0.45	0/3969	0.75	0/5414
1	D	0.45	0/3970	0.76	0/5417
All	All	0.46	0/15892	0.77	5/21679 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	179	LEU	N-CA-C	8.46	122.89	112.23
1	A	205	GLY	CA-C-N	5.81	126.21	119.47
1	A	205	GLY	C-N-CA	5.81	126.21	119.47
1	A	80	LEU	CA-C-N	5.44	125.14	119.64
1	A	80	LEU	C-N-CA	5.44	125.14	119.64

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	3882	0	3735	24	0
1	B	3875	0	3711	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3871	0	3718	16	0
1	D	3872	0	3708	10	0
2	A	53	0	33	0	0
2	B	53	0	32	0	0
2	C	53	0	32	0	0
2	D	53	0	33	0	0
3	A	50	0	22	6	0
3	B	46	0	22	2	0
3	C	15	0	8	0	0
3	D	15	0	8	0	0
4	A	30	0	0	1	0
4	B	30	0	0	0	0
4	C	35	0	0	0	0
4	D	35	0	0	0	0
5	A	8	0	12	0	0
5	B	12	0	18	0	0
5	C	12	0	18	0	0
5	D	12	0	18	1	0
6	A	141	0	0	0	0
6	B	173	0	0	0	0
6	C	155	0	0	1	0
6	D	171	0	0	0	0
All	All	16652	0	15128	59	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 2.

All (59) 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:183:VAL:HG22	3:A:602:UDP:H1'	1.74	0.70
1:A:107:GLN:HB3	1:A:150:MET:HE1	1.73	0.69
1:A:107:GLN:CB	1:A:150:MET:HE1	2.29	0.61
1:A:269:MET:HE2	1:A:273:PHE:HB3	1.83	0.60
1:A:146:ILE:O	1:A:150:MET:HG3	2.04	0.58
1:B:125:MET:HE1	1:B:191:VAL:HG11	1.85	0.58
1:C:125:MET:HG2	1:C:188:LEU:HD13	1.89	0.55
1:D:69:TYR:CD1	1:D:463:MET:HG3	2.43	0.54
1:D:69:TYR:CG	1:D:463:MET:HG3	2.43	0.54
1:A:69:TYR:CG	1:A:463:MET:HG3	2.45	0.52
1:A:187:ASN:OD1	1:A:190:ALA:N	2.43	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:MET:HG2	1:A:188:LEU:HD13	1.91	0.52
1:B:327:ARG:NH1	3:B:602:UDP:O2B	2.34	0.51
1:C:69:TYR:CG	1:C:463:MET:HG3	2.45	0.51
1:A:327:ARG:NH1	3:A:602:UDP:O3B	2.35	0.51
1:A:150:MET:HE3	1:A:186:PRO:HG3	1.92	0.50
1:C:69:TYR:CD1	1:C:463:MET:HG3	2.46	0.50
1:C:245:VAL:HG22	1:C:252:VAL:HG22	1.93	0.50
1:C:125:MET:HE3	1:C:154:ILE:HD12	1.94	0.49
1:A:69:TYR:CD1	1:A:463:MET:HG3	2.49	0.48
1:B:69:TYR:CG	1:B:463:MET:HG3	2.50	0.47
1:A:192:THR:HG21	1:D:122:ILE:HG21	1.98	0.45
1:A:455:VAL:HG13	1:A:484:PRO:HB3	1.98	0.45
1:B:348:THR:O	1:B:357:PRO:HG3	2.17	0.45
1:C:455:VAL:HG13	1:C:484:PRO:HB3	1.99	0.45
1:C:148:ARG:HD3	6:C:773:HOH:O	2.17	0.45
1:B:183:VAL:HG22	3:B:602:UDP:H1'	1.99	0.45
1:D:384:GLN:HG3	1:D:412:HIS:HE1	1.81	0.44
1:A:162:TYR:O	1:A:166:VAL:HG23	2.17	0.44
1:B:130:LEU:HD23	1:C:130:LEU:HD23	1.99	0.44
1:B:37:VAL:HG12	1:B:235:ARG:HB3	1.98	0.44
1:C:14:GLY:O	1:C:19:GLY:HA3	2.17	0.44
1:B:470:ASP:HB3	1:B:476:ALA:HB3	2.00	0.43
1:A:150:MET:HE2	1:A:150:MET:HB3	1.58	0.43
1:C:149:MET:HE3	1:C:149:MET:HB3	1.89	0.43
1:D:14:GLY:O	1:D:19:GLY:HA3	2.19	0.43
1:A:158:PHE:HE2	3:A:602:UDP:N3	2.16	0.43
1:D:149:MET:HG3	5:D:612:EDO:H12	2.01	0.43
1:B:192:THR:HG21	1:C:122:ILE:HG21	2.01	0.43
1:D:242:VAL:HG13	1:D:252:VAL:HG13	2.01	0.43
1:A:183:VAL:HG13	3:A:602:UDP:O2	2.19	0.42
1:A:117:GLU:HG2	1:A:157:LEU:HD21	2.00	0.42
1:B:269:MET:HE2	1:B:273:PHE:HB3	2.00	0.42
1:D:434:LEU:HB2	1:D:435:PRO:HD3	2.01	0.42
1:A:179:LEU:HA	1:A:179:LEU:HD23	1.66	0.42
1:A:453:TYR:OH	3:A:602:UDP:O1B	2.29	0.42
1:A:125:MET:HE3	1:A:154:ILE:HD12	2.02	0.42
1:C:125:MET:HG3	1:C:186:PRO:HB3	2.01	0.41
1:A:158:PHE:CE2	3:A:602:UDP:C4	3.08	0.41
1:C:3:HIS:HA	1:C:4:PRO:HD3	1.92	0.41
1:B:18:THR:OG1	1:B:461:SER:HB3	2.21	0.41
1:C:37:VAL:HG12	1:C:235:ARG:HB3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:ILE:HD12	1:D:192:THR:HG22	2.03	0.41
1:B:162:TYR:HB2	1:B:319:PRO:HB3	2.03	0.40
1:C:122:ILE:HD13	1:C:122:ILE:HA	1.95	0.40
1:D:254:LEU:HD12	1:D:258:THR:HB	2.03	0.40
1:C:365:GLY:HA3	1:C:366:PRO:HA	1.95	0.40
1:A:139:PRO:HB3	1:A:148:ARG:HD2	2.03	0.40
1:A:312:ASP:HB3	4:A:607:SO4:O4	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	503/513 (98%)	488 (97%)	10 (2%)	5 (1%)	12	15
1	B	503/513 (98%)	489 (97%)	14 (3%)	0	100	100
1	C	502/513 (98%)	495 (99%)	7 (1%)	0	100	100
1	D	503/513 (98%)	492 (98%)	11 (2%)	0	100	100
All	All	2011/2052 (98%)	1964 (98%)	42 (2%)	5 (0%)	43	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	111	SER
1	A	107	GLN
1	A	180	GLY
1	A	110	ILE
1	A	108	ASN

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	407/431 (94%)	399 (98%)	8 (2%)	48	67
1	B	406/431 (94%)	404 (100%)	2 (0%)	81	90
1	C	405/431 (94%)	400 (99%)	5 (1%)	63	79
1	D	405/431 (94%)	402 (99%)	3 (1%)	76	87
All	All	1623/1724 (94%)	1605 (99%)	18 (1%)	65	81

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	SER
1	A	117	GLU
1	A	147	VAL
1	A	150	MET
1	A	175	GLN
1	A	232	GLU
1	A	421	THR
1	A	470	ASP
1	B	175	GLN
1	B	232	GLU
1	C	147	VAL
1	C	175	GLN
1	C	252	VAL
1	C	360	THR
1	C	470	ASP
1	D	7	SER
1	D	175	GLN
1	D	470	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	482	ASN
1	B	27	ASN
1	C	246	ASN
1	C	474	ASN
1	C	482	ASN
1	D	27	ASN
1	D	384	GLN
1	D	482	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

47 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	603	-	4,4,4	0.21	0	6,6,6	0.23	0
4	SO4	C	605	-	4,4,4	0.24	0	6,6,6	0.11	0
4	SO4	C	606	-	4,4,4	0.25	0	6,6,6	0.18	0
3	UDP	D	609	-	16,16,26	2.49	8 (50%)	22,23,40	2.19	6 (27%)
5	EDO	B	612	-	3,3,3	0.52	0	2,2,2	0.30	0
5	EDO	B	610	-	3,3,3	0.55	0	2,2,2	0.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	B	603	-	4,4,4	0.26	0	6,6,6	0.25	0
4	SO4	D	605	-	4,4,4	0.24	0	6,6,6	0.11	0
4	SO4	D	606	-	4,4,4	0.25	0	6,6,6	0.10	0
2	FDA	B	601	-	57,58,58	2.83	24 (42%)	78,89,89	2.00	19 (24%)
2	FDA	A	601	-	57,58,58	2.94	23 (40%)	78,89,89	2.10	22 (28%)
5	EDO	A	610	-	3,3,3	0.57	0	2,2,2	0.41	0
5	EDO	C	612	-	3,3,3	0.52	0	2,2,2	0.35	0
4	SO4	B	607	-	4,4,4	0.25	0	6,6,6	0.11	0
4	SO4	B	604	-	4,4,4	0.26	0	6,6,6	0.07	0
4	SO4	A	607	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	C	602	-	4,4,4	0.22	0	6,6,6	0.19	0
5	EDO	D	612	-	3,3,3	0.59	0	2,2,2	0.39	0
4	SO4	A	604	-	4,4,4	0.27	0	6,6,6	0.08	0
4	SO4	C	608	-	4,4,4	0.24	0	6,6,6	0.12	0
4	SO4	B	605	-	4,4,4	0.26	0	6,6,6	0.16	0
2	FDA	C	601	-	57,58,58	2.88	24 (42%)	78,89,89	2.05	22 (28%)
5	EDO	B	611	-	3,3,3	0.49	0	2,2,2	0.27	0
4	SO4	D	607	-	4,4,4	0.25	0	6,6,6	0.09	0
5	EDO	D	610	-	3,3,3	0.50	0	2,2,2	0.24	0
4	SO4	A	608	-	4,4,4	0.25	0	6,6,6	0.11	0
5	EDO	C	611	-	3,3,3	0.55	0	2,2,2	0.33	0
4	SO4	D	604	-	4,4,4	0.25	0	6,6,6	0.15	0
4	SO4	B	608	-	4,4,4	0.24	0	6,6,6	0.11	0
5	EDO	D	611	-	3,3,3	0.53	0	2,2,2	0.11	0
3	UDP	B	602	-	25,26,26	2.05	9 (36%)	38,40,40	1.79	10 (26%)
3	UDP	C	609	-	16,16,26	2.42	8 (50%)	22,23,40	2.25	6 (27%)
4	SO4	D	603	-	4,4,4	0.24	0	6,6,6	0.24	0
3	UDP	B	609	-	22,22,26	2.08	8 (36%)	32,33,40	2.30	11 (34%)
3	UDP	A	602	-	25,26,26	1.93	8 (32%)	38,40,40	2.07	9 (23%)
3	UDP	A	609	-	25,26,26	1.90	8 (32%)	38,40,40	2.23	12 (31%)
4	SO4	C	603	-	4,4,4	0.21	0	6,6,6	0.14	0
5	EDO	A	611	-	3,3,3	0.47	0	2,2,2	0.12	0
2	FDA	D	601	-	57,58,58	2.87	22 (38%)	78,89,89	1.99	23 (29%)
4	SO4	B	606	-	4,4,4	0.21	0	6,6,6	0.12	0
4	SO4	D	602	-	4,4,4	0.26	0	6,6,6	0.18	0
4	SO4	C	607	-	4,4,4	0.22	0	6,6,6	0.16	0
5	EDO	C	610	-	3,3,3	0.50	0	2,2,2	0.29	0
4	SO4	C	604	-	4,4,4	0.27	0	6,6,6	0.10	0
4	SO4	A	606	-	4,4,4	0.24	0	6,6,6	0.10	0
4	SO4	D	608	-	4,4,4	0.24	0	6,6,6	0.22	0
4	SO4	A	605	-	4,4,4	0.21	0	6,6,6	0.12	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	UDP	D	609	-	-	0/4/17/32	0/2/2/2
5	EDO	B	612	-	-	1/1/1/1	-
5	EDO	B	610	-	-	1/1/1/1	-
2	FDA	B	601	-	-	4/34/50/50	0/6/6/6
2	FDA	A	601	-	-	1/34/50/50	0/6/6/6
5	EDO	A	610	-	-	0/1/1/1	-
5	EDO	C	612	-	-	0/1/1/1	-
5	EDO	D	612	-	-	0/1/1/1	-
5	EDO	B	611	-	-	0/1/1/1	-
2	FDA	C	601	-	-	4/34/50/50	0/6/6/6
5	EDO	D	610	-	-	0/1/1/1	-
5	EDO	C	611	-	-	1/1/1/1	-
5	EDO	D	611	-	-	1/1/1/1	-
3	UDP	B	602	-	-	0/16/32/32	0/2/2/2
3	UDP	C	609	-	-	0/4/17/32	0/2/2/2
3	UDP	B	609	-	-	1/10/26/32	0/2/2/2
3	UDP	A	602	-	-	0/16/32/32	0/2/2/2
3	UDP	A	609	-	-	3/16/32/32	0/2/2/2
5	EDO	A	611	-	-	0/1/1/1	-
2	FDA	D	601	-	-	4/34/50/50	0/6/6/6
5	EDO	C	610	-	-	0/1/1/1	-

All (142) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FDA	PA-O3P	-9.60	1.49	1.59
2	D	601	FDA	PA-O3P	-8.55	1.50	1.59
2	C	601	FDA	PA-O3P	-8.14	1.50	1.59
2	B	601	FDA	O4-C4	7.74	1.38	1.23
2	D	601	FDA	O4-C4	7.55	1.37	1.23
2	A	601	FDA	O4-C4	7.54	1.37	1.23
2	C	601	FDA	O4-C4	7.35	1.37	1.23
2	C	601	FDA	O2-C2	6.99	1.38	1.23
2	A	601	FDA	O2-C2	6.98	1.38	1.23
2	B	601	FDA	O2-C2	6.93	1.38	1.23
2	D	601	FDA	O2-C2	6.83	1.37	1.23
2	B	601	FDA	PA-O3P	-6.52	1.52	1.59
2	A	601	FDA	C6-C5X	6.38	1.49	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FDA	C6-C5X	6.34	1.49	1.39
2	B	601	FDA	C9-C9A	6.31	1.49	1.39
2	B	601	FDA	C6-C5X	6.14	1.49	1.39
2	C	601	FDA	C6-C5X	6.13	1.49	1.39
2	A	601	FDA	C9-C9A	5.61	1.48	1.39
2	C	601	FDA	C9-C9A	5.35	1.48	1.39
2	D	601	FDA	C9-C9A	5.32	1.48	1.39
3	B	602	UDP	C2-N1	5.29	1.46	1.38
2	C	601	FDA	C4X-N5	5.12	1.46	1.35
2	C	601	FDA	C10-N1	5.10	1.46	1.37
3	D	609	UDP	C2-N1	5.08	1.46	1.38
3	A	602	UDP	C2-N1	5.05	1.46	1.38
3	C	609	UDP	C2-N1	4.99	1.46	1.38
2	D	601	FDA	C4X-N5	4.83	1.45	1.35
3	B	609	UDP	C2-N1	4.82	1.46	1.38
2	B	601	FDA	C4X-N5	4.81	1.45	1.35
3	D	609	UDP	C3'-C2'	-4.68	1.45	1.53
2	A	601	FDA	C10-N1	4.67	1.45	1.37
3	C	609	UDP	C3'-C2'	-4.51	1.46	1.53
2	B	601	FDA	C10-N1	4.45	1.45	1.37
2	B	601	FDA	C5X-C9A	-4.41	1.35	1.40
2	A	601	FDA	C4X-N5	4.38	1.44	1.35
2	A	601	FDA	C5X-C9A	-4.33	1.35	1.40
3	A	609	UDP	C2-N1	4.25	1.45	1.38
2	C	601	FDA	C6A-N6A	4.24	1.45	1.34
2	C	601	FDA	C5X-C9A	-4.17	1.36	1.40
2	A	601	FDA	C6A-N6A	4.12	1.44	1.34
2	D	601	FDA	P-O3P	4.11	1.63	1.59
2	B	601	FDA	C6A-N6A	4.09	1.44	1.34
2	D	601	FDA	C10-N1	4.05	1.44	1.37
2	D	601	FDA	C6A-N6A	4.04	1.44	1.34
2	D	601	FDA	C5X-N5	4.02	1.46	1.39
2	C	601	FDA	P-O3P	3.98	1.63	1.59
2	D	601	FDA	C5X-C9A	-3.83	1.36	1.40
2	B	601	FDA	C5X-N5	3.63	1.46	1.39
2	A	601	FDA	C5X-N5	3.57	1.46	1.39
2	B	601	FDA	C2-N1	3.56	1.43	1.37
2	C	601	FDA	C2-N1	3.54	1.43	1.37
3	B	602	UDP	C2-N3	3.48	1.44	1.38
2	D	601	FDA	C2-N1	3.46	1.43	1.37
2	A	601	FDA	P-O3P	3.45	1.63	1.59
2	A	601	FDA	C2-N1	3.45	1.43	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	FDA	C5X-N5	3.43	1.45	1.39
2	B	601	FDA	P-O3P	3.42	1.63	1.59
3	A	609	UDP	C2-N3	3.36	1.43	1.38
2	A	601	FDA	C9A-N10	3.35	1.47	1.41
3	D	609	UDP	C2-N3	3.35	1.43	1.38
3	A	602	UDP	C5-C4	3.31	1.50	1.43
3	A	602	UDP	C2-N3	3.23	1.43	1.38
3	C	609	UDP	C2-N3	3.22	1.43	1.38
2	C	601	FDA	C10-N10	3.22	1.44	1.38
2	B	601	FDA	C9A-N10	3.22	1.46	1.41
3	A	609	UDP	C5-C4	3.21	1.50	1.43
2	C	601	FDA	C9A-N10	3.16	1.46	1.41
3	D	609	UDP	C6-N1	3.14	1.45	1.38
3	B	602	UDP	C5-C4	3.13	1.50	1.43
3	B	609	UDP	C2-N3	3.13	1.43	1.38
3	D	609	UDP	C5-C4	3.10	1.50	1.43
3	B	609	UDP	C6-N1	3.10	1.45	1.38
3	C	609	UDP	C6-N1	3.10	1.45	1.38
3	A	609	UDP	C6-N1	3.08	1.45	1.38
3	B	609	UDP	C5-C4	3.07	1.50	1.43
3	B	609	UDP	PA-O1A	3.02	1.59	1.50
2	D	601	FDA	C2-N3	2.99	1.42	1.37
3	C	609	UDP	C5-C4	2.97	1.50	1.43
3	A	602	UDP	C6-N1	2.86	1.44	1.38
3	B	602	UDP	C6-N1	2.85	1.44	1.38
2	D	601	FDA	C9A-N10	2.84	1.46	1.41
3	A	609	UDP	C3'-C2'	-2.82	1.45	1.53
3	B	602	UDP	PA-O1A	2.78	1.60	1.50
3	B	609	UDP	C3'-C2'	-2.76	1.45	1.53
2	C	601	FDA	C2-N3	2.76	1.42	1.37
2	A	601	FDA	PA-O5B	-2.73	1.48	1.59
2	B	601	FDA	C10-N10	2.72	1.43	1.38
2	C	601	FDA	PA-O5B	-2.70	1.48	1.59
2	D	601	FDA	PA-O5B	-2.69	1.48	1.59
3	A	602	UDP	PA-O1A	2.68	1.60	1.50
2	D	601	FDA	C10-N10	2.68	1.43	1.38
2	B	601	FDA	PA-O5B	-2.66	1.49	1.59
2	B	601	FDA	C2-N3	2.64	1.41	1.37
2	A	601	FDA	C4A-N9A	2.61	1.43	1.37
2	A	601	FDA	C10-N10	2.56	1.42	1.38
2	A	601	FDA	C9-C8	2.55	1.43	1.39
3	A	609	UDP	PA-O1A	2.52	1.59	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FDA	C4X-C4	2.50	1.49	1.41
2	C	601	FDA	O3B-C3B	-2.49	1.36	1.43
3	B	602	UDP	C3'-C2'	-2.48	1.46	1.53
2	B	601	FDA	O3B-C3B	-2.47	1.36	1.43
2	B	601	FDA	C5A-C4A	2.44	1.43	1.39
2	A	601	FDA	P-O1P	2.43	1.59	1.50
2	A	601	FDA	O3B-C3B	-2.41	1.37	1.43
2	B	601	FDA	P-O1P	2.39	1.59	1.50
2	A	601	FDA	C2-N3	2.38	1.41	1.37
3	B	602	UDP	O2'-C2'	-2.37	1.37	1.43
2	B	601	FDA	O3'-C3'	-2.36	1.37	1.43
2	D	601	FDA	PA-O2A	-2.34	1.44	1.55
3	B	602	UDP	C6-C5	2.31	1.40	1.35
2	B	601	FDA	C4X-C4	2.31	1.48	1.41
2	D	601	FDA	C4A-N9A	2.31	1.42	1.37
3	A	609	UDP	O2'-C2'	-2.29	1.37	1.43
2	C	601	FDA	C4X-C4	2.29	1.48	1.41
3	A	609	UDP	C6-C5	2.29	1.40	1.35
3	D	609	UDP	C6-C5	2.25	1.40	1.35
2	C	601	FDA	O2'-C2'	-2.25	1.38	1.43
3	A	602	UDP	C3'-C2'	-2.23	1.47	1.53
2	D	601	FDA	P-O1P	2.23	1.58	1.50
2	A	601	FDA	PA-O2A	-2.23	1.45	1.55
3	A	602	UDP	C6-C5	2.23	1.40	1.35
2	B	601	FDA	PA-O2A	-2.23	1.45	1.55
2	C	601	FDA	C2B-C3B	-2.21	1.47	1.53
3	D	609	UDP	O2'-C2'	-2.19	1.37	1.43
3	B	609	UDP	O2'-C2'	-2.19	1.37	1.43
3	D	609	UDP	O3'-C3'	-2.17	1.38	1.43
3	B	602	UDP	C4-N3	2.16	1.42	1.38
3	B	609	UDP	C6-C5	2.14	1.40	1.35
3	C	609	UDP	O3'-C3'	-2.14	1.38	1.43
2	D	601	FDA	O2'-C2'	-2.13	1.38	1.43
2	C	601	FDA	P-O1P	2.13	1.58	1.50
2	D	601	FDA	O3B-C3B	-2.12	1.37	1.43
3	C	609	UDP	O2'-C2'	-2.12	1.37	1.43
2	B	601	FDA	C4A-N9A	2.11	1.42	1.37
2	B	601	FDA	C2B-C3B	-2.09	1.47	1.53
2	C	601	FDA	PA-O2A	-2.09	1.45	1.55
2	A	601	FDA	C5A-C4A	2.08	1.42	1.39
3	C	609	UDP	C6-C5	2.06	1.39	1.35
2	C	601	FDA	C5A-C4A	2.06	1.42	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FDA	O3'-C3'	-2.05	1.37	1.43
3	A	602	UDP	O2'-C2'	-2.01	1.38	1.43
2	C	601	FDA	C4A-N9A	2.01	1.41	1.37

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	FDA	O2P-P-O3P	-6.18	90.56	107.27
2	C	601	FDA	N3A-C2A-N1A	-5.86	119.71	128.58
3	A	609	UDP	C4-N3-C2	-5.84	119.36	126.61
2	A	601	FDA	C5A-C4A-N3A	-5.76	118.79	126.72
3	A	602	UDP	O3A-PA-O1A	-5.61	93.81	110.70
2	D	601	FDA	N3A-C2A-N1A	-5.58	120.13	128.58
3	C	609	UDP	C4-N3-C2	-5.56	119.71	126.61
2	B	601	FDA	N3A-C2A-N1A	-5.55	120.18	128.58
3	B	609	UDP	C4-N3-C2	-5.55	119.72	126.61
3	A	609	UDP	O3A-PA-O1A	-5.50	94.16	110.70
3	D	609	UDP	C4-N3-C2	-5.47	119.83	126.61
3	A	609	UDP	O2A-PA-O3A	5.43	121.95	107.27
3	A	602	UDP	C4-N3-C2	-5.35	119.97	126.61
2	D	601	FDA	C5A-C4A-N3A	-5.27	119.45	126.72
3	A	602	UDP	O2A-PA-O3A	5.21	121.36	107.27
2	A	601	FDA	N3A-C2A-N1A	-5.20	120.72	128.58
3	B	602	UDP	C4-N3-C2	-5.19	120.16	126.61
2	B	601	FDA	C5A-C4A-N3A	-5.07	119.73	126.72
3	B	609	UDP	O2A-PA-O5'	5.07	119.90	106.67
2	D	601	FDA	N3A-C4A-N9A	4.88	135.46	127.17
2	C	601	FDA	C5A-C4A-N3A	-4.75	120.18	126.72
2	A	601	FDA	O2A-PA-O3P	-4.71	94.54	107.27
2	A	601	FDA	N3A-C4A-N9A	4.69	135.15	127.17
2	B	601	FDA	O4B-C1B-N9A	4.67	117.05	108.09
2	A	601	FDA	C4-N3-C2	-4.63	120.00	126.37
2	D	601	FDA	C4-N3-C2	-4.57	120.07	126.37
3	A	609	UDP	N3-C2-N1	4.50	120.75	114.89
3	B	609	UDP	O3A-PA-O1A	-4.40	93.69	110.83
3	C	609	UDP	N3-C2-N1	4.38	120.59	114.89
2	C	601	FDA	N3A-C4A-N9A	4.35	134.56	127.17
2	B	601	FDA	C4-N3-C2	-4.31	120.44	126.37
2	C	601	FDA	C4-N3-C2	-4.23	120.54	126.37
2	B	601	FDA	O2P-P-O3P	-4.19	95.95	107.27
3	B	609	UDP	N3-C2-N1	4.16	120.31	114.89
2	B	601	FDA	N3A-C4A-N9A	4.13	134.20	127.17

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	FDA	C4'-C3'-C2'	4.12	120.43	113.57
3	D	609	UDP	N3-C2-N1	4.10	120.22	114.89
3	D	609	UDP	C5-C4-N3	3.99	120.40	114.80
2	A	601	FDA	O4B-C1B-N9A	3.96	115.70	108.09
2	A	601	FDA	O4-C4-C4X	-3.95	117.73	127.26
2	A	601	FDA	C5A-N7A-C8A	3.95	109.65	103.45
3	B	609	UDP	C5-C4-N3	3.93	120.31	114.80
3	A	609	UDP	C5-C4-N3	3.89	120.25	114.80
2	C	601	FDA	O3P-P-O1P	3.89	122.41	110.70
2	D	601	FDA	C5A-N7A-C8A	3.86	109.52	103.45
3	C	609	UDP	C5-C4-N3	3.77	120.08	114.80
2	B	601	FDA	C5A-N7A-C8A	3.74	109.33	103.45
2	A	601	FDA	C2A-N3A-C4A	3.66	120.78	111.83
3	A	602	UDP	C5-C4-N3	3.66	119.93	114.80
2	D	601	FDA	O2P-P-O5'	-3.65	91.05	107.57
3	A	602	UDP	N3-C2-N1	3.64	119.63	114.89
3	B	602	UDP	N3-C2-N1	3.60	119.58	114.89
2	D	601	FDA	C2A-N3A-C4A	3.60	120.63	111.83
2	B	601	FDA	C2A-N3A-C4A	3.56	120.52	111.83
2	B	601	FDA	O3P-P-O1P	3.52	121.30	110.70
2	D	601	FDA	C4'-C3'-C2'	3.50	119.40	113.57
2	A	601	FDA	O2P-P-O3P	-3.47	97.88	107.27
2	C	601	FDA	C2A-N3A-C4A	3.47	120.30	111.83
2	B	601	FDA	O4-C4-C4X	-3.44	118.95	127.26
3	D	609	UDP	C3'-C2'-C1'	3.44	105.30	101.76
3	B	602	UDP	C5-C4-N3	3.44	119.61	114.80
2	C	601	FDA	C5A-N7A-C8A	3.44	108.85	103.45
2	D	601	FDA	N9A-C8A-N7A	-3.43	109.07	113.94
3	C	609	UDP	C3'-C2'-C1'	3.40	105.26	101.76
2	C	601	FDA	O4-C4-C4X	-3.34	119.20	127.26
2	B	601	FDA	C4'-C3'-C2'	3.34	119.12	113.57
3	B	609	UDP	O3A-PA-O5'	-3.22	98.29	106.67
2	B	601	FDA	N3-C2-N1	3.19	120.76	115.74
2	D	601	FDA	N3-C2-N1	3.19	120.75	115.74
3	C	609	UDP	O4'-C1'-N1	3.15	112.91	108.90
2	A	601	FDA	N9A-C8A-N7A	-3.15	109.47	113.94
3	B	609	UDP	O3A-PA-O2A	3.15	119.60	107.80
2	A	601	FDA	N3-C2-N1	3.11	120.63	115.74
3	A	609	UDP	O2-C2-N1	-3.11	118.75	122.80
2	D	601	FDA	O4-C4-C4X	-3.09	119.82	127.26
2	B	601	FDA	N9A-C8A-N7A	-3.06	109.59	113.94
2	A	601	FDA	O2P-P-O5'	-3.06	93.70	107.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FDA	O3P-PA-O1A	3.05	119.87	110.70
3	B	602	UDP	O2A-PA-O3A	3.04	115.50	107.27
2	B	601	FDA	C4A-C5A-N7A	-3.03	107.11	110.58
2	C	601	FDA	N9A-C8A-N7A	-3.03	109.64	113.94
3	C	609	UDP	O4-C4-C5	-2.96	120.06	125.16
2	C	601	FDA	O4B-C1B-N9A	2.92	113.70	108.09
3	D	609	UDP	O4-C4-C5	-2.89	120.17	125.16
2	A	601	FDA	C4'-C3'-C2'	2.88	118.36	113.57
2	A	601	FDA	C4A-C5A-N7A	-2.85	107.33	110.58
2	D	601	FDA	C4A-N9A-C8A	2.83	108.71	105.74
3	B	602	UDP	O4-C4-C5	-2.82	120.30	125.16
2	D	601	FDA	O2A-PA-O5B	-2.80	94.86	107.57
2	C	601	FDA	C4X-C4-N3	2.80	119.82	112.13
2	D	601	FDA	O4B-C1B-N9A	2.80	113.47	108.09
2	B	601	FDA	O2A-PA-O3P	-2.79	99.72	107.27
3	B	602	UDP	O3A-PA-O1A	-2.78	102.35	110.70
2	C	601	FDA	N3-C2-N1	2.77	120.10	115.74
2	A	601	FDA	C4X-C4-N3	2.75	119.68	112.13
3	A	609	UDP	O2A-PA-O5'	2.74	119.97	107.57
3	A	609	UDP	O4-C4-C5	-2.73	120.46	125.16
3	A	609	UDP	O5'-PA-O1A	-2.65	98.42	108.94
3	B	602	UDP	O5'-PA-O1A	-2.63	98.50	108.94
3	B	609	UDP	O4-C4-C5	-2.63	120.62	125.16
3	D	609	UDP	O4'-C1'-N1	2.62	112.23	108.90
2	D	601	FDA	C4X-C4-N3	2.61	119.31	112.13
2	C	601	FDA	C5X-C9A-N10	2.61	120.97	118.01
2	C	601	FDA	O2A-PA-O3P	-2.60	100.24	107.27
2	D	601	FDA	C4A-C5A-N7A	-2.59	107.62	110.58
2	B	601	FDA	C4X-C4-N3	2.59	119.23	112.13
3	A	609	UDP	C3'-C2'-C1'	2.57	106.33	101.46
3	B	609	UDP	O5'-PA-O1A	-2.56	99.51	106.44
2	D	601	FDA	O5'-P-O1P	2.55	119.05	108.94
2	A	601	FDA	O5B-PA-O1A	2.55	119.05	108.94
2	C	601	FDA	O2A-PA-O5B	-2.55	96.01	107.57
3	B	602	UDP	C3'-C2'-C1'	2.53	106.25	101.46
3	A	602	UDP	O4-C4-C5	-2.52	120.81	125.16
2	D	601	FDA	O2P-P-O3P	-2.51	100.48	107.27
2	A	601	FDA	O5'-P-O1P	2.49	118.82	108.94
3	B	609	UDP	O2A-PA-O1A	2.47	120.45	110.83
2	C	601	FDA	C4A-N9A-C8A	2.46	108.33	105.74
2	D	601	FDA	C5X-C9A-N10	2.45	120.78	118.01
2	A	601	FDA	O2A-PA-O5B	-2.43	96.55	107.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	UDP	O3B-PB-O3A	2.40	112.68	104.64
3	A	609	UDP	O4'-C1'-N1	2.34	113.66	108.36
3	B	602	UDP	O2A-PA-O5'	2.33	118.14	107.57
2	C	601	FDA	C4A-C5A-N7A	-2.33	107.92	110.58
2	A	601	FDA	C5X-C9A-N10	2.29	120.61	118.01
2	C	601	FDA	O5B-PA-O1A	2.29	118.01	108.94
2	C	601	FDA	C2A-N1A-C6A	2.28	122.48	118.73
3	B	602	UDP	O2B-PB-O3A	2.24	112.16	104.64
2	A	601	FDA	O3P-P-O1P	2.22	117.39	110.70
3	B	609	UDP	C3'-C2'-C1'	2.21	105.64	101.46
2	B	601	FDA	O2-C2-N1	-2.21	117.94	121.86
2	D	601	FDA	O4'-C4'-C3'	2.19	114.38	109.25
3	A	602	UDP	O5'-PA-O1A	-2.14	100.46	108.94
3	A	602	UDP	O2A-PA-O5'	2.14	117.25	107.57
2	D	601	FDA	O2-C2-N1	-2.13	118.08	121.86
2	B	601	FDA	C4A-N9A-C1B	-2.13	121.65	126.63
2	C	601	FDA	C4A-N9A-C1B	-2.07	121.80	126.63
2	D	601	FDA	C9-C9A-N10	-2.05	119.10	121.85
2	B	601	FDA	C4A-N9A-C8A	2.05	107.89	105.74
2	D	601	FDA	C5'-C4'-C3'	-2.04	108.37	112.22
3	A	609	UDP	O3B-PB-O3A	2.03	111.44	104.64

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	FDA	C5'-O5'-P-O3P
3	B	609	UDP	C5'-O5'-PA-O1A
5	B	610	EDO	O1-C1-C2-O2
2	C	601	FDA	C3'-C4'-C5'-O5'
2	D	601	FDA	P-O3P-PA-O1A
2	A	601	FDA	PA-O3P-P-O5'
2	C	601	FDA	P-O3P-PA-O5B
2	D	601	FDA	PA-O3P-P-O5'
3	A	609	UDP	C3'-C4'-C5'-O5'
3	A	609	UDP	O4'-C4'-C5'-O5'
2	D	601	FDA	P-O3P-PA-O2A
2	B	601	FDA	C2'-C3'-C4'-O4'
3	A	609	UDP	C4'-C5'-O5'-PA
2	B	601	FDA	O3'-C3'-C4'-O4'
2	B	601	FDA	O3'-C3'-C4'-C5'
5	B	612	EDO	O1-C1-C2-O2

Continued on next page...

Continued from previous page...

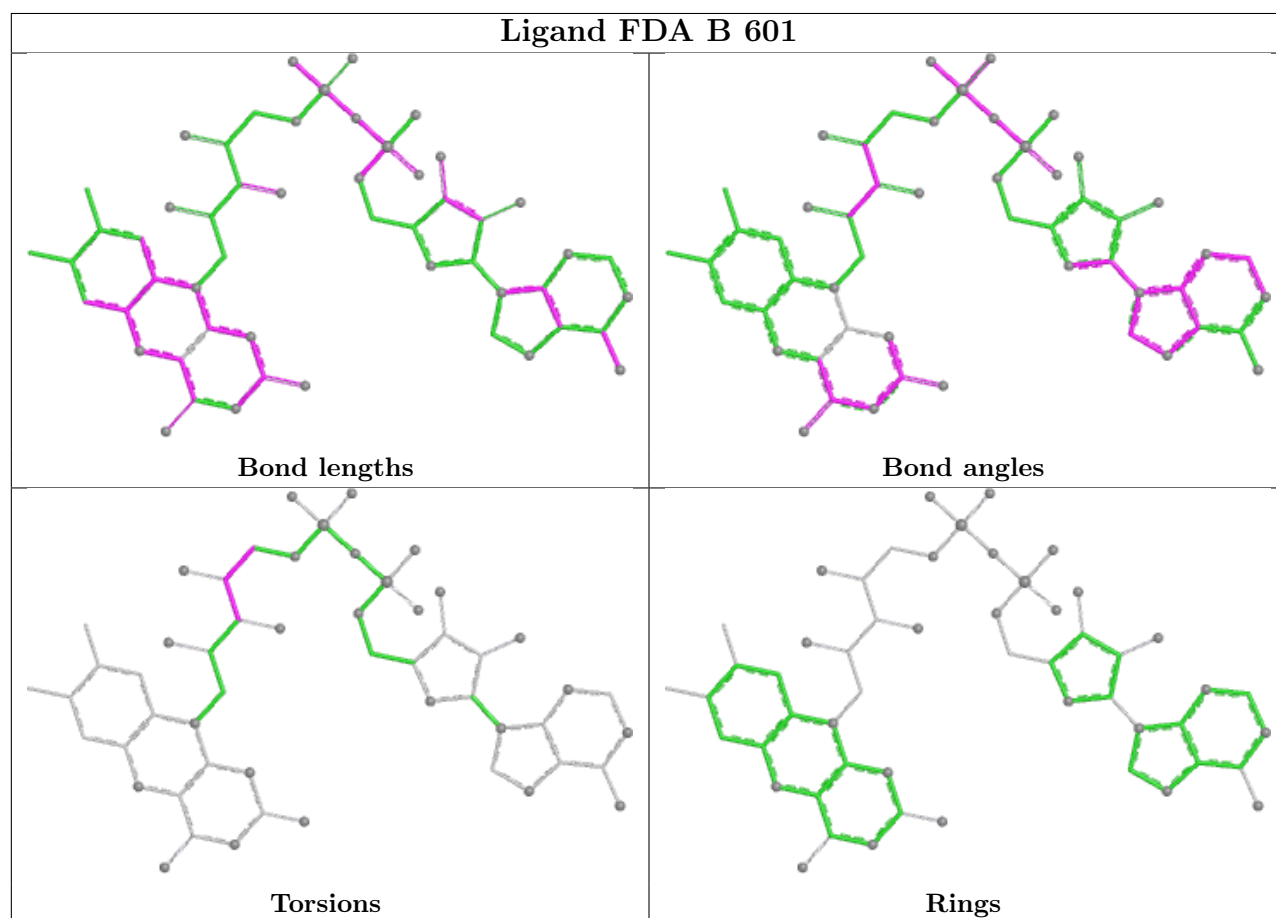
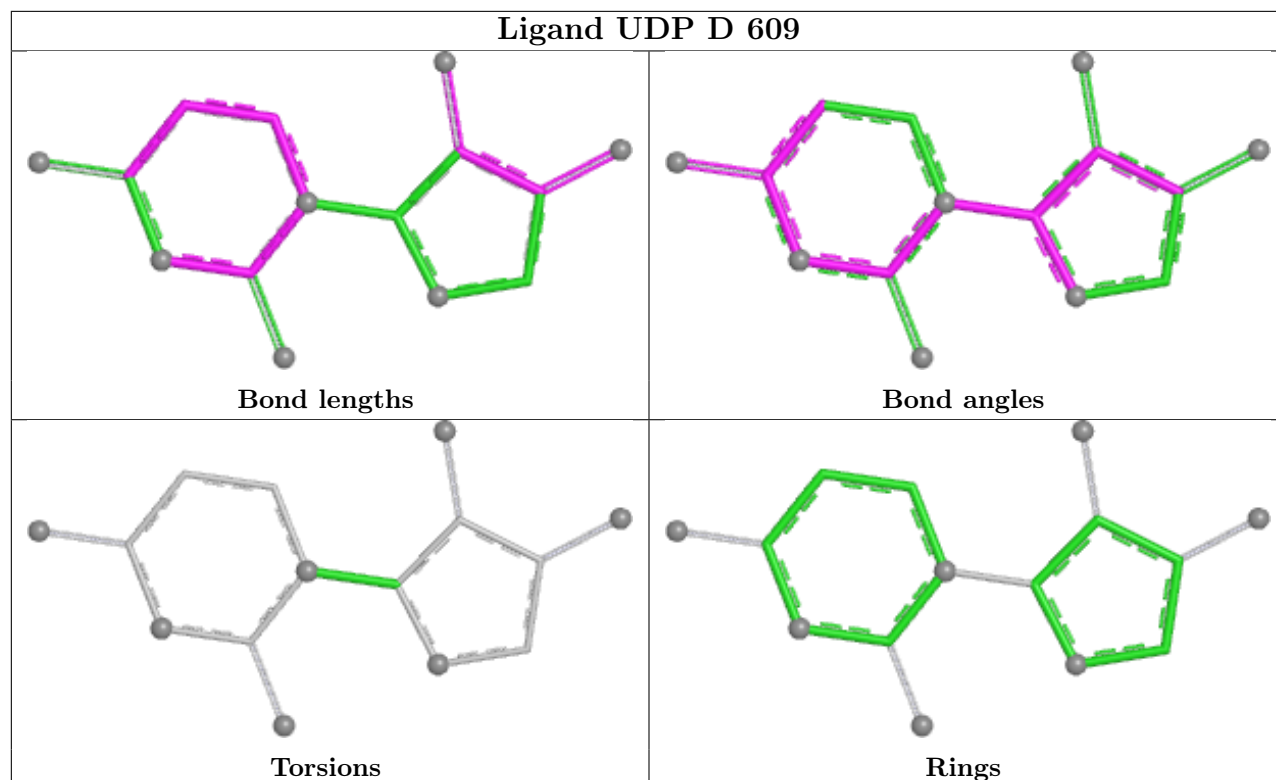
Mol	Chain	Res	Type	Atoms
5	C	611	EDO	O1-C1-C2-O2
5	D	611	EDO	O1-C1-C2-O2
2	C	601	FDA	C2'-C3'-C4'-O4'
2	B	601	FDA	C3'-C4'-C5'-O5'
2	D	601	FDA	O4B-C4B-C5B-O5B

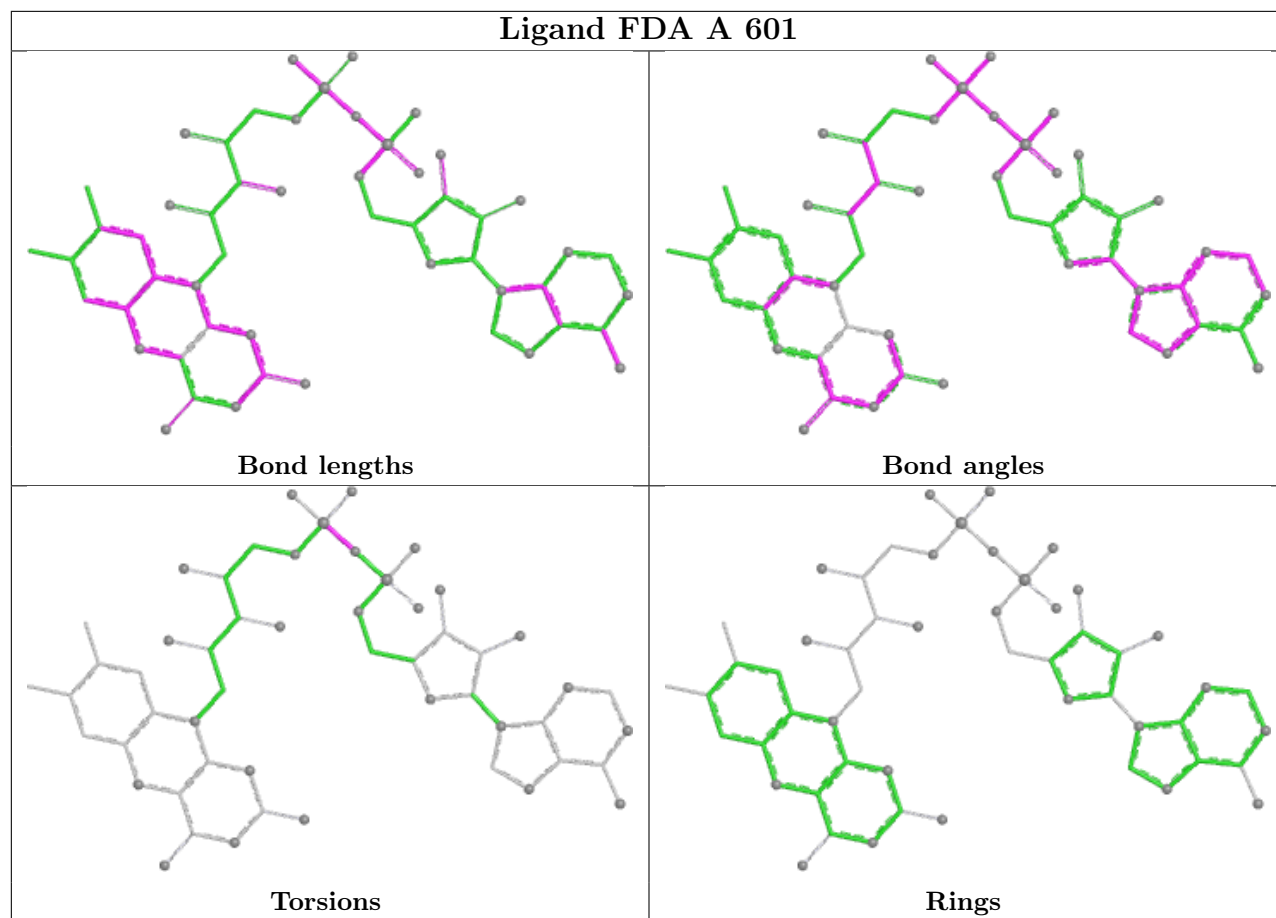
There are no ring outliers.

4 monomers are involved in 10 short contacts:

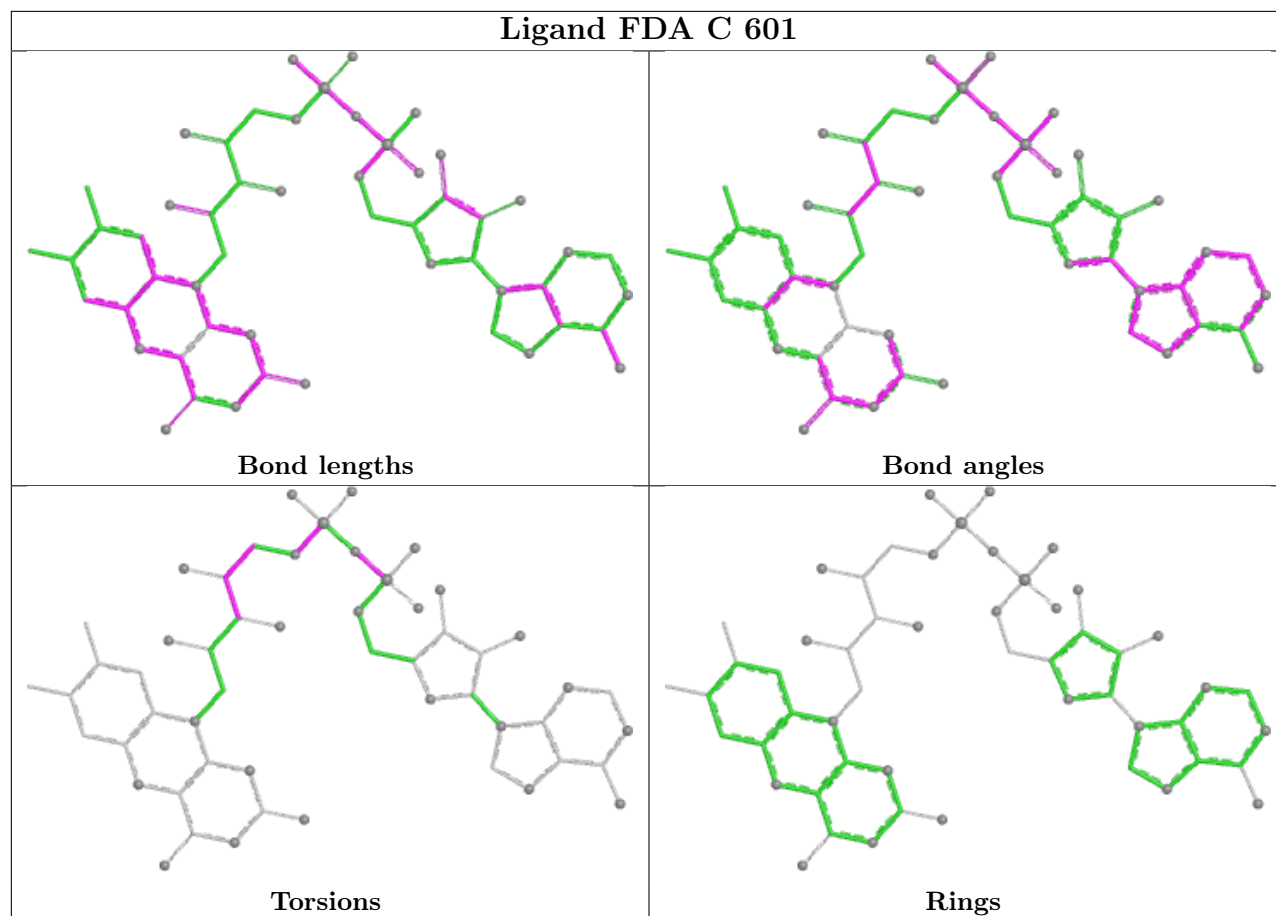
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	607	SO4	1	0
5	D	612	EDO	1	0
3	B	602	UDP	2	0
3	A	602	UDP	6	0

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.

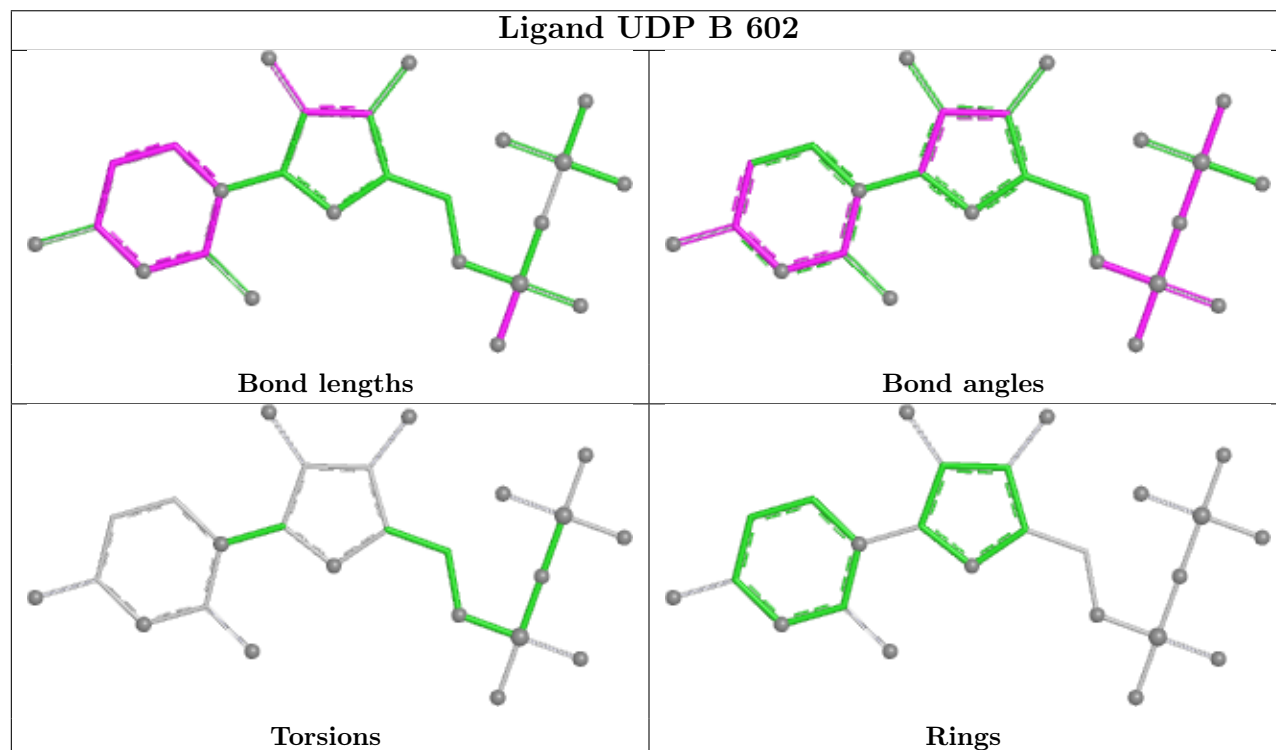


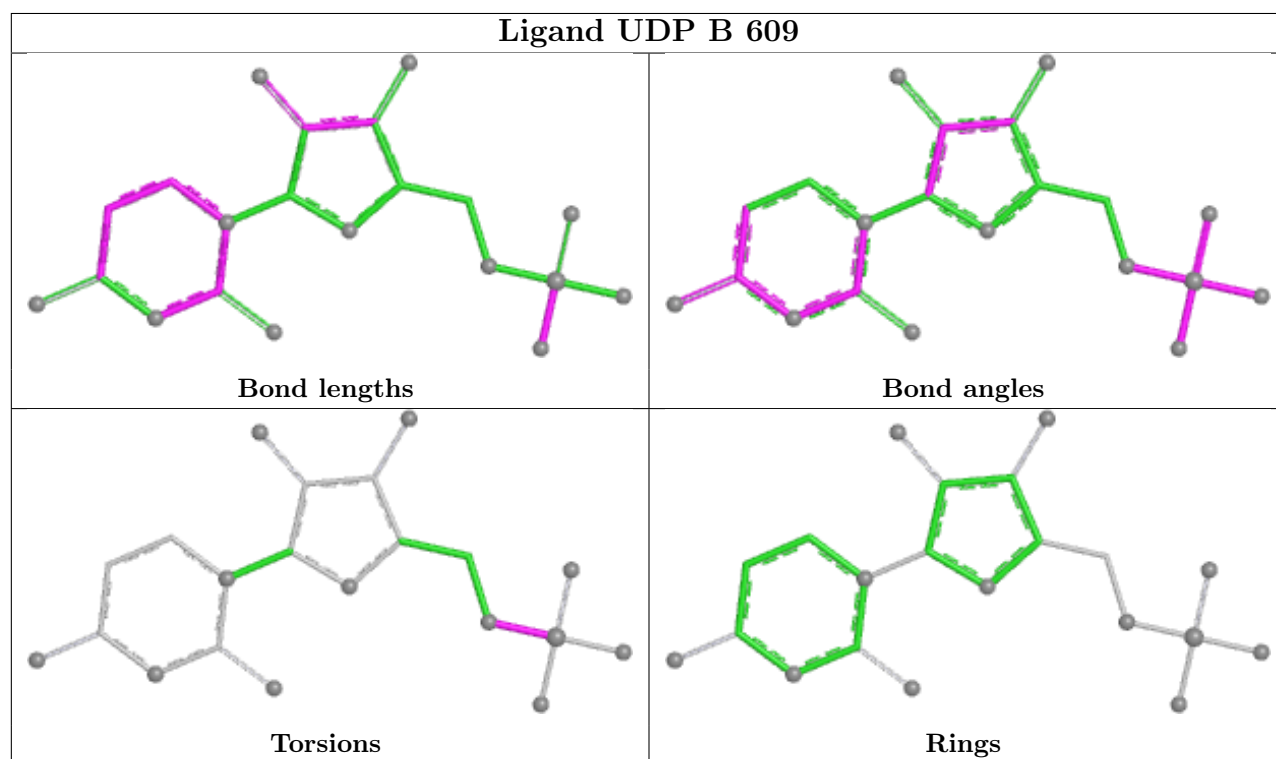
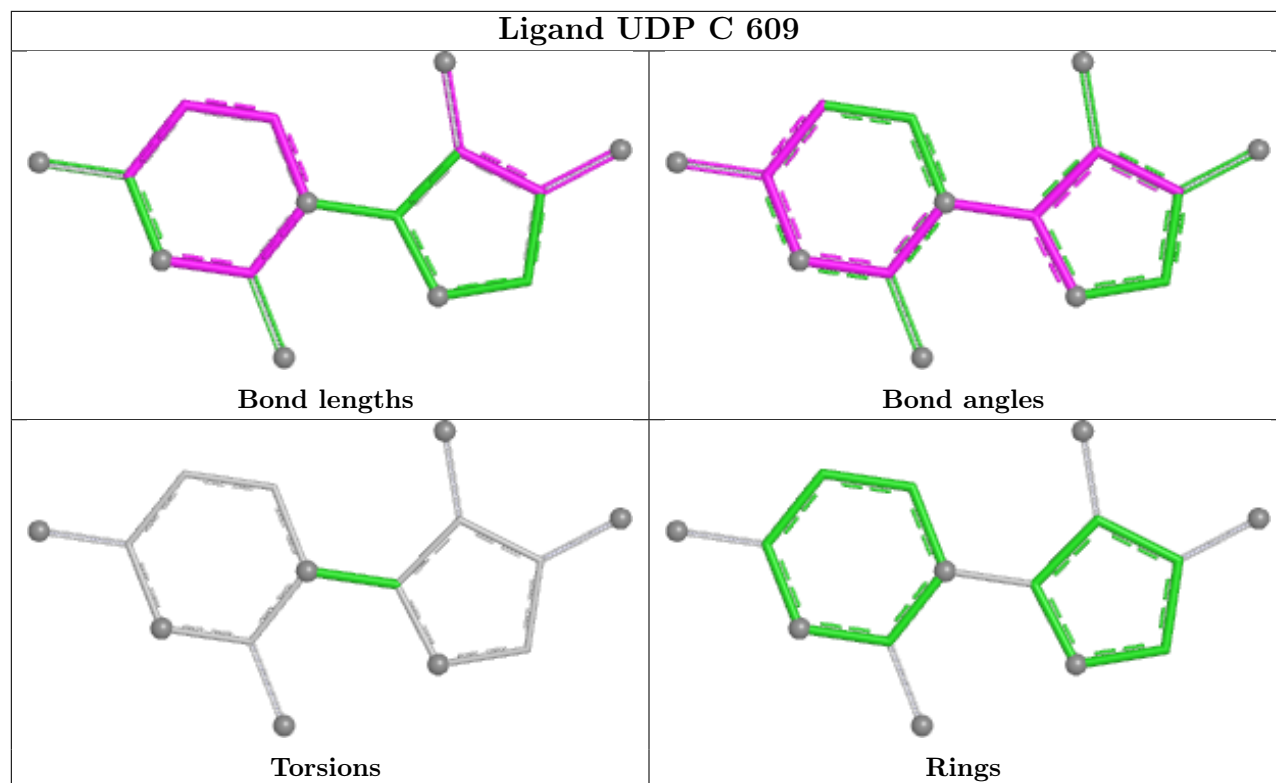


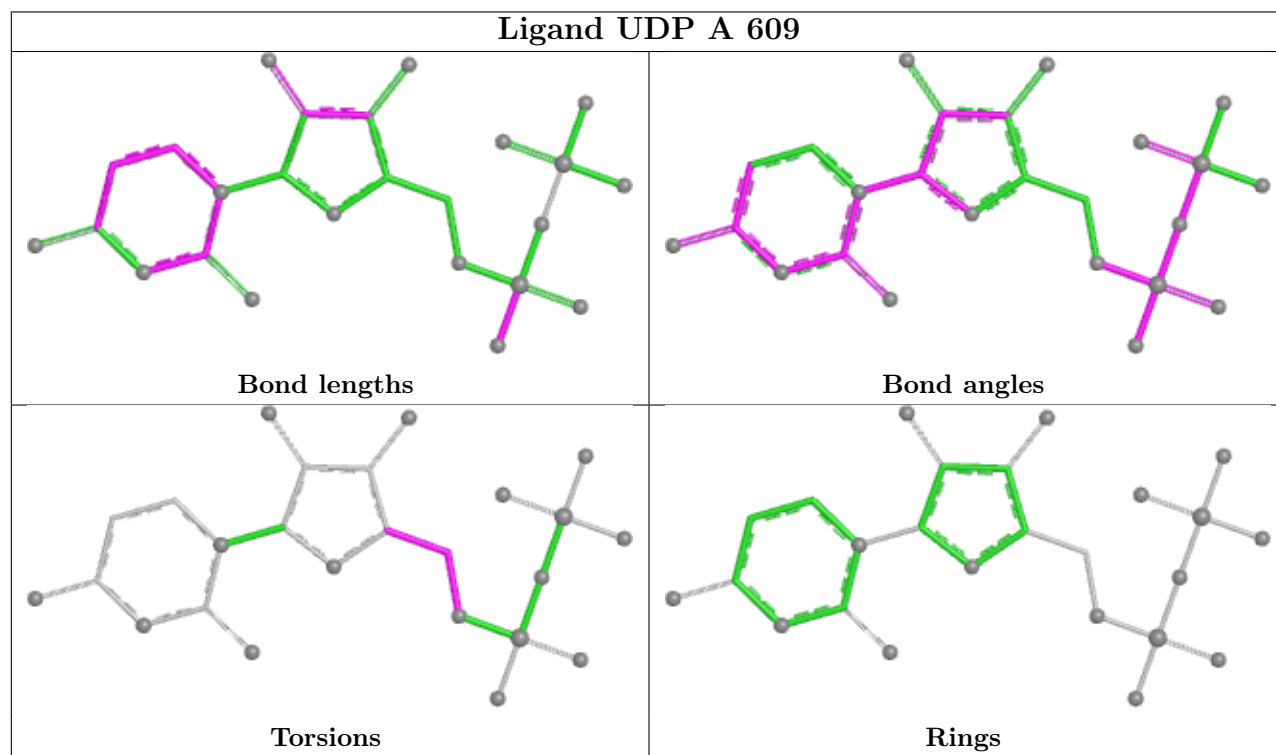
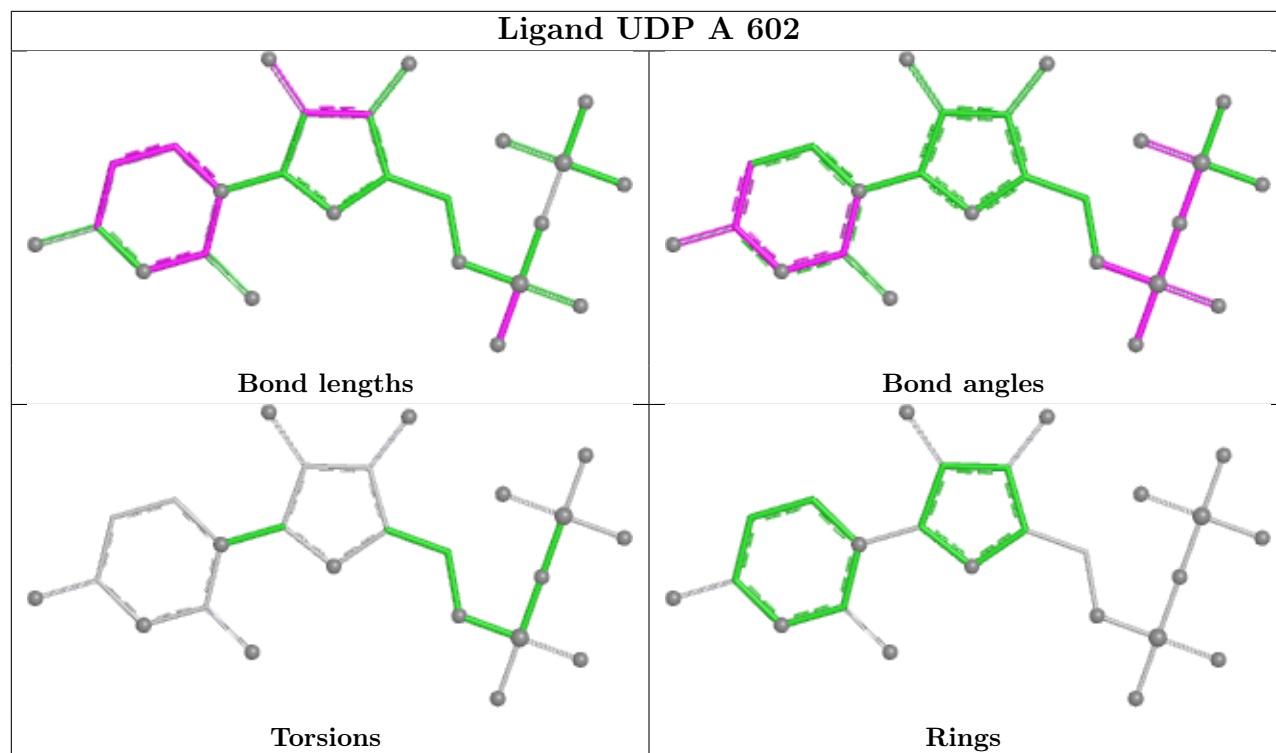
Ligand FDA C 601

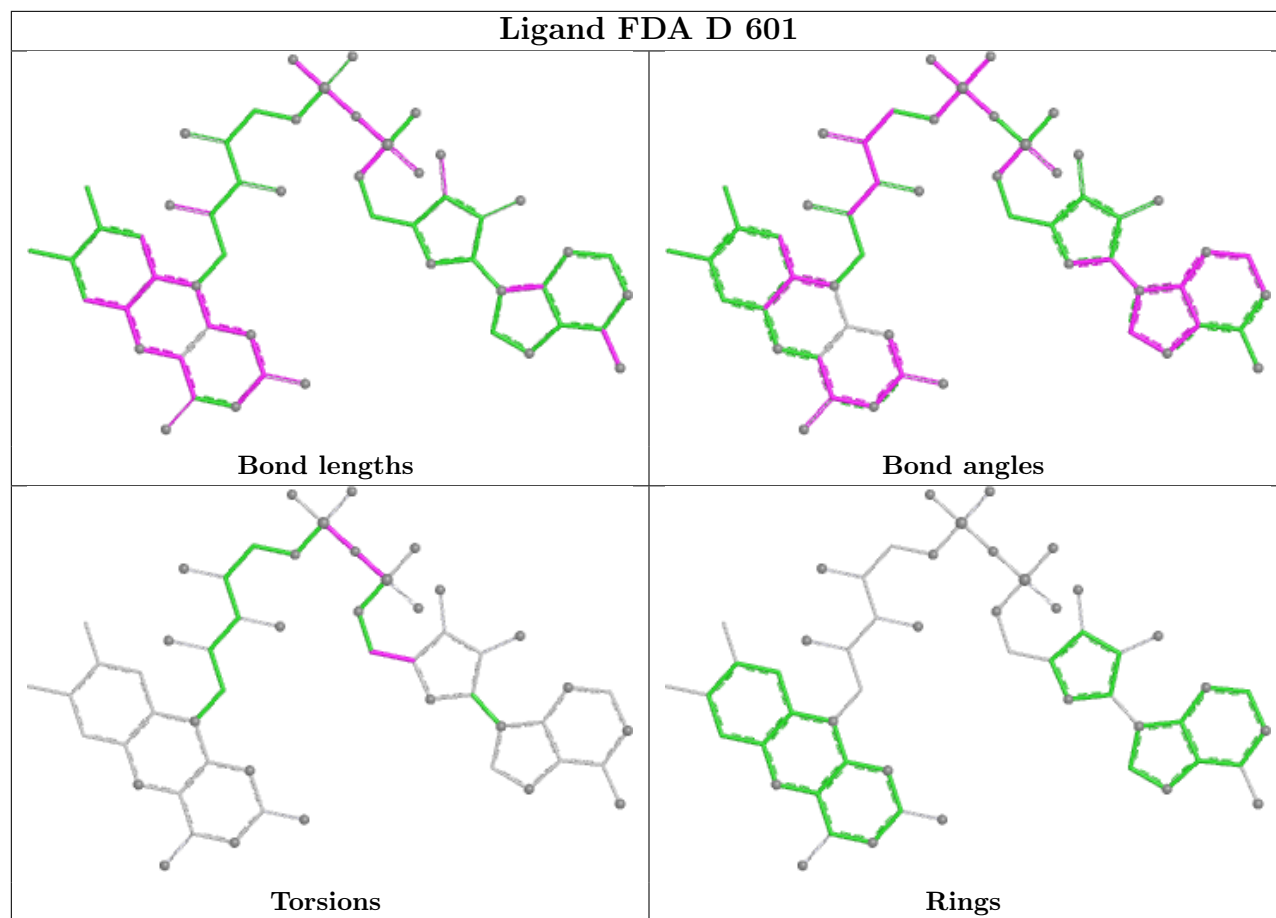


Ligand UDP B 602









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	505/513 (98%)	-0.09	26 (5%) 33 35	29, 40, 60, 102	18 (3%)
1	B	505/513 (98%)	-0.21	15 (2%) 52 54	29, 39, 61, 95	0
1	C	504/513 (98%)	-0.19	9 (1%) 67 69	29, 43, 65, 82	0
1	D	505/513 (98%)	-0.29	8 (1%) 70 72	27, 41, 63, 90	0
All	All	2019/2052 (98%)	-0.20	58 (2%) 53 56	27, 41, 63, 102	18 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	203	ASN	8.9
1	A	201	ALA	8.7
1	B	206	PRO	6.8
1	B	358	GLN	6.8
1	A	507	SER	6.6
1	B	207	ALA	6.4
1	A	3	HIS	6.2
1	B	202	GLY	5.7
1	D	507	SER	5.7
1	C	506	LYS	5.7
1	B	3	HIS	5.4
1	A	207	ALA	5.2
1	B	507	SER	5.1
1	D	3	HIS	5.1
1	A	206	PRO	4.9
1	C	3	HIS	4.7
1	A	203	ASN	4.7
1	A	180	GLY	4.4
1	A	185	ALA	4.0
1	B	201	ALA	3.9
1	A	202	GLY	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	108	ASN	3.9
1	D	273	PHE	3.8
1	A	184	ALA	3.7
1	C	182	ARG	3.7
1	C	273	PHE	3.6
1	A	183	VAL	3.5
1	A	200	THR	3.5
1	A	111	SER	3.4
1	B	506	LYS	3.4
1	A	157	LEU	3.3
1	A	506	LYS	3.3
1	C	183	VAL	3.2
1	C	491	GLN	3.1
1	B	273	PHE	3.1
1	A	179	LEU	3.1
1	A	205	GLY	3.1
1	A	358	GLN	3.0
1	C	185	ALA	3.0
1	B	200	THR	3.0
1	B	205	GLY	3.0
1	D	207	ALA	2.7
1	B	356	ARG	2.7
1	D	506	LYS	2.6
1	D	491	GLN	2.6
1	A	273	PHE	2.6
1	C	181	GLU	2.5
1	A	436	LYS	2.5
1	A	110	ILE	2.5
1	B	360	THR	2.3
1	C	149	MET	2.3
1	B	204	TRP	2.3
1	A	199	LYS	2.3
1	A	107	GLN	2.2
1	A	249	ASN	2.2
1	D	77	ASP	2.1
1	D	238	GLU	2.1
1	A	182	ARG	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

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
4	SO4	D	607	5/5	0.68	0.21	103,105,105,106	5
4	SO4	A	608	5/5	0.69	0.14	106,108,109,109	0
4	SO4	C	607	5/5	0.73	0.16	86,92,95,97	0
4	SO4	A	606	5/5	0.73	0.15	91,93,95,97	0
4	SO4	A	607	5/5	0.77	0.19	100,101,102,105	5
4	SO4	B	606	5/5	0.77	0.14	78,85,87,87	0
4	SO4	D	604	5/5	0.80	0.20	73,79,84,86	5
4	SO4	D	606	5/5	0.80	0.14	102,107,107,108	0
4	SO4	B	608	5/5	0.80	0.13	93,97,98,100	5
3	UDP	A	609	25/25	0.81	0.17	42,65,123,150	25
4	SO4	C	606	5/5	0.81	0.19	84,90,91,94	0
4	SO4	B	607	5/5	0.81	0.16	90,91,95,97	0
4	SO4	C	605	5/5	0.82	0.13	95,96,98,99	0
4	SO4	A	604	5/5	0.82	0.18	94,95,96,98	5
4	SO4	D	605	5/5	0.83	0.17	100,105,106,106	0
4	SO4	B	605	5/5	0.84	0.16	96,98,99,101	5
3	UDP	C	609	15/25	0.85	0.20	44,62,71,74	15
3	UDP	D	609	15/25	0.86	0.19	52,67,74,74	15
4	SO4	C	604	5/5	0.86	0.17	96,97,98,99	5
4	SO4	A	605	5/5	0.86	0.19	70,80,83,88	5
4	SO4	C	608	5/5	0.87	0.14	91,92,95,95	5
4	SO4	D	608	5/5	0.87	0.15	75,75,79,81	5
4	SO4	B	604	5/5	0.88	0.15	94,95,97,100	5
3	UDP	B	609	21/25	0.88	0.15	36,66,85,153	21
3	UDP	A	602	25/25	0.88	0.18	45,64,78,157	25
5	EDO	A	611	4/4	0.89	0.16	44,50,55,58	0
4	SO4	C	603	5/5	0.90	0.16	65,72,76,76	5
5	EDO	B	612	4/4	0.91	0.19	58,59,64,65	0
4	SO4	D	603	5/5	0.92	0.10	68,73,76,82	5
5	EDO	A	610	4/4	0.92	0.14	49,56,56,57	0
5	EDO	C	612	4/4	0.92	0.17	50,56,60,60	0
5	EDO	B	610	4/4	0.93	0.15	47,47,55,58	0

Continued on next page...

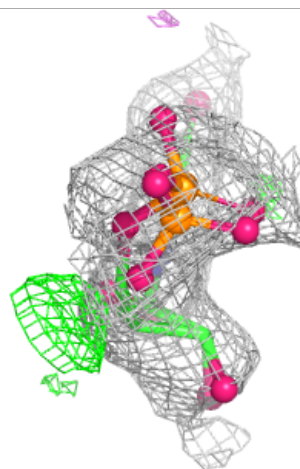
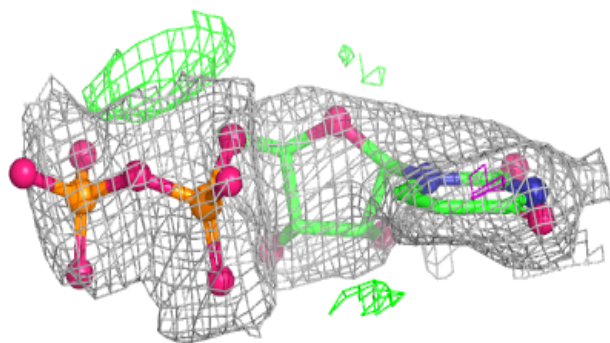
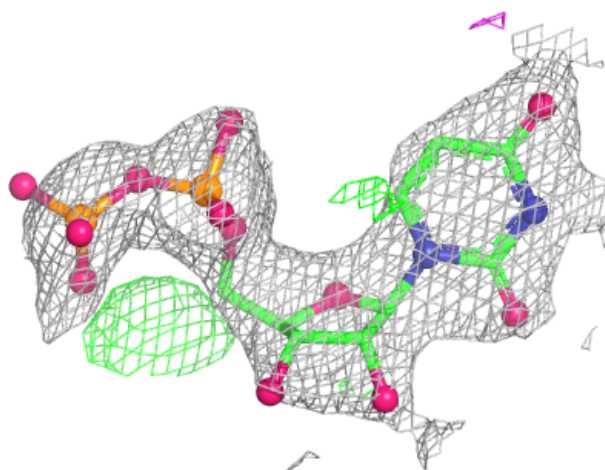
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	C	610	4/4	0.93	0.14	47,47,50,51	0
5	EDO	B	611	4/4	0.93	0.16	52,53,53,55	0
5	EDO	D	611	4/4	0.93	0.17	59,65,65,66	0
5	EDO	D	610	4/4	0.94	0.12	48,49,50,50	0
5	EDO	C	611	4/4	0.94	0.13	49,56,60,66	0
4	SO4	B	603	5/5	0.95	0.10	51,55,62,64	0
3	UDP	B	602	25/25	0.95	0.10	35,42,56,75	0
4	SO4	A	603	5/5	0.96	0.09	61,61,69,73	0
5	EDO	D	612	4/4	0.96	0.14	47,51,51,54	0
4	SO4	C	602	5/5	0.97	0.09	45,50,51,62	5
2	FDA	C	601	53/53	0.97	0.07	26,37,46,49	0
2	FDA	D	601	53/53	0.97	0.07	26,37,47,53	0
4	SO4	D	602	5/5	0.98	0.07	45,45,52,52	5
2	FDA	B	601	53/53	0.98	0.06	23,32,40,46	0
2	FDA	A	601	53/53	0.98	0.07	20,32,43,49	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.

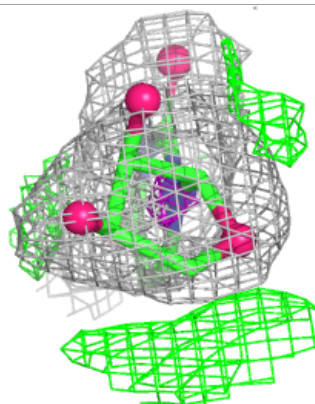
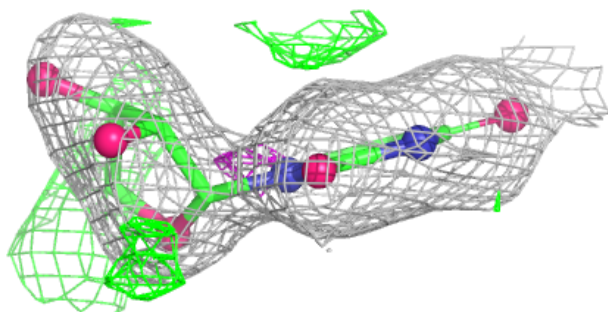
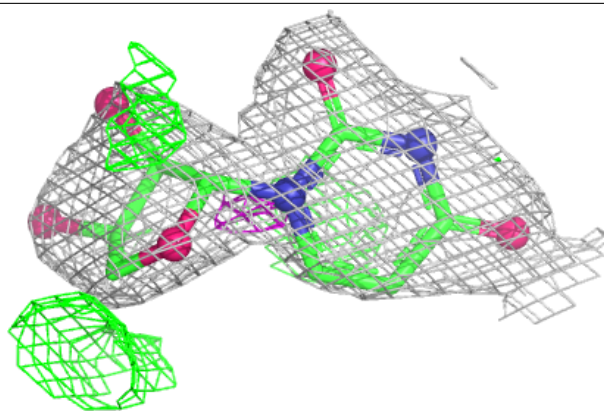
Electron density around UDP A 609:

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

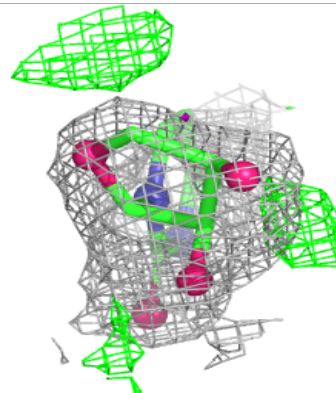
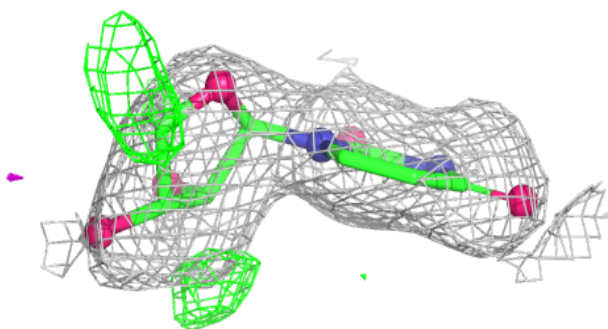
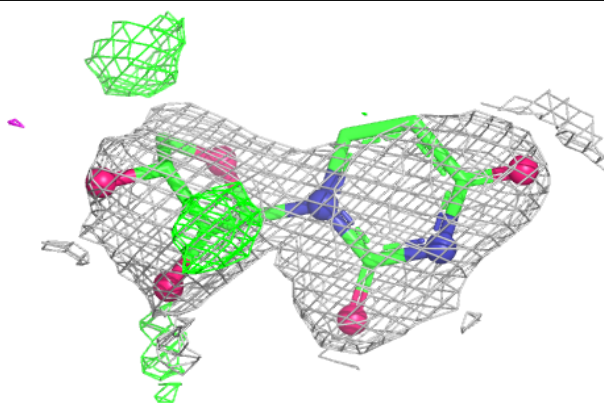


Electron density around UDP C 609:

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

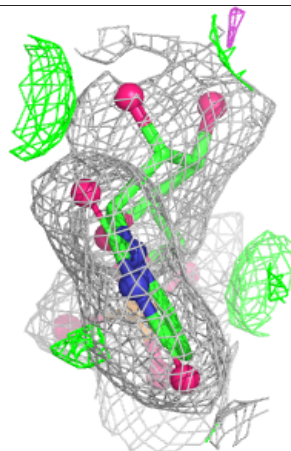
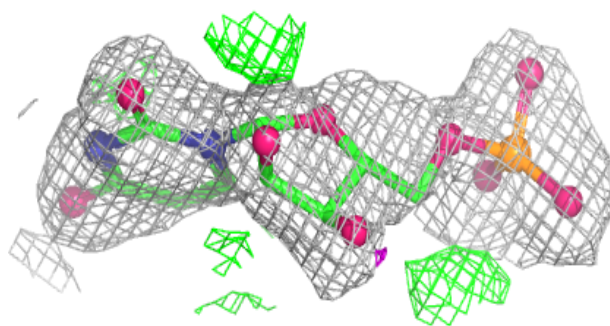
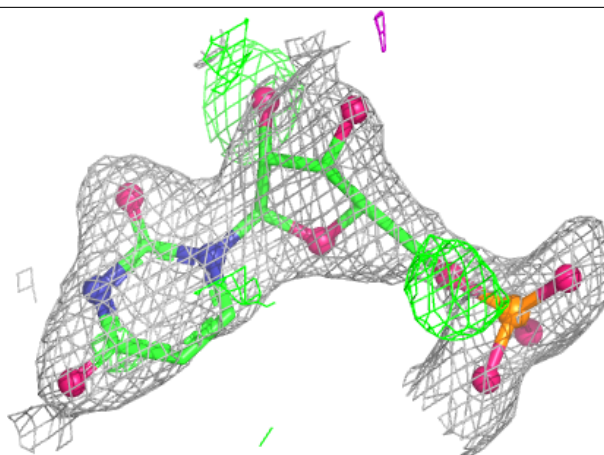
**Electron density around UDP D 609:**

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

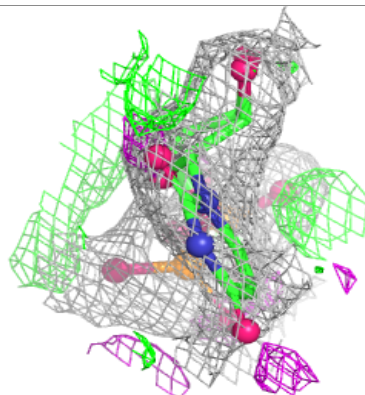
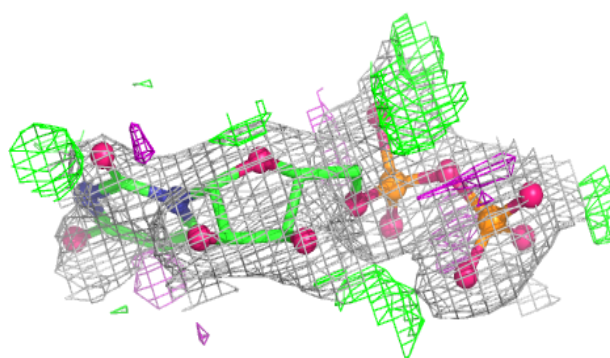
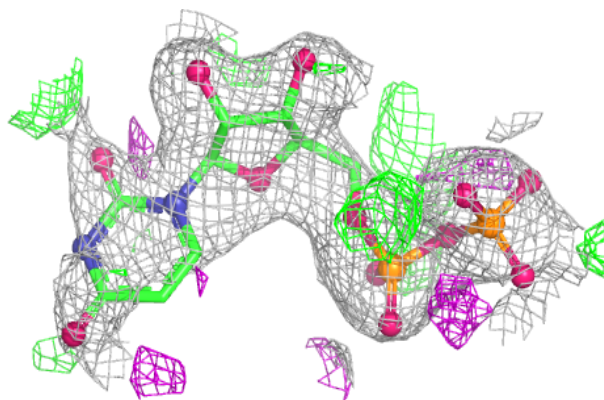


Electron density around UDP B 609:

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

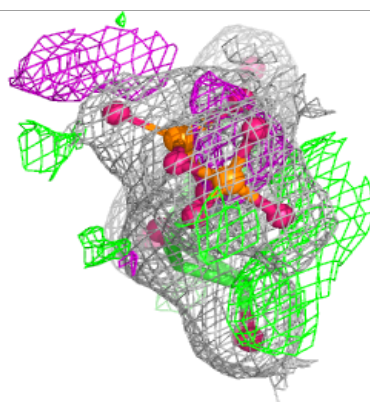
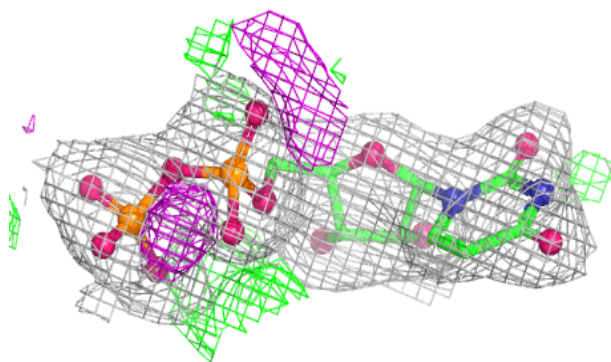
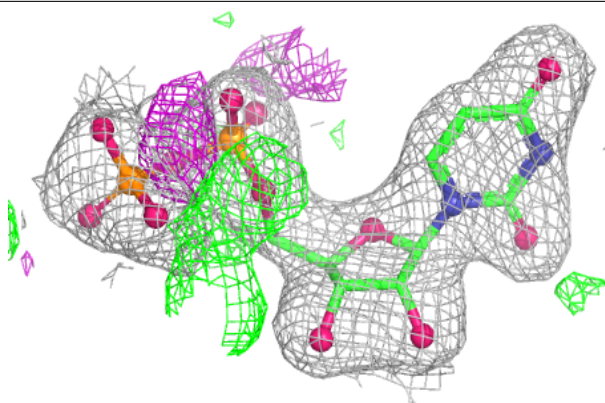
**Electron density around UDP A 602:**

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

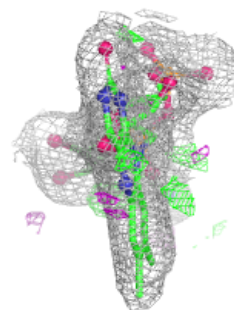
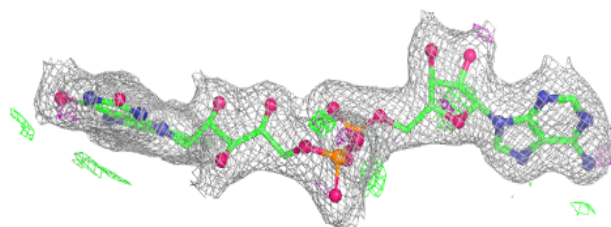
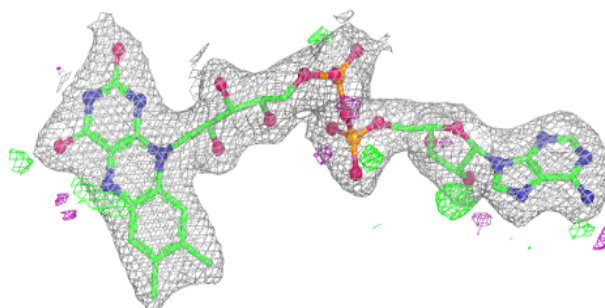


Electron density around UDP B 602:

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

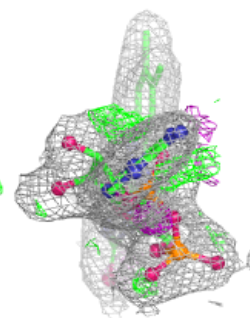
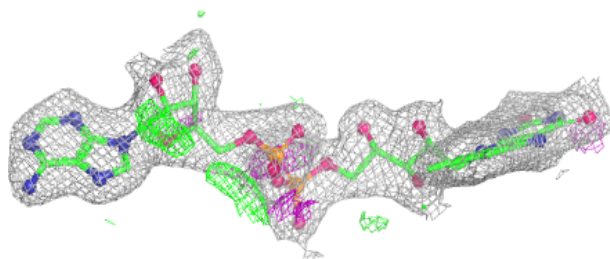
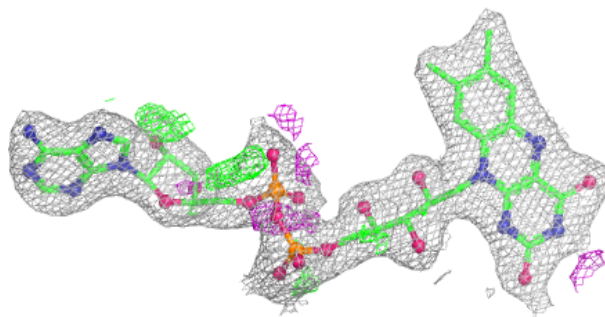
**Electron density around FDA C 601:**

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

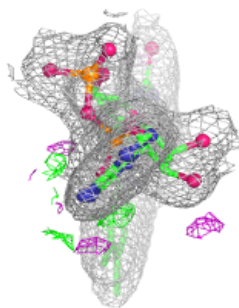
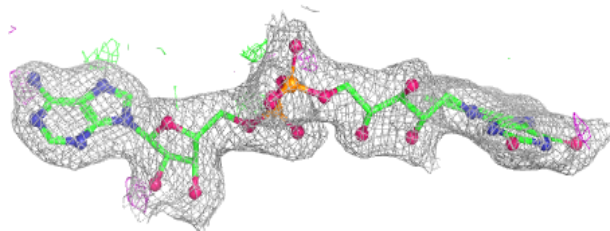
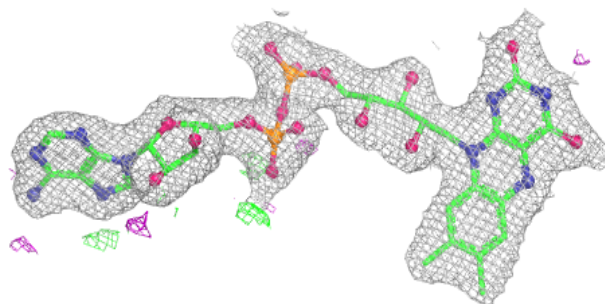


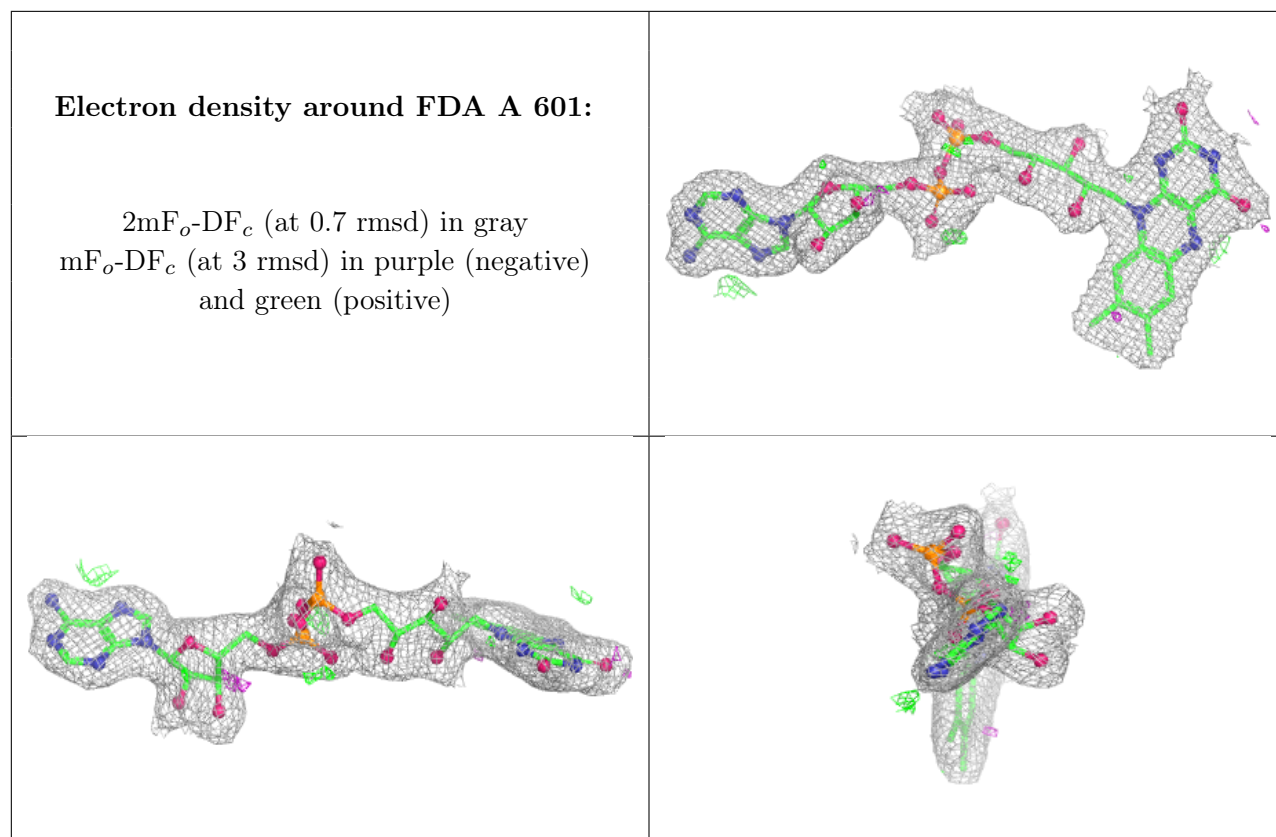
Electron density around FDA D 601:

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

**Electron density around FDA B 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.