



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:20 pm BST

PDB ID : 5MQJ
Title : Crystal structure of dCK mutant C3S
Authors : Saez-Ayala, M.; Rebuffet, E.; Hammam, K.; Gros, L.; Lopez, S.; Hajem, B.;
Humbert, M.; Baudalet, E.; Audebert, S.; Betzi, S.; Lugari, A.; Combes, S.;
Pez, D.; Letard, S.; Mansfield, C.; Moussy, A.; de Sepulveda, P.; Morelli, X.;
Dubreuil, P.
Deposited on : 2016-12-20
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

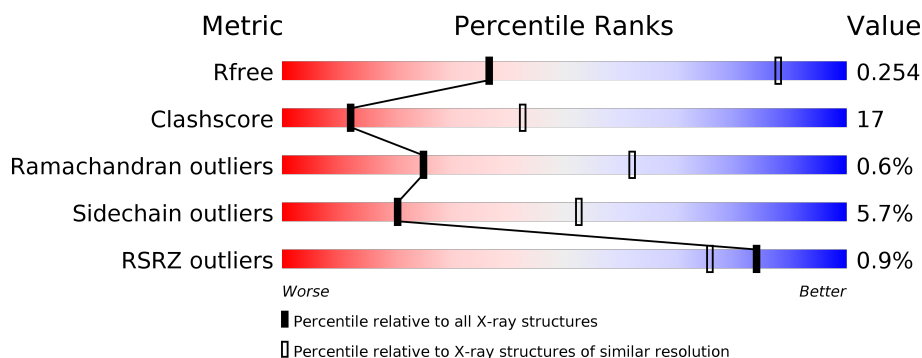
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	281	<div> <div>60%</div> <div>22%</div> <div>•</div> <div>17%</div> </div>
1	B	281	<div> <div>58%</div> <div>22%</div> <div>•</div> <div>19%</div> </div>
1	C	281	<div> <div>2%</div> <div>62%</div> <div>19%</div> <div>•</div> <div>18%</div> </div>
1	D	281	<div> <div>58%</div> <div>22%</div> <div>•</div> <div>19%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7447 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 Deoxycytidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1850	1184	305	354	7			
1	B	228	Total	C	N	O	S	0	0	0
			1793	1155	291	340	7			
1	C	230	Total	C	N	O	S	0	1	0
			1811	1163	301	340	7			
1	D	229	Total	C	N	O	S	0	0	0
			1809	1164	296	342	7			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP P27707
A	-19	SER	-	expression tag	UNP P27707
A	-18	TYR	-	expression tag	UNP P27707
A	-17	TYR	-	expression tag	UNP P27707
A	-16	HIS	-	expression tag	UNP P27707
A	-15	HIS	-	expression tag	UNP P27707
A	-14	HIS	-	expression tag	UNP P27707
A	-13	HIS	-	expression tag	UNP P27707
A	-12	HIS	-	expression tag	UNP P27707
A	-11	HIS	-	expression tag	UNP P27707
A	-10	LEU	-	expression tag	UNP P27707
A	-9	GLU	-	expression tag	UNP P27707
A	-8	SER	-	expression tag	UNP P27707
A	-7	THR	-	expression tag	UNP P27707
A	-6	SER	-	expression tag	UNP P27707
A	-5	LEU	-	expression tag	UNP P27707
A	-4	TYR	-	expression tag	UNP P27707
A	-3	LYS	-	expression tag	UNP P27707
A	-2	LYS	-	expression tag	UNP P27707
A	-1	ALA	-	expression tag	UNP P27707
A	0	GLY	-	expression tag	UNP P27707

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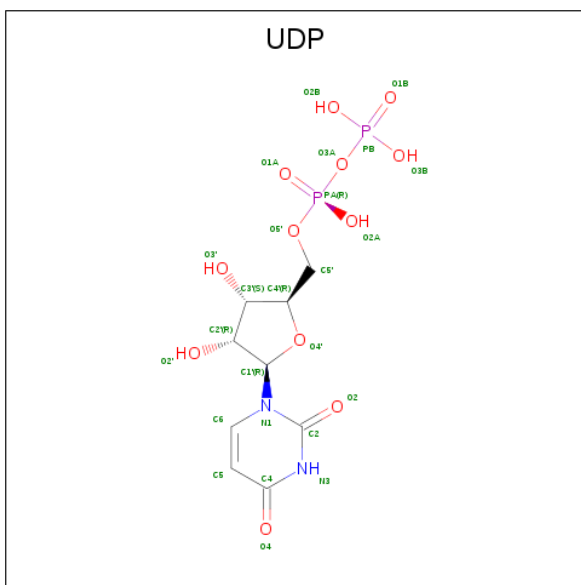
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	LEU	-	expression tag	UNP P27707
A	9	SER	CYS	engineered mutation	UNP P27707
A	45	SER	CYS	engineered mutation	UNP P27707
A	59	SER	CYS	engineered mutation	UNP P27707
B	-20	MET	-	initiating methionine	UNP P27707
B	-19	SER	-	expression tag	UNP P27707
B	-18	TYR	-	expression tag	UNP P27707
B	-17	TYR	-	expression tag	UNP P27707
B	-16	HIS	-	expression tag	UNP P27707
B	-15	HIS	-	expression tag	UNP P27707
B	-14	HIS	-	expression tag	UNP P27707
B	-13	HIS	-	expression tag	UNP P27707
B	-12	HIS	-	expression tag	UNP P27707
B	-11	HIS	-	expression tag	UNP P27707
B	-10	LEU	-	expression tag	UNP P27707
B	-9	GLU	-	expression tag	UNP P27707
B	-8	SER	-	expression tag	UNP P27707
B	-7	THR	-	expression tag	UNP P27707
B	-6	SER	-	expression tag	UNP P27707
B	-5	LEU	-	expression tag	UNP P27707
B	-4	TYR	-	expression tag	UNP P27707
B	-3	LYS	-	expression tag	UNP P27707
B	-2	LYS	-	expression tag	UNP P27707
B	-1	ALA	-	expression tag	UNP P27707
B	0	GLY	-	expression tag	UNP P27707
B	1	LEU	-	expression tag	UNP P27707
B	9	SER	CYS	engineered mutation	UNP P27707
B	45	SER	CYS	engineered mutation	UNP P27707
B	59	SER	CYS	engineered mutation	UNP P27707
C	-20	MET	-	initiating methionine	UNP P27707
C	-19	SER	-	expression tag	UNP P27707
C	-18	TYR	-	expression tag	UNP P27707
C	-17	TYR	-	expression tag	UNP P27707
C	-16	HIS	-	expression tag	UNP P27707
C	-15	HIS	-	expression tag	UNP P27707
C	-14	HIS	-	expression tag	UNP P27707
C	-13	HIS	-	expression tag	UNP P27707
C	-12	HIS	-	expression tag	UNP P27707
C	-11	HIS	-	expression tag	UNP P27707
C	-10	LEU	-	expression tag	UNP P27707
C	-9	GLU	-	expression tag	UNP P27707
C	-8	SER	-	expression tag	UNP P27707

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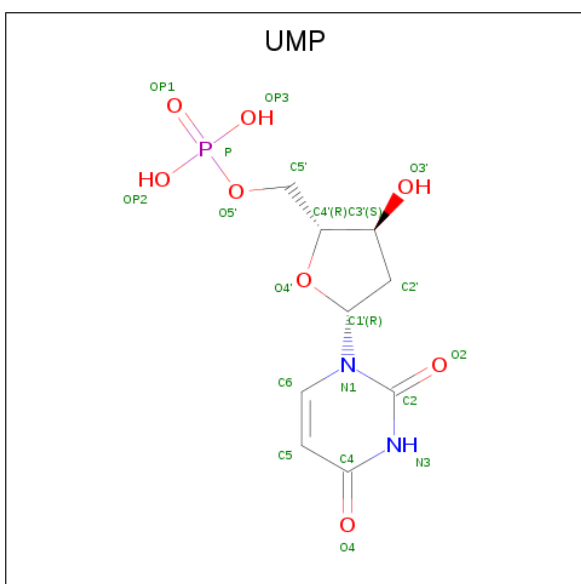
Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	THR	-	expression tag	UNP P27707
C	-6	SER	-	expression tag	UNP P27707
C	-5	LEU	-	expression tag	UNP P27707
C	-4	TYR	-	expression tag	UNP P27707
C	-3	LYS	-	expression tag	UNP P27707
C	-2	LYS	-	expression tag	UNP P27707
C	-1	ALA	-	expression tag	UNP P27707
C	0	GLY	-	expression tag	UNP P27707
C	1	LEU	-	expression tag	UNP P27707
C	9	SER	CYS	engineered mutation	UNP P27707
C	45	SER	CYS	engineered mutation	UNP P27707
C	59	SER	CYS	engineered mutation	UNP P27707
D	-20	MET	-	initiating methionine	UNP P27707
D	-19	SER	-	expression tag	UNP P27707
D	-18	TYR	-	expression tag	UNP P27707
D	-17	TYR	-	expression tag	UNP P27707
D	-16	HIS	-	expression tag	UNP P27707
D	-15	HIS	-	expression tag	UNP P27707
D	-14	HIS	-	expression tag	UNP P27707
D	-13	HIS	-	expression tag	UNP P27707
D	-12	HIS	-	expression tag	UNP P27707
D	-11	HIS	-	expression tag	UNP P27707
D	-10	LEU	-	expression tag	UNP P27707
D	-9	GLU	-	expression tag	UNP P27707
D	-8	SER	-	expression tag	UNP P27707
D	-7	THR	-	expression tag	UNP P27707
D	-6	SER	-	expression tag	UNP P27707
D	-5	LEU	-	expression tag	UNP P27707
D	-4	TYR	-	expression tag	UNP P27707
D	-3	LYS	-	expression tag	UNP P27707
D	-2	LYS	-	expression tag	UNP P27707
D	-1	ALA	-	expression tag	UNP P27707
D	0	GLY	-	expression tag	UNP P27707
D	1	LEU	-	expression tag	UNP P27707
D	9	SER	CYS	engineered mutation	UNP P27707
D	45	SER	CYS	engineered mutation	UNP P27707
D	59	SER	CYS	engineered mutation	UNP P27707

- Molecule 2 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).



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

- Molecule 3 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: $\text{C}_9\text{H}_{13}\text{N}_2\text{O}_8\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

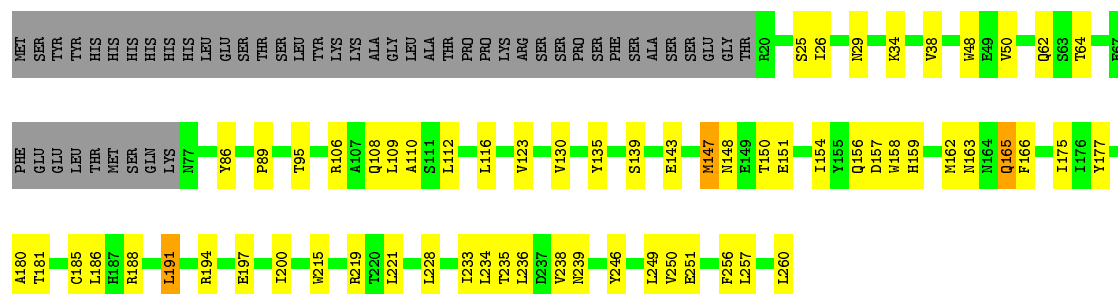
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

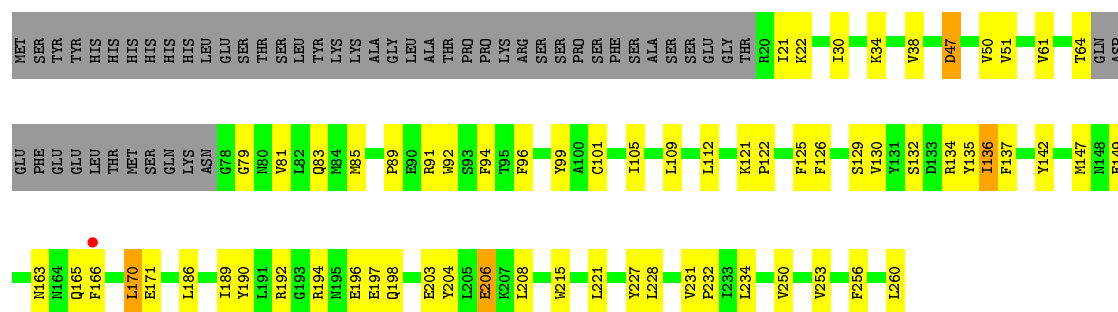
• Molecule 1: Deoxycytidine kinase

Chain A: 



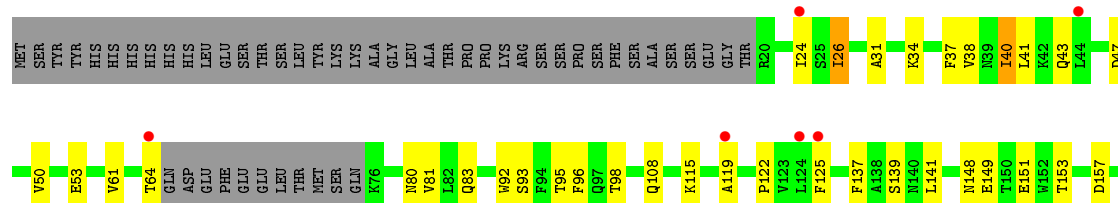
• Molecule 1: Deoxycytidine kinase

Chain B: 



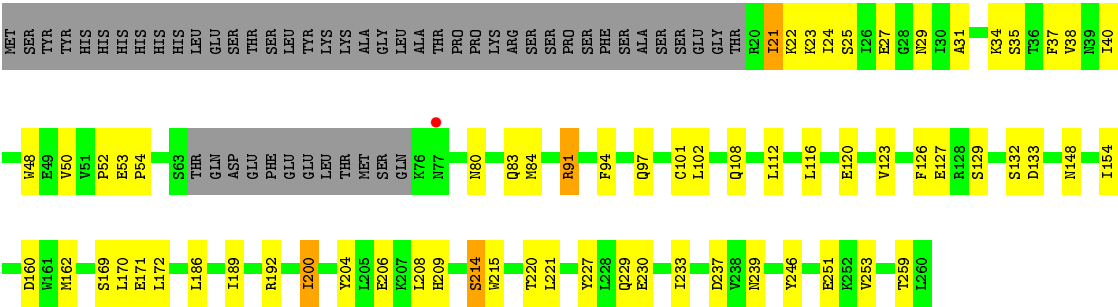
• Molecule 1: Deoxycytidine kinase

Chain C: 





● Molecule 1: Deoxycytidine kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.69 Å 92.69 Å 338.08 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.06 – 3.70 46.35 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.06-3.70) 99.9 (46.35-3.70)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 3.66 Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.181 , 0.251 0.191 , 0.254	Depositor DCC
R_{free} test set	830 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	108.0	Xtriage
Anisotropy	0.613	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 143.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7447	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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: UDP, MG, UMP

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	0.53	0/1896	0.72	0/2584
1	B	0.53	0/1839	0.78	0/2512
1	C	0.52	0/1856	0.76	0/2533
1	D	0.56	0/1855	0.75	0/2532
All	All	0.54	0/7446	0.75	0/10161

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	1850	0	1695	78	0
1	B	1793	0	1628	76	0
1	C	1811	0	1651	64	0
1	D	1809	0	1652	48	0
2	A	25	0	11	0	0
2	B	25	0	11	1	0
2	C	25	0	11	3	0
2	D	25	0	11	6	0
3	A	20	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	20	0	11	2	0
3	C	20	0	11	0	0
3	D	20	0	11	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	7447	0	6714	242	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 17.

All (242) 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:158:TRP:CZ2	1:A:162:MET:HE1	1.44	1.49
1:C:38:VAL:CG2	1:C:50:VAL:HG11	1.62	1.28
1:A:158:TRP:CE2	1:A:162:MET:CE	2.27	1.18
1:A:158:TRP:CZ2	1:A:162:MET:CE	2.28	1.15
1:C:186:LEU:HA	1:C:189:ILE:HD12	1.29	1.13
1:A:158:TRP:CE2	1:A:162:MET:HE1	1.84	1.11
1:A:148:ASN:OD1	1:A:151:GLU:OE2	1.69	1.11
1:C:38:VAL:HG23	1:C:50:VAL:HG11	1.22	1.09
1:D:38:VAL:HG21	1:D:50:VAL:HG21	1.27	1.09
1:C:189:ILE:HD13	1:C:200:ILE:HD11	1.13	1.06
1:C:38:VAL:CG2	1:C:50:VAL:CG1	2.37	1.02
1:D:38:VAL:HG21	1:D:50:VAL:CG2	1.90	1.02
1:C:189:ILE:HD13	1:C:200:ILE:CD1	1.89	1.00
1:D:38:VAL:CG2	1:D:50:VAL:HG21	1.92	1.00
1:C:137:PHE:O	1:C:141:LEU:CD1	2.11	0.99
1:D:29:ASN:O	1:D:34:LYS:NZ	1.95	0.98
1:A:148:ASN:OD1	1:A:151:GLU:HB2	1.65	0.97
1:D:35:SER:HB2	2:D:301:UDP:O1A	1.62	0.96
1:C:38:VAL:HG22	1:C:50:VAL:HG21	1.49	0.95
1:B:232:PRO:HG2	1:B:260:LEU:HD21	1.44	0.94
1:B:194:ARG:HH12	3:B:302:UMP:H5'	1.34	0.92
1:A:148:ASN:OD1	1:A:151:GLU:CG	2.18	0.91
1:C:137:PHE:O	1:C:141:LEU:HD12	1.69	0.91
1:A:158:TRP:CE2	1:A:162:MET:HE2	2.03	0.91
1:B:21:ILE:HG23	1:B:122:PRO:HG2	1.54	0.89
1:B:190:TYR:HD1	1:B:198:GLN:OE1	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:VAL:HG22	1:C:50:VAL:HG11	1.56	0.87
1:A:157:ASP:OD1	1:B:64:THR:HB	1.74	0.85
1:A:165:GLN:HB3	1:B:166:PHE:HE1	1.40	0.85
1:C:141:LEU:H	1:C:141:LEU:HD12	1.41	0.85
1:A:148:ASN:OD1	1:A:151:GLU:CB	2.25	0.84
1:C:38:VAL:HG23	1:C:50:VAL:CG1	2.03	0.84
1:A:38:VAL:HG12	1:A:50:VAL:HG11	1.59	0.82
1:B:232:PRO:HG2	1:B:260:LEU:CD2	2.10	0.81
1:C:93:SER:OG	1:C:141:LEU:HD23	1.81	0.80
1:D:91:ARG:HH21	1:D:91:ARG:HG2	1.47	0.80
1:B:171:GLU:HG3	1:B:227:TYR:CZ	2.16	0.80
1:A:148:ASN:OD1	1:A:151:GLU:CD	2.20	0.79
1:C:185:CYS:O	1:C:189:ILE:HG13	1.83	0.79
1:B:130:VAL:HG11	1:B:163:ASN:HD21	1.49	0.78
1:A:38:VAL:CG1	1:A:50:VAL:HG11	2.13	0.77
1:C:38:VAL:HG21	1:C:50:VAL:HB	1.66	0.77
1:B:21:ILE:HG23	1:B:122:PRO:CG	2.15	0.77
1:C:38:VAL:CG2	1:C:50:VAL:CB	2.63	0.76
1:C:95:THR:CG2	1:D:154:ILE:HD11	2.14	0.76
1:C:31:ALA:HB2	1:C:192:ARG:NH2	2.02	0.74
1:C:141:LEU:HD12	1:C:141:LEU:N	2.02	0.74
1:A:165:GLN:HG2	1:B:166:PHE:CD1	2.22	0.74
1:A:112:LEU:N	1:A:112:LEU:HD12	2.03	0.73
1:B:171:GLU:HG3	1:B:227:TYR:CE2	2.24	0.72
1:C:38:VAL:HG21	1:C:50:VAL:CB	2.19	0.72
1:A:34:LYS:O	1:A:38:VAL:HG23	1.89	0.71
1:A:175:ILE:HB	1:A:233:ILE:HG22	1.71	0.71
1:A:197:GLU:HB2	1:A:200:ILE:HD12	1.72	0.70
1:D:35:SER:N	2:D:301:UDP:O2B	2.22	0.70
1:C:38:VAL:CG2	1:C:50:VAL:HG21	2.22	0.69
1:A:246:TYR:O	1:A:250:VAL:HG13	1.93	0.69
1:A:165:GLN:HB3	1:B:166:PHE:CE1	2.27	0.69
1:B:231:VAL:HG23	1:B:232:PRO:CD	2.23	0.68
1:A:112:LEU:HD12	1:A:112:LEU:H	1.56	0.68
1:C:38:VAL:HG22	1:C:50:VAL:CG2	2.23	0.68
1:B:21:ILE:CG2	1:B:122:PRO:HB2	2.24	0.68
1:A:165:GLN:CB	1:B:166:PHE:HE1	2.07	0.67
1:A:165:GLN:HG2	1:B:166:PHE:CE1	2.30	0.67
1:B:192:ARG:NH1	1:B:197:GLU:OE1	2.28	0.66
1:B:190:TYR:CD1	1:B:198:GLN:OE1	2.45	0.66
1:B:231:VAL:CG2	1:B:232:PRO:CD	2.73	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:VAL:HG23	1:A:251:GLU:OE2	1.94	0.66
1:A:25:SER:HB3	1:A:175:ILE:HG23	1.78	0.66
1:D:35:SER:CB	2:D:301:UDP:O1A	2.41	0.66
1:A:148:ASN:HD21	1:B:92:TRP:HH2	1.44	0.66
1:C:189:ILE:HD11	1:C:205:LEU:HD21	1.78	0.66
1:D:91:ARG:HH21	1:D:91:ARG:CG	2.10	0.65
1:A:250:VAL:CG2	1:A:251:GLU:N	2.60	0.65
1:A:38:VAL:CG1	1:A:50:VAL:CG1	2.74	0.65
1:B:21:ILE:HG23	1:B:122:PRO:HB2	1.77	0.64
1:B:186:LEU:O	1:B:189:ILE:HG13	1.98	0.64
1:B:234:LEU:HD13	1:B:256:PHE:HB2	1.78	0.64
1:B:21:ILE:HG23	1:B:122:PRO:CB	2.28	0.64
1:C:38:VAL:HA	1:C:41:LEU:HD12	1.80	0.64
1:C:50:VAL:HG12	1:C:125:PHE:HB2	1.80	0.64
1:A:116:LEU:O	1:A:116:LEU:HG	1.97	0.63
1:B:50:VAL:HG12	1:B:125:PHE:HB2	1.79	0.62
1:C:177:TYR:HD2	1:C:235:THR:HG22	1.63	0.62
1:C:40:ILE:O	1:C:43:GLN:HB2	1.99	0.62
1:C:61:VAL:O	1:C:61:VAL:HG23	1.99	0.62
1:C:31:ALA:HA	2:C:301:UDP:O2B	1.99	0.61
1:B:231:VAL:HG23	1:B:232:PRO:HD2	1.81	0.61
1:C:137:PHE:O	1:C:141:LEU:HD13	1.96	0.61
1:C:31:ALA:HA	2:C:301:UDP:PB	2.40	0.61
1:A:250:VAL:CG2	1:A:251:GLU:OE2	2.49	0.61
1:A:135:TYR:HB3	1:A:221:LEU:HD21	1.82	0.60
1:D:27:GLU:OE2	1:D:132:SER:HB2	2.02	0.60
1:A:26:ILE:HG13	1:A:38:VAL:HG22	1.83	0.60
1:C:141:LEU:CD1	1:C:141:LEU:H	2.11	0.60
1:A:148:ASN:ND2	1:B:92:TRP:HH2	1.99	0.59
1:A:197:GLU:HB2	1:A:200:ILE:CD1	2.33	0.59
1:B:197:GLU:HG3	1:B:197:GLU:O	2.02	0.59
1:C:95:THR:HG23	1:D:154:ILE:HD11	1.84	0.58
1:A:250:VAL:HG23	1:A:251:GLU:N	2.18	0.58
1:D:34:LYS:N	2:D:301:UDP:O2B	2.37	0.58
1:B:231:VAL:HG22	1:B:232:PRO:N	2.18	0.58
1:B:165:GLN:NE2	1:B:165:GLN:H	2.02	0.58
1:C:31:ALA:HB2	1:C:192:ARG:HH21	1.68	0.58
1:C:186:LEU:HA	1:C:189:ILE:CD1	2.18	0.57
1:D:97:GLN:HE22	3:D:302:UMP:HN3	1.52	0.57
1:B:130:VAL:HG11	1:B:163:ASN:ND2	2.16	0.57
1:D:38:VAL:CG2	1:D:50:VAL:CG2	2.64	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ASN:ND2	1:B:92:TRP:CH2	2.71	0.57
1:D:25:SER:HB3	1:D:172:LEU:HD21	1.85	0.57
1:A:157:ASP:O	1:A:158:TRP:C	2.43	0.57
1:A:139:SER:O	1:A:143:GLU:HG3	2.05	0.56
1:B:231:VAL:CG2	1:B:232:PRO:HD2	2.36	0.56
1:C:92:TRP:HH2	1:D:148:ASN:HD21	1.54	0.56
1:C:38:VAL:CG2	1:C:50:VAL:CG2	2.83	0.56
1:D:23:LYS:HE3	1:D:169:SER:O	2.05	0.56
1:A:112:LEU:H	1:A:112:LEU:CD1	2.19	0.56
1:B:64:THR:O	1:B:64:THR:HG23	2.06	0.55
1:C:81:VAL:HG13	1:C:96:PHE:HD1	1.70	0.55
1:A:158:TRP:NE1	1:A:162:MET:HE2	2.21	0.55
1:A:38:VAL:HG13	1:A:50:VAL:CG1	2.36	0.55
1:D:215:TRP:HB2	1:D:221:LEU:HD13	1.87	0.55
1:A:148:ASN:OD1	1:A:148:ASN:N	2.39	0.55
1:C:179:GLN:O	1:C:238:VAL:HG22	2.06	0.55
1:C:47:ASP:OD1	1:C:47:ASP:O	2.24	0.55
1:B:101:CYS:O	1:B:105:ILE:HG22	2.06	0.55
1:D:129:SER:HB2	1:D:132:SER:H	1.71	0.55
1:B:34:LYS:HB2	2:B:301:UDP:O2B	2.07	0.55
1:C:189:ILE:CD1	1:C:200:ILE:CD1	2.77	0.55
1:A:64:THR:HG21	1:A:106:ARG:HH12	1.71	0.54
1:B:194:ARG:HB3	1:B:197:GLU:HG2	1.89	0.54
1:D:229:GLN:CG	1:D:230:GLU:N	2.71	0.54
1:C:108:GLN:HE21	1:C:170:LEU:HD22	1.73	0.54
1:C:47:ASP:CG	1:C:119:ALA:HB1	2.28	0.54
1:A:165:GLN:HG2	1:B:166:PHE:HD1	1.70	0.53
1:D:229:GLN:HG2	1:D:230:GLU:H	1.73	0.53
1:A:157:ASP:OD1	1:B:64:THR:CB	2.52	0.53
1:B:194:ARG:HB3	1:B:197:GLU:CG	2.39	0.52
1:A:86:TYR:O	1:A:89:PRO:HD3	2.10	0.52
1:C:95:THR:CG2	1:D:154:ILE:CD1	2.87	0.52
1:C:162:MET:O	1:C:165:GLN:O	2.26	0.52
1:A:165:GLN:CG	1:B:166:PHE:CE1	2.92	0.52
1:B:21:ILE:HG22	1:B:22:LYS:H	1.75	0.51
1:B:204:TYR:CE2	1:B:208:LEU:HD11	2.46	0.51
1:D:40:ILE:CD1	1:D:246:TYR:CD2	2.93	0.51
1:A:48:TRP:CD1	1:A:123:VAL:HG22	2.45	0.51
1:B:47:ASP:HB3	1:B:121:LYS:O	2.09	0.51
1:C:189:ILE:CD1	1:C:205:LEU:HD11	2.41	0.51
1:A:194:ARG:HB3	1:A:197:GLU:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:GLU:HG3	1:D:220:THR:HB	1.91	0.51
1:D:22:LYS:O	1:D:123:VAL:HA	2.10	0.51
1:C:26:ILE:CG2	1:C:34:LYS:HG2	2.40	0.51
1:A:130:VAL:HG21	1:A:163:ASN:HD21	1.76	0.51
1:A:165:GLN:CG	1:B:166:PHE:HE1	2.22	0.51
1:A:236:LEU:HD22	1:A:249:LEU:HD22	1.93	0.51
1:D:204:TYR:CE2	1:D:208:LEU:HD11	2.45	0.51
1:B:129:SER:HB2	1:B:132:SER:H	1.76	0.50
1:A:150:THR:HG21	1:B:79:GLY:HA3	1.93	0.50
1:C:38:VAL:HG22	1:C:50:VAL:CG1	2.28	0.50
1:D:38:VAL:HG22	1:D:50:VAL:HG21	1.88	0.50
1:C:177:TYR:CD2	1:C:235:THR:HG22	2.43	0.49
1:A:147:MET:HG2	1:A:151:GLU:HB3	1.94	0.49
1:A:159:HIS:O	1:A:163:ASN:HB2	2.12	0.49
1:B:231:VAL:CG2	1:B:232:PRO:N	2.74	0.49
1:B:81:VAL:HG13	1:B:96:PHE:HD1	1.77	0.49
1:B:171:GLU:CG	1:B:227:TYR:CE2	2.96	0.49
1:C:31:ALA:HA	2:C:301:UDP:O3A	2.13	0.49
1:D:237:ASP:OD1	1:D:239:ASN:HB2	2.13	0.48
1:A:158:TRP:CH2	1:A:162:MET:CE	2.91	0.48
1:D:38:VAL:HG21	1:D:50:VAL:HG23	1.90	0.48
1:A:158:TRP:CD2	1:A:162:MET:CE	2.93	0.48
1:A:215:TRP:O	1:A:219:ARG:HA	2.14	0.47
1:C:186:LEU:O	1:C:189:ILE:HB	2.13	0.47
1:A:156:GLN:O	1:A:157:ASP:C	2.48	0.47
1:C:37:PHE:CD2	1:C:41:LEU:HD11	2.50	0.47
1:D:40:ILE:HD13	1:D:246:TYR:CD2	2.49	0.47
1:A:108:GLN:O	1:A:109:LEU:C	2.49	0.47
1:A:234:LEU:HD13	1:A:256:PHE:HB2	1.97	0.47
1:B:61:VAL:H	1:B:79:GLY:H	1.63	0.47
1:C:47:ASP:OD1	1:C:119:ALA:HB1	2.14	0.47
1:A:177:TYR:HB3	1:A:235:THR:HG22	1.97	0.47
1:B:228:LEU:O	1:B:231:VAL:HG12	2.15	0.46
1:D:37:PHE:HZ	1:D:253:VAL:HG21	1.79	0.46
1:B:83:GLN:HB2	1:B:196:GLU:HG2	1.97	0.46
1:D:80:ASN:O	1:D:84:MET:HG2	2.15	0.46
1:C:153:THR:O	1:C:157:ASP:HB2	2.15	0.46
1:A:95:THR:HG23	1:B:94:PHE:CE2	2.52	0.45
2:D:301:UDP:H6	2:D:301:UDP:H5'2	1.81	0.45
1:B:132:SER:HA	1:B:136:ILE:HG23	1.98	0.45
1:B:206:GLU:OE1	1:D:214:SER:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:108:GLN:HB3	1:D:170:LEU:HD11	1.98	0.45
1:D:206:GLU:HA	1:D:209:HIS:HB3	1.98	0.45
1:C:240:GLU:O	1:C:241:ASP:C	2.53	0.45
1:B:134:ARG:HD3	1:B:135:TYR:CE2	2.52	0.45
1:B:30:ILE:HG22	1:B:189:ILE:CG2	2.47	0.45
1:A:154:ILE:HG12	1:B:99:TYR:CD1	2.52	0.44
1:A:38:VAL:HG13	1:A:50:VAL:HG11	1.94	0.44
1:A:108:GLN:O	1:A:110:ALA:N	2.51	0.44
1:D:48:TRP:CD1	1:D:123:VAL:HG12	2.53	0.44
1:A:188:ARG:HA	1:A:191:LEU:HB2	1.99	0.44
1:B:89:PRO:C	1:B:91:ARG:H	2.21	0.43
1:A:165:GLN:CB	1:B:166:PHE:CE1	2.94	0.43
1:B:194:ARG:NH1	3:B:302:UMP:H5'	2.15	0.43
1:B:21:ILE:HG21	1:B:122:PRO:HB2	2.01	0.43
1:B:231:VAL:HG22	1:B:232:PRO:CD	2.47	0.43
1:D:23:LYS:HB2	1:D:126:PHE:CE2	2.54	0.43
1:A:257:LEU:HD23	1:A:260:LEU:HD12	1.99	0.43
1:C:192:ARG:HD3	1:C:197:GLU:OE1	2.18	0.43
1:D:34:LYS:HD2	2:D:301:UDP:O3B	2.19	0.43
1:B:51:VAL:HB	1:B:126:PHE:HD1	1.83	0.43
1:B:142:TYR:HA	1:B:147:MET:HB2	2.00	0.43
1:B:21:ILE:HG22	1:B:22:LYS:N	2.32	0.43
1:A:181:THR:HG23	1:A:239:ASN:OD1	2.19	0.42
1:C:179:GLN:HG3	1:C:180:ALA:N	2.33	0.42
1:A:154:ILE:HG13	1:B:61:VAL:HG11	2.01	0.42
1:C:80:ASN:ND2	1:C:83:GLN:CB	2.82	0.42
1:D:31:ALA:HB2	1:D:192:ARG:NH2	2.35	0.42
1:A:166:PHE:CD2	1:A:166:PHE:N	2.87	0.42
1:C:148:ASN:HB3	1:C:151:GLU:HG3	2.00	0.42
1:B:215:TRP:HB2	1:B:221:LEU:HD13	2.02	0.42
1:C:247:GLU:HA	1:C:250:VAL:HG22	2.01	0.42
1:D:102:LEU:HD13	1:D:162:MET:HE3	2.02	0.42
1:A:148:ASN:O	1:A:151:GLU:HB2	2.19	0.42
1:A:180:ALA:HA	1:A:239:ASN:ND2	2.35	0.41
1:B:109:LEU:HG	1:B:170:LEU:HD13	2.02	0.41
1:C:26:ILE:HG22	1:C:34:LYS:HG2	2.01	0.41
1:C:37:PHE:CE2	1:C:41:LEU:HD11	2.55	0.41
1:D:21:ILE:H	1:D:21:ILE:HD12	1.85	0.41
1:A:148:ASN:OD1	1:A:151:GLU:HG3	2.13	0.41
1:D:171:GLU:HG2	1:D:227:TYR:CZ	2.56	0.41
1:D:34:LYS:H	1:D:34:LYS:HG3	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:LEU:O	1:A:116:LEU:CG	2.65	0.41
1:C:24:ILE:O	1:C:125:PHE:HA	2.20	0.41
1:A:29:ASN:HB3	1:A:185:CYS:SG	2.61	0.41
1:D:189:ILE:HD13	1:D:200:ILE:HG21	2.03	0.41
1:D:52:PRO:HA	1:D:127:GLU:HB2	2.03	0.41
1:B:192:ARG:CZ	1:B:197:GLU:OE1	2.69	0.41
1:C:95:THR:HG23	1:D:94:PHE:CE2	2.56	0.40
1:B:136:ILE:HG13	1:B:137:PHE:CD2	2.56	0.40
1:D:229:GLN:HG2	1:D:230:GLU:N	2.35	0.40
1:B:250:VAL:HA	1:B:253:VAL:HG22	2.02	0.40
1:B:234:LEU:HB2	1:B:256:PHE:CD1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/281 (81%)	209 (92%)	18 (8%)	1 (0%)	34	69
1	B	224/281 (80%)	194 (87%)	29 (13%)	1 (0%)	34	69
1	C	227/281 (81%)	203 (89%)	22 (10%)	2 (1%)	17	54
1	D	225/281 (80%)	202 (90%)	22 (10%)	1 (0%)	34	69
All	All	904/1124 (80%)	808 (89%)	91 (10%)	5 (1%)	25	62

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	170	LEU
1	C	115	LYS
1	C	170	LEU
1	D	120	GLU

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Mol	Chain	Res	Type
1	A	238	VAL

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	191/258 (74%)	185 (97%)	6 (3%)	40	65
1	B	181/258 (70%)	174 (96%)	7 (4%)	32	60
1	C	181/258 (70%)	169 (93%)	12 (7%)	16	48
1	D	184/258 (71%)	167 (91%)	17 (9%)	9	36
All	All	737/1032 (71%)	695 (94%)	42 (6%)	20	52

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	147	MET
1	A	165	GLN
1	A	186	LEU
1	A	191	LEU
1	A	228	LEU
1	B	38	VAL
1	B	47	ASP
1	B	85	MET
1	B	112	LEU
1	B	136	ILE
1	B	149	GLU
1	B	206	GLU
1	C	26	ILE
1	C	40	ILE
1	C	53	GLU
1	C	64	THR
1	C	98	THR
1	C	122	PRO
1	C	139	SER

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Mol	Chain	Res	Type
1	C	149	GLU
1	C	163	ASN
1	C	171	GLU
1	C	216	LEU
1	C	235	THR
1	D	21	ILE
1	D	24	ILE
1	D	53	GLU
1	D	54	PRO
1	D	83	GLN
1	D	91	ARG
1	D	101	CYS
1	D	112	LEU
1	D	116	LEU
1	D	133	ASP
1	D	160	ASP
1	D	186	LEU
1	D	200	ILE
1	D	214	SER
1	D	233	ILE
1	D	251	GLU
1	D	259	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	163	ASN
1	A	165	GLN
1	A	198	GLN
1	A	218	HIS
1	B	108	GLN
1	B	156	GLN
1	B	163	ASN
1	B	165	GLN
1	B	179	GLN
1	B	198	GLN
1	C	60	ASN
1	C	62	GLN
1	C	97	GLN
1	C	108	GLN
1	D	60	ASN

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Mol	Chain	Res	Type
1	D	97	GLN
1	D	229	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\# Z > 2$
2	UDP	A	301	-	20,26,26	1.16	3 (15%)	25,40,40	1.08	1 (4%)
2	UDP	D	301	4	20,26,26	1.23	3 (15%)	25,40,40	1.04	1 (4%)
2	UDP	B	301	-	20,26,26	1.13	2 (10%)	25,40,40	1.22	2 (8%)
3	UMP	D	302	4	18,21,21	2.14	3 (16%)	21,31,31	1.02	1 (4%)
3	UMP	B	302	4	18,21,21	2.00	2 (11%)	21,31,31	1.18	3 (14%)
3	UMP	A	302	4	18,21,21	2.41	4 (22%)	21,31,31	1.05	1 (4%)
3	UMP	C	302	4	18,21,21	1.89	3 (16%)	21,31,31	1.00	1 (4%)
2	UDP	C	301	-	20,26,26	1.08	2 (10%)	25,40,40	1.14	2 (8%)

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
2	UDP	A	301	-	-	0/14/32/32	0/2/2/2
2	UDP	D	301	4	-	7/14/32/32	0/2/2/2
2	UDP	B	301	-	-	2/14/32/32	0/2/2/2
3	UMP	D	302	4	-	3/7/22/22	0/2/2/2
3	UMP	B	302	4	-	0/7/22/22	0/2/2/2
3	UMP	A	302	4	-	5/7/22/22	0/2/2/2
3	UMP	C	302	4	-	4/7/22/22	0/2/2/2
2	UDP	C	301	-	-	1/14/32/32	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	UMP	C6-N1	7.05	1.44	1.35
3	D	302	UMP	C6-N1	6.02	1.43	1.35
3	B	302	UMP	C6-N1	5.88	1.43	1.35
3	A	302	UMP	C4-N3	5.59	1.42	1.33
3	C	302	UMP	C6-N1	5.20	1.42	1.35
3	B	302	UMP	C4-N3	5.08	1.41	1.33
3	D	302	UMP	C4-N3	5.03	1.41	1.33
3	C	302	UMP	C4-N3	4.69	1.41	1.33
2	A	301	UDP	C4-N3	3.25	1.38	1.33
2	D	301	UDP	C4-N3	3.18	1.38	1.33
2	C	301	UDP	C4-N3	3.07	1.38	1.33
2	B	301	UDP	C4-N3	2.99	1.38	1.33
2	D	301	UDP	PB-O2B	-2.88	1.43	1.54
3	D	302	UMP	O4'-C1'	2.84	1.48	1.42
2	D	301	UDP	C6-N1	2.77	1.39	1.35
2	A	301	UDP	C6-N1	2.68	1.39	1.35
3	A	302	UMP	O4'-C1'	2.63	1.48	1.42
2	C	301	UDP	C6-N1	2.50	1.38	1.35
2	A	301	UDP	PB-O2B	-2.42	1.45	1.54
2	B	301	UDP	C6-N1	2.31	1.38	1.35
3	C	302	UMP	O4'-C1'	2.05	1.46	1.42
3	A	302	UMP	P-OP3	-2.01	1.47	1.54

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	UDP	C5-C4-N3	-3.94	114.63	123.31
2	B	301	UDP	C5-C4-N3	-3.91	114.70	123.31
2	A	301	UDP	C5-C4-N3	-3.90	114.72	123.31
2	D	301	UDP	C5-C4-N3	-3.88	114.77	123.31
2	B	301	UDP	O2B-PB-O3A	2.39	112.63	104.64
2	C	301	UDP	PA-O3A-PB	-2.36	124.74	132.83
3	D	302	UMP	OP3-P-OP2	2.25	116.22	107.64
3	B	302	UMP	O5'-P-OP1	-2.22	100.24	106.47
3	B	302	UMP	O4'-C4'-C5'	-2.20	102.13	109.37
3	C	302	UMP	OP3-P-OP2	2.20	116.03	107.64
3	A	302	UMP	O5'-P-OP1	-2.18	100.35	106.47
3	B	302	UMP	O4'-C1'-C2'	-2.00	102.47	106.25

There are no chirality outliers.

All (22) torsion outliers are listed below:

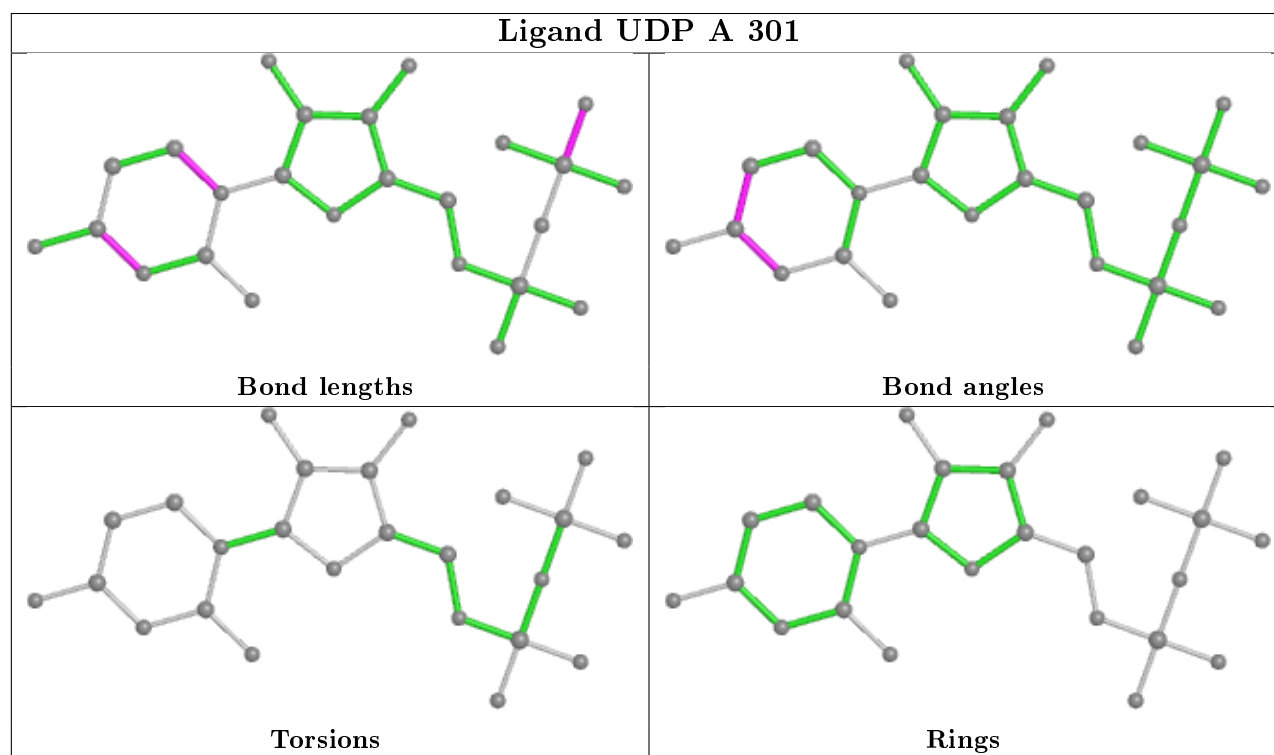
Mol	Chain	Res	Type	Atoms
2	D	301	UDP	O4'-C4'-C5'-O5'
2	D	301	UDP	PA-O3A-PB-O2B
3	D	302	UMP	O4'-C4'-C5'-O5'
3	A	302	UMP	C5'-O5'-P-OP1
3	A	302	UMP	C5'-O5'-P-OP2
3	A	302	UMP	C5'-O5'-P-OP3
3	C	302	UMP	C5'-O5'-P-OP1
3	C	302	UMP	C5'-O5'-P-OP2
3	C	302	UMP	C5'-O5'-P-OP3
3	D	302	UMP	C3'-C4'-C5'-O5'
2	D	301	UDP	C5'-O5'-PA-O3A
2	C	301	UDP	C5'-O5'-PA-O3A
3	D	302	UMP	C4'-C5'-O5'-P
2	D	301	UDP	C5'-O5'-PA-O1A
2	D	301	UDP	C3'-C4'-C5'-O5'
3	A	302	UMP	C4'-C5'-O5'-P
2	D	301	UDP	PA-O3A-PB-O3B
2	B	301	UDP	PB-O3A-PA-O2A
2	D	301	UDP	C5'-O5'-PA-O2A
2	B	301	UDP	C5'-O5'-PA-O1A
3	A	302	UMP	O4'-C4'-C5'-O5'
3	C	302	UMP	O4'-C4'-C5'-O5'

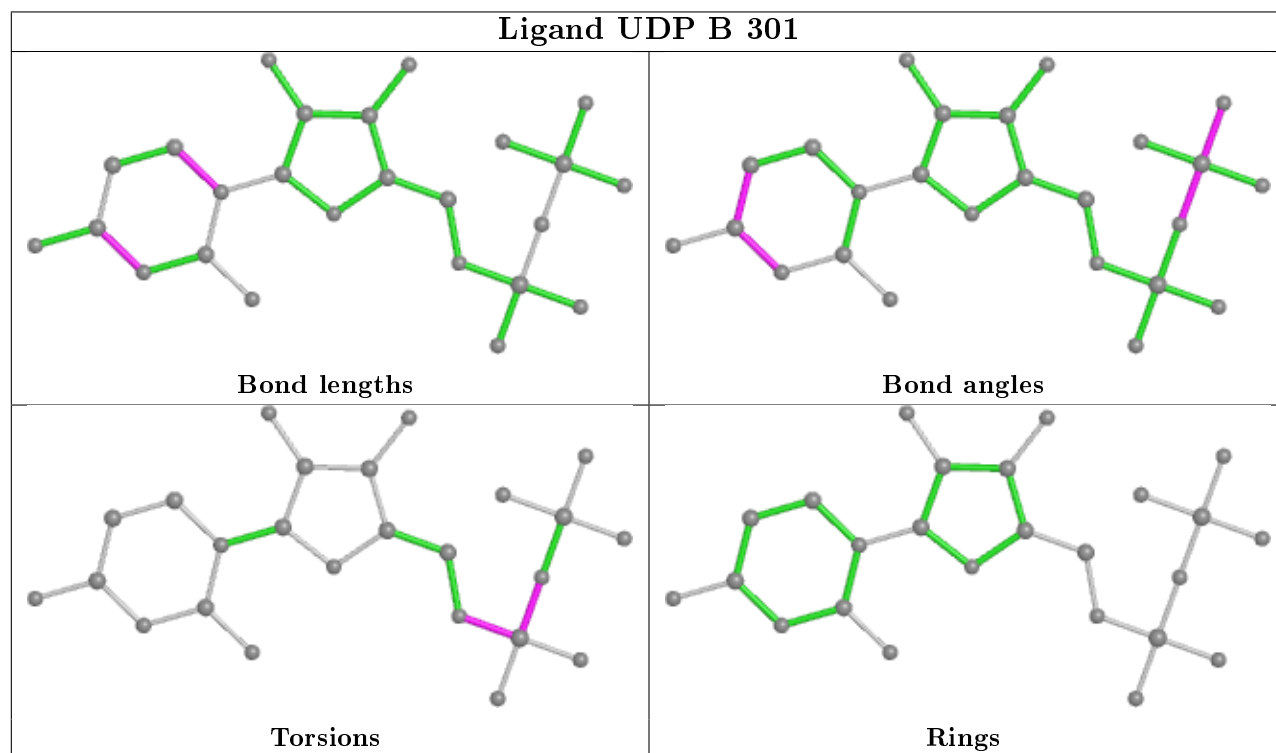
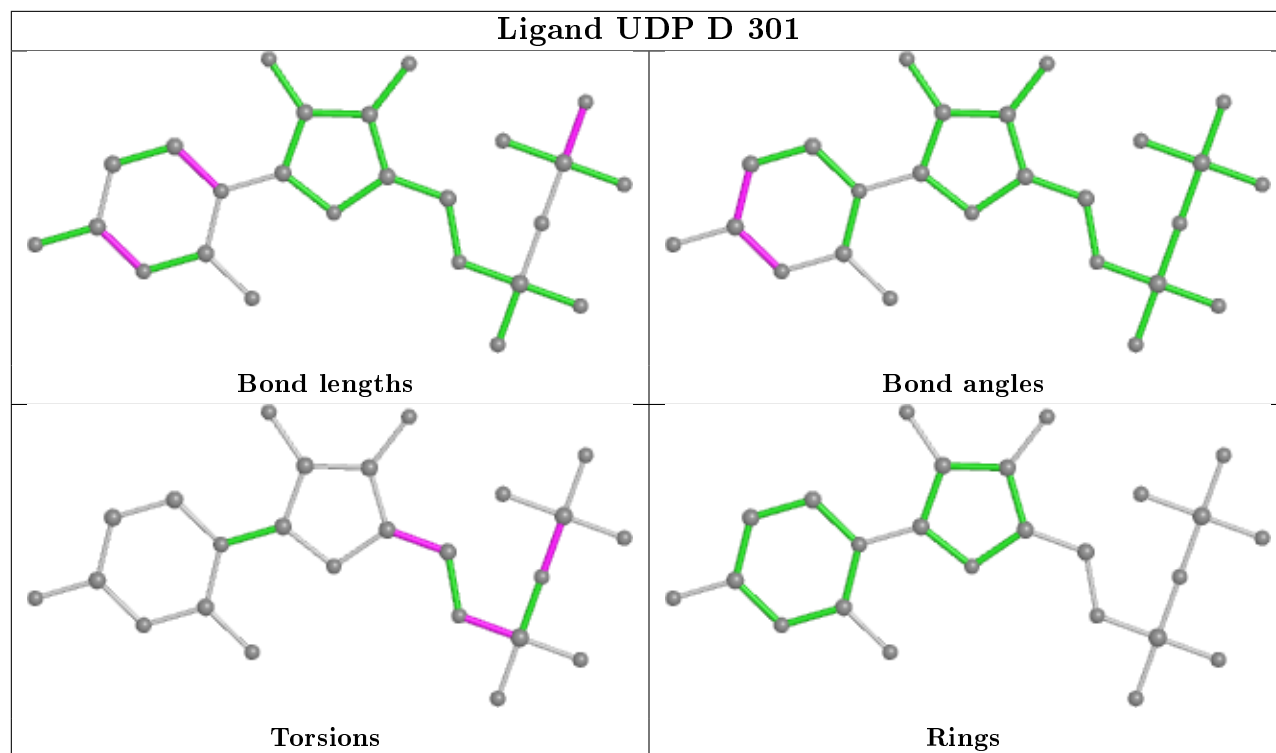
There are no ring outliers.

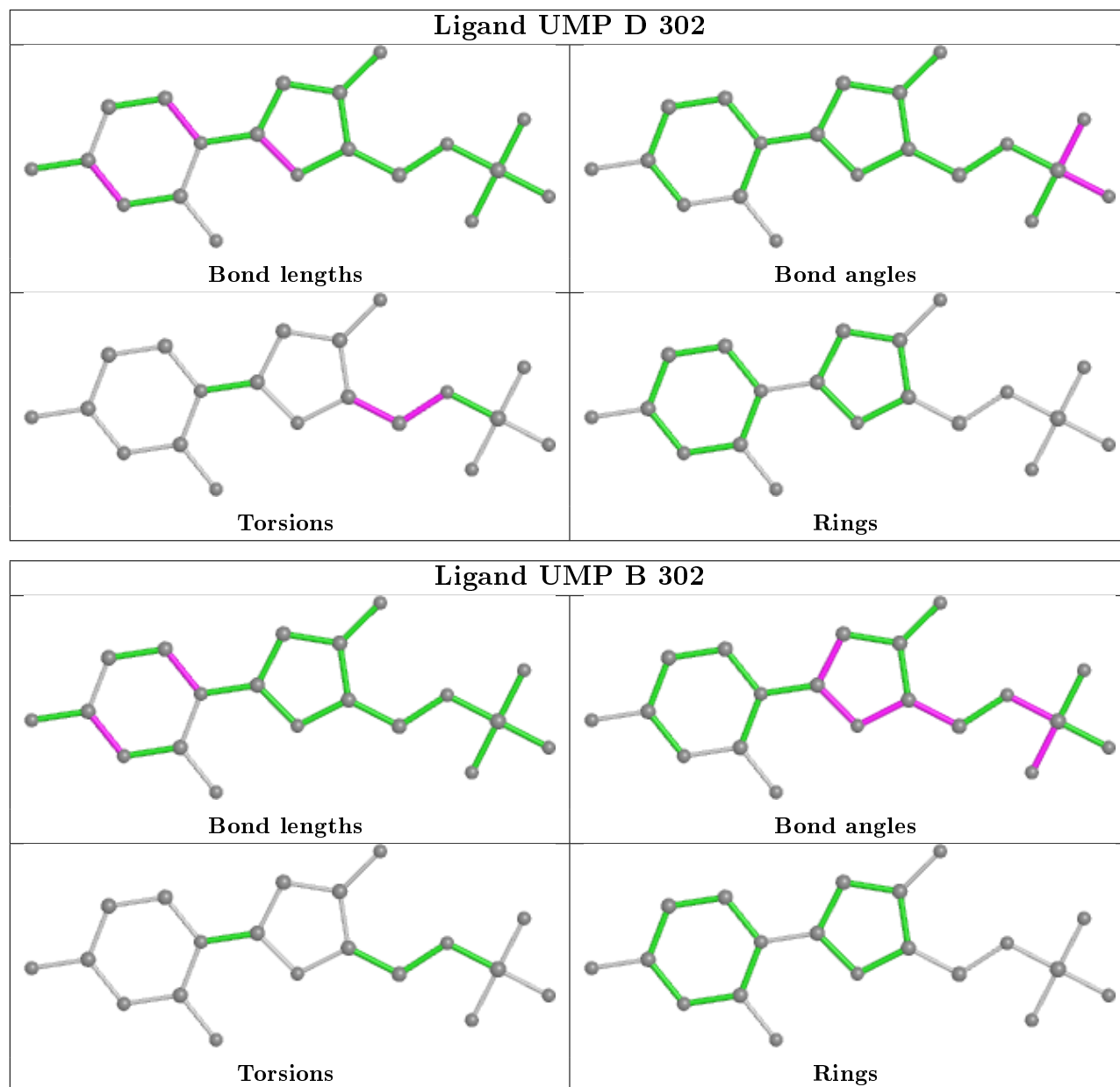
5 monomers are involved in 13 short contacts:

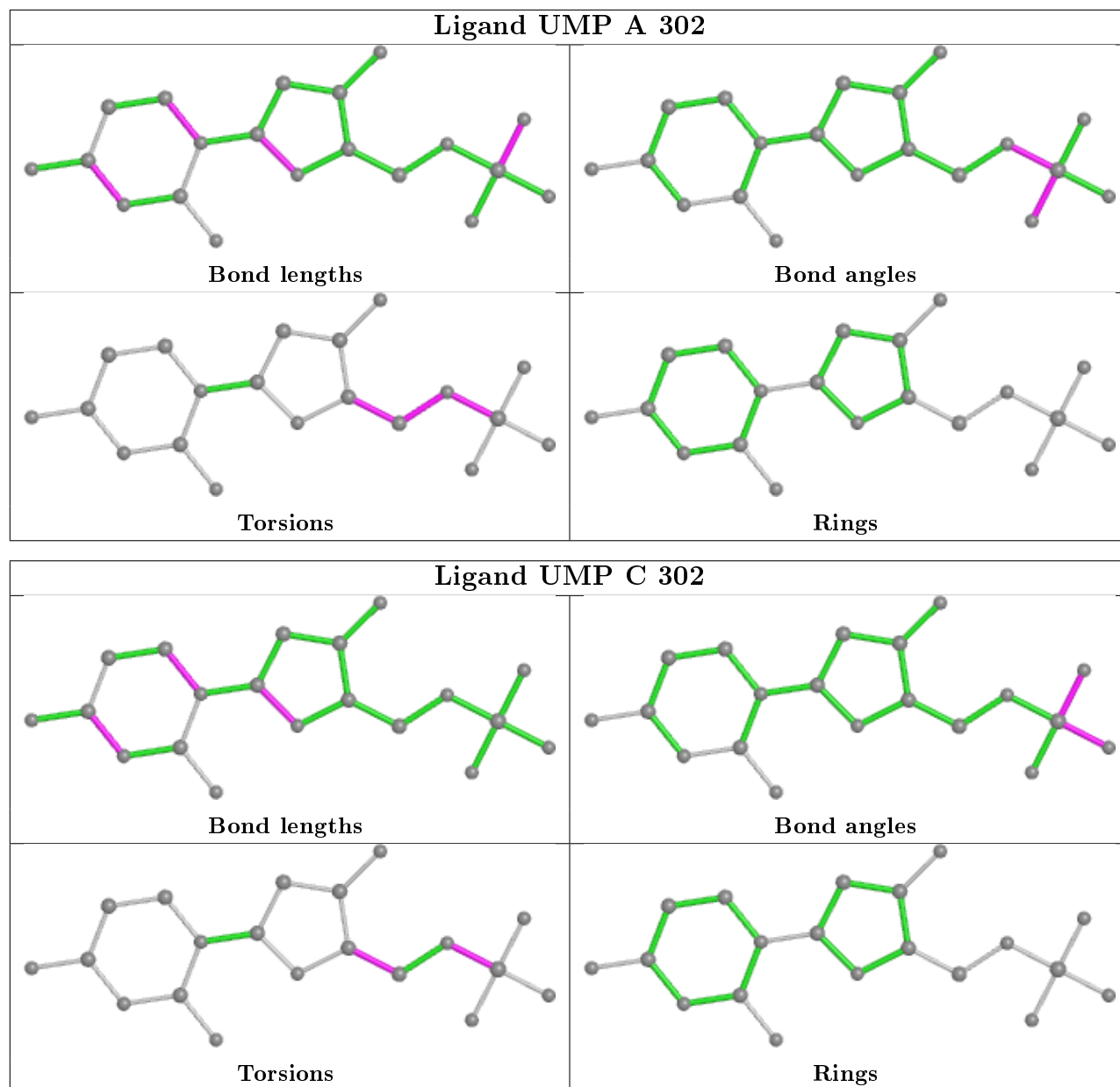
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	UDP	6	0
2	B	301	UDP	1	0
3	D	302	UMP	1	0
3	B	302	UMP	2	0
2	C	301	UDP	3	0

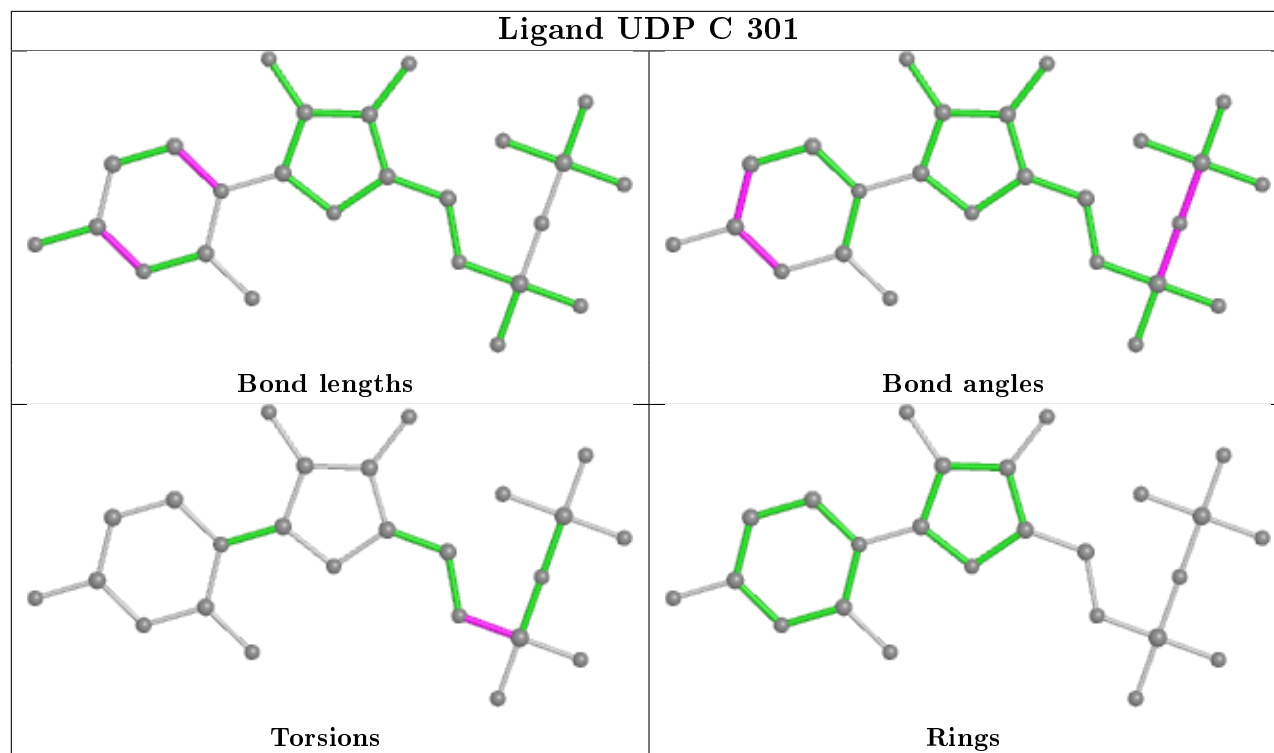
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	232/281 (82%)	-0.36	0 100 100	88, 120, 187, 234	0
1	B	228/281 (81%)	-0.31	1 (0%) 92 88	91, 127, 163, 193	0
1	C	230/281 (81%)	0.08	6 (2%) 56 43	87, 135, 194, 222	0
1	D	229/281 (81%)	-0.24	1 (0%) 92 88	89, 126, 180, 208	0
All	All	919/1124 (81%)	-0.21	8 (0%) 84 76	87, 127, 185, 234	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	119	ALA	3.8
1	C	64	THR	2.9
1	C	125	PHE	2.8
1	B	166	PHE	2.6
1	C	124	LEU	2.4
1	D	77	ASN	2.2
1	C	24	ILE	2.1
1	C	44	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands

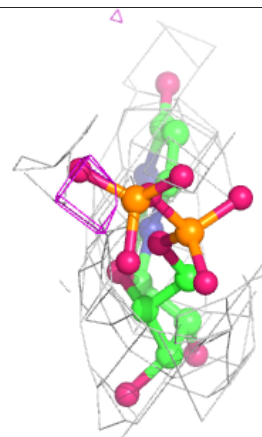
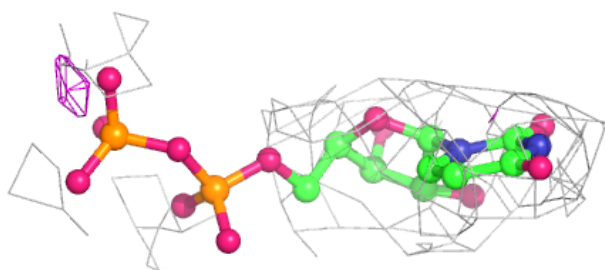
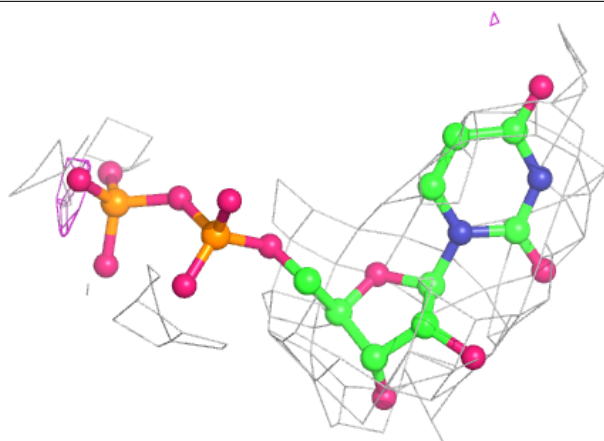
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	UDP	B	301	25/25	0.89	0.22	119,134,144,147	0
2	UDP	D	301	25/25	0.93	0.19	123,147,160,167	0
2	UDP	A	301	25/25	0.94	0.20	115,131,151,157	0
2	UDP	C	301	25/25	0.94	0.13	128,150,166,173	0
3	UMP	B	302	20/20	0.95	0.20	124,134,148,149	0
4	MG	D	303	1/1	0.97	0.13	66,66,66,66	0
4	MG	B	303	1/1	0.97	0.11	55,55,55,55	0
3	UMP	A	302	20/20	0.98	0.22	104,113,124,125	0
3	UMP	C	302	20/20	0.98	0.21	113,122,144,146	0
3	UMP	D	302	20/20	0.98	0.20	92,110,125,128	0
4	MG	C	303	1/1	0.98	0.09	91,91,91,91	0
4	MG	A	303	1/1	0.98	0.22	64,64,64,64	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.

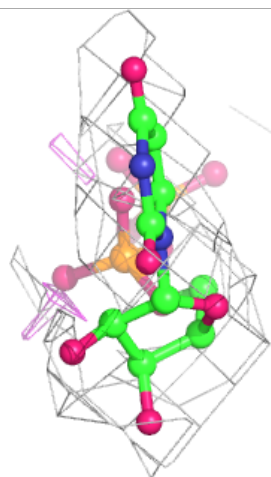
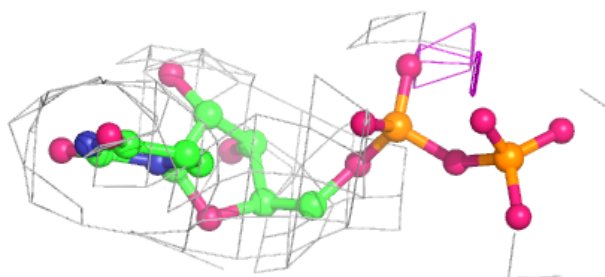
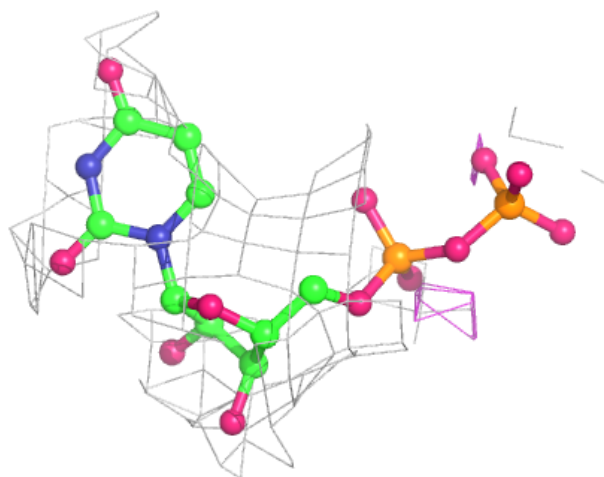
Electron density around UDP B 301:

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



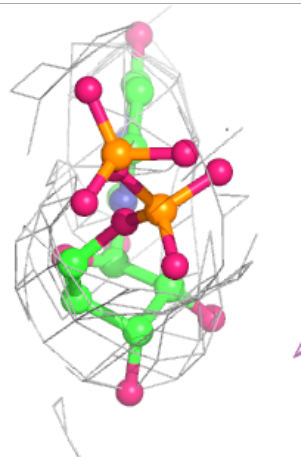
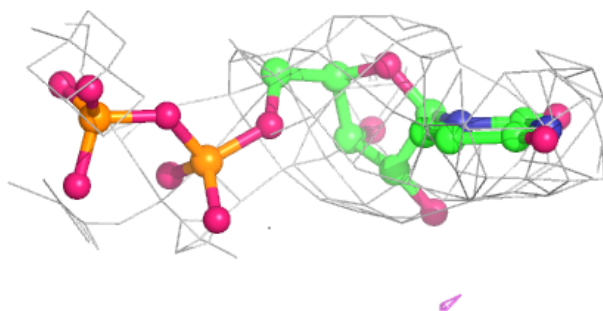
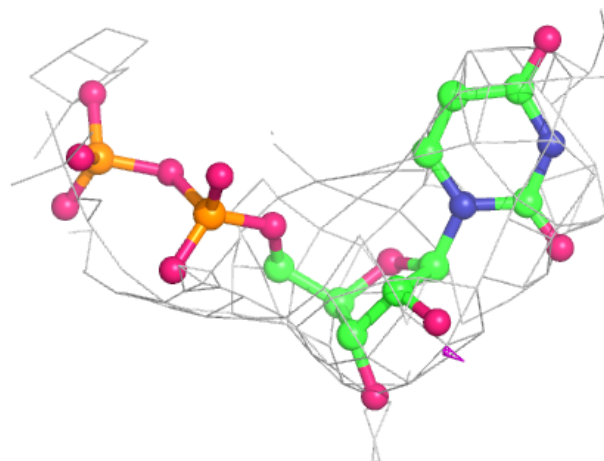
Electron density around UDP D 301:

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



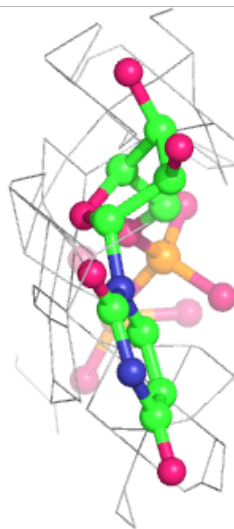
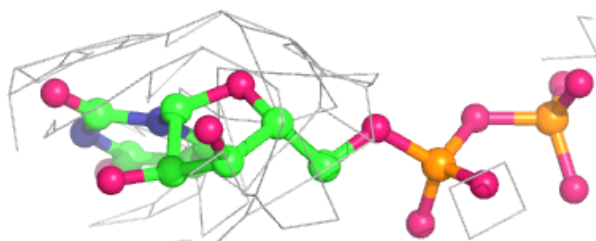
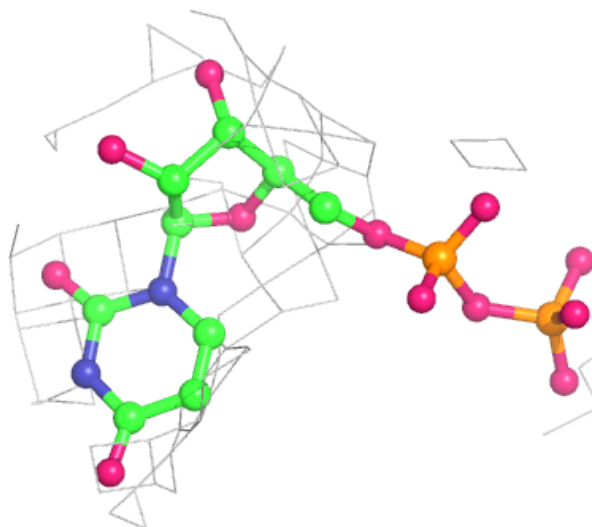
Electron density around UDP A 301:

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



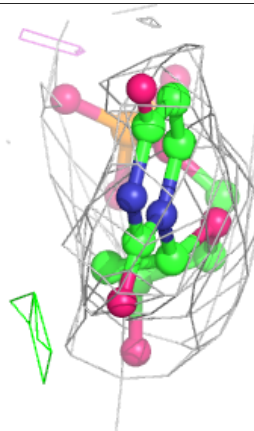
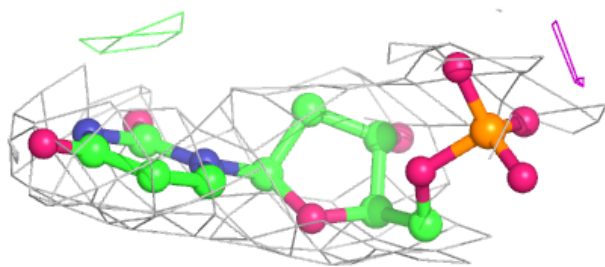
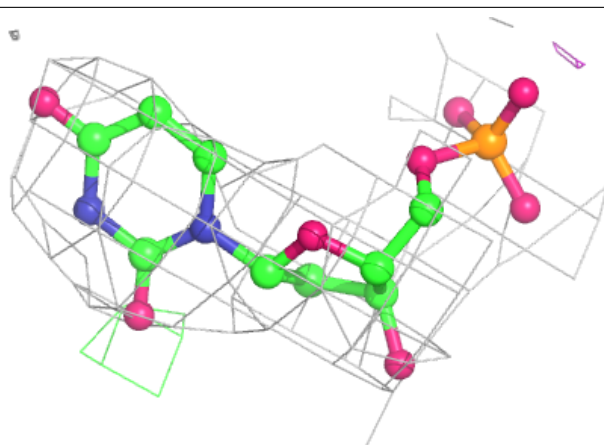
Electron density around UDP C 301:

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

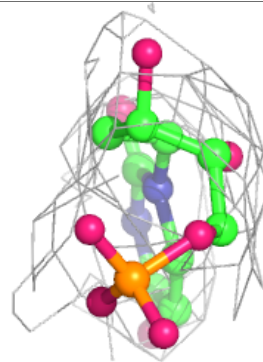
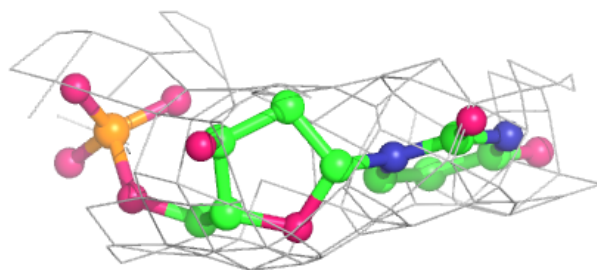
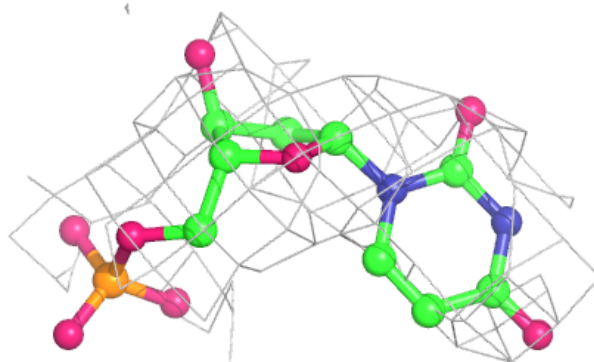


Electron density around UMP B 302:

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

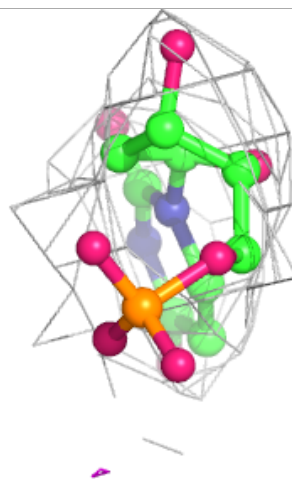
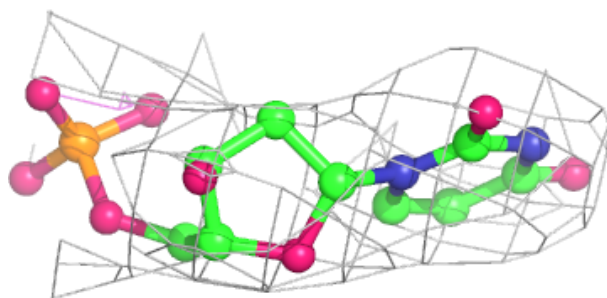
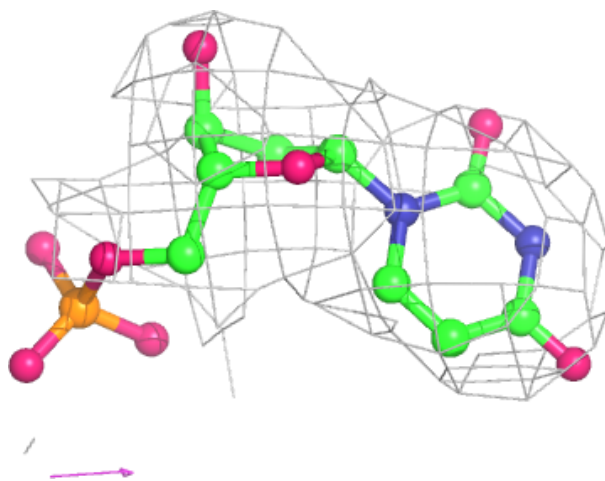
**Electron density around UMP A 302:**

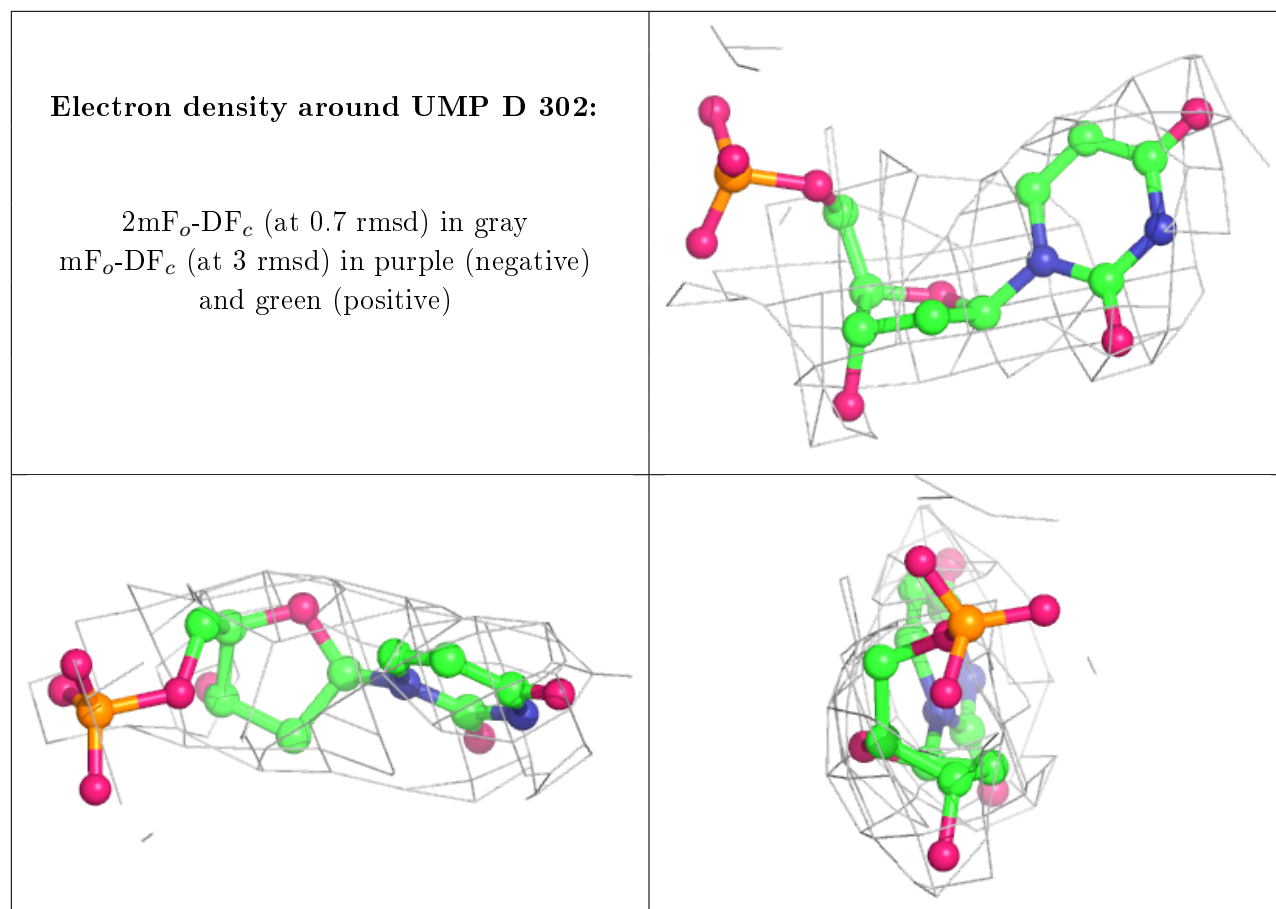
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around UMP C 302:

$2mF_o-DF_c$ (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.