



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:12 AM UTC

PDB ID : 6QXH / pdb_00006qhx
Title : Crystal structure of His-tag human thymidylate synthase (HT-hTS) in complex with dUMP
Authors : Pozzi, C.; Mangani, M.
Deposited on : 2019-03-07
Resolution : 2.04 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

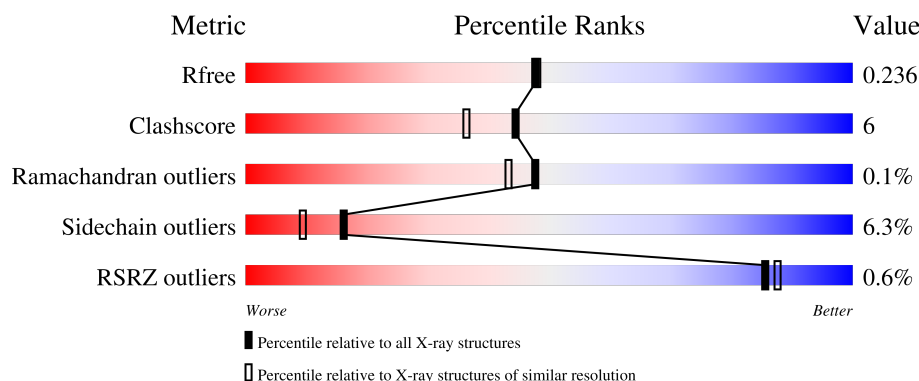
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	325	74% 14% • 12%
1	B	325	74% 13% • 12%
1	C	325	% 70% 18% • 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7082 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 Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2264	1452	383	415	14			
1	B	287	Total	C	N	O	S	0	0	0
			2267	1455	389	409	14			
1	C	288	Total	C	N	O	S	0	0	0
			2273	1456	387	416	14			

There are 36 discrepancies between the modelled and reference sequences:

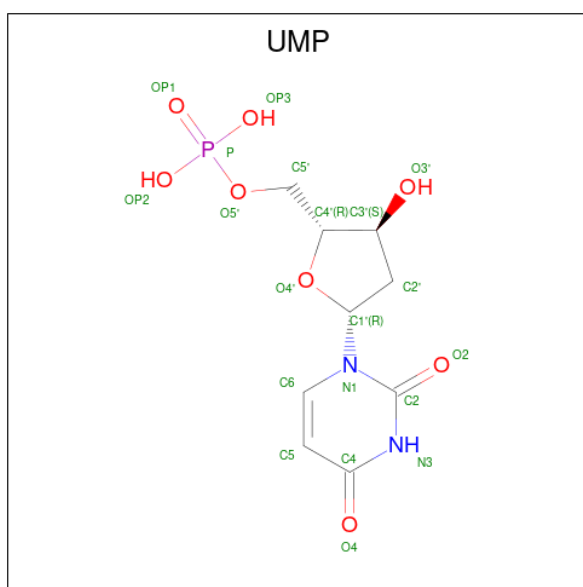
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P04818
A	-10	ARG	-	expression tag	UNP P04818
A	-9	GLY	-	expression tag	UNP P04818
A	-8	SER	-	expression tag	UNP P04818
A	-7	HIS	-	expression tag	UNP P04818
A	-6	HIS	-	expression tag	UNP P04818
A	-5	HIS	-	expression tag	UNP P04818
A	-4	HIS	-	expression tag	UNP P04818
A	-3	HIS	-	expression tag	UNP P04818
A	-2	HIS	-	expression tag	UNP P04818
A	-1	GLY	-	expression tag	UNP P04818
A	0	SER	-	expression tag	UNP P04818
B	-11	MET	-	initiating methionine	UNP P04818
B	-10	ARG	-	expression tag	UNP P04818
B	-9	GLY	-	expression tag	UNP P04818
B	-8	SER	-	expression tag	UNP P04818
B	-7	HIS	-	expression tag	UNP P04818
B	-6	HIS	-	expression tag	UNP P04818
B	-5	HIS	-	expression tag	UNP P04818
B	-4	HIS	-	expression tag	UNP P04818
B	-3	HIS	-	expression tag	UNP P04818
B	-2	HIS	-	expression tag	UNP P04818
B	-1	GLY	-	expression tag	UNP P04818

Continued on next page...

Continued from previous page...

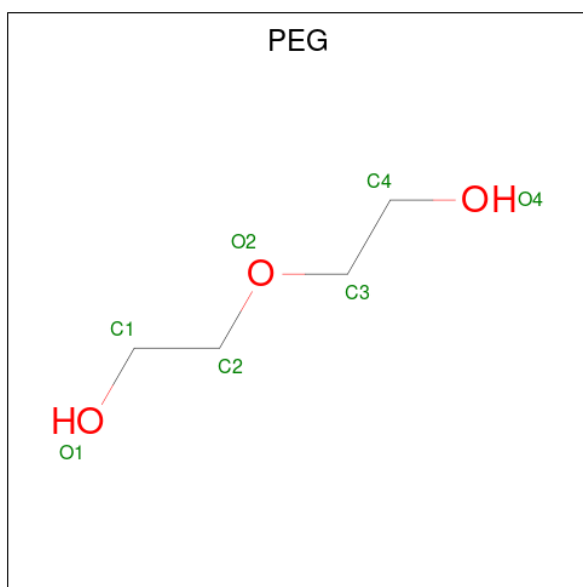
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP P04818
C	-11	MET	-	initiating methionine	UNP P04818
C	-10	ARG	-	expression tag	UNP P04818
C	-9	GLY	-	expression tag	UNP P04818
C	-8	SER	-	expression tag	UNP P04818
C	-7	HIS	-	expression tag	UNP P04818
C	-6	HIS	-	expression tag	UNP P04818
C	-5	HIS	-	expression tag	UNP P04818
C	-4	HIS	-	expression tag	UNP P04818
C	-3	HIS	-	expression tag	UNP P04818
C	-2	HIS	-	expression tag	UNP P04818
C	-1	GLY	-	expression tag	UNP P04818
C	0	SER	-	expression tag	UNP P04818

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (CCD ID: UMP) (formula: $C_9H_{13}N_2O_8P$).



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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).

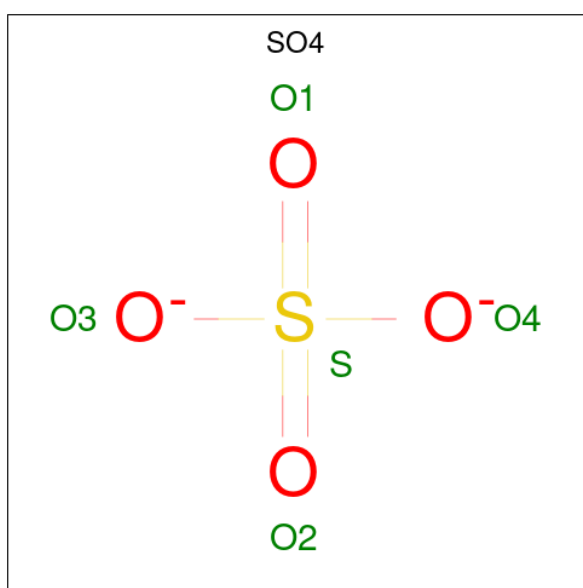


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

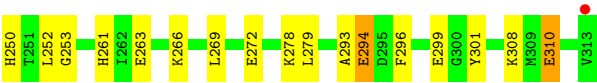
- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	66	Total	O	0	0
			66	66		
6	B	63	Total	O	0	0
			63	63		
6	C	76	Total	O	0	0
			76	76		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.11Å 61.59Å 101.10Å 90.00° 115.38° 90.00°	Depositor
Resolution (Å)	34.19 – 2.04 34.19 – 2.04	Depositor EDS
% Data completeness (in resolution range)	96.7 (34.19-2.04) 96.7 (34.19-2.04)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.187 , 0.237 0.185 , 0.236	Depositor DCC
R_{free} test set	4434 reflections (6.85%)	wwPDB-VP
Wilson B-factor (Å ²)	56.8	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.1	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	0.98	EDS
Total number of atoms	7082	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, SCH, PEG, CL, 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	0.75	0/2315	1.30	7/3141 (0.2%)
1	B	0.71	1/2318 (0.0%)	1.30	8/3143 (0.3%)
1	C	0.76	1/2324 (0.0%)	1.32	8/3150 (0.3%)
All	All	0.74	2/6957 (0.0%)	1.30	23/9434 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	261	HIS	CE1-NE2	10.73	1.43	1.32
1	B	196	HIS	CE1-NE2	5.69	1.38	1.32

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	272	GLU	CB-CA-C	8.05	118.97	109.47
1	A	196	HIS	CA-CB-CG	-6.71	107.09	113.80
1	B	247	ASP	CA-C-N	-6.67	113.91	122.77
1	B	247	ASP	C-N-CA	-6.67	113.91	122.77
1	A	91	PHE	CA-CB-CG	6.15	119.95	113.80
1	B	128	GLU	CB-CA-C	6.12	120.11	109.65
1	C	294	GLU	CB-CG-CD	-6.08	102.26	112.60
1	C	263	GLU	CB-CG-CD	6.06	122.90	112.60
1	A	69	ASP	CA-CB-CG	-5.96	106.64	112.60
1	B	205	ASN	CB-CA-C	-5.86	103.15	111.95
1	C	293	ALA	CA-C-N	-5.63	113.64	122.65
1	C	293	ALA	C-N-CA	-5.63	113.64	122.65
1	B	58	VAL	CA-C-N	-5.56	115.37	122.77
1	B	58	VAL	C-N-CA	-5.56	115.37	122.77
1	B	196	HIS	CA-CB-CG	-5.54	108.25	113.80
1	C	278	LYS	CB-CA-C	5.43	118.68	109.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	ILE	CA-C-N	-5.41	113.97	122.73
1	A	298	ILE	C-N-CA	-5.41	113.97	122.73
1	A	170	THR	CB-CA-C	5.24	117.46	109.34
1	C	47	LYS	CB-CA-C	5.23	118.81	109.65
1	C	53	THR	CA-CB-OG1	-5.23	101.75	109.60
1	A	186	ASP	CA-CB-CG	5.17	117.77	112.60
1	C	71	PHE	CB-CA-C	5.04	116.88	110.13

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2264	0	2155	25	0
1	B	2267	0	2184	31	0
1	C	2273	0	2165	29	0
2	A	20	0	11	2	0
2	B	20	0	11	1	0
2	C	20	0	11	0	0
3	A	7	0	10	0	0
4	A	1	0	0	0	0
5	C	5	0	0	0	0
6	A	66	0	0	0	0
6	B	63	0	0	0	0
6	C	76	0	0	2	0
All	All	7082	0	6547	80	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (80) 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:C:250:HIS:CE1	1:C:252:LEU:HD21	2.03	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ASP:O	1:A:170:THR:HG23	1.82	0.80
1:A:70:GLU:OE2	1:A:276:PHE:HD2	1.79	0.66
1:B:196:HIS:HB3	1:B:212:LEU:HD11	1.77	0.65
1:A:195:CYS:SG	2:A:401:UMP:C6	2.91	0.64
1:B:147:ARG:NH2	1:B:151:SER:HB3	2.14	0.62
1:C:160:GLN:HB3	1:C:179:MET:HG3	1.82	0.62
1:A:198:LEU:HD23	1:B:198:LEU:HD23	1.82	0.61
1:C:236:MET:HE2	1:C:296:PHE:CZ	2.36	0.61
1:C:214:GLN:HB3	1:C:252:LEU:HD23	1.83	0.60
1:A:166:ASP:O	1:A:170:THR:CG2	2.50	0.59
1:B:147:ARG:NH1	1:B:156:GLN:OE1	2.35	0.59
1:B:126:ARG:HD3	1:B:130:ASP:HB3	1.86	0.58
1:C:38:GLN:HE21	1:C:269:LEU:HD22	1.71	0.56
1:C:250:HIS:NE2	1:C:252:LEU:HD21	2.20	0.55
1:A:236:MET:HE2	1:A:296:PHE:CZ	2.42	0.54
1:C:59:PHE:HA	1:C:253:GLY:O	2.07	0.54
1:B:86:GLU:HG2	1:B:104:LYS:HB3	1.90	0.54
1:C:266:LYS:HE2	6:C:566:HOH:O	2.07	0.53
1:B:271:ARG:HH11	1:B:304:HIS:HB2	1.75	0.52
1:C:198:LEU:C	1:C:198:LEU:HD12	2.35	0.51
1:A:195:CYS:SG	2:A:401:UMP:C5	3.03	0.51
1:B:279:LEU:HD13	1:B:298:ILE:CD1	2.40	0.51
1:A:204:VAL:HG21	1:B:45:VAL:CG2	2.42	0.49
1:B:147:ARG:HH21	1:B:151:SER:HB3	1.76	0.49
1:B:86:GLU:OE2	1:B:86:GLU:HA	2.12	0.49
1:C:141:HIS:O	1:C:142:PHE:C	2.56	0.49
1:B:196:HIS:HB3	1:B:212:LEU:CD1	2.43	0.49
1:B:99:LYS:HE3	1:B:128:GLU:HG3	1.94	0.48
1:C:34:LEU:HD22	1:C:269:LEU:HD23	1.93	0.48
1:C:126:ARG:HG2	1:C:130:ASP:HB3	1.96	0.48
1:C:301:TYR:HA	6:C:516:HOH:O	2.14	0.48
1:B:86:GLU:CG	1:B:104:LYS:HB3	2.44	0.47
1:C:186:ASP:O	1:C:187:LEU:C	2.57	0.47
1:A:167:THR:HG21	1:A:177:ILE:HG12	1.97	0.47
1:C:151:SER:HB2	1:C:153:TYR:CZ	2.50	0.47
1:B:118:LEU:HD13	1:B:126:ARG:HB3	1.97	0.46
1:A:187:LEU:N	1:A:188:PRO:CD	2.79	0.46
1:C:90:TRP:HA	1:C:93:LYS:HD3	1.98	0.46
1:B:69:ASP:OD1	1:B:278:LYS:HE3	2.16	0.45
1:C:223:VAL:HG13	1:C:250:HIS:CE1	2.51	0.45
1:C:207:GLU:HA	1:C:244:LYS:O	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:LEU:HD11	1:A:236:MET:HE3	1.99	0.45
1:B:274:ARG:HD3	1:B:302:ASN:O	2.16	0.45
1:B:85:LEU:HD21	1:B:293:ALA:HA	1.99	0.45
1:C:140:ARG:NH2	1:C:159:ASP:OD2	2.43	0.44
1:A:126:ARG:HG2	1:A:130:ASP:HB3	2.00	0.44
1:C:34:LEU:HD11	1:C:76:THR:HG21	2.00	0.43
1:C:308:LYS:HD3	1:C:310:GLU:OE1	2.18	0.43
1:A:153:TYR:O	1:A:154:SER:C	2.61	0.43
1:B:279:LEU:HD13	1:B:298:ILE:HD11	2.00	0.43
1:C:235:TYR:CD2	1:C:279:LEU:HD23	2.53	0.43
1:B:195:CYS:SG	2:B:401:UMP:C6	3.11	0.43
1:A:182:TRP:CZ2	1:A:187:LEU:HD11	2.54	0.43
1:B:88:LEU:HD23	1:B:232:LEU:HG	2.01	0.43
1:A:176:ARG:HG3	1:B:215:ARG:NH1	2.34	0.42
1:A:202:TYR:CE1	1:B:47:LYS:HE3	2.54	0.42
1:C:212:LEU:HD22	1:C:230:TYR:CD1	2.53	0.42
1:C:38:GLN:NE2	1:C:269:LEU:HD22	2.34	0.42
1:B:279:LEU:CD1	1:B:298:ILE:HD13	2.50	0.42
1:A:86:GLU:HB2	1:A:106:VAL:HG21	2.01	0.42
1:A:152:ASP:OD1	1:A:152:ASP:C	2.62	0.42
1:B:279:LEU:HD13	1:B:298:ILE:HD13	2.01	0.42
1:A:130:ASP:OD1	1:A:146:TYR:OH	2.34	0.42
1:B:71:PHE:CD1	1:B:71:PHE:C	2.97	0.42
1:A:44:GLY:HA2	1:A:58:VAL:HG23	2.02	0.42
1:A:167:THR:CG2	1:A:177:ILE:HG12	2.50	0.42
1:C:199:CYS:HA	1:C:211:GLN:O	2.18	0.42
1:B:254:ASP:C	1:B:254:ASP:OD1	2.62	0.41
1:B:274:ARG:O	1:B:275:PRO:C	2.63	0.41
1:A:204:VAL:HG21	1:B:45:VAL:HG23	2.02	0.41
1:B:212:LEU:HD22	1:B:230:TYR:CD1	2.54	0.41
1:C:26:PRO:HA	1:C:27:PRO:HD3	1.85	0.41
1:C:269:LEU:HD23	1:C:269:LEU:HA	1.91	0.41
1:A:71:PHE:CD1	1:A:71:PHE:C	2.99	0.41
1:B:118:LEU:HD23	1:B:118:LEU:HA	1.92	0.41
1:A:272:GLU:O	1:A:273:PRO:C	2.64	0.40
1:C:140:ARG:HH21	1:C:159:ASP:CG	2.26	0.40
1:A:145:GLU:OE1	1:A:185:ARG:NH1	2.54	0.40
1:C:203:VAL:HA	1:C:207:GLU:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	284/325 (87%)	276 (97%)	8 (3%)	0	100	100
1	B	284/325 (87%)	271 (95%)	13 (5%)	0	100	100
1	C	285/325 (88%)	269 (94%)	15 (5%)	1 (0%)	30	22
All	All	853/975 (88%)	816 (96%)	36 (4%)	1 (0%)	48	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	134	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	231/280 (82%)	216 (94%)	15 (6%)	15	9
1	B	233/280 (83%)	219 (94%)	14 (6%)	17	10
1	C	231/280 (82%)	216 (94%)	15 (6%)	15	9
All	All	695/840 (83%)	651 (94%)	44 (6%)	16	9

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	49	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	69	ASP
1	A	96	THR
1	A	100	GLU
1	A	170	THR
1	A	176	ARG
1	A	185	ARG
1	A	221	LEU
1	A	229	SER
1	A	240	ILE
1	A	288	ILE
1	A	306	THR
1	A	309	MET
1	A	311	MET
1	B	49	ASP
1	B	69	ASP
1	B	86	GLU
1	B	150	GLU
1	B	164	VAL
1	B	176	ARG
1	B	198	LEU
1	B	221	LEU
1	B	272	GLU
1	B	286	GLU
1	B	288	ILE
1	B	289	ASP
1	B	306	THR
1	B	311	MET
1	C	38	GLN
1	C	49	ASP
1	C	56	LEU
1	C	69	ASP
1	C	74	LEU
1	C	126	ARG
1	C	150	GLU
1	C	164	VAL
1	C	176	ARG
1	C	204	VAL
1	C	221	LEU
1	C	272	GLU
1	C	294	GLU
1	C	299	GLU
1	C	310	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	141	HIS
1	A	302	ASN
1	B	268	GLN
1	C	38	GLN
1	C	171	ASN
1	C	196	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	$\# Z > 2$
1	SCH	C	43	1	6,7,8	0.55	0	4,7,9	0.33	0
1	SCH	A	43	1	6,7,8	0.55	0	4,7,9	0.66	0
1	SCH	B	43	1	6,7,8	0.62	0	4,7,9	0.65	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
1	SCH	C	43	1	-	0/2/6/8	-
1	SCH	A	43	1	-	0/2/6/8	-
1	SCH	B	43	1	-	0/2/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	UMP	C	401	-	21,21,21	0.55	0	30,31,31	0.60	0
3	PEG	A	402	-	6,6,6	0.12	0	5,5,5	0.18	0
5	SO4	C	402	-	4,4,4	0.32	0	6,6,6	0.07	0
2	UMP	B	401	-	21,21,21	0.40	0	30,31,31	0.65	0
2	UMP	A	401	-	21,21,21	0.52	0	30,31,31	0.64	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
2	UMP	B	401	-	-	2/10/22/22	0/2/2/2
2	UMP	C	401	-	-	1/10/22/22	0/2/2/2
2	UMP	A	401	-	-	4/10/22/22	0/2/2/2
3	PEG	A	402	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

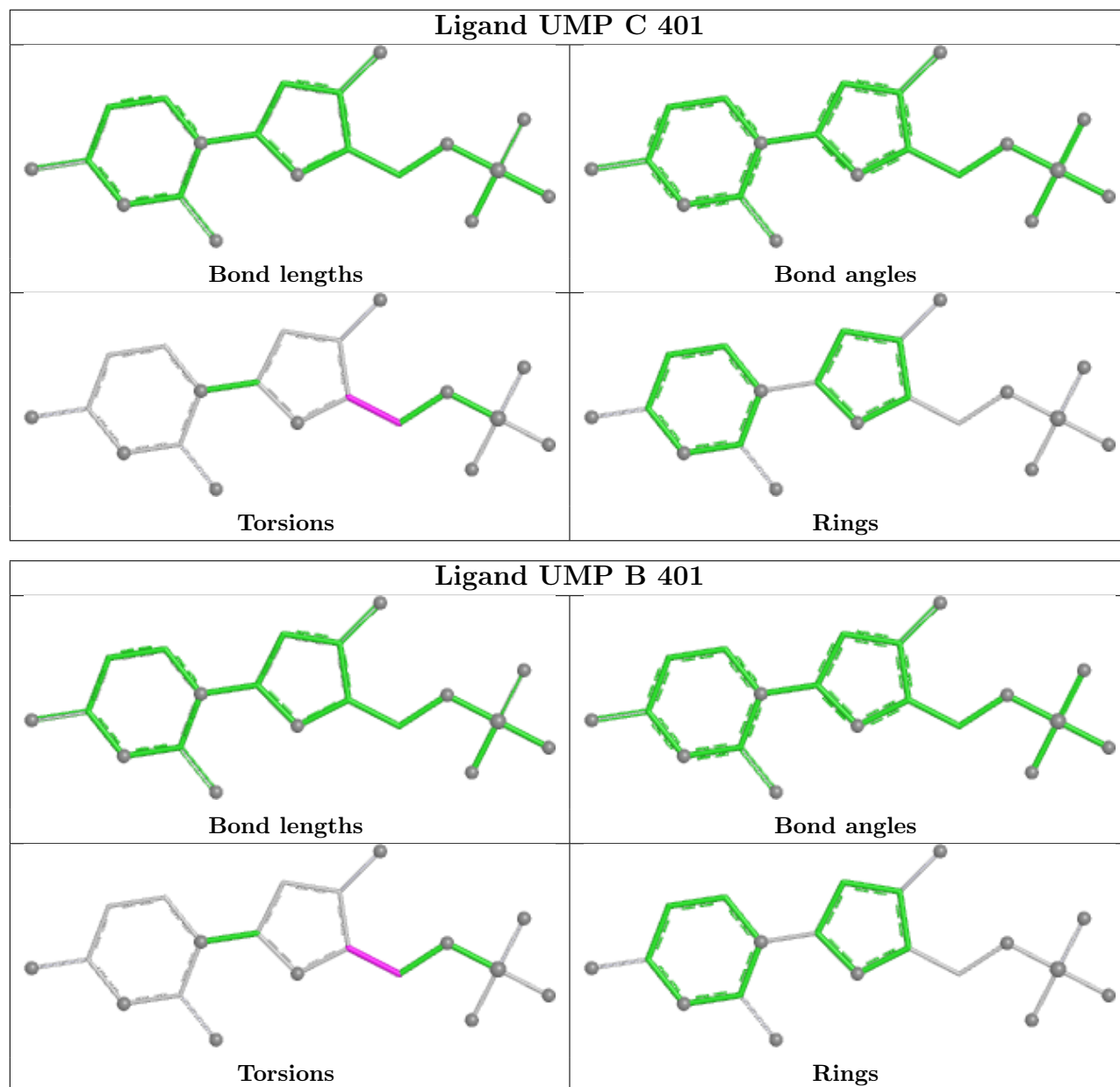
Mol	Chain	Res	Type	Atoms
3	A	402	PEG	O2-C3-C4-O4
2	B	401	UMP	O4'-C4'-C5'-O5'
2	B	401	UMP	C3'-C4'-C5'-O5'
3	A	402	PEG	O1-C1-C2-O2
2	A	401	UMP	O4'-C4'-C5'-O5'
2	A	401	UMP	C5'-O5'-P-OP3
2	C	401	UMP	O4'-C4'-C5'-O5'
2	A	401	UMP	C3'-C4'-C5'-O5'
2	A	401	UMP	C4'-C5'-O5'-P

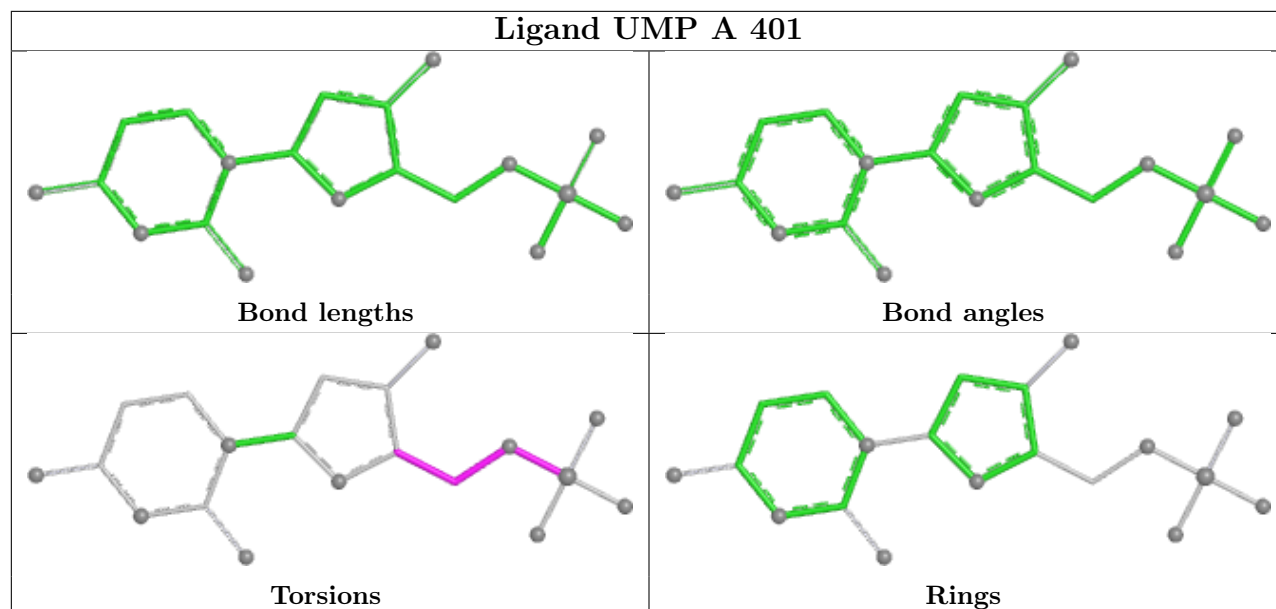
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	UMP	1	0
2	A	401	UMP	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 [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	286/325 (88%)	-0.12	1 (0%) 90 92	47, 69, 91, 104	0
1	B	286/325 (88%)	-0.11	1 (0%) 90 92	45, 72, 93, 103	2 (0%)
1	C	287/325 (88%)	-0.11	3 (1%) 79 81	53, 69, 88, 126	1 (0%)
All	All	859/975 (88%)	-0.11	5 (0%) 85 87	45, 69, 92, 126	3 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	312	ALA	5.0
1	A	96	THR	2.3
1	C	313	VAL	2.3
1	C	163	ARG	2.3
1	C	113	GLY	2.1

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
1	SCH	A	43	8/9	0.89	0.11	74,78,99,101	2
1	SCH	C	43	8/9	0.89	0.08	68,74,101,112	0
1	SCH	B	43	8/9	0.90	0.08	70,76,102,106	0

6.3 Carbohydrates [i](#)

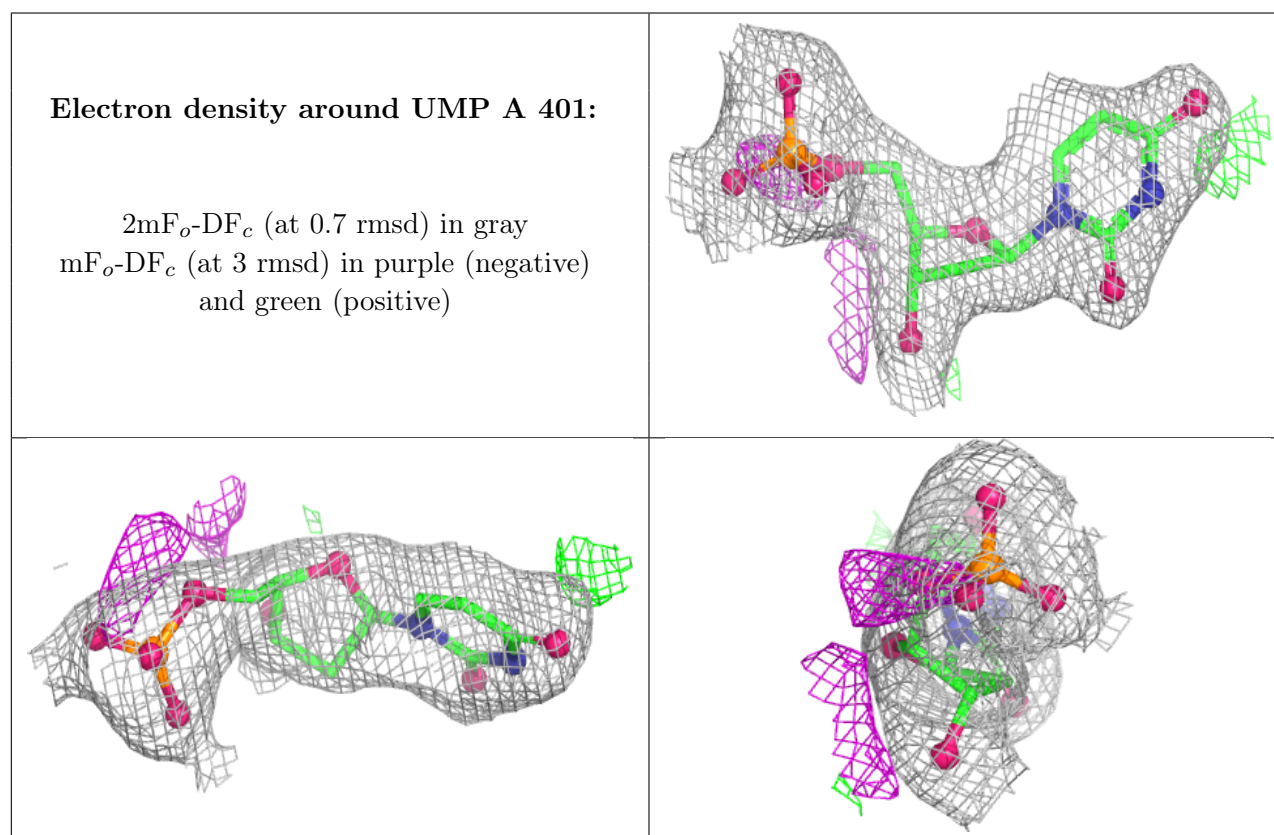
There are no oligosaccharides in this entry.

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.

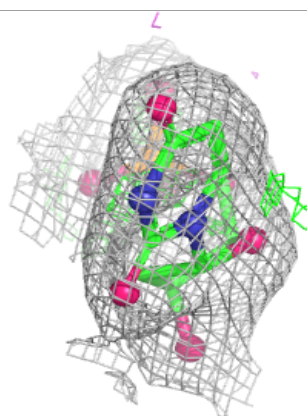
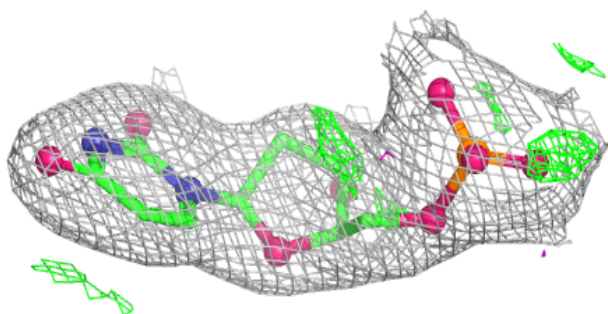
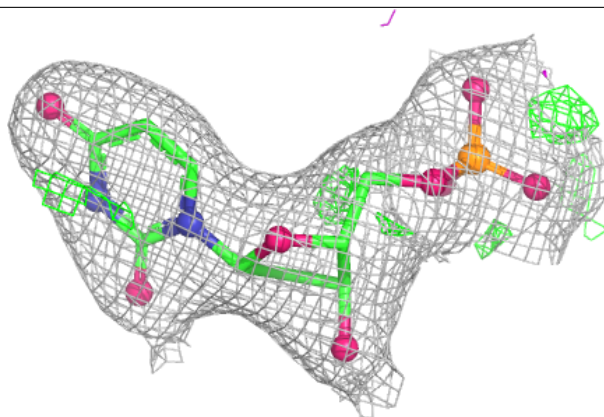
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PEG	A	402	7/7	0.81	0.21	91,97,107,110	0
5	SO4	C	402	5/5	0.92	0.07	91,94,97,100	0
4	CL	A	403	1/1	0.93	0.09	69,69,69,69	0
2	UMP	A	401	20/20	0.95	0.07	53,64,71,74	0
2	UMP	C	401	20/20	0.96	0.06	52,59,67,74	0
2	UMP	B	401	20/20	0.96	0.06	51,62,69,75	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.

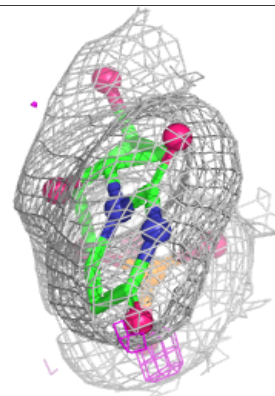
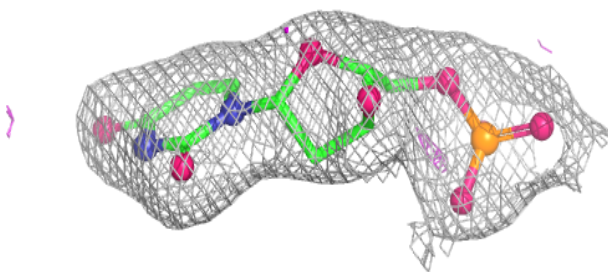
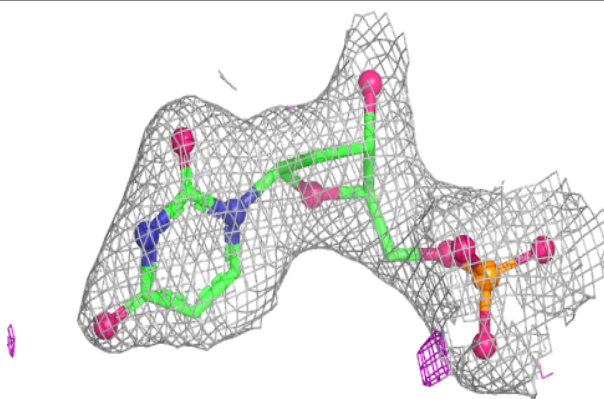


Electron density around UMP C 401:

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

**Electron density around UMP B 401:**

$2mF_o-DF_c$ (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.