



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 11:28 AM UTC

PDB ID : 1RXC / pdb_00001rxc
Title : E. COLI uridine phosphorylase: 5-fluorouracil ribose-1-phosphate complex
Authors : Caradoc-Davies, T.T.; Cutfield, S.M.; Lamont, I.L.; Cutfield, J.F.
Deposited on : 2003-12-18
Resolution : 2.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

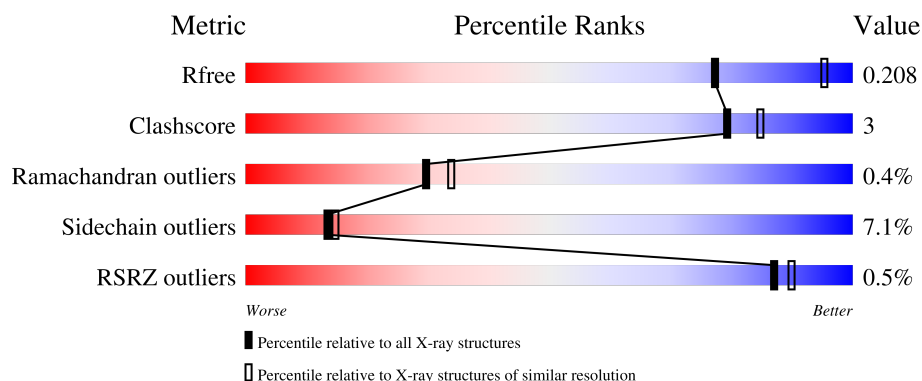
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	253	0% 86% 11% .
1	B	253	87% 12% .
1	C	253	2% 84% 12% . .
1	D	253	86% 11% ..
1	E	253	2% 90% 8% ..

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Mol	Chain	Length	Quality of chain
1	F	253	 % 87% 11% .
1	G	253	 83% 13% .
1	H	253	 81% 13% 5%
1	I	253	 88% 10% ..
1	J	253	 87% 10% ..
1	K	253	 81% 15% .
1	L	253	 87% 10% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	URF	B	2011	-	X	-	-
4	URF	C	2081	-	X	-	-
4	URF	D	2021	-	X	-	-
4	URF	E	2031	-	X	-	-
4	URF	F	2001	-	X	-	-
4	URF	I	2041	-	X	-	-
4	URF	K	2061	-	X	-	-
4	URF	L	2071	-	X	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 23681 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 Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	0	0
			1847	1158	323	356	10			
1	B	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	C	246	Total	C	N	O	S	0	0	0
			1851	1162	323	355	11			
1	D	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	E	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	F	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	G	245	Total	C	N	O	S	0	0	0
			1839	1153	321	354	11			
1	H	240	Total	C	N	O	S	0	0	0
			1801	1130	315	346	10			
1	I	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	J	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			
1	K	243	Total	C	N	O	S	0	0	0
			1822	1144	319	349	10			
1	L	250	Total	C	N	O	S	0	0	0
			1880	1178	328	363	11			

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

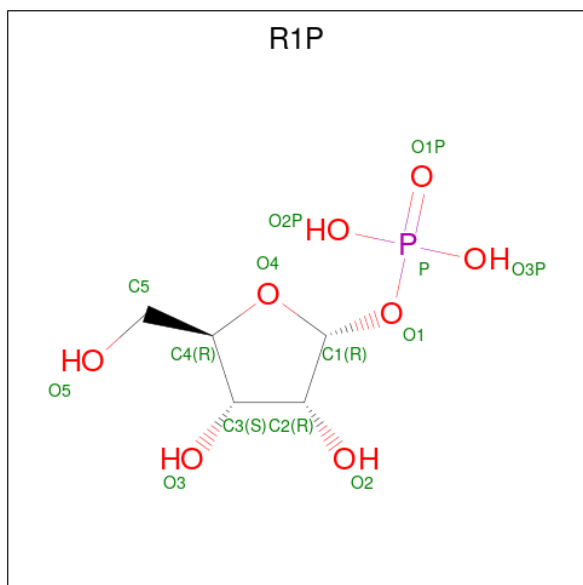
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		
2	C	1	Total	K	0	0
			1	1		

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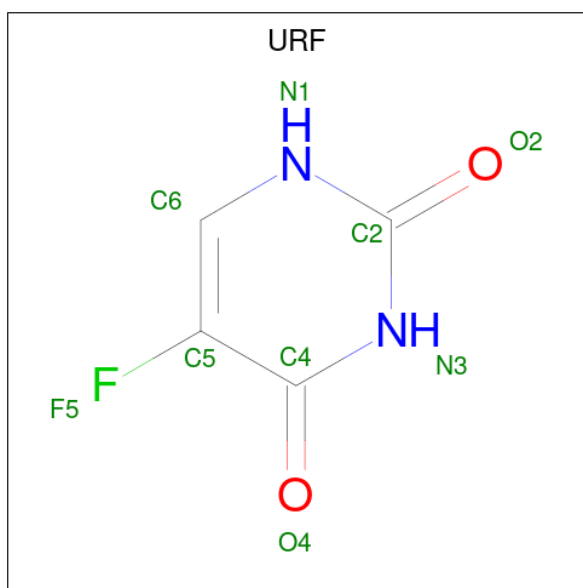
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	1	Total K 1 1	0	0
2	I	1	Total K 1 1	0	0
2	K	1	Total K 1 1	0	0

- Molecule 3 is 1-O-phosphono-alpha-D-ribofuranose (CCD ID: R1P) (formula: $C_5H_{11}O_8P$).



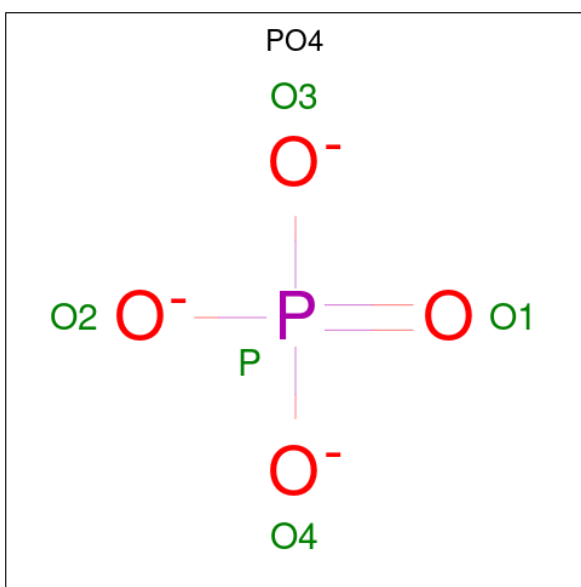
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O P 14 5 8 1	0	0
3	C	1	Total C O P 14 5 8 1	0	0
3	D	1	Total C O P 14 5 8 1	0	0
3	E	1	Total C O P 14 5 8 1	0	0
3	F	1	Total C O P 14 5 8 1	0	0
3	I	1	Total C O P 14 5 8 1	0	0
3	K	1	Total C O P 14 5 8 1	0	0
3	L	1	Total C O P 14 5 8 1	0	0

- Molecule 4 is 5-FLUOROURACIL (CCD ID: URF) (formula: $C_4H_3FN_2O_2$).



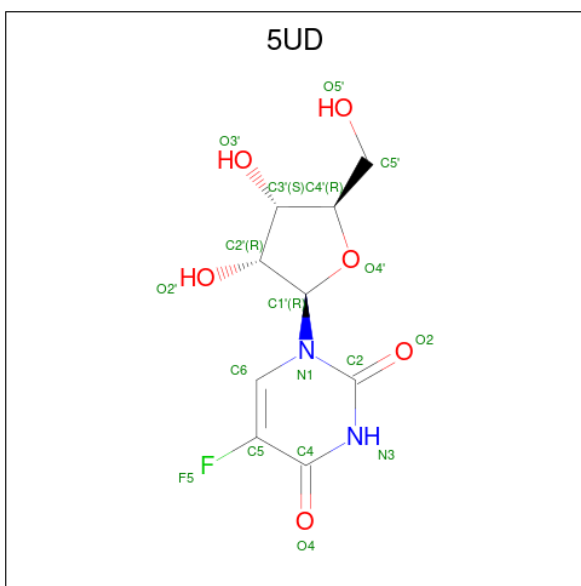
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	C	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	D	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	E	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	F	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	I	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	K	1	Total	C	F	N	O	0	0
			9	4	1	2	2		
4	L	1	Total	C	F	N	O	0	0
			9	4	1	2	2		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	J	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is 5-FLUOROURIDINE (CCD ID: 5UD) (formula: $C_9H_{11}FN_2O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	J	1	Total	C	F	N	O	0	0
			18	9	1	2	6		

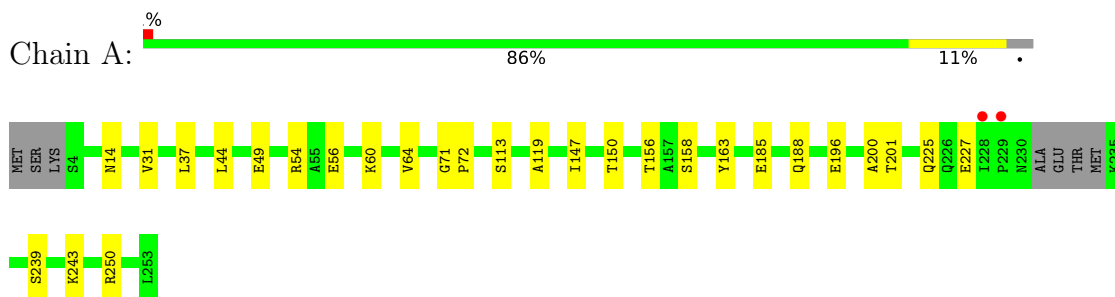
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	90	Total 90	O 90	0	0
7	B	101	Total 101	O 101	0	0
7	C	85	Total 85	O 85	0	0
7	D	88	Total 88	O 88	0	0
7	E	98	Total 98	O 98	0	0
7	F	96	Total 96	O 96	0	0
7	G	89	Total 89	O 89	0	0
7	H	113	Total 113	O 113	0	0
7	I	95	Total 95	O 95	0	0
7	J	120	Total 120	O 120	0	0
7	K	90	Total 90	O 90	0	0
7	L	84	Total 84	O 84	0	0

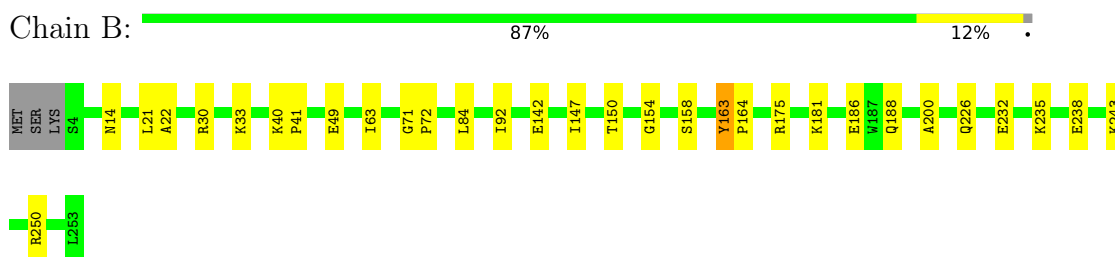
3 Residue-property plots [i](#)

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.

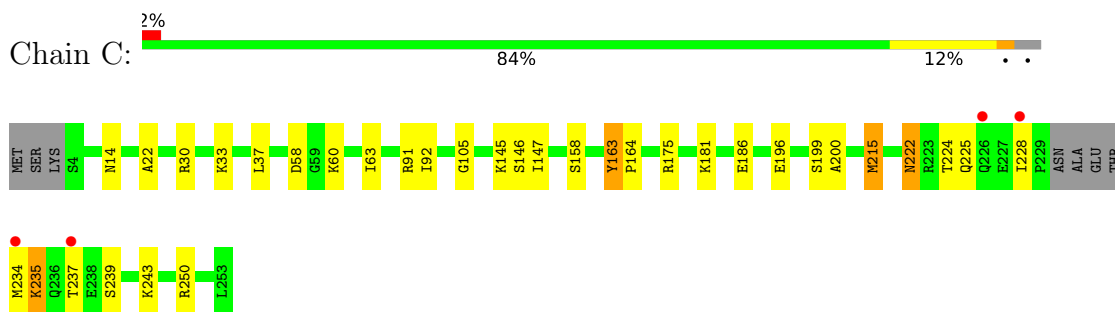
- Molecule 1: Uridine phosphorylase



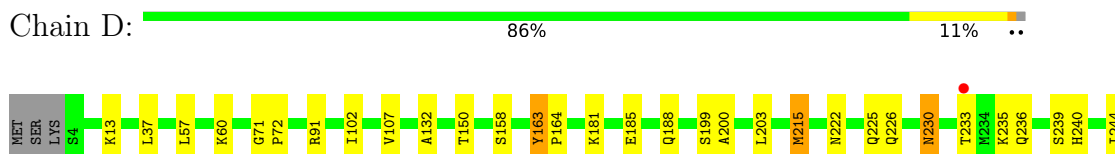
- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase

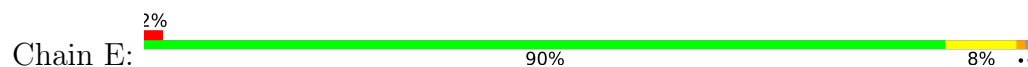


- Molecule 1: Uridine phosphorylase

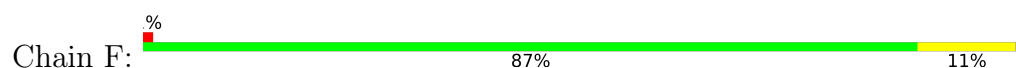




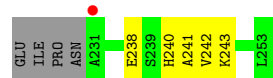
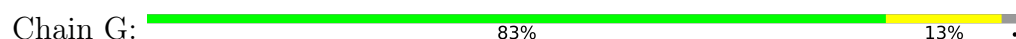
- Molecule 1: Uridine phosphorylase



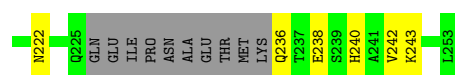
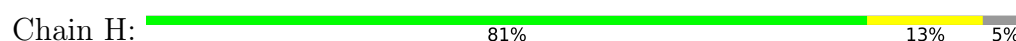
- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase

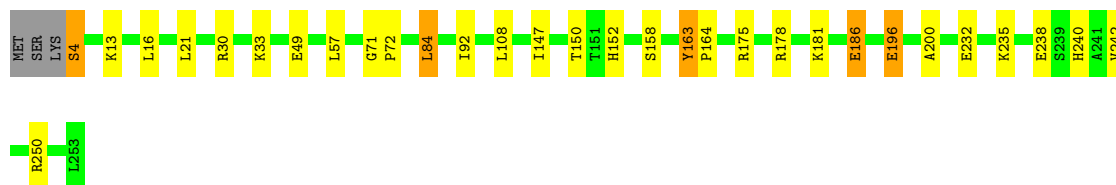


- Molecule 1: Uridine phosphorylase



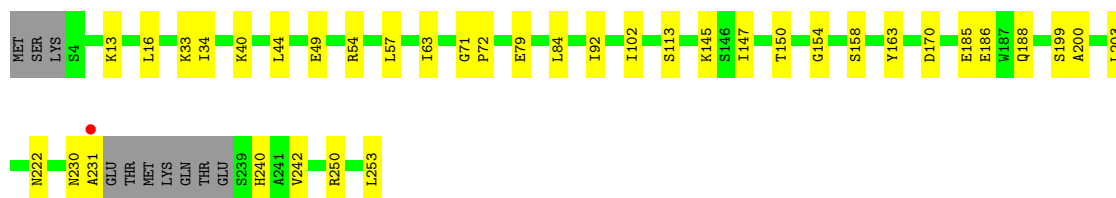
- Molecule 1: Uridine phosphorylase

Chain J:  87% 10% ..



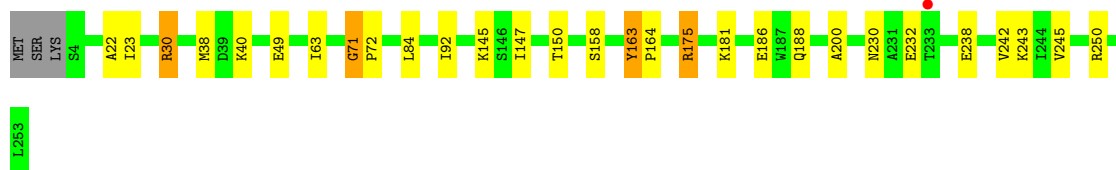
- Molecule 1: Uridine phosphorylase

Chain K:  81% 15% .



- Molecule 1: Uridine phosphorylase

Chain L:  87% 10% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.19Å 191.70Å 91.91Å 90.00° 118.50° 90.00°	Depositor
Resolution (Å)	16.93 – 2.35 16.93 – 2.35	Depositor EDS
% Data completeness (in resolution range)	92.7 (16.93-2.35) 92.5 (16.93-2.35)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 2.35Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.150 , 0.203 0.161 , 0.208	Depositor DCC
R_{free} test set	5294 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.002 for -h-l,k,h 0.002 for l,k,-h-l 0.015 for h,-k,-h-l 0.018 for -h-l,-k,l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23681	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: R1P, K, URF, PO4, 5UD

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	0.61	0/1878	0.86	0/2549
1	B	0.61	0/1912	0.87	1/2595 (0.0%)
1	C	0.59	0/1882	0.84	0/2552
1	D	0.61	0/1912	0.84	0/2595
1	E	0.62	0/1912	0.84	1/2595 (0.0%)
1	F	0.60	0/1912	0.84	1/2595 (0.0%)
1	G	0.59	0/1869	0.84	0/2534
1	H	0.60	0/1831	0.85	0/2484
1	I	0.61	0/1912	0.87	0/2595
1	J	0.62	0/1912	0.88	0/2595
1	K	0.62	0/1853	0.88	1/2515 (0.0%)
1	L	0.59	0/1912	0.86	2/2595 (0.1%)
All	All	0.60	0/22697	0.86	6/30799 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	232	GLU	N-CA-C	5.37	117.14	111.28
1	K	154	GLY	N-CA-C	5.34	117.40	110.45
1	L	71	GLY	O-C-N	5.25	122.96	121.07
1	B	154	GLY	N-CA-C	5.22	117.63	110.69
1	F	194	ASN	N-CA-C	5.12	116.08	108.60

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	1847	0	1845	8	0
1	B	1880	0	1884	9	0
1	C	1851	0	1859	12	0
1	D	1880	0	1884	13	0
1	E	1880	0	1884	6	0
1	F	1880	0	1884	9	0
1	G	1839	0	1846	9	0
1	H	1801	0	1806	13	0
1	I	1880	0	1884	12	0
1	J	1880	0	1884	12	0
1	K	1822	0	1827	14	0
1	L	1880	0	1884	10	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	E	1	0	0	0	0
2	I	1	0	0	0	0
2	K	1	0	0	0	0
3	B	14	0	0	0	0
3	C	14	0	0	0	0
3	D	14	0	0	0	0
3	E	14	0	0	0	0
3	F	14	0	0	0	0
3	I	14	0	0	0	0
3	K	14	0	0	0	0
3	L	14	0	0	0	0
4	B	9	0	3	0	0
4	C	9	0	3	0	0
4	D	9	0	3	0	0
4	E	9	0	3	0	0
4	F	9	0	3	0	0
4	I	9	0	3	0	0
4	K	9	0	3	0	0
4	L	9	0	3	0	0
5	J	5	0	0	0	0
6	J	18	0	10	0	0
7	A	90	0	0	0	0
7	B	101	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	85	0	0	0	0
7	D	88	0	0	0	0
7	E	98	0	0	0	0
7	F	96	0	0	1	0
7	G	89	0	0	2	0
7	H	113	0	0	2	0
7	I	95	0	0	2	0
7	J	120	0	0	3	0
7	K	90	0	0	1	0
7	L	84	0	0	0	0
All	All	23681	0	22405	121	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 3.

The worst 5 of 121 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:G:185:GLU:HA	1:G:188:GLN:HE21	1.50	0.76
1:C:58:ASP:OD2	1:C:250:ARG:HD3	1.87	0.73
7:G:310:HOH:O	1:I:186:GLU:HG3	1.92	0.68
1:G:152:HIS:HD2	7:G:335:HOH:O	1.80	0.65
1:K:170:ASP:HB2	7:K:1147:HOH:O	1.99	0.63

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	242/253 (96%)	239 (99%)	2 (1%)	1 (0%)	30 34
1	B	248/253 (98%)	242 (98%)	5 (2%)	1 (0%)	30 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	242/253 (96%)	232 (96%)	9 (4%)	1 (0%)	30	34
1	D	248/253 (98%)	241 (97%)	6 (2%)	1 (0%)	30	34
1	E	248/253 (98%)	242 (98%)	5 (2%)	1 (0%)	30	34
1	F	248/253 (98%)	244 (98%)	3 (1%)	1 (0%)	30	34
1	G	241/253 (95%)	235 (98%)	5 (2%)	1 (0%)	30	34
1	H	236/253 (93%)	234 (99%)	1 (0%)	1 (0%)	30	34
1	I	248/253 (98%)	245 (99%)	2 (1%)	1 (0%)	30	34
1	J	248/253 (98%)	245 (99%)	2 (1%)	1 (0%)	30	34
1	K	239/253 (94%)	233 (98%)	5 (2%)	1 (0%)	30	34
1	L	248/253 (98%)	245 (99%)	2 (1%)	1 (0%)	30	34
All	All	2936/3036 (97%)	2877 (98%)	47 (2%)	12 (0%)	30	34

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	163	TYR
1	C	163	TYR
1	F	163	TYR
1	G	163	TYR
1	I	163	TYR

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	197/204 (97%)	185 (94%)	12 (6%)	17	20
1	B	201/204 (98%)	186 (92%)	15 (8%)	12	13
1	C	198/204 (97%)	177 (89%)	21 (11%)	6	6
1	D	201/204 (98%)	189 (94%)	12 (6%)	17	21
1	E	201/204 (98%)	189 (94%)	12 (6%)	17	21
1	F	201/204 (98%)	186 (92%)	15 (8%)	12	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	196/204 (96%)	179 (91%)	17 (9%)	9	10
1	H	192/204 (94%)	180 (94%)	12 (6%)	16	19
1	I	201/204 (98%)	191 (95%)	10 (5%)	22	27
1	J	201/204 (98%)	184 (92%)	17 (8%)	10	11
1	K	194/204 (95%)	183 (94%)	11 (6%)	18	23
1	L	201/204 (98%)	186 (92%)	15 (8%)	12	13
All	All	2384/2448 (97%)	2215 (93%)	169 (7%)	13	15

5 of 169 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	243	LYS
1	K	13	LYS
1	I	92	ILE
1	J	84	LEU
1	K	150	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	17	GLN
1	I	188	GLN
1	K	188	GLN
1	E	188	GLN
1	D	226	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 23 ligands modelled in this entry, 5 are monoatomic - leaving 18 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
4	URF	L	2071	-	9,9,9	2.35	3 (33%)	12,12,12	4.22	7 (58%)
3	R1P	D	2022	-	13,14,14	0.73	0	21,21,21	4.68	10 (47%)
3	R1P	K	2062	-	13,14,14	0.75	0	21,21,21	4.81	10 (47%)
3	R1P	L	2072	-	13,14,14	0.68	0	21,21,21	4.64	11 (52%)
4	URF	B	2011	-	9,9,9	2.36	3 (33%)	12,12,12	3.50	7 (58%)
4	URF	C	2081	-	9,9,9	2.74	3 (33%)	12,12,12	3.84	7 (58%)
3	R1P	I	2042	-	13,14,14	0.83	0	21,21,21	4.83	9 (42%)
4	URF	K	2061	-	9,9,9	2.39	3 (33%)	12,12,12	3.85	7 (58%)
3	R1P	C	2082	-	13,14,14	0.84	1 (7%)	21,21,21	5.11	10 (47%)
4	URF	F	2001	-	9,9,9	2.38	3 (33%)	12,12,12	3.98	7 (58%)
3	R1P	B	2012	-	13,14,14	0.65	0	21,21,21	4.84	11 (52%)
3	R1P	E	2032	-	13,14,14	0.67	0	21,21,21	5.03	12 (57%)
4	URF	D	2021	-	9,9,9	2.84	3 (33%)	12,12,12	3.96	7 (58%)
4	URF	I	2041	-	9,9,9	2.38	3 (33%)	12,12,12	4.16	8 (66%)
6	5UD	J	2051	-	19,19,19	1.98	3 (15%)	28,28,28	3.69	22 (78%)
5	PO4	J	2052	-	4,4,4	0.98	0	6,6,6	0.81	0
3	R1P	F	2002	-	13,14,14	0.74	0	21,21,21	5.00	9 (42%)
4	URF	E	2031	-	9,9,9	2.67	4 (44%)	12,12,12	3.77	7 (58%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	URF	L	2071	-	-	-	0/1/1/1
3	R1P	D	2022	-	-	0/6/23/23	0/1/1/1
3	R1P	K	2062	-	-	0/6/23/23	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	R1P	L	2072	-	-	0/6/23/23	0/1/1/1
4	URF	B	2011	-	-	-	0/1/1/1
4	URF	C	2081	-	-	-	0/1/1/1
3	R1P	I	2042	-	-	0/6/23/23	0/1/1/1
4	URF	K	2061	-	-	-	0/1/1/1
3	R1P	C	2082	-	-	0/6/23/23	0/1/1/1
4	URF	F	2001	-	-	-	0/1/1/1
3	R1P	B	2012	-	-	1/6/23/23	0/1/1/1
3	R1P	E	2032	-	-	0/6/23/23	0/1/1/1
4	URF	D	2021	-	-	-	0/1/1/1
4	URF	I	2041	-	-	-	0/1/1/1
6	5UD	J	2051	-	-	3/6/22/22	0/2/2/2
3	R1P	F	2002	-	-	1/6/23/23	0/1/1/1
4	URF	E	2031	-	-	-	0/1/1/1

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	2021	URF	C6-C5	6.90	1.39	1.33
4	C	2081	URF	C6-C5	6.59	1.39	1.33
6	J	2051	5UD	C6-C5	6.42	1.42	1.33
4	E	2031	URF	C6-C5	6.19	1.39	1.33
4	F	2001	URF	C6-C5	5.68	1.38	1.33

The worst 5 of 161 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2032	R1P	O4-C1-C2	-14.24	86.87	104.98
3	F	2002	R1P	O4-C1-C2	-14.13	87.01	104.98
3	C	2082	R1P	O4-C1-C2	-13.70	87.55	104.98
3	K	2062	R1P	O4-C1-C2	-13.06	88.36	104.98
3	B	2012	R1P	O4-C1-C2	-13.02	88.42	104.98

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	J	2051	5UD	C2'-C1'-N1-C6
6	J	2051	5UD	C2'-C1'-N1-C2
6	J	2051	5UD	C3'-C4'-C5'-O5'
3	F	2002	R1P	C3-C4-C5-O5

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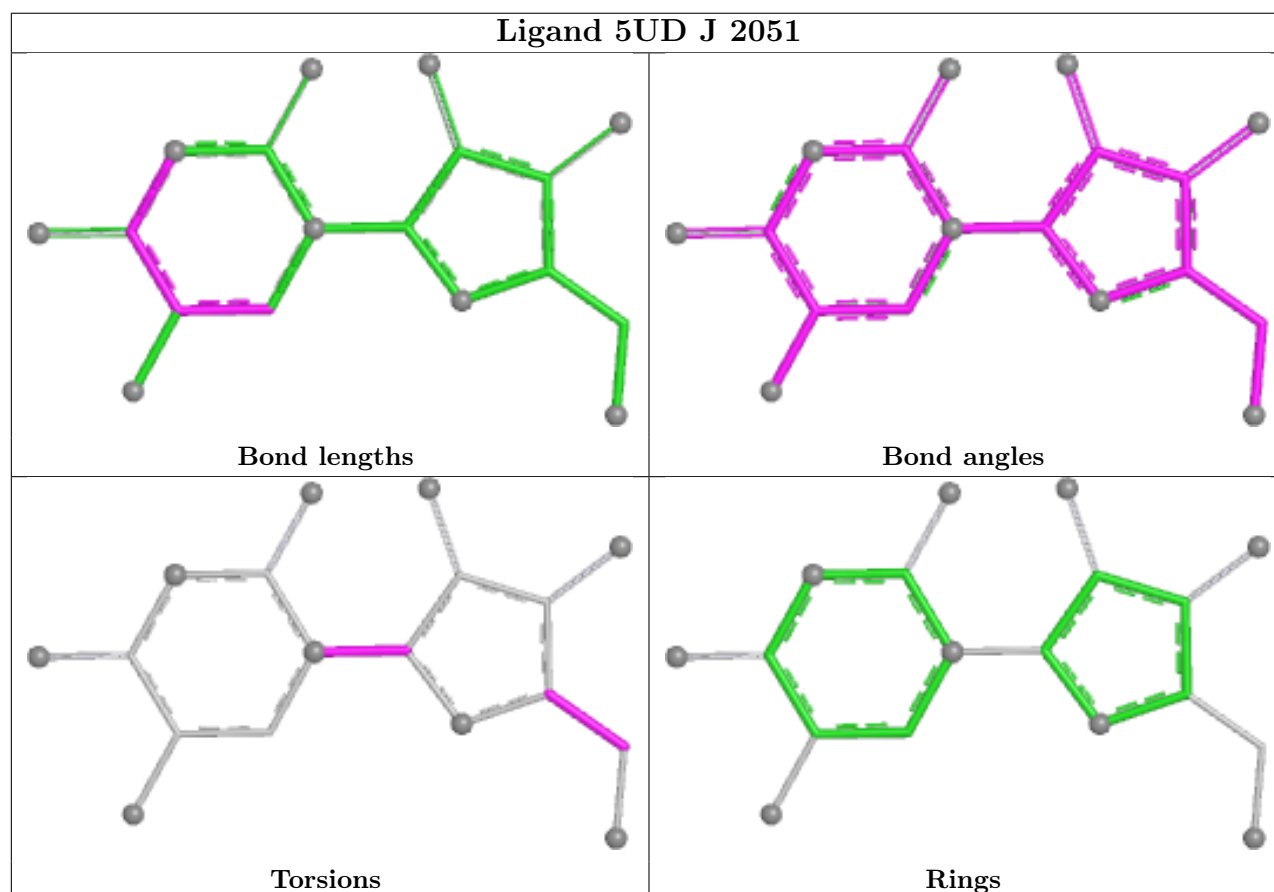
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Mol	Chain	Res	Type	Atoms
3	B	2012	R1P	C1-O1-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	246/253 (97%)	-0.40	2 (0%) 82 86	11, 19, 36, 63	0
1	B	250/253 (98%)	-0.56	0 100 100	10, 18, 29, 35	0
1	C	246/253 (97%)	-0.30	4 (1%) 70 76	11, 19, 38, 66	0
1	D	250/253 (98%)	-0.33	1 (0%) 88 91	11, 20, 44, 63	0
1	E	250/253 (98%)	-0.50	4 (1%) 70 76	11, 17, 32, 50	0
1	F	250/253 (98%)	-0.59	2 (0%) 82 86	10, 15, 31, 58	0
1	G	245/253 (96%)	-0.37	1 (0%) 88 91	15, 23, 35, 62	0
1	H	240/253 (94%)	-0.53	0 100 100	12, 19, 29, 42	0
1	I	250/253 (98%)	-0.49	0 100 100	10, 17, 31, 51	0
1	J	250/253 (98%)	-0.58	0 100 100	9, 15, 25, 41	0
1	K	243/253 (96%)	-0.58	1 (0%) 88 91	9, 16, 28, 39	0
1	L	250/253 (98%)	-0.39	1 (0%) 88 91	15, 21, 35, 54	0
All	All	2970/3036 (97%)	-0.47	16 (0%) 87 90	9, 19, 33, 66	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	228	ILE	3.1
1	C	234	MET	2.8
1	A	229	PRO	2.8
1	G	231	ALA	2.7
1	L	233	THR	2.6

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 ⓘ

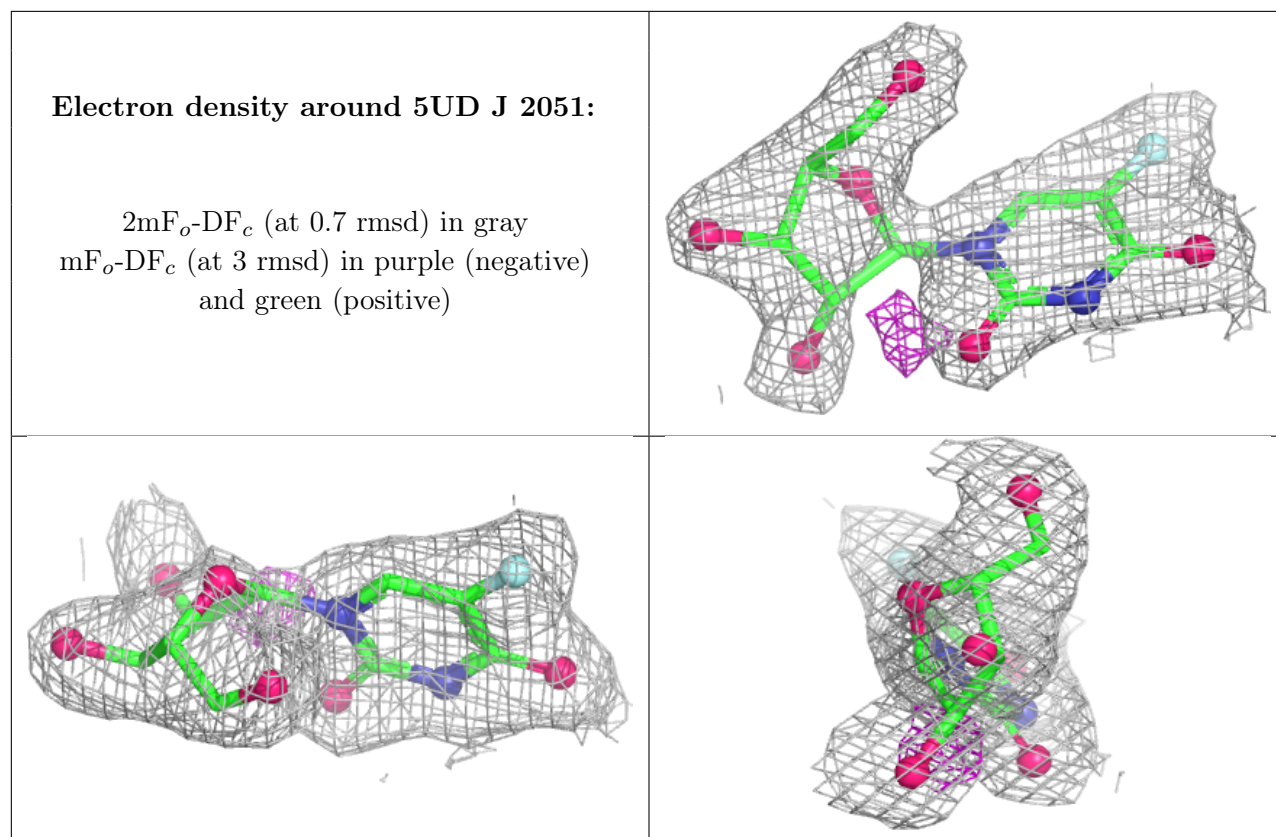
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	R1P	C	2082	14/14	0.80	0.15	42,44,50,50	2
3	R1P	D	2022	14/14	0.84	0.12	38,39,43,43	3
4	URF	C	2081	9/9	0.86	0.12	41,44,44,45	1
3	R1P	K	2062	14/14	0.87	0.12	31,32,39,40	2
3	R1P	E	2032	14/14	0.90	0.10	31,34,39,39	2
4	URF	D	2021	9/9	0.91	0.08	30,32,33,33	0
4	URF	L	2071	9/9	0.91	0.07	27,28,29,32	0
6	5UD	J	2051	18/18	0.91	0.09	29,31,33,35	2
4	URF	I	2041	9/9	0.92	0.06	19,20,21,22	0
3	R1P	F	2002	14/14	0.92	0.10	30,32,38,39	2
4	URF	B	2011	9/9	0.92	0.09	11,13,15,17	0
4	URF	K	2061	9/9	0.93	0.06	19,21,22,27	0
3	R1P	I	2042	14/14	0.93	0.10	27,29,33,33	2
3	R1P	L	2072	14/14	0.93	0.09	38,38,41,42	2
4	URF	E	2031	9/9	0.95	0.06	25,27,28,29	0
4	URF	F	2001	9/9	0.95	0.06	18,22,23,25	0
3	R1P	B	2012	14/14	0.95	0.09	26,29,30,30	2
5	PO4	J	2052	5/5	0.97	0.09	18,18,19,19	0
2	K	C	2102	1/1	0.97	0.10	21,21,21,21	0
2	K	E	2103	1/1	0.98	0.07	16,16,16,16	0
2	K	A	2101	1/1	0.99	0.09	20,20,20,20	0
2	K	I	2104	1/1	0.99	0.06	16,16,16,16	0
2	K	K	2105	1/1	0.99	0.07	17,17,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.