



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:07 PM UTC

PDB ID : 3C74 / pdb_00003c74
Title : X-ray structure of the uridine phosphorylase from salmonella typhimurium in complex with 2,2'-anhydrouridine at 2.38a resolution
Authors : Lashkov, A.A.; Mikhailov, A.M.
Deposited on : 2008-02-06
Resolution : 2.38 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
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

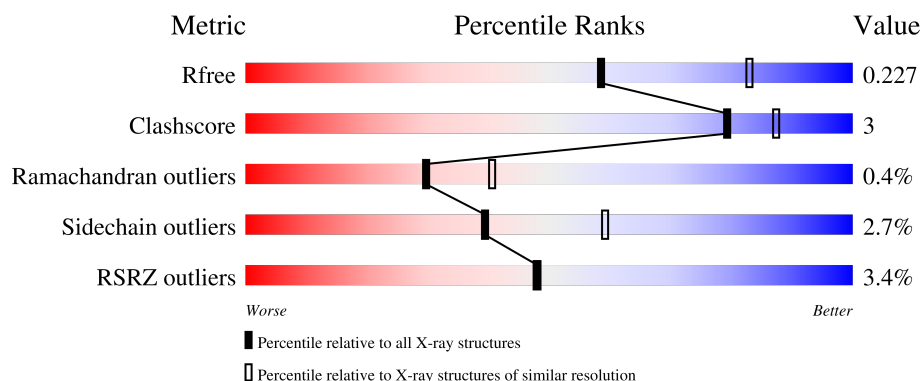
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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.



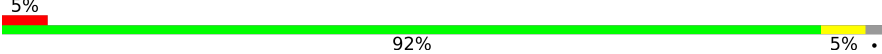
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	2% 91% 5%
1	B	253	4% 84% 10%
1	C	253	2% 85% 10%
1	D	253	3% 90% 8%
1	E	253	4% 88% 6% 5%

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Mol	Chain	Length	Quality of chain
1	F	253	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment at the beginning labeled '5%', a long green segment in the middle labeled '92%', and a yellow segment at the end labeled '5%'. A small grey dot is visible at the far right end of the bar.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11475 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.

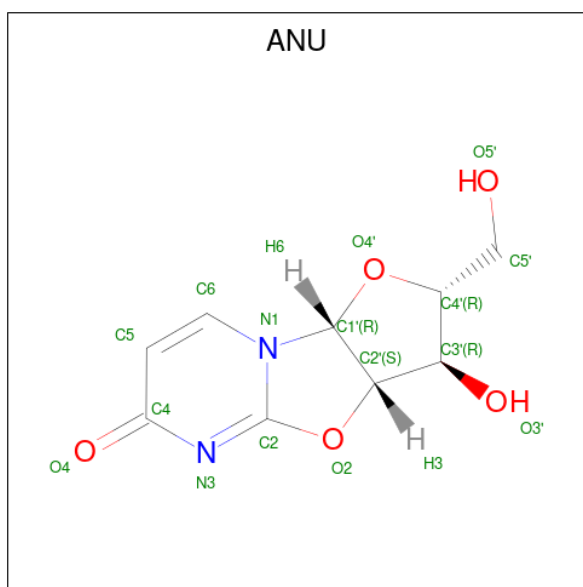
- Molecule 1 is a protein called Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1814	1138	319	346	11			
1	B	244	Total	C	N	O	S	0	0	0
			1827	1145	322	349	11			
1	C	243	Total	C	N	O	S	0	0	0
			1818	1140	321	346	11			
1	D	251	Total	C	N	O	S	0	0	0
			1885	1180	332	361	12			
1	E	241	Total	C	N	O	S	0	0	0
			1805	1133	318	343	11			
1	F	248	Total	C	N	O	S	0	0	0
			1856	1163	327	354	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1001	LYS	-	expression tag	UNP P0A1F6
B	2001	LYS	-	expression tag	UNP P0A1F6
C	3001	LYS	-	expression tag	UNP P0A1F6
D	4001	LYS	-	expression tag	UNP P0A1F6
E	5001	LYS	-	expression tag	UNP P0A1F6
F	6001	LYS	-	expression tag	UNP P0A1F6

- Molecule 2 is 2,2'-Anhydro-(1-beta-D-arabinofuranosyl)uracil (CCD ID: ANU) (formula: $C_9H_{10}N_2O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	9	2	5		
2	B	1	Total	C	N	O	0	0
			16	9	2	5		
2	C	1	Total	C	N	O	0	0
			16	9	2	5		
2	D	1	Total	C	N	O	0	0
			16	9	2	5		
2	E	1	Total	C	N	O	0	0
			16	9	2	5		
2	F	1	Total	C	N	O	0	0
			16	9	2	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total	O	0	0
			57	57		
3	B	48	Total	O	0	0
			48	48		
3	C	59	Total	O	0	0
			59	59		
3	D	82	Total	O	0	0
			82	82		
3	E	61	Total	O	0	0
			61	61		
3	F	67	Total	O	0	0
			67	67		

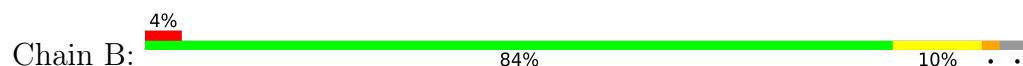
3 Residue-property plots [i](#)

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.

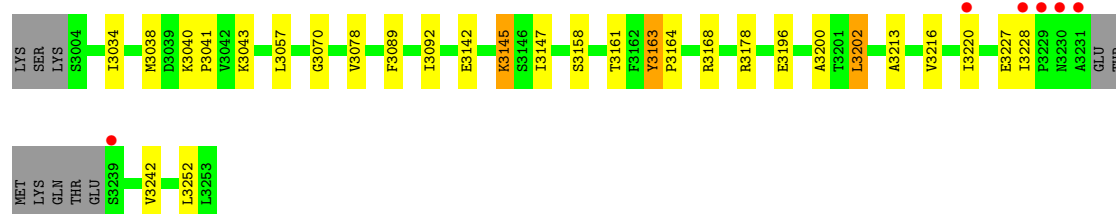
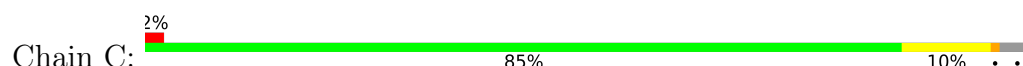
• Molecule 1: Uridine phosphorylase



• Molecule 1: Uridine phosphorylase



• Molecule 1: Uridine phosphorylase

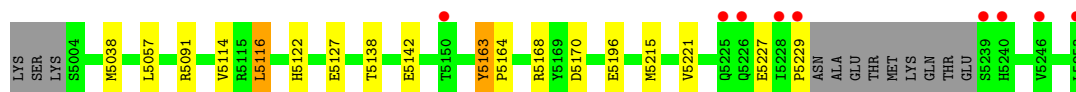


• Molecule 1: Uridine phosphorylase

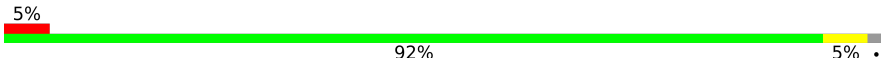


● Molecule 1: Uridine phosphorylase

Chain E:  4% 88% 6% • 5%



● Molecule 1: Uridine phosphorylase

Chain F:  5% 92% 5% •



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.37Å 125.31Å 135.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 2.38 19.94 – 2.38	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.94-2.38) 98.2 (19.94-2.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.38Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.208 , 0.258 (Not available) , 0.227	Depositor DCC
R_{free} test set	1849 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11475	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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: ANU

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	0.51	0/1843	0.79	1/2498 (0.0%)
1	B	0.52	0/1856	0.83	0/2516
1	C	0.52	0/1847	0.85	3/2504 (0.1%)
1	D	0.51	0/1915	0.82	0/2595
1	E	0.52	0/1834	0.81	0/2486
1	F	0.53	0/1885	0.79	1/2554 (0.0%)
All	All	0.52	0/11180	0.82	5/15153 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3228	ILE	CA-C-N	6.91	126.16	118.97
1	C	3228	ILE	C-N-CA	6.91	126.16	118.97
1	F	6194	ASN	N-CA-C	5.48	117.17	108.79
1	C	3070	GLY	N-CA-C	5.35	117.03	111.95
1	A	1194	ASN	N-CA-C	5.08	116.01	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	1814	0	1825	6	0
1	B	1827	0	1833	17	0
1	C	1818	0	1830	13	0
1	D	1885	0	1900	14	0
1	E	1805	0	1819	9	0
1	F	1856	0	1867	8	0
2	A	16	0	10	0	0
2	B	16	0	10	0	0
2	C	16	0	10	0	0
2	D	16	0	10	0	0
2	E	16	0	10	0	0
2	F	16	0	10	0	0
3	A	57	0	0	0	0
3	B	48	0	0	0	0
3	C	59	0	0	0	0
3	D	82	0	0	0	0
3	E	61	0	0	0	0
3	F	67	0	0	0	0
All	All	11475	0	11134	61	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.

All (61) 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:B:2163:TYR:HB2	1:B:2164:PRO:HD3	1.65	0.79
1:E:5163:TYR:HB2	1:E:5164:PRO:HD3	1.65	0.78
1:F:6163:TYR:HB2	1:F:6164:PRO:HD3	1.69	0.74
1:F:6221:VAL:HB	1:F:6229:PRO:HG3	1.73	0.71
1:C:3163:TYR:HB2	1:C:3164:PRO:HD3	1.71	0.70
1:B:2091:ARG:HG2	1:B:2215:MET:SD	2.34	0.67
1:F:6032:GLU:HG3	1:F:6033:LYS:HE3	1.78	0.64
1:D:4030:ARG:NH1	1:D:4033:LYS:HD3	2.16	0.61
1:E:5221:VAL:HB	1:E:5229:PRO:HG3	1.84	0.60
1:A:1049:GLU:HG3	1:F:6049:GLU:HG3	1.83	0.59
1:D:4230:ASN:HD22	1:D:4230:ASN:H	1.54	0.55
1:A:1125:PRO:HB2	1:A:1127:GLU:OE2	2.05	0.55
1:C:3034:ILE:HG12	1:C:3242:VAL:HG13	1.88	0.55
1:C:3040:LYS:N	1:C:3041:PRO:HD3	2.21	0.55
1:E:5163:TYR:CB	1:E:5164:PRO:HD3	2.36	0.55
1:B:2077:ALA:O	1:B:2081:LEU:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:5091:ARG:HG2	1:E:5215:MET:SD	2.48	0.54
1:E:5114:VAL:HG12	1:E:5116:LEU:HD13	1.90	0.54
1:B:2051:THR:H	1:B:2066:SER:HB3	1.75	0.51
1:A:1178:ARG:O	1:C:3178:ARG:NH2	2.43	0.51
1:C:3158:SER:HB3	1:C:3200:ALA:HB2	1.93	0.50
1:C:3078:VAL:HG21	1:C:3202:LEU:HD23	1.93	0.50
1:B:2125:PRO:HB2	1:B:2127:GLU:OE2	2.12	0.50
1:E:5138:THR:O	1:E:5142:GLU:HG2	2.12	0.50
1:D:4038:MET:HG2	1:D:4057:LEU:HD13	1.93	0.49
1:E:5168:ARG:NH1	1:E:5227:GLU:O	2.46	0.49
1:D:4030:ARG:HH21	1:D:4242:VAL:HG21	1.77	0.48
1:A:1049:GLU:HG3	1:F:6049:GLU:CG	2.44	0.48
1:F:6163:TYR:CB	1:F:6164:PRO:HD3	2.43	0.48
1:B:2223:ARG:HA	1:B:2226:GLN:O	2.13	0.48
1:C:3038:MET:HG2	1:C:3057:LEU:HD13	1.96	0.48
1:D:4163:TYR:HB2	1:D:4164:PRO:HD3	1.96	0.48
1:B:2163:TYR:CB	1:B:2164:PRO:HD3	2.41	0.47
1:A:1038:MET:HG2	1:A:1057:LEU:HD13	1.98	0.45
1:C:3142:GLU:O	1:C:3145:LYS:HD3	2.15	0.45
1:A:1049:GLU:HG2	1:A:1068:GLY:HA3	1.99	0.45
1:F:6016:LEU:HA	1:F:6063:ILE:HD11	1.99	0.44
1:B:2163:TYR:HA	1:B:2168:ARG:HD2	2.00	0.44
1:B:2049:GLU:HB3	1:D:4049:GLU:HB3	1.99	0.44
1:C:3161:THR:OG1	1:E:5122:HIS:HD2	2.00	0.44
1:D:4091:ARG:CZ	1:D:4198:GLU:HG3	2.48	0.44
1:B:2016:LEU:HG	1:B:2063:ILE:HD11	2.01	0.43
1:C:3089:PHE:O	1:C:3213:ALA:HA	2.19	0.43
1:B:2122:HIS:HD2	1:D:4161:THR:OG1	2.02	0.42
1:C:3163:TYR:CB	1:C:3164:PRO:HD3	2.45	0.42
1:C:3168:ARG:NH1	1:C:3227:GLU:O	2.52	0.42
1:B:2222:ASN:HD22	1:B:2224:THR:H	1.67	0.42
1:D:4238:GLU:O	1:D:4242:VAL:HG23	2.20	0.42
1:B:2044:LEU:HD11	1:B:2054:ARG:HB2	2.02	0.42
1:E:5038:MET:HG2	1:E:5057:LEU:HD13	2.01	0.41
1:C:3092:ILE:HA	1:C:3216:VAL:O	2.20	0.41
1:F:6038:MET:HE3	1:F:6057:LEU:HD22	2.02	0.41
1:B:2226:GLN:NE2	1:B:2228:ILE:O	2.52	0.41
1:D:4158:SER:HB3	1:D:4200:ALA:HB2	2.02	0.41
1:D:4222:ASN:HB3	1:D:4225:GLN:HG2	2.02	0.41
1:D:4163:TYR:HB2	1:D:4164:PRO:CD	2.51	0.41
1:B:2228:ILE:HA	1:B:2229:PRO:HD3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2099:GLN:HA	1:B:2100:PRO:HD3	1.91	0.41
1:D:4166:GLN:OE1	1:D:4168:ARG:NH1	2.55	0.40
1:B:2024:VAL:O	1:B:2091:ARG:HD2	2.22	0.40
1:D:4049:GLU:HG3	1:D:4068:GLY:HA3	2.03	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	238/253 (94%)	234 (98%)	3 (1%)	1 (0%)	30	40
1	B	240/253 (95%)	235 (98%)	4 (2%)	1 (0%)	30	40
1	C	239/253 (94%)	234 (98%)	4 (2%)	1 (0%)	30	40
1	D	249/253 (98%)	246 (99%)	2 (1%)	1 (0%)	30	40
1	E	237/253 (94%)	231 (98%)	5 (2%)	1 (0%)	30	40
1	F	244/253 (96%)	238 (98%)	5 (2%)	1 (0%)	30	40
All	All	1447/1518 (95%)	1418 (98%)	23 (2%)	6 (0%)	30	40

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	4163	TYR
1	A	1163	TYR
1	C	3163	TYR
1	B	2163	TYR
1	E	5163	TYR
1	F	6163	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	192/202 (95%)	188 (98%)	4 (2%)	47	67
1	B	193/202 (96%)	184 (95%)	9 (5%)	23	37
1	C	192/202 (95%)	185 (96%)	7 (4%)	31	49
1	D	200/202 (99%)	195 (98%)	5 (2%)	42	61
1	E	191/202 (95%)	187 (98%)	4 (2%)	47	67
1	F	196/202 (97%)	194 (99%)	2 (1%)	68	82
All	All	1164/1212 (96%)	1133 (97%)	31 (3%)	39	59

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1092	ILE
1	A	1140	LEU
1	A	1196	GLU
1	A	1228	ILE
1	B	2081	LEU
1	B	2092	ILE
1	B	2127	GLU
1	B	2147	ILE
1	B	2196	GLU
1	B	2202	LEU
1	B	2222	ASN
1	B	2228	ILE
1	B	2230	ASN
1	C	3043	LYS
1	C	3145	LYS
1	C	3147	ILE
1	C	3196	GLU
1	C	3202	LEU
1	C	3220	ILE
1	C	3252	LEU
1	D	4196	GLU
1	D	4198	GLU

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Mol	Chain	Res	Type
1	D	4230	ASN
1	D	4235	LYS
1	D	4236	GLN
1	E	5116	LEU
1	E	5127	GLU
1	E	5170	ASP
1	E	5196	GLU
1	F	6092	ILE
1	F	6202	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1083	GLN
1	A	1101	HIS
1	A	1152	HIS
1	A	1188	GLN
1	A	1226	GLN
1	B	2017	GLN
1	B	2103	ASN
1	B	2122	HIS
1	B	2209	GLN
1	B	2222	ASN
1	B	2230	ASN
1	C	3047	HIS
1	C	3122	HIS
1	C	3188	GLN
1	C	3226	GLN
1	D	4047	HIS
1	D	4083	GLN
1	D	4103	ASN
1	D	4122	HIS
1	D	4209	GLN
1	D	4225	GLN
1	D	4230	ASN
1	D	4236	GLN
1	E	5122	HIS
1	E	5166	GLN
1	F	6083	GLN
1	F	6226	GLN
1	F	6240	HIS

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 ⓘ

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	ANU	C	1516	-	18,18,18	3.24	4 (22%)	23,27,27	4.24	10 (43%)
2	ANU	F	1516	-	18,18,18	3.24	4 (22%)	23,27,27	4.25	9 (39%)
2	ANU	B	1516	-	18,18,18	3.11	5 (27%)	23,27,27	4.30	8 (34%)
2	ANU	A	1516	-	18,18,18	3.19	6 (33%)	23,27,27	4.33	7 (30%)
2	ANU	D	1516	-	18,18,18	3.20	4 (22%)	23,27,27	4.49	8 (34%)
2	ANU	E	1516	-	18,18,18	3.22	5 (27%)	23,27,27	4.46	9 (39%)

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	ANU	C	1516	-	-	0/2/26/26	0/3/3/3
2	ANU	F	1516	-	-	1/2/26/26	0/3/3/3
2	ANU	B	1516	-	-	2/2/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANU	A	1516	-	-	0/2/26/26	0/3/3/3
2	ANU	D	1516	-	-	2/2/26/26	0/3/3/3
2	ANU	E	1516	-	-	2/2/26/26	0/3/3/3

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1516	ANU	C2-N3	9.42	1.47	1.30
2	D	1516	ANU	C2-N3	9.40	1.47	1.30
2	C	1516	ANU	C2-N3	9.32	1.47	1.30
2	E	1516	ANU	C2-N3	9.30	1.47	1.30
2	A	1516	ANU	C2-N3	9.25	1.47	1.30
2	B	1516	ANU	C2-N3	9.16	1.47	1.30
2	F	1516	ANU	C2-N1	7.04	1.45	1.34
2	C	1516	ANU	C2-N1	7.01	1.45	1.34
2	E	1516	ANU	C2-N1	6.99	1.45	1.34
2	A	1516	ANU	C2-N1	6.84	1.45	1.34
2	D	1516	ANU	C2-N1	6.83	1.45	1.34
2	B	1516	ANU	C2-N1	6.56	1.44	1.34
2	C	1516	ANU	O2-C2	5.75	1.43	1.34
2	E	1516	ANU	O2-C2	5.68	1.42	1.34
2	A	1516	ANU	O2-C2	5.65	1.42	1.34
2	F	1516	ANU	O2-C2	5.62	1.42	1.34
2	D	1516	ANU	O2-C2	5.57	1.42	1.34
2	B	1516	ANU	O2-C2	5.26	1.42	1.34
2	B	1516	ANU	C4-N3	-2.20	1.34	1.38
2	A	1516	ANU	C6-C5	2.18	1.40	1.35
2	F	1516	ANU	C6-C5	2.16	1.40	1.35
2	B	1516	ANU	C6-C5	2.09	1.39	1.35
2	C	1516	ANU	C6-C5	2.09	1.39	1.35
2	E	1516	ANU	C6-C5	2.07	1.39	1.35
2	A	1516	ANU	C4-N3	-2.04	1.34	1.38
2	D	1516	ANU	C6-C5	2.04	1.39	1.35
2	A	1516	ANU	C5-C4	-2.01	1.40	1.44
2	E	1516	ANU	C4-N3	-2.01	1.35	1.38

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1516	ANU	N1-C2-N3	-14.94	114.04	127.09
2	C	1516	ANU	N1-C2-N3	-14.70	114.25	127.09
2	A	1516	ANU	N1-C2-N3	-14.61	114.33	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1516	ANU	N1-C2-N3	-14.61	114.34	127.09
2	D	1516	ANU	N1-C2-N3	-14.57	114.37	127.09
2	F	1516	ANU	N1-C2-N3	-14.52	114.41	127.09
2	D	1516	ANU	O2-C2-N1	-13.72	101.66	111.82
2	E	1516	ANU	O2-C2-N1	-12.59	102.49	111.82
2	A	1516	ANU	O2-C2-N1	-12.31	102.70	111.82
2	B	1516	ANU	O2-C2-N1	-11.93	102.98	111.82
2	F	1516	ANU	O2-C2-N1	-11.23	103.50	111.82
2	C	1516	ANU	O2-C2-N1	-10.67	103.91	111.82
2	B	1516	ANU	C2'-O2-C2	-4.09	103.63	108.67
2	A	1516	ANU	C2-N3-C4	4.03	120.77	116.66
2	E	1516	ANU	C2-N3-C4	3.90	120.63	116.66
2	D	1516	ANU	C2-N3-C4	3.75	120.48	116.66
2	C	1516	ANU	O4'-C1'-N1	-3.70	108.04	111.94
2	C	1516	ANU	C2'-O2-C2	-3.70	104.11	108.67
2	A	1516	ANU	C2'-O2-C2	-3.67	104.14	108.67
2	F	1516	ANU	O4'-C1'-N1	-3.64	108.11	111.94
2	C	1516	ANU	C2-N3-C4	3.63	120.35	116.66
2	E	1516	ANU	O4'-C1'-N1	-3.61	108.14	111.94
2	F	1516	ANU	C2-N3-C4	3.61	120.33	116.66
2	B	1516	ANU	C2-N3-C4	3.58	120.31	116.66
2	F	1516	ANU	C2'-O2-C2	-3.43	104.43	108.67
2	D	1516	ANU	C2'-O2-C2	-3.43	104.44	108.67
2	E	1516	ANU	C2'-O2-C2	-3.39	104.48	108.67
2	C	1516	ANU	O2-C2'-C1'	2.65	108.66	105.47
2	F	1516	ANU	O2-C2-N3	2.64	125.05	121.24
2	B	1516	ANU	C5-C4-N3	2.60	121.71	118.48
2	E	1516	ANU	O2-C2'-C1'	2.57	108.56	105.47
2	F	1516	ANU	O2-C2'-C1'	2.51	108.49	105.47
2	C	1516	ANU	O2-C2-N3	2.50	124.84	121.24
2	C	1516	ANU	C5-C4-N3	2.46	121.53	118.48
2	E	1516	ANU	C5-C4-N3	2.45	121.52	118.48
2	A	1516	ANU	O2-C2'-C1'	2.42	108.38	105.47
2	B	1516	ANU	O2-C2'-C1'	2.38	108.33	105.47
2	C	1516	ANU	C5'-C4'-C3'	-2.37	109.50	115.10
2	D	1516	ANU	C5-C4-N3	2.31	121.34	118.48
2	F	1516	ANU	O4-C4-C5	-2.27	118.77	122.29
2	A	1516	ANU	C5-C4-N3	2.23	121.25	118.48
2	F	1516	ANU	C5-C4-N3	2.22	121.24	118.48
2	D	1516	ANU	C5'-C4'-C3'	-2.22	109.85	115.10
2	B	1516	ANU	C5'-C4'-C3'	-2.19	109.93	115.10
2	C	1516	ANU	O4-C4-C5	-2.17	118.91	122.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1516	ANU	O2-C2'-C1'	2.15	108.06	105.47
2	A	1516	ANU	C3'-C2'-C1'	2.15	106.92	102.81
2	E	1516	ANU	C5'-C4'-C3'	-2.09	110.16	115.10
2	D	1516	ANU	O4-C4-C5	-2.04	119.11	122.29
2	B	1516	ANU	C5-C6-N1	-2.04	118.52	121.84
2	E	1516	ANU	O4-C4-C5	-2.01	119.17	122.29

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1516	ANU	C3'-C4'-C5'-O5'
2	B	1516	ANU	O4'-C4'-C5'-O5'
2	D	1516	ANU	C3'-C4'-C5'-O5'
2	D	1516	ANU	O4'-C4'-C5'-O5'
2	E	1516	ANU	O4'-C4'-C5'-O5'
2	F	1516	ANU	O4'-C4'-C5'-O5'
2	E	1516	ANU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	242/253 (95%)	0.42	6 (2%) 58 58	27, 36, 49, 60	0
1	B	244/253 (96%)	0.36	9 (3%) 45 45	24, 34, 48, 58	0
1	C	243/253 (96%)	0.25	6 (2%) 58 58	24, 31, 42, 56	0
1	D	251/253 (99%)	0.25	7 (2%) 55 54	24, 31, 53, 64	0
1	E	241/253 (95%)	0.44	9 (3%) 45 45	25, 34, 45, 55	0
1	F	248/253 (98%)	0.42	13 (5%) 33 32	24, 32, 47, 63	0
All	All	1469/1518 (96%)	0.36	50 (3%) 48 48	24, 33, 48, 64	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	6233	THR	5.0
1	A	1238	GLU	4.5
1	A	1239	SER	4.3
1	F	6234	MET	4.3
1	F	6231	ALA	4.2
1	C	3231	ALA	4.2
1	A	1228	ILE	4.1
1	F	6239	SER	3.9
1	D	4233	THR	3.9
1	F	6232	GLU	3.8
1	C	3230	ASN	3.6
1	A	1229	PRO	3.5
1	F	6235	LYS	3.4
1	B	2007	PHE	3.3
1	C	3228	ILE	3.3
1	E	5150	THR	3.3
1	D	4231	ALA	3.2
1	F	6238	GLU	3.1
1	E	5225	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	4232	GLU	3.0
1	B	2036	ALA	2.9
1	D	4230	ASN	2.9
1	F	6029	GLU	2.9
1	D	4237	THR	2.8
1	E	5240	HIS	2.8
1	B	2230	ASN	2.6
1	E	5239	SER	2.6
1	C	3229	PRO	2.5
1	C	3239	SER	2.5
1	B	2238	GLU	2.5
1	E	5228	ILE	2.4
1	B	2228	ILE	2.4
1	F	6049	GLU	2.4
1	A	1250	ARG	2.4
1	E	5246	VAL	2.3
1	D	4236	GLN	2.3
1	B	2226	GLN	2.2
1	B	2004	SER	2.2
1	F	6037	LEU	2.2
1	E	5226	GLN	2.2
1	E	5229	PRO	2.2
1	C	3220	ILE	2.1
1	E	5253	LEU	2.1
1	F	6042	VAL	2.1
1	B	2225	GLN	2.1
1	F	6004	SER	2.1
1	A	1240	HIS	2.1
1	B	2229	PRO	2.1
1	F	6010	GLY	2.1
1	D	4235	LYS	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ANU	E	1516	16/16	0.79	0.14	41,42,42,43	0
2	ANU	C	1516	16/16	0.84	0.12	37,37,38,38	0
2	ANU	D	1516	16/16	0.87	0.12	41,42,42,42	0
2	ANU	A	1516	16/16	0.88	0.10	32,33,33,33	0
2	ANU	F	1516	16/16	0.88	0.11	32,33,34,34	0
2	ANU	B	1516	16/16	0.91	0.09	36,36,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.