WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 30, 2023 – 07:31 PM JST

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PDB ID	:	4YMU
Title	:	Crystal structure of an amino acid ABC transporter complex with arginines and ATPs
Authors	:	Ge, J.; Yu, J.; Yang, M.
Deposited on	:	2015-03-07
Resolution	:	2.50 Å(reported)

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 2.50 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.
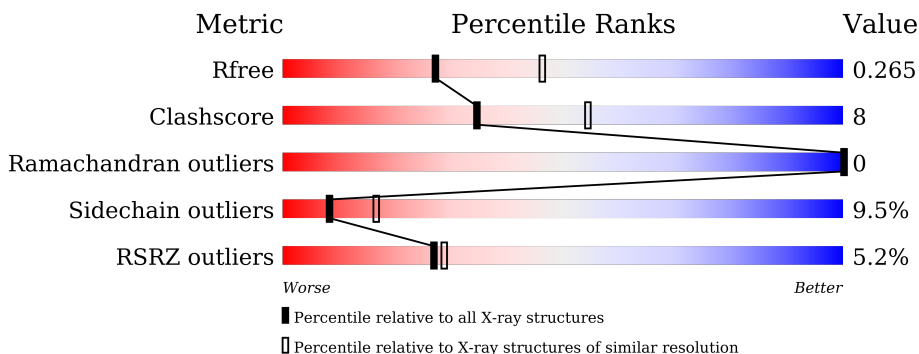
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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 <=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	240	5% / 82% / 14% / •
1	J	240	% / 79% / 17% / •
2	C	220	8% / 75% / 19% / • •
2	D	220	8% / 75% / 20% / • •

2 Entity composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7135 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 ABC-type polar amino acid transport system, ATPase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	J	240	Total 1872	C 1198	N 317	O 345	S 12	0	0	0
1	A	240	Total 1868	C 1195	N 316	O 345	S 12	0	0	0

- Molecule 2 is a protein called ABC-type amino acid transport system, permease component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	215	Total 1659	C 1096	N 264	O 286	S 13	0	0	0
2	C	214	Total 1648	C 1090	N 260	O 285	S 13	0	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).
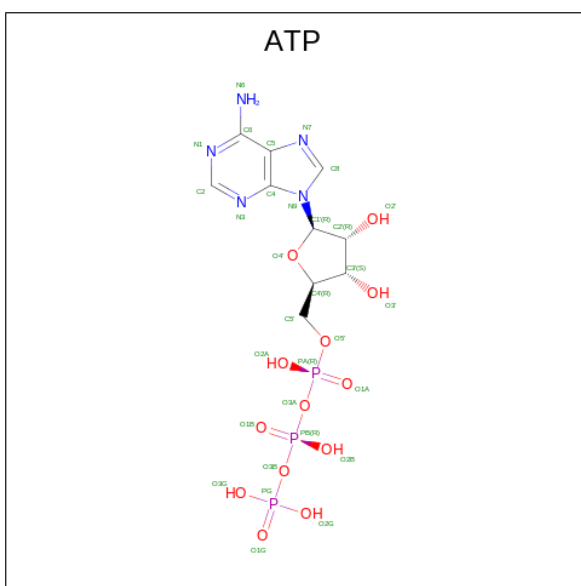
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	J	1	Total 31	C 10	N 5	O 13	P 3	0	0
3	A	1	Total 31	C 10	N 5	O 13	P 3	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	J	1	Total 1	Mg 1	0	0
4	A	1	Total 1	Mg 1	0	0

- Molecule 5 is ARGININE (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).
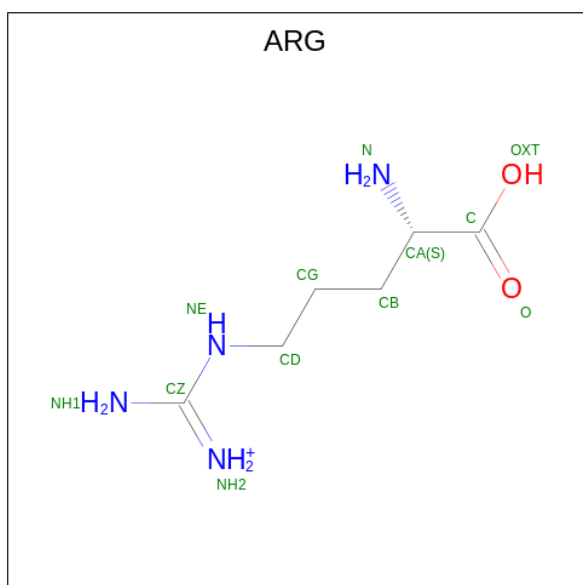
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total 12	C 6	N 4	O 2	0	0
5	C	1	Total 12	C 6	N 4	O 2	0	0

3 Residue-property plots ⓘ

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: ABC-type polar amino acid transport system, ATPase component
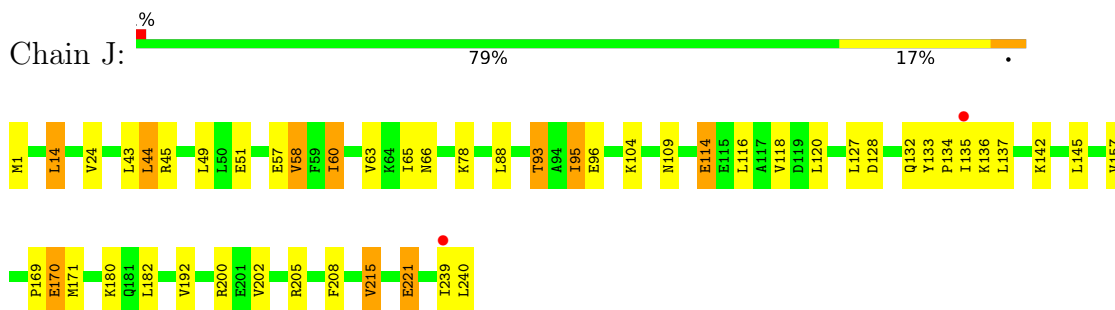
- Molecule 1: ABC-type polar amino acid transport system, ATPase component
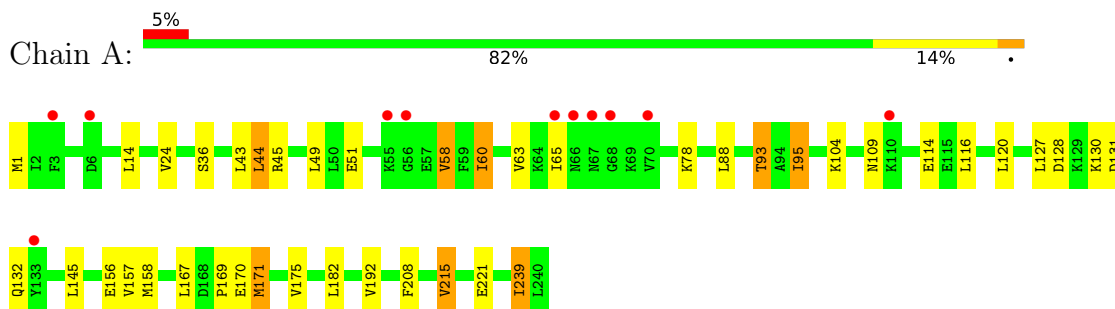
- Molecule 2: ABC-type amino acid transport system, permease component

- Molecule 2: ABC-type amino acid transport system, permease component

M1 T2 V3 D4 F5 T12 L25 G33 F39 L42 M43 S46 S47 I48 K49 P50 T65 P66 L67 L68 L71 Y75 Q80 I85 P86 A87 F88 S100 E105 R108 N119 E120 T128 M131 I137 P147 M156 E159 S160

A161 I162 V163 S164 V165 I166 L171 Q179 Y185 F186 E187 I191 I195 Y196 F197 V198 M199 T202 F203 L206 L207 S208 L209 F210 E211 R212 R213 L214 ARG ALA GLY ASP ILE ARG
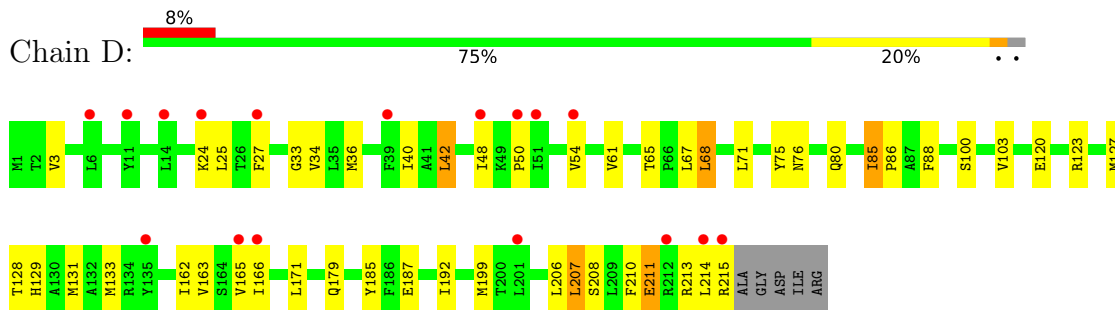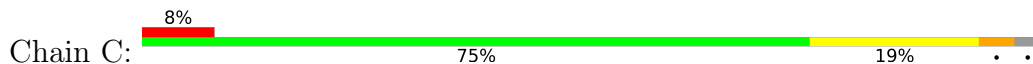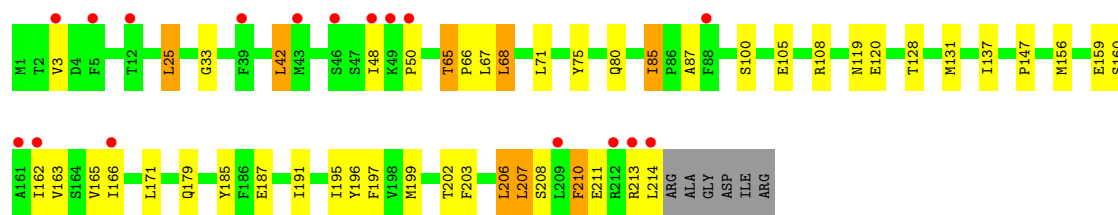
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	96.77Å 114.10Å 298.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.50 – 2.50 49.50 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.4 (49.50-2.50) 94.5 (49.50-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.28 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.224 , 0.260 0.230 , 0.265	Depositor DCC
R_{free} test set	2766 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å^2)	57.1	Xtriage
Anisotropy	0.811	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 73.1	EDS
L-test for twinning[2]	$<|L|> = 0.50, <L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7135	wwPDB-VP
Average B, all atoms (Å^2)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<|L|>$, $<L^2>$ 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: MG, ATP

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	0.45	0/1893	0.62	0/2548
1	J	0.51	1/1897 (0.1%)	0.66	1/2552 (0.0%)
2	C	0.42	0/1677	0.57	0/2274
2	D	0.42	0/1688	0.55	0/2288
All	All	0.45	1/7155 (0.0%)	0.60	1/9662 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	134	PRO	N-CD	5.17	1.55	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	J	133	TYR	C-N-CD	5.59	140.14	128.40

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	1868	0	1949	25	0
1	J	1872	0	1959	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1648	0	1761	47	0
2	D	1659	0	1774	35	0
3	A	31	0	12	1	0
3	J	31	0	12	0	0
4	A	1	0	0	0	0
4	J	1	0	0	0	0
5	C	12	0	12	0	0
5	D	12	0	12	0	0
All	All	7135	0	7491	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 8.

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:A:130:LYS:NZ	1:A:131:ASP:OD1	1.88	1.04
2:D:208:SER:HA	2:D:211:GLU:HG3	1.46	0.96
2:C:207:LEU:HD23	2:C:208:SER:N	1.82	0.94
2:C:206:LEU:HD12	2:C:206:LEU:H	1.34	0.93
2:D:208:SER:HA	2:D:211:GLU:CG	2.04	0.86

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	238/240 (99%)	232 (98%)	6 (2%)	0	100	100
1	J	238/240 (99%)	234 (98%)	4 (2%)	0	100	100
2	C	212/220 (96%)	204 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	213/220 (97%)	204 (96%)	9 (4%)	0	100	100
All	All	901/920 (98%)	874 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	207/209 (99%)	185 (89%)	22 (11%)	6	13
1	J	208/209 (100%)	185 (89%)	23 (11%)	6	11
2	C	179/184 (97%)	167 (93%)	12 (7%)	16	31
2	D	180/184 (98%)	163 (91%)	17 (9%)	8	17
All	All	774/786 (98%)	700 (90%)	74 (10%)	8	16

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	207	LEU
2	C	206	LEU
2	D	213	ARG
2	C	65	THR
1	A	24	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	J	84	GLN
1	A	132	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
3	ATP	A	301	4	26,33,33	0.89	1 (3%)	31,52,52	1.51	7 (22%)
5	ARG	D	301	-	10,11,11	0.75	1 (10%)	11,13,13	0.99	2 (18%)
3	ATP	J	301	4	26,33,33	0.94	1 (3%)	31,52,52	1.35	3 (9%)
5	ARG	C	301	-	10,11,11	0.68	0	11,13,13	1.01	2 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	A	301	4	-	4/18/38/38	0/3/3/3
5	ARG	D	301	-	-	0/11/11/11	-
3	ATP	J	301	4	-	4/18/38/38	0/3/3/3
5	ARG	C	301	-	-	0/11/11/11	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	301	ATP	C5-C4	2.50	1.47	1.40
3	A	301	ATP	C5-C4	2.30	1.47	1.40
5	D	301	ARG	OXT-C	-2.14	1.23	1.30

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	301	ATP	N3-C2-N1	-3.48	123.23	128.68
3	J	301	ATP	N3-C2-N1	-3.14	123.77	128.68
3	A	301	ATP	PA-O3A-PB	-2.88	122.95	132.83
3	A	301	ATP	PB-O3B-PG	-2.85	123.06	132.83
3	J	301	ATP	PA-O3A-PB	-2.83	123.12	132.83

There are no chirality outliers.
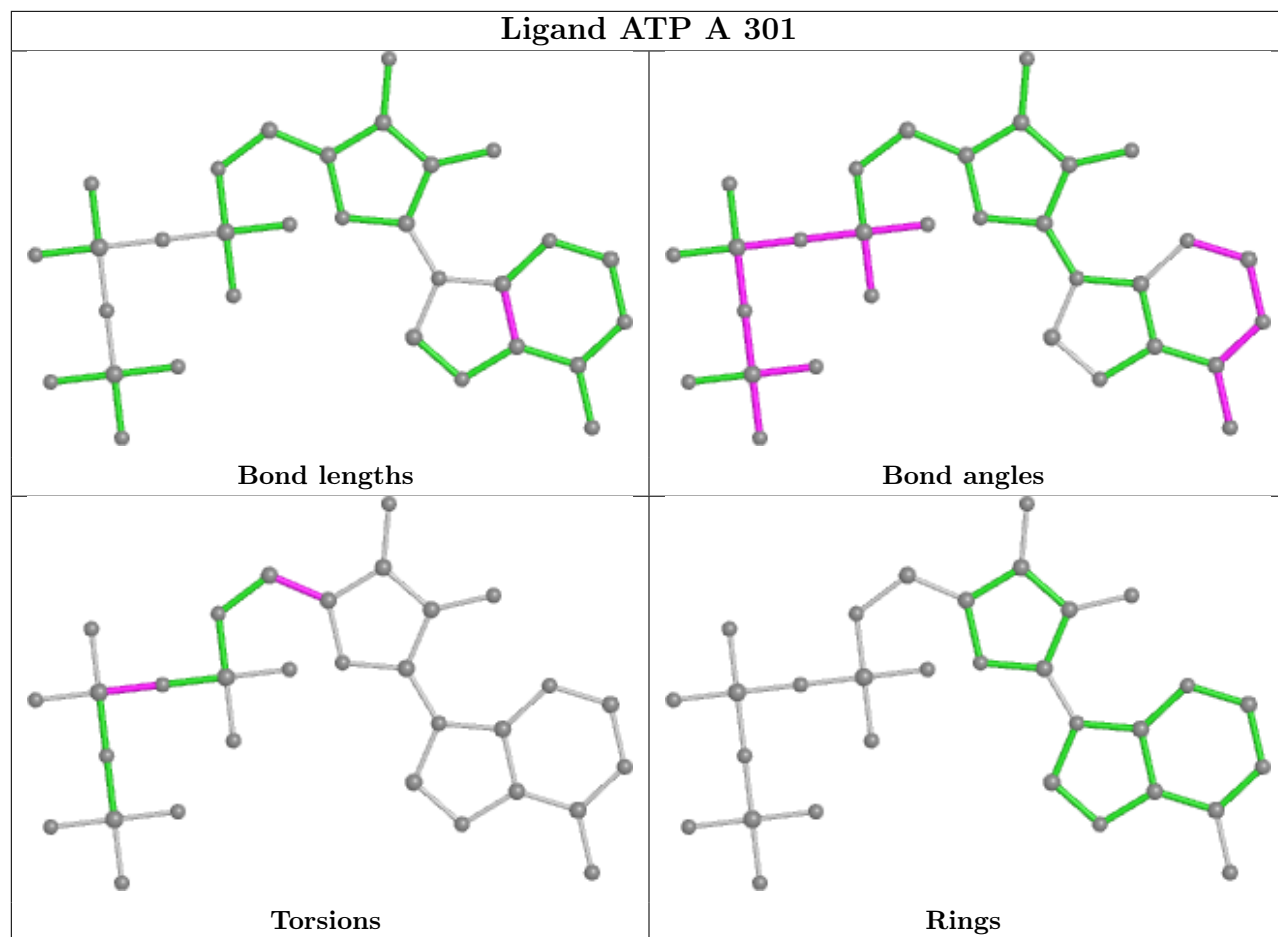
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	ATP	O4'-C4'-C5'-O5'
3	A	301	ATP	C3'-C4'-C5'-O5'
3	J	301	ATP	PA-O3A-PB-O1B
3	A	301	ATP	PA-O3A-PB-O1B
3	J	301	ATP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	ATP	1	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ATP A 301

Bond lengths

Bond angles

Torsions

Rings

Ligand ATP J 301

Bond lengths

Bond angles

Torsions

Rings
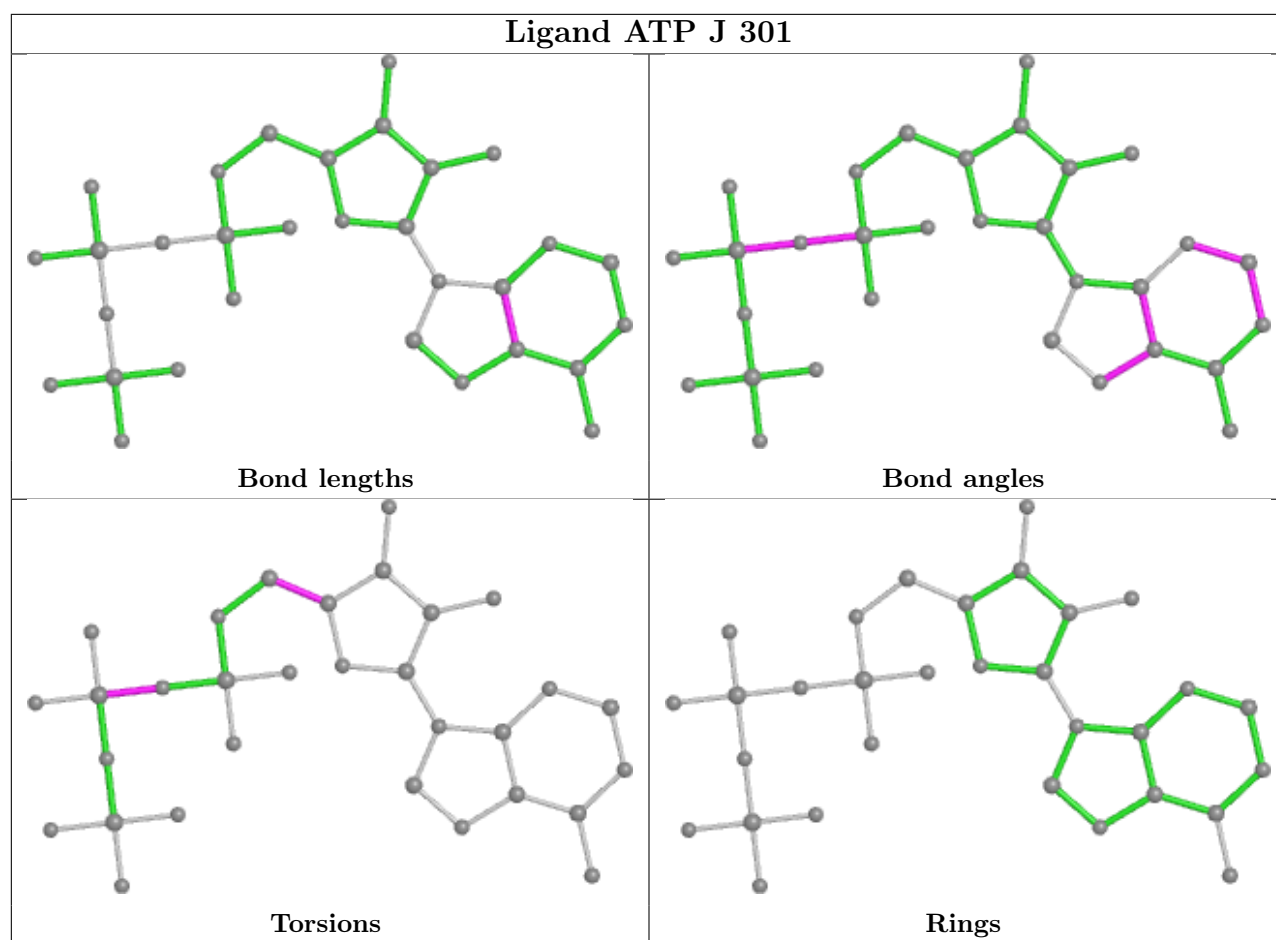
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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(Å²)	Q<0.9
1	A	240/240 (100%)	0.37	11 (4%)	32	34	52, 81, 109, 129	0
1	J	240/240 (100%)	0.13	2 (0%)	86	87	50, 74, 100, 121	0
2	C	214/220 (97%)	0.63	17 (7%)	12	12	63, 92, 123, 149	0
2	D	215/220 (97%)	0.56	17 (7%)	12	12	72, 96, 131, 155	0
All	All	909/920 (98%)	0.41	47 (5%)	27	29	50, 87, 119, 155	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	212	ARG	7.4
2	C	50	PRO	4.7
2	D	50	PRO	4.4
2	D	215	ARG	4.3
2	C	209	LEU	4.3

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

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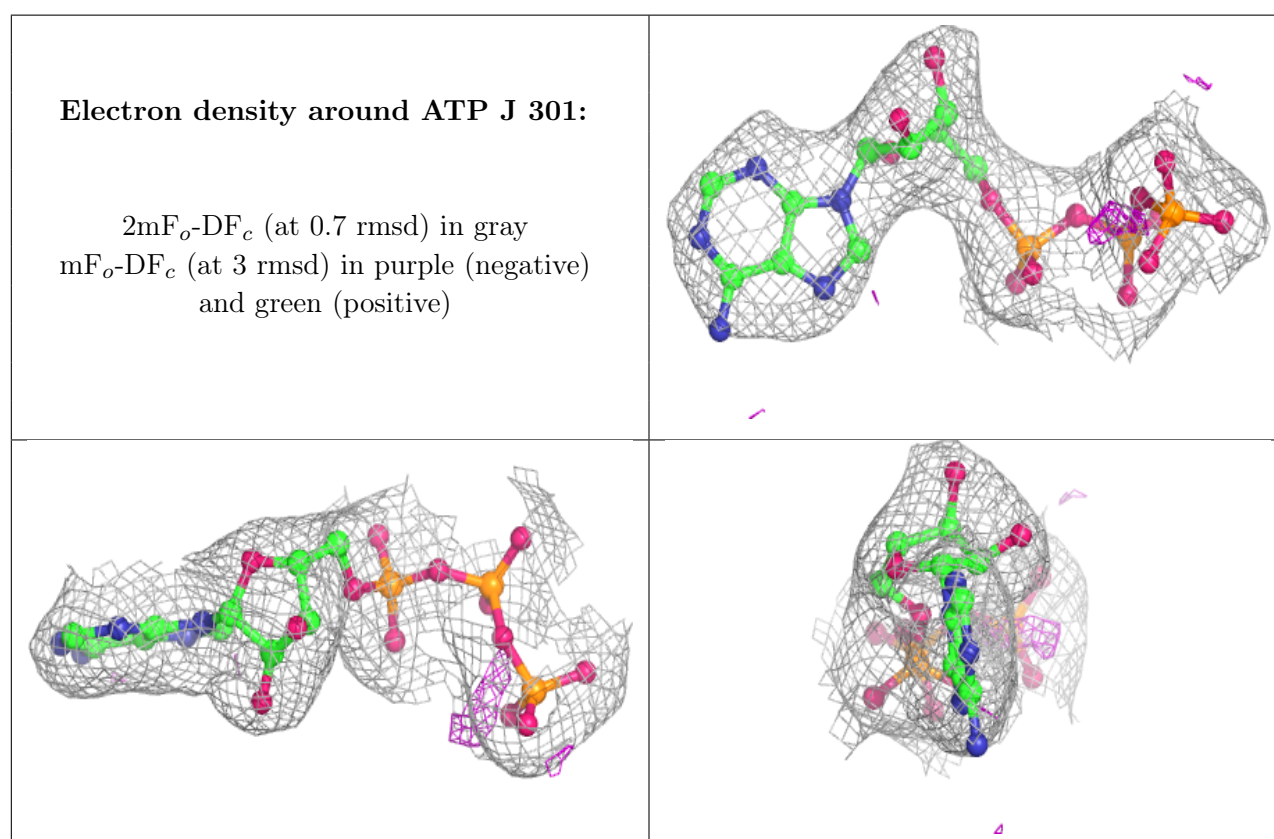
6.3   Carbohydrates ⓘ

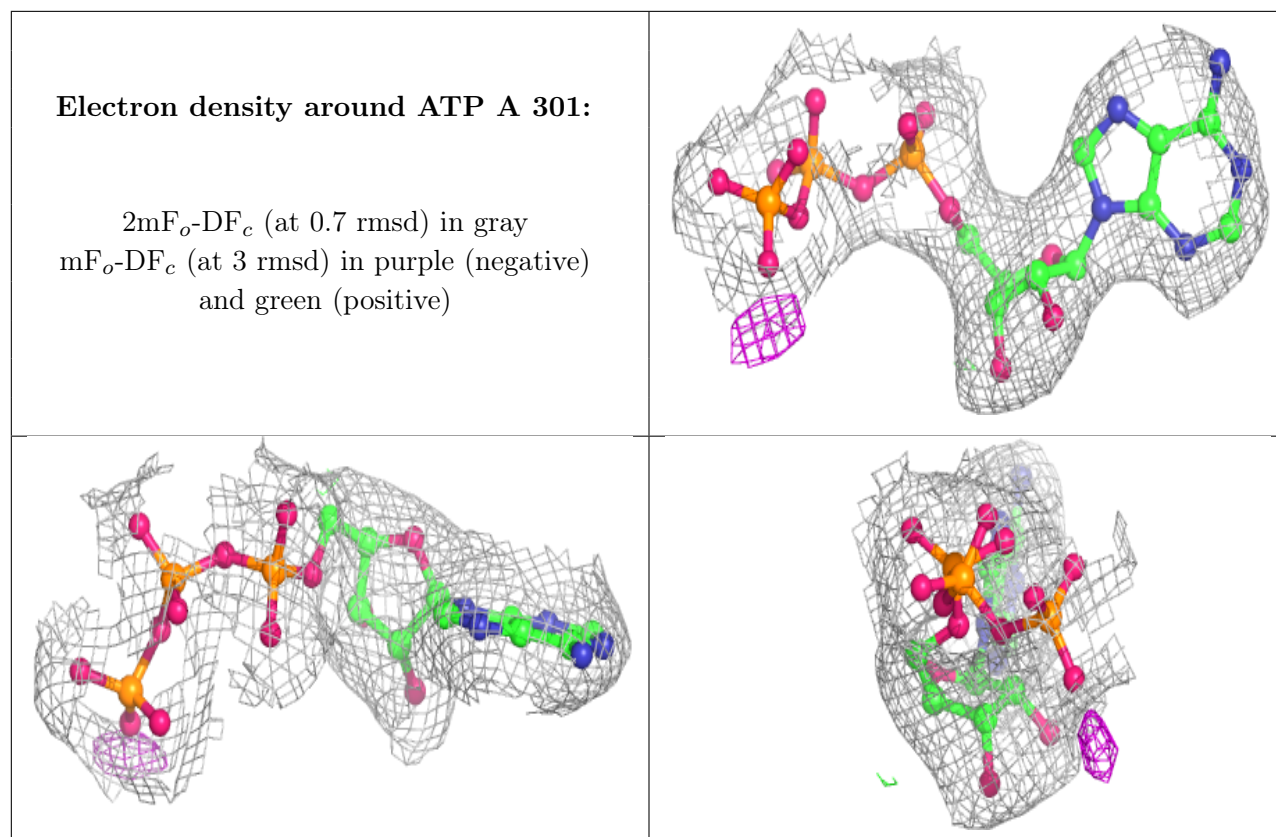There are no monosaccharides in this entry.

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
4	MG	J	302	1/1	0.69	0.11	84,84,84,84	0
4	MG	A	302	1/1	0.81	0.24	96,96,96,96	0
5	ARG	D	301	12/12	0.89	0.25	79,93,104,106	0
5	ARG	C	301	12/12	0.96	0.17	80,89,101,101	0
3	ATP	J	301	31/31	0.97	0.14	64,80,93,102	0
3	ATP	A	301	31/31	0.97	0.14	72,89,106,108	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 ATP J 301:

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

Electron density around ATP 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)

6.5 Other polymers ⓘ

There are no such residues in this entry.