



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2023 – 04:16 AM EDT

PDB ID : 4JXX
Title : Crystal structure of E coli E. coli glutamyl-tRNA synthetase bound to tRNA(Gln)(CUG) and ATP from novel cryostabilization conditions
Authors : Perona, J.J.; Rodriguez-Hernandez, A.
Deposited on : 2013-03-28
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

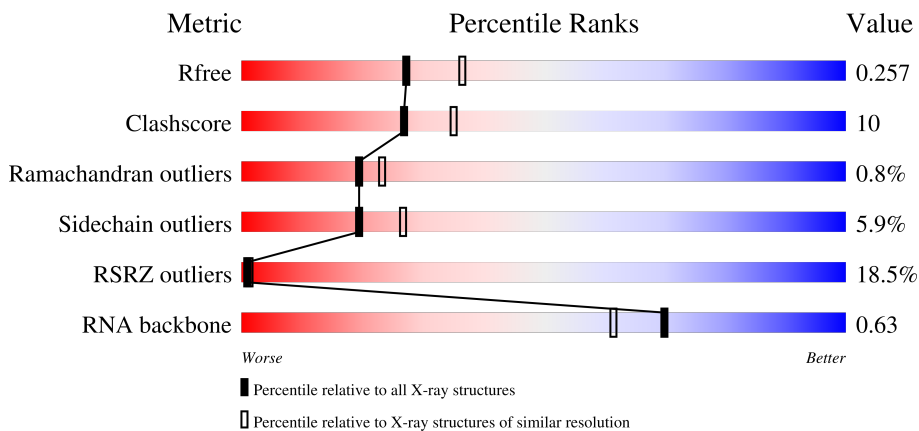
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

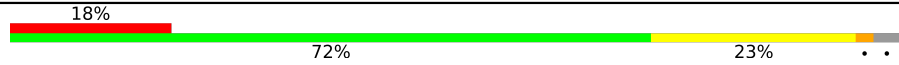
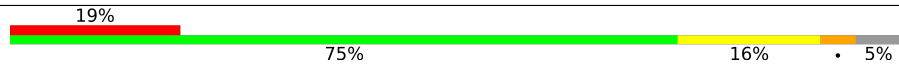
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)
RNA backbone	3102	1090 (2.70-1.90)

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	553	
2	B	75	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6050 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.

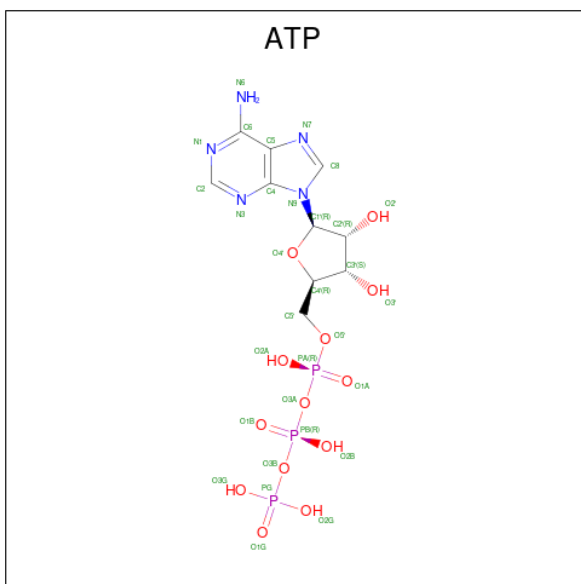
- Molecule 1 is a protein called Glutamine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	536	4295	2715	755	804	21	0	0	0

- Molecule 2 is a RNA chain called RNA (71-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	71	1511	674	270	496	71	0	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

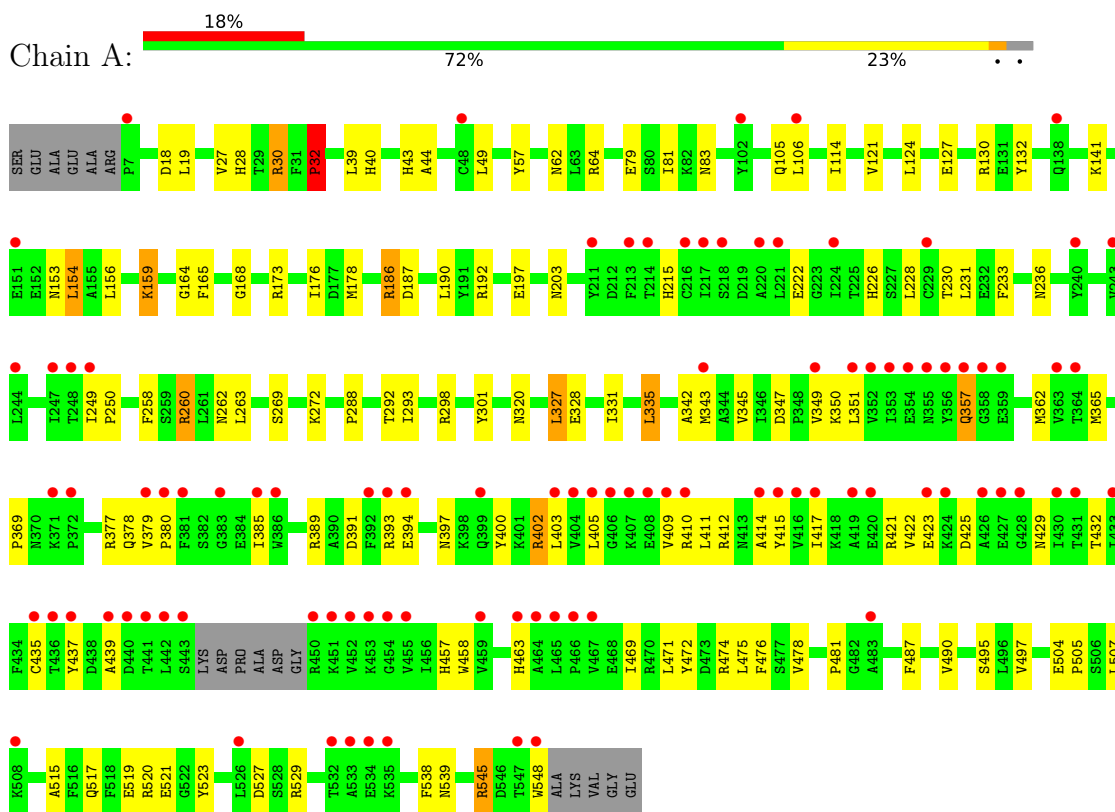
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	179	Total	O	0	0
			179	179		
5	B	29	Total	O	0	0
			29	29		

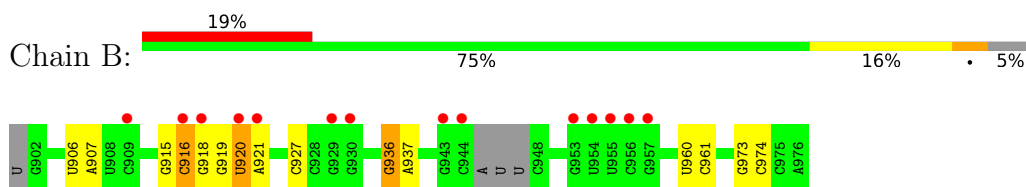
3 Residue-property plots [i](#)

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: Glutamine-tRNA ligase



- Molecule 2: RNA (71-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	93.66Å 234.28Å 113.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.10 – 2.30 41.13 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (41.10-2.30) 99.2 (41.13-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.29Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.226 , 0.258 0.221 , 0.257	Depositor DCC
R_{free} test set	10451 reflections (9.80%)	wwPDB-VP
Wilson B-factor (Å ²)	49.9	Xtrriage
Anisotropy	0.385	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6050	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 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	0.39	0/4398	0.59	0/5962
2	B	0.34	0/1686	0.69	0/2623
All	All	0.37	0/6084	0.62	0/8585

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	915	G	Sidechain

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	4295	0	4133	103	0
2	B	1511	0	770	11	0
3	A	31	0	12	0	0
4	A	5	0	0	0	0
5	A	179	0	0	6	0
5	B	29	0	0	1	0
All	All	6050	0	4915	110	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 10.

All (110) 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:39:LEU:HD13	1:A:81:ILE:HG12	1.41	1.02
1:A:40:HIS:H	1:A:43:HIS:HD2	1.12	0.96
1:A:394:GLU:HA	1:A:405:LEU:HD23	1.58	0.85
1:A:40:HIS:H	1:A:43:HIS:CD2	2.02	0.74
1:A:435:CYS:HB3	5:A:842:HOH:O	1.85	0.74
1:A:159:LYS:HD3	1:A:164:GLY:HA3	1.69	0.74
1:A:380:PRO:HB2	1:A:463:HIS:CD2	2.24	0.72
1:A:83:ASN:HB2	5:A:808:HOH:O	1.89	0.72
1:A:517:GLN:HG3	1:A:523:TYR:CE1	2.26	0.71
1:A:39:LEU:CD1	1:A:81:ILE:HG12	2.21	0.68
1:A:471:LEU:HB2	1:A:497:VAL:HG13	1.76	0.67
1:A:40:HIS:HA	1:A:292:THR:HA	1.76	0.67
1:A:393:ARG:HD3	1:A:400:TYR:CZ	2.29	0.67
1:A:487:PHE:O	1:A:490:VAL:HG12	1.96	0.65
1:A:365:MET:HE2	1:A:379:VAL:HG11	1.81	0.63
1:A:114:ILE:HG21	1:A:154:LEU:HD13	1.80	0.63
1:A:515:ALA:HB2	5:A:875:HOH:O	1.98	0.63
1:A:349:VAL:HB	1:A:389:ARG:HG2	1.80	0.62
1:A:178:MET:O	1:A:186:ARG:HD2	2.02	0.59
1:A:40:HIS:N	1:A:43:HIS:HD2	1.92	0.59
1:A:30:ARG:NH2	1:A:228:LEU:O	2.37	0.57
1:A:394:GLU:HA	1:A:405:LEU:CD2	2.34	0.57
1:A:417:ILE:HB	5:A:842:HOH:O	2.04	0.57
1:A:114:ILE:CG2	1:A:154:LEU:HD13	2.35	0.56
1:A:357:GLN:H	1:A:357:GLN:CD	2.09	0.56
1:A:32:PRO:HA	1:A:64:ARG:O	2.05	0.56
1:A:173:ARG:HD2	1:A:187:ASP:O	2.05	0.55
1:A:520:ARG:NH1	2:B:936:G:OP1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ARG:HG2	1:A:422:VAL:H	1.70	0.55
1:A:437:TYR:CE2	1:A:439:ALA:HA	2.42	0.55
1:A:260:ARG:HG2	1:A:260:ARG:HH11	1.70	0.55
1:A:343:MET:HE1	1:A:458:TRP:H	1.72	0.55
1:A:471:LEU:HB2	1:A:497:VAL:CG1	2.36	0.55
1:A:391:ASP:HA	1:A:402:ARG:HG2	1.90	0.54
1:A:159:LYS:HD2	1:A:165:PHE:CD2	2.43	0.53
1:A:377:ARG:HH11	1:A:377:ARG:HG2	1.74	0.53
1:A:351:LEU:HD23	1:A:351:LEU:O	2.09	0.52
1:A:298:ARG:NH1	1:A:529:ARG:NH1	2.57	0.52
1:A:545:ARG:HG2	1:A:545:ARG:NH1	2.25	0.52
1:A:520:ARG:HG2	1:A:520:ARG:HH11	1.75	0.52
1:A:545:ARG:HG2	1:A:545:ARG:HH11	1.73	0.52
1:A:132:TYR:CD2	1:A:141:LYS:HG3	2.45	0.51
1:A:422:VAL:HG12	1:A:423:GLU:N	2.25	0.51
1:A:403:LEU:HD13	1:A:409:VAL:HG22	1.93	0.51
2:B:936:G:H3'	2:B:937:A:H5'	1.93	0.51
1:A:365:MET:CE	1:A:379:VAL:HG11	2.41	0.51
1:A:504:GLU:HB2	1:A:505:PRO:HD2	1.93	0.50
1:A:393:ARG:HD3	1:A:400:TYR:CE1	2.46	0.50
1:A:298:ARG:HH12	1:A:529:ARG:NH1	2.10	0.50
2:B:920:U:H2'	2:B:920:U:O2	2.10	0.49
1:A:39:LEU:HA	1:A:43:HIS:CD2	2.47	0.49
1:A:18:ASP:OD2	1:A:226:HIS:HE1	1.94	0.49
1:A:357:GLN:H	1:A:357:GLN:NE2	2.10	0.49
1:A:421:ARG:HG2	1:A:422:VAL:N	2.28	0.49
1:A:30:ARG:NH1	1:A:215:HIS:NE2	2.60	0.48
1:A:411:LEU:HB2	1:A:414:ALA:HB3	1.95	0.48
1:A:197:GLU:HG3	1:A:203:ASN:ND2	2.29	0.48
1:A:410:ARG:HD3	1:A:415:TYR:O	2.14	0.48
2:B:960:U:H5''	2:B:961:C:H5	1.77	0.48
1:A:121:VAL:H	1:A:153:ASN:ND2	2.12	0.47
1:A:342:ALA:HB1	1:A:507:LEU:HD21	1.96	0.47
1:A:457:HIS:HE1	5:A:809:HOH:O	1.98	0.47
1:A:402:ARG:HB3	1:A:403:LEU:H	1.58	0.47
1:A:345:VAL:HA	5:A:809:HOH:O	2.14	0.46
1:A:350:LYS:HG3	1:A:351:LEU:N	2.31	0.46
1:A:331:ILE:HG13	1:A:335:LEU:HD22	1.98	0.45
1:A:343:MET:HG3	1:A:365:MET:CE	2.47	0.45
1:A:472:TYR:HA	1:A:495:SER:O	2.16	0.45
1:A:362:MET:CG	1:A:378:GLN:HG3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:VAL:O	1:A:481:PRO:HD3	2.17	0.45
1:A:288:PRO:HD3	1:A:298:ARG:CZ	2.47	0.45
1:A:507:LEU:HD12	1:A:538:PHE:CZ	2.52	0.44
1:A:377:ARG:HG2	1:A:377:ARG:NH1	2.32	0.44
1:A:349:VAL:HG23	1:A:389:ARG:NH1	2.33	0.44
1:A:425:ASP:OD1	1:A:429:ASN:HB2	2.17	0.44
1:A:347:ASP:OD2	1:A:389:ARG:HD3	2.17	0.44
1:A:64:ARG:HD3	1:A:222:GLU:OE2	2.17	0.44
1:A:130:ARG:HG3	2:B:973:G:OP2	2.18	0.44
2:B:936:G:H3'	2:B:937:A:C5'	2.48	0.44
1:A:260:ARG:HH11	1:A:260:ARG:CG	2.31	0.43
1:A:351:LEU:HD22	1:A:385:ILE:HD11	2.00	0.43
1:A:44:ALA:HB2	1:A:293:ILE:HD11	2.00	0.43
1:A:269:SER:OG	1:A:272:LYS:HG3	2.19	0.43
1:A:301:TYR:HE2	1:A:327:LEU:HD22	1.83	0.42
1:A:28:HIS:HE1	1:A:62:ASN:OD1	2.02	0.42
1:A:400:TYR:CE2	1:A:402:ARG:HB2	2.54	0.42
2:B:916:C:H5'	2:B:960:U:O2	2.20	0.42
1:A:27:VAL:HG21	1:A:57:TYR:HB2	2.01	0.42
1:A:262:ASN:HB2	1:A:320:ASN:O	2.18	0.42
1:A:349:VAL:HG13	1:A:349:VAL:O	2.20	0.42
1:A:469:ILE:HD12	1:A:469:ILE:N	2.34	0.42
1:A:474:ARG:HD3	1:A:476:PHE:O	2.19	0.42
1:A:301:TYR:CE2	1:A:327:LEU:HD22	2.55	0.42
2:B:906:U:O2'	2:B:907:A:H5'	2.19	0.41
1:A:249:ILE:HG13	1:A:250:PRO:HD2	2.02	0.41
2:B:920:U:H3'	5:B:1021:HOH:O	2.19	0.41
1:A:400:TYR:CZ	1:A:402:ARG:HB2	2.55	0.41
1:A:168:GLY:HA2	2:B:974:C:N3	2.35	0.41
1:A:328:GLU:O	1:A:331:ILE:HG22	2.19	0.41
1:A:527:ASP:HB2	1:A:539:ASN:ND2	2.35	0.41
1:A:343:MET:HG3	1:A:365:MET:HE1	2.02	0.41
1:A:519:GLU:C	1:A:521:GLU:H	2.24	0.41
1:A:362:MET:HG2	1:A:378:GLN:HG3	2.03	0.40
1:A:545:ARG:NH2	2:B:927:C:OP2	2.49	0.40
1:A:154:LEU:HD12	1:A:154:LEU:HA	1.94	0.40
1:A:230:THR:HA	1:A:258:PHE:O	2.21	0.40
1:A:233:PHE:HA	1:A:236:ASN:HD22	1.87	0.40
1:A:349:VAL:HG23	1:A:389:ARG:HH12	1.86	0.40
1:A:394:GLU:CA	1:A:405:LEU:HD23	2.41	0.40
1:A:335:LEU:HD23	1:A:523:TYR:HB3	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	532/553 (96%)	501 (94%)	27 (5%)	4 (1%)	19 23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	PRO
1	A	397	ASN
1	A	369	PRO
1	A	176	ILE

5.3.2 Protein sidechains [i](#)

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	457/481 (95%)	430 (94%)	27 (6%)	19 27

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	30	ARG
1	A	32	PRO
1	A	49	LEU

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Mol	Chain	Res	Type
1	A	79	GLU
1	A	105	GLN
1	A	106	LEU
1	A	124	LEU
1	A	127	GLU
1	A	154	LEU
1	A	156	LEU
1	A	159	LYS
1	A	186	ARG
1	A	190	LEU
1	A	192	ARG
1	A	231	LEU
1	A	260	ARG
1	A	263	LEU
1	A	327	LEU
1	A	335	LEU
1	A	357	GLN
1	A	402	ARG
1	A	412	ARG
1	A	432	THR
1	A	475	LEU
1	A	545	ARG
1	A	548	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	HIS
1	A	43	HIS
1	A	60	GLN
1	A	105	GLN
1	A	115	ASN
1	A	142	ASN
1	A	153	ASN
1	A	203	ASN
1	A	226	HIS
1	A	236	ASN
1	A	355	ASN
1	A	357	GLN
1	A	367	ASN
1	A	413	ASN
1	A	429	ASN

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Mol	Chain	Res	Type
1	A	457	HIS
1	A	463	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	69/75 (92%)	6 (8%)	2 (2%)

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	916	C
2	B	918	G
2	B	919	G
2	B	920	U
2	B	921	A
2	B	936	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	916	C
2	B	920	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
4	SO4	A	602	-	4,4,4	0.27	0	6,6,6	0.05	0
3	ATP	A	601	-	26,33,33	1.71	5 (19%)	31,52,52	1.79	4 (12%)

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	601	-	-	2/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	ATP	C2-N3	5.11	1.40	1.32
3	A	601	ATP	C2-N1	3.50	1.40	1.33
3	A	601	ATP	C5-C4	-2.71	1.33	1.40
3	A	601	ATP	C6-C5	-2.64	1.33	1.43
3	A	601	ATP	O4'-C1'	2.18	1.44	1.41

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	ATP	N3-C2-N1	-6.94	117.84	128.68
3	A	601	ATP	PB-O3B-PG	-3.23	121.73	132.83
3	A	601	ATP	PA-O3A-PB	-3.14	122.06	132.83
3	A	601	ATP	C5-C6-N6	-2.61	116.38	120.35

There are no chirality outliers.

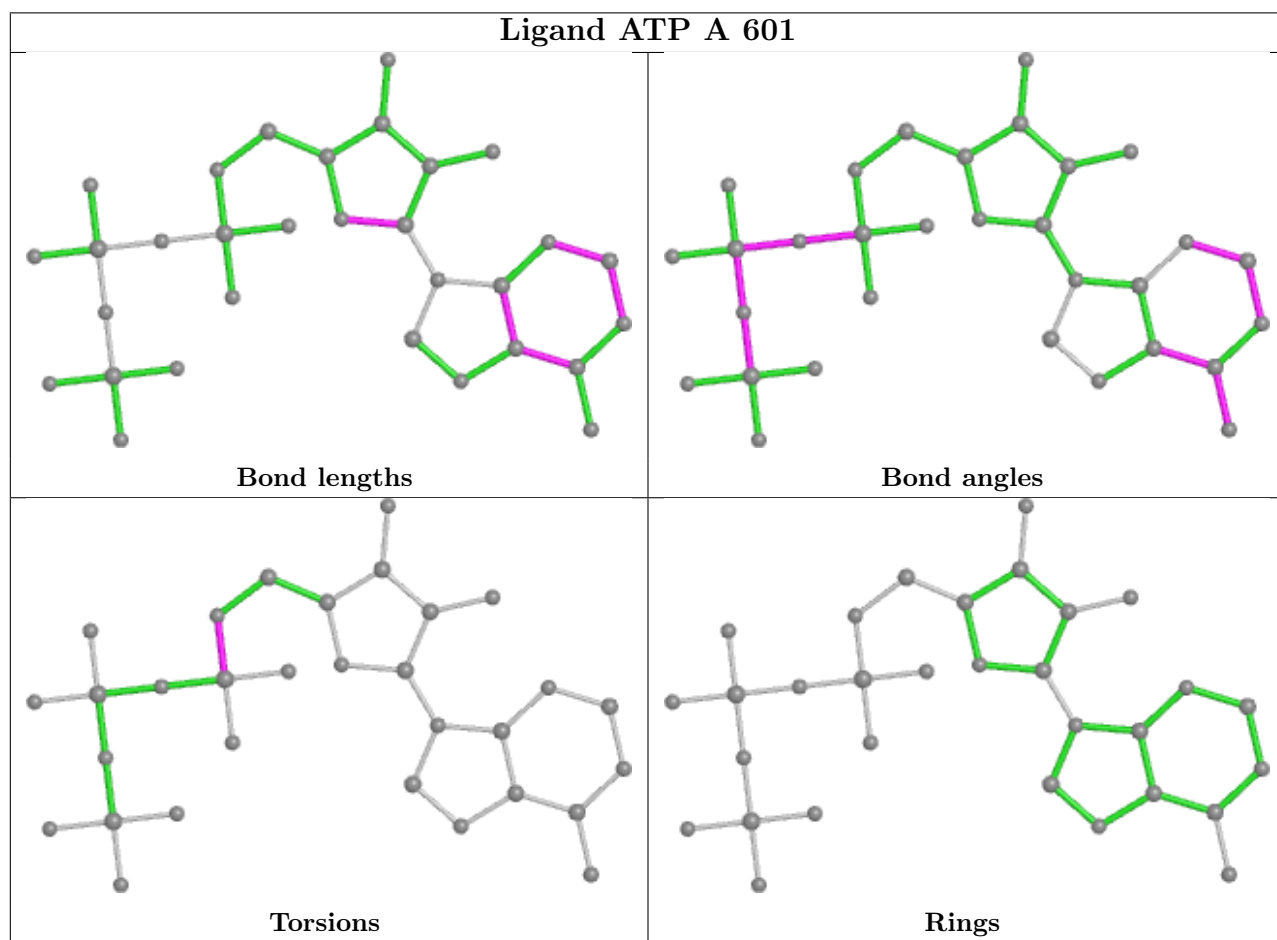
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	ATP	C5'-O5'-PA-O3A
3	A	601	ATP	C5'-O5'-PA-O1A

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

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	536/553 (96%)	1.11	98 (18%) 1 1	30, 49, 93, 105	0
2	B	71/75 (94%)	1.12	14 (19%) 1 1	41, 77, 105, 118	0
All	All	607/628 (96%)	1.11	112 (18%) 1 1	30, 50, 96, 118	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	406	GLY	7.6
1	A	404	VAL	6.6
1	A	452	VAL	6.4
1	A	426	ALA	5.8
1	A	358	GLY	5.8
1	A	381	PHE	5.7
1	A	439	ALA	5.6
1	A	407	LYS	5.6
1	A	419	ALA	5.5
1	A	428	GLY	5.3
1	A	356	TYR	5.2
1	A	440	ASP	5.2
1	A	443	SER	4.9
1	A	357	GLN	4.8
1	A	415	TYR	4.6
2	B	921	A	4.6
1	A	441	THR	4.5
1	A	454	GLY	4.5
1	A	414	ALA	4.4
1	A	453	LYS	4.4
1	A	392	PHE	4.4
1	A	399	GLN	4.4
1	A	408	GLU	4.3
1	A	534	GLU	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	355	ASN	4.3
1	A	483	ALA	4.1
2	B	956	C	4.1
1	A	353	ILE	4.1
1	A	437	TYR	3.9
1	A	430	ILE	3.8
2	B	920	U	3.7
1	A	427	GLU	3.7
1	A	548	TRP	3.7
1	A	463	HIS	3.7
1	A	403	LEU	3.6
1	A	363	VAL	3.5
1	A	533	ALA	3.5
1	A	351	LEU	3.5
1	A	405	LEU	3.5
1	A	416	VAL	3.5
1	A	420	GLU	3.4
1	A	464	ALA	3.4
1	A	433	ILE	3.4
1	A	383	GLY	3.2
2	B	954	U	3.2
1	A	467	VAL	3.2
1	A	354	GLU	3.2
1	A	409	VAL	3.2
1	A	532	THR	3.1
1	A	450	ARG	3.1
1	A	424	LYS	3.1
1	A	244	LEU	3.0
1	A	455	VAL	3.0
2	B	953	G	3.0
1	A	442	LEU	3.0
1	A	372	PRO	3.0
1	A	535	LYS	3.0
2	B	957	G	2.9
1	A	349	VAL	2.8
1	A	216	CYS	2.8
1	A	217	ILE	2.8
1	A	410	ARG	2.8
1	A	379	VAL	2.7
1	A	211	TYR	2.7
1	A	247	ILE	2.7
1	A	547	THR	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	909	C	2.7
1	A	436	THR	2.6
1	A	451	LYS	2.6
1	A	218	SER	2.6
2	B	916	C	2.6
1	A	243	VAL	2.6
1	A	221	LEU	2.5
1	A	435	CYS	2.5
1	A	352	VAL	2.5
2	B	944	C	2.5
1	A	364	THR	2.5
1	A	213	PHE	2.4
2	B	929	G	2.4
2	B	930	G	2.4
2	B	943	G	2.4
1	A	385	ILE	2.4
1	A	380	PRO	2.4
1	A	220	ALA	2.4
1	A	7	PRO	2.4
1	A	343	MET	2.4
1	A	138	GLN	2.4
2	B	955	U	2.3
1	A	102	TYR	2.3
1	A	459	VAL	2.3
1	A	240	TYR	2.3
1	A	466	PRO	2.3
1	A	526	LEU	2.3
1	A	106	LEU	2.2
1	A	214	THR	2.2
1	A	431	THR	2.2
1	A	151	GLU	2.2
1	A	417	ILE	2.2
1	A	359	GLU	2.2
1	A	249	ILE	2.2
1	A	423	GLU	2.2
1	A	508	LYS	2.2
1	A	393	ARG	2.1
1	A	465	LEU	2.1
1	A	229	CYS	2.1
1	A	248	THR	2.1
2	B	918	G	2.0
1	A	394	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	386	TRP	2.0
1	A	371	LYS	2.0
1	A	224	ILE	2.0
1	A	48	CYS	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](#)

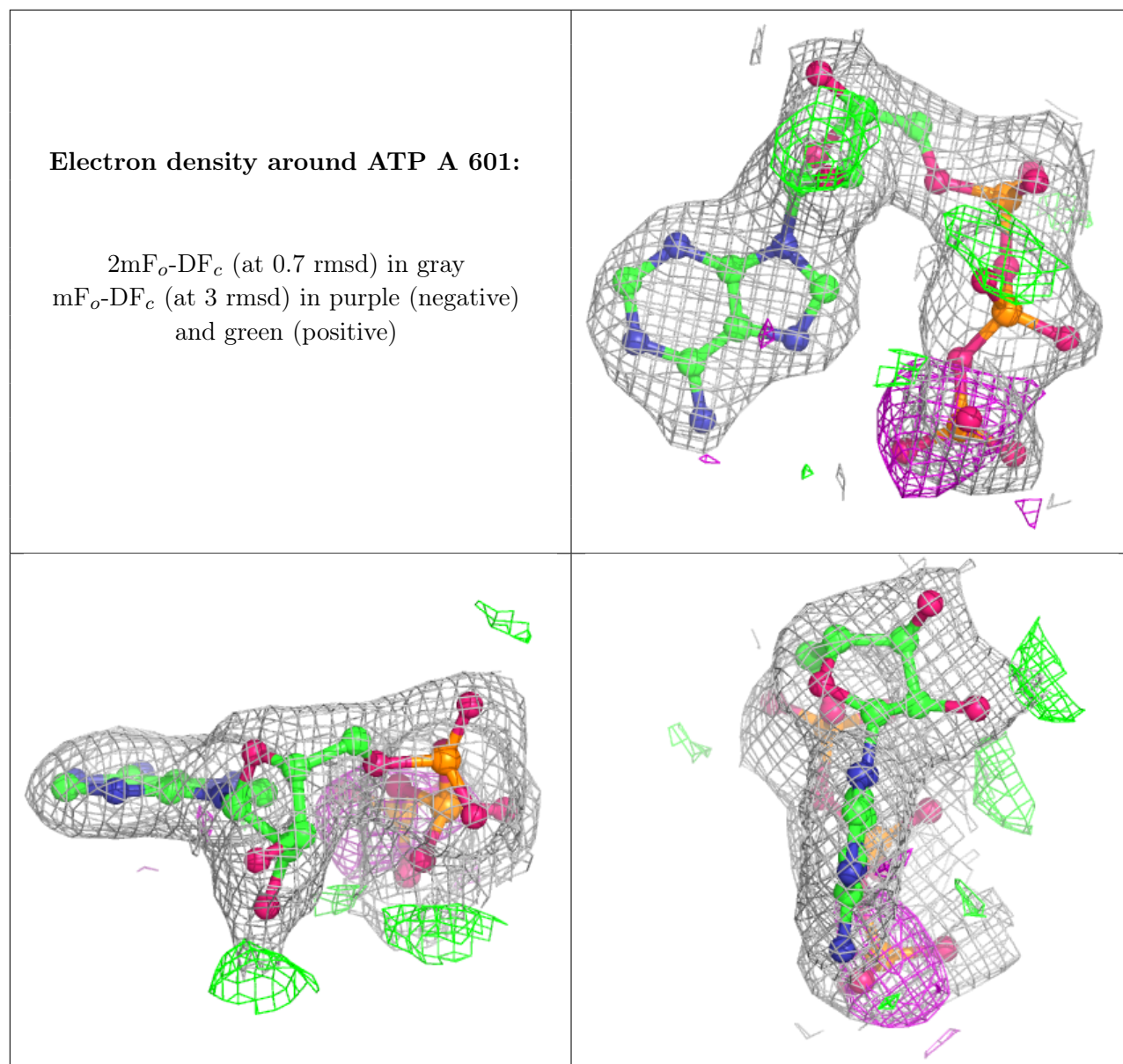
There are no monosaccharides in this entry.

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(Å ²)	Q < 0.9
4	SO4	A	602	5/5	0.69	0.34	150,150,150,151	0
3	ATP	A	601	31/31	0.93	0.22	37,42,71,73	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.