wwPDB X-ray Structure Validation Summary Report (i)

Jan 27, 2024 – 09:13 AM EST

PDB ID	:	1ASZ
Title	:	THE ACTIVE SITE OF YEAST ASPARTYL-TRNA SYNTHETASE: STRUCTURAL AND FUNCTIONAL ASPECTS OF THE AMINOACYLATION REACTION
Authors	:	Cavarelli, J.; Rees, B.; Thierry, J.C.; Moras, D.
Deposited on	:	1995-01-19
Resolution	:	3.00 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 (i) 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 (1)) were used in the production of this report:

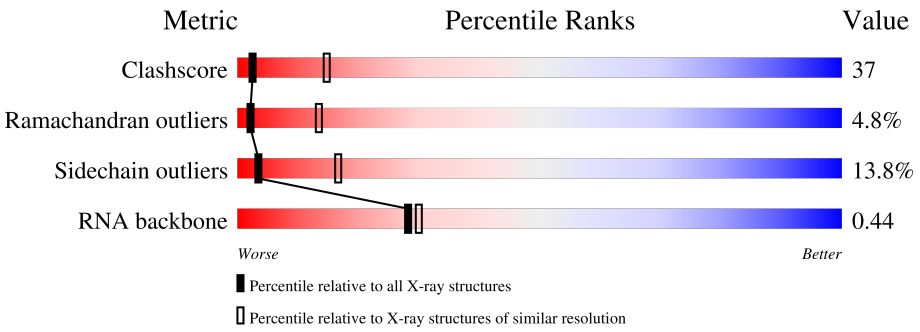
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	R	75	15% 32% 39% 15%
1	S	75	8% 47% 36% 9%
2	A	490	34% 55% 9% •
2	B	490	33% 54% 13% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11158 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.

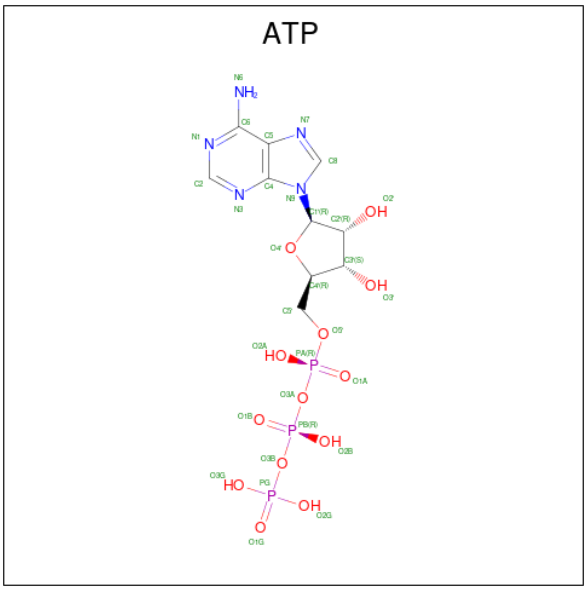
- Molecule 1 is a RNA chain called T-RNA (75-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	R	75	1602	715	280	532	75	0	0	0
1	S	75	1602	715	280	532	75	0	0	0

- Molecule 2 is a protein called ASPARTYL-tRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	490	3946	2513	679	741	13	0	0	0
2	B	490	3946	2513	679	741	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
			Total	C	N	O	P		
3	A	1	31	10	5	13	3	0	0
			Total	C	N	O	P		
3	B	1	31	10	5	13	3	0	0

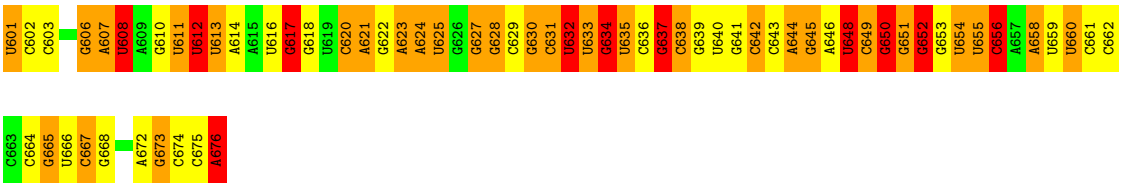
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

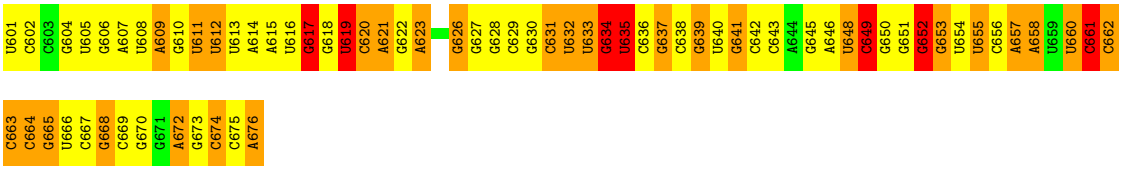
• Molecule 1: T-RNA (75-MER)

Chain R:



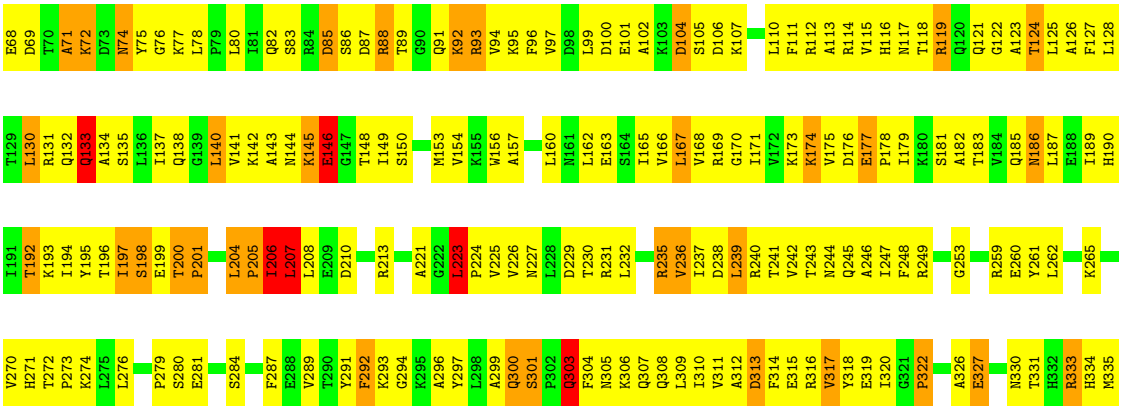
• Molecule 1: T-RNA (75-MER)

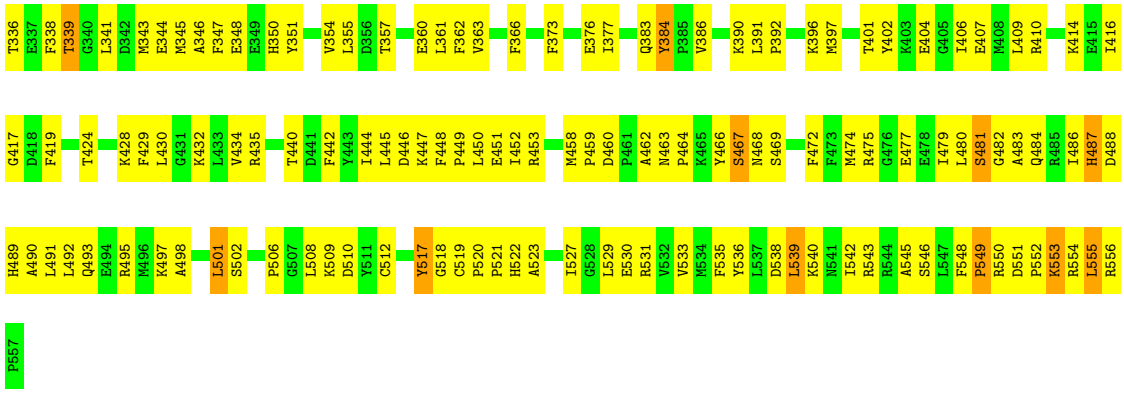
Chain S:



• Molecule 2: ASPARTYL-tRNA SYNTHETASE

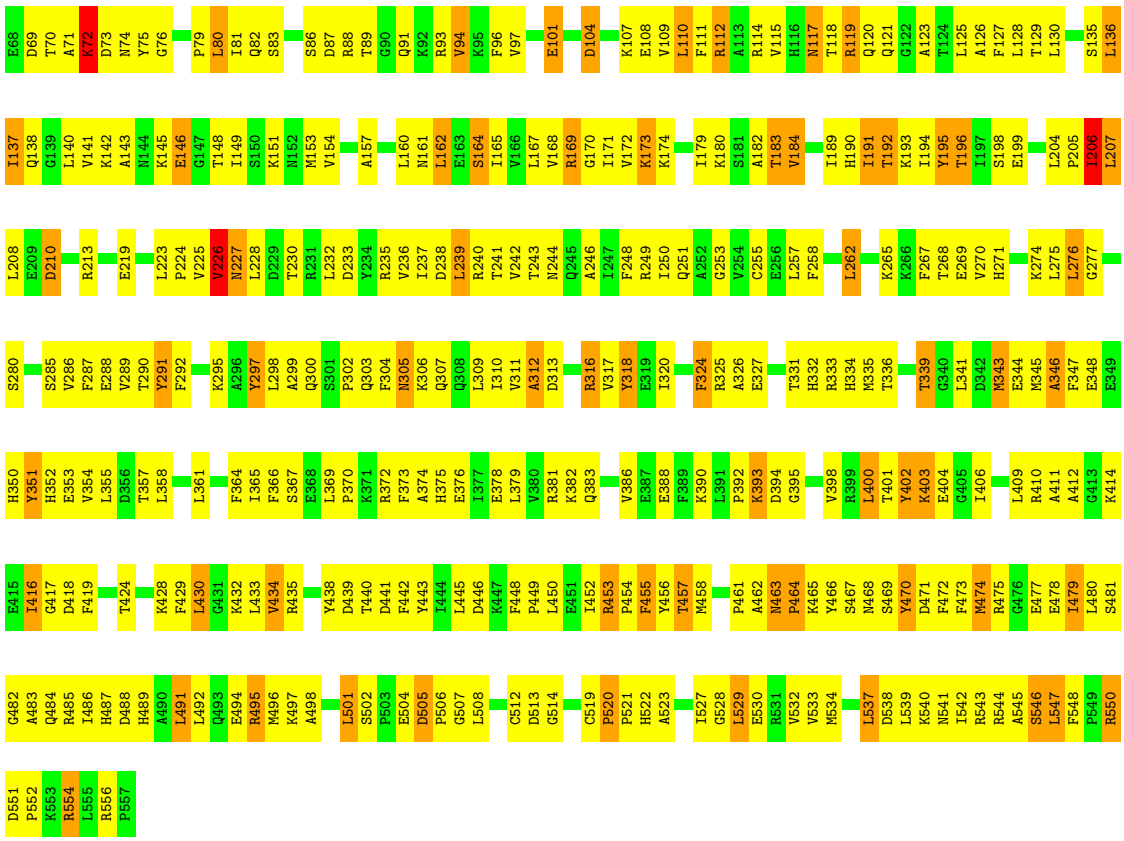
Chain A:





• Molecule 2: ASPARTYL-tRNA SYNTHETASE

Chain B: 33% 54% 13%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	211.27Å 145.35Å 86.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 3.00	Depositor
% Data completeness (in resolution range)	80.0 (7.00-3.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.203 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11158	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

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: 5MU, 1MG, 5MC, ATP, H2U, PSU

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	R	1.09	0/1605	1.93	56/2500 (2.2%)
1	S	1.09	0/1605	1.93	57/2500 (2.3%)
2	A	0.58	0/4029	0.84	3/5433 (0.1%)
2	B	0.61	0/4029	0.88	2/5433 (0.0%)
All	All	0.77	0/11268	1.30	118/15866 (0.7%)

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	3

There are no bond length outliers.

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	S	609	A	OP1-P-O3'	12.46	132.62	105.20
1	S	611	U	OP1-P-O3'	10.94	129.27	105.20
1	S	633	U	P-O3'-C3'	10.65	132.48	119.70
1	R	614	A	OP1-P-O3'	9.66	126.46	105.20
1	R	645	G	OP1-P-O3'	8.97	124.94	105.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	291	TYR	Sidechain

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Mol	Chain	Res	Type	Group
2	B	297	TYR	Sidechain
2	B	402	TYR	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	R	1602	0	815	70	0
1	S	1602	0	814	59	0
2	A	3946	0	3939	321	0
2	B	3946	0	3939	380	0
3	A	31	0	12	1	0
3	B	31	0	12	1	0
All	All	11158	0	9531	769	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 37.

The worst 5 of 769 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)
2:B:386:VAL:HG11	2:B:538:ASP:HB3	1.33	1.02
2:B:453:ARG:HB3	2:B:457:THR:HG21	1.42	0.97
2:A:227:ASN:O	2:A:231:ARG:HG3	1.65	0.97
2:B:424:THR:HG22	2:B:428:LYS:HE3	1.44	0.95
2:A:119:ARG:HH11	2:A:119:ARG:HB3	1.29	0.95

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
2	A	488/490 (100%)	395 (81%)	66 (14%)	27 (6%)	2 10
2	B	488/490 (100%)	412 (84%)	56 (12%)	20 (4%)	3 16
All	All	976/980 (100%)	807 (83%)	122 (12%)	47 (5%)	2 13

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	88	ARG
2	A	124	THR
2	B	80	LEU
2	B	162	LEU
2	B	206	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
2	A	427/427 (100%)	375 (88%)	52 (12%)	5 21
2	B	427/427 (100%)	361 (84%)	66 (16%)	2 13
All	All	854/854 (100%)	736 (86%)	118 (14%)	3 17

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	110	LEU
2	B	501	LEU
2	B	184	VAL
2	B	495	ARG
2	B	416	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	484	GLN
2	B	121	GLN
2	B	489	HIS
2	B	117	ASN
2	B	303	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	74/75 (98%)	17 (22%)	1 (1%)
1	S	74/75 (98%)	17 (22%)	2 (2%)
All	All	148/150 (98%)	34 (22%)	3 (2%)

5 of 34 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	606	G
1	R	608	U
1	R	612	U
1	R	617	G
1	R	618	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	R	634	G
1	S	633	U
1	S	634	G

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

16 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	H2U	S	619	1	18,21,22	0.50	0	21,30,33	0.91	1 (4%)
1	H2U	R	619	1	18,21,22	0.59	0	21,30,33	0.85	0
1	PSU	S	632	1	18,21,22	0.52	0	22,30,33	0.74	0
1	PSU	R	632	1	18,21,22	0.61	0	22,30,33	1.07	2 (9%)
1	1MG	R	637	1	18,26,27	0.93	1 (5%)	19,39,42	1.10	2 (10%)
1	PSU	R	613	1	18,21,22	0.62	0	22,30,33	1.09	2 (9%)
1	1MG	S	637	1	18,26,27	1.05	1 (5%)	19,39,42	1.48	3 (15%)
1	5MC	S	649	1	18,22,23	0.54	0	26,32,35	0.96	1 (3%)
1	5MU	R	654	1	19,22,23	0.56	0	28,32,35	0.95	2 (7%)
1	PSU	S	655	1	18,21,22	0.90	1 (5%)	22,30,33	1.13	2 (9%)
1	H2U	S	616	1	18,21,22	0.42	0	21,30,33	0.75	0
1	PSU	S	613	1	18,21,22	0.62	0	22,30,33	1.19	3 (13%)
1	5MC	R	649	1	18,22,23	0.50	0	26,32,35	0.91	1 (3%)
1	5MU	S	654	1	19,22,23	0.44	0	28,32,35	1.12	3 (10%)
1	PSU	R	655	1	18,21,22	0.63	0	22,30,33	1.23	3 (13%)
1	H2U	R	616	1	18,21,22	0.50	0	21,30,33	1.06	2 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	H2U	S	619	1	-	3/7/38/39	0/2/2/2
1	H2U	R	619	1	-	2/7/38/39	0/2/2/2
1	PSU	S	632	1	-	0/7/25/26	0/2/2/2
1	PSU	R	632	1	-	2/7/25/26	0/2/2/2
1	1MG	R	637	1	-	0/3/25/26	0/3/3/3
1	PSU	R	613	1	-	0/7/25/26	0/2/2/2
1	1MG	S	637	1	-	0/3/25/26	0/3/3/3
1	5MC	S	649	1	-	2/7/25/26	0/2/2/2
1	5MU	R	654	1	-	0/7/25/26	0/2/2/2
1	PSU	S	655	1	-	2/7/25/26	0/2/2/2
1	H2U	S	616	1	-	1/7/38/39	0/2/2/2
1	PSU	S	613	1	-	1/7/25/26	0/2/2/2
1	5MC	R	649	1	-	2/7/25/26	0/2/2/2
1	5MU	S	654	1	-	0/7/25/26	0/2/2/2
1	PSU	R	655	1	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	H2U	R	616	1	-	0/7/38/39	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S	655	PSU	O4'-C1'	-2.44	1.40	1.43
1	R	637	1MG	C8-N7	-2.41	1.30	1.35
1	S	637	1MG	C8-N7	-2.18	1.31	1.35

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	S	637	1MG	C2-N1-C6	4.49	124.60	120.95
1	S	655	PSU	C6-C5-C4	3.34	120.53	118.20
1	S	654	5MU	C6-C5-C4	3.32	120.81	118.03
1	R	637	1MG	C2-N1-C6	3.28	123.61	120.95
1	R	632	PSU	O4'-C1'-C2'	3.16	109.59	105.14

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	R	619	H2U	O4'-C1'-N1-C2
1	R	619	H2U	O4'-C1'-N1-C6
1	S	613	PSU	C2'-C1'-C5-C4
1	S	619	H2U	O4'-C4'-C5'-O5'
1	S	649	5MC	O4'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	S	619	H2U	4	0
1	S	632	PSU	1	0
1	R	632	PSU	4	0
1	R	637	1MG	3	0
1	R	613	PSU	1	0
1	S	637	1MG	1	0
1	S	649	5MC	4	0
1	R	654	5MU	1	0
1	S	655	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	S	616	H2U	1	0
1	R	649	5MC	2	0
1	R	655	PSU	3	0

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	$\#\|Z\| > 2$
3	ATP	A	701	-	26,33,33	0.78	0	31,52,52	0.88	0
3	ATP	B	701	-	26,33,33	0.76	0	31,52,52	0.97	1 (3%)

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	701	-	-	10/18/38/38	0/3/3/3
3	ATP	B	701	-	-	3/18/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	701	ATP	O4'-C1'-C2'	-2.45	103.34	106.93

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	ATP	PG-O3B-PB-O1B
3	A	701	ATP	O4'-C4'-C5'-O5'
3	A	701	ATP	PB-O3B-PG-O1G
3	B	701	ATP	PB-O3A-PA-O2A
3	A	701	ATP	PA-O3A-PB-O2B

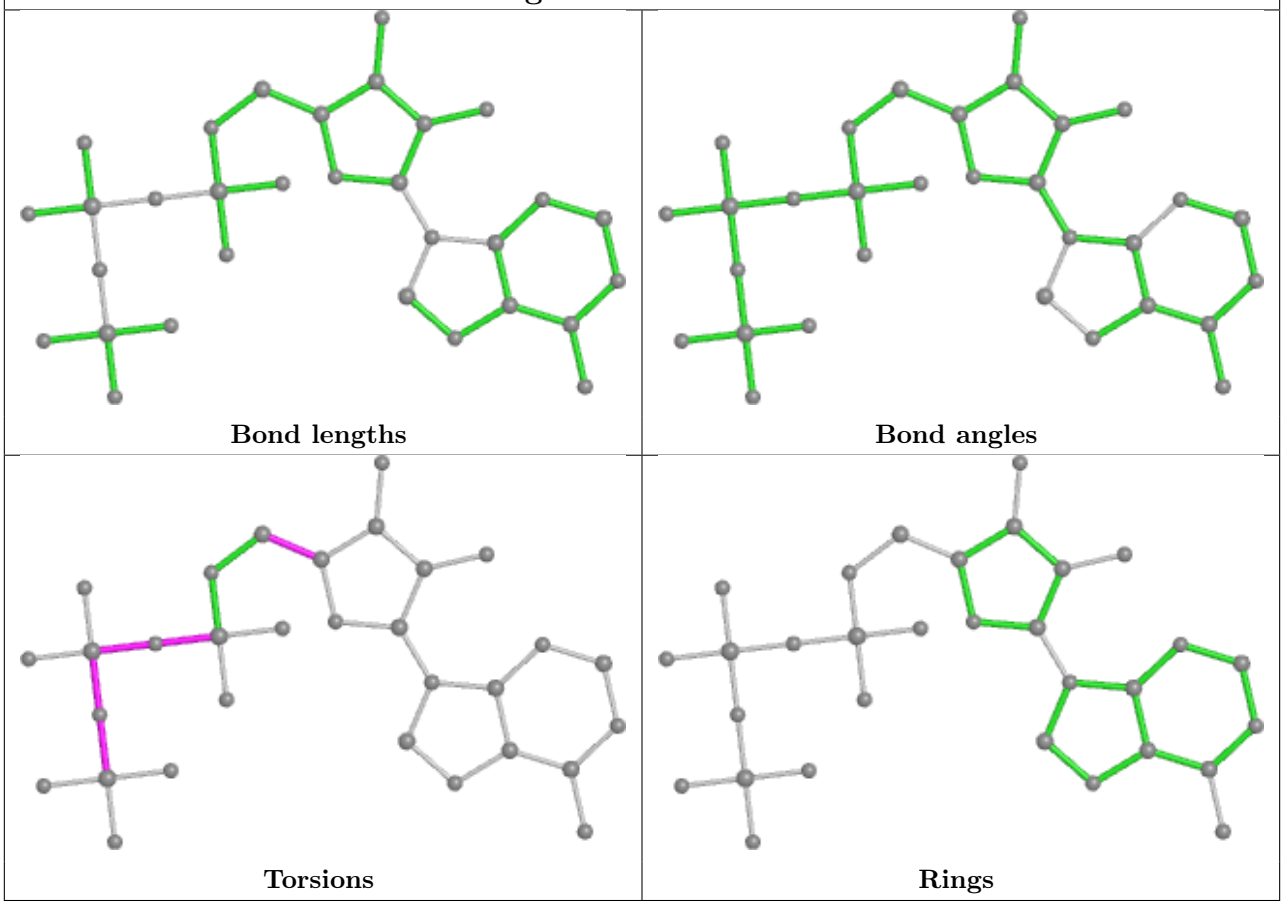
There are no ring outliers.

2 monomers are involved in 2 short contacts:

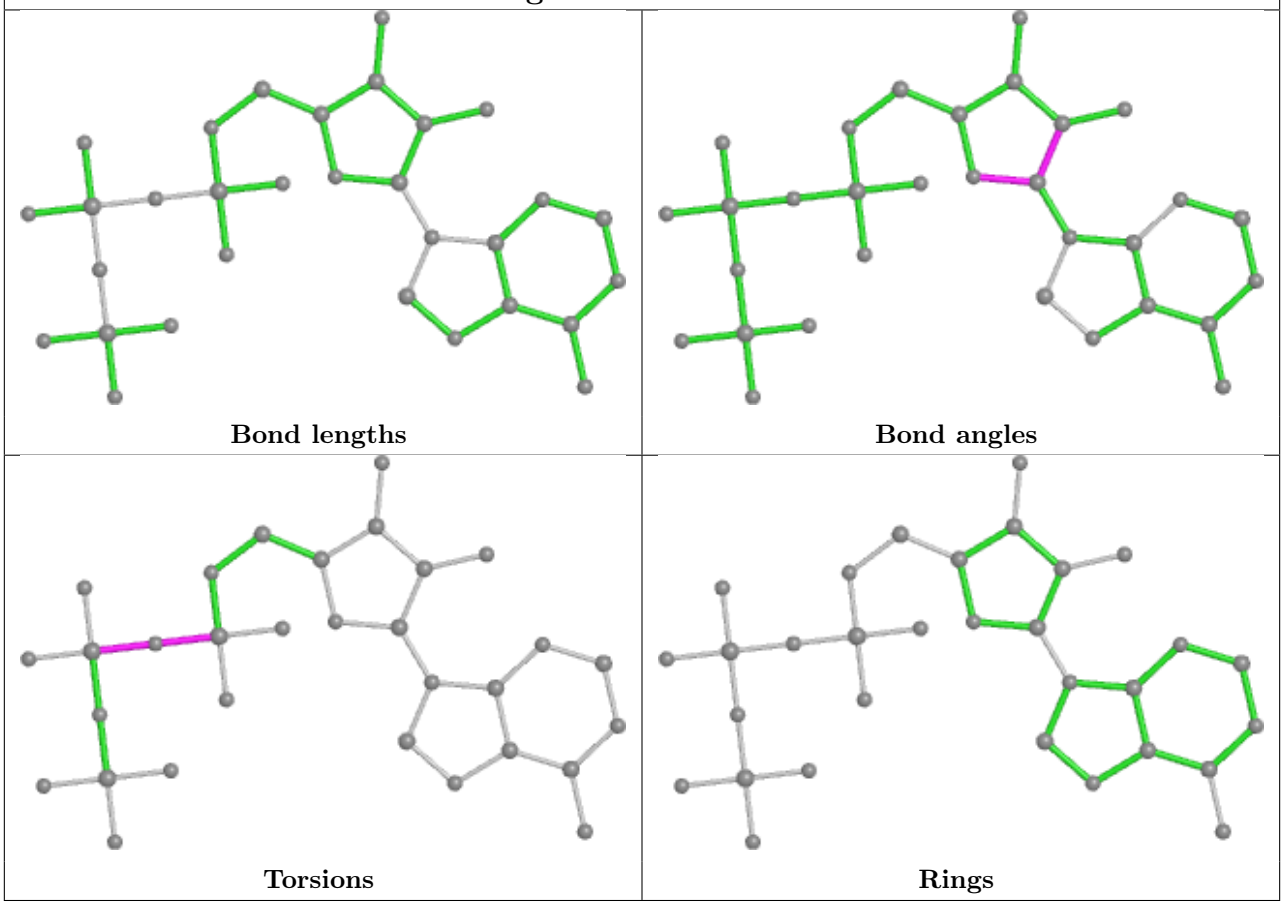
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	ATP	1	0
3	B	701	ATP	1	0

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 701



Ligand ATP B 701



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.