



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 15, 2020 – 11:24 pm BST

PDB ID : 3H0R  
Title : Structure of trna-dependent amidotransferase gatcab from aquifex aeolicus  
Authors : Wu, J.; Bu, W.; Sheppard, K.; Kitabatake, M.; Soll, D.; Smith, J.L.  
Deposited on : 2009-04-10  
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](mailto: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.

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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)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

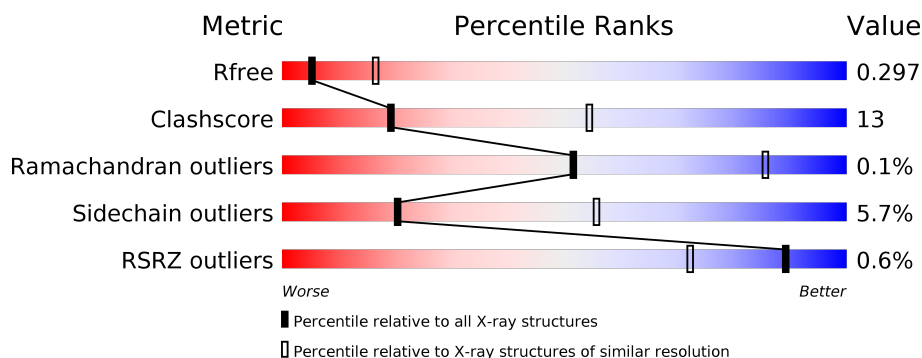
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	478	<div> <div>72%</div> <div>24%</div> <div>.</div> </div>
1	D	478	<div> <div>73%</div> <div>24%</div> <div>.</div> </div>
1	G	478	<div> <div>77%</div> <div>21%</div> <div>.</div> </div>
1	J	478	<div> <div>73%</div> <div>23%</div> <div>.</div> </div>
1	M	478	<div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	P	478	<div> <div>71%</div> <div>24%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	S	478	
1	V	478	
2	B	478	
2	E	478	
2	H	478	
2	K	478	
2	N	478	
2	Q	478	
2	T	478	
2	W	478	
3	C	94	
3	F	94	
3	I	94	
3	L	94	
3	O	94	
3	R	94	
3	U	94	
3	X	94	

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	ASN	A	901	-	-	-	X
4	ASN	D	902	-	-	X	-
4	ASN	S	907	-	-	X	-
4	ASN	V	908	-	-	X	-
9	ASP	H	482	-	-	X	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 63243 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 Glutamyl-tRNA(Gln) amidotransferase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	D	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	G	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	J	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	M	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	P	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	S	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			
1	V	478	Total	C	N	O	S	0	0	0
			3784	2450	615	712	7			

- Molecule 2 is a protein called Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	E	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	H	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	K	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	N	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	Q	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			

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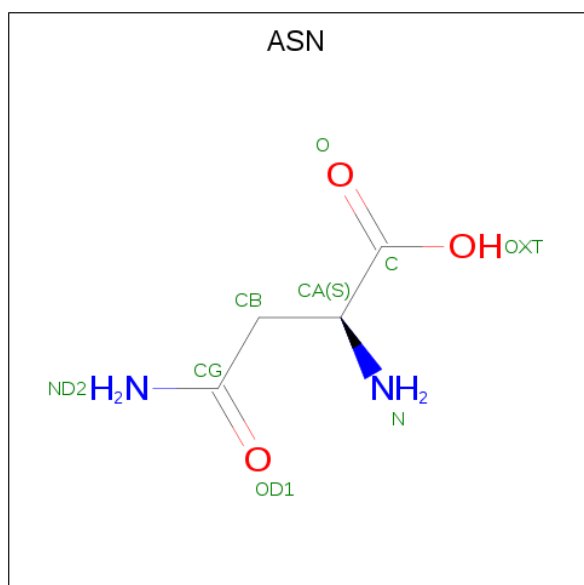
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			
2	W	410	Total	C	N	O	S	0	0	0
			3308	2104	567	622	15			

- Molecule 3 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	F	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	I	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	L	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	O	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	R	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	U	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			
3	X	91	Total	C	N	O	S	0	0	0
			764	487	125	150	2			

- Molecule 4 is ASPARAGINE (three-letter code: ASN) (formula:  $C_4H_8N_2O_3$ ).

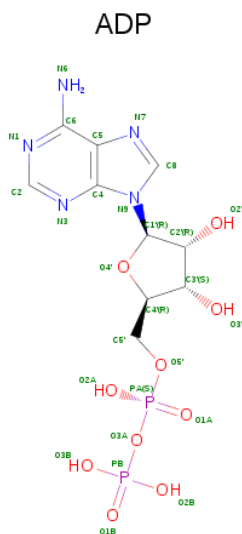


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		
4	D	1	Total	C	N	O	0	0
			8	4	1	3		
4	G	1	Total	C	N	O	0	0
			8	4	1	3		
4	J	1	Total	C	N	O	0	0
			8	4	1	3		
4	M	1	Total	C	N	O	0	0
			8	4	1	3		
4	P	1	Total	C	N	O	0	0
			8	4	1	3		
4	S	1	Total	C	N	O	0	0
			8	4	1	3		
4	V	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	Q	1	Total	Zn	0	0
			1	1		
5	K	1	Total	Zn	0	0
			1	1		
5	E	1	Total	Zn	0	0
			1	1		
5	H	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		
5	W	1	Total	Zn	0	0
			1	1		
5	T	1	Total	Zn	0	0
			1	1		
5	N	1	Total	Zn	0	0
			1	1		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).

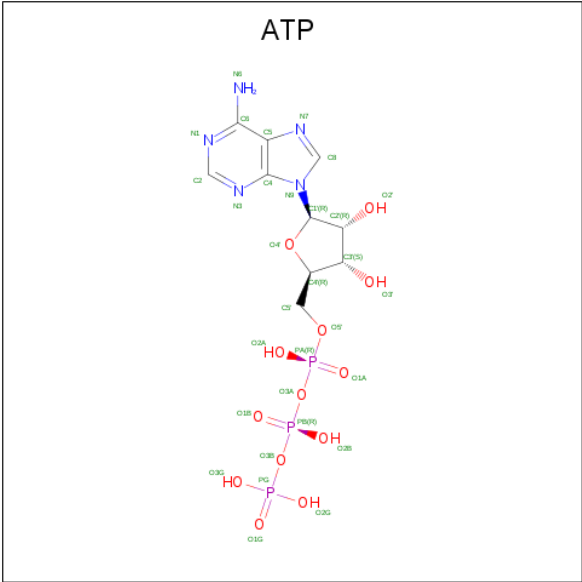


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
6	T	1	Total 27	C 10	N 5	O 10	P 2	0	0

- Molecule 7 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	Q	2	Total Mn 2 2	0	0
7	K	2	Total Mn 2 2	0	0
7	E	2	Total Mn 2 2	0	0
7	H	2	Total Mn 2 2	0	0
7	B	2	Total Mn 2 2	0	0
7	W	2	Total Mn 2 2	0	0
7	T	2	Total Mn 2 2	0	0
7	N	2	Total Mn 2 2	0	0

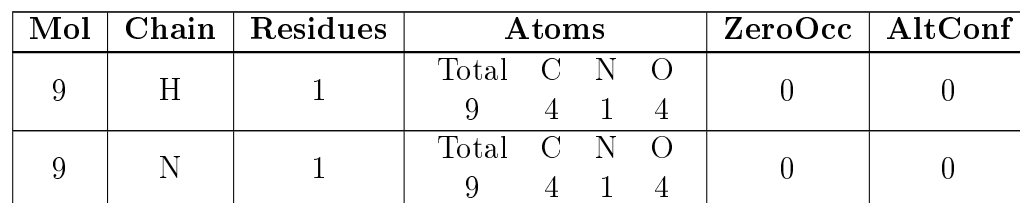
- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
8	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
8	K	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
8	N	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
8	Q	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
8	W	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 9 is ASPARTIC ACID (three-letter code: ASP) (formula: C<sub>4</sub>H<sub>7</sub>NO<sub>4</sub>).





- | Mol | Chain | Residues | Atoms          | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 10  | A     | 1        | Total O<br>1 1 | 0       | 0       |
| 10  | B     | 4        | Total O<br>4 4 | 0       | 0       |
| 10  | E     | 3        | Total O<br>3 3 | 0       | 0       |
| 10  | G     | 2        | Total O<br>2 2 | 0       | 0       |
| 10  | H     | 3        | Total O<br>3 3 | 0       | 0       |
| 10  | J     | 2        | Total O<br>2 2 | 0       | 0       |
| 10  | K     | 5        | Total O<br>5 5 | 0       | 0       |
| 10  | M     | 3        | Total O<br>3 3 | 0       | 0       |
| 10  | N     | 5        | Total O<br>5 5 | 0       | 0       |
| 10  | P     | 2        | Total O<br>2 2 | 0       | 0       |



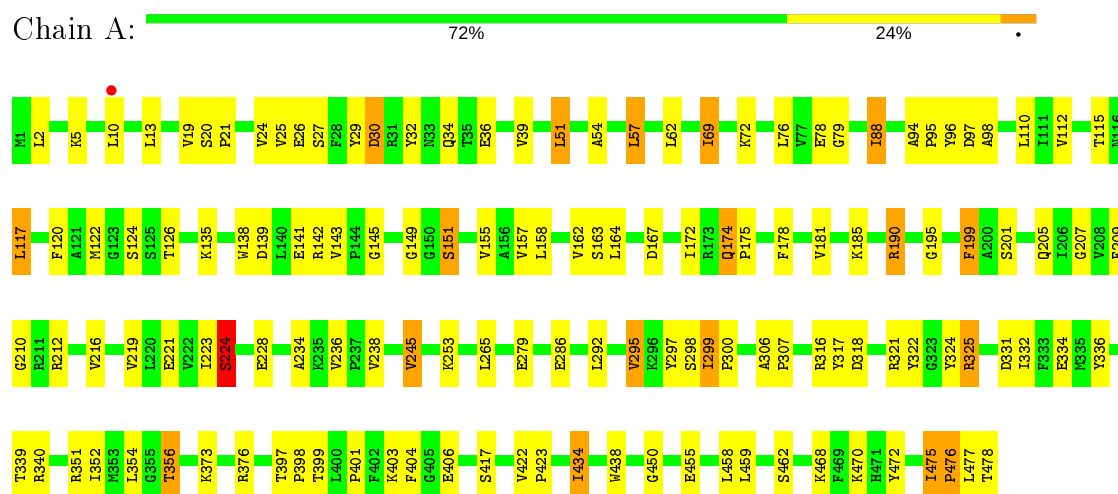
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	Q	7	Total 7	O 7	0	0
10	T	5	Total 5	O 5	0	0
10	V	1	Total 1	O 1	0	0
10	W	6	Total 6	O 6	0	0

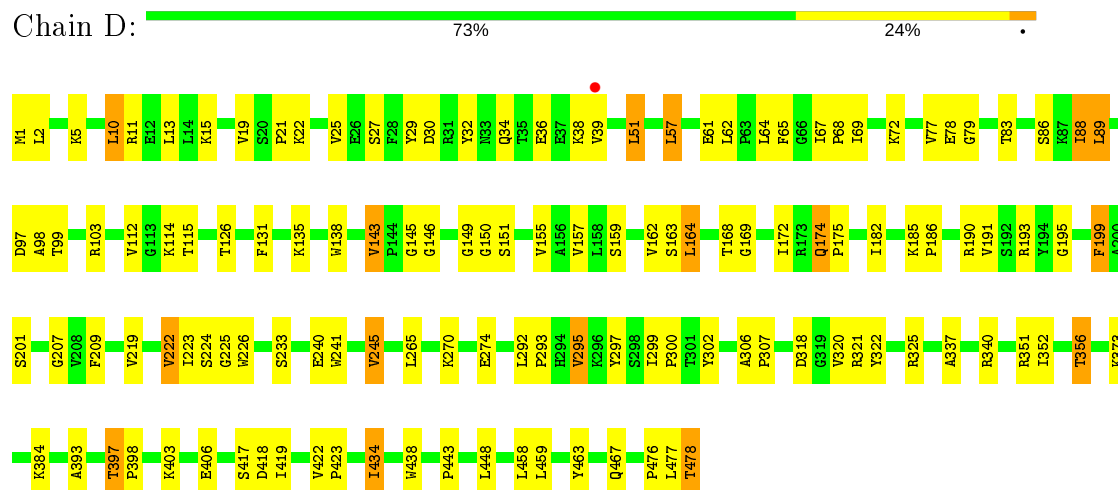
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

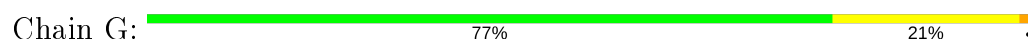
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

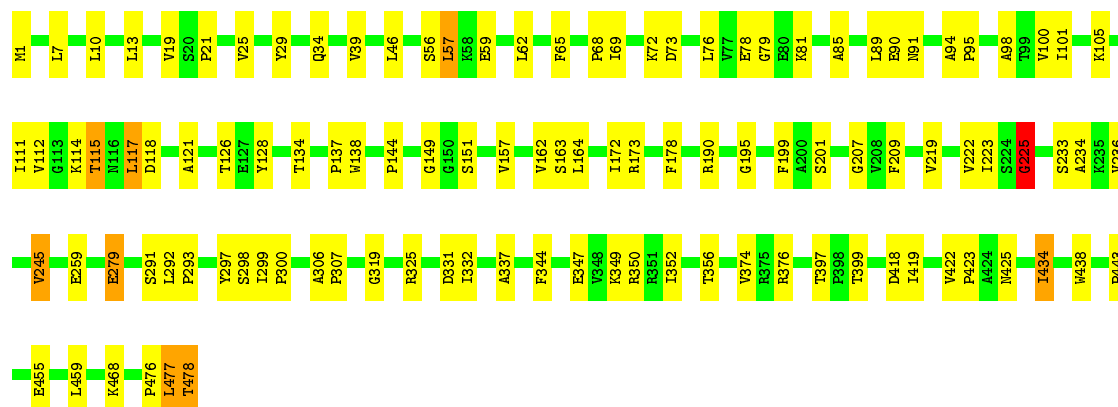


- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A



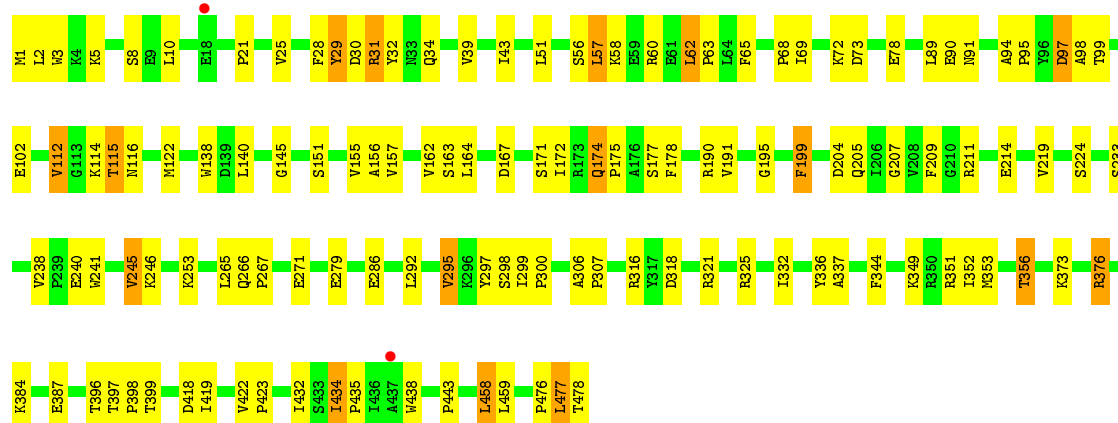
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A





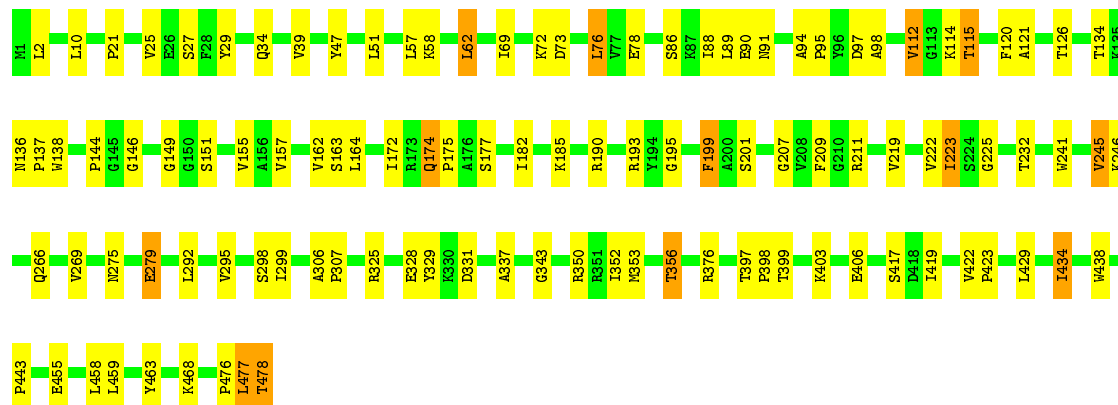
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain J: 73% 23% •



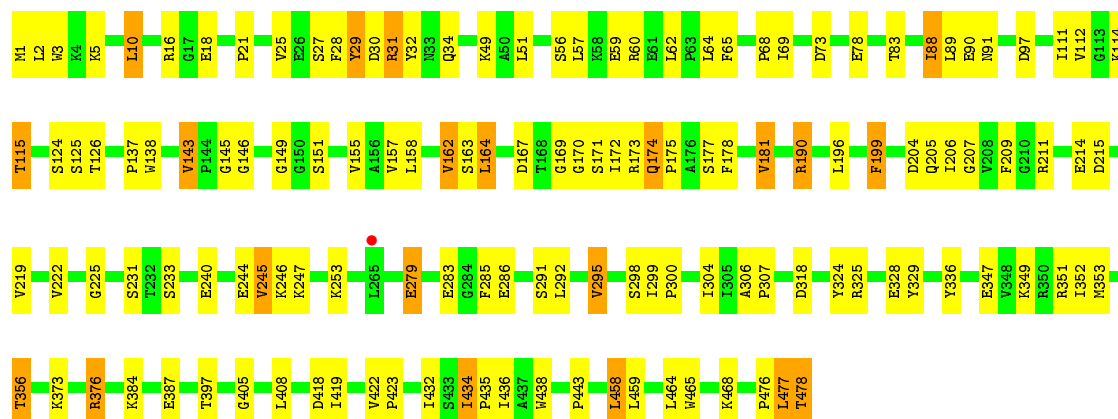
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain M: 77% 20% •



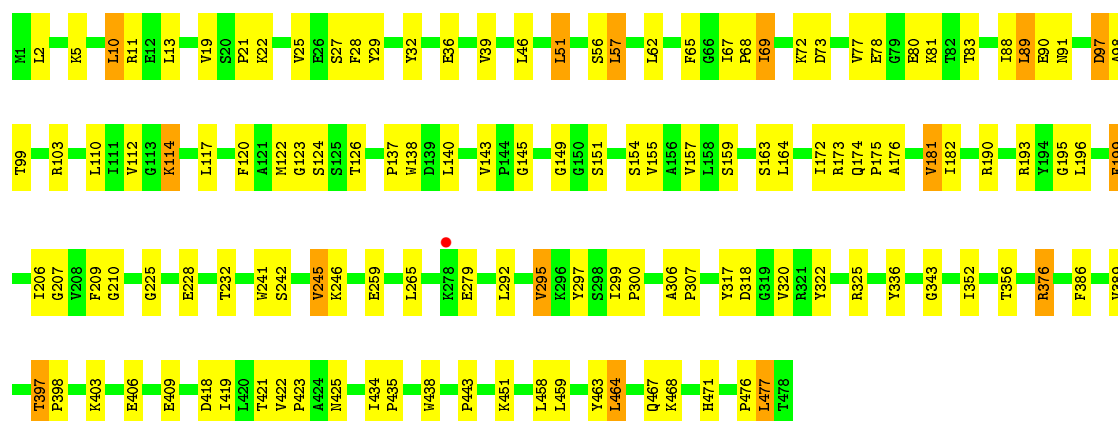
- Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain P: 71% 24% •



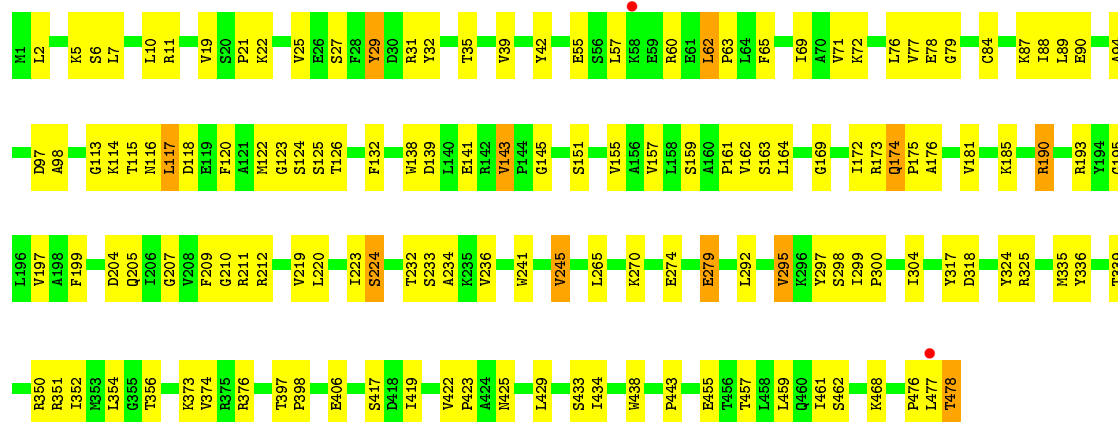
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain S: 73% 24%



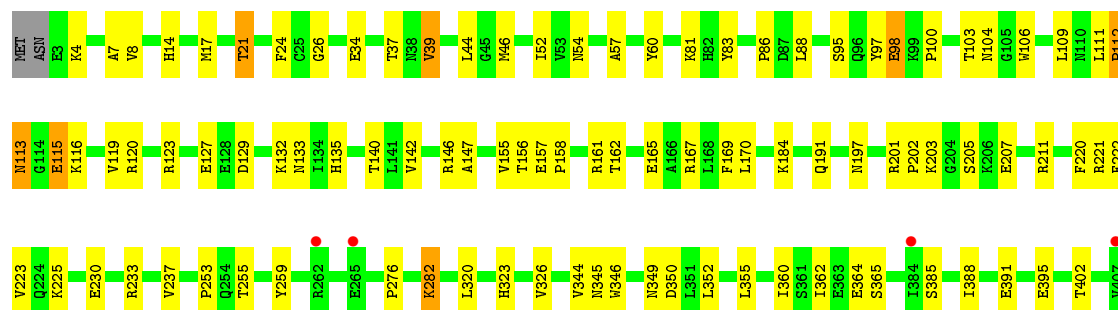
• Molecule 1: Glutamyl-tRNA(Gln) amidotransferase subunit A

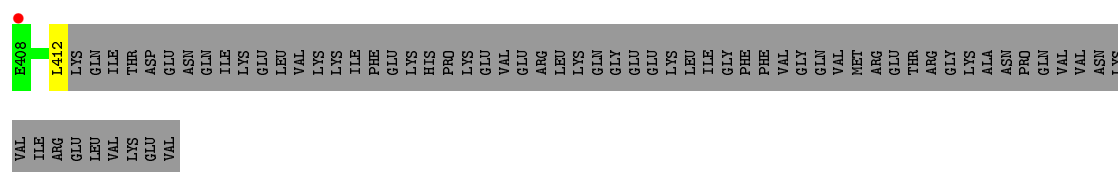
Chain V: 70% 27%



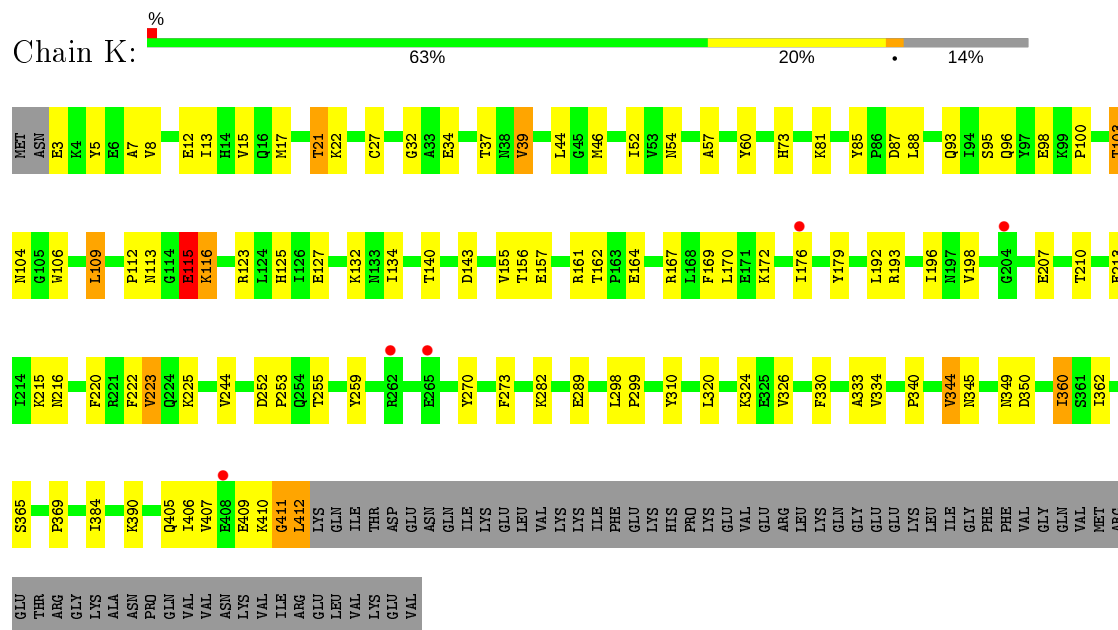
• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

Chain B: 62% 21% 14%

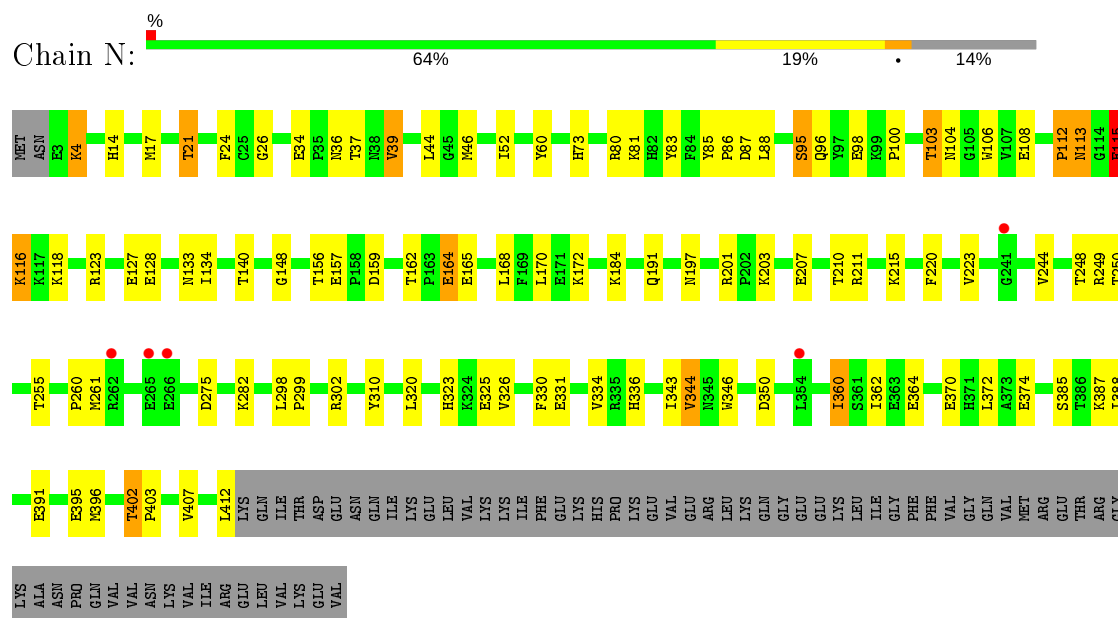




• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

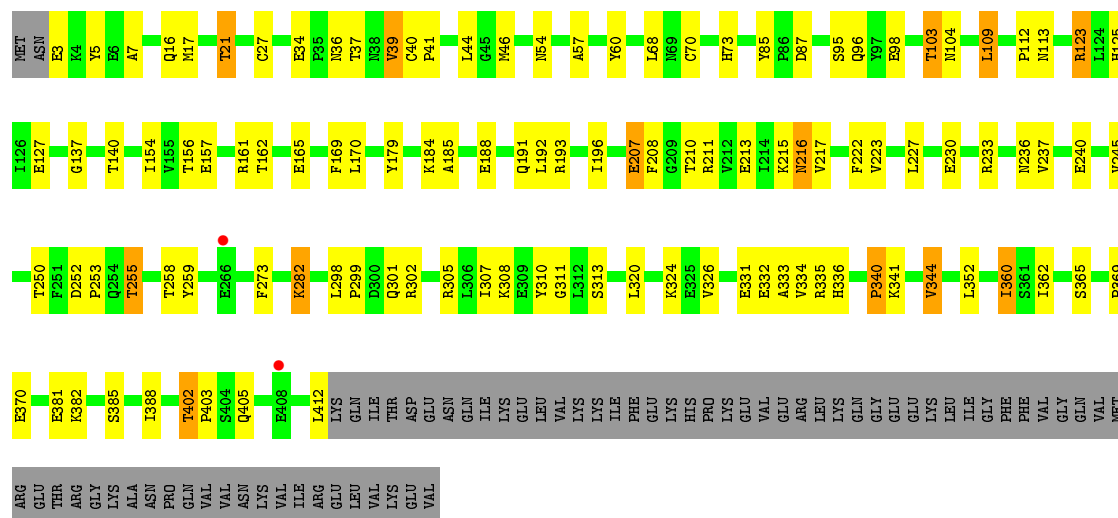


• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

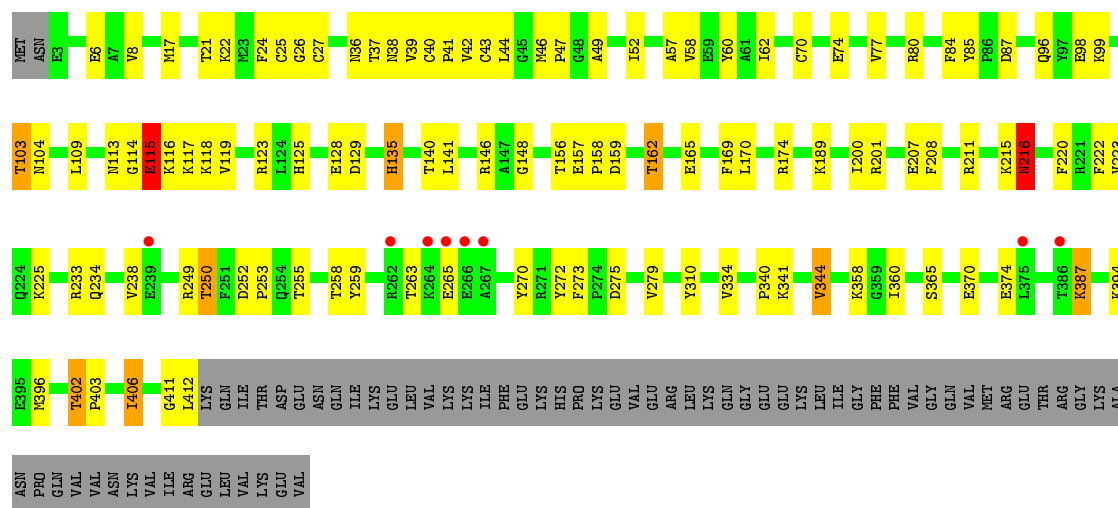


• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

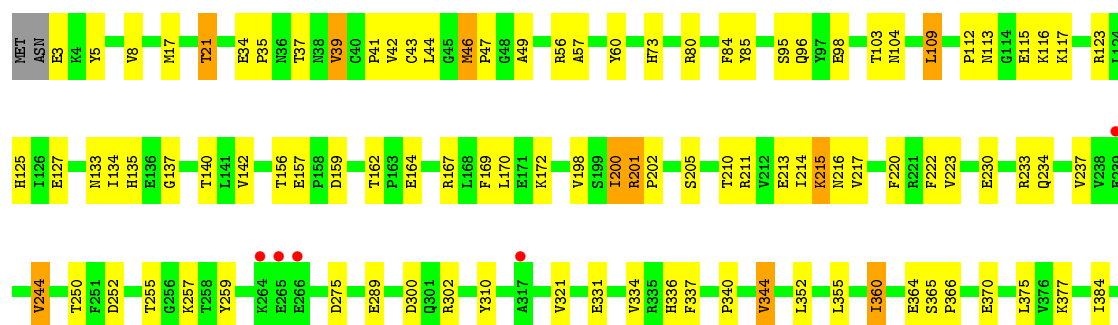




• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B



• Molecule 2: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

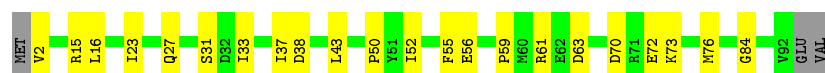






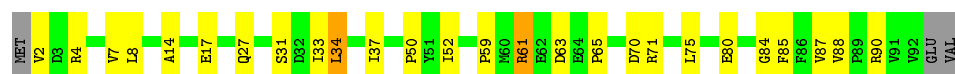
- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain C: 73% 23%



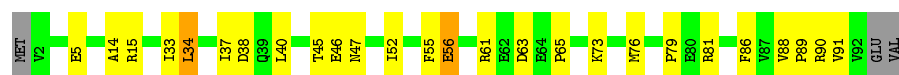
- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain F: 69% 26%



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain I: 69% 26%



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain L: 69% 27%



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain O: 80% 16%



- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain R: 73% 23%

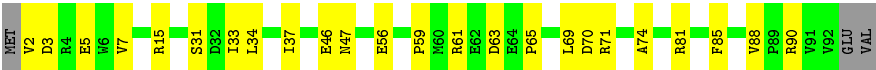


- Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain U: 

71%

26%

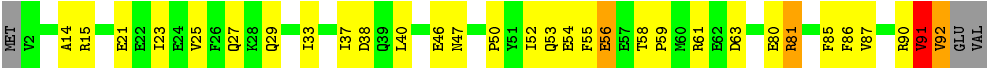


● Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain X: 

64%

29%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	127.38Å 130.41Å 153.97Å 89.89° 90.21° 89.95°	Depositor
Resolution (Å)	48.97 – 3.00 48.98 – 2.79	Depositor EDS
% Data completeness (in resolution range)	96.0 (48.97-3.00) 93.8 (48.98-2.79)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.263 , 0.306 0.258 , 0.297	Depositor DCC
$R_{free}$ test set	11760 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.3	Xtriage
Anisotropy	0.988	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 16.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -k,h,l 0.000 for k,-h,l 0.140 for h,-k,-l 0.439 for -h,k,-l 0.145 for -h,-k,l 0.000 for -k,-h,-l 0.000 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	63243	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.61 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.6768e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: ZN, MN, ATP, ADP

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	0.66	0/3874	0.71	1/5244 (0.0%)
1	D	0.65	0/3874	0.69	1/5244 (0.0%)
1	G	0.62	0/3874	0.68	0/5244
1	J	0.62	0/3874	0.70	1/5244 (0.0%)
1	M	0.63	0/3874	0.70	1/5244 (0.0%)
1	P	0.62	0/3874	0.67	1/5244 (0.0%)
1	S	0.64	0/3874	0.69	2/5244 (0.0%)
1	V	0.67	0/3874	0.72	2/5244 (0.0%)
2	B	0.60	0/3371	0.66	0/4541
2	E	0.61	0/3371	0.65	0/4541
2	H	0.62	1/3371 (0.0%)	0.70	1/4541 (0.0%)
2	K	0.63	1/3371 (0.0%)	0.69	0/4541
2	N	0.60	0/3371	0.68	0/4541
2	Q	0.62	1/3371 (0.0%)	0.69	0/4541
2	T	0.66	1/3371 (0.0%)	0.68	2/4541 (0.0%)
2	W	0.62	2/3371 (0.1%)	0.69	0/4541
3	C	0.59	0/778	0.74	0/1050
3	F	0.60	0/778	0.75	0/1050
3	I	0.62	0/778	0.69	0/1050
3	L	0.70	1/778 (0.1%)	0.76	0/1050
3	O	0.62	0/778	0.73	0/1050
3	R	0.61	0/778	0.73	0/1050
3	U	0.63	0/778	0.76	0/1050
3	X	0.60	0/778	0.76	0/1050
All	All	0.63	7/64184 (0.0%)	0.69	12/86680 (0.0%)

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
1	A	0	4
1	D	0	2
1	G	0	3
1	M	0	4
1	P	0	1
1	S	0	1
2	B	0	4
2	E	0	3
2	H	0	2
2	K	0	4
2	N	0	2
2	Q	0	2
2	T	0	2
2	W	0	3
3	I	0	1
3	R	0	1
All	All	0	39

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	43	CYS	CB-SG	-5.94	1.72	1.81
2	W	43	CYS	CB-SG	-5.74	1.72	1.81
2	W	289	GLU	CG-CD	5.47	1.60	1.51
2	K	289	GLU	CG-CD	5.19	1.59	1.51
2	H	98	GLU	CG-CD	5.18	1.59	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	174	ARG	NE-CZ-NH1	5.72	123.16	120.30
2	H	120	ARG	NE-CZ-NH2	-5.60	117.50	120.30
2	T	129	ASP	CB-CG-OD1	5.37	123.13	118.30
1	M	97	ASP	CB-CG-OD2	5.23	123.01	118.30
1	V	97	ASP	CB-CG-OD2	5.22	123.00	118.30

There are no chirality outliers.

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	223	ILE	Peptide
1	A	224	SER	Peptide

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Mol	Chain	Res	Type	Group
1	A	475	ILE	Peptide
1	A	477	LEU	Peptide
2	B	32	GLY	Peptide

## 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	3784	0	3816	110	0
1	D	3784	0	3816	116	0
1	G	3784	0	3816	95	0
1	J	3784	0	3816	106	0
1	M	3784	0	3816	88	0
1	P	3784	0	3816	115	0
1	S	3784	0	3816	103	0
1	V	3784	0	3816	107	0
2	B	3308	0	3354	112	0
2	E	3308	0	3353	116	0
2	H	3308	0	3353	91	0
2	K	3308	0	3353	84	0
2	N	3308	0	3353	81	0
2	Q	3308	0	3353	89	0
2	T	3308	0	3353	93	0
2	W	3308	0	3353	92	0
3	C	764	0	755	21	0
3	F	764	0	755	23	0
3	I	764	0	755	30	0
3	L	764	0	755	22	0
3	O	764	0	755	17	0
3	R	764	0	755	17	0
3	U	764	0	755	17	0
3	X	764	0	755	32	0
4	A	8	0	3	1	0
4	D	8	0	3	5	0
4	G	8	0	3	0	0
4	J	8	0	3	0	0
4	M	8	0	3	1	0
4	P	8	0	3	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	S	8	0	3	4	0
4	V	8	0	3	4	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	H	1	0	0	0	0
5	K	1	0	0	0	0
5	N	1	0	0	0	0
5	Q	1	0	0	0	0
5	T	1	0	0	0	0
5	W	1	0	0	0	0
6	B	27	0	12	0	0
6	T	27	0	12	2	0
7	B	2	0	0	0	0
7	E	2	0	0	0	0
7	H	2	0	0	0	0
7	K	2	0	0	0	0
7	N	2	0	0	0	0
7	Q	2	0	0	0	0
7	T	2	0	0	0	0
7	W	2	0	0	0	0
8	E	31	0	12	1	0
8	H	31	0	12	7	0
8	K	31	0	12	1	0
8	N	31	0	12	1	0
8	Q	31	0	12	3	0
8	W	31	0	12	3	0
9	H	9	0	3	5	0
9	N	9	0	3	3	0
10	A	1	0	0	0	0
10	B	4	0	0	0	0
10	E	3	0	0	0	0
10	G	2	0	0	1	0
10	H	3	0	0	2	0
10	J	2	0	0	1	0
10	K	5	0	0	0	0
10	M	3	0	0	2	0
10	N	5	0	0	1	0
10	P	2	0	0	1	0
10	Q	7	0	0	0	0
10	T	5	0	0	0	0
10	V	1	0	0	0	0
10	W	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	63243	0	63519	1639	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 13.

The worst 5 of 1639 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:W:384:ILE:HG22	2:W:412:LEU:CD2	1.62	1.28
1:D:83:THR:HG21	1:D:131:PHE:CZ	1.78	1.19
2:B:280:PRO:HD2	3:C:55:PHE:CZ	1.85	1.12
2:K:115:GLU:OE2	2:K:115:GLU:HA	1.48	1.10
1:V:190:ARG:HH11	1:V:190:ARG:HG3	1.11	1.10

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	476/478 (100%)	455 (96%)	20 (4%)	1 (0%)	47	82
1	D	476/478 (100%)	457 (96%)	19 (4%)	0	100	100
1	G	476/478 (100%)	454 (95%)	21 (4%)	1 (0%)	47	82
1	J	476/478 (100%)	458 (96%)	17 (4%)	1 (0%)	47	82
1	M	476/478 (100%)	454 (95%)	22 (5%)	0	100	100
1	P	476/478 (100%)	455 (96%)	21 (4%)	0	100	100
1	S	476/478 (100%)	458 (96%)	18 (4%)	0	100	100
1	V	476/478 (100%)	458 (96%)	18 (4%)	0	100	100
2	B	408/478 (85%)	388 (95%)	19 (5%)	1 (0%)	47	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	408/478 (85%)	381 (93%)	27 (7%)	0	100	100
2	H	408/478 (85%)	385 (94%)	23 (6%)	0	100	100
2	K	408/478 (85%)	381 (93%)	27 (7%)	0	100	100
2	N	408/478 (85%)	388 (95%)	20 (5%)	0	100	100
2	Q	408/478 (85%)	383 (94%)	24 (6%)	1 (0%)	47	82
2	T	408/478 (85%)	375 (92%)	32 (8%)	1 (0%)	47	82
2	W	408/478 (85%)	388 (95%)	19 (5%)	1 (0%)	47	82
3	C	89/94 (95%)	82 (92%)	7 (8%)	0	100	100
3	F	89/94 (95%)	84 (94%)	5 (6%)	0	100	100
3	I	89/94 (95%)	80 (90%)	8 (9%)	1 (1%)	14	50
3	L	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
3	O	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
3	R	89/94 (95%)	82 (92%)	7 (8%)	0	100	100
3	U	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
3	X	89/94 (95%)	78 (88%)	10 (11%)	1 (1%)	14	50
All	All	7784/8400 (93%)	7379 (95%)	396 (5%)	9 (0%)	51	85

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	56	GLU
2	B	113	ASN
2	T	216	ASN
2	W	216	ASN
1	J	477	LEU

### 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	406/406 (100%)	379 (93%)	27 (7%)	16	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	406/406 (100%)	381 (94%)	25 (6%)	18	52
1	G	406/406 (100%)	388 (96%)	18 (4%)	28	65
1	J	406/406 (100%)	378 (93%)	28 (7%)	15	48
1	M	406/406 (100%)	383 (94%)	23 (6%)	20	56
1	P	406/406 (100%)	372 (92%)	34 (8%)	11	38
1	S	406/406 (100%)	380 (94%)	26 (6%)	17	51
1	V	406/406 (100%)	384 (95%)	22 (5%)	22	57
2	B	364/427 (85%)	342 (94%)	22 (6%)	19	53
2	E	364/427 (85%)	346 (95%)	18 (5%)	25	61
2	H	364/427 (85%)	350 (96%)	14 (4%)	33	69
2	K	364/427 (85%)	346 (95%)	18 (5%)	25	61
2	N	364/427 (85%)	341 (94%)	23 (6%)	18	51
2	Q	364/427 (85%)	344 (94%)	20 (6%)	21	57
2	T	364/427 (85%)	345 (95%)	19 (5%)	23	59
2	W	364/427 (85%)	345 (95%)	19 (5%)	23	59
3	C	86/89 (97%)	82 (95%)	4 (5%)	26	63
3	F	86/89 (97%)	82 (95%)	4 (5%)	26	63
3	I	86/89 (97%)	81 (94%)	5 (6%)	20	55
3	L	86/89 (97%)	81 (94%)	5 (6%)	20	55
3	O	86/89 (97%)	81 (94%)	5 (6%)	20	55
3	R	86/89 (97%)	83 (96%)	3 (4%)	36	71
3	U	86/89 (97%)	81 (94%)	5 (6%)	20	55
3	X	86/89 (97%)	79 (92%)	7 (8%)	11	40
All	All	6848/7376 (93%)	6454 (94%)	394 (6%)	20	55

5 of 394 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	223	VAL
2	N	134	ILE
1	V	354	LEU
3	L	34	LEU
1	M	199	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	322	ASN
2	N	216	ASN
2	Q	216	ASN
2	K	216	ASN
1	P	174	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 carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

Of 42 ligands modelled in this entry, 24 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	$\# Z  > 2$
6	ADP	T	479	-	24,29,29	0.95	1 (4%)	29,45,45	1.45	5 (17%)
8	ATP	Q	479	-	26,33,33	1.10	1 (3%)	31,52,52	1.62	4 (12%)
8	ATP	K	479	-	26,33,33	0.99	2 (7%)	31,52,52	1.65	6 (19%)
8	ATP	W	479	-	26,33,33	1.30	2 (7%)	31,52,52	2.08	11 (35%)
8	ATP	E	479	-	26,33,33	0.91	1 (3%)	31,52,52	1.40	4 (12%)
6	ADP	B	479	-	24,29,29	1.03	2 (8%)	29,45,45	1.71	7 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	ATP	N	479	-	26,33,33	1.02	2 (7%)	31,52,52	1.52	6 (19%)
8	ATP	H	479	-	26,33,33	1.02	1 (3%)	31,52,52	1.73	7 (22%)

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
6	ADP	T	479	-	-	5/12/32/32	0/3/3/3
8	ATP	Q	479	-	-	4/18/38/38	0/3/3/3
8	ATP	K	479	-	-	4/18/38/38	0/3/3/3
8	ATP	W	479	-	-	5/18/38/38	0/3/3/3
8	ATP	E	479	-	-	5/18/38/38	0/3/3/3
6	ADP	B	479	-	-	0/12/32/32	0/3/3/3
8	ATP	N	479	-	-	7/18/38/38	0/3/3/3
8	ATP	H	479	-	-	5/18/38/38	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	W	479	ATP	C2'-C1'	-3.29	1.48	1.53
8	Q	479	ATP	C2'-C1'	-3.15	1.49	1.53
8	N	479	ATP	C5-C4	2.61	1.47	1.40
8	W	479	ATP	O4'-C1'	2.50	1.44	1.41
6	B	479	ADP	C2'-C1'	-2.45	1.50	1.53

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	Q	479	ATP	PA-O3A-PB	-4.44	117.60	132.83
8	K	479	ATP	PA-O3A-PB	-4.41	117.68	132.83
8	W	479	ATP	O3'-C3'-C4'	-4.36	98.44	111.05
8	W	479	ATP	PA-O3A-PB	-4.35	117.90	132.83
8	Q	479	ATP	N3-C2-N1	-4.27	122.01	128.68

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

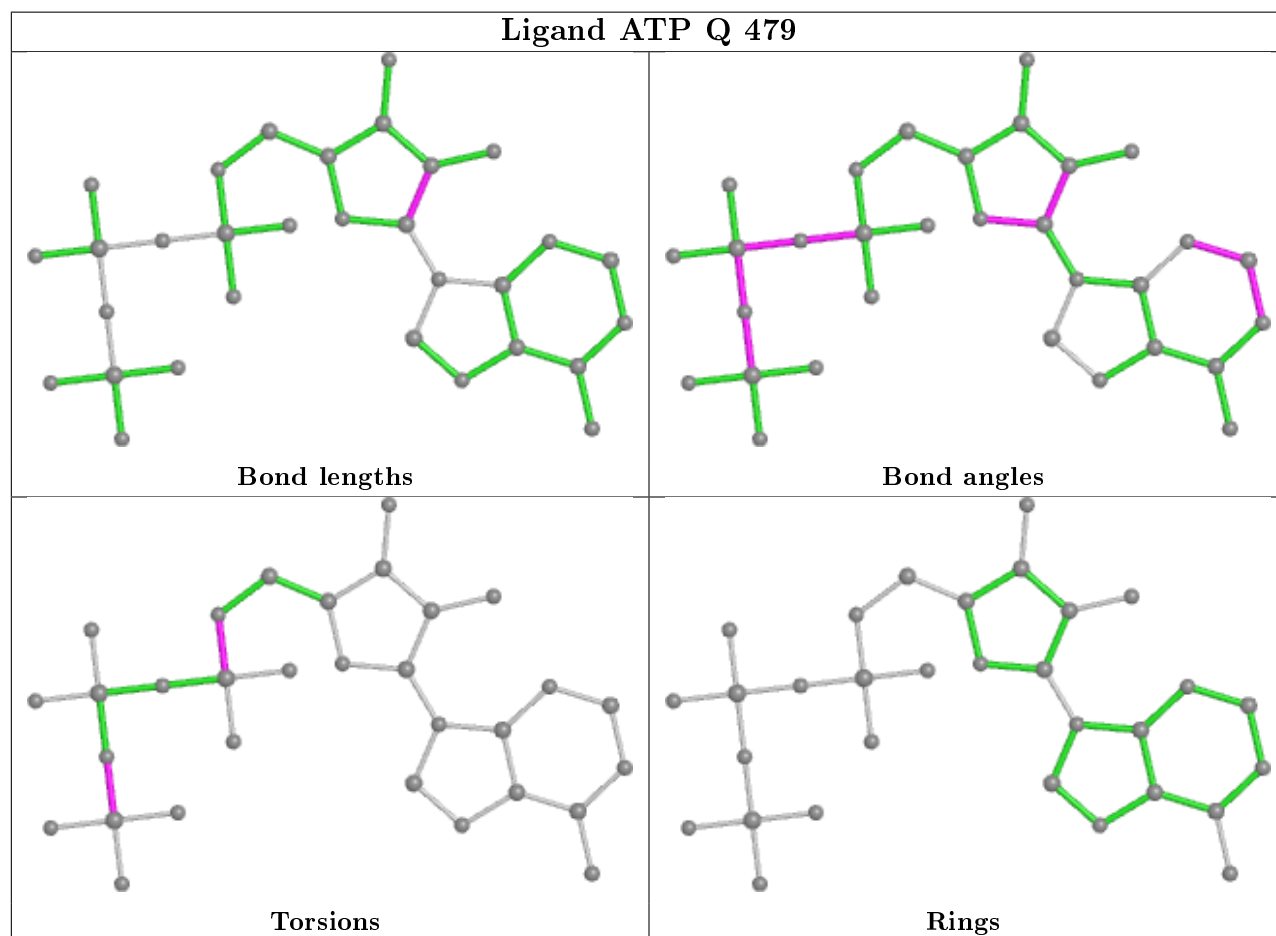
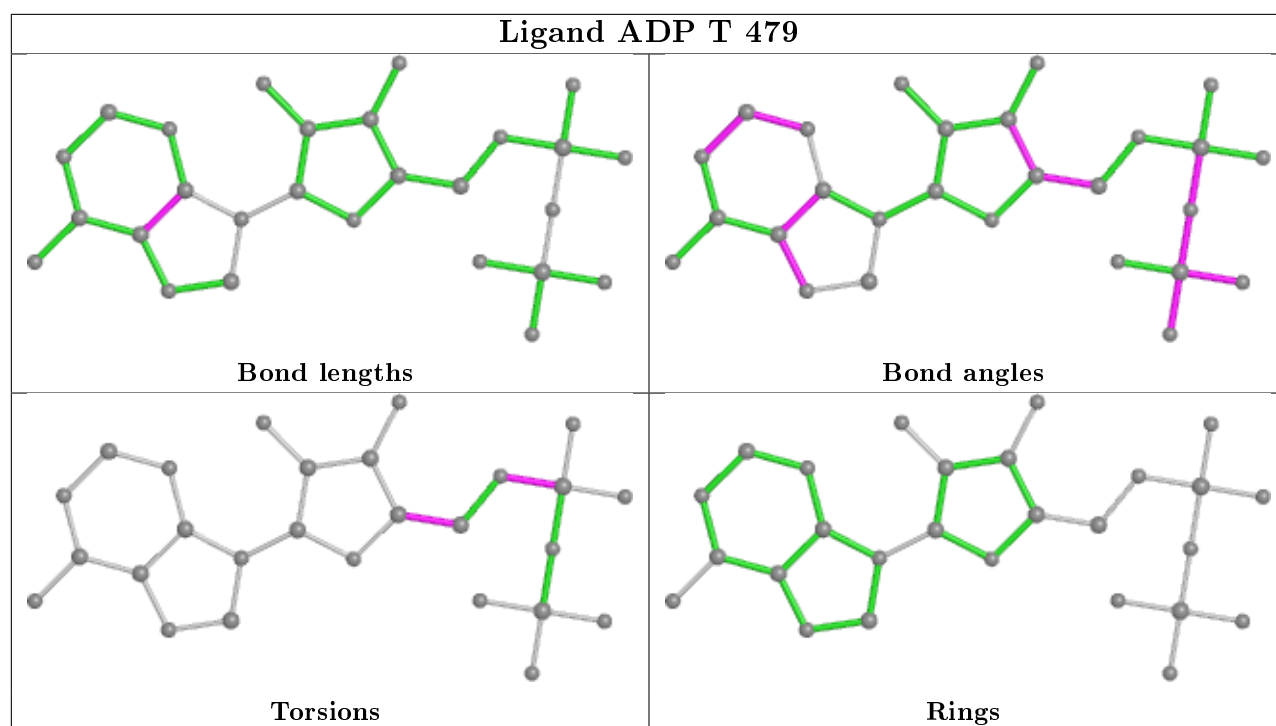
Mol	Chain	Res	Type	Atoms
6	T	479	ADP	C5'-O5'-PA-O1A
6	T	479	ADP	C5'-O5'-PA-O2A
6	T	479	ADP	C5'-O5'-PA-O3A
6	T	479	ADP	O4'-C4'-C5'-O5'
6	T	479	ADP	C3'-C4'-C5'-O5'

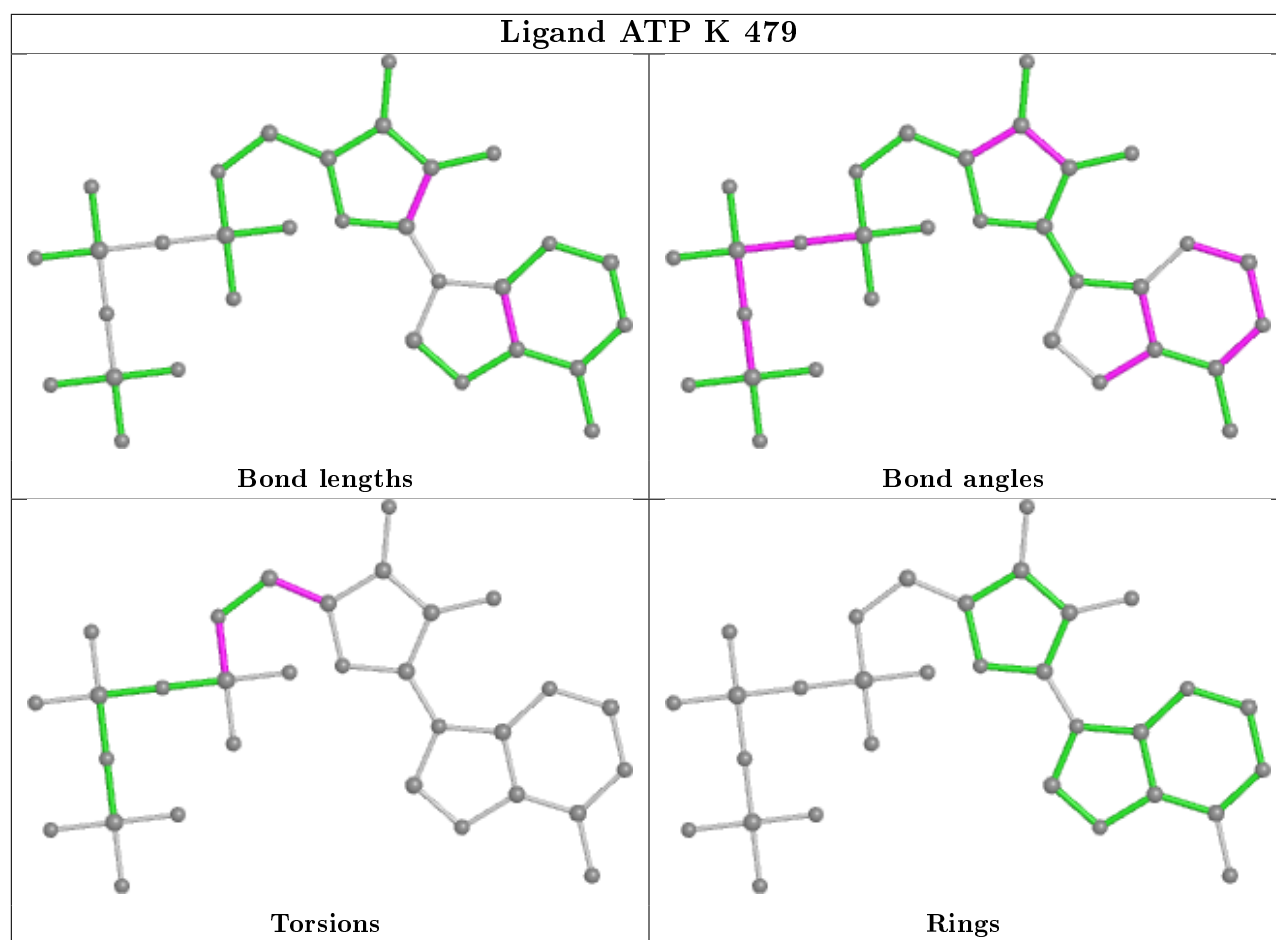
There are no ring outliers.

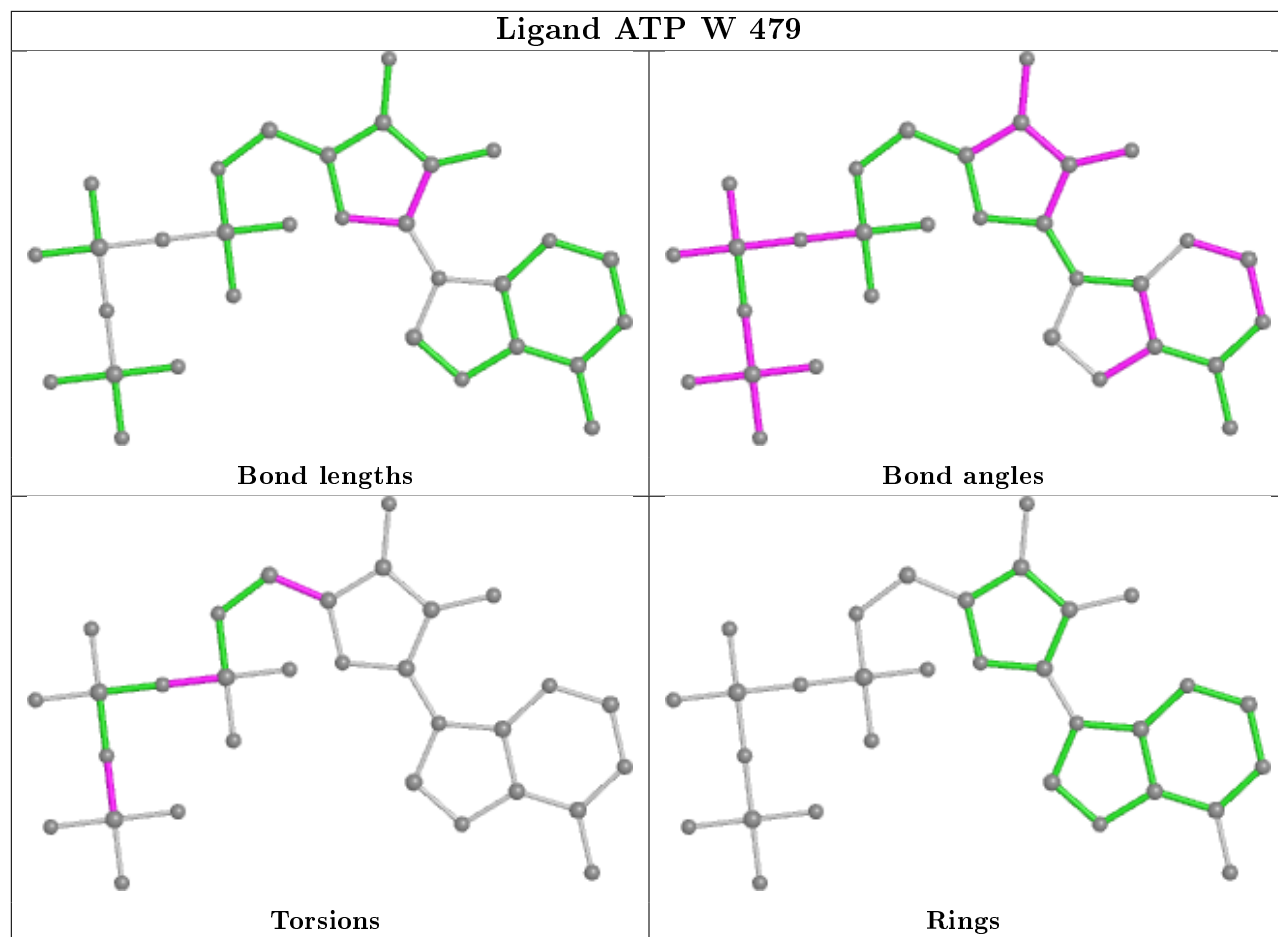
7 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	T	479	ADP	2	0
8	Q	479	ATP	3	0
8	K	479	ATP	1	0
8	W	479	ATP	3	0
8	E	479	ATP	1	0
8	N	479	ATP	1	0
8	H	479	ATP	7	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 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.

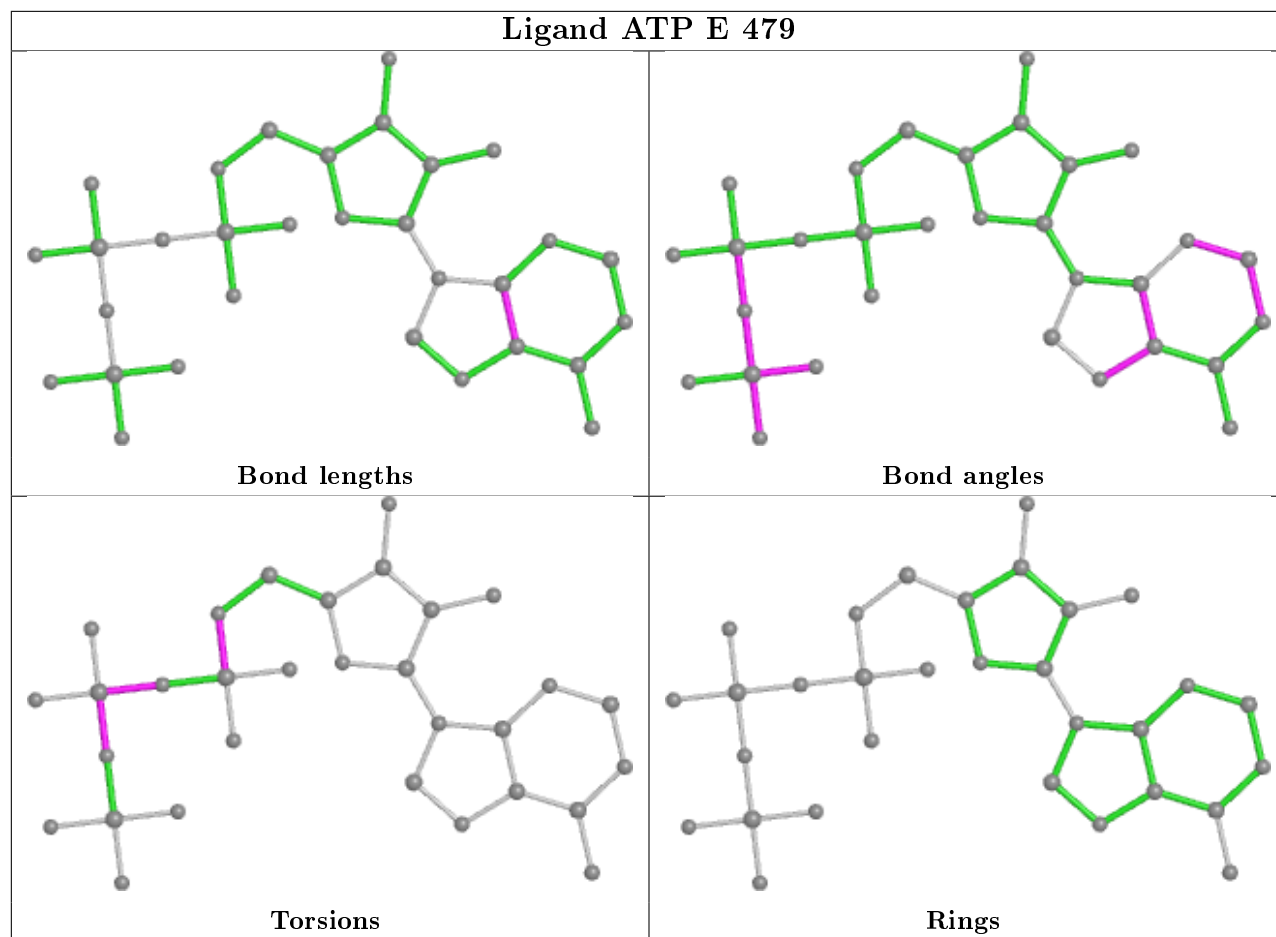




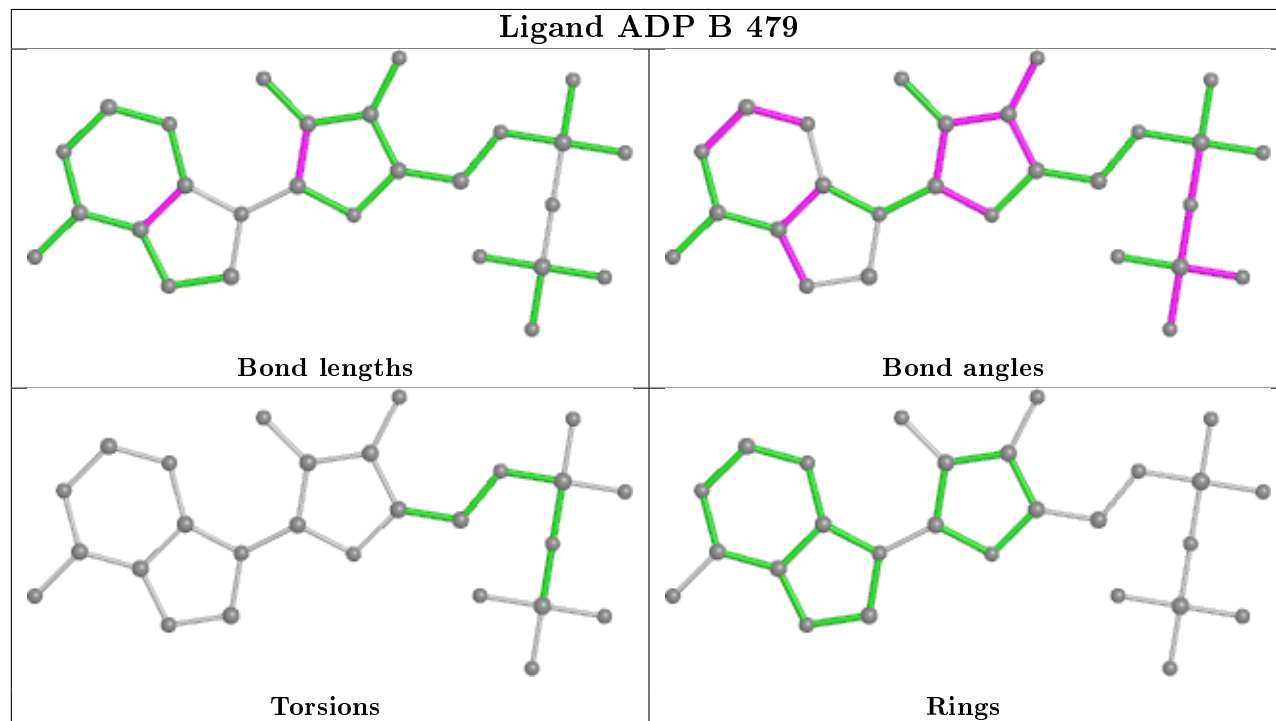


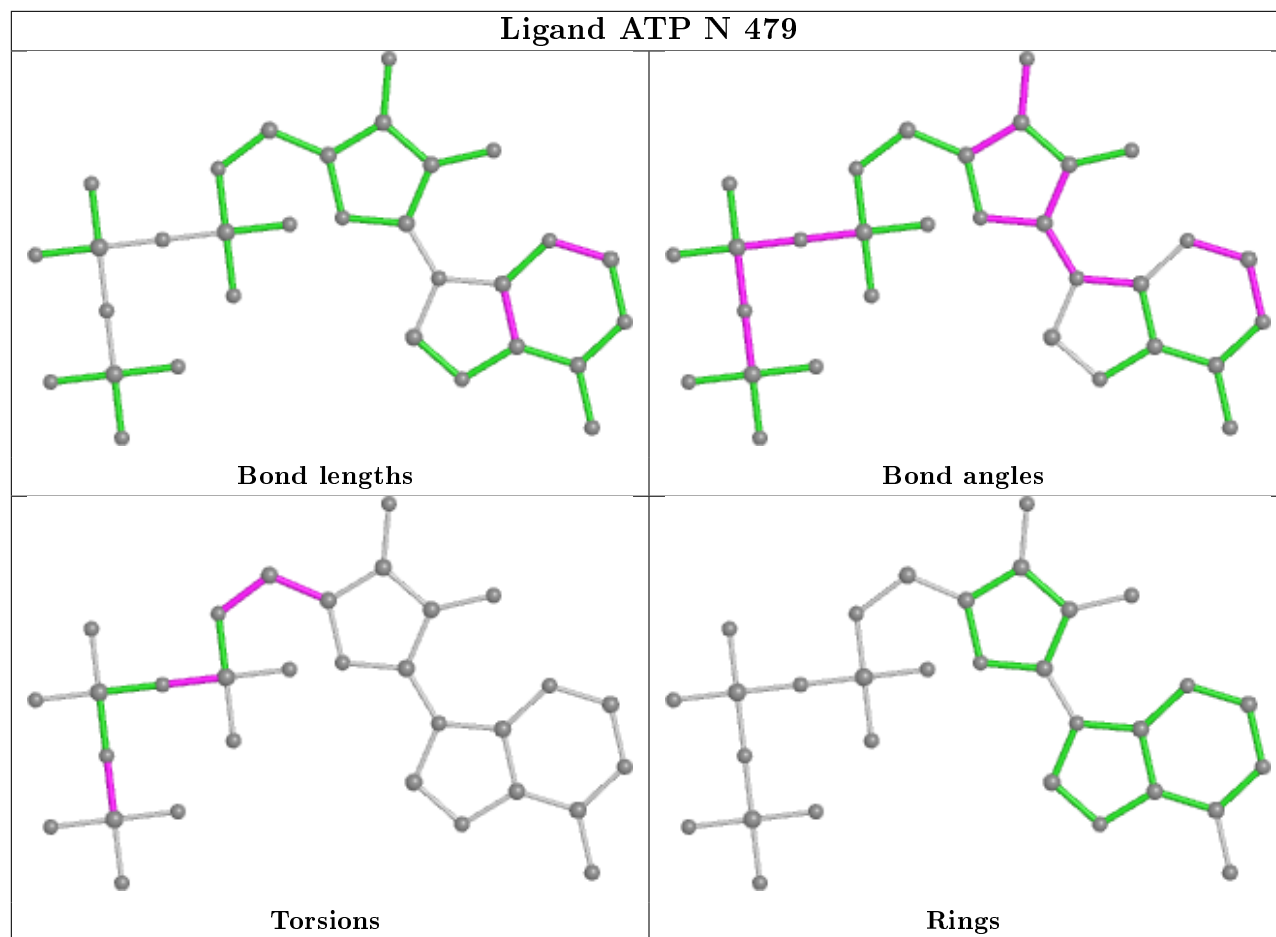


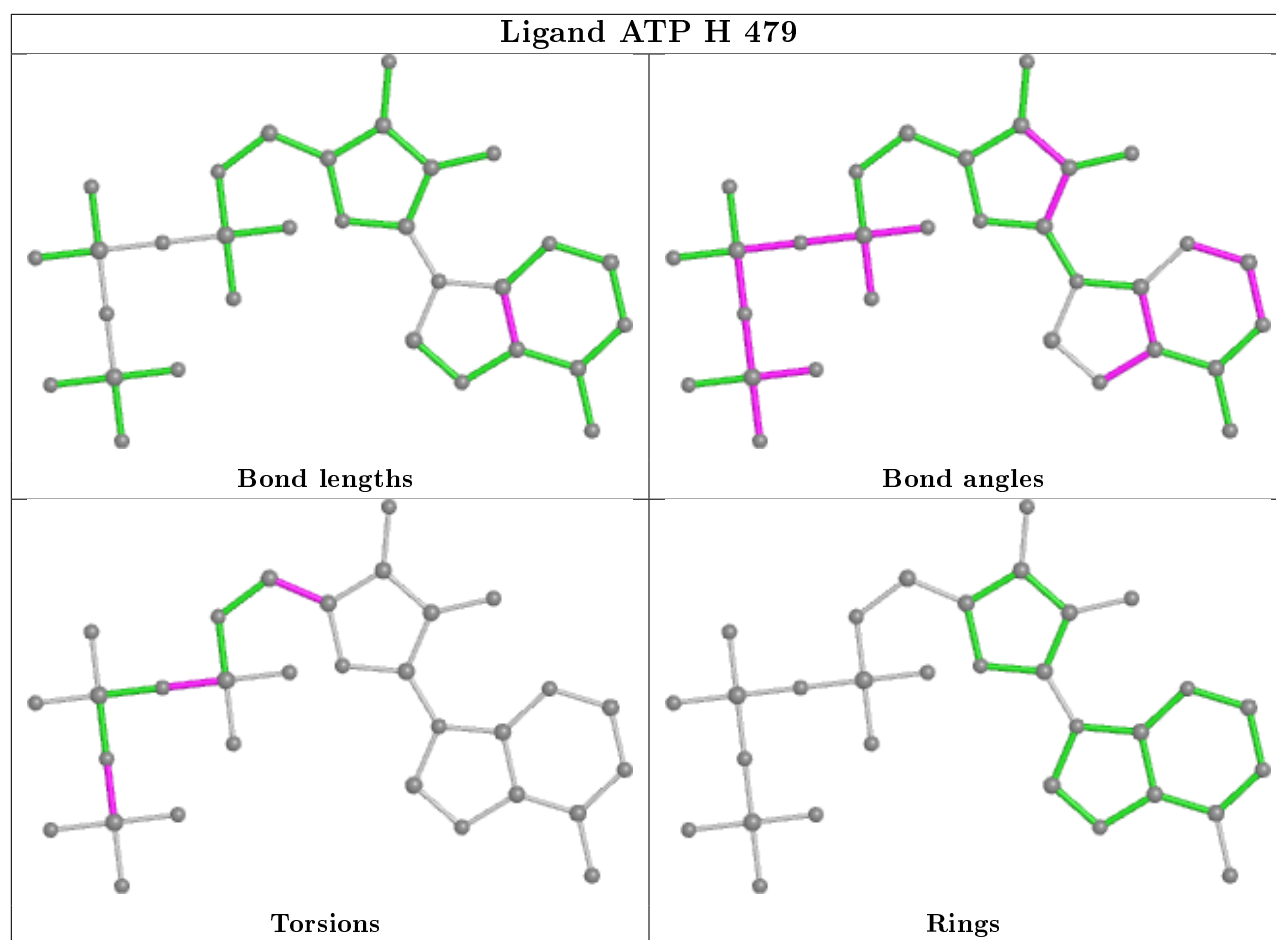
## Ligand ATP E 479



## Ligand ADP B 479







## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	478/478 (100%)	-0.24	1 (0%) 95 87	23, 53, 79, 88	0
1	D	478/478 (100%)	-0.25	1 (0%) 95 87	23, 53, 79, 88	0
1	G	478/478 (100%)	-0.26	0 100 100	23, 53, 78, 88	0
1	J	478/478 (100%)	-0.24	2 (0%) 92 79	23, 53, 78, 88	0
1	M	478/478 (100%)	-0.26	0 100 100	23, 53, 79, 88	0
1	P	478/478 (100%)	-0.24	1 (0%) 95 87	23, 53, 78, 88	0
1	S	478/478 (100%)	-0.25	1 (0%) 95 87	23, 53, 79, 88	0
1	V	478/478 (100%)	-0.26	2 (0%) 92 79	23, 53, 79, 88	0
2	B	410/478 (85%)	-0.22	2 (0%) 91 75	31, 63, 93, 112	0
2	E	410/478 (85%)	-0.16	8 (1%) 65 36	31, 63, 94, 112	0
2	H	410/478 (85%)	-0.18	5 (1%) 79 54	31, 63, 93, 112	0
2	K	410/478 (85%)	-0.19	5 (1%) 79 54	31, 63, 93, 112	0
2	N	410/478 (85%)	-0.20	5 (1%) 79 54	31, 63, 93, 112	0
2	Q	410/478 (85%)	-0.18	2 (0%) 91 75	31, 63, 93, 112	0
2	T	410/478 (85%)	-0.16	8 (1%) 65 36	31, 63, 93, 112	0
2	W	410/478 (85%)	-0.17	5 (1%) 79 54	31, 63, 93, 112	0
3	C	91/94 (96%)	-0.23	0 100 100	25, 60, 72, 76	0
3	F	91/94 (96%)	-0.24	0 100 100	25, 60, 72, 76	0
3	I	91/94 (96%)	-0.25	0 100 100	25, 59, 72, 76	0
3	L	91/94 (96%)	-0.23	0 100 100	25, 59, 71, 76	0
3	O	91/94 (96%)	-0.24	1 (1%) 80 56	25, 59, 71, 76	0
3	R	91/94 (96%)	-0.15	0 100 100	25, 59, 71, 76	0
3	U	91/94 (96%)	-0.22	0 100 100	25, 60, 72, 76	0
3	X	91/94 (96%)	-0.23	0 100 100	25, 59, 72, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	7832/8400 (93%)	-0.22	49 (0%) 89 72	23, 56, 88, 112	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	262	ARG	4.9
2	H	262	ARG	4.2
2	N	262	ARG	4.0
1	J	18	GLU	3.8
2	T	265	GLU	3.6

## 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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
7	MN	W	481	1/1	0.30	0.28	82,82,82,82	1
7	MN	B	481	1/1	0.69	0.13	56,56,56,56	1
4	ASN	A	901	8/9	0.75	0.49	31,32,34,35	8
7	MN	Q	481	1/1	0.76	0.23	64,64,64,64	1
8	ATP	E	479	31/31	0.78	0.36	34,40,85,85	31
7	MN	H	481	1/1	0.80	0.24	75,75,75,75	1
9	ASP	N	482	9/9	0.81	0.19	71,79,81,82	0
4	ASN	V	908	8/9	0.82	0.39	28,29,29,30	8
9	ASP	H	482	9/9	0.82	0.19	71,79,81,82	0
8	ATP	K	479	31/31	0.83	0.35	24,35,57,58	31
7	MN	N	481	1/1	0.83	0.28	86,86,86,86	1
4	ASN	M	905	8/9	0.83	0.36	31,31,32,32	8
8	ATP	H	479	31/31	0.83	0.31	21,28,49,51	31

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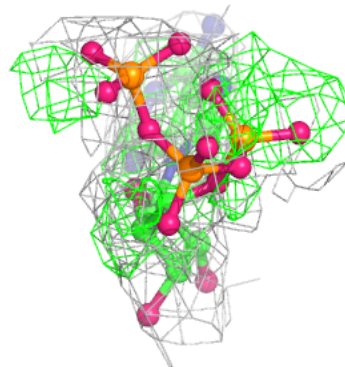
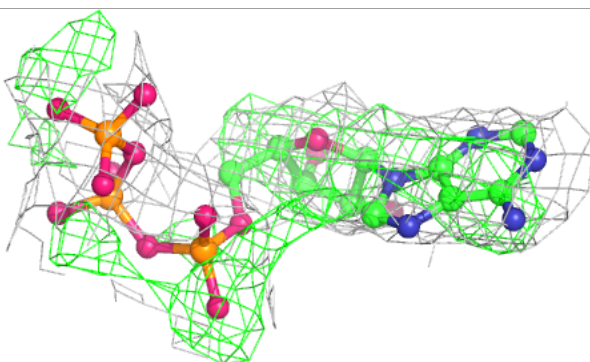
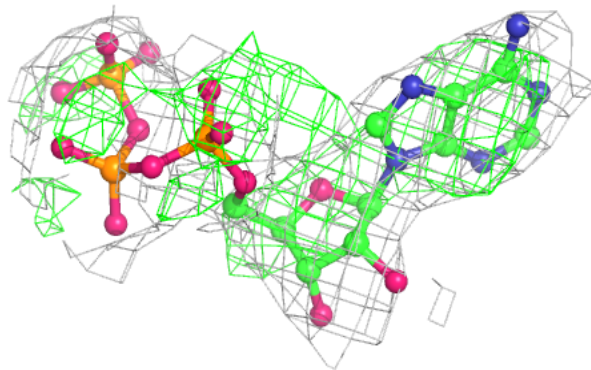
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
8	ATP	N	479	31/31	0.84	0.32	35,39,66,66	31
4	ASN	G	903	8/9	0.84	0.39	27,29,30,31	8
8	ATP	Q	479	31/31	0.84	0.38	30,37,49,50	31
6	ADP	B	479	27/27	0.85	0.30	70,71,82,82	27
7	MN	T	480	1/1	0.85	0.08	55,55,55,55	0
8	ATP	W	479	31/31	0.86	0.30	14,21,28,32	31
6	ADP	T	479	27/27	0.87	0.30	75,76,87,88	27
4	ASN	J	904	8/9	0.88	0.23	52,53,54,54	0
4	ASN	P	906	8/9	0.88	0.35	28,28,29,29	8
7	MN	T	481	1/1	0.89	0.23	75,75,75,75	0
7	MN	W	480	1/1	0.91	0.17	52,52,52,52	0
4	ASN	S	907	8/9	0.91	0.24	53,53,55,57	0
7	MN	E	481	1/1	0.91	0.31	85,85,85,85	1
7	MN	E	480	1/1	0.92	0.12	53,53,53,53	0
7	MN	K	481	1/1	0.92	0.30	63,63,63,63	1
7	MN	B	480	1/1	0.92	0.23	44,44,44,44	0
4	ASN	D	902	8/9	0.94	0.20	62,62,62,62	0
7	MN	Q	480	1/1	0.95	0.17	51,51,51,51	0
5	ZN	K	904	1/1	0.95	0.21	50,50,50,50	0
5	ZN	Q	906	1/1	0.96	0.21	51,51,51,51	0
7	MN	H	480	1/1	0.97	0.15	50,50,50,50	0
5	ZN	N	905	1/1	0.97	0.20	53,53,53,53	0
5	ZN	B	901	1/1	0.97	0.24	57,57,57,57	0
7	MN	N	480	1/1	0.97	0.14	49,49,49,49	0
5	ZN	W	908	1/1	0.97	0.21	55,55,55,55	0
7	MN	K	480	1/1	0.98	0.15	45,45,45,45	0
5	ZN	T	907	1/1	0.98	0.18	55,55,55,55	0
5	ZN	H	903	1/1	0.99	0.18	53,53,53,53	0
5	ZN	E	902	1/1	0.99	0.20	59,59,59,59	0

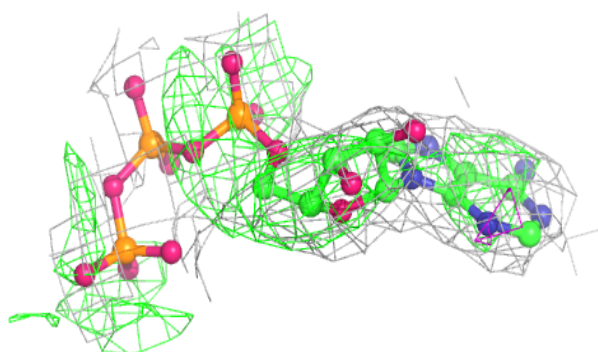
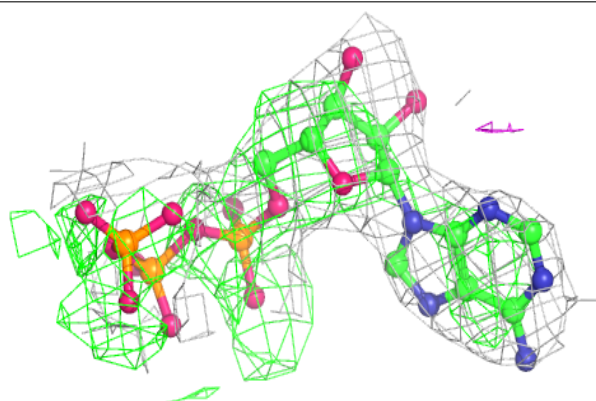
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around ATP E 479:**

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

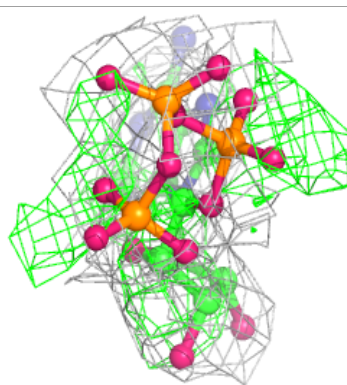
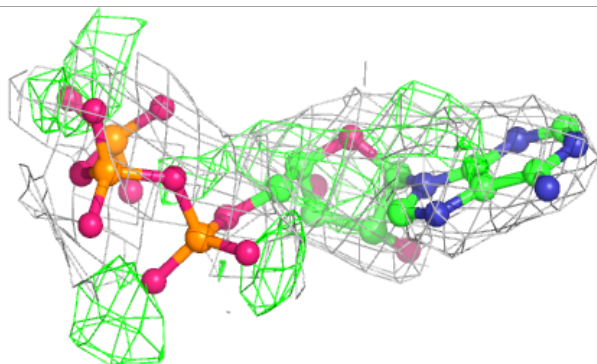
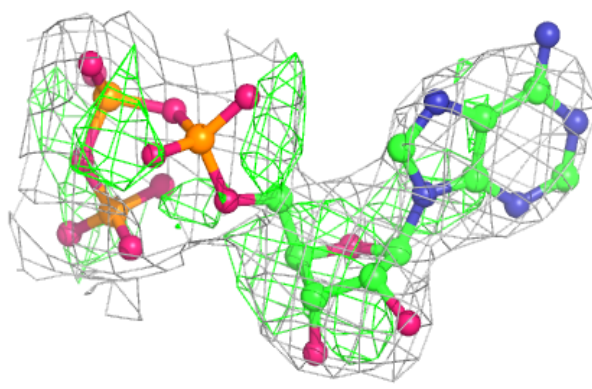
**Electron density around ATP K 479:**

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

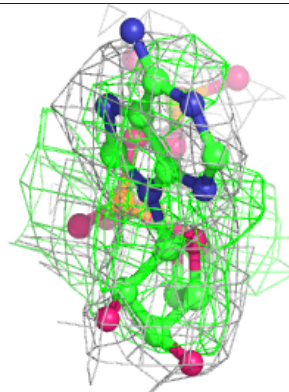
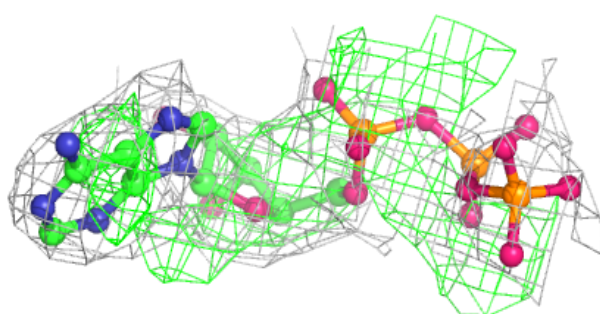
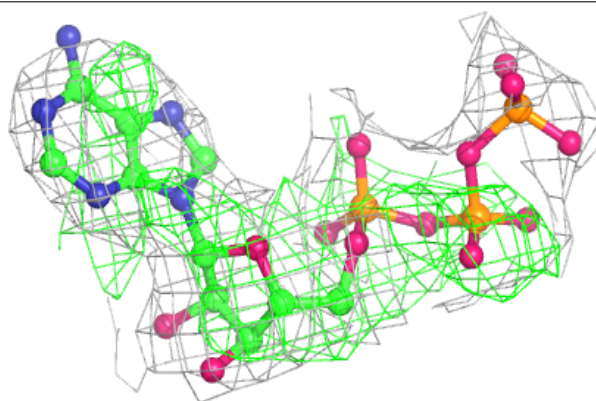


**Electron density around ATP H 479:**

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

**Electron density around ATP N 479:**

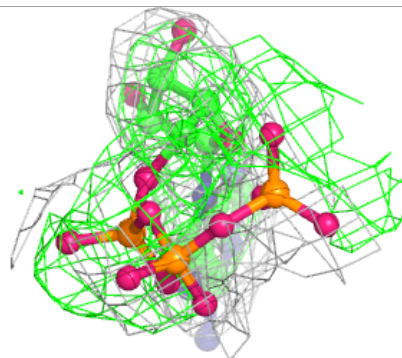
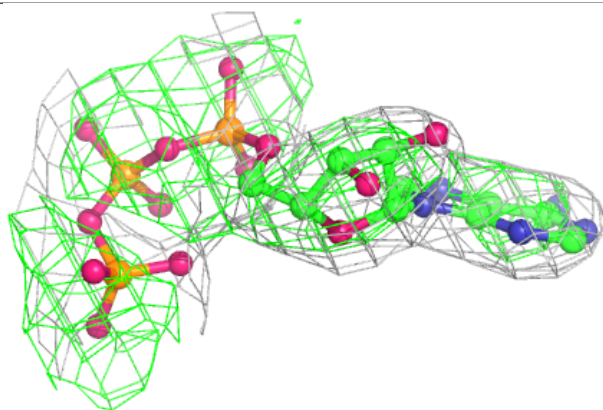
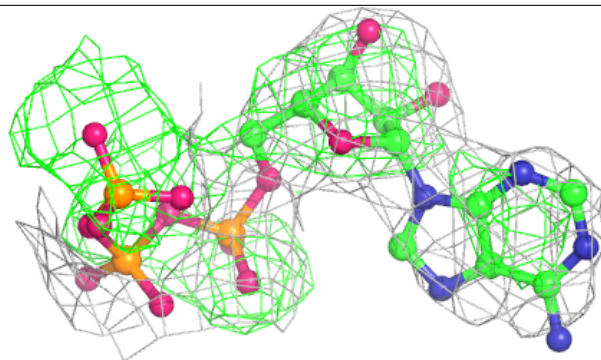
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



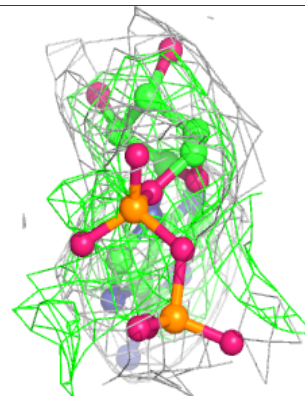
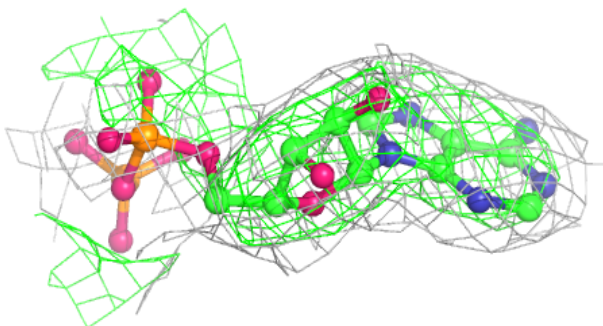
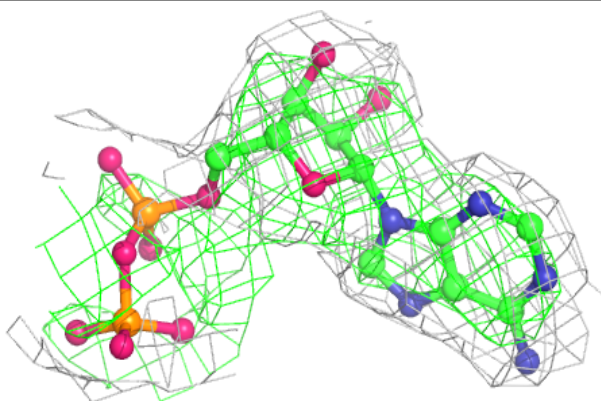


**Electron density around ATP Q 479:**

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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

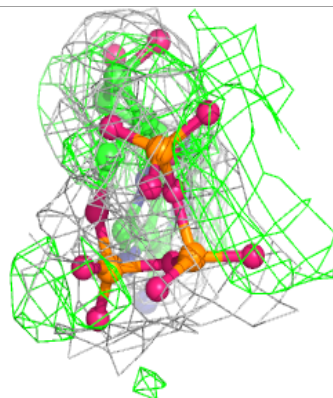
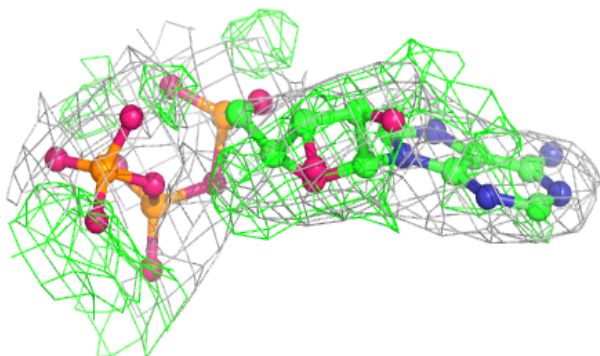
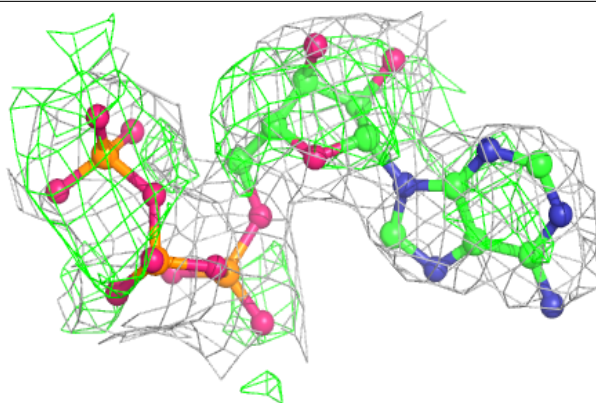
**Electron density around ADP B 479:**

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

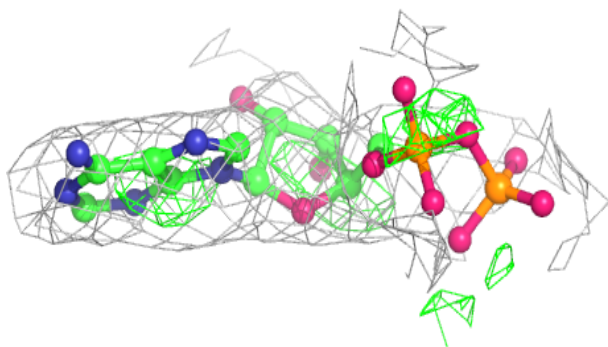
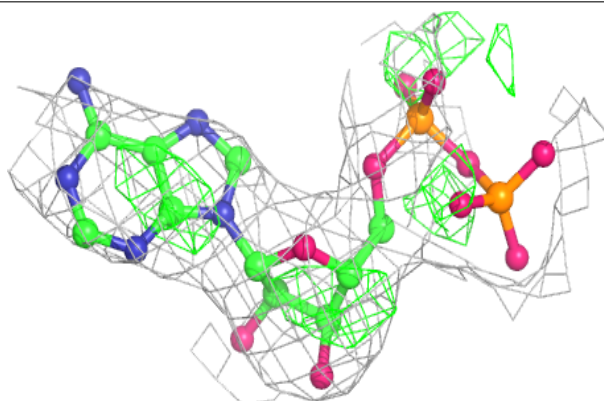


**Electron density around ATP W 479:**

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

**Electron density around ADP T 479:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.