



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 24, 2023 – 01:23 PM EDT

PDB ID : 3E1Y  
Title : Crystal structure of human eRF1/eRF3 complex  
Authors : Cheng, Z.; Lim, M.; Kong, C.; Song, H.  
Deposited on : 2008-08-05  
Resolution : 3.80 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.

The types of validation reports are described at

<https://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.36  
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) : 2.36

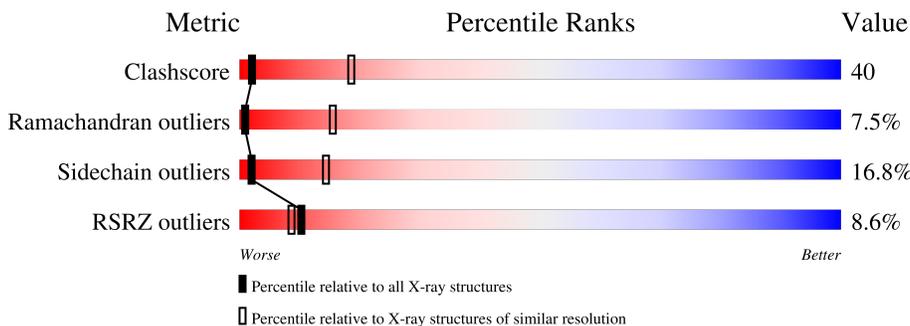
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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  $\geq 3$ , 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	451	
1	B	451	
1	C	451	
1	D	451	
2	E	204	
2	F	204	
2	G	204	

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Mol	Chain	Length	Quality of chain
2	H	204	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment (13%), a green segment (31%), a yellow segment (47%), and an orange segment (15%). The orange segment ends with two small black dots. The percentages are labeled below the segments.</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17110 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 Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	380	2987	1908	511	558	10	0	0	0
1	B	380	2987	1908	511	558	10	0	0	0
1	C	318	2511	1617	414	470	10	0	0	0
1	D	318	2511	1617	414	470	10	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	expression tag	UNP P62495
A	-12	ARG	-	expression tag	UNP P62495
A	-11	GLY	-	expression tag	UNP P62495
A	-10	SER	-	expression tag	UNP P62495
A	-9	HIS	-	expression tag	UNP P62495
A	-8	HIS	-	expression tag	UNP P62495
A	-7	HIS	-	expression tag	UNP P62495
A	-6	HIS	-	expression tag	UNP P62495
A	-5	HIS	-	expression tag	UNP P62495
A	-4	HIS	-	expression tag	UNP P62495
A	-3	GLY	-	expression tag	UNP P62495
A	-2	MET	-	expression tag	UNP P62495
A	-1	ALA	-	expression tag	UNP P62495
A	0	SER	-	expression tag	UNP P62495
B	-13	MET	-	expression tag	UNP P62495
B	-12	ARG	-	expression tag	UNP P62495
B	-11	GLY	-	expression tag	UNP P62495
B	-10	SER	-	expression tag	UNP P62495
B	-9	HIS	-	expression tag	UNP P62495
B	-8	HIS	-	expression tag	UNP P62495
B	-7	HIS	-	expression tag	UNP P62495

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	expression tag	UNP P62495
B	-5	HIS	-	expression tag	UNP P62495
B	-4	HIS	-	expression tag	UNP P62495
B	-3	GLY	-	expression tag	UNP P62495
B	-2	MET	-	expression tag	UNP P62495
B	-1	ALA	-	expression tag	UNP P62495
B	0	SER	-	expression tag	UNP P62495
C	-13	MET	-	expression tag	UNP P62495
C	-12	ARG	-	expression tag	UNP P62495
C	-11	GLY	-	expression tag	UNP P62495
C	-10	SER	-	expression tag	UNP P62495
C	-9	HIS	-	expression tag	UNP P62495
C	-8	HIS	-	expression tag	UNP P62495
C	-7	HIS	-	expression tag	UNP P62495
C	-6	HIS	-	expression tag	UNP P62495
C	-5	HIS	-	expression tag	UNP P62495
C	-4	HIS	-	expression tag	UNP P62495
C	-3	GLY	-	expression tag	UNP P62495
C	-2	MET	-	expression tag	UNP P62495
C	-1	ALA	-	expression tag	UNP P62495
C	0	SER	-	expression tag	UNP P62495
D	-13	MET	-	expression tag	UNP P62495
D	-12	ARG	-	expression tag	UNP P62495
D	-11	GLY	-	expression tag	UNP P62495
D	-10	SER	-	expression tag	UNP P62495
D	-9	HIS	-	expression tag	UNP P62495
D	-8	HIS	-	expression tag	UNP P62495
D	-7	HIS	-	expression tag	UNP P62495
D	-6	HIS	-	expression tag	UNP P62495
D	-5	HIS	-	expression tag	UNP P62495
D	-4	HIS	-	expression tag	UNP P62495
D	-3	GLY	-	expression tag	UNP P62495
D	-2	MET	-	expression tag	UNP P62495
D	-1	ALA	-	expression tag	UNP P62495
D	0	SER	-	expression tag	UNP P62495

- Molecule 2 is a protein called Eukaryotic peptide chain release factor GTP-binding subunit ERF3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	195	1513	960	261	280	12	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	195	Total	C	N	O	S	0	0	0
			1513	960	261	280	12			
2	G	195	Total	C	N	O	S	0	0	0
			1513	960	261	280	12			
2	H	195	Total	C	N	O	S	0	0	0
			1513	960	261	280	12			

There are 20 discrepancies between the modelled and reference sequences:

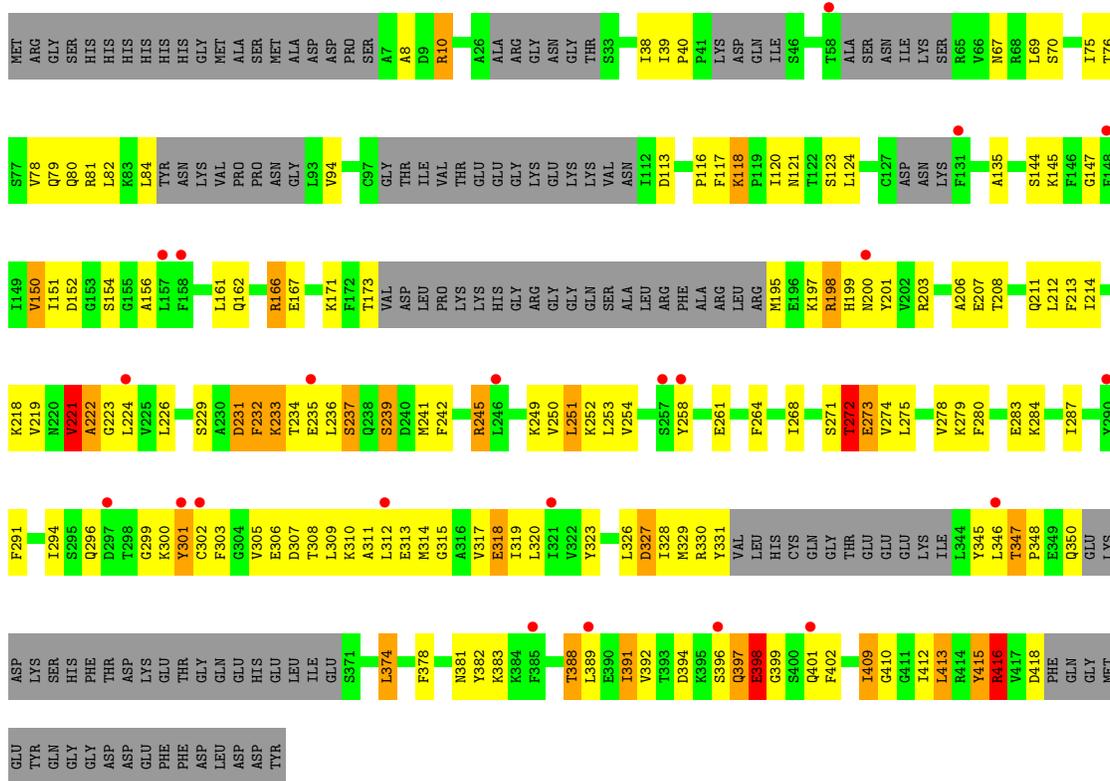
Chain	Residue	Modelled	Actual	Comment	Reference
E	434	GLY	-	expression tag	UNP P15170
E	435	PRO	-	expression tag	UNP P15170
E	436	LEU	-	expression tag	UNP P15170
E	437	GLY	-	expression tag	UNP P15170
E	438	SER	-	expression tag	UNP P15170
F	434	GLY	-	expression tag	UNP P15170
F	435	PRO	-	expression tag	UNP P15170
F	436	LEU	-	expression tag	UNP P15170
F	437	GLY	-	expression tag	UNP P15170
F	438	SER	-	expression tag	UNP P15170
G	434	GLY	-	expression tag	UNP P15170
G	435	PRO	-	expression tag	UNP P15170
G	436	LEU	-	expression tag	UNP P15170
G	437	GLY	-	expression tag	UNP P15170
G	438	SER	-	expression tag	UNP P15170
H	434	GLY	-	expression tag	UNP P15170
H	435	PRO	-	expression tag	UNP P15170
H	436	LEU	-	expression tag	UNP P15170
H	437	GLY	-	expression tag	UNP P15170
H	438	SER	-	expression tag	UNP P15170

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

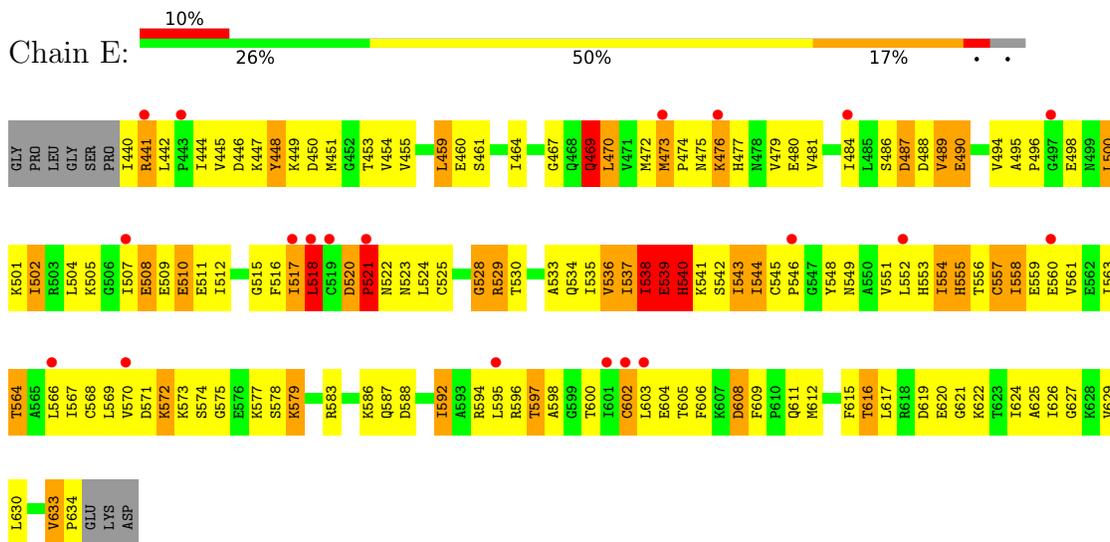




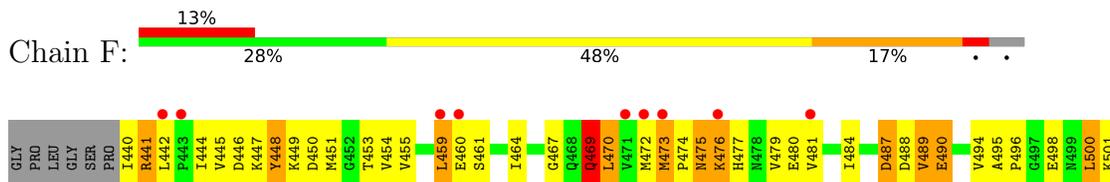


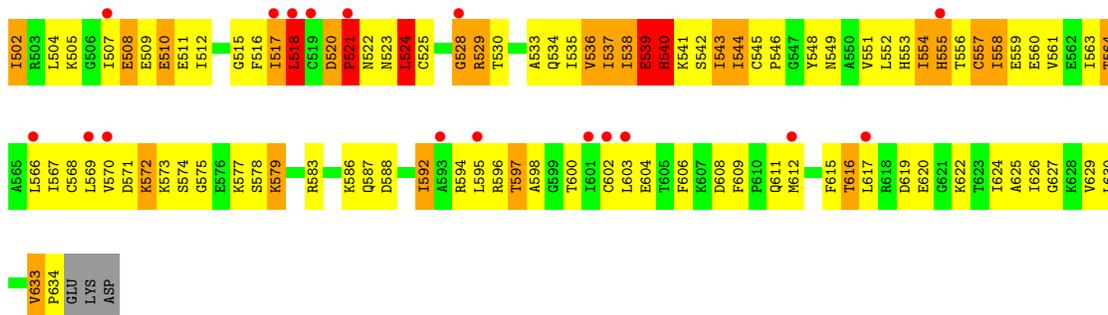


• Molecule 2: Eukaryotic peptide chain release factor GTP-binding subunit ERF3A

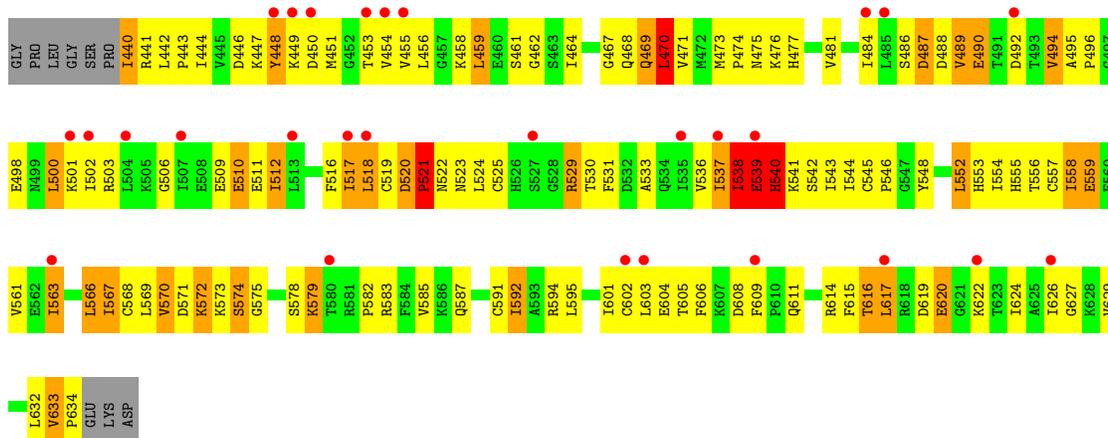


• Molecule 2: Eukaryotic peptide chain release factor GTP-binding subunit ERF3A

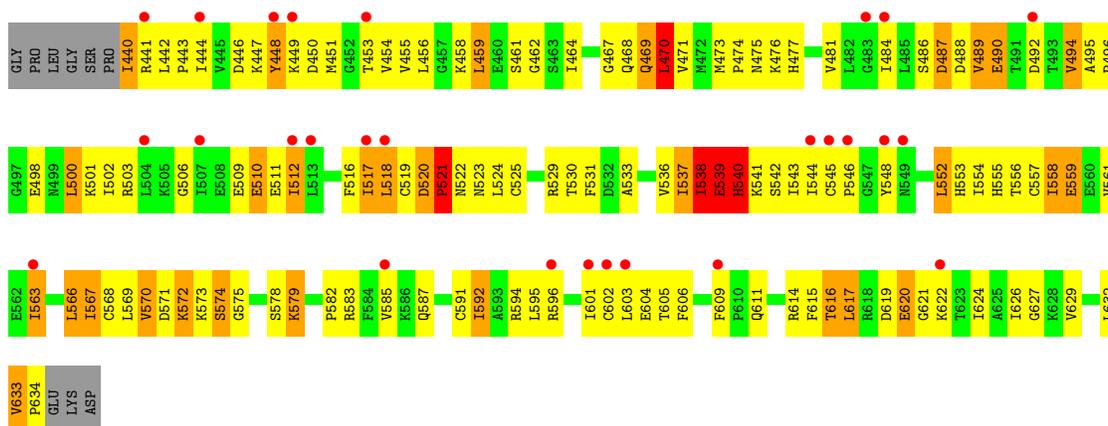




● Molecule 2: Eukaryotic peptide chain release factor GTP-binding subunit ERF3A



● Molecule 2: Eukaryotic peptide chain release factor GTP-binding subunit ERF3A



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	173.97Å 173.97Å 119.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.80 85.83 – 3.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.80) 99.9 (85.83-3.60)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 3.58Å)	Xtrriage
Refinement program	REFMAC 5.4.0077	Depositor
R, $R_{free}$	0.260 , 0.304 0.280 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	151.8	Xtrriage
Anisotropy	0.032	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 143.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.430 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	17110	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.51	2/3033 (0.1%)	0.67	3/4077 (0.1%)
1	B	0.50	0/3033	0.70	4/4077 (0.1%)
1	C	0.37	0/2544	0.55	0/3413
1	D	0.38	0/2544	0.55	0/3413
2	E	0.52	0/1534	0.84	4/2068 (0.2%)
2	F	0.53	0/1534	0.83	3/2068 (0.1%)
2	G	0.45	0/1534	0.79	4/2068 (0.2%)
2	H	0.45	0/1534	0.80	4/2068 (0.2%)
All	All	0.47	2/17290 (0.0%)	0.70	22/23252 (0.1%)

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	B	0	1
2	E	0	10
2	F	0	10
2	G	0	5
2	H	0	5
All	All	0	31

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	416	ARG	CD-NE	6.51	1.57	1.46
1	A	416	ARG	CZ-NH2	-5.40	1.26	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	539	GLU	N-CA-C	-10.60	82.38	111.00
2	H	539	GLU	N-CA-C	-10.26	83.31	111.00
2	E	539	GLU	N-CA-C	-9.96	84.12	111.00
1	B	299	GLY	N-CA-C	-9.82	88.55	113.10
2	E	537	ILE	N-CA-C	-7.47	90.82	111.00

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	298	THR	Peptide
2	E	469	GLN	Peptide
2	E	473	MET	Peptide
2	E	517	ILE	Peptide
2	E	521	PRO	Peptide

## 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	2987	0	3054	224	0
1	B	2987	0	3054	217	0
1	C	2511	0	2552	119	0
1	D	2511	0	2552	120	0
2	E	1513	0	1582	178	0
2	F	1513	0	1582	180	0
2	G	1513	0	1582	190	0
2	H	1513	0	1582	187	0
3	A	31	0	12	3	0
3	B	31	0	12	0	0
All	All	17110	0	17564	1402	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 40.

The worst 5 of 1402 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:G:541:LYS:HG2	2:G:587:GLN:NE2	1.21	1.53
2:H:541:LYS:HG2	2:H:587:GLN:NE2	1.20	1.45
2:E:541:LYS:HG2	2:E:587:GLN:NE2	1.27	1.41
2:F:541:LYS:HG2	2:F:587:GLN:NE2	1.30	1.38
2:F:540:HIS:HB3	2:F:541:LYS:CA	1.50	1.37

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	374/451 (83%)	289 (77%)	55 (15%)	30 (8%)	1	14
1	B	374/451 (83%)	290 (78%)	51 (14%)	33 (9%)	1	12
1	C	298/451 (66%)	230 (77%)	51 (17%)	17 (6%)	1	21
1	D	298/451 (66%)	229 (77%)	52 (17%)	17 (6%)	1	21
2	E	193/204 (95%)	143 (74%)	34 (18%)	16 (8%)	1	13
2	F	193/204 (95%)	146 (76%)	30 (16%)	17 (9%)	1	12
2	G	193/204 (95%)	148 (77%)	31 (16%)	14 (7%)	1	16
2	H	193/204 (95%)	148 (77%)	31 (16%)	14 (7%)	1	16
All	All	2116/2620 (81%)	1623 (77%)	335 (16%)	158 (8%)	1	15

5 of 158 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	ARG
1	A	108	LYS
1	A	115	GLU
1	A	116	PRO
1	A	118	LYS

### 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	325/387 (84%)	268 (82%)	57 (18%)	2	13
1	B	325/387 (84%)	267 (82%)	58 (18%)	2	12
1	C	275/387 (71%)	239 (87%)	36 (13%)	4	23
1	D	275/387 (71%)	238 (86%)	37 (14%)	4	22
2	E	173/180 (96%)	142 (82%)	31 (18%)	2	12
2	F	173/180 (96%)	141 (82%)	32 (18%)	1	11
2	G	173/180 (96%)	140 (81%)	33 (19%)	1	10
2	H	173/180 (96%)	140 (81%)	33 (19%)	1	10
All	All	1892/2268 (83%)	1575 (83%)	317 (17%)	2	14

5 of 317 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	505	LYS
2	H	449	LYS
2	F	570	VAL
2	G	494	VAL
2	H	540	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	499	ASN
2	G	549	ASN
2	H	549	ASN
1	C	121	ASN
1	C	67	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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
3	ATP	B	1526	-	26,33,33	0.99	2 (7%)	31,52,52	1.40	4 (12%)
3	ATP	A	1526	-	26,33,33	0.97	1 (3%)	31,52,52	1.61	5 (16%)

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	B	1526	-	-	1/18/38/38	0/3/3/3
3	ATP	A	1526	-	-	3/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1526	ATP	C5-C4	2.76	1.48	1.40
3	B	1526	ATP	C5-C4	2.70	1.48	1.40
3	B	1526	ATP	O4'-C1'	2.27	1.44	1.41

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1526	ATP	PA-O3A-PB	-3.56	120.61	132.83
3	A	1526	ATP	C3'-C2'-C1'	3.42	106.12	100.98
3	A	1526	ATP	PB-O3B-PG	-3.17	121.94	132.83
3	B	1526	ATP	N3-C2-N1	-3.00	123.99	128.68
3	A	1526	ATP	N3-C2-N1	-2.97	124.04	128.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

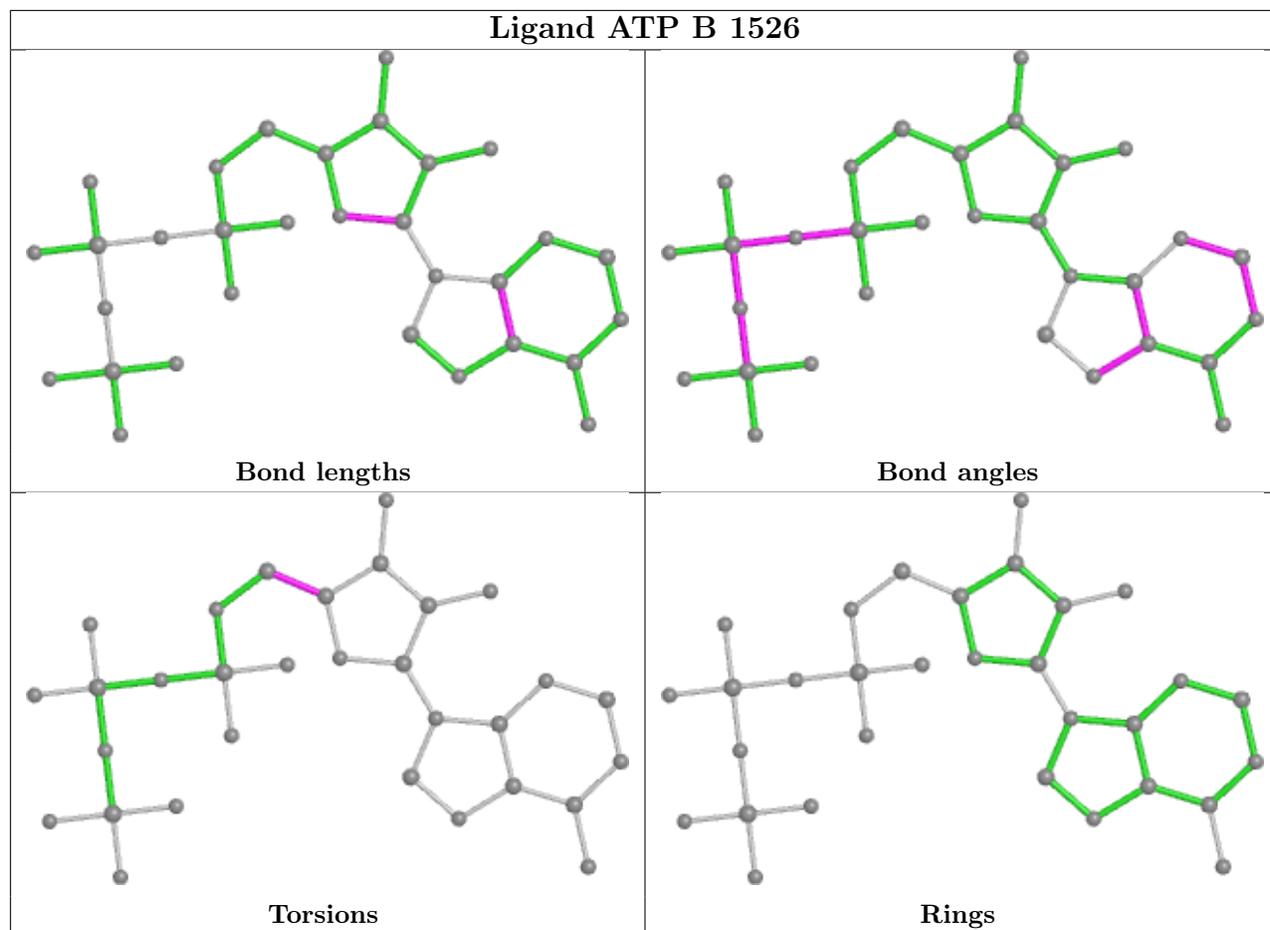
Mol	Chain	Res	Type	Atoms
3	A	1526	ATP	C3'-C4'-C5'-O5'
3	A	1526	ATP	O4'-C4'-C5'-O5'
3	A	1526	ATP	C4'-C5'-O5'-PA
3	B	1526	ATP	O4'-C4'-C5'-O5'

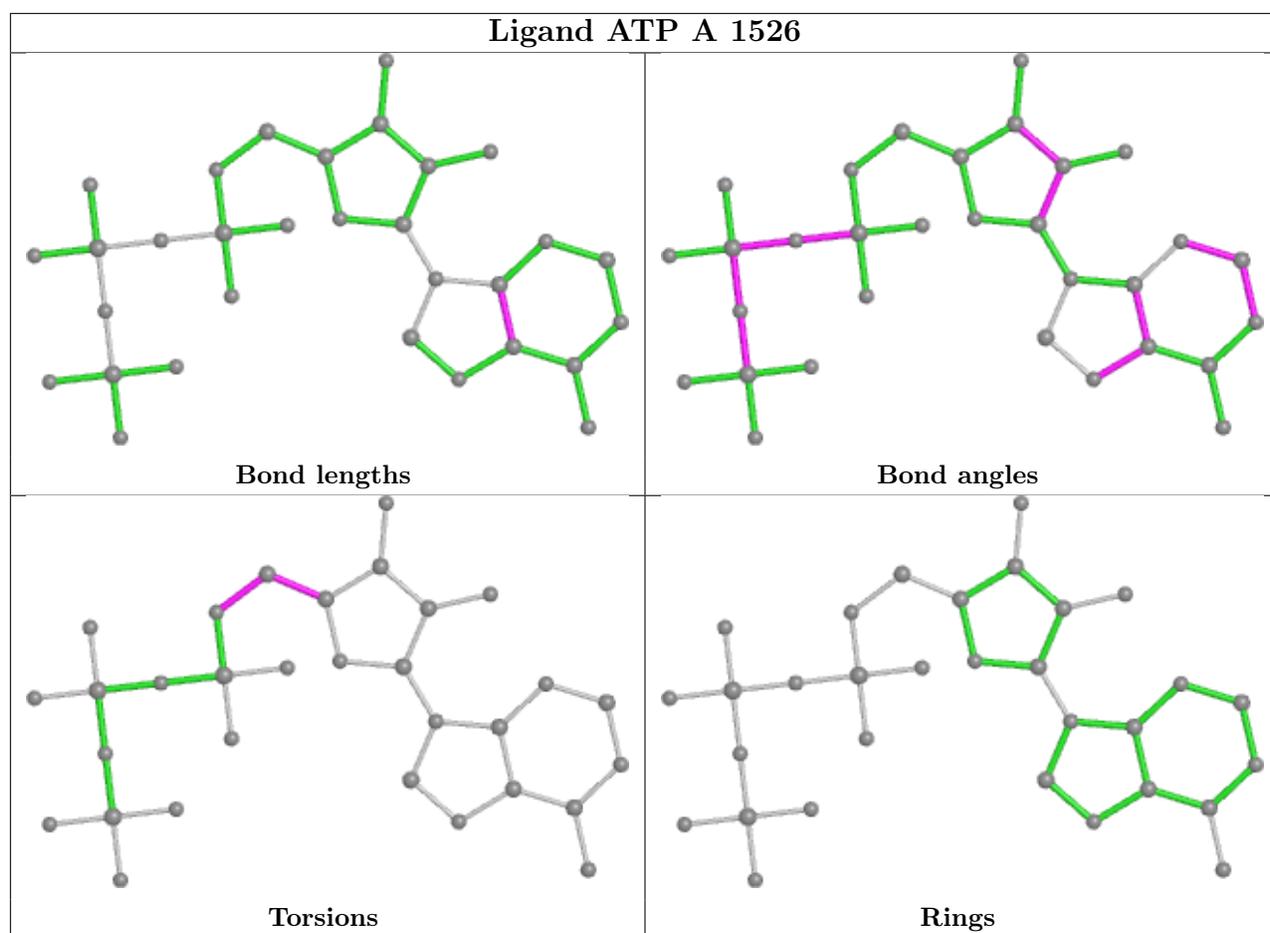
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1526	ATP	3	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.





## 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](#)

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	380/451 (84%)	0.58	20 (5%) 26 23	71, 89, 96, 100	0
1	B	380/451 (84%)	0.62	23 (6%) 21 17	71, 89, 96, 100	0
1	C	318/451 (70%)	0.48	22 (6%) 16 13	73, 90, 93, 100	0
1	D	318/451 (70%)	0.47	22 (6%) 16 13	73, 90, 93, 100	0
2	E	195/204 (95%)	0.80	20 (10%) 6 6	56, 87, 93, 97	0
2	F	195/204 (95%)	0.81	26 (13%) 3 3	56, 87, 93, 97	0
2	G	195/204 (95%)	0.84	28 (14%) 2 3	55, 87, 92, 96	0
2	H	195/204 (95%)	0.79	27 (13%) 2 3	55, 87, 92, 96	0
All	All	2176/2620 (83%)	0.64	188 (8%) 10 8	55, 89, 95, 100	0

The worst 5 of 188 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	GLY	6.4
1	A	181	GLY	5.9
2	F	570	VAL	5.6
2	G	502	ILE	5.5
1	B	184	GLY	5.4

### 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](#)

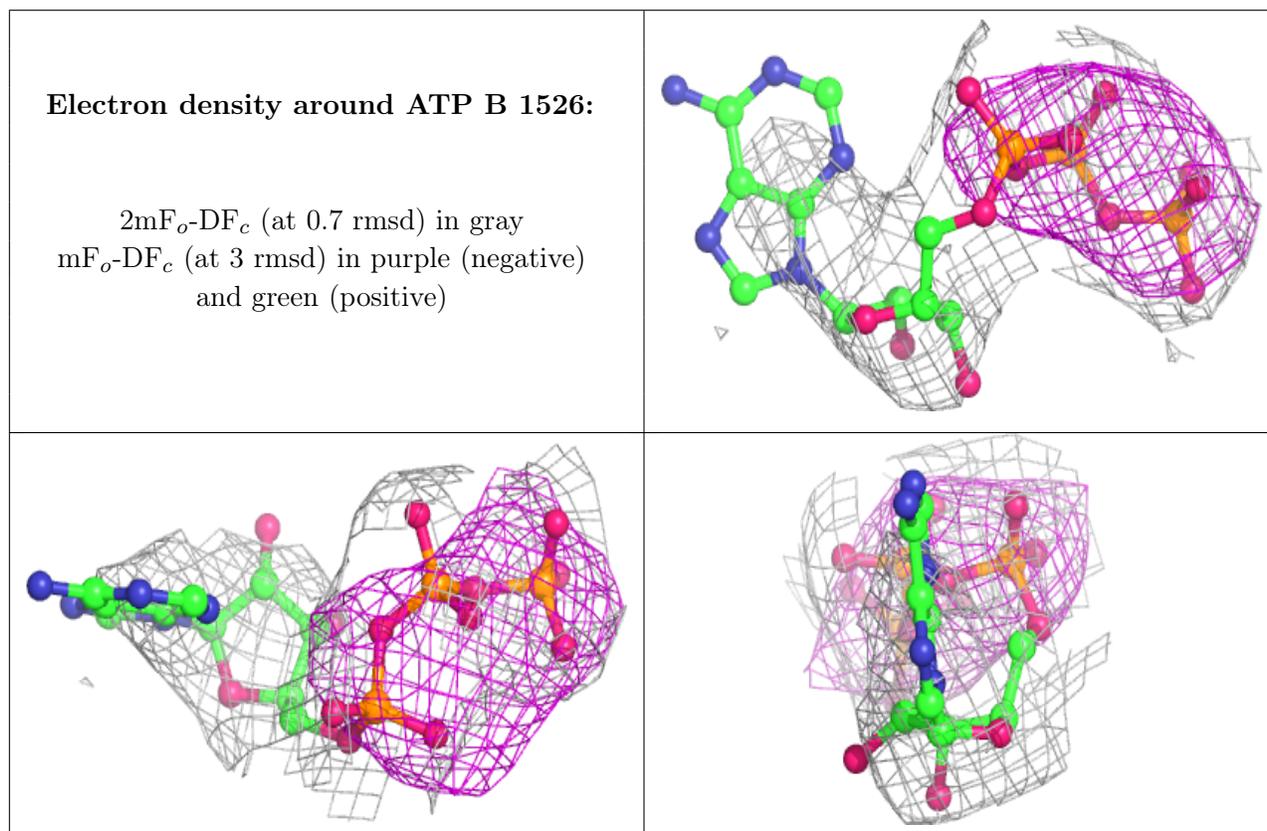
There are no monosaccharides in this entry.

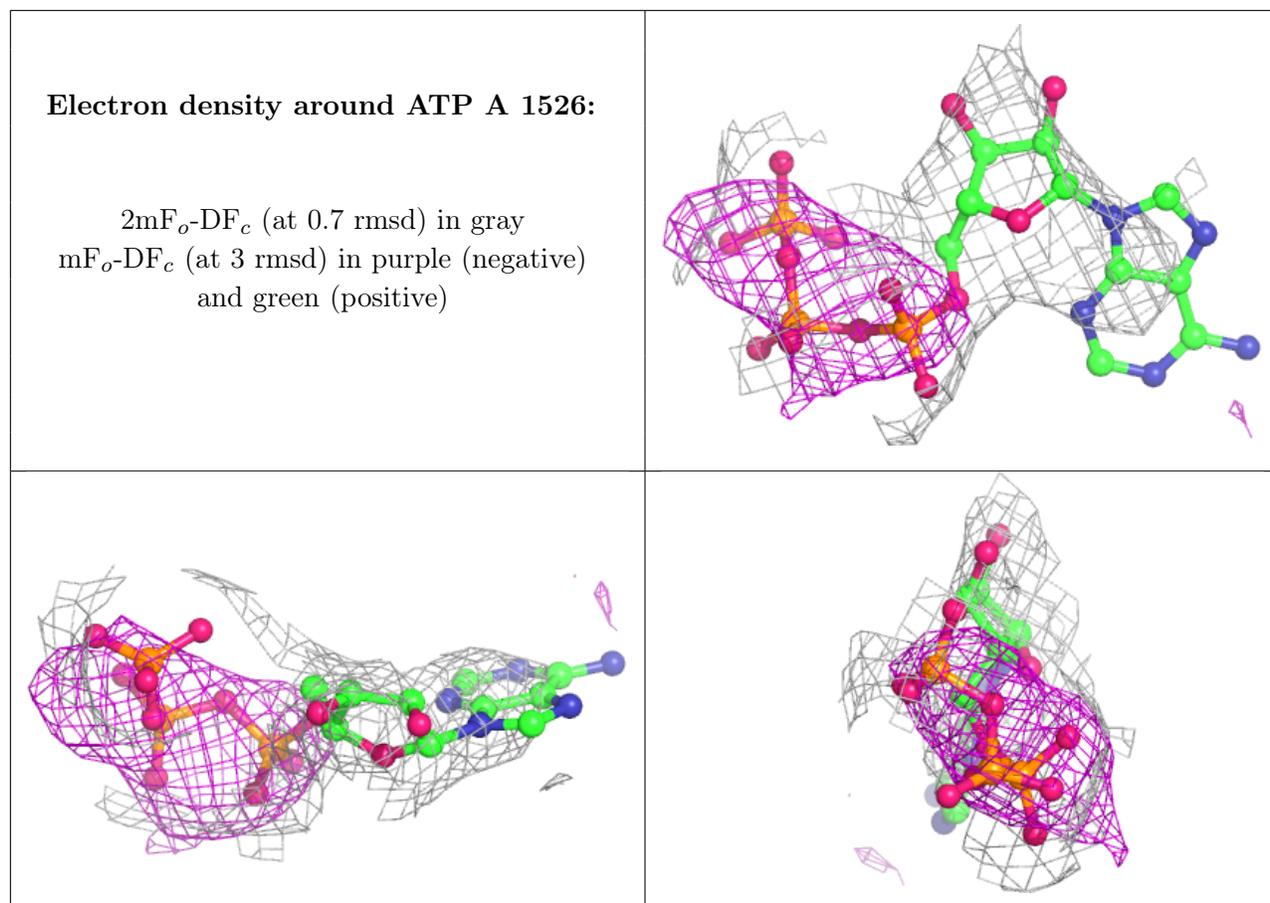
## 6.4 Ligands [i](#)

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, 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
3	ATP	B	1526	31/31	0.75	0.34	169,171,179,179	0
3	ATP	A	1526	31/31	0.78	0.36	171,173,180,180	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.