



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 07:51 pm BST

PDB ID : 6C9J
Title : AMP-activated protein kinase bound to pharmacological activator R734
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Deposited on : 2018-01-26
Resolution : 3.05 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 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

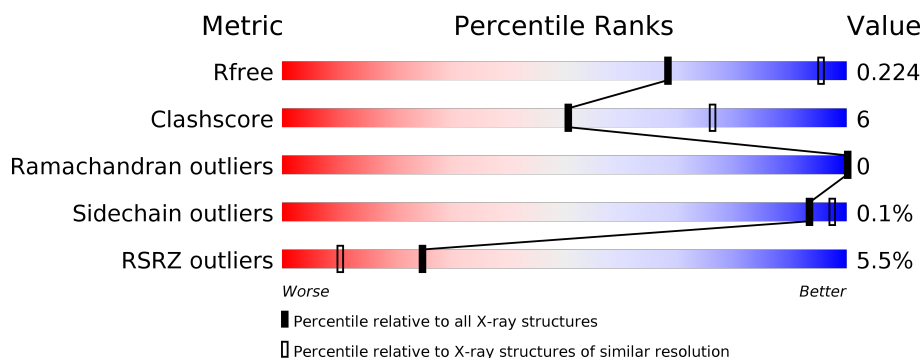
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)

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 ≥ 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	494	<div> <div>4%</div> <div>69% 9% 22%</div> </div>
2	B	204	<div> <div>3%</div> <div>75% 11% 15%</div> </div>
3	C	325	<div> <div>7%</div> <div>80% 12% 8%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7034 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 5'-AMP-activated protein kinase catalytic subunit alpha-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	386	3133	2010	548	556	1	18	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	MET	-	expression tag	UNP Q13131
A	4	GLY	-	expression tag	UNP Q13131
A	5	HIS	-	expression tag	UNP Q13131
A	6	HIS	-	expression tag	UNP Q13131
A	7	HIS	-	expression tag	UNP Q13131
A	8	HIS	-	expression tag	UNP Q13131
A	9	HIS	-	expression tag	UNP Q13131
A	10	HIS	-	expression tag	UNP Q13131
A	11	GLY	-	expression tag	UNP Q13131
A	12	SER	-	expression tag	UNP Q13131

- Molecule 2 is a protein called 5'-AMP-activated protein kinase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	174	1391	900	234	252	5	0	0	0

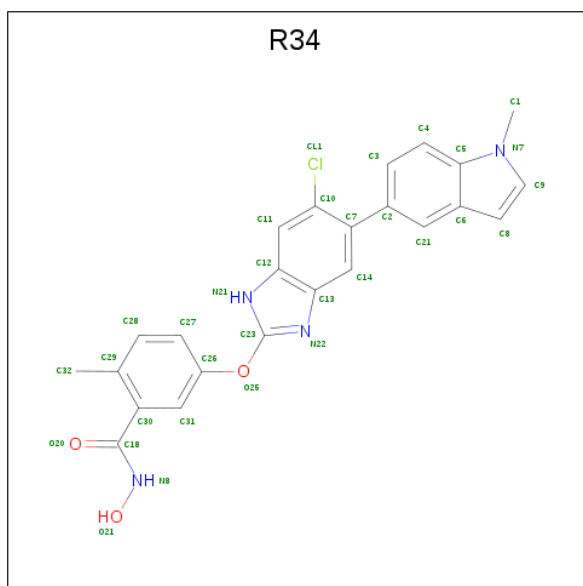
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MET	-	expression tag	UNP Q9Y478
B	108	ASP	SER	engineered mutation	UNP Q9Y478

- Molecule 3 is a protein called 5'-AMP-activated protein kinase subunit gamma-1.

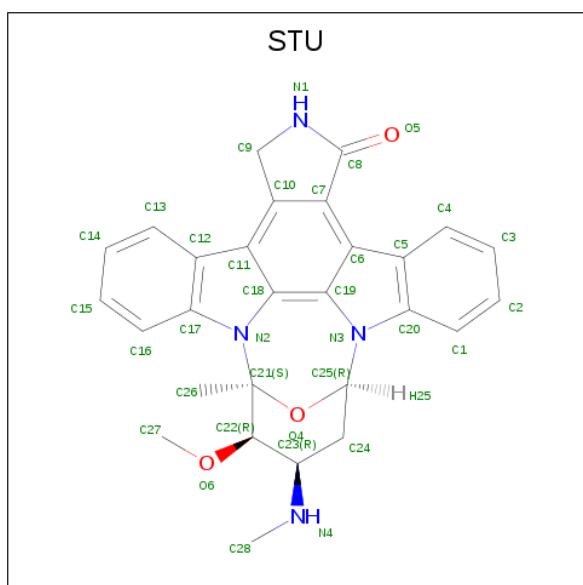
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	300	Total	C	N	O	S	0	0	0
			2420	1572	402	439	7			

- Molecule 4 is 5-{[6-chloro-5-(1-methyl-1H-indol-5-yl)-1H-benzimidazol-2-yl]oxy}-N-hydroxy-2-methylbenzamide (three-letter code: R34) (formula: C₂₄H₁₉ClN₄O₃).



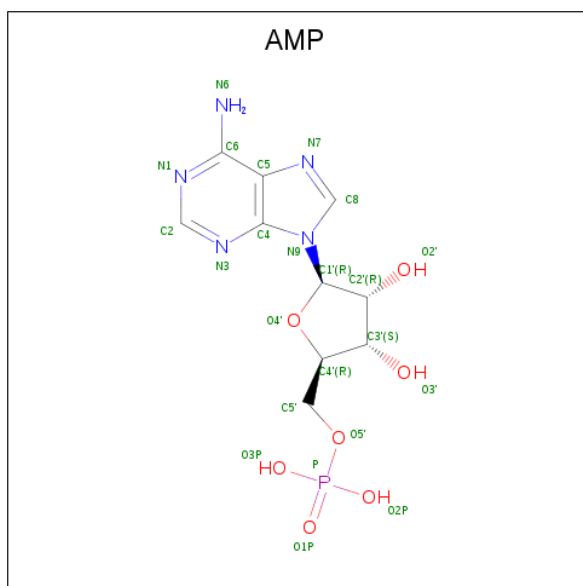
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	0	0
			32	24	1	4	3		

- Molecule 5 is STAUROSPORINE (three-letter code: STU) (formula: C₂₈H₂₆N₄O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			35	28	4	3		

- Molecule 6 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).




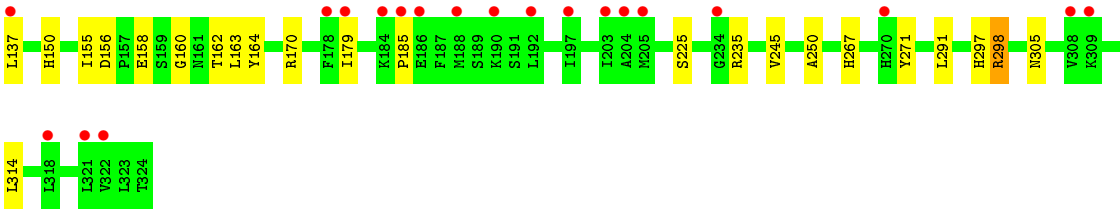
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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.

- [illegible]

- Chain B:
-
- | Color | Residues |
|--------|---|
| Green | D218, T219, G220, D224, P225, A226, L227, L239, R236, K259, K260, Y261, I270 |
| Yellow | T106, D108, H109, N110, F112, E120, F160, Q174, E188, F189, Y190, C192 |
| Grey | MET, GLU, VAL, ASN, ASP, LYS, ALA, P74, A75, Q76, A77, A78, T107, D108, H109, N110, F112, E120, K157, F160, Q174, LYS, CYS, SER, ASP, VAL, SER, SER, SER, SER, SER, PRO, PRO, GLY, PRO, TYR, HIS, Q187, E188, F189, Y190, C192, LYS, PRO, GLU, GLU, ARG, ARG, PHE, R201, A202, P203 |

- Chain C: 
- | Residue | Category |
|---------|----------|
| MET | Grey |
| THR | Grey |
| GLU | Grey |
| VAL | Grey |
| ILE | Grey |
| SER | Grey |
| ASP | Red |
| SER | Red |
| SER | Red |
| PRO | Red |
| ALA | Red |
| VAL | Red |
| GLU | Red |
| GLU | Red |
| ASN | Red |
| HIS | Red |
| PRO | Red |
| GLN | Red |
| GLU | Red |
| THR | Red |
| PRO | Red |
| GLU | Red |
| SER | Red |
| ASN | Red |
| N25 | Red |
| S26 | Red |
| Y27 | Red |
| Y28 | Red |
| P32 | Red |
| L40 | Yellow |
| T43 | Yellow |
| V48 | Yellow |
| P72 | Yellow |
| L73 | Yellow |
| G83 | Yellow |
| P84 | Yellow |
| L86 | Yellow |
| I91 | Yellow |
| I113 | Yellow |
| R117 | Yellow |
| E118 | Yellow |
| V119 | Yellow |
| Y120 | Yellow |
| L121 | Yellow |
| Q122 | Yellow |
| L128 | Yellow |
| V129 | Yellow |
| C130 | Yellow |



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.30Å 123.30Å 404.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.65 – 3.05 49.65 – 3.05	Depositor EDS
% Data completeness (in resolution range)	91.3 (49.65-3.05) 91.4 (49.65-3.05)	Depositor EDS
R_{merge}	0.81	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 3.07Å)	Xtriage
Refinement program	PHENIX (1.13 _2998: ???)	Depositor
R, R_{free}	0.214 , 0.225 0.216 , 0.224	Depositor DCC
R_{free} test set	2368 reflections (7.23%)	wwPDB-VP
Wilson B-factor (Å ²)	71.2	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 74.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7034	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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: TPO, STU, R34, AMP

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	0.28	0/3195	0.47	0/4313
2	B	0.28	0/1430	0.48	0/1949
3	C	0.26	0/2471	0.43	0/3355
All	All	0.27	0/7096	0.46	0/9617

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3133	0	3171	41	0
2	B	1391	0	1385	23	0
3	C	2420	0	2489	34	0
4	A	32	0	0	1	0
5	A	35	0	26	3	0
6	C	23	0	12	1	0
All	All	7034	0	7083	80	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 6.

All (80) 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:370:VAL:HG21	3:C:267:HIS:HD2	1.32	0.93
3:C:130:CYS:HB3	3:C:155:ILE:HD12	1.55	0.86
1:A:33:LYS:NZ	2:B:108:ASP:OD2	2.14	0.79
3:C:120:TYR:HD2	3:C:121:LEU:HD12	1.48	0.79
1:A:370:VAL:HG21	3:C:267:HIS:CD2	2.19	0.76
1:A:470:ASP:OD2	1:A:529:ARG:NH1	2.20	0.75
4:A:601:R34:C8	2:B:108:ASP:HB2	2.24	0.67
1:A:362:HIS:CD2	1:A:364:GLU:HB2	2.29	0.67
3:C:164:TYR:OH	3:C:170:ARG:NE	2.29	0.66
1:A:368:PHE:O	1:A:371:ALA:HB3	1.99	0.63
3:C:117:ARG:O	3:C:121:LEU:HB2	1.98	0.62
1:A:173:ARG:HB2	1:A:191:LEU:HD23	1.82	0.61
3:C:155:ILE:HG12	3:C:162:THR:HA	1.83	0.60
3:C:27:VAL:HB	3:C:185:PRO:HD3	1.82	0.60
1:A:469:ASP:OD1	1:A:470:ASP:N	2.36	0.59
3:C:150:HIS:NE2	6:C:401:AMP:O1P	2.23	0.59
2:B:260:LYS:CD	3:C:43:THR:HA	2.33	0.59
3:C:130:CYS:CB	3:C:155:ILE:HD12	2.32	0.59
2:B:260:LYS:HD2	3:C:43:THR:HA	1.86	0.58
1:A:138:VAL:HG12	1:A:140:ARG:HG3	1.85	0.57
1:A:140:ARG:NH1	1:A:192:TYR:OH	2.32	0.56
1:A:95:MET:HE3	5:A:602:STU:H92	1.88	0.56
1:A:365:ARG:NH1	2:B:220:GLY:O	2.39	0.55
1:A:139:HIS:CE1	1:A:141:ASP:HB3	2.42	0.55
3:C:118:GLU:O	3:C:122:GLN:HB2	2.07	0.55
1:A:365:ARG:HG3	2:B:225:PRO:HD3	1.89	0.53
1:A:443:THR:HB	1:A:530:PRO:HG2	1.91	0.53
1:A:427:LYS:HG3	2:B:188:GLU:HA	1.92	0.52
3:C:156:ASP:HB2	3:C:163:LEU:HD11	1.90	0.52
1:A:139:HIS:HE1	1:A:141:ASP:HB3	1.74	0.52
1:A:365:ARG:O	1:A:369:LEU:HD13	2.11	0.51
1:A:527:THR:O	1:A:529:ARG:HG3	2.10	0.51
3:C:120:TYR:CD2	3:C:121:LEU:HD12	2.37	0.50
1:A:403:ARG:HE	1:A:462:LEU:HD12	1.77	0.50
1:A:370:VAL:HG11	3:C:267:HIS:HB2	1.94	0.50
5:A:602:STU:H261	5:A:602:STU:H16	1.94	0.50
1:A:145:GLU:N	1:A:145:GLU:OE1	2.45	0.49
1:A:528:PRO:HG3	3:C:158:GLU:OE1	2.12	0.49
3:C:91:ILE:HG12	3:C:245:VAL:HG11	1.93	0.49
2:B:78:ARG:NH1	2:B:120:GLU:OE2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:PHE:HB2	2:B:239:LEU:HB3	1.95	0.48
3:C:225:SER:OG	3:C:298:ARG:NH2	2.44	0.48
1:A:102:GLU:OE2	5:A:602:STU:N4	2.46	0.47
2:B:109:HIS:O	2:B:110:ASN:CG	2.52	0.47
1:A:426:TRP:CZ3	2:B:190:TYR:HB3	2.49	0.47
2:B:78:ARG:HB3	2:B:160:PHE:CE1	2.50	0.47
1:A:395:LYS:NZ	2:B:218:ASP:OD1	2.48	0.47
1:A:98:VAL:HG21	1:A:148:LEU:HB3	1.97	0.47
3:C:297:HIS:O	3:C:314:LEU:HG	2.15	0.47
3:C:73:LEU:HD21	3:C:85:LEU:HB2	1.97	0.47
1:A:148:LEU:O	1:A:156:LYS:N	2.49	0.46
2:B:224:ASP:HB3	2:B:227:LEU:HG	1.98	0.46
3:C:117:ARG:HH11	3:C:121:LEU:HD22	1.81	0.46
1:A:370:VAL:CG1	3:C:267:HIS:HB2	2.45	0.46
1:A:546:LYS:O	1:A:550:GLN:HG2	2.16	0.46
3:C:40:LEU:HD13	3:C:137:LEU:HD21	1.98	0.45
2:B:106:THR:O	2:B:112:PHE:HA	2.16	0.45
2:B:78:ARG:HB3	2:B:160:PHE:CZ	2.50	0.45
2:B:259:LYS:O	2:B:259:LYS:HG2	2.17	0.45
3:C:83:GLY:HA2	3:C:128:LEU:CD2	2.47	0.45
1:A:98:VAL:HG11	1:A:156:LYS:HG3	1.99	0.45
3:C:235:ARG:NE	3:C:305:ASN:O	2.50	0.45
3:C:73:LEU:HD22	3:C:113:ILE:HG21	1.99	0.45
2:B:107:ARG:HD3	2:B:112:PHE:CZ	2.52	0.44
2:B:256:ARG:HE	2:B:261:TYR:HE2	1.65	0.43
3:C:117:ARG:NH1	3:C:121:LEU:HD22	2.33	0.43
1:A:371:ALA:HB2	3:C:250:ALA:HB1	1.99	0.43
2:B:109:HIS:ND1	2:B:109:HIS:O	2.52	0.42
1:A:451:LEU:HB3	1:A:463:LEU:HD11	2.01	0.42
1:A:425:GLU:HG2	2:B:188:GLU:C	2.40	0.42
1:A:415:VAL:O	1:A:419:ILE:HG13	2.19	0.42
1:A:531:GLY:O	3:C:160:GLY:HA3	2.20	0.41
3:C:48:VAL:O	3:C:72:PRO:HD2	2.21	0.41
1:A:362:HIS:O	1:A:366:VAL:HG23	2.20	0.41
3:C:28:TYR:CZ	3:C:179:ILE:HG21	2.56	0.41
3:C:291:LEU:HD13	3:C:314:LEU:HD23	2.02	0.41
1:A:542:ALA:HB1	2:B:270:ILE:HD11	2.02	0.41
1:A:252:GLN:HB2	1:A:258:ARG:HA	2.03	0.41
2:B:107:ARG:HB2	2:B:112:PHE:CE2	2.56	0.40
1:A:366:VAL:HG13	3:C:271:TYR:OH	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	379/494 (77%)	372 (98%)	7 (2%)	0	100	100
2	B	168/204 (82%)	165 (98%)	3 (2%)	0	100	100
3	C	298/325 (92%)	293 (98%)	5 (2%)	0	100	100
All	All	845/1023 (83%)	830 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	347/447 (78%)	347 (100%)	0	100	100
2	B	157/185 (85%)	157 (100%)	0	100	100
3	C	276/300 (92%)	275 (100%)	1 (0%)	91	95
All	All	780/932 (84%)	779 (100%)	1 (0%)	93	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	298	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	267	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	TPO	A	174	1	8,10,11	1.05	0	10,14,16	1.76	3 (30%)

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	TPO	A	174	1	-	2/9/11/13	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	TPO	P-OG1-CB	-4.27	110.31	123.21
1	A	174	TPO	CG2-CB-CA	-2.58	108.08	113.16
1	A	174	TPO	O-C-CA	-2.00	119.53	124.78

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	174	TPO	CB-OG1-P-O2P
1	A	174	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
5	STU	A	602	-	30,42,42	3.07	5 (16%)	31,68,68	1.58	6 (19%)
4	R34	A	601	-	35,36,36	1.77	4 (11%)	39,53,53	1.22	3 (7%)
6	AMP	C	401	-	22,25,25	0.90	1 (4%)	25,38,38	1.26	2 (8%)

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
5	STU	A	602	-	-	1/4/42/42	-
4	R34	A	601	-	-	3/12/14/14	0/5/5/5
6	AMP	C	401	-	-	1/6/26/26	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	602	STU	C8-N1	11.95	1.44	1.35
5	A	602	STU	O5-C8	8.56	1.40	1.23
4	A	601	R34	C18-N8	8.02	1.43	1.32
5	A	602	STU	C22-C23	-4.13	1.48	1.52
5	A	602	STU	C9-C10	3.79	1.53	1.50
4	A	601	R34	C9-N7	-3.11	1.32	1.37
4	A	601	R34	C7-C2	2.82	1.54	1.49
6	C	401	AMP	C5-C4	2.45	1.47	1.40
4	A	601	R34	C11-C10	2.38	1.40	1.36
5	A	602	STU	C24-C25	2.37	1.56	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	STU	C9-N1-C8	-5.64	108.43	113.85
4	A	601	R34	O21-N8-C18	-3.70	110.50	119.64
6	C	401	AMP	N3-C2-N1	-3.29	123.54	128.68
5	A	602	STU	O5-C8-C7	-3.23	125.48	129.32
4	A	601	R34	C11-C10-C7	-3.09	119.73	121.92
4	A	601	R34	C29-C30-C18	2.71	122.59	120.56
6	C	401	AMP	C4-C5-N7	-2.70	106.58	109.40
5	A	602	STU	C26-C21-C22	-2.47	107.83	112.64
5	A	602	STU	C7-C8-N1	2.27	108.67	106.37
5	A	602	STU	C7-C10-C11	-2.19	119.47	122.42
5	A	602	STU	C1-C20-N3	-2.05	129.80	132.25

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	R34	C30-C18-N8-O21
4	A	601	R34	O20-C18-N8-O21
5	A	602	STU	C24-C23-N4-C28
6	C	401	AMP	C5'-O5'-P-O1P
4	A	601	R34	O20-C18-C30-C31

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602	STU	3	0
4	A	601	R34	1	0

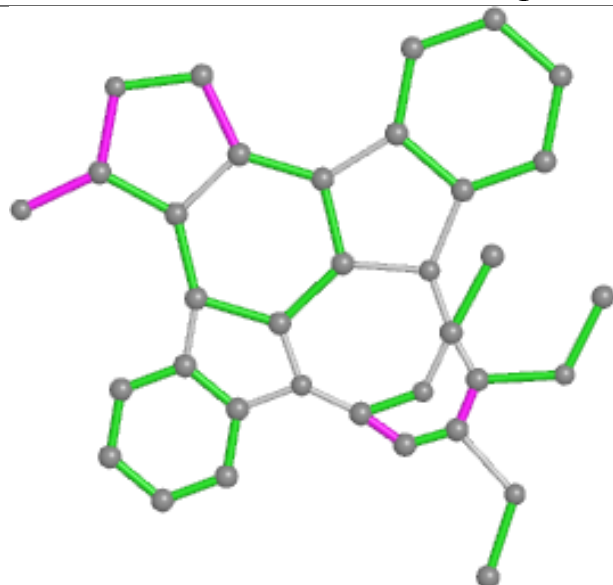
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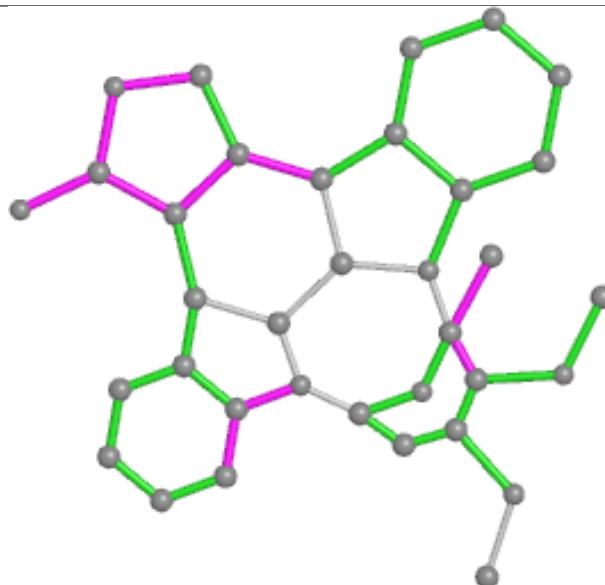
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	401	AMP	1	0

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 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.

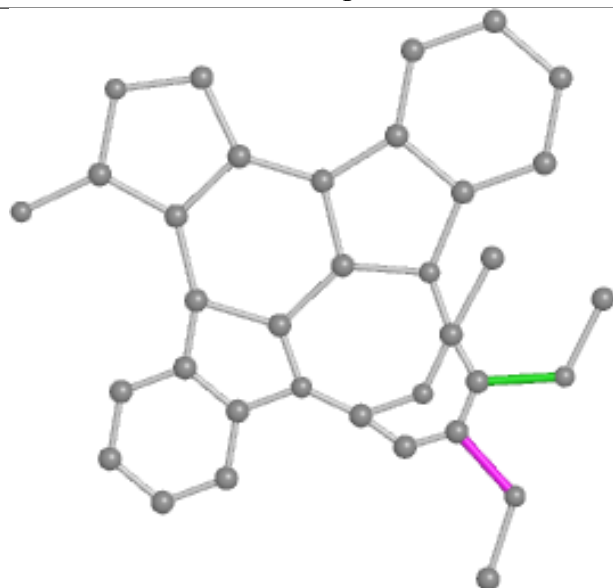
Ligand STU A 602



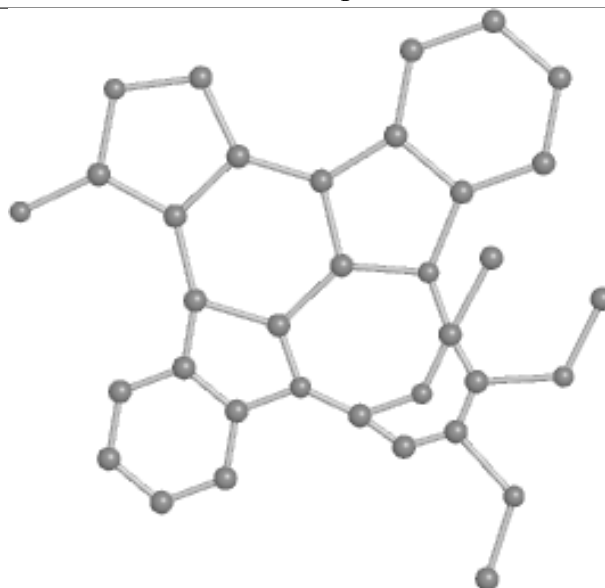
Bond lengths



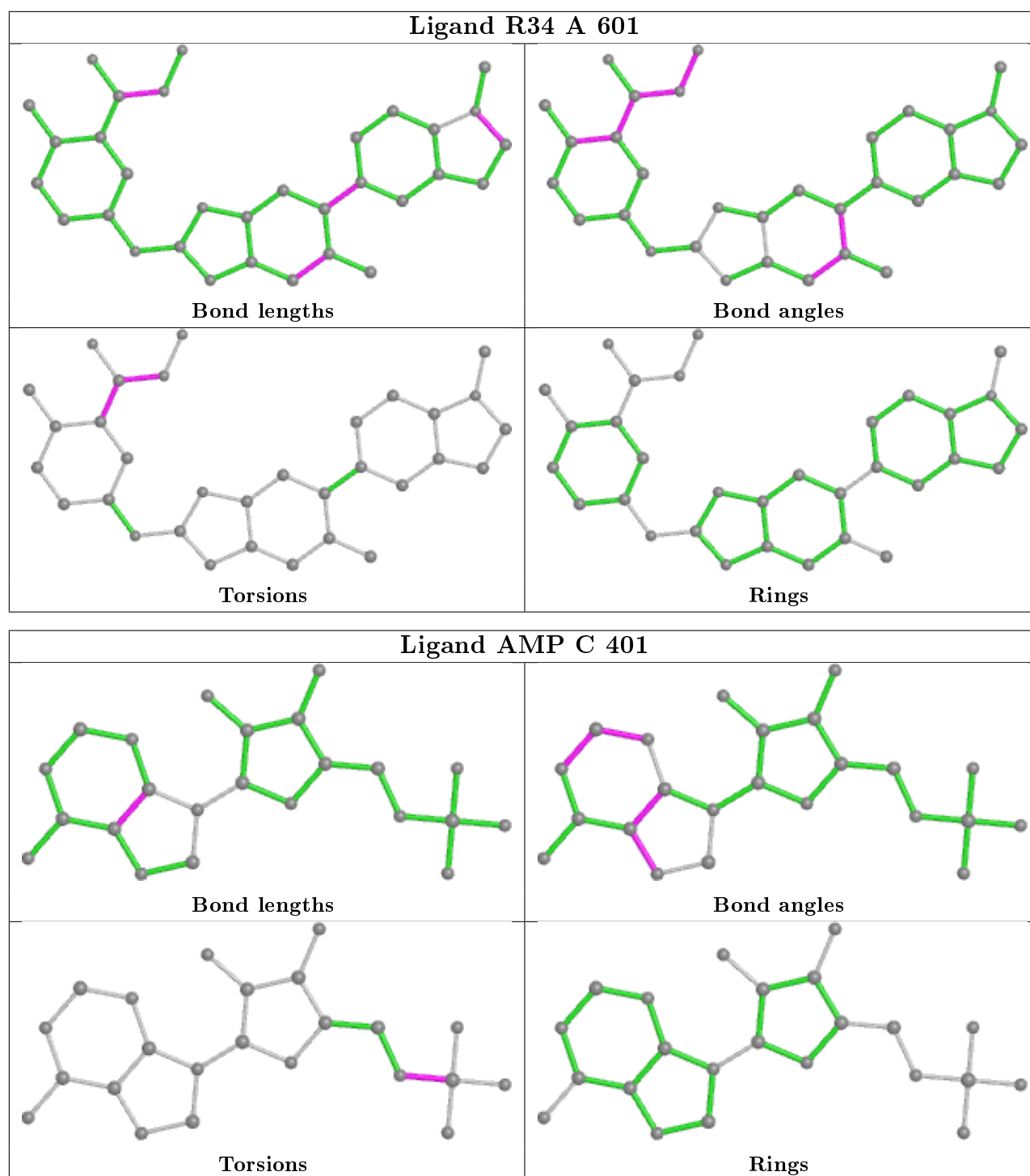
Bond angles



Torsions



Rings



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	385/494 (77%)	0.21	18 (4%) 31 14	33, 68, 178, 254	0
2	B	174/204 (85%)	0.19	6 (3%) 45 22	40, 83, 167, 203	0
3	C	300/325 (92%)	0.40	23 (7%) 13 4	62, 122, 180, 207	0
All	All	859/1023 (83%)	0.27	47 (5%) 25 10	33, 92, 178, 254	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	308	VAL	5.9
1	A	367	PRO	5.6
3	C	28	TYR	4.9
3	C	270	HIS	4.5
3	C	184	LYS	4.4
1	A	359	THR	4.2
1	A	360	ARG	4.0
3	C	186	GLU	3.7
1	A	426	TRP	3.7
3	C	190	LYS	3.7
2	B	76	GLN	3.7
3	C	178	PHE	3.6
2	B	203	PRO	3.4
3	C	203	ILE	3.3
1	A	415	VAL	3.3
3	C	192	LEU	3.2
3	C	188	MET	3.2
3	C	25	ASN	3.0
1	A	436	VAL	3.0
1	A	370	VAL	2.8
1	A	443	THR	2.8
3	C	137	LEU	2.7
2	B	190	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	321	LEU	2.7
3	C	234	GLY	2.6
3	C	185	PRO	2.6
3	C	205	MET	2.6
1	A	366	VAL	2.6
1	A	368	PHE	2.5
1	A	471	GLU	2.5
1	A	451	LEU	2.4
2	B	187	GLN	2.4
3	C	179	ILE	2.3
3	C	309	LYS	2.3
1	A	548	LEU	2.2
3	C	318	LEU	2.2
3	C	32	MET	2.2
1	A	434	LEU	2.1
2	B	256	ARG	2.1
1	A	411	ILE	2.1
3	C	204	ALA	2.1
1	A	173	ARG	2.1
1	A	422	LEU	2.1
1	A	449	MET	2.1
3	C	322	VAL	2.0
3	C	197	ILE	2.0
2	B	157	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	A	174	11/12	0.97	0.17	59,67,84,129	0

6.3 Carbohydrates [i](#)

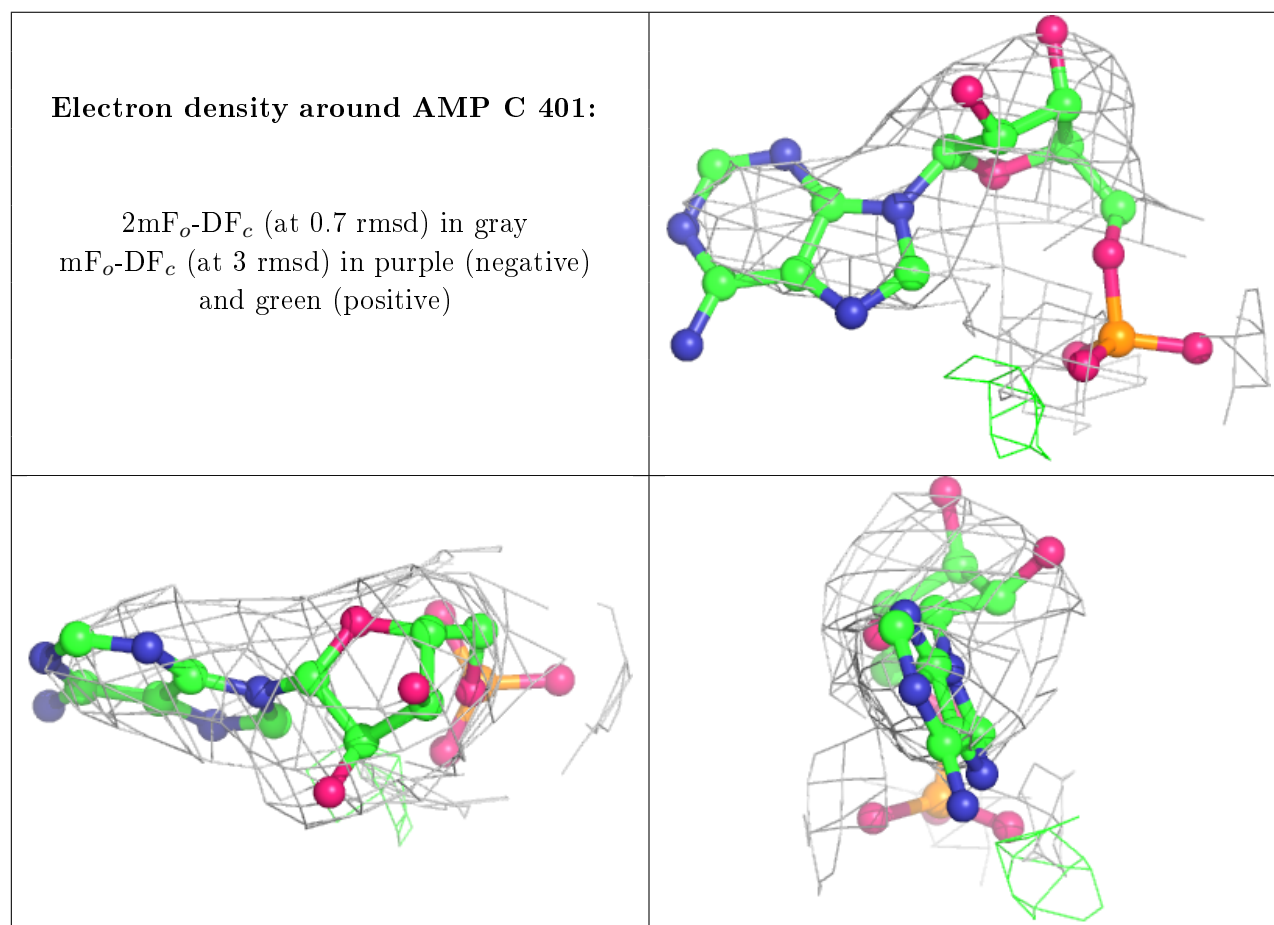
There are no carbohydrates in this entry.

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, 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.

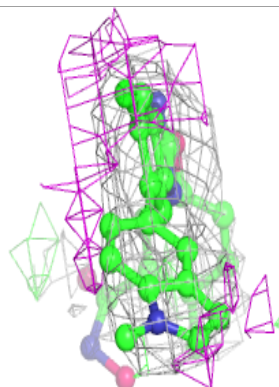
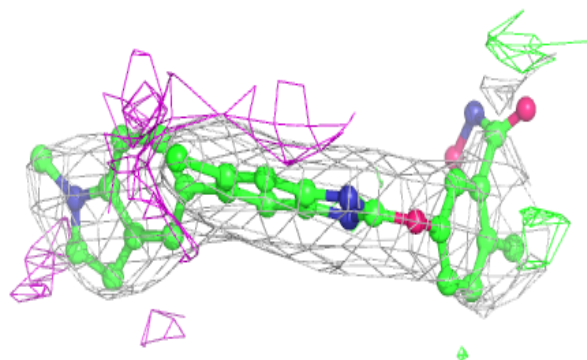
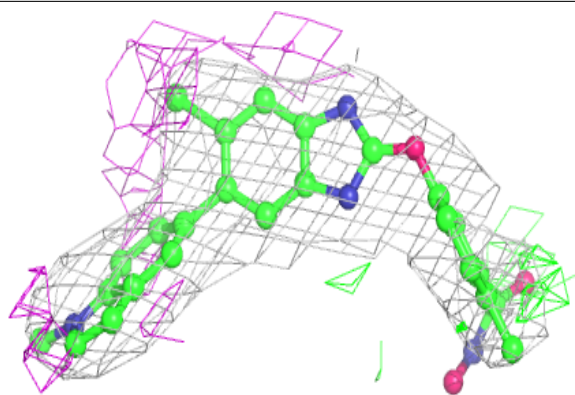
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	AMP	C	401	23/23	0.67	0.31	133,149,160,161	0
4	R34	A	601	32/32	0.89	0.30	40,59,146,149	0
5	STU	A	602	35/35	0.98	0.24	28,39,50,59	0

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.



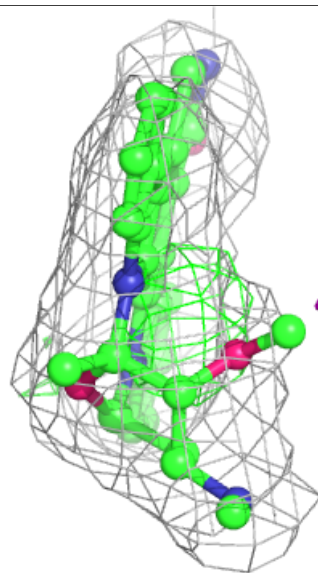
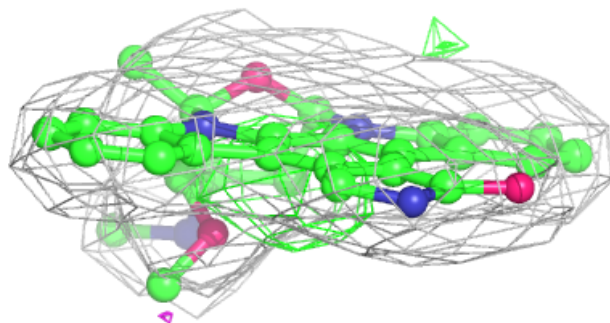
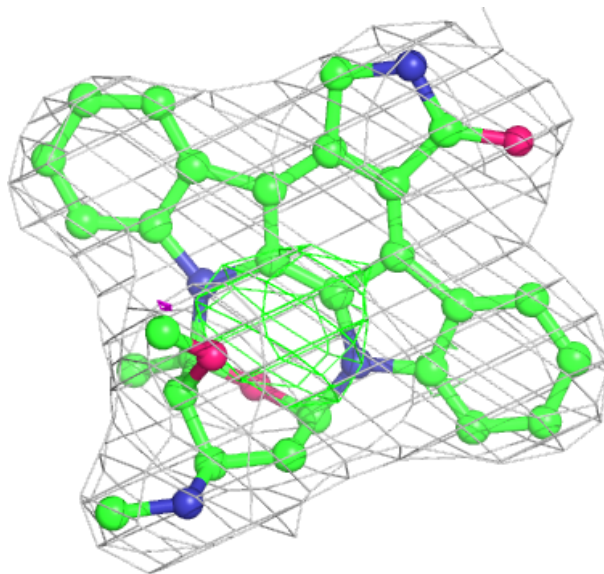
Electron density around R34 A 601:

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



Electron density around STU A 602:

$2mF_o-DF_c$ (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.