



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 10:52 AM UTC

PDB ID : 5UFU / pdb_00005ufu
Title : Structure of AMPK bound to activator
Authors : Calabrese, M.F.; Kurumbail, R.G.
Deposited on : 2017-01-05
Resolution : 3.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

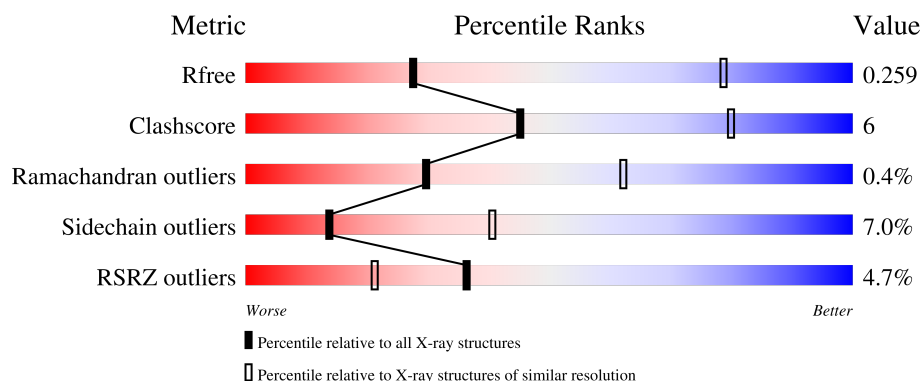
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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}	180053	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	503	
2	B	204	
3	C	330	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6125 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	369	2802	1793	481	510	1	17	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P54645
A	517	ALA	-	see remark 999	UNP P54645
A	518	SER	-	see remark 999	UNP P54645
A	519	GLY	-	see remark 999	UNP P54645
A	520	GLY	-	see remark 999	UNP P54645
A	521	PRO	-	see remark 999	UNP P54645
A	522	GLY	-	see remark 999	UNP P54645
A	523	GLY	-	see remark 999	UNP P54645
A	524	SER	-	see remark 999	UNP P54645

- 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	159	1172	762	198	210	2	0	0	0

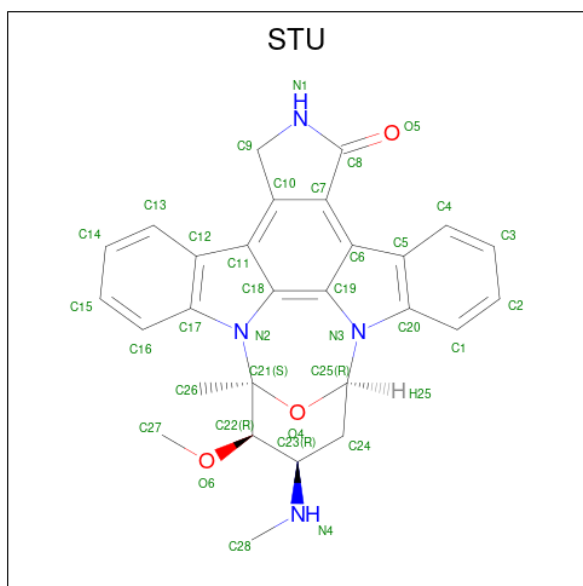
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MET	-	initiating methionine	UNP P80386
B	108	ASP	SER	engineered mutation	UNP P80386

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

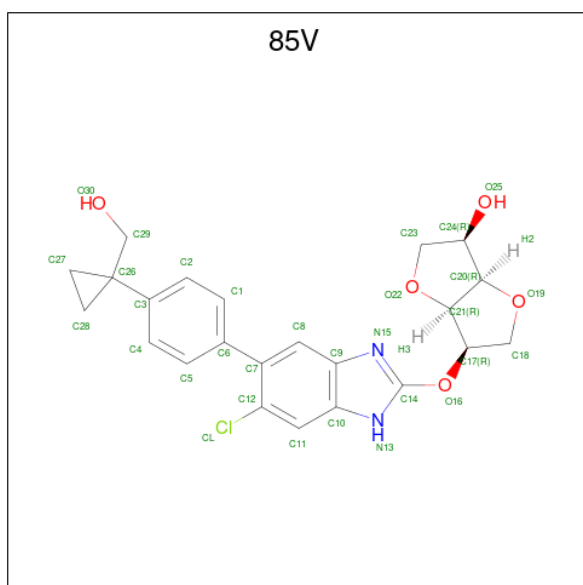
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	289	Total	C	N	O	S	0	0	0
			1999	1276	344	373	6			

- Molecule 4 is STAUROSPORINE (CCD ID: STU) (formula: $C_{28}H_{26}N_4O_3$).



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

- Molecule 5 is 1,4:3,6-dianhydro-2-O-(6-chloro-5-{4-[1-(hydroxymethyl)cyclopropyl]phenyl}-1H-benzimidazol-2-yl)-D-mannitol (CCD ID: 85V) (formula: $C_{23}H_{23}ClN_2O_5$).

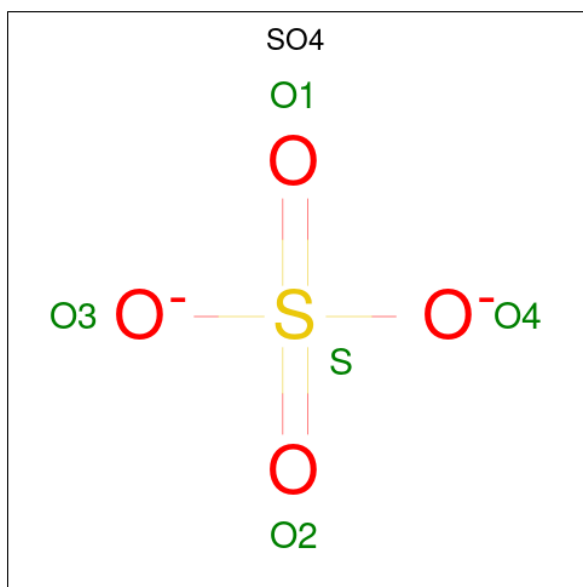


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	O	0	0
			31	23	1	2	5		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

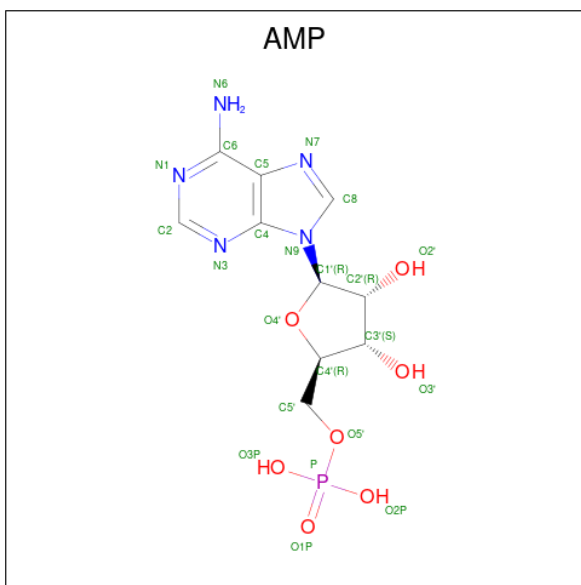
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	Cl	0	0
			3	3		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



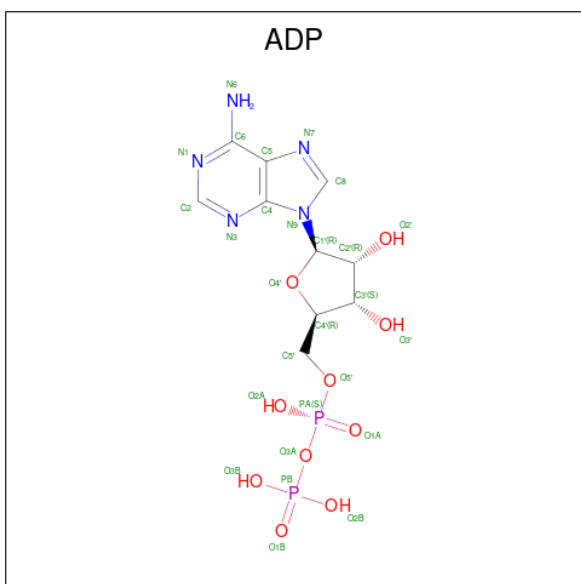
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



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

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

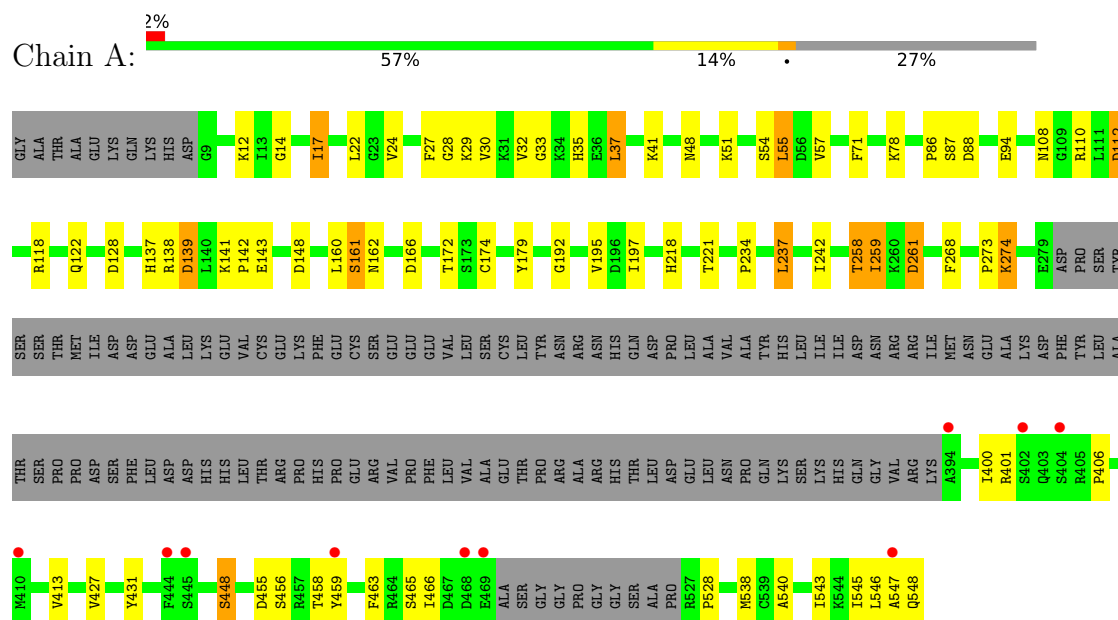


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

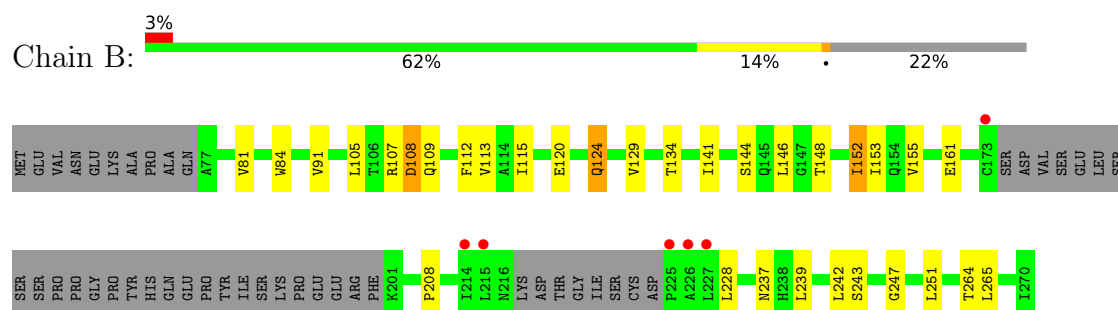
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

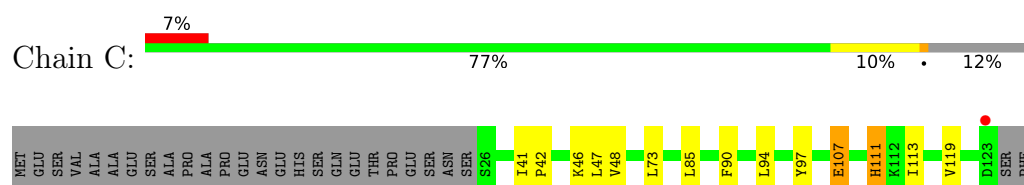
- Molecule 1: 5'-AMP-activated protein kinase catalytic subunit alpha-1

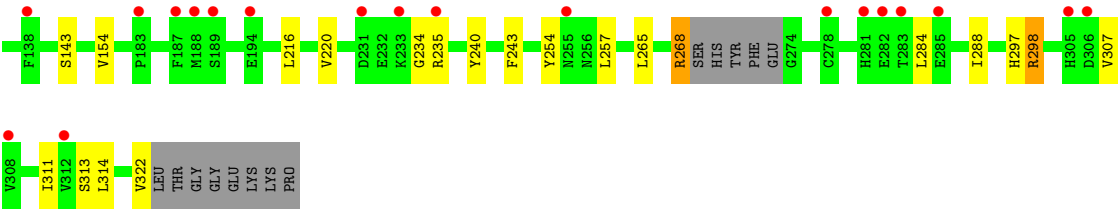


- Molecule 2: 5'-AMP-activated protein kinase subunit beta-1



- Molecule 3: 5'-AMP-activated protein kinase subunit gamma-1





4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	124.26 Å 124.26 Å 401.57 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.43 – 3.45 47.43 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.43-3.45) 99.8 (47.43-3.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 3.48 Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.193 , 0.238 0.217 , 0.259	Depositor DCC
R_{free} test set	1242 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	83.1	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 119.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6125	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 85V, SO4, AMP, STU, CL, ADP, TPO

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	0.86	0/2856	1.40	17/3886 (0.4%)
2	B	0.88	0/1206	1.30	6/1663 (0.4%)
3	C	0.89	0/2039	1.44	6/2809 (0.2%)
All	All	0.87	0/6101	1.39	29/8358 (0.3%)

There are no bond length outliers.

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	PRO	CA-C-N	7.48	130.17	120.44
1	A	273	PRO	C-N-CA	7.48	130.17	120.44
2	B	108	ASP	CA-CB-CG	7.05	119.65	112.60
1	A	71	PHE	CA-CB-CG	6.59	120.39	113.80
3	C	119	VAL	CA-C-N	6.51	129.32	120.54
3	C	119	VAL	C-N-CA	6.51	129.32	120.54
1	A	112	ASP	CA-CB-CG	6.29	118.89	112.60
1	A	148	ASP	CA-CB-CG	6.17	118.77	112.60
1	A	261	ASP	CA-CB-CG	5.80	118.40	112.60
1	A	139	ASP	CA-CB-CG	5.78	118.38	112.60
1	A	547	ALA	N-CA-C	5.70	117.59	108.41
3	C	42	PRO	CA-C-N	5.70	128.19	120.38
3	C	42	PRO	C-N-CA	5.70	128.19	120.38
3	C	313	SER	CA-C-N	5.54	127.97	120.38
3	C	313	SER	C-N-CA	5.54	127.97	120.38
1	A	546	LEU	CA-C-N	5.48	129.71	122.42
1	A	546	LEU	C-N-CA	5.48	129.71	122.42
2	B	161	GLU	CA-C-N	5.43	127.61	120.60
2	B	161	GLU	C-N-CA	5.43	127.61	120.60
1	A	55	LEU	N-CA-C	-5.42	101.99	110.17
1	A	14	GLY	N-CA-C	-5.40	100.39	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	ASN	N-CA-C	-5.38	102.49	110.46
1	A	28	GLY	N-CA-C	5.37	119.05	111.42
2	B	113	VAL	N-CA-C	5.33	116.53	108.96
1	A	268	PHE	CA-C-N	5.32	128.15	120.38
1	A	268	PHE	C-N-CA	5.32	128.15	120.38
1	A	166	ASP	CA-CB-CG	5.04	117.64	112.60
2	B	208	PRO	CA-C-N	5.02	127.01	120.28
2	B	208	PRO	C-N-CA	5.02	127.01	120.28

There are no chirality outliers.

There are no planarity outliers.

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	2802	0	2617	36	0
2	B	1172	0	1070	17	0
3	C	1999	0	1720	20	0
4	A	35	0	26	1	0
5	A	31	0	0	0	0
6	A	3	0	0	0	0
7	A	5	0	0	0	0
7	C	5	0	0	0	0
8	C	46	0	24	2	0
9	C	27	0	12	0	0
All	All	6125	0	5469	68	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 (68) 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)
3:C:107:GLU:O	3:C:111:HIS:HB2	1.92	0.70
1:A:427:VAL:HB	1:A:431:TYR:HD2	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:HG3	1:A:143:GLU:HB2	1.78	0.64
1:A:160:LEU:HD13	1:A:174:CYS:HB2	1.81	0.62
3:C:97:TYR:CD1	3:C:107:GLU:HG3	2.35	0.62
1:A:78:LYS:H	1:A:94:GLU:HG2	1.65	0.61
4:A:601:STU:H261	4:A:601:STU:H16	1.81	0.61
3:C:90:PHE:O	3:C:94:LEU:HB2	2.01	0.60
1:A:128:ASP:HB2	1:A:259:ILE:HG21	1.84	0.59
3:C:97:TYR:CG	3:C:107:GLU:HG3	2.38	0.58
1:A:274:LYS:H	1:A:274:LYS:HD3	1.69	0.57
2:B:107:ARG:HD2	2:B:112:PHE:CZ	2.40	0.57
1:A:48:ASN:HB3	1:A:51:LYS:HB3	1.87	0.56
1:A:218:HIS:HD2	1:A:221:THR:HG23	1.70	0.56
3:C:243:PHE:HB3	8:C:402:AMP:H5'1	1.86	0.56
1:A:455:ASP:HB3	1:A:458:THR:HG22	1.87	0.55
2:B:239:LEU:HD11	2:B:251:LEU:HD22	1.88	0.55
3:C:235:ARG:HA	3:C:307:VAL:HA	1.88	0.55
1:A:218:HIS:CD2	1:A:221:THR:HG23	2.41	0.54
1:A:24:VAL:HG12	1:A:29:LYS:HA	1.90	0.53
1:A:427:VAL:HB	1:A:431:TYR:CD2	2.45	0.52
2:B:107:ARG:HB3	2:B:112:PHE:CD2	2.44	0.52
1:A:401:ARG:O	1:A:548:GLN:HB3	2.10	0.52
1:A:465:SER:HB3	2:B:237:ASN:HB3	1.93	0.51
2:B:144:SER:HB3	2:B:148:THR:H	1.75	0.51
2:B:124:GLN:HG3	2:B:152:ILE:HD12	1.94	0.50
3:C:297:HIS:HA	3:C:314:LEU:HD22	1.94	0.50
3:C:94:LEU:HD11	3:C:254:TYR:HB2	1.93	0.49
2:B:265:LEU:HD12	3:C:48:VAL:HG22	1.93	0.49
1:A:137:HIS:HA	1:A:161:SER:HB2	1.96	0.48
1:A:22:LEU:HD12	1:A:30:VAL:HG12	1.96	0.48
2:B:84:TRP:CE2	2:B:129:VAL:HG21	2.49	0.47
3:C:94:LEU:HG	3:C:257:LEU:HD11	1.97	0.47
1:A:448:SER:HB3	1:A:466:ILE:HD11	1.97	0.47
1:A:543:ILE:C	1:A:545:ILE:H	2.22	0.47
2:B:91:VAL:HG22	2:B:129:VAL:HG13	1.96	0.47
1:A:137:HIS:HE1	1:A:139:ASP:O	1.97	0.46
1:A:540:ALA:HB2	2:B:251:LEU:HD11	1.97	0.46
3:C:265:LEU:HD22	3:C:268:ARG:NH1	2.30	0.46
1:A:455:ASP:CG	1:A:456:SER:H	2.23	0.46
3:C:265:LEU:HD22	3:C:268:ARG:HH12	1.80	0.46
1:A:234:PRO:HD2	1:A:237:LEU:HD22	1.97	0.46
2:B:228:LEU:HD11	3:C:46:LYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:HIS:HE1	1:A:37:LEU:HD12	1.82	0.45
1:A:258:THR:H	1:A:261:ASP:HB2	1.81	0.44
1:A:463:PHE:HB2	2:B:239:LEU:HB3	1.98	0.44
1:A:33:GLY:O	1:A:41:LYS:HA	2.17	0.44
1:A:12:LYS:HG2	1:A:17:ILE:HG22	1.98	0.44
3:C:298:ARG:HH11	8:C:402:AMP:H8	1.66	0.44
1:A:27:PHE:CE1	1:A:57:VAL:HG11	2.53	0.43
1:A:86:PRO:HG3	2:B:155:VAL:HG23	2.00	0.43
3:C:216:LEU:O	3:C:220:VAL:HG23	2.18	0.43
2:B:91:VAL:HG12	2:B:105:LEU:HD12	2.00	0.42
3:C:73:LEU:HD21	3:C:85:LEU:HB2	2.01	0.42
1:A:118:ARG:O	1:A:122:GLN:HG3	2.19	0.42
3:C:97:TYR:HB3	3:C:107:GLU:HG3	2.01	0.42
3:C:73:LEU:HD22	3:C:113:ILE:HG21	2.01	0.42
1:A:138:ARG:NH2	1:A:162:ASN:HB2	2.35	0.42
1:A:237:LEU:HB3	1:A:242:ILE:HD11	2.02	0.41
3:C:240:TYR:CD1	3:C:265:LEU:HD21	2.54	0.41
1:A:406:PRO:HG3	1:A:459:TYR:CZ	2.55	0.41
3:C:41:ILE:HD11	3:C:154:VAL:HG11	2.01	0.41
1:A:197:ILE:HD11	1:A:259:ILE:HG13	2.03	0.41
1:A:142:PRO:HD2	1:A:179:TYR:CE1	2.55	0.41
1:A:192:GLY:O	1:A:195:VAL:HG22	2.21	0.41
2:B:120:GLU:HA	2:B:155:VAL:HG13	2.02	0.40
2:B:107:ARG:HD2	2:B:112:PHE:CE2	2.56	0.40
2:B:81:VAL:HG22	2:B:115:ILE:HG12	2.03	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	362/503 (72%)	333 (92%)	28 (8%)	1 (0%)	36 67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	153/204 (75%)	141 (92%)	11 (7%)	1 (1%)	18	51
3	C	283/330 (86%)	270 (95%)	12 (4%)	1 (0%)	30	62
All	All	798/1037 (77%)	744 (93%)	51 (6%)	3 (0%)	30	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	528	PRO
2	B	247	GLY
3	C	234	GLY

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	281/448 (63%)	263 (94%)	18 (6%)	16	43
2	B	115/185 (62%)	104 (90%)	11 (10%)	8	31
3	C	174/299 (58%)	163 (94%)	11 (6%)	16	44
All	All	570/932 (61%)	530 (93%)	40 (7%)	14	40

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ILE
1	A	32	VAL
1	A	37	LEU
1	A	54	SER
1	A	55	LEU
1	A	87	SER
1	A	88	ASP
1	A	110	ARG
1	A	112	ASP
1	A	161	SER
1	A	237	LEU

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Mol	Chain	Res	Type
1	A	258	THR
1	A	259	ILE
1	A	274	LYS
1	A	400	ILE
1	A	413	VAL
1	A	448	SER
1	A	538	MET
2	B	108	ASP
2	B	109	GLN
2	B	124	GLN
2	B	134	THR
2	B	141	ILE
2	B	146	LEU
2	B	152	ILE
2	B	153	ILE
2	B	242	LEU
2	B	243	SER
2	B	264	THR
3	C	47	LEU
3	C	107	GLU
3	C	111	HIS
3	C	128	LEU
3	C	143	SER
3	C	268	ARG
3	C	284	LEU
3	C	288	ILE
3	C	298	ARG
3	C	311	ILE
3	C	322	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	218	HIS
1	A	247	HIS
1	A	397	HIS
1	A	531	HIS
3	C	168	HIS
3	C	297	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	172	1	8,10,11	1.62	1 (12%)	10,14,16	1.82	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	172	1	-	3/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	TPO	P-OG1	-3.85	1.52	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TPO	P-OG1-CB	-2.93	115.36	123.33
1	A	172	TPO	O2P-P-OG1	2.47	115.46	105.85
1	A	172	TPO	O3P-P-O1P	2.02	118.69	110.83

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	172	TPO	CB-OG1-P-O3P
1	A	172	TPO	CB-OG1-P-O1P
1	A	172	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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
4	STU	A	601	-	39,42,42	0.94	2 (5%)	50,68,68	0.78	2 (4%)
9	ADP	C	403	-	28,29,29	0.44	0	43,45,45	0.67	0
8	AMP	C	402	-	25,25,25	0.35	0	37,38,38	0.67	1 (2%)
7	SO4	A	606	-	4,4,4	0.27	0	6,6,6	0.09	0
8	AMP	C	401	-	25,25,25	0.28	0	37,38,38	0.48	0
7	SO4	C	404	-	4,4,4	0.25	0	6,6,6	0.17	0
5	85V	A	602	-	35,36,36	0.62	1 (2%)	49,55,55	1.85	5 (10%)

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
4	STU	A	601	-	-	2/4/42/42	-
9	ADP	C	403	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	AMP	C	402	-	-	2/10/26/26	0/3/3/3
8	AMP	C	401	-	-	0/10/26/26	0/3/3/3
5	85V	A	602	-	-	0/15/43/43	0/6/6/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	STU	C8-N1	4.81	1.38	1.35
5	A	602	85V	C14-N15	3.10	1.35	1.30
4	A	601	STU	C9-C10	-2.10	1.48	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	85V	O16-C14-N15	-10.12	120.19	127.04
5	A	602	85V	C17-O16-C14	4.46	123.52	117.18
5	A	602	85V	C9-C10-N13	3.58	110.02	105.71
4	A	601	STU	C9-C10-C7	3.31	111.10	109.88
8	C	402	AMP	O2P-P-O5'	2.89	114.22	106.67
5	A	602	85V	C10-C9-N15	-2.63	105.82	109.42
5	A	602	85V	C10-N13-C14	-2.25	103.59	107.85
4	A	601	STU	C11-C10-C7	-2.07	119.88	121.25

There are no chirality outliers.

All (6) torsion outliers are listed below:

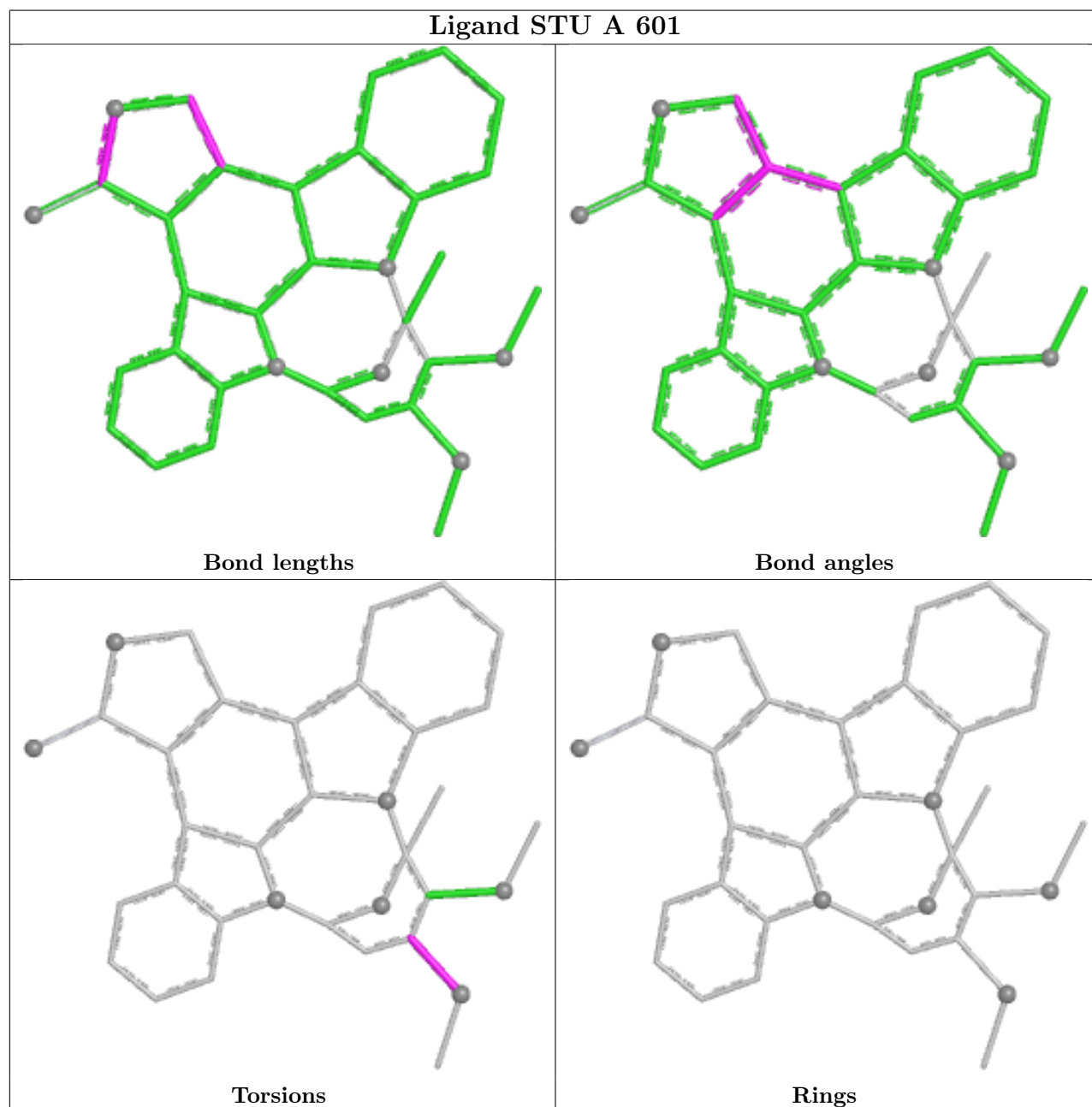
Mol	Chain	Res	Type	Atoms
8	C	402	AMP	C3'-C4'-C5'-O5'
9	C	403	ADP	C5'-O5'-PA-O1A
9	C	403	ADP	C5'-O5'-PA-O3A
4	A	601	STU	C24-C23-N4-C28
8	C	402	AMP	O4'-C4'-C5'-O5'
4	A	601	STU	C22-C23-N4-C28

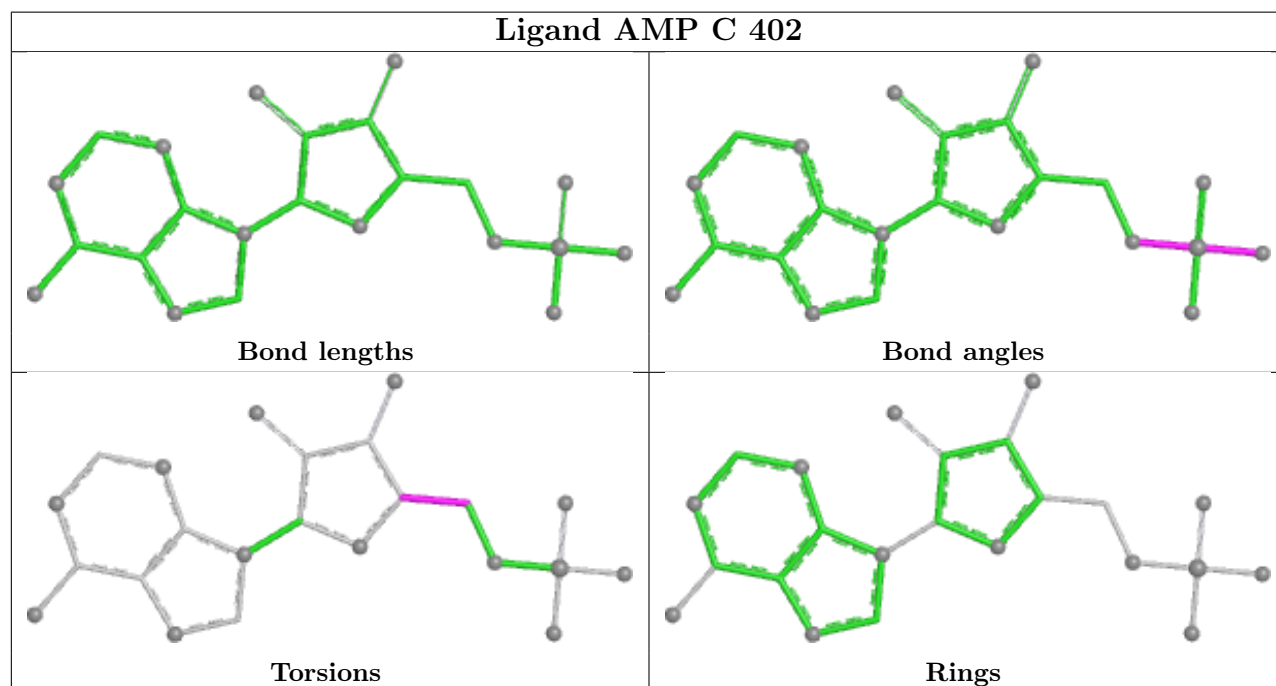
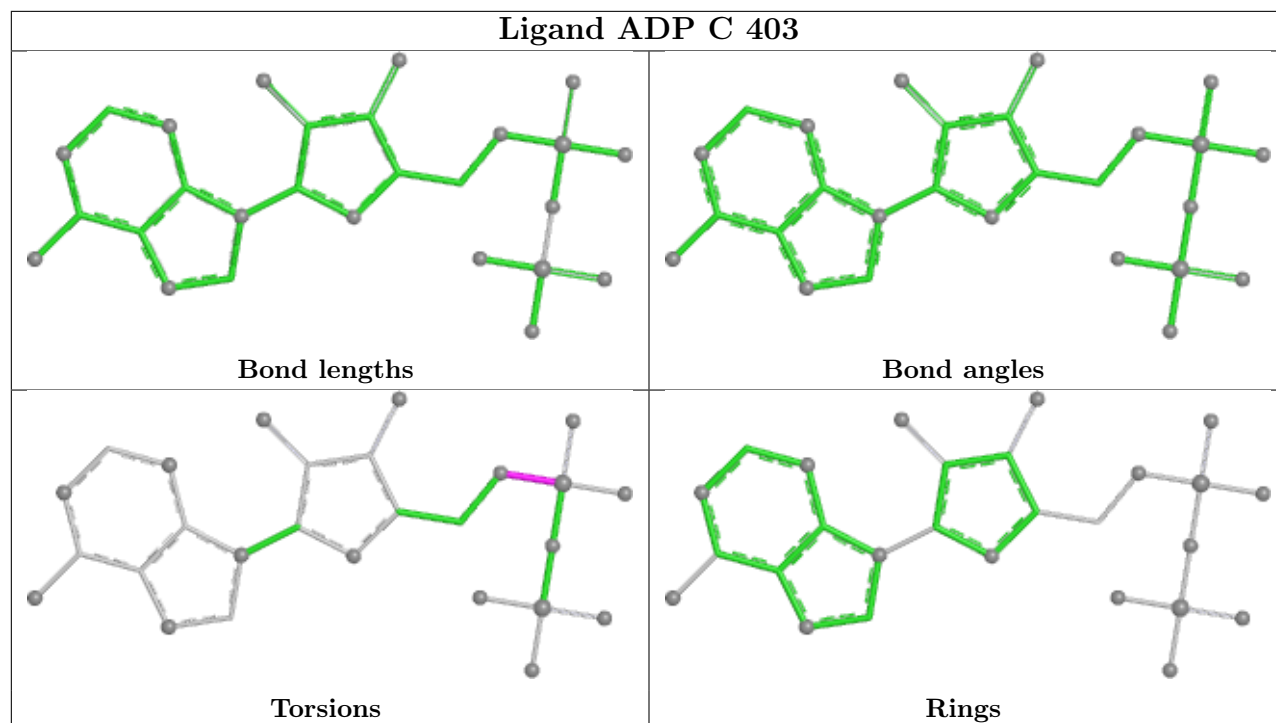
There are no ring outliers.

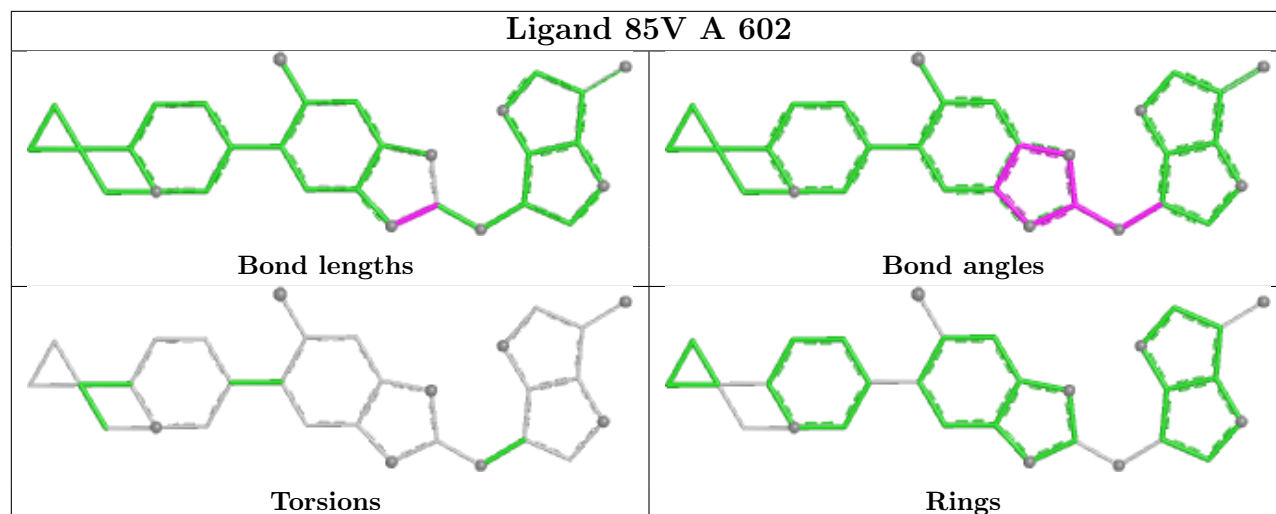
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	STU	1	0
8	C	402	AMP	2	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

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	368/503 (73%)	-0.02	10 (2%) 56 33	40, 69, 131, 152	0
2	B	159/204 (77%)	0.23	6 (3%) 44 26	49, 81, 112, 136	0
3	C	289/330 (87%)	0.56	22 (7%) 20 14	69, 110, 171, 180	0
All	All	816/1037 (78%)	0.23	38 (4%) 36 21	40, 87, 159, 180	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	173	CYS	4.9
3	C	278	CYS	4.6
3	C	189	SER	4.5
3	C	283	THR	4.5
1	A	547	ALA	4.2
3	C	188	MET	4.1
3	C	282	GLU	3.7
2	B	215	LEU	3.6
2	B	225	PRO	3.5
1	A	394	ALA	3.3
3	C	123	ASP	3.3
1	A	445	SER	3.1
3	C	281	HIS	3.0
3	C	187	PHE	3.0
3	C	183	PRO	2.7
3	C	231	ASP	2.7
3	C	305	HIS	2.6
3	C	308	VAL	2.6
3	C	194	GLU	2.6
1	A	468	ASP	2.6
3	C	127	PRO	2.6
1	A	469	GLU	2.5
3	C	306	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	131	ILE	2.4
3	C	312	VAL	2.4
1	A	444	PHE	2.3
3	C	255	ASN	2.3
1	A	410	MET	2.3
1	A	404	SER	2.3
3	C	138	PHE	2.3
3	C	235	ARG	2.3
2	B	214	ILE	2.3
1	A	402	SER	2.3
3	C	233	LYS	2.3
3	C	285	GLU	2.2
2	B	226	ALA	2.1
2	B	227	LEU	2.1
1	A	459	TYR	2.1

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	172	11/12	0.94	0.09	70,74,79,80	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

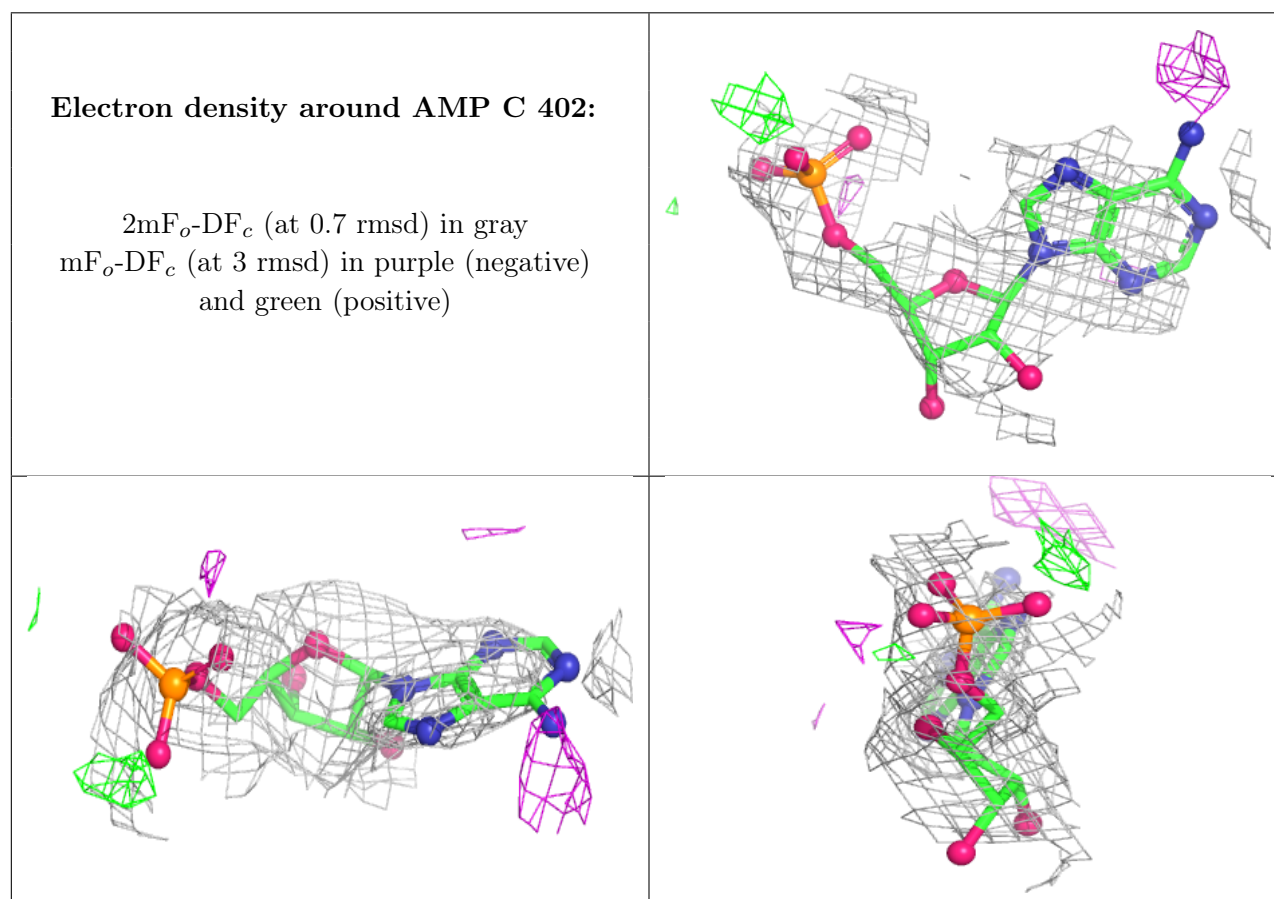
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	AMP	C	402	23/23	0.74	0.15	181,193,209,212	0
7	SO4	A	606	5/5	0.77	0.11	174,174,174,174	0

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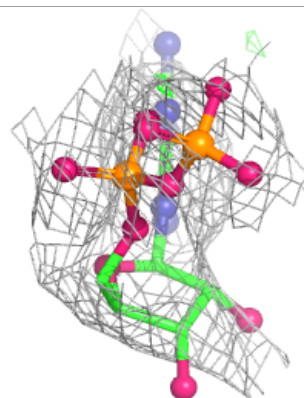
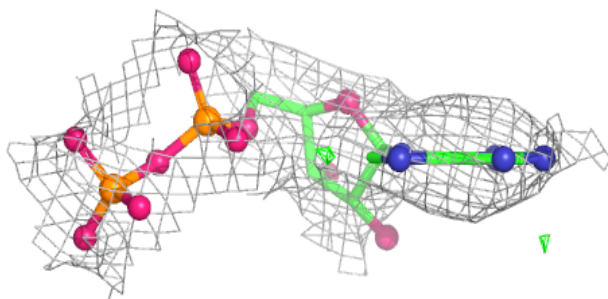
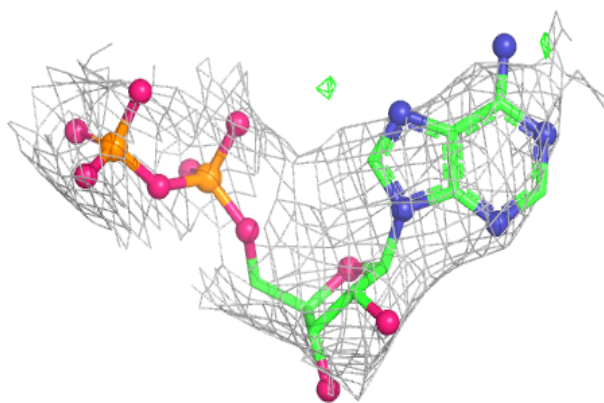
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	SO4	C	404	5/5	0.84	0.13	141,141,141,142	0
8	AMP	C	401	23/23	0.88	0.15	128,143,148,153	0
9	ADP	C	403	27/27	0.88	0.15	157,160,179,181	0
6	CL	A	604	1/1	0.96	0.07	75,75,75,75	0
5	85V	A	602	31/31	0.97	0.08	46,52,56,58	0
6	CL	A	605	1/1	0.98	0.07	53,53,53,53	0
6	CL	A	603	1/1	0.98	0.11	51,51,51,51	0
4	STU	A	601	35/35	0.98	0.09	48,53,60,64	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.

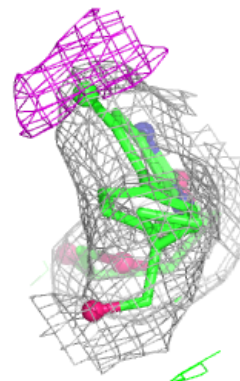
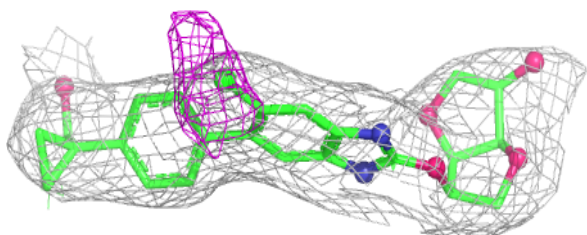
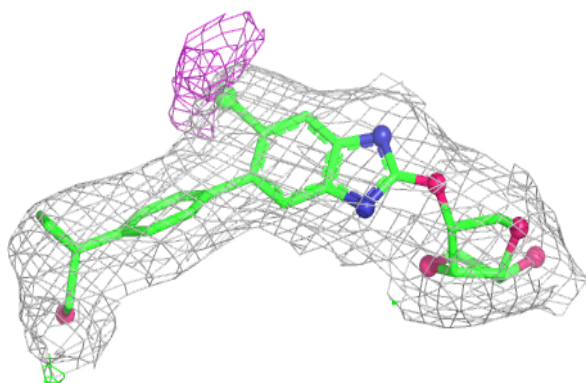


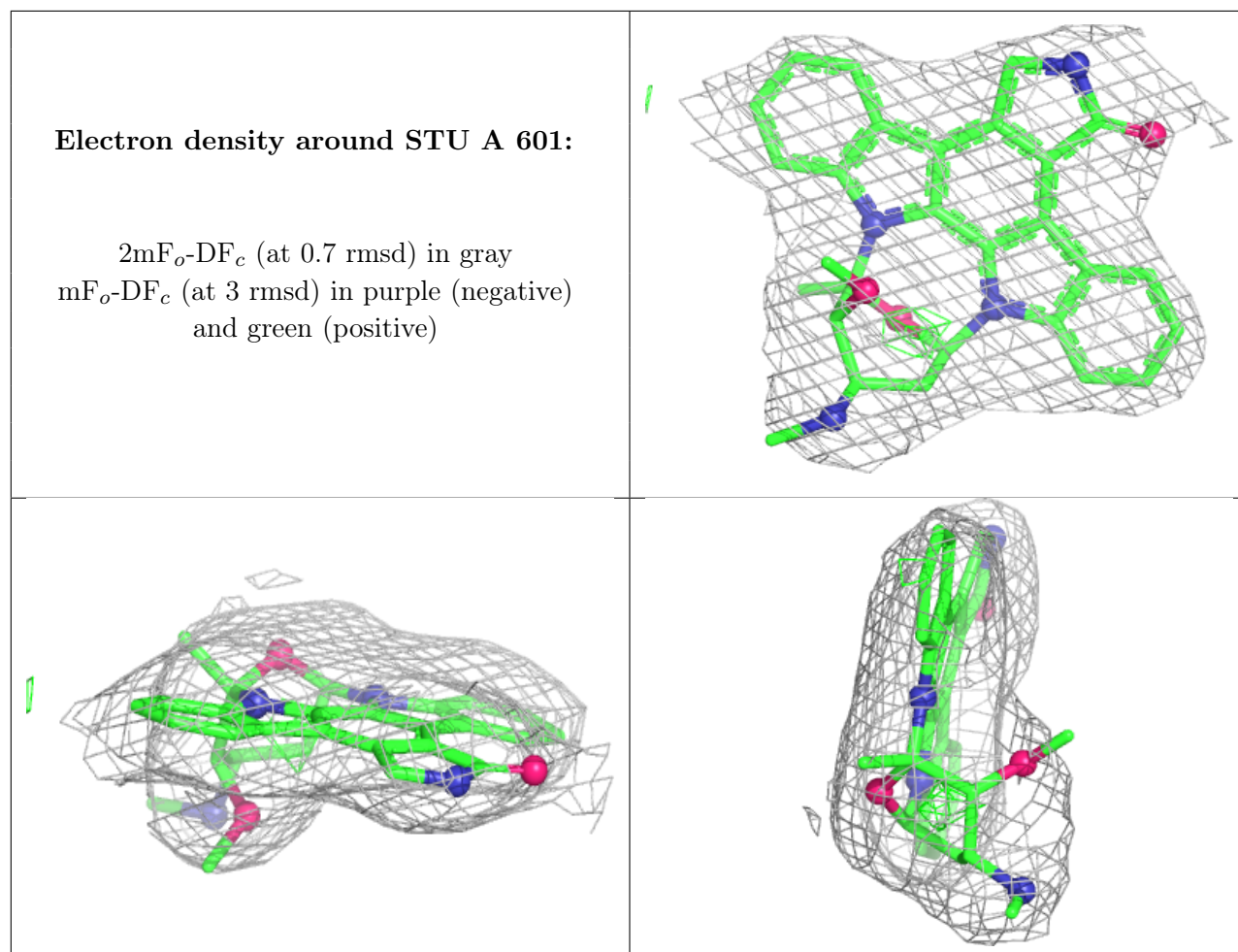
Electron density around ADP C 403:

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

**Electron density around 85V 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.