



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:52 PM UTC

PDB ID : 5KQ5 / pdb_00005kq5
Title : AMPK bound to allosteric activator
Authors : Calabrese, M.F.; Kurumbail, R.G.
Deposited on : 2016-07-05
Resolution : 3.41 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

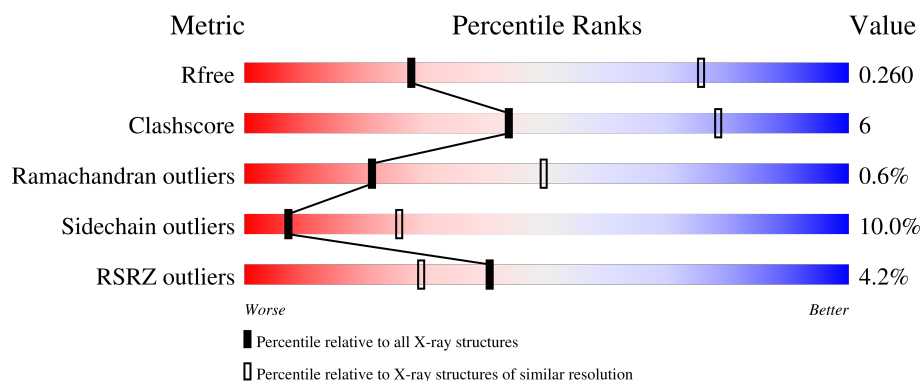
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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	1210 (3.48-3.36)
Clashscore	190562	1234 (3.48-3.36)
Ramachandran outliers	187476	1222 (3.48-3.36)
Sidechain outliers	187428	1222 (3.48-3.36)
RSRZ outliers	180081	1210 (3.48-3.36)

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% 56% 13% 28%
2	B	204	 2% 57% 19% 22%
3	C	330	 6% 71% 13% 15%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6230 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
1	A	363	Total	C	N	O	P	S	0	0	0
			2832	1820	483	511	1	17			

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P54645
A	?	-	ILE	deletion	UNP P54645
A	?	-	THR	deletion	UNP P54645
A	?	-	GLU	deletion	UNP P54645
A	?	-	ALA	deletion	UNP P54645
A	?	-	LYS	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	GLY	deletion	UNP P54645
A	?	-	THR	deletion	UNP P54645
A	?	-	ALA	deletion	UNP P54645
A	?	-	THR	deletion	UNP P54645
A	?	-	PRO	deletion	UNP P54645
A	?	-	GLN	deletion	UNP P54645
A	?	-	ARG	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	GLY	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	ILE	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	ASN	deletion	UNP P54645
A	?	-	TYR	deletion	UNP P54645
A	?	-	ARG	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	CYS	deletion	UNP P54645
A	?	-	GLN	deletion	UNP P54645
A	?	-	ARG	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	ASP	deletion	UNP P54645
A	?	-	ALA	deletion	UNP P54645
A	?	-	GLU	deletion	UNP P54645
A	?	-	ALA	deletion	UNP P54645
A	?	-	GLN	deletion	UNP P54645
A	?	-	GLY	deletion	UNP P54645
A	?	-	LYS	deletion	UNP P54645
A	?	-	PRO	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	GLU	deletion	UNP P54645
A	?	-	VAL	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	LEU	deletion	UNP P54645
A	?	-	THR	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	?	-	VAL	deletion	UNP P54645
A	?	-	THR	deletion	UNP P54645
A	?	-	SER	deletion	UNP P54645
A	517	ALA	LEU	linker	UNP P54645
A	518	SER	ASP	linker	UNP P54645
A	519	GLY	SER	linker	UNP P54645
A	520	GLY	SER	linker	UNP P54645
A	522	GLY	VAL	linker	UNP P54645
A	523	GLY	ASP	linker	UNP P54645
A	524	SER	VAL	linker	UNP P54645

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	160	Total	C	N	O	S	0	0	0
			1227	799	207	218	3			

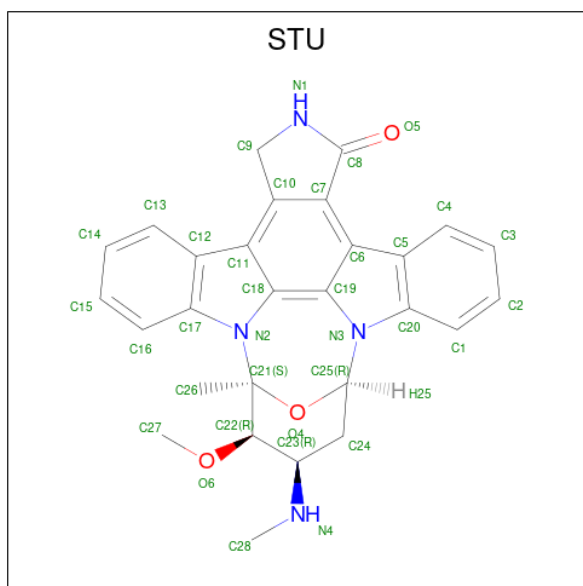
There are 2 discrepancies between the modelled and reference sequences:

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.

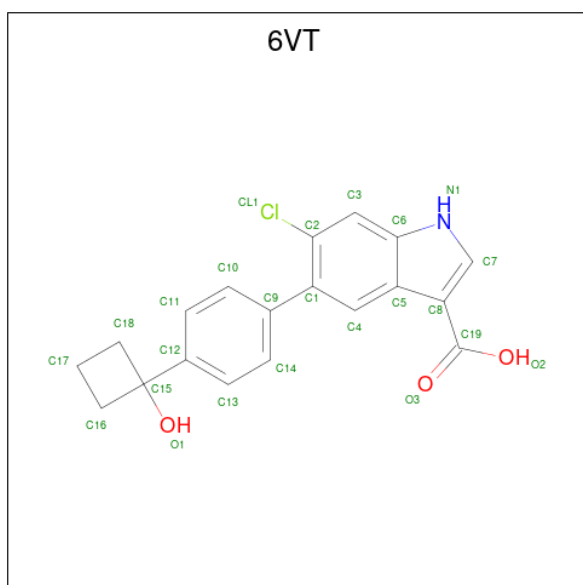
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	281	Total	C	N	O	S	0	0	0
			2030	1316	339	369	6			

- 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 6-chloranyl-5-[4-(1-oxidanylcyclobutyl)phenyl]-1 {H}-indole-3-carboxylic acid (CCD ID: 6VT) (formula: $C_{19}H_{16}ClNO_3$).

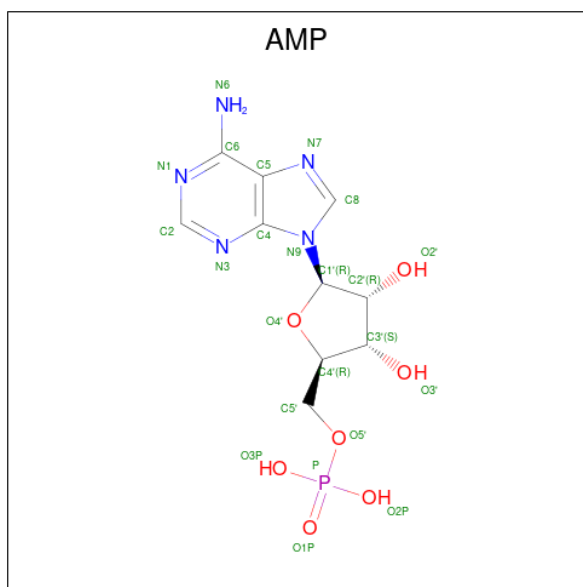


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	O	0	0
			24	19	1	1	3		

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

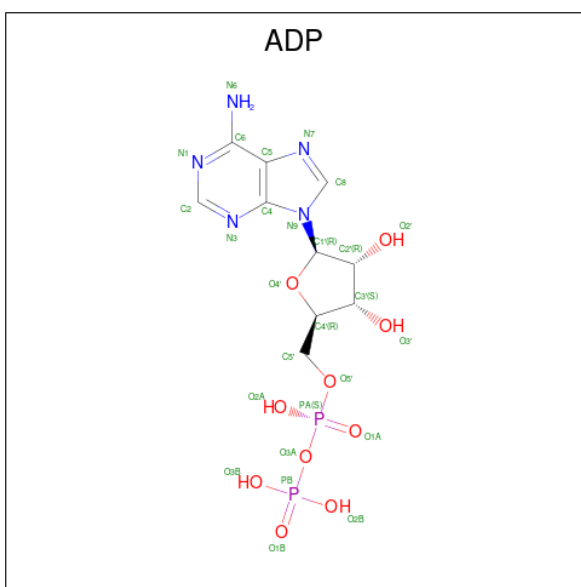
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	Cl	0	0
			4	4		

- Molecule 7 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



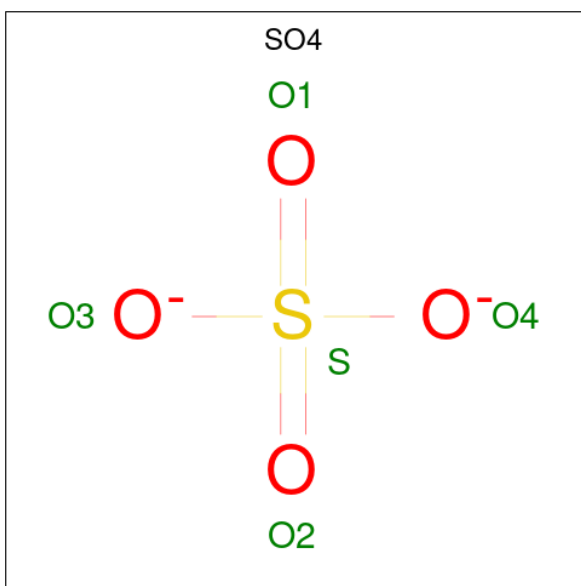
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
7	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

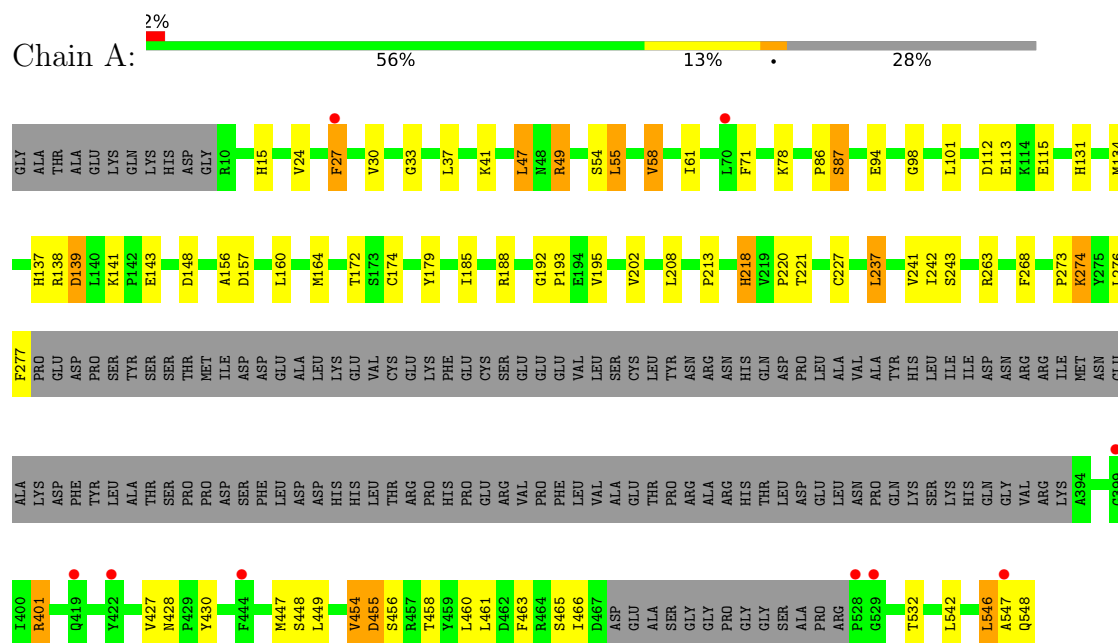


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	C	1	Total	O S		
			5	4 1	0	0

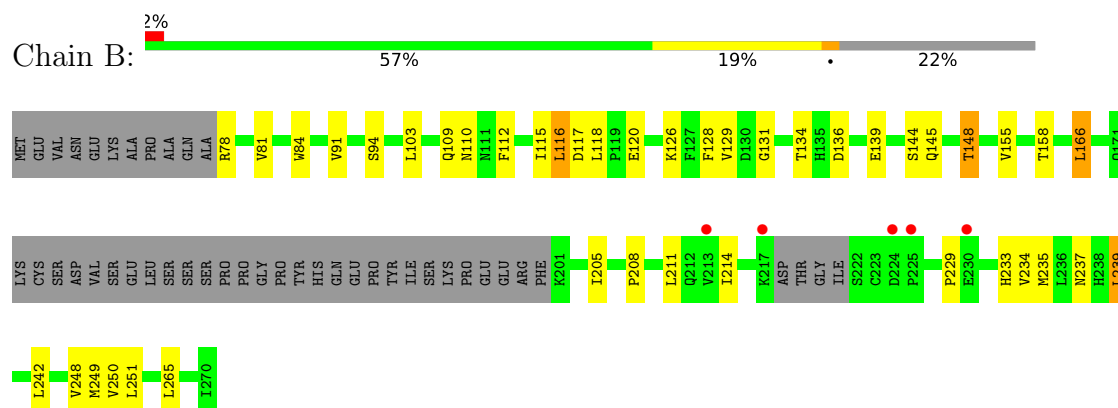
3 Residue-property plots

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

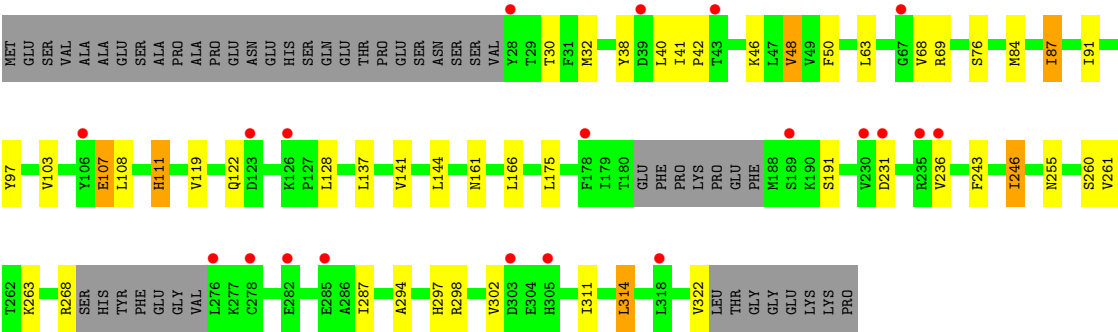


• Molecule 2: 5'-AMP-activated protein kinase subunit beta-1



• 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	124.50Å 124.50Å 402.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.90 – 3.41 29.90 – 3.41	Depositor EDS
% Data completeness (in resolution range)	96.5 (29.90-3.41) 96.2 (29.90-3.41)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 3.39Å)	Xtriage
Refinement program	BUSTER-TNT 2.11.6	Depositor
R, R_{free}	0.221 , 0.259 0.223 , 0.260	Depositor DCC
R_{free} test set	1248 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	86.4	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 116.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6230	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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: SO4, ADP, TPO, CL, AMP, STU, 6VT

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	0.80	0/2886	1.39	20/3917 (0.5%)
2	B	0.79	0/1261	1.21	2/1727 (0.1%)
3	C	0.83	0/2069	1.40	5/2844 (0.2%)
All	All	0.81	0/6216	1.36	27/8488 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	SER	N-CA-C	-8.20	103.06	113.23
1	A	139	ASP	CA-CB-CG	8.16	120.76	112.60
1	A	273	PRO	CA-C-N	6.59	129.00	120.44
1	A	273	PRO	C-N-CA	6.59	129.00	120.44
1	A	101	LEU	N-CA-C	-6.46	104.31	111.36
1	A	156	ALA	N-CA-C	6.38	121.67	113.18
1	A	268	PHE	CA-C-N	6.38	129.12	120.38
1	A	268	PHE	C-N-CA	6.38	129.12	120.38
1	A	55	LEU	N-CA-C	-6.06	100.69	110.32
1	A	138	ARG	N-CA-C	-5.90	103.15	110.41
1	A	148	ASP	CA-CB-CG	5.68	118.28	112.60
3	C	119	VAL	CA-C-N	5.68	127.89	120.28
3	C	119	VAL	C-N-CA	5.68	127.89	120.28
3	C	50	PHE	CA-CB-CG	5.65	119.45	113.80
1	A	547	ALA	N-CA-C	5.46	117.64	108.96
1	A	218	HIS	CA-C-N	5.35	125.57	120.43
1	A	218	HIS	C-N-CA	5.35	125.57	120.43
1	A	546	LEU	CA-C-N	5.35	129.52	122.30
1	A	546	LEU	C-N-CA	5.35	129.52	122.30
1	A	455	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	98	GLY	N-CA-C	5.30	120.31	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	42	PRO	CA-C-N	5.29	127.63	120.38
3	C	42	PRO	C-N-CA	5.29	127.63	120.38
2	B	233	HIS	CA-C-N	5.20	128.82	120.30
2	B	233	HIS	C-N-CA	5.20	128.82	120.30
1	A	27	PHE	CA-CB-CG	5.09	118.89	113.80
1	A	71	PHE	CA-CB-CG	5.07	118.87	113.80

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	2832	0	2747	38	0
2	B	1227	0	1190	22	0
3	C	2030	0	1900	19	0
4	A	35	0	26	5	0
5	A	24	0	0	1	0
6	A	4	0	0	0	0
7	C	46	0	24	2	0
8	C	27	0	12	0	0
9	C	5	0	0	0	0
All	All	6230	0	5899	74	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 (74) 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)
4:A:601:STU:H261	4:A:601:STU:H16	1.52	0.90
3:C:69:ARG:HD2	3:C:243:PHE:HD1	1.54	0.72
1:A:532:THR:H	3:C:161:ASN:HD21	1.39	0.71
1:A:455:ASP:HB2	1:A:458:THR:H	1.58	0.68
1:A:274:LYS:H	1:A:274:LYS:HD3	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:243:PHE:HB3	7:C:402:AMP:H5'1	1.75	0.67
1:A:134:MET:HA	1:A:164:MET:HE3	1.76	0.67
2:B:208:PRO:HA	2:B:211:LEU:HD12	1.78	0.65
1:A:49:ARG:HH21	1:A:86:PRO:HA	1.61	0.65
1:A:185:ILE:HD11	1:A:227:CYS:SG	2.38	0.63
3:C:32:MET:HE3	3:C:175:LEU:HD12	1.80	0.62
2:B:214:ILE:HB	2:B:229:PRO:HD2	1.82	0.62
2:B:116:LEU:HD12	2:B:118:LEU:HD21	1.83	0.61
3:C:97:TYR:CG	3:C:107:GLU:HG3	2.36	0.60
1:A:448:SER:HB3	1:A:466:ILE:HD11	1.84	0.60
1:A:141:LYS:HG3	1:A:143:GLU:HB2	1.84	0.59
1:A:237:LEU:HB3	1:A:242:ILE:HD11	1.85	0.58
3:C:97:TYR:CD1	3:C:107:GLU:HG3	2.37	0.58
1:A:218:HIS:HD2	1:A:221:THR:H	1.51	0.57
3:C:69:ARG:HD2	3:C:243:PHE:CD1	2.37	0.56
1:A:188:ARG:HG2	2:B:205:ILE:HD13	1.88	0.56
3:C:63:LEU:HD23	3:C:68:VAL:HG13	1.88	0.54
3:C:69:ARG:HG2	3:C:87:ILE:HD11	1.90	0.54
1:A:532:THR:H	3:C:161:ASN:ND2	2.03	0.53
2:B:81:VAL:HG22	2:B:115:ILE:HG12	1.91	0.52
4:A:601:STU:H261	4:A:601:STU:C16	2.24	0.52
1:A:27:PHE:O	1:A:47:LEU:HD23	2.11	0.51
1:A:179:TYR:HD1	1:A:202:VAL:CG2	2.24	0.51
1:A:463:PHE:HB2	2:B:239:LEU:HB3	1.92	0.50
1:A:274:LYS:H	1:A:274:LYS:CD	2.24	0.49
2:B:145:GLN:H	2:B:145:GLN:CD	2.20	0.49
4:A:601:STU:C16	4:A:601:STU:C26	2.89	0.48
1:A:179:TYR:HD1	1:A:202:VAL:HG23	1.79	0.47
1:A:58:VAL:HG23	2:B:166:LEU:HD12	1.95	0.47
3:C:243:PHE:CB	7:C:402:AMP:H5'1	2.41	0.47
2:B:249:MET:HE2	2:B:251:LEU:HD21	1.96	0.47
3:C:243:PHE:O	3:C:246:ILE:HG13	2.14	0.47
2:B:265:LEU:HD12	3:C:48:VAL:HG22	1.97	0.47
2:B:128:PHE:CZ	2:B:131:GLY:HA2	2.49	0.47
3:C:107:GLU:O	3:C:111:HIS:HB2	2.15	0.47
5:A:602:6VT:CL1	5:A:602:6VT:C14	3.00	0.47
1:A:160:LEU:HD13	1:A:174:CYS:HB2	1.97	0.46
3:C:260:SER:H	3:C:263:LYS:HD2	1.81	0.46
1:A:465:SER:HB3	2:B:237:ASN:HB3	1.98	0.46
1:A:87:SER:OG	2:B:81:VAL:HB	2.16	0.45
3:C:141:VAL:HA	3:C:144:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:109:GLN:HB3	2:B:110:ASN:H	1.66	0.45
1:A:263:ARG:HD3	1:A:277:PHE:CD1	2.52	0.45
2:B:84:TRP:HB3	2:B:112:PHE:HB2	1.98	0.45
1:A:78:LYS:H	1:A:94:GLU:HG2	1.82	0.45
2:B:265:LEU:HD11	3:C:46:LYS:HD2	1.99	0.45
1:A:137:HIS:HE1	1:A:139:ASP:O	2.00	0.44
3:C:297:HIS:HA	3:C:314:LEU:HD22	1.98	0.44
1:A:179:TYR:CD1	1:A:202:VAL:CG2	3.01	0.44
2:B:144:SER:HB3	2:B:148:THR:H	1.83	0.44
1:A:401:ARG:O	1:A:548:GLN:HB3	2.18	0.44
2:B:136:ASP:HB3	2:B:139:GLU:HB2	1.99	0.44
2:B:91:VAL:HG22	2:B:129:VAL:HG13	2.00	0.43
1:A:208:LEU:HD11	1:A:241:VAL:HG21	2.00	0.43
1:A:401:ARG:HH22	1:A:454:VAL:HG11	1.84	0.43
2:B:239:LEU:HD11	2:B:251:LEU:HD22	2.00	0.42
1:A:192:GLY:O	1:A:195:VAL:HG22	2.19	0.42
2:B:78:ARG:O	2:B:117:ASP:HA	2.19	0.42
1:A:202:VAL:HG12	1:A:213:PRO:HG2	2.02	0.42
1:A:449:LEU:HD23	1:A:461:LEU:HD11	2.01	0.41
1:A:131:HIS:CE1	1:A:193:PRO:HA	2.55	0.41
1:A:218:HIS:CD2	1:A:220:PRO:HD2	2.55	0.41
3:C:38:TYR:HA	3:C:41:ILE:HD12	2.03	0.41
1:A:428:ASN:C	1:A:430:TYR:H	2.29	0.41
1:A:143:GLU:HB3	4:A:601:STU:H281	2.02	0.41
1:A:33:GLY:O	1:A:41:LYS:HA	2.21	0.40
1:A:112:ASP:O	1:A:113:GLU:C	2.64	0.40
2:B:84:TRP:CE2	2:B:129:VAL:HG21	2.56	0.40
1:A:30:VAL:HG21	4:A:601:STU:C17	2.52	0.40

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	356/503 (71%)	329 (92%)	26 (7%)	1 (0%)	36	65
2	B	154/204 (76%)	142 (92%)	11 (7%)	1 (1%)	21	49
3	C	275/330 (83%)	257 (94%)	15 (6%)	3 (1%)	11	37
All	All	785/1037 (76%)	728 (93%)	52 (7%)	5 (1%)	21	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	294	ALA
2	B	120	GLU
3	C	231	ASP
3	C	122	GLN
1	A	427	VAL

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	299/448 (67%)	277 (93%)	22 (7%)	13	37
2	B	131/185 (71%)	116 (88%)	15 (12%)	5	20
3	C	198/299 (66%)	172 (87%)	26 (13%)	4	16
All	All	628/932 (67%)	565 (90%)	63 (10%)	7	25

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	24	VAL
1	A	37	LEU
1	A	47	LEU
1	A	49	ARG
1	A	54	SER
1	A	55	LEU
1	A	58	VAL

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Mol	Chain	Res	Type
1	A	61	ILE
1	A	87	SER
1	A	115	GLU
1	A	157	ASP
1	A	237	LEU
1	A	243	SER
1	A	274	LYS
1	A	276	LEU
1	A	401	ARG
1	A	447	MET
1	A	454	VAL
1	A	460	LEU
1	A	542	LEU
1	A	546	LEU
2	B	94	SER
2	B	103	LEU
2	B	116	LEU
2	B	126	LYS
2	B	134	THR
2	B	148	THR
2	B	155	VAL
2	B	158	THR
2	B	166	LEU
2	B	234	VAL
2	B	235	MET
2	B	239	LEU
2	B	242	LEU
2	B	248	VAL
2	B	250	VAL
3	C	30	THR
3	C	40	LEU
3	C	48	VAL
3	C	76	SER
3	C	84	MET
3	C	87	ILE
3	C	91	ILE
3	C	103	VAL
3	C	107	GLU
3	C	108	LEU
3	C	111	HIS
3	C	128	LEU
3	C	137	LEU

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Mol	Chain	Res	Type
3	C	166	LEU
3	C	191	SER
3	C	236	VAL
3	C	246	ILE
3	C	255	ASN
3	C	261	VAL
3	C	268	ARG
3	C	287	ILE
3	C	298	ARG
3	C	302	VAL
3	C	311	ILE
3	C	314	LEU
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	218	HIS
1	A	247	HIS
2	B	212	GLN
2	B	232	ASN
3	C	161	ASN
3	C	221	GLN
3	C	319	GLN

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	1.18	1 (12%)	10,14,16	1.60	2 (20%)

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	-	0/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	TPO	P-OG1	-2.81	1.54	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TPO	P-OG1-CB	-3.06	115.00	123.33
1	A	172	TPO	O3P-P-O1P	-2.23	102.14	110.83

There are no chirality outliers.

There are no torsion outliers.

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, 4 are monoatomic - leaving 6 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	$\# Z > 2$
7	AMP	C	402	-	25,25,25	0.34	0	37,38,38	0.60	1 (2%)
7	AMP	C	401	-	25,25,25	0.21	0	37,38,38	0.42	0
4	STU	A	601	-	39,42,42	2.56	14 (35%)	50,68,68	2.87	19 (38%)
5	6VT	A	602	-	25,27,27	0.93	2 (8%)	35,41,41	1.14	5 (14%)
8	ADP	C	403	-	28,29,29	0.48	0	43,45,45	0.65	0
9	SO4	C	404	-	4,4,4	0.23	0	6,6,6	0.17	0

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
7	AMP	C	402	-	-	2/10/26/26	0/3/3/3
7	AMP	C	401	-	-	0/10/26/26	0/3/3/3
4	STU	A	601	-	-	1/4/42/42	-
5	6VT	A	602	-	-	3/14/22/22	0/4/4/4
8	ADP	C	403	-	-	3/16/32/32	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	STU	C9-C10	-5.25	1.46	1.50
4	A	601	STU	C12-C17	5.21	1.49	1.41
4	A	601	STU	C5-C20	5.10	1.48	1.41
4	A	601	STU	C11-C10	4.92	1.49	1.40
4	A	601	STU	C6-C7	4.68	1.49	1.40
4	A	601	STU	C19-C18	4.10	1.49	1.40
4	A	601	STU	C7-C10	4.00	1.46	1.39
5	A	602	6VT	O3-C19	3.94	1.32	1.22
4	A	601	STU	C9-N1	3.83	1.49	1.45
4	A	601	STU	C25-N3	3.79	1.48	1.45
4	A	601	STU	C11-C18	3.54	1.47	1.41
4	A	601	STU	C18-N2	-3.52	1.36	1.40
4	A	601	STU	C6-C19	2.83	1.46	1.41
4	A	601	STU	C17-N2	-2.72	1.37	1.40
4	A	601	STU	O5-C8	2.42	1.29	1.23
5	A	602	6VT	O2-C19	-2.21	1.24	1.30

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	601	STU	C11-C10-C7	-7.00	116.64	121.25
4	A	601	STU	C7-C8-N1	5.83	111.94	106.38
4	A	601	STU	C6-C7-C10	5.68	124.72	120.76
4	A	601	STU	C9-C10-C11	5.46	132.88	128.73
4	A	601	STU	C18-N2-C17	5.44	113.94	107.37
4	A	601	STU	C9-N1-C8	-5.38	108.96	113.86
4	A	601	STU	C10-C7-C8	-5.13	103.80	108.09
4	A	601	STU	C12-C17-N2	-4.70	105.85	108.94
4	A	601	STU	C28-N4-C23	4.64	119.93	114.39
4	A	601	STU	C1-C20-C5	-4.10	116.80	121.59
4	A	601	STU	C16-C17-N2	4.07	136.33	130.22
4	A	601	STU	C4-C5-C20	3.77	123.60	119.24
5	A	602	6VT	O3-C19-C8	-3.35	114.95	121.51
4	A	601	STU	C16-C17-C12	-3.23	117.81	121.59
4	A	601	STU	C10-C9-N1	3.15	104.82	101.75
5	A	602	6VT	C7-C8-C19	3.05	128.12	124.82
4	A	601	STU	O5-C8-C7	-3.04	124.06	128.47
4	A	601	STU	C13-C12-C17	3.01	122.72	119.24
5	A	602	6VT	O2-C19-C8	2.92	121.62	115.83
4	A	601	STU	C1-C20-N3	2.77	134.44	129.73
5	A	602	6VT	C17-C18-C15	2.40	90.57	88.97
7	C	402	AMP	O2P-P-O5'	2.32	112.72	106.67
4	A	601	STU	C3-C4-C5	-2.24	116.52	120.23
5	A	602	6VT	C17-C16-C15	2.08	90.36	88.97
4	A	601	STU	C14-C13-C12	-2.08	116.78	120.23

There are no chirality outliers.

All (9) torsion outliers are listed below:

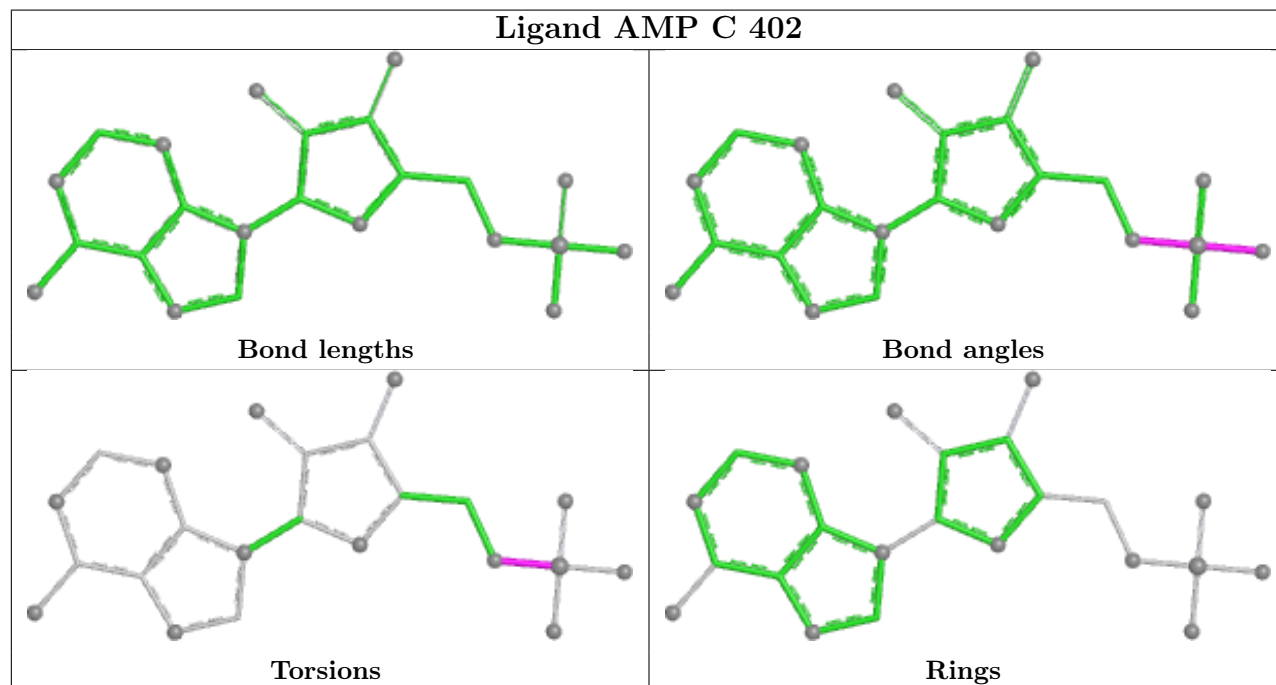
Mol	Chain	Res	Type	Atoms
8	C	403	ADP	C5'-O5'-PA-O1A
8	C	403	ADP	C5'-O5'-PA-O2A
8	C	403	ADP	C5'-O5'-PA-O3A
7	C	402	AMP	C5'-O5'-P-O3P
7	C	402	AMP	C5'-O5'-P-O2P
5	A	602	6VT	C13-C12-C15-C18
5	A	602	6VT	C11-C12-C15-C18
5	A	602	6VT	C11-C12-C15-O1
4	A	601	STU	C24-C23-N4-C28

There are no ring outliers.

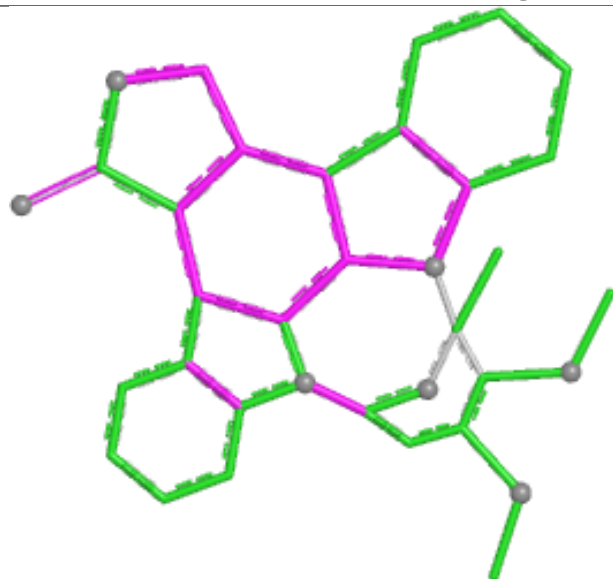
3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	402	AMP	2	0
4	A	601	STU	5	0
5	A	602	6VT	1	0

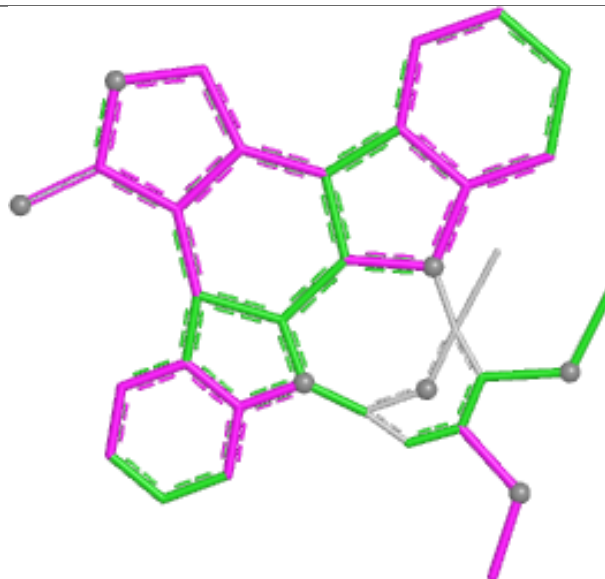
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



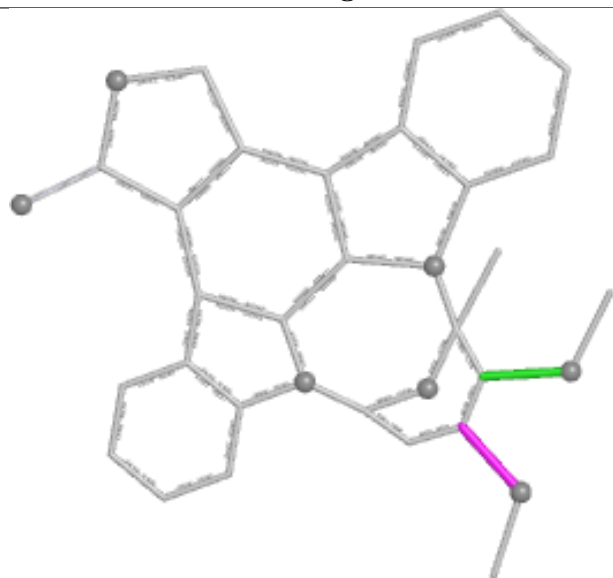
Ligand STU A 601



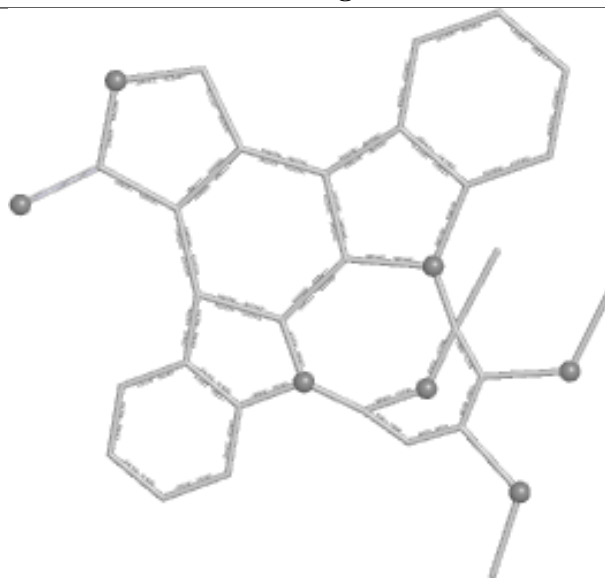
Bond lengths



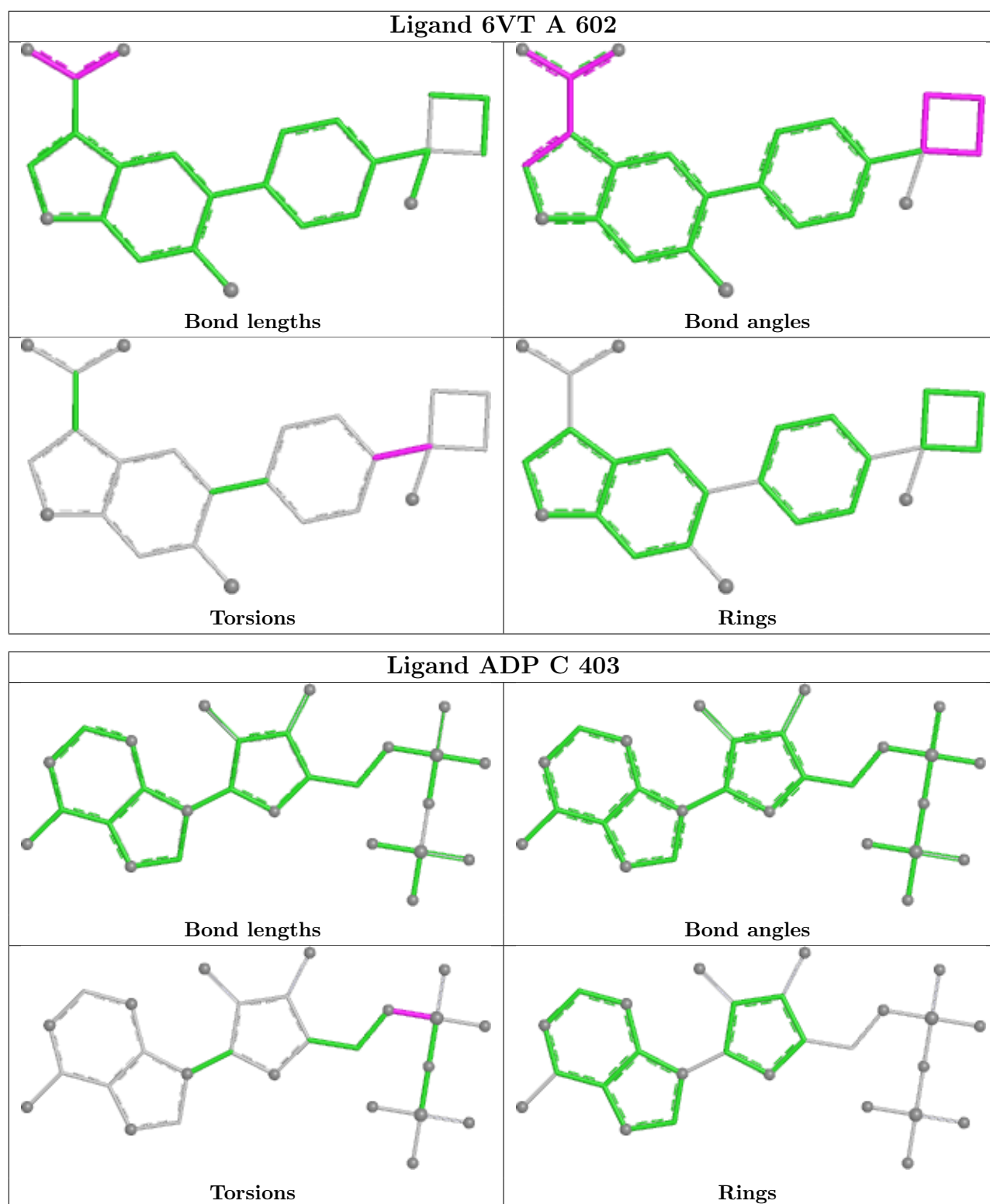
Bond angles



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	362/503 (71%)	0.11	9 (2%)	58	43	64, 92, 163, 188	0
2	B	160/204 (78%)	0.24	5 (3%)	51	38	72, 103, 144, 178	0
3	C	281/330 (85%)	0.60	20 (7%)	22	18	86, 138, 192, 198	0
All	All	803/1037 (77%)	0.31	34 (4%)	40	29	64, 108, 184, 198	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	285	GLU	5.1
3	C	303	ASP	4.7
1	A	547	ALA	4.5
3	C	189	SER	4.3
3	C	278	CYS	4.2
3	C	231	ASP	3.4
1	A	422	TYR	3.4
3	C	276	LEU	3.2
3	C	43	THR	3.1
3	C	235	ARG	3.0
1	A	444	PHE	3.0
3	C	28	TYR	2.9
2	B	224	ASP	2.8
2	B	213	VAL	2.8
3	C	230	VAL	2.7
3	C	282	GLU	2.7
2	B	217	LYS	2.6
3	C	126	LYS	2.5
1	A	528	PRO	2.5
3	C	305	HIS	2.5
3	C	236	VAL	2.5
2	B	225	PRO	2.4
1	A	70	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	27	PHE	2.3
3	C	39	ASP	2.3
3	C	123	ASP	2.3
3	C	106	TYR	2.3
1	A	419	GLN	2.2
1	A	529	GLY	2.2
3	C	178	PHE	2.1
3	C	67	GLY	2.1
2	B	230	GLU	2.1
1	A	399	GLY	2.0
3	C	318	LEU	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	172	11/12	0.95	0.08	99,102,106,107	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.

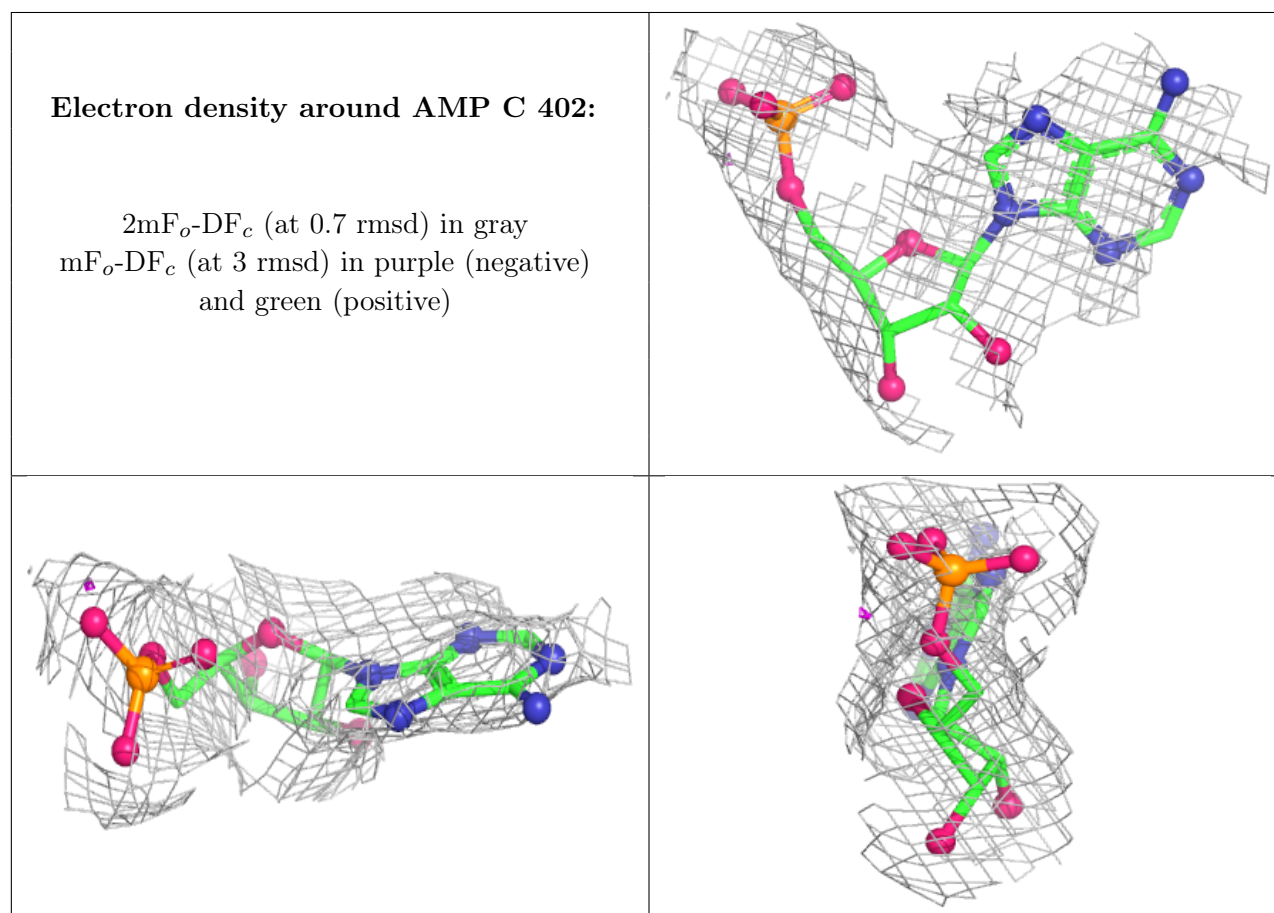
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	SO4	C	404	5/5	0.80	0.14	158,159,159,159	0
6	CL	A	606	1/1	0.84	0.07	115,115,115,115	0
7	AMP	C	402	23/23	0.88	0.13	168,180,198,200	0
7	AMP	C	401	23/23	0.88	0.15	153,172,179,182	0
8	ADP	C	403	27/27	0.93	0.12	182,189,194,194	0
5	6VT	A	602	24/24	0.93	0.12	57,64,72,73	0

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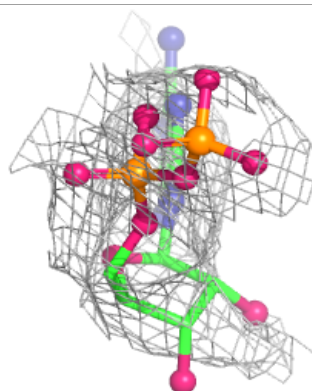
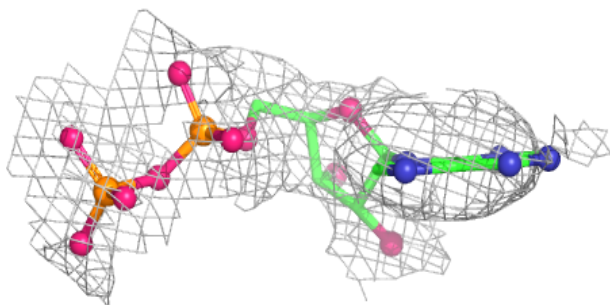
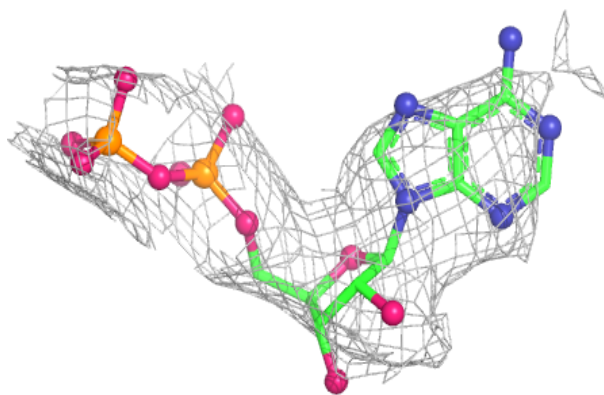
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	CL	A	605	1/1	0.95	0.07	90,90,90,90	0
6	CL	A	604	1/1	0.95	0.11	69,69,69,69	0
4	STU	A	601	35/35	0.97	0.09	66,70,73,74	0
6	CL	A	603	1/1	0.98	0.07	64,64,64,64	0

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.

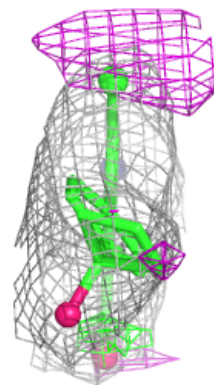
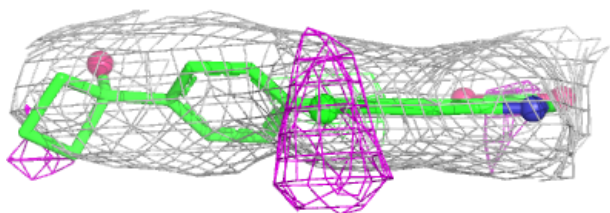
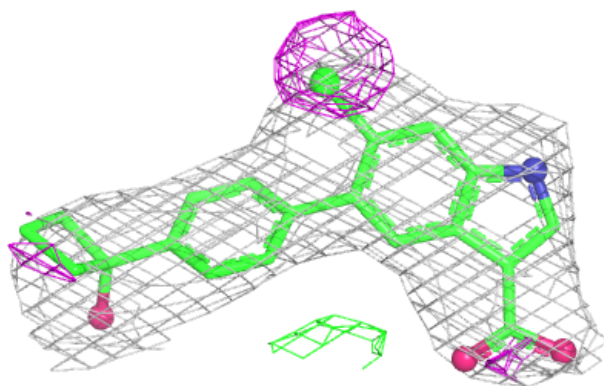


Electron density around ADP C 403:

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

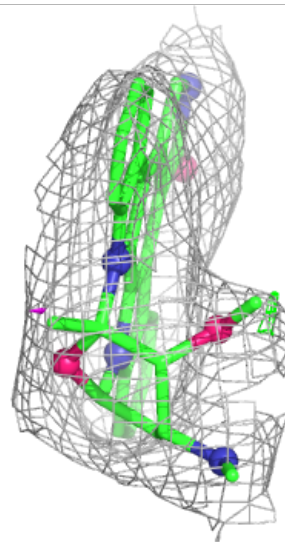
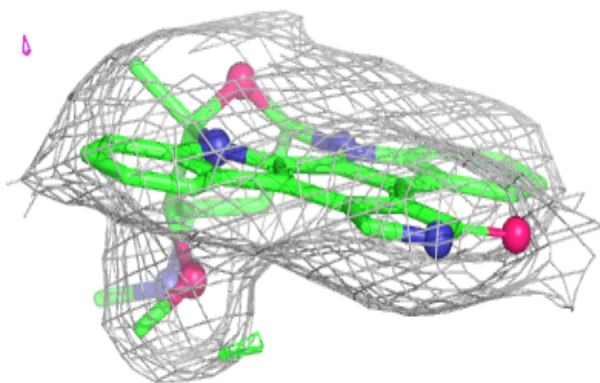
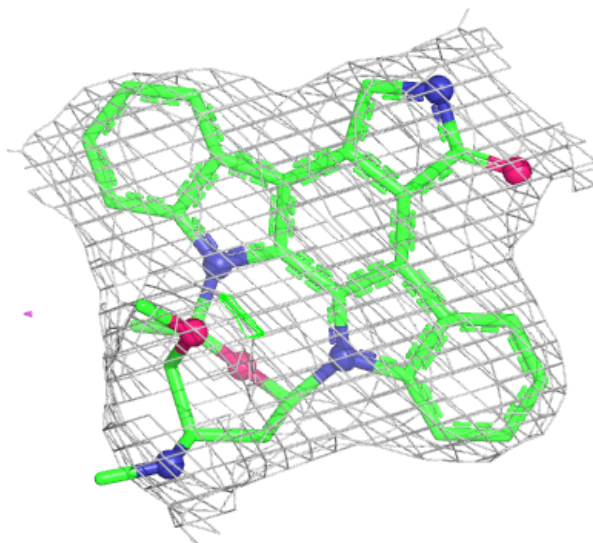
**Electron density around 6VT A 602:**

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



Electron density around STU 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.