wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 04:01 AM EDT

PDB ID	:	4QFG
Title	:	Structure of AMPK in complex with STAUROSPORINE inhibitor and in the absence of a synthetic activator
Authors	:	Calabrese, M.F.; Kurumbail, R.G.
Deposited on	:	2014-05-20
Resolution	:	3.46 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

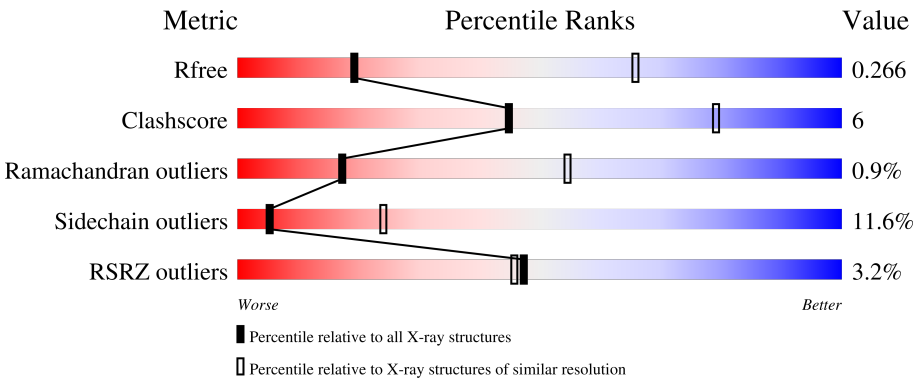
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.46 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	1291 (3.52-3.40)
Clashscore	141614	1372 (3.52-3.40)
Ramachandran outliers	138981	1337 (3.52-3.40)
Sidechain outliers	138945	1338 (3.52-3.40)
RSRZ outliers	127900	1205 (3.52-3.40)

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 <=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% 52% 19% • 27%
2	B	204	4% 61% 15% • 21%
3	C	330	2% 68% 18% • 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SO4	C	403	-	-	-	X

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6593 atoms, of which 26 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	366	2970	1905	518	528	1	18	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	161	1271	828	215	225	3	0	0	0

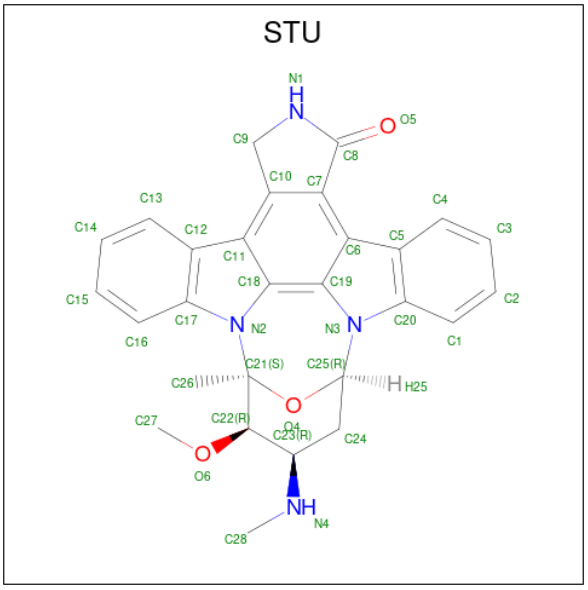
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MET	-	EXPRESSION TAG	UNP 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
			Total	C	N	O	S			
3	C	287	2250	1463	376	404	7	0	0	0

- Molecule 4 is STAUROSPORINE (three-letter code: STU) (formula: $C_{28}H_{26}N_4O_3$).

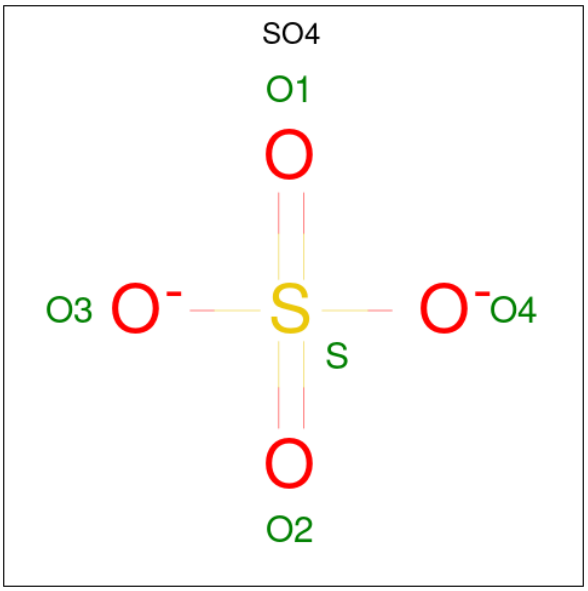


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	61	28	26	4	3	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

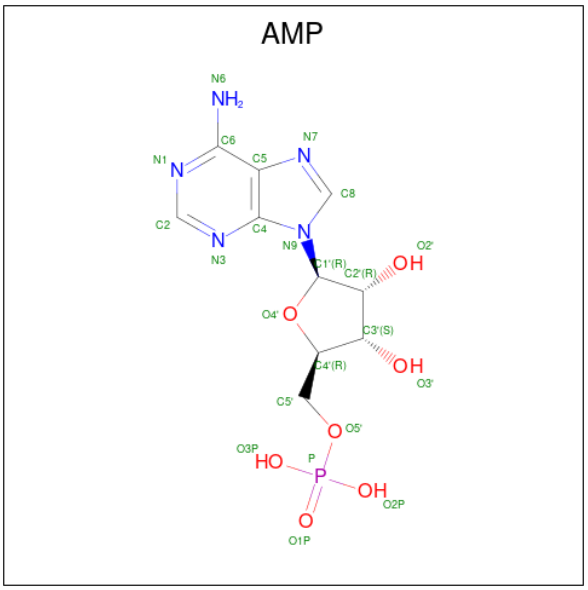
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
5	A	3	3	3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 7 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



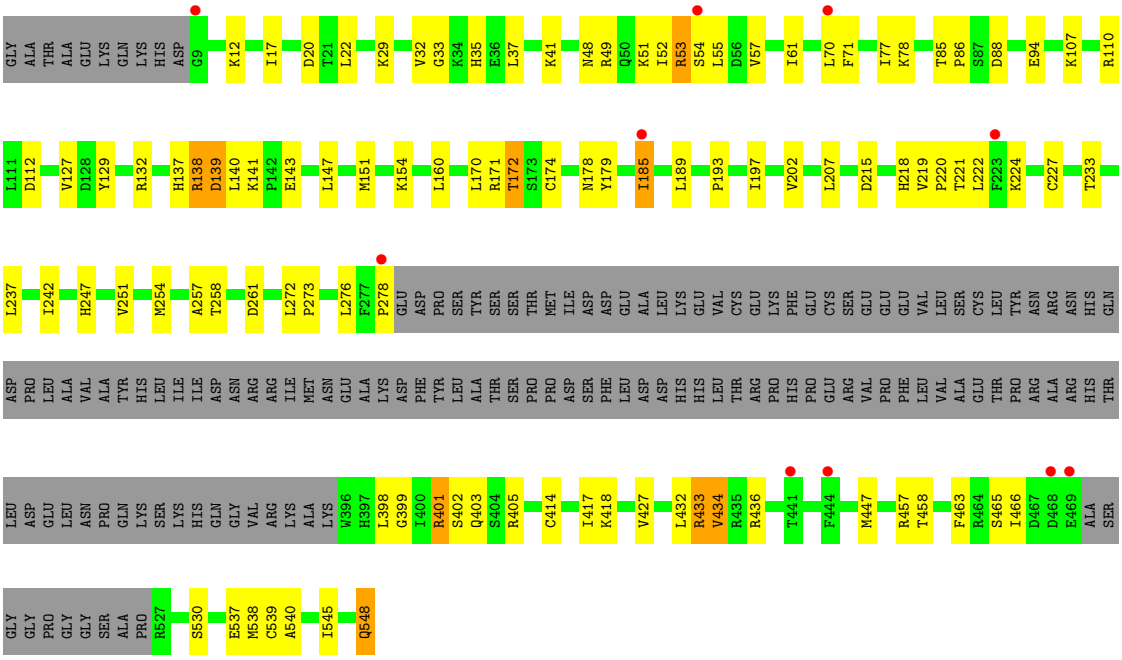
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C N O P 23 10 5 7 1	0	0

3 Residue-property plots (i)

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.

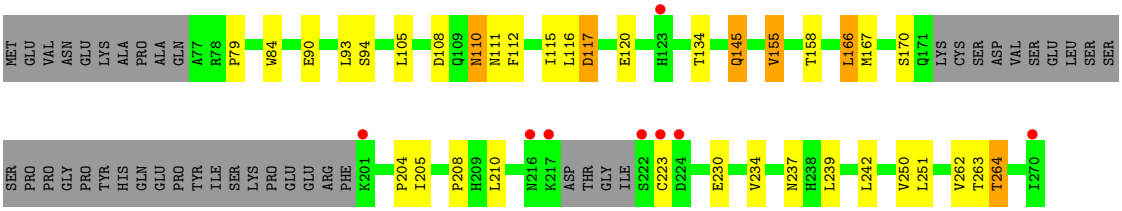
• Molecule 1: 5'-AMP-activated protein kinase catalytic subunit alpha-1

Chain A:



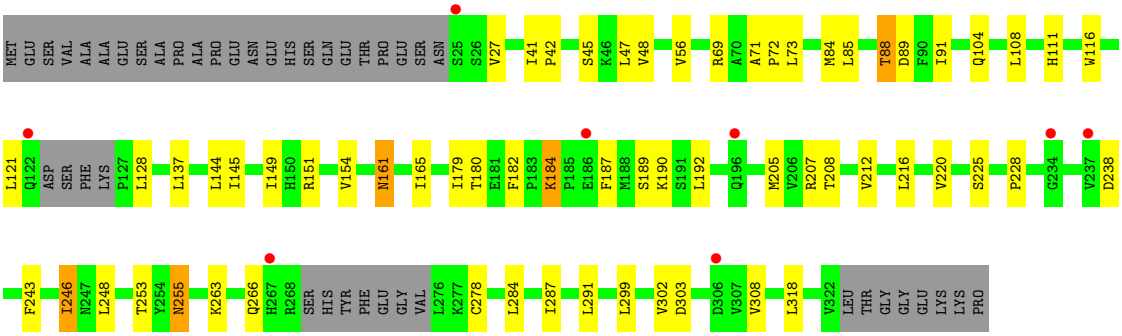
• Molecule 2: 5'-AMP-activated protein kinase subunit beta-1

Chain B:



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

Chain C:


MET GLU SER VAL ALA ALA GLU SER ALA PRO ALA PRO GLU ASN GLU HIS SER GLN GLU THR PRO GLU SER ASN S25 S26 V27 I41 P42 S45 K46 L47 V48 V56 R69 A70 A71 P72 L73 M84 L85 T88 D89 F90 I91 Q104 L108 H111 W116
L121 Q122 ASP SER PHE LYS P127 L128 L137 L144 I145 I149 H150 R151 V154 N161 I165 I179 T180 E181 F182 P183 K184 P185 E186 F187 M188 S189 K190 S191 L192 Q196 M205 V206 R207 T208 V212 L216 V220 S225 P228 G234 V237 D238
F243 I246 N247 L248 T253 Y254 N255 K263 Q266 H267 R268 SER HIS TYR PHE GLU GLY VAL L276 K277 C278 L284 I287 L291 L299 V302 D303 D306 V307 V308 L318 V322 LEU THR GLY GLY GLU LYS LYS PRO

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	124.37Å 124.37Å 404.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.86 – 3.46 29.86 – 3.46	Depositor EDS
% Data completeness (in resolution range)	97.0 (29.86-3.46) 96.3 (29.86-3.46)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.42 (at 3.47Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.11.5, BUSTER 2.11.5	Depositor
R, R_{free}	0.222 , 0.267 0.218 , 0.266	Depositor DCC
R_{free} test set	1210 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	79.2	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 85.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6593	wwPDB-VP
Average B, all atoms (Å^2)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CL, SO4, STU, AMP, 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	0.48	0/3026	0.76	0/4081
2	B	0.48	0/1306	0.73	0/1779
3	C	0.47	0/2294	0.66	0/3119
All	All	0.48	0/6626	0.72	0/8979

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	2970	0	2996	48	0
2	B	1271	0	1268	19	0
3	C	2250	0	2283	24	0
4	A	35	26	26	6	0
5	A	3	0	0	0	0
6	A	5	0	0	0	0
6	C	10	0	0	0	0
7	C	23	0	12	0	0
All	All	6567	26	6585	85	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.

The worst 5 of 85 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:79:PRO:HB2	2:B:115:ILE:HG22	1.44	0.99
4:A:601:STU:H261	4:A:601:STU:H16	1.60	0.82
2:B:120:GLU:HA	2:B:155:VAL:HG22	1.72	0.70
1:A:51:LYS:O	1:A:54:SER:HB3	1.96	0.65
1:A:141:LYS:HG3	1:A:143:GLU:HB2	1.79	0.64

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	359/503 (71%)	333 (93%)	22 (6%)	4 (1%)	14	50
2	B	155/204 (76%)	143 (92%)	10 (6%)	2 (1%)	12	46
3	C	281/330 (85%)	265 (94%)	15 (5%)	1 (0%)	34	70
All	All	795/1037 (77%)	741 (93%)	47 (6%)	7 (1%)	17	54

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	108	ASP
3	C	303	ASP
1	A	139	ASP
2	B	223	CYS
1	A	399	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	328/448 (73%)	288 (88%)	40 (12%)	5	22
2	B	140/185 (76%)	121 (86%)	19 (14%)	3	18
3	C	247/299 (83%)	223 (90%)	24 (10%)	8	32
All	All	715/932 (77%)	632 (88%)	83 (12%)	5	24

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	263	THR
3	C	189	SER
3	C	56	VAL
3	C	128	LEU
3	C	225	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	266	GLN
3	C	255	ASN
2	B	232	ASN
2	B	145	GLN
2	B	233	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	1.38	2 (25%)	10,14,16	2.37	5 (50%)

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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	TPO	P-O1P	2.05	1.57	1.50
1	A	172	TPO	CG2-CB	2.04	1.56	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	172	TPO	P-OG1-CB	-4.21	110.50	123.21
1	A	172	TPO	O3P-P-O2P	-3.33	94.91	107.64
1	A	172	TPO	CG2-CB-CA	2.87	118.83	113.16
1	A	172	TPO	O2P-P-OG1	2.55	117.40	105.99
1	A	172	TPO	OG1-P-O1P	-2.03	101.55	109.39

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	172	TPO	CB-OG1-P-O1P
1	A	172	TPO	CB-OG1-P-O2P
1	A	172	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	172	TPO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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	-	30,42,42	2.47	10 (33%)	31,68,68	2.09	11 (35%)
6	SO4	C	403	-	4,4,4	0.12	0	6,6,6	0.35	0
6	SO4	C	402	-	4,4,4	0.21	0	6,6,6	0.19	0
7	AMP	C	401	-	22,25,25	0.65	0	25,38,38	1.22	2 (8%)
6	SO4	A	605	-	4,4,4	0.18	0	6,6,6	0.15	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
4	STU	A	601	-	-	1/4/42/42	-
7	AMP	C	401	-	-	3/6/26/26	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	STU	C9-C10	-5.79	1.46	1.50
4	A	601	STU	C12-C17	4.61	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	STU	C5-C20	4.49	1.48	1.41
4	A	601	STU	C10-C11	4.27	1.49	1.42
4	A	601	STU	C11-C18	4.16	1.47	1.42

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	C	401	AMP	P-O5'-C5'	4.56	130.84	118.30
4	A	601	STU	C16-C17-N2	4.48	137.70	132.29
4	A	601	STU	C7-C10-C11	-4.34	116.58	122.42
4	A	601	STU	O5-C8-C7	-3.68	124.95	129.32
4	A	601	STU	C7-C8-N1	3.67	110.08	106.37

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	401	AMP	C5'-O5'-P-O3P
7	C	401	AMP	C5'-O5'-P-O1P
7	C	401	AMP	C5'-O5'-P-O2P
4	A	601	STU	C24-C23-N4-C28

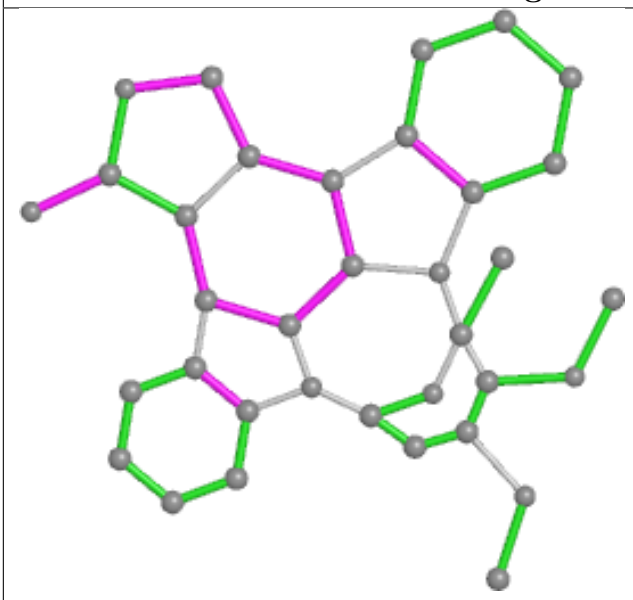
There are no ring outliers.

1 monomer is involved in 6 short contacts:

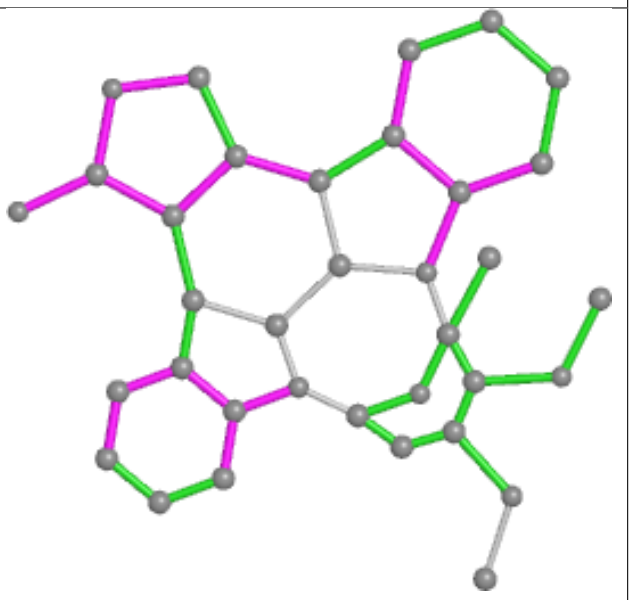
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	STU	6	0

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 then 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.

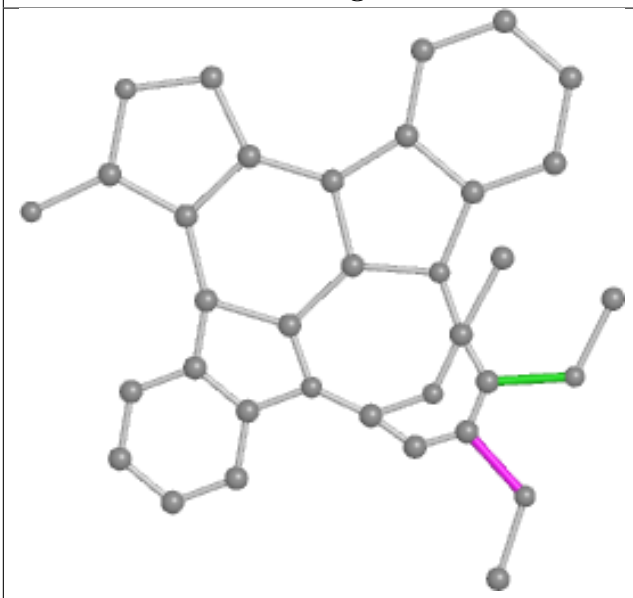
Ligand STU A 601



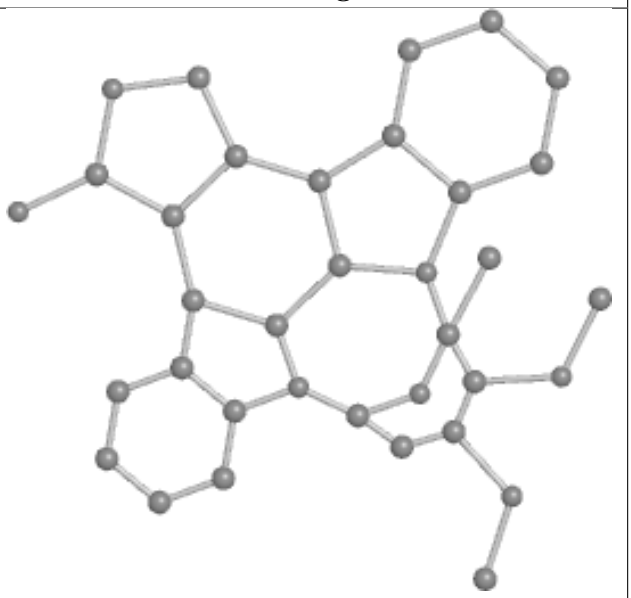
Bond lengths



Bond angles

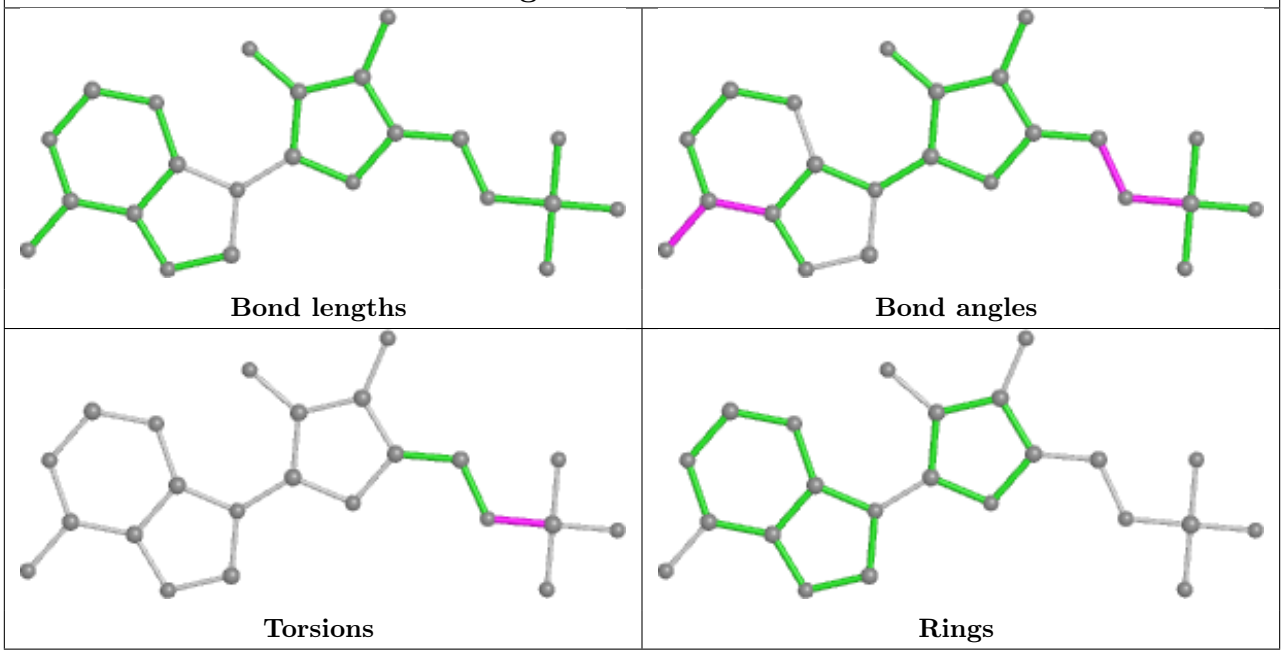


Torsions



Rings

Ligand AMP C 401



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	365/503 (72%)	0.06	10 (2%)	54	52	38, 70, 125, 160	0
2	B	161/204 (78%)	0.30	8 (4%)	28	28	52, 80, 116, 144	0
3	C	287/330 (86%)	0.05	8 (2%)	53	51	65, 95, 126, 173	0
All	All	813/1037 (78%)	0.11	26 (3%)	47	46	38, 84, 125, 173	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	469	GLU	4.6
1	A	278	PRO	3.7
2	B	222	SER	3.4
1	A	444	PHE	3.2
2	B	201	LYS	3.2

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	0.93	0.18	74,76,84,87	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

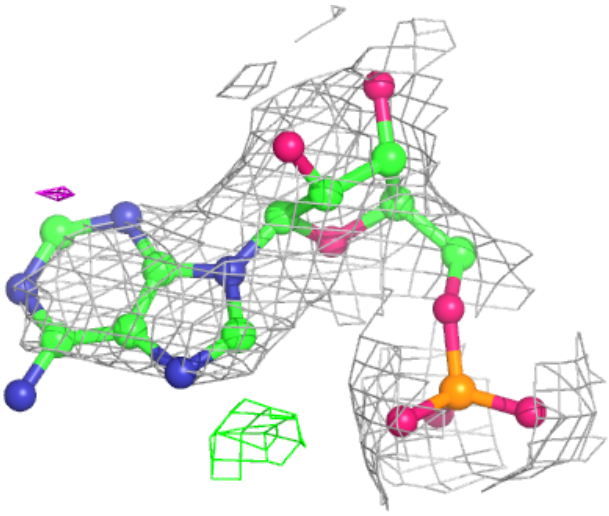
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

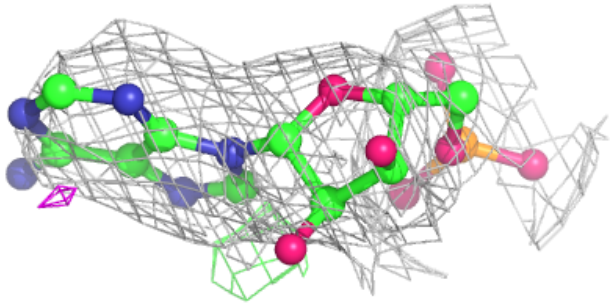
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	CL	A	603	1/1	0.62	0.16	95,95,95,95	0
6	SO4	C	403	5/5	0.69	0.42	145,145,145,146	0
7	AMP	C	401	23/23	0.79	0.32	139,151,154,156	0
6	SO4	C	402	5/5	0.83	0.48	144,145,145,146	0
5	CL	A	604	1/1	0.90	0.19	52,52,52,52	0
5	CL	A	602	1/1	0.95	0.18	65,65,65,65	0
6	SO4	A	605	5/5	0.96	0.21	76,78,79,79	0
4	STU	A	601	35/35	0.96	0.24	41,50,59,61	0

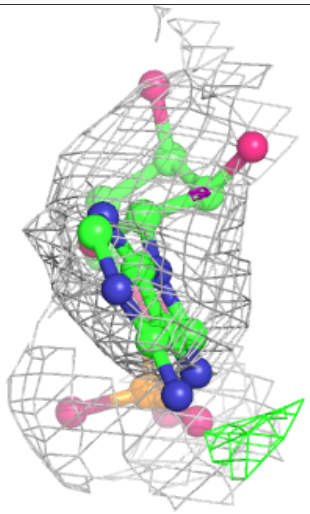
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around AMP C 401:

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

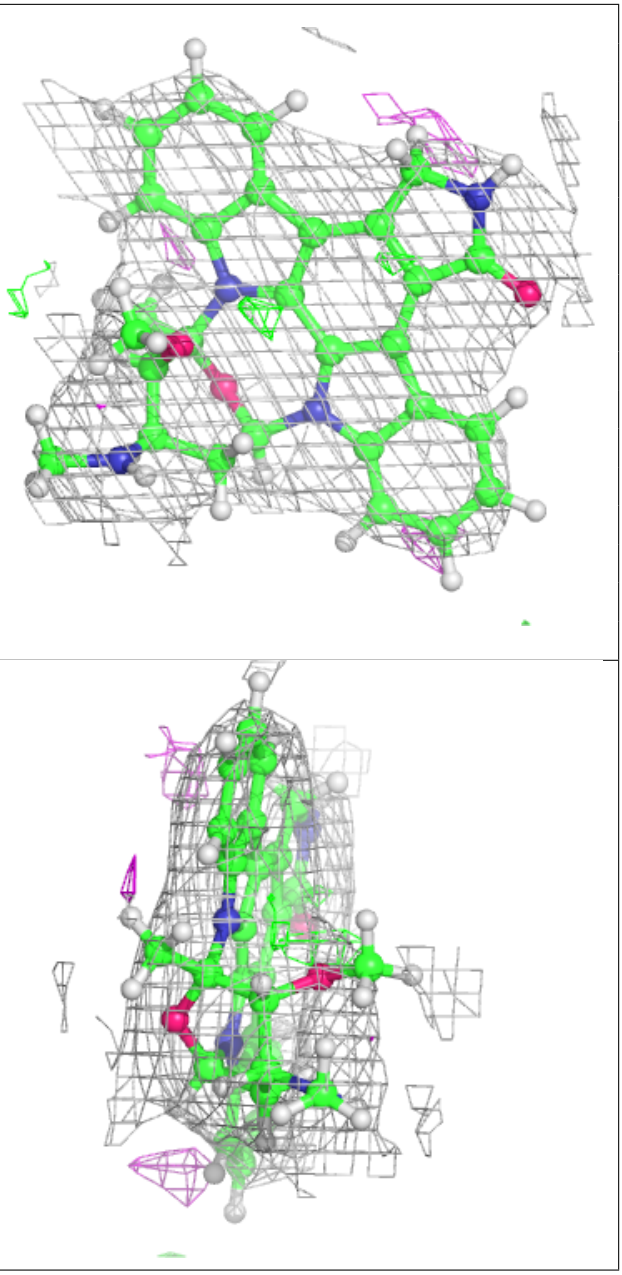






Electron density around STU A 601:

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.