



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:54 PM UTC

PDB ID : 4GXQ / pdb_00004gxq
Title : Crystal Structure of ATP bound RpMatB-BxBclM chimera B1
Authors : Rank, K.C.; Crosby, H.A.; Escalante-Semerena, J.C.; Rayment, I.
Deposited on : 2012-09-04
Resolution : 2.00 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 ⓘ 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

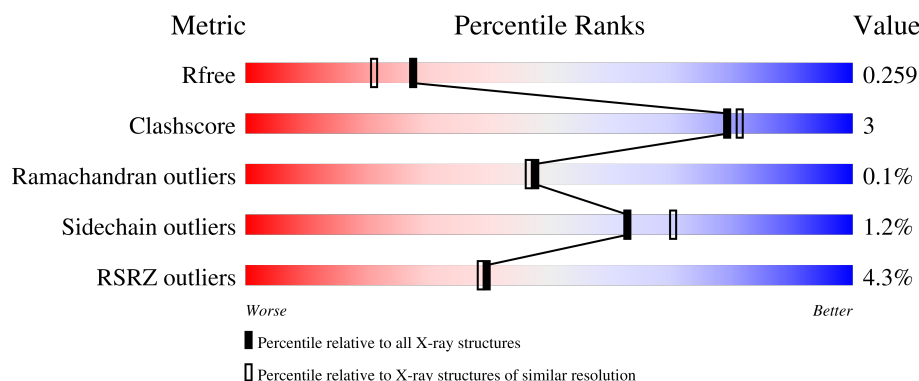
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	506	2% 94% 5%
1	B	506	2% 94% 5%
1	C	506	9% 93% 7%

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
1	MLY	A	62	-	-	X	-
1	MLY	C	62	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13557 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.

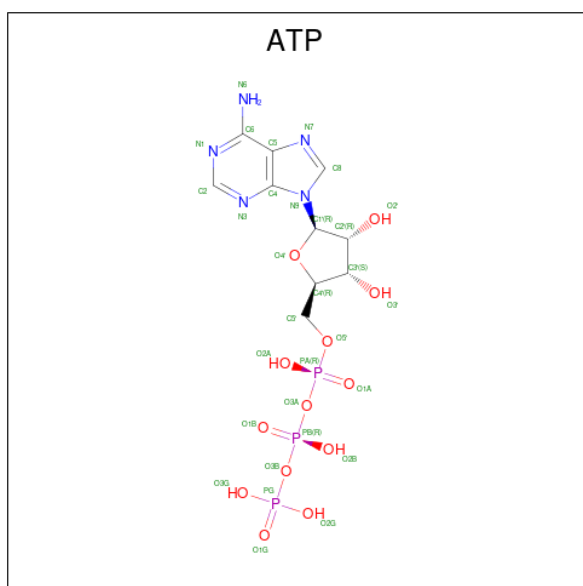
- Molecule 1 is a protein called Malonyl CoA synthetase, Benzoate-CoA ligase Chimeric protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	506	Total	C	N	O	S	0	1	0
			3944	2532	669	729	14			
1	B	506	Total	C	N	O	S	0	6	0
			3972	2550	673	735	14			
1	C	506	Total	C	N	O	S	0	2	0
			3947	2534	669	730	14			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	491	ALA	LYS	engineered mutation	UNP Q6ND88
B	491	ALA	LYS	engineered mutation	UNP Q6ND88
C	491	ALA	LYS	engineered mutation	UNP Q6ND88

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

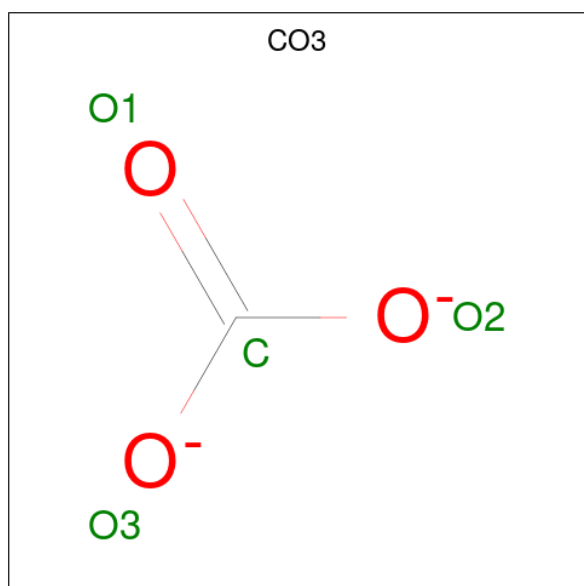


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	1	3		
4	B	1	Total	C	O	0	0
			4	1	3		
4	C	1	Total	C	O	0	0
			4	1	3		

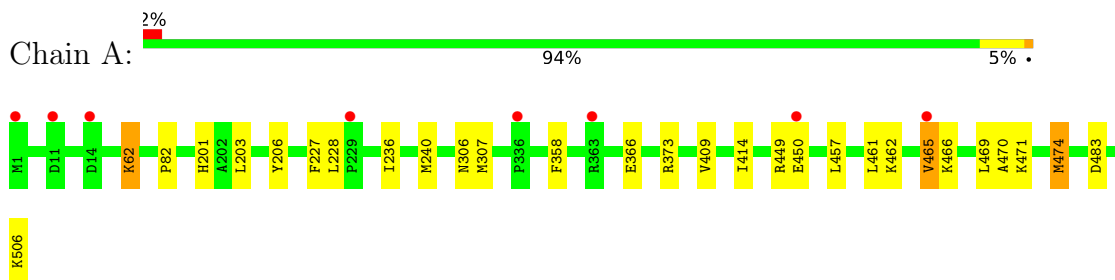
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	476	Total 476	O 476	0	0
5	B	668	Total 668	O 668	0	0
5	C	442	Total 442	O 442	0	0

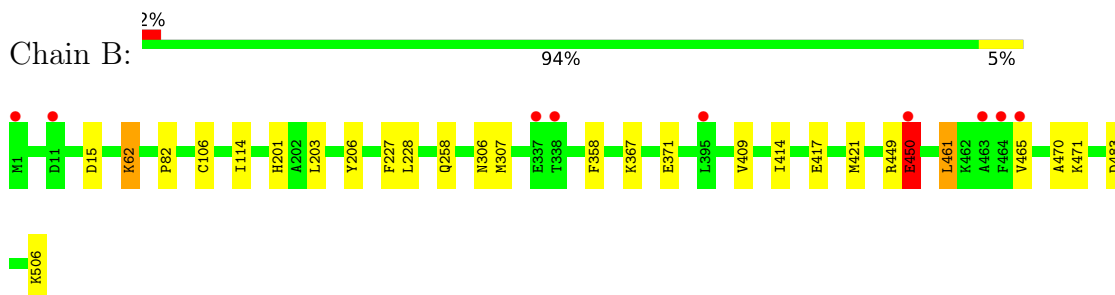
3 Residue-property plots [i](#)

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.

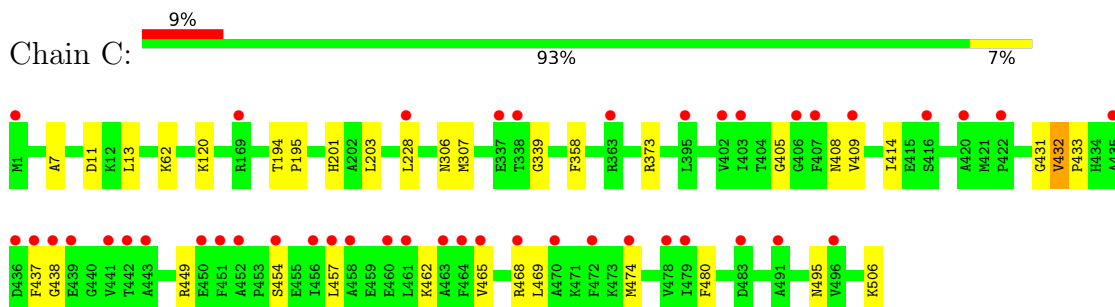
- Molecule 1: Malonyl CoA synthetase, Benzoate-CoA ligase Chimeric protein



- Molecule 1: Malonyl CoA synthetase, Benzoate-CoA ligase Chimeric protein



- Molecule 1: Malonyl CoA synthetase, Benzoate-CoA ligase Chimeric protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	299.31Å 299.31Å 47.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.95 – 2.00 24.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (24.95-2.00) 99.5 (24.95-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.219 , 0.254 0.225 , 0.259	Depositor DCC
R_{free} test set	8392 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13557	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 81.78 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.2680e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ATP, MG, MLY, CO3

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	0.52	0/3696	0.70	0/5048
1	B	0.67	0/3739	0.76	0/5105
1	C	0.53	0/3702	0.71	0/5056
All	All	0.58	0/11137	0.72	0/15209

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

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	3944	0	3996	19	0
1	B	3972	0	4033	19	0
1	C	3947	0	4002	27	0
2	A	31	0	12	0	0
2	B	31	0	12	0	0
2	C	31	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	4	0	0	0	0
4	C	4	0	0	0	0
5	A	476	0	0	1	0
5	B	668	0	0	3	0
5	C	442	0	0	4	0
All	All	13557	0	12067	65	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 3.

The worst 5 of 65 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:C:438:GLY:HA2	5:C:1112:HOH:O	1.75	0.85
1:A:62:MLY:HH23	1:A:203:LEU:O	1.83	0.78
1:A:461:LEU:O	1:A:465:VAL:HG23	1.84	0.78
1:C:495:ASN:HB2	5:C:1046:HOH:O	1.86	0.74
1:A:465:VAL:CG1	1:A:469:LEU:HD12	2.18	0.73

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	476/506 (94%)	472 (99%)	3 (1%)	1 (0%)	43	42
1	B	481/506 (95%)	478 (99%)	2 (0%)	1 (0%)	43	42
1	C	477/506 (94%)	473 (99%)	4 (1%)	0	100	100
All	All	1434/1518 (94%)	1423 (99%)	9 (1%)	2 (0%)	48	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	465	VAL
1	B	450	GLU

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	378/377 (100%)	371 (98%)	7 (2%)	50	56
1	B	383/377 (102%)	380 (99%)	3 (1%)	73	80
1	C	379/377 (100%)	375 (99%)	4 (1%)	65	73
All	All	1140/1131 (101%)	1126 (99%)	14 (1%)	63	70

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	358	PHE
1	B	450	GLU
1	C	449	ARG
1	C	358	PHE
1	C	432	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	216	ASN
1	C	408	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

90 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MLY	C	359	1	9,10,11	0.58	0	6,11,13	0.45	0
1	MLY	A	506	1	10,11,11	0.84	1 (10%)	10,13,13	1.07	1 (10%)
1	MLY	A	18	1	9,10,11	0.58	0	6,11,13	0.57	0
1	MLY	C	102	1	9,10,11	0.64	0	6,11,13	0.43	0
1	MLY	B	264	1	9,10,11	0.61	0	6,11,13	0.59	0
1	MLY	B	12	1	9,10,11	0.57	0	6,11,13	0.56	0
1	MLY	B	62	1	9,10,11	1.05	1 (11%)	6,11,13	1.67	2 (33%)
1	MLY	B	477	1	9,10,11	0.60	0	6,11,13	0.63	0
1	MLY	B	448	1	9,10,11	0.52	0	6,11,13	0.74	0
1	MLY	A	399	1	9,10,11	0.46	0	6,11,13	0.53	0
1	MLY	A	367	1	9,10,11	0.56	0	6,11,13	0.37	0
1	MLY	C	230	1	9,10,11	0.48	0	6,11,13	0.60	0
1	MLY	B	28	1	9,10,11	0.63	0	6,11,13	0.76	0
1	MLY	A	171	1	9,10,11	0.49	0	6,11,13	0.32	0
1	MLY	B	473	1	9,10,11	0.49	0	6,11,13	0.68	0
1	MLY	C	462	1	9,10,11	0.49	0	6,11,13	0.69	0
1	MLY	A	385	1	9,10,11	0.57	0	6,11,13	0.52	0
1	MLY	A	448	1	9,10,11	0.60	0	6,11,13	0.64	0
1	MLY	A	291	1	9,10,11	0.57	0	6,11,13	0.55	0
1	MLY	C	466	1	9,10,11	0.49	0	6,11,13	0.49	0
1	MLY	A	477	1	9,10,11	0.47	0	6,11,13	0.58	0
1	MLY	B	120	1	9,10,11	0.49	0	6,11,13	0.51	0
1	MLY	A	28	1	9,10,11	0.59	0	6,11,13	0.67	0
1	MLY	B	230	1	9,10,11	0.48	0	6,11,13	0.46	0
1	MLY	C	12	1	9,10,11	0.53	0	6,11,13	0.45	0
1	MLY	C	62	1	9,10,11	0.53	0	6,11,13	0.86	0
1	MLY	A	110	1	9,10,11	0.51	0	6,11,13	0.53	0
1	MLY	B	353	1	9,10,11	0.57	0	6,11,13	0.65	0
1	MLY	B	471	1	9,10,11	0.50	0	6,11,13	0.43	0
1	MLY	A	369	1	9,10,11	0.50	0	6,11,13	0.35	0
1	MLY	C	18	1	9,10,11	0.52	0	6,11,13	0.54	0
1	MLY	C	506	1	10,11,11	0.82	1 (10%)	10,13,13	1.12	1 (10%)
1	MLY	B	502	1	9,10,11	0.47	0	6,11,13	0.43	0
1	MLY	B	476	1	9,10,11	0.49	0	6,11,13	0.53	0
1	MLY	C	353	1	9,10,11	0.64	0	6,11,13	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	B	412	1	9,10,11	0.57	0	6,11,13	0.52	0
1	MLY	B	102	1	9,10,11	0.68	0	6,11,13	0.75	0
1	MLY	C	476	1	9,10,11	0.57	0	6,11,13	0.51	0
1	MLY	A	264	1	9,10,11	0.67	0	6,11,13	0.50	0
1	MLY	C	235	1	9,10,11	0.46	0	6,11,13	0.45	0
1	MLY	A	102	1	9,10,11	0.55	0	6,11,13	0.46	0
1	MLY	A	12	1	9,10,11	0.53	0	6,11,13	0.71	0
1	MLY	C	502	1	9,10,11	0.37	0	6,11,13	0.81	0
1	MLY	A	462	1	9,10,11	0.46	0	6,11,13	0.66	0
1	MLY	C	385	1	9,10,11	0.48	0	6,11,13	0.77	0
1	MLY	C	120	1	9,10,11	0.43	0	6,11,13	0.88	1 (16%)
1	MLY	B	340	1	9,10,11	0.53	0	6,11,13	0.64	0
1	MLY	C	412	1	9,10,11	0.58	0	6,11,13	0.44	0
1	MLY	B	18	1	9,10,11	0.53	0	6,11,13	0.45	0
1	MLY	A	230	1	9,10,11	0.47	0	6,11,13	0.56	0
1	MLY	B	235	1	9,10,11	0.49	0	6,11,13	0.52	0
1	MLY	A	359	1	9,10,11	0.50	0	6,11,13	0.39	0
1	MLY	B	385	1	9,10,11	0.64	0	6,11,13	0.34	0
1	MLY	B	506	1	10,11,11	0.78	1 (10%)	10,13,13	1.24	1 (10%)
1	MLY	B	369	1	9,10,11	0.46	0	6,11,13	0.64	0
1	MLY	B	494	1	9,10,11	0.65	0	6,11,13	0.61	0
1	MLY	C	291	1	9,10,11	0.59	0	6,11,13	0.42	0
1	MLY	C	340	1	9,10,11	0.55	0	6,11,13	0.86	0
1	MLY	C	477	1	9,10,11	0.58	0	6,11,13	0.56	0
1	MLY	C	367	1	9,10,11	0.59	0	6,11,13	0.53	0
1	MLY	A	340	1	9,10,11	0.63	0	6,11,13	0.70	0
1	MLY	A	62	1	9,10,11	0.93	1 (11%)	6,11,13	1.22	1 (16%)
1	MLY	A	353	1	9,10,11	0.57	0	6,11,13	0.58	0
1	MLY	A	235	1	9,10,11	0.41	0	6,11,13	0.45	0
1	MLY	B	367	1	9,10,11	0.60	0	6,11,13	0.43	0
1	MLY	A	473	1	9,10,11	0.52	0	6,11,13	0.72	0
1	MLY	A	120	1	9,10,11	0.46	0	6,11,13	0.60	0
1	MLY	C	473	1	9,10,11	0.49	0	6,11,13	0.90	0
1	MLY	B	171	1	9,10,11	0.54	0	6,11,13	0.47	0
1	MLY	B	110	1	9,10,11	0.74	0	6,11,13	0.46	0
1	MLY	C	448	1	9,10,11	0.52	0	6,11,13	0.34	0
1	MLY	C	369	1	9,10,11	0.42	0	6,11,13	0.67	0
1	MLY	C	399	1	9,10,11	0.42	0	6,11,13	0.59	0
1	MLY	B	359	1	9,10,11	0.51	0	6,11,13	0.49	0
1	MLY	B	462	1	9,10,11	0.48	0	6,11,13	0.67	0
1	MLY	B	291	1	9,10,11	0.59	0	6,11,13	0.46	0
1	MLY	A	466	1	9,10,11	0.57	0	6,11,13	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	C	110	1	9,10,11	0.49	0	6,11,13	0.47	0
1	MLY	C	471	1	9,10,11	0.53	0	6,11,13	0.29	0
1	MLY	C	171	1	9,10,11	0.58	0	6,11,13	0.65	0
1	MLY	A	476	1	9,10,11	0.53	0	6,11,13	0.55	0
1	MLY	A	502	1	9,10,11	0.47	0	6,11,13	0.92	0
1	MLY	C	494	1	9,10,11	0.54	0	6,11,13	0.55	0
1	MLY	A	494	1	9,10,11	0.63	0	6,11,13	0.62	0
1	MLY	C	28	1	9,10,11	0.63	0	6,11,13	0.53	0
1	MLY	B	399	1	9,10,11	0.54	0	6,11,13	0.36	0
1	MLY	A	412	1	9,10,11	0.42	0	6,11,13	0.58	0
1	MLY	B	466	1	9,10,11	0.48	0	6,11,13	0.59	0
1	MLY	A	471	1	9,10,11	0.52	0	6,11,13	0.41	0
1	MLY	C	264	1	9,10,11	0.55	0	6,11,13	0.62	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
1	MLY	C	359	1	-	2/8/9/11	-
1	MLY	A	506	1	-	2/11/11/11	-
1	MLY	A	18	1	-	5/8/9/11	-
1	MLY	C	102	1	-	3/8/9/11	-
1	MLY	B	264	1	-	1/8/9/11	-
1	MLY	B	12	1	-	3/8/9/11	-
1	MLY	B	62	1	-	5/8/9/11	-
1	MLY	B	477	1	-	0/8/9/11	-
1	MLY	B	448	1	-	5/8/9/11	-
1	MLY	A	399	1	-	2/8/9/11	-
1	MLY	A	367	1	-	0/8/9/11	-
1	MLY	C	230	1	-	1/8/9/11	-
1	MLY	B	28	1	-	2/8/9/11	-
1	MLY	A	171	1	-	1/8/9/11	-
1	MLY	B	473	1	-	0/8/9/11	-
1	MLY	C	462	1	-	2/8/9/11	-
1	MLY	A	385	1	-	1/8/9/11	-
1	MLY	A	448	1	-	1/8/9/11	-
1	MLY	A	291	1	-	2/8/9/11	-
1	MLY	C	466	1	-	1/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	477	1	-	1/8/9/11	-
1	MLY	B	120	1	-	0/8/9/11	-
1	MLY	A	28	1	-	1/8/9/11	-
1	MLY	B	230	1	-	0/8/9/11	-
1	MLY	C	12	1	-	3/8/9/11	-
1	MLY	C	62	1	-	3/8/9/11	-
1	MLY	A	110	1	-	0/8/9/11	-
1	MLY	B	353	1	-	0/8/9/11	-
1	MLY	B	471	1	-	3/8/9/11	-
1	MLY	A	369	1	-	4/8/9/11	-
1	MLY	C	18	1	-	2/8/9/11	-
1	MLY	C	506	1	-	3/11/11/11	-
1	MLY	B	502	1	-	0/8/9/11	-
1	MLY	B	476	1	-	0/8/9/11	-
1	MLY	C	353	1	-	0/8/9/11	-
1	MLY	B	412	1	-	0/8/9/11	-
1	MLY	B	102	1	-	1/8/9/11	-
1	MLY	C	476	1	-	2/8/9/11	-
1	MLY	A	264	1	-	1/8/9/11	-
1	MLY	C	235	1	-	2/8/9/11	-
1	MLY	A	102	1	-	3/8/9/11	-
1	MLY	A	12	1	-	3/8/9/11	-
1	MLY	C	502	1	-	0/8/9/11	-
1	MLY	A	462	1	-	0/8/9/11	-
1	MLY	C	385	1	-	1/8/9/11	-
1	MLY	C	120	1	-	4/8/9/11	-
1	MLY	B	340	1	-	2/8/9/11	-
1	MLY	C	412	1	-	0/8/9/11	-
1	MLY	B	18	1	-	4/8/9/11	-
1	MLY	A	230	1	-	2/8/9/11	-
1	MLY	B	235	1	-	0/8/9/11	-
1	MLY	A	359	1	-	1/8/9/11	-
1	MLY	B	385	1	-	1/8/9/11	-
1	MLY	B	506	1	-	4/11/11/11	-
1	MLY	B	369	1	-	5/8/9/11	-
1	MLY	B	494	1	-	2/8/9/11	-
1	MLY	C	291	1	-	2/8/9/11	-
1	MLY	C	340	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	C	477	1	-	1/8/9/11	-
1	MLY	C	367	1	-	0/8/9/11	-
1	MLY	A	340	1	-	1/8/9/11	-
1	MLY	A	62	1	-	3/8/9/11	-
1	MLY	A	353	1	-	1/8/9/11	-
1	MLY	A	235	1	-	0/8/9/11	-
1	MLY	B	367	1	-	1/8/9/11	-
1	MLY	A	473	1	-	0/8/9/11	-
1	MLY	A	120	1	-	1/8/9/11	-
1	MLY	C	473	1	-	4/8/9/11	-
1	MLY	B	171	1	-	0/8/9/11	-
1	MLY	B	110	1	-	0/8/9/11	-
1	MLY	C	448	1	-	2/8/9/11	-
1	MLY	C	369	1	-	1/8/9/11	-
1	MLY	C	399	1	-	2/8/9/11	-
1	MLY	B	359	1	-	1/8/9/11	-
1	MLY	B	462	1	-	3/8/9/11	-
1	MLY	B	291	1	-	3/8/9/11	-
1	MLY	A	466	1	-	1/8/9/11	-
1	MLY	C	110	1	-	0/8/9/11	-
1	MLY	C	471	1	-	3/8/9/11	-
1	MLY	C	171	1	-	3/8/9/11	-
1	MLY	A	476	1	-	1/8/9/11	-
1	MLY	A	502	1	-	0/8/9/11	-
1	MLY	C	494	1	-	2/8/9/11	-
1	MLY	A	494	1	-	3/8/9/11	-
1	MLY	C	28	1	-	0/8/9/11	-
1	MLY	B	399	1	-	1/8/9/11	-
1	MLY	A	412	1	-	0/8/9/11	-
1	MLY	B	466	1	-	5/8/9/11	-
1	MLY	A	471	1	-	2/8/9/11	-
1	MLY	C	264	1	-	0/8/9/11	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	62	MLY	CB-CA	-2.45	1.49	1.53
1	A	506	MLY	OXT-C	-2.38	1.23	1.30
1	C	506	MLY	OXT-C	-2.23	1.23	1.30
1	B	506	MLY	OXT-C	-2.19	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	62	MLY	CB-CA	-2.17	1.50	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	506	MLY	OXT-C-O	-3.15	116.93	124.08
1	C	506	MLY	OXT-C-O	-3.00	117.28	124.08
1	A	506	MLY	OXT-C-O	-2.61	118.16	124.08
1	B	62	MLY	CD-CG-CB	-2.41	104.53	113.62
1	A	62	MLY	CD-CG-CB	-2.23	105.22	113.62

There are no chirality outliers.

5 of 146 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	12	MLY	O-C-CA-CB
1	A	18	MLY	O-C-CA-CB
1	A	102	MLY	O-C-CA-CB
1	A	171	MLY	O-C-CA-CB
1	A	340	MLY	O-C-CA-CB

There are no ring outliers.

9 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	62	MLY	6	0
1	C	462	MLY	1	0
1	C	62	MLY	7	0
1	B	471	MLY	1	0
1	A	462	MLY	2	0
1	A	62	MLY	8	0
1	B	367	MLY	1	0
1	A	466	MLY	1	0
1	A	471	MLY	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 3 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
2	ATP	B	601	3	32,33,33	1.54	7 (21%)	48,52,52	1.65	11 (22%)
4	CO3	C	603	-	3,3,3	1.01	0	2,3,3	0.27	0
4	CO3	A	603	-	3,3,3	1.02	0	2,3,3	0.24	0
2	ATP	C	601	3	32,33,33	1.35	7 (21%)	48,52,52	1.79	9 (18%)
2	ATP	A	601	3	32,33,33	1.52	8 (25%)	48,52,52	1.66	11 (22%)
4	CO3	B	603	-	3,3,3	0.95	0	2,3,3	0.10	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
2	ATP	A	601	3	-	7/22/38/38	0/3/3/3
2	ATP	B	601	3	-	7/22/38/38	0/3/3/3
2	ATP	C	601	3	-	6/22/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ATP	C5-C4	4.91	1.47	1.39
2	B	601	ATP	C5-C4	4.78	1.47	1.39
2	C	601	ATP	C5-C4	4.21	1.46	1.39
2	A	601	ATP	PA-O3A	2.86	1.62	1.59
2	A	601	ATP	C4-N9	-2.77	1.31	1.37

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	ATP	C5-C4-N3	-5.77	118.78	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	ATP	N3-C4-N9	5.26	136.11	127.17
2	A	601	ATP	C5-C4-N3	-4.78	120.14	126.72
2	B	601	ATP	C5-C4-N3	-4.11	121.05	126.72
2	A	601	ATP	N3-C4-N9	3.95	133.88	127.17

There are no chirality outliers.

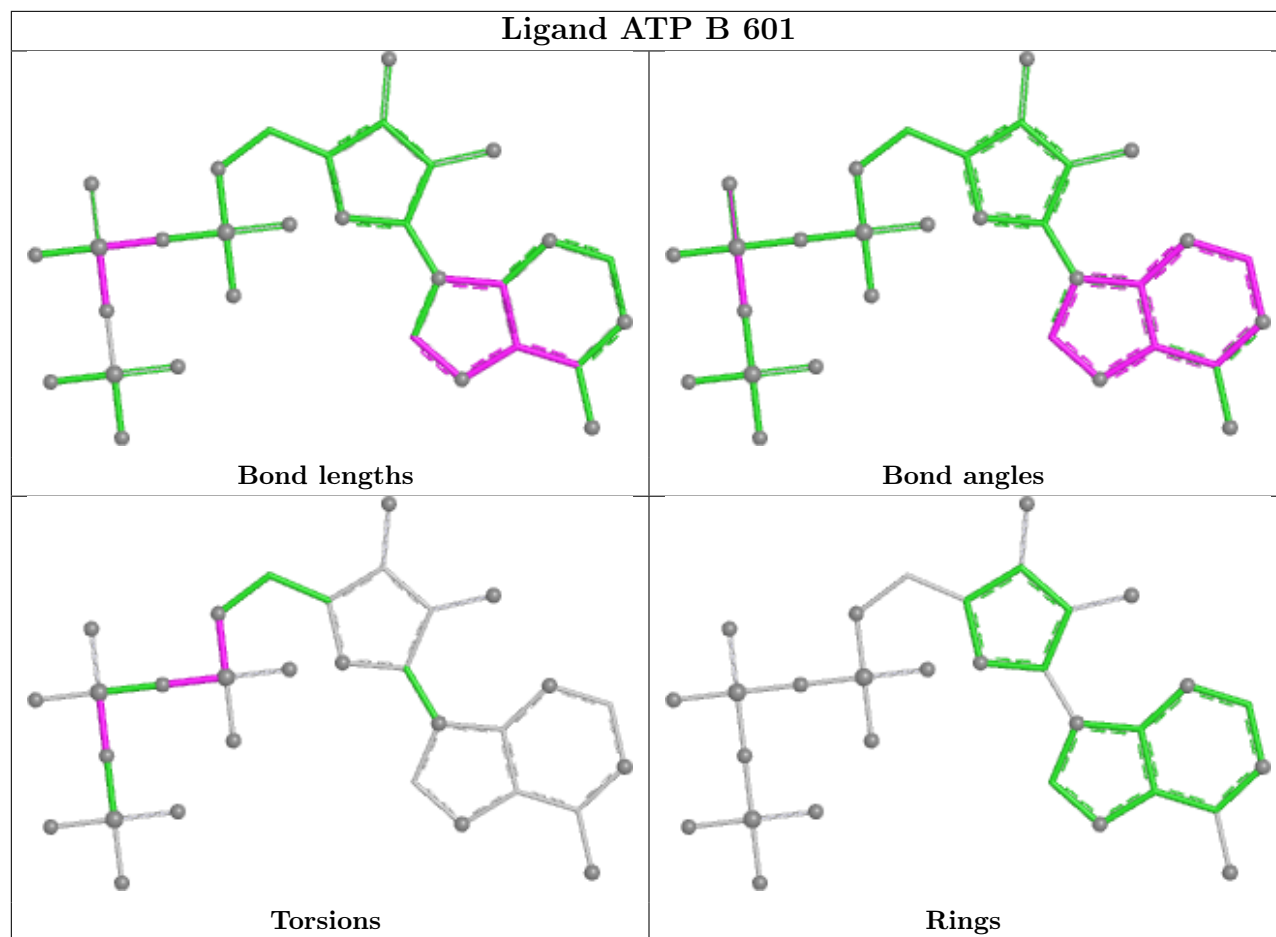
5 of 20 torsion outliers are listed below:

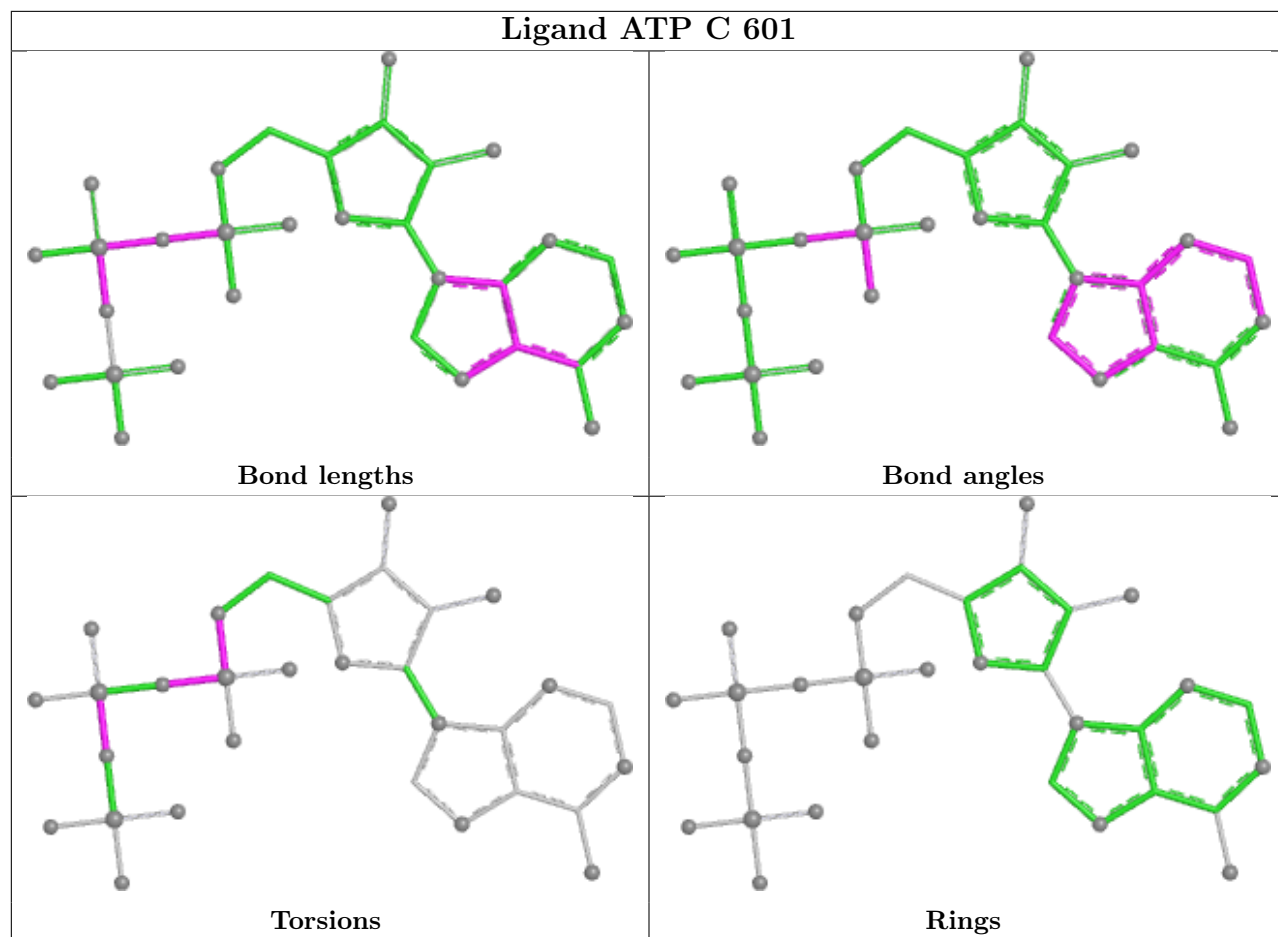
Mol	Chain	Res	Type	Atoms
2	A	601	ATP	C5'-O5'-PA-O1A
2	A	601	ATP	C5'-O5'-PA-O3A
2	B	601	ATP	PB-O3A-PA-O5'
2	B	601	ATP	C5'-O5'-PA-O1A
2	B	601	ATP	C5'-O5'-PA-O3A

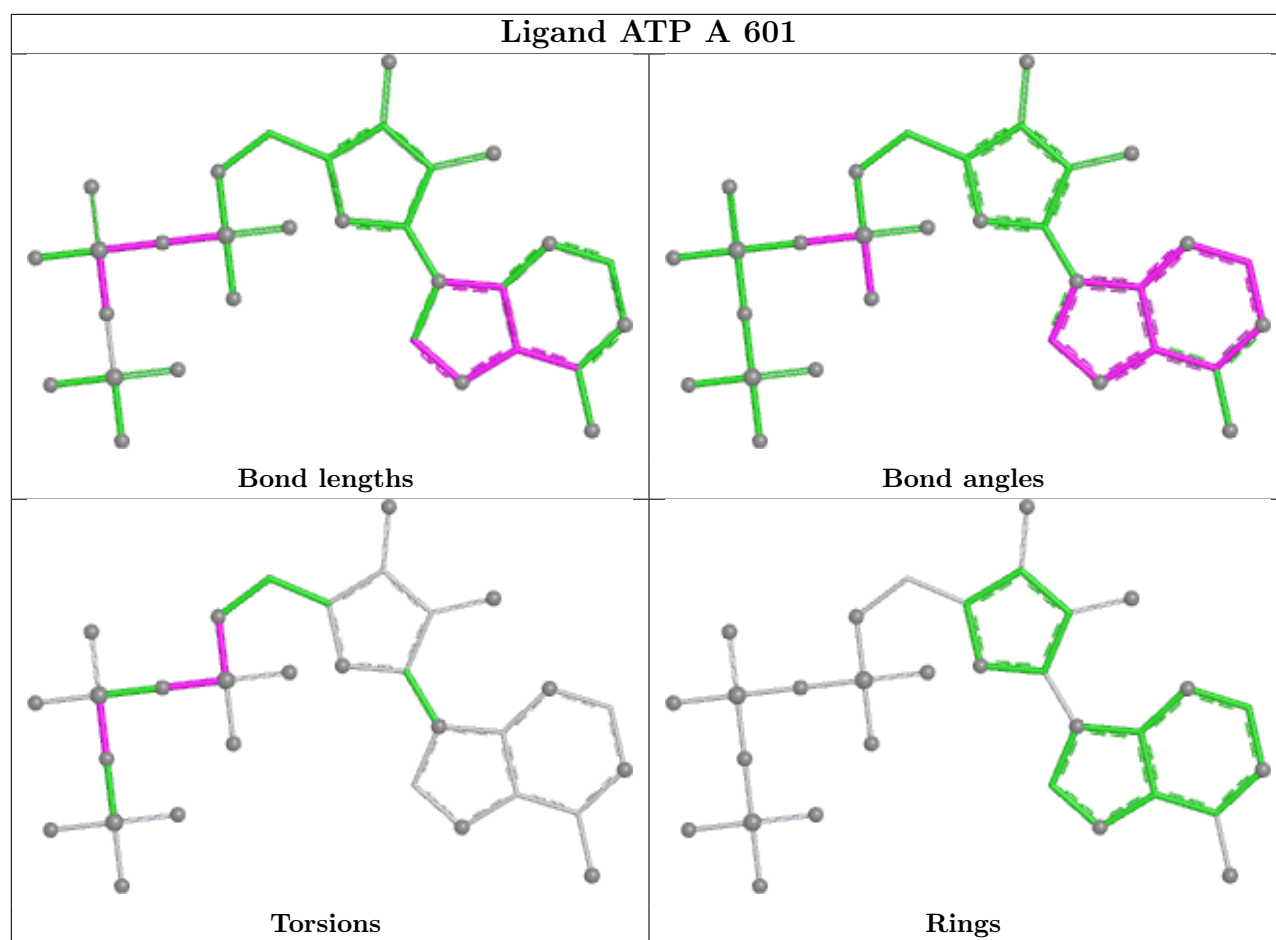
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	476/506 (94%)	-0.04	8 (1%) 69 68	21, 29, 49, 79	1 (0%)
1	B	476/506 (94%)	-0.25	9 (1%) 66 66	11, 19, 43, 82	6 (1%)
1	C	476/506 (94%)	0.30	44 (9%) 14 13	19, 30, 70, 107	2 (0%)
All	All	1428/1518 (94%)	0.00	61 (4%) 40 39	11, 27, 61, 107	9 (0%)

The worst 5 of 61 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	465	VAL	6.2
1	C	461	LEU	4.9
1	C	464	PHE	4.5
1	C	451	PHE	4.2
1	C	409	VAL	3.7

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	MLY	C	471	11/12	0.70	0.24	65,99,124,128	0
1	MLY	C	506	12/12	0.77	0.18	72,85,104,107	0
1	MLY	C	462	11/12	0.78	0.23	71,81,93,106	0
1	MLY	A	466	11/12	0.79	0.25	38,55,90,98	0
1	MLY	C	476	11/12	0.80	0.21	55,68,84,94	0
1	MLY	C	448	11/12	0.81	0.20	53,61,78,79	0
1	MLY	C	466	11/12	0.83	0.28	61,84,139,141	0
1	MLY	C	340	11/12	0.83	0.18	39,63,93,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	MLY	C	473	11/12	0.83	0.15	61,65,82,89	0
1	MLY	A	235	11/12	0.83	0.23	29,41,120,122	0
1	MLY	A	471	11/12	0.83	0.23	33,65,103,113	0
1	MLY	A	12	11/12	0.84	0.20	37,47,91,100	0
1	MLY	C	230	11/12	0.84	0.15	32,43,72,77	0
1	MLY	A	448	11/12	0.85	0.19	32,40,92,95	0
1	MLY	A	369	11/12	0.85	0.19	40,59,93,101	0
1	MLY	C	369	11/12	0.86	0.20	39,57,105,112	0
1	MLY	A	230	11/12	0.87	0.18	33,49,96,102	0
1	MLY	A	399	11/12	0.87	0.21	31,54,117,123	0
1	MLY	C	412	11/12	0.87	0.15	53,59,70,74	0
1	MLY	A	473	11/12	0.87	0.10	29,33,42,44	0
1	MLY	A	506	12/12	0.87	0.15	29,56,90,91	0
1	MLY	B	12	11/12	0.87	0.25	33,46,112,123	0
1	MLY	B	230	11/12	0.87	0.17	26,38,80,90	0
1	MLY	B	471	11/12	0.87	0.17	37,59,89,94	0
1	MLY	C	120	11/12	0.87	0.14	35,47,82,83	0
1	MLY	C	477	11/12	0.87	0.17	51,54,77,90	0
1	MLY	A	340	11/12	0.87	0.16	35,55,84,94	0
1	MLY	B	466	11/12	0.88	0.18	42,54,88,89	0
1	MLY	A	359	11/12	0.88	0.16	29,43,68,70	0
1	MLY	C	399	11/12	0.88	0.19	38,62,100,102	0
1	MLY	A	120	11/12	0.88	0.12	38,56,75,79	0
1	MLY	B	462	11/12	0.88	0.14	37,45,53,59	0
1	MLY	C	291	11/12	0.88	0.20	38,44,99,103	0
1	MLY	C	359	11/12	0.89	0.17	28,40,64,69	0
1	MLY	A	18	11/12	0.89	0.16	23,32,64,69	0
1	MLY	C	502	11/12	0.89	0.15	54,58,92,96	0
1	MLY	C	12	11/12	0.89	0.16	36,56,93,99	0
1	MLY	C	494	11/12	0.90	0.13	52,56,63,63	0
1	MLY	C	102	11/12	0.90	0.15	26,30,57,64	0
1	MLY	B	473	11/12	0.90	0.11	29,31,50,61	0
1	MLY	B	235	11/12	0.91	0.19	18,30,86,96	0
1	MLY	B	359	11/12	0.91	0.13	18,34,53,55	0
1	MLY	C	171	11/12	0.91	0.15	31,37,54,72	0
1	MLY	B	369	11/12	0.91	0.19	24,35,98,109	0
1	MLY	A	291	11/12	0.91	0.17	29,41,82,84	0
1	MLY	A	102	11/12	0.91	0.13	27,33,55,57	0
1	MLY	A	28	11/12	0.91	0.10	27,38,54,54	0
1	MLY	A	462	11/12	0.91	0.11	32,37,42,48	0
1	MLY	B	506	12/12	0.91	0.12	33,53,74,81	0
1	MLY	A	367	11/12	0.91	0.10	34,39,54,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	MLY	C	62	11/12	0.92	0.16	26,31,63,93	0
1	MLY	B	399	11/12	0.92	0.14	22,32,81,82	0
1	MLY	C	110	11/12	0.92	0.11	31,40,56,59	0
1	MLY	C	367	11/12	0.92	0.12	36,42,69,75	0
1	MLY	B	448	11/12	0.92	0.14	28,35,77,82	0
1	MLY	C	385	11/12	0.92	0.11	35,40,64,67	0
1	MLY	A	62	11/12	0.92	0.12	30,32,50,52	0
1	MLY	B	120	11/12	0.92	0.11	29,35,50,53	0
1	MLY	C	235	11/12	0.92	0.16	27,42,89,97	0
1	MLY	B	494	11/12	0.93	0.09	19,21,31,32	0
1	MLY	B	367	11/12	0.93	0.12	25,30,60,73	0
1	MLY	A	110	11/12	0.93	0.11	33,38,53,55	0
1	MLY	B	291	11/12	0.93	0.16	21,30,69,74	0
1	MLY	A	385	11/12	0.93	0.11	29,35,60,66	0
1	MLY	C	264	11/12	0.93	0.09	27,30,35,41	0
1	MLY	B	28	11/12	0.94	0.10	23,29,55,64	0
1	MLY	C	18	11/12	0.94	0.14	20,29,66,74	0
1	MLY	A	353	11/12	0.94	0.10	25,30,58,60	0
1	MLY	B	385	11/12	0.94	0.11	17,20,48,54	0
1	MLY	B	340	11/12	0.94	0.10	28,41,74,78	0
1	MLY	B	412	11/12	0.94	0.09	21,24,30,32	0
1	MLY	A	494	11/12	0.94	0.07	25,27,32,32	0
1	MLY	A	477	11/12	0.95	0.08	20,23,31,31	0
1	MLY	B	264	11/12	0.95	0.07	18,19,23,24	0
1	MLY	B	18	11/12	0.95	0.12	19,26,58,62	0
1	MLY	A	264	11/12	0.95	0.08	25,35,39,39	0
1	MLY	B	62	11/12	0.95	0.11	17,19,33,49	0
1	MLY	B	476	11/12	0.95	0.09	23,28,48,59	0
1	MLY	B	102	11/12	0.95	0.10	16,18,36,44	0
1	MLY	B	502	11/12	0.95	0.10	21,29,58,61	0
1	MLY	B	110	11/12	0.95	0.08	19,22,35,43	0
1	MLY	C	353	11/12	0.95	0.10	25,28,56,58	0
1	MLY	A	502	11/12	0.95	0.11	24,32,72,72	0
1	MLY	B	171	11/12	0.95	0.09	16,19,33,35	0
1	MLY	A	171	11/12	0.95	0.09	30,32,48,51	0
1	MLY	C	28	11/12	0.96	0.08	27,35,48,54	0
1	MLY	B	477	11/12	0.96	0.08	20,22,32,33	0
1	MLY	A	476	11/12	0.96	0.10	20,24,55,70	0
1	MLY	B	353	11/12	0.96	0.08	16,18,40,45	0
1	MLY	A	412	11/12	0.97	0.07	22,27,43,45	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

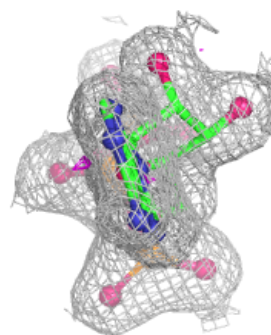
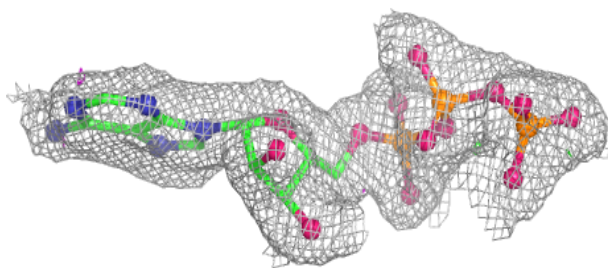
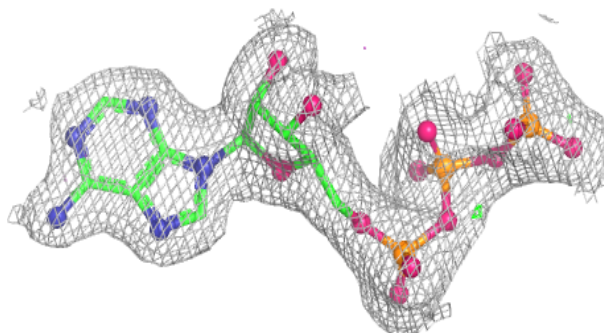
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CO3	B	603	4/4	0.94	0.16	9,28,32,43	0
4	CO3	C	603	4/4	0.95	0.10	23,39,45,50	0
4	CO3	A	603	4/4	0.96	0.09	21,38,45,48	0
2	ATP	A	601	31/31	0.97	0.06	22,27,32,36	0
2	ATP	C	601	31/31	0.97	0.07	22,30,37,43	0
3	MG	C	602	1/1	0.97	0.04	27,27,27,27	0
3	MG	A	602	1/1	0.98	0.06	29,29,29,29	0
3	MG	B	602	1/1	0.98	0.05	16,16,16,16	0
2	ATP	B	601	31/31	0.99	0.05	10,16,23,27	0

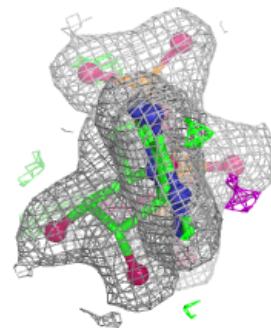
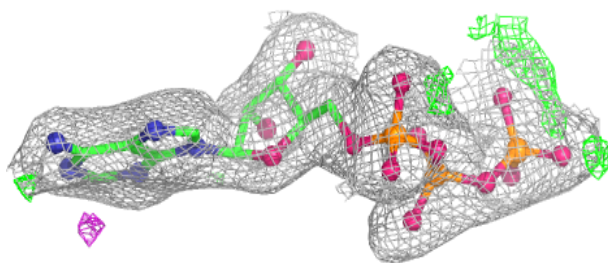
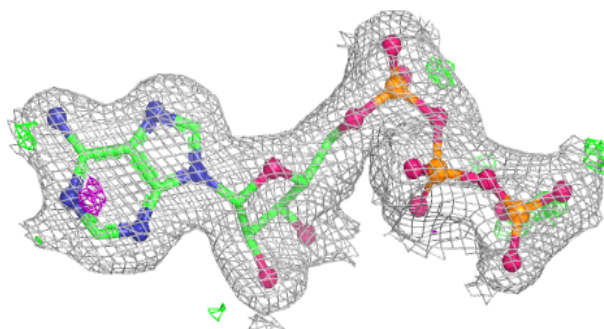
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP 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)

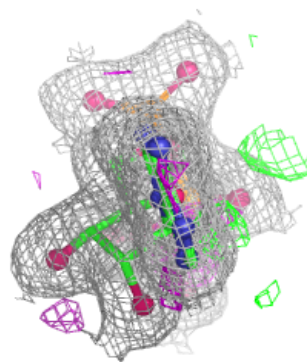
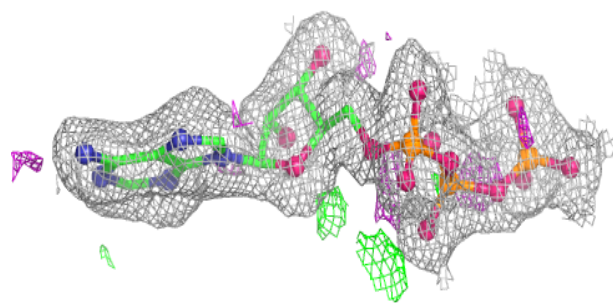
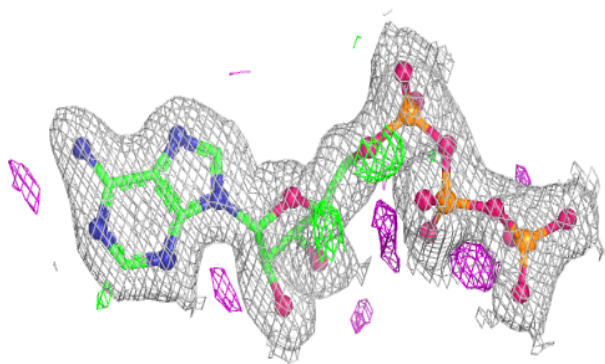
**Electron density around ATP C 601:**

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



Electron density around ATP B 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.