



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 01:23 PM BST

PDB ID : 6B2E
Title : Structure of full length human AMPK (a2b2g1) in complex with a small molecule activator SC4.
Authors : Ngoei, K.R.W.; Langendorf, C.G.; Ling, N.X.Y.; Hoque, A.; Johnson, S.; Camerino, M.C.; Walker, S.R.; Bozikis, Y.E.; Dite, T.A.; Ovens, A.J.; Smiles, W.J.; Jacobs, R.; Huang, H.; Parker, M.W.; Scott, J.W.; Rider, M.H.; Kemp, B.E.; Foitzik, R.C.; Baell, J.B.; Oakhill, J.S.
Deposited on : 2017-09-19
Resolution : 3.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
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)	:	2.13.1

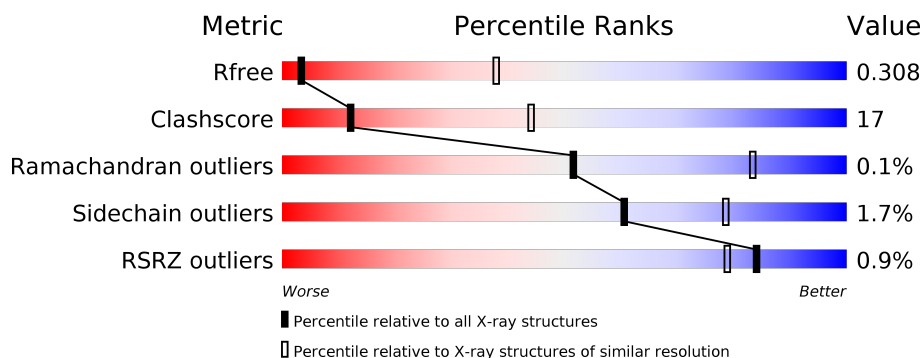
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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

Mol	Chain	Length	Quality of chain
1	A	565	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 65%, grey 22%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 65% 13% • 22% </div> </div>
2	B	272	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 57%, grey 29%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 57% 13% • 29% </div> </div>
3	C	336	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 15%, green 73%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 73% 15% 12% </div> </div>
4	D	7	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 14%, yellow 71%, orange 14%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 14% 71% 14% </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SEP	B	108	-	-	X	-
4	GLC	D	1	-	-	-	X
4	GLC	D	4	-	-	X	X
4	GLC	D	5	-	-	X	X
4	GLC	D	6	-	-	-	X
4	GLC	D	7	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6720 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-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	P	S	0	0	0
			3206	2062	533	588	1	22			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	initiating methionine	UNP P54646
A	-11	GLY	-	expression tag	UNP P54646
A	-10	SER	-	expression tag	UNP P54646
A	-9	SER	-	expression tag	UNP P54646
A	-8	HIS	-	expression tag	UNP P54646
A	-7	HIS	-	expression tag	UNP P54646
A	-6	HIS	-	expression tag	UNP P54646
A	-5	HIS	-	expression tag	UNP P54646
A	-4	HIS	-	expression tag	UNP P54646
A	-3	HIS	-	expression tag	UNP P54646
A	-2	SER	-	expression tag	UNP P54646
A	-1	GLN	-	expression tag	UNP P54646
A	0	ASP	-	expression tag	UNP P54646
A	1	PRO	-	expression tag	UNP P54646
A	271	GLY	ASP	conflict	UNP P54646

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	193	Total	C	N	O	P	S	0	0	0
			1258	782	220	252	1	3			

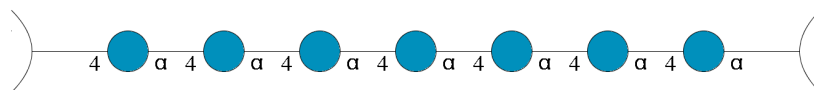
- Molecule 3 is a protein called 5'-AMP-activated protein kinase subunit gamma-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	295	Total	C	N	O	S	0	0	0
			2064	1335	343	382	4			

There are 6 discrepancies between the modelled and reference sequences:

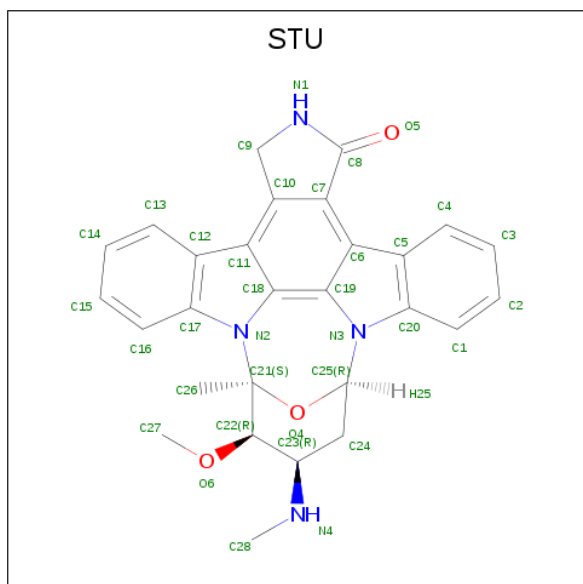
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	MET	-	initiating methionine	UNP P54619
C	-3	ALA	-	expression tag	UNP P54619
C	-2	ASP	-	expression tag	UNP P54619
C	-1	LEU	-	expression tag	UNP P54619
C	0	ASN	-	expression tag	UNP P54619
C	1	TRP	-	expression tag	UNP P54619

- Molecule 4 is an oligosaccharide called Cycloheptakis-(1-4)-(alpha-D-glucopyranose).



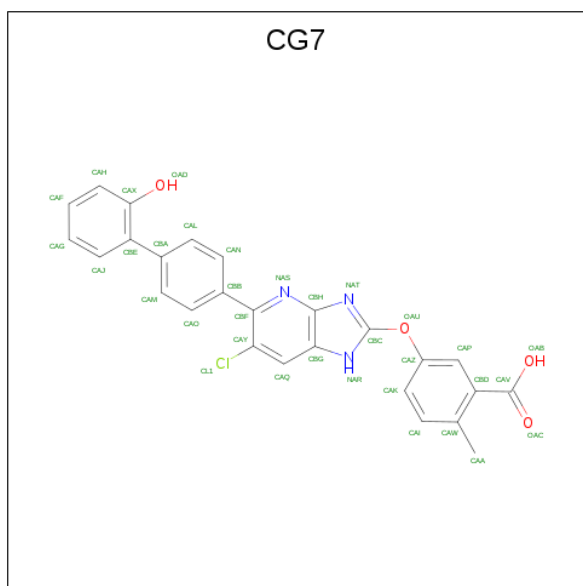
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	D	7	Total	C	O	0	0	0
			77	42	35			

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



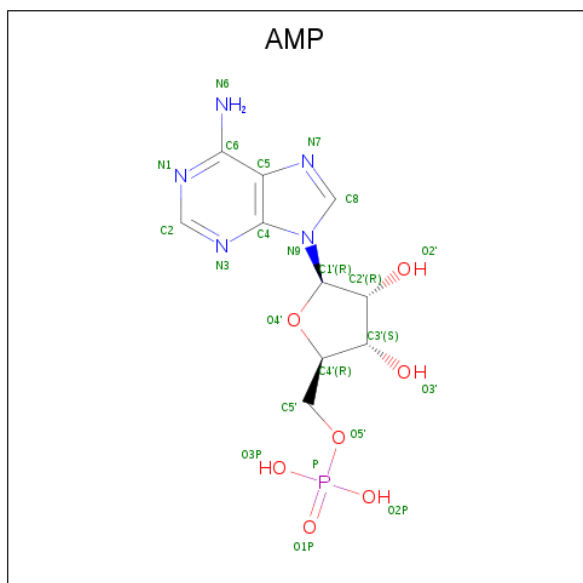
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			35	28	4	3		

- Molecule 6 is 5-{{6-chloro-5-(2'-hydroxy[1,1'-biphenyl]-4-yl)-1H-imidazo[4,5-b]pyridin-2-yl}oxy}-2-methylbenzoic acid (three-letter code: CG7) (formula: C₂₆H₁₈ClN₃O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	Cl	N	O	0
			34	26	1	3	4	0

- Molecule 7 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).

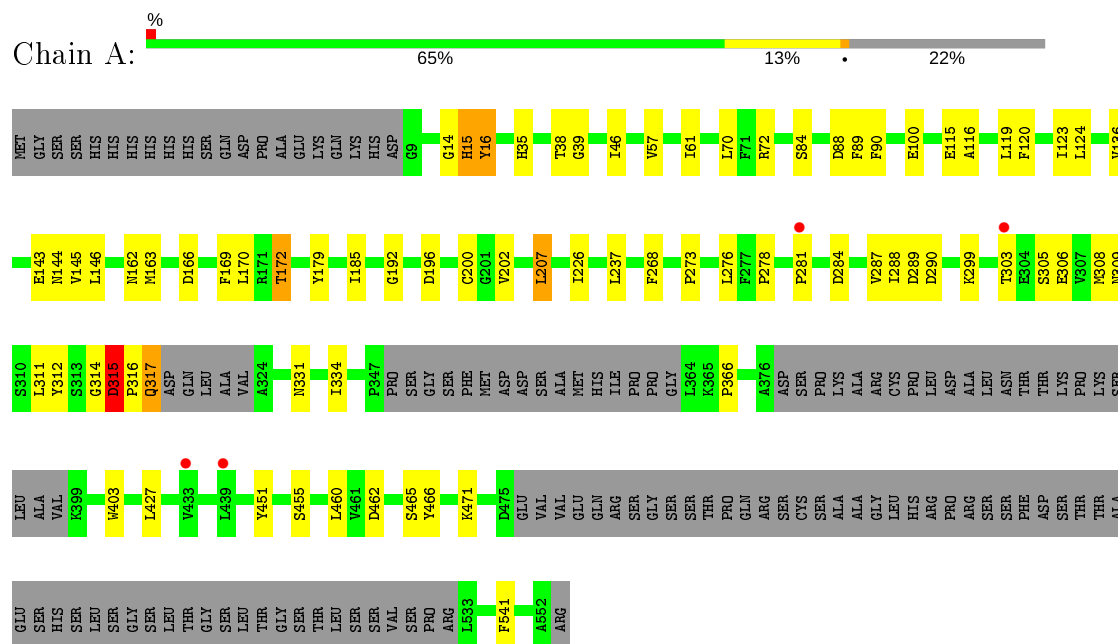


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
7	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

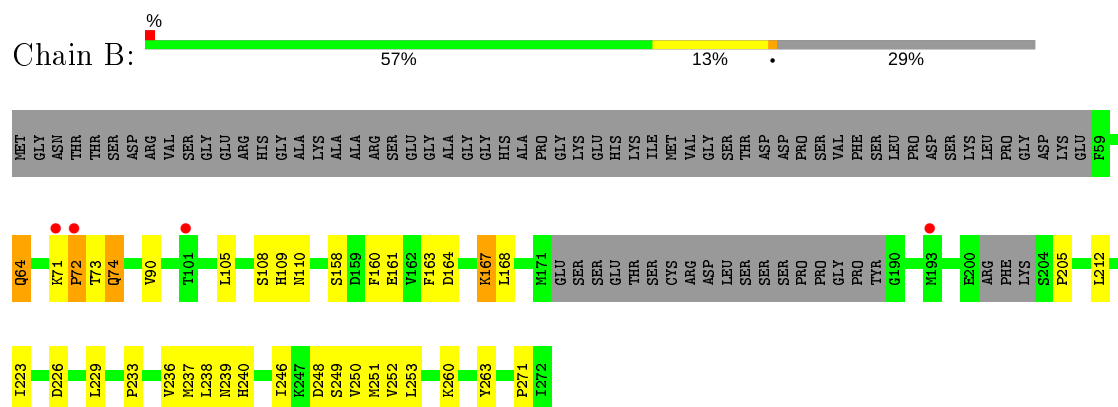
3 Residue-property plots [i](#)

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-2

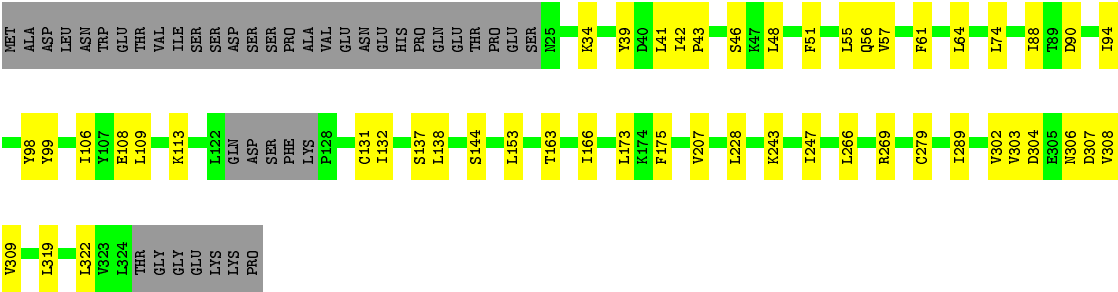


- Molecule 2: 5'-AMP-activated protein kinase subunit beta-2

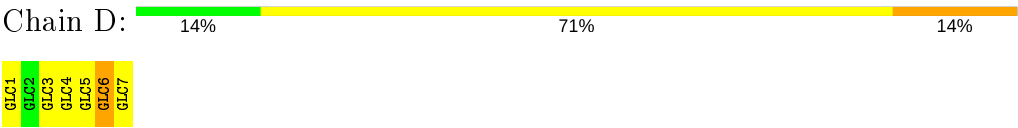


- Molecule 3: 5'-AMP-activated protein kinase subunit gamma-1





- Molecule 4: Cycloheptakis-(1-4)-(alpha-D-glucopyranose)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.94Å 118.85Å 138.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 3.80 48.15 – 3.80	Depositor EDS
% Data completeness (in resolution range)	93.3 (48.15-3.80) 93.3 (48.15-3.80)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 3.77Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.244 , 0.277 0.280 , 0.308	Depositor DCC
R_{free} test set	920 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	121.5	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 138.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.031 for k,h,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6720	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, TPO, GLC, STU, AMP, CG7

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	0.39	0/3270	0.55	1/4470 (0.0%)
2	B	0.40	1/1272 (0.1%)	0.56	1/1756 (0.1%)
3	C	0.39	0/2104	0.54	0/2903
All	All	0.39	1/6646 (0.0%)	0.55	2/9129 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	72	PRO	N-CD	5.21	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ASP	C-N-CD	5.92	140.84	128.40
2	B	71	LYS	C-N-CD	5.71	140.39	128.40

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	3206	0	2866	106	0
2	B	1258	0	992	55	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2064	0	1858	55	0
4	D	77	0	63	10	0
5	A	35	0	26	10	0
6	A	34	0	0	0	0
7	C	46	0	24	0	0
All	All	6720	0	5829	214	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 17.

The worst 5 of 214 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ALA:HB1	1:A:207:LEU:CD2	1.41	1.48
1:A:308:MET:CB	1:A:311:LEU:HD12	1.59	1.31
1:A:273:PRO:HD2	1:A:276:LEU:CD1	1.57	1.31
3:C:88:ILE:CG1	3:C:247:ILE:HD11	1.72	1.19
1:A:116:ALA:CB	1:A:207:LEU:CD2	2.21	1.17

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	432/565 (76%)	415 (96%)	16 (4%)	1 (0%)	47	79
2	B	186/272 (68%)	181 (97%)	5 (3%)	0	100	100
3	C	291/336 (87%)	280 (96%)	11 (4%)	0	100	100
All	All	909/1173 (78%)	876 (96%)	32 (4%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	315	ASP

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	298/497 (60%)	291 (98%)	7 (2%)	50	72
2	B	101/242 (42%)	98 (97%)	3 (3%)	41	66
3	C	190/308 (62%)	190 (100%)	0	100	100
All	All	589/1047 (56%)	579 (98%)	10 (2%)	60	78

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	317	GLN
1	A	451	TYR
2	B	64	GLN
1	A	207	LEU
1	A	460	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	64	GLN
2	B	240	HIS
3	C	223	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](#)

2 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	$\# Z > 2$
2	SEP	B	108	2	8,9,10	0.84	0	8,12,14	1.12	0
1	TPO	A	172	1	8,10,11	0.87	0	10,14,16	1.22	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	B	108	2	-	5/5/8/10	-
1	TPO	A	172	1	-	3/9/11/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	172	TPO	O-C-CA	-2.02	119.48	124.78

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	108	SEP	N-CA-CB-OG
2	B	108	SEP	CB-OG-P-O2P
2	B	108	SEP	CB-OG-P-O3P
1	A	172	TPO	O-C-CA-CB
1	A	172	TPO	CG2-CB-OG1-P

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	108	SEP	4	0
1	A	172	TPO	1	0

5.5 Carbohydrates ⓘ

7 monosaccharides 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
4	GLC	D	1	4	11,11,12	0.37	0	15,15,17	1.40	3 (20%)
4	GLC	D	2	4	11,11,12	0.24	0	15,15,17	0.58	0
4	GLC	D	3	4	11,11,12	0.24	0	15,15,17	0.57	0
4	GLC	D	4	4	11,11,12	0.21	0	15,15,17	0.70	0
4	GLC	D	5	4	11,11,12	0.28	0	15,15,17	0.77	0
4	GLC	D	6	4	11,11,12	0.25	0	15,15,17	1.12	1 (6%)
4	GLC	D	7	4	11,11,12	0.21	0	15,15,17	0.72	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	GLC	D	1	4	-	1/2/19/22	0/1/1/1
4	GLC	D	2	4	-	1/2/19/22	0/1/1/1
4	GLC	D	3	4	-	0/2/19/22	0/1/1/1
4	GLC	D	4	4	-	0/2/19/22	0/1/1/1
4	GLC	D	5	4	-	1/2/19/22	0/1/1/1
4	GLC	D	6	4	-	0/2/19/22	0/1/1/1
4	GLC	D	7	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	D	1	GLC	C1-O5-C5	3.48	116.90	112.19
4	D	6	GLC	C1-O5-C5	2.50	115.58	112.19
4	D	1	GLC	C3-C4-C5	2.19	114.14	110.24
4	D	1	GLC	O5-C1-C2	2.05	113.94	110.77

There are no chirality outliers.

All (3) torsion outliers are listed below:

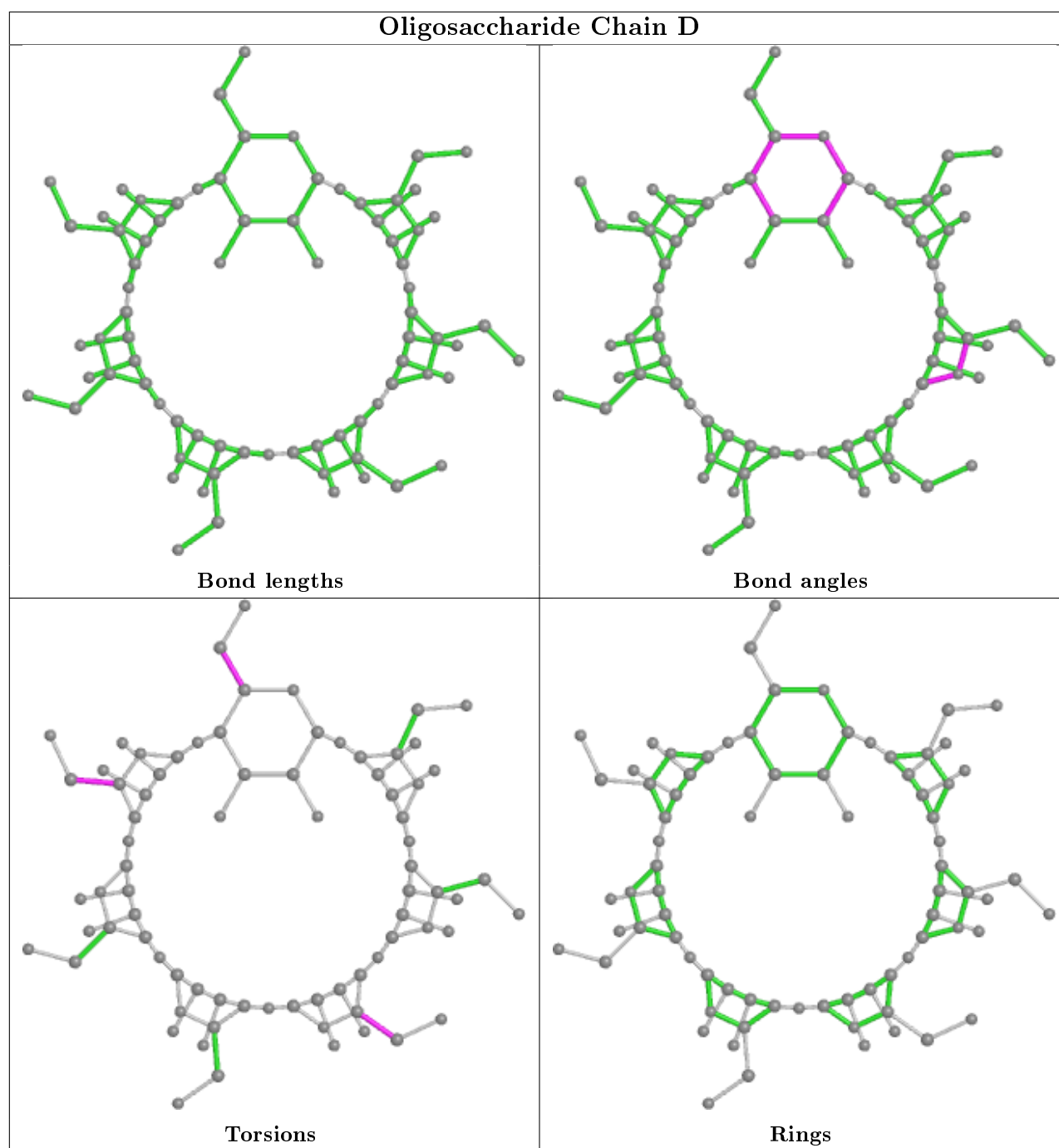
Mol	Chain	Res	Type	Atoms
4	D	2	GLC	O5-C5-C6-O6
4	D	1	GLC	O5-C5-C6-O6
4	D	5	GLC	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	6	GLC	2	0
4	D	7	GLC	2	0
4	D	3	GLC	2	0
4	D	4	GLC	8	0
4	D	5	GLC	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 oligosaccharide.



5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection.

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	AMP	C	401	-	22,25,25	1.08	2 (9%)	25,38,38	1.44	3 (12%)
5	STU	A	601	-	30,42,42	2.52	10 (33%)	31,68,68	2.44	13 (41%)
6	CG7	A	602	-	35,38,38	2.52	7 (20%)	39,55,55	1.13	3 (7%)
7	AMP	C	400	-	22,25,25	1.08	2 (9%)	25,38,38	1.37	3 (12%)

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	401	-	-	0/6/26/26	0/3/3/3
5	STU	A	601	-	-	0/4/42/42	-
6	CG7	A	602	-	-	0/10/16/16	0/5/5/5
7	AMP	C	400	-	-	0/6/26/26	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	602	CG7	CBD-CAV	-7.73	1.40	1.47
6	A	602	CG7	CBB-CBF	-7.46	1.40	1.49
5	A	601	STU	C9-C10	-5.89	1.46	1.50
6	A	602	CG7	CAA-CAW	-5.36	1.40	1.51
6	A	602	CG7	CAQ-CBG	-4.97	1.34	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	601	STU	C7-C8-N1	5.47	111.91	106.37
5	A	601	STU	C9-N1-C8	-5.04	109.01	113.85
5	A	601	STU	O5-C8-C7	-4.48	124.00	129.32
5	A	601	STU	C7-C10-C11	-4.26	116.68	122.42
6	A	602	CG7	CBF-NAS-CBH	3.74	121.51	117.99

There are no chirality outliers.

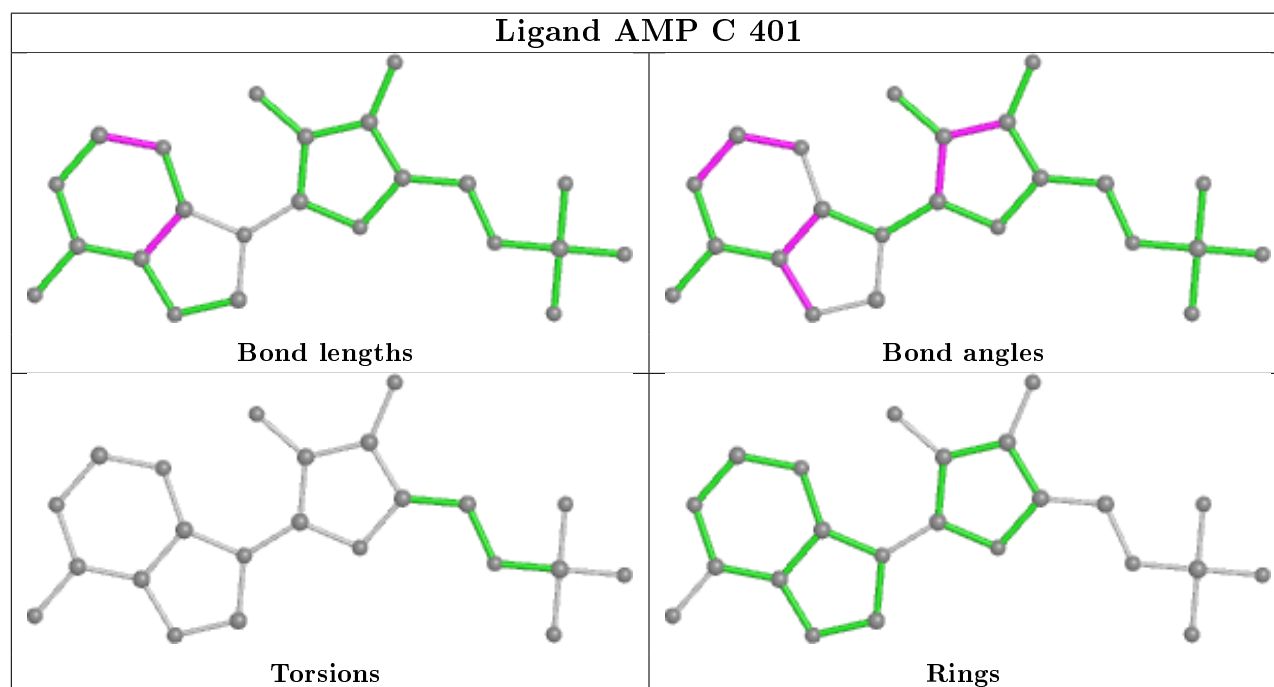
There are no torsion outliers.

There are no ring outliers.

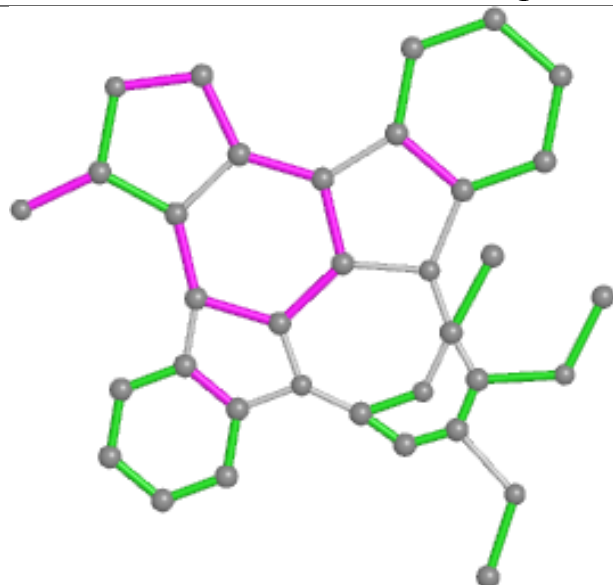
1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	601	STU	10	0

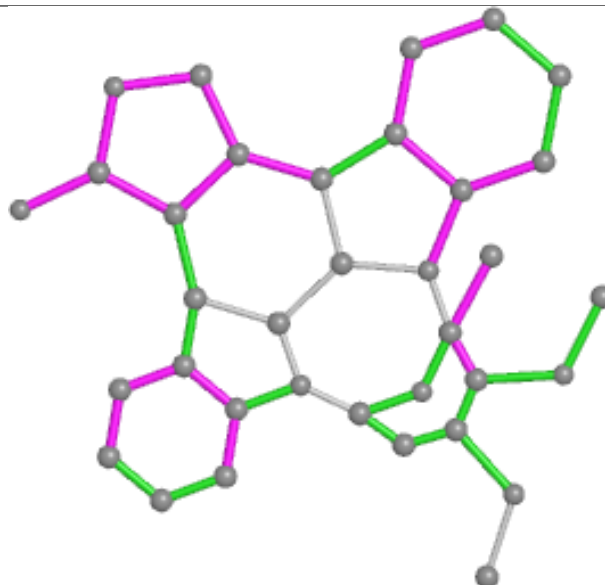
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



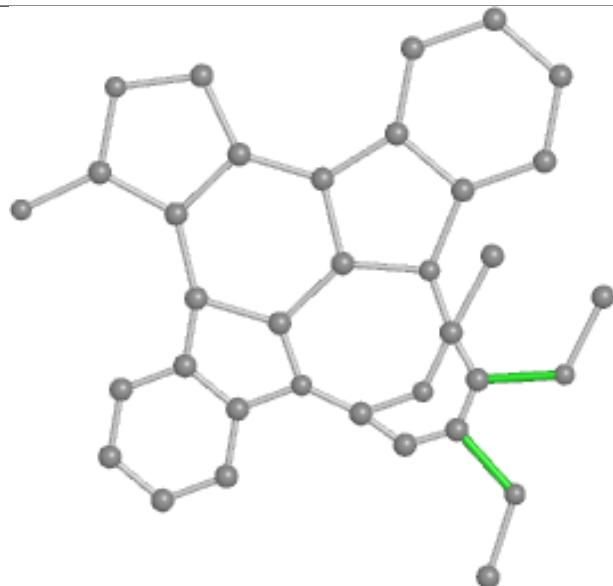
Ligand STU A 601



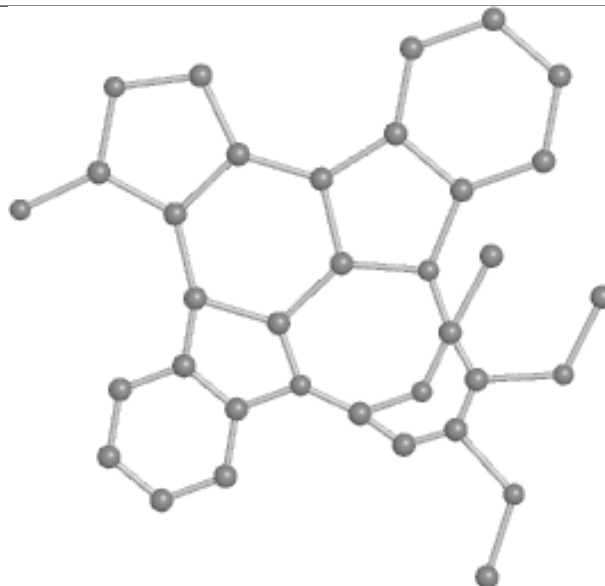
Bond lengths



Bond angles

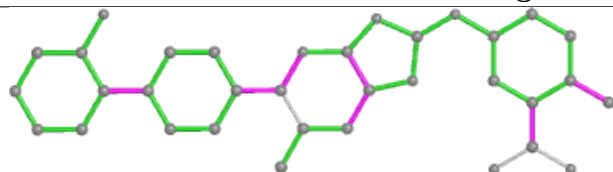


Torsions

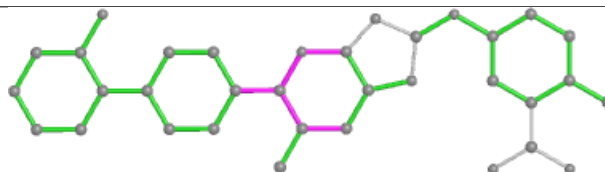


Rings

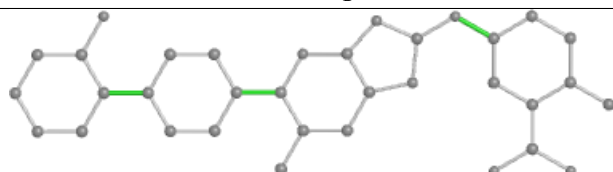
Ligand CG7 A 602



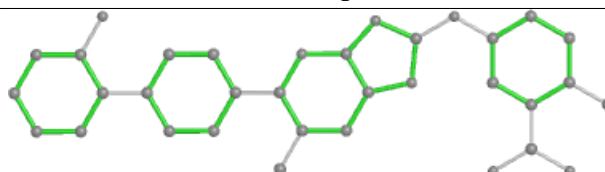
Bond lengths



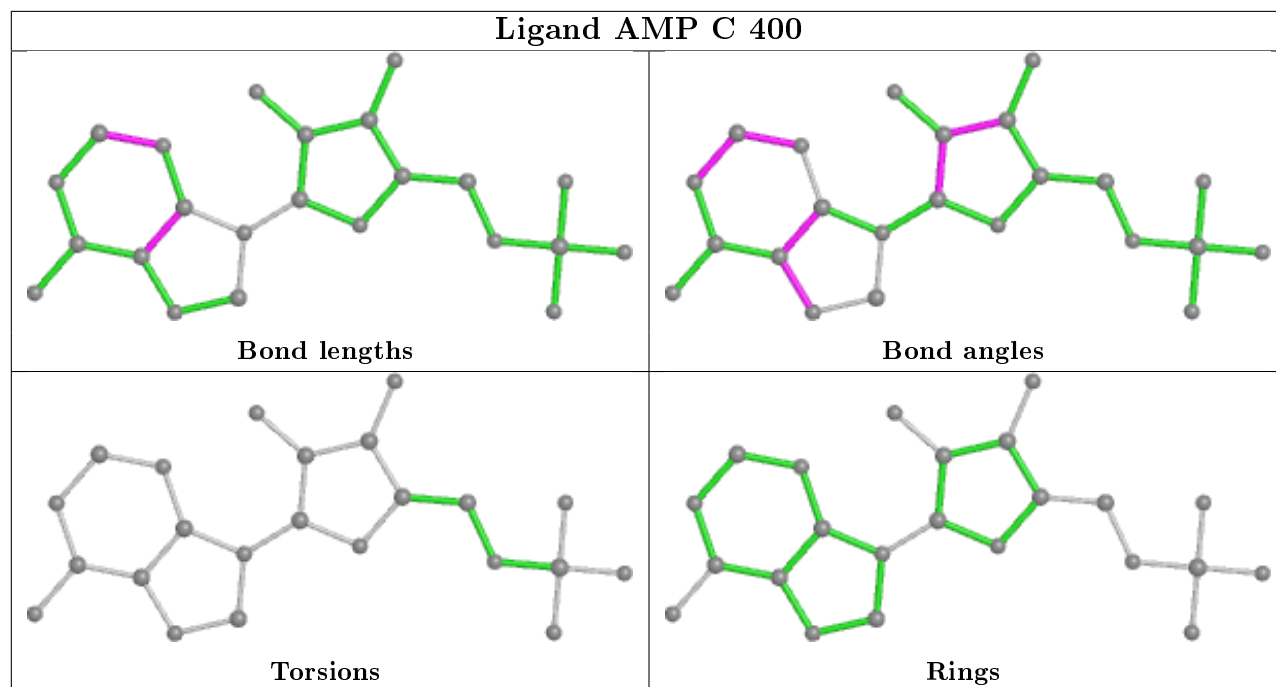
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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	442/565 (78%)	-0.04	4 (0%) 84 79	26, 124, 197, 252	0
2	B	192/272 (70%)	-0.10	4 (2%) 63 55	28, 145, 198, 243	0
3	C	295/336 (87%)	-0.20	0 100 100	87, 135, 194, 210	0
All	All	929/1173 (79%)	-0.10	8 (0%) 84 79	26, 130, 195, 252	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	PRO	3.6
1	A	433	VAL	2.8
2	B	72	PRO	2.7
2	B	71	LYS	2.3
2	B	101	THR	2.3

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	0.80	0.27	144,145,147,149	0
2	SEP	B	108	10/11	0.90	0.13	151,154,163,163	0

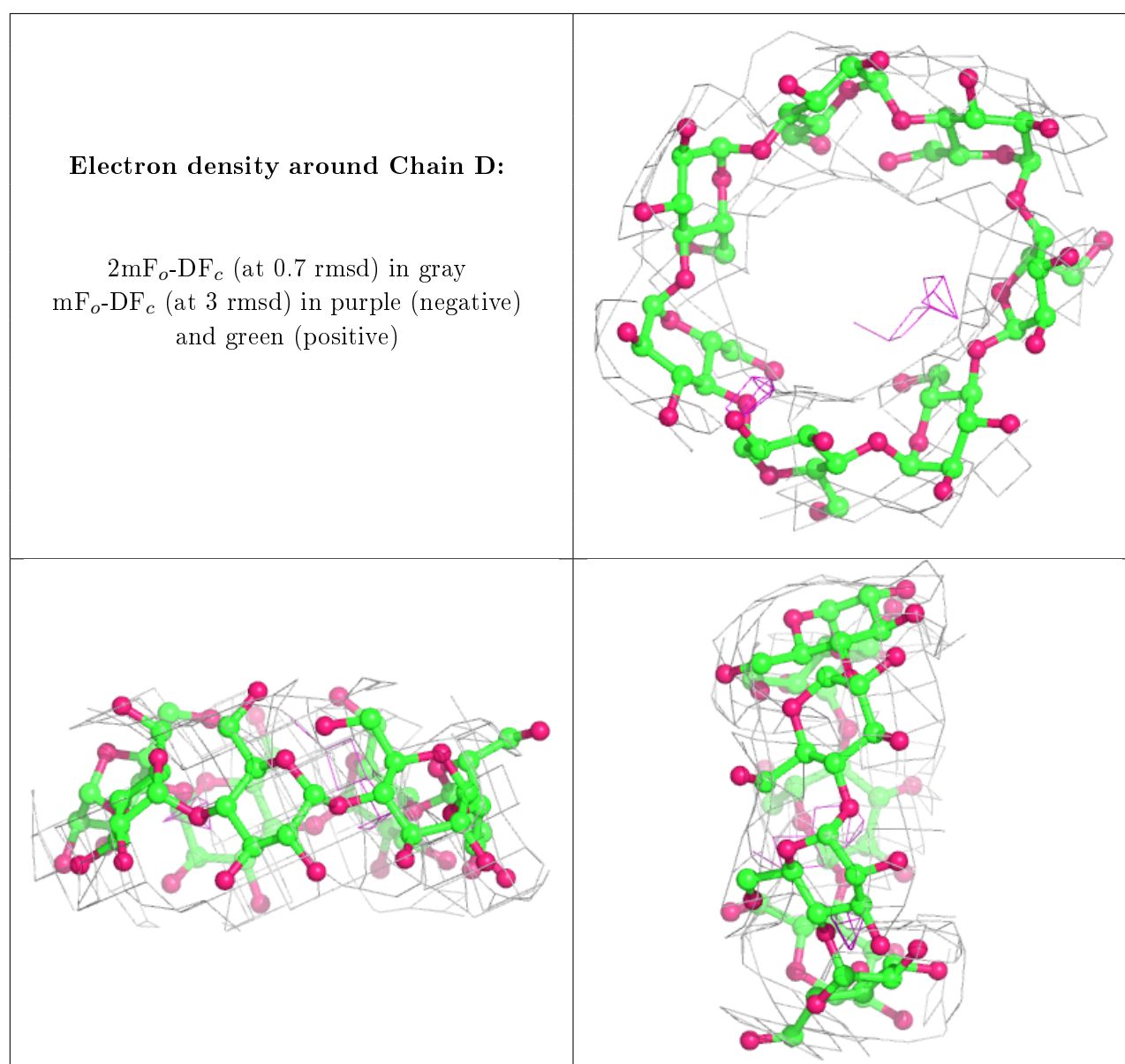
6.3 Carbohydrates [i](#)

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(\AA^2)	Q<0.9
4	GLC	D	4	11/12	0.74	0.41	212,212,213,213	0
4	GLC	D	7	11/12	0.76	0.45	213,213,213,213	0
4	GLC	D	2	11/12	0.76	0.36	212,212,212,212	0
4	GLC	D	1	11/12	0.77	0.48	212,213,213,213	0
4	GLC	D	6	11/12	0.79	0.44	212,212,213,213	0
4	GLC	D	5	11/12	0.79	0.48	213,213,213,213	0
4	GLC	D	3	11/12	0.88	0.34	212,212,212,212	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

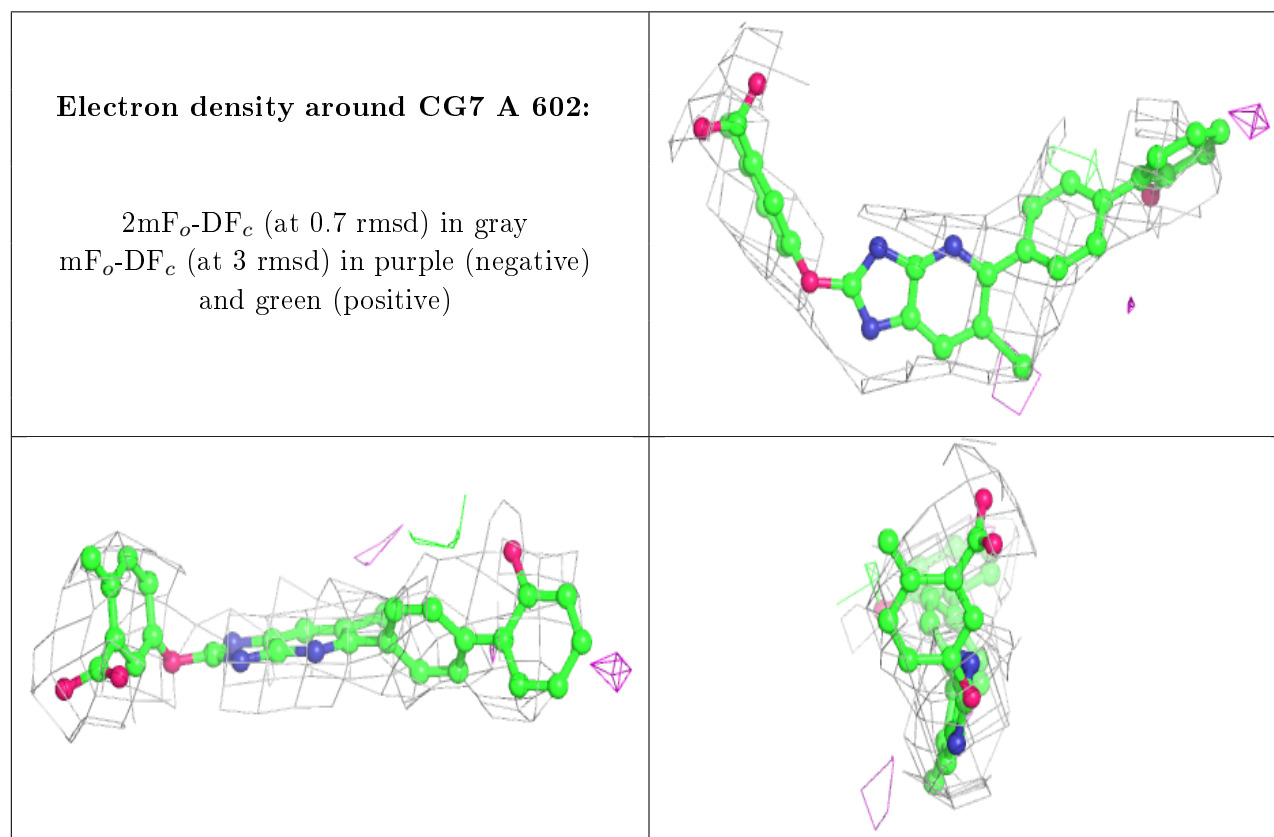


6.4 Ligands [i](#)

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.

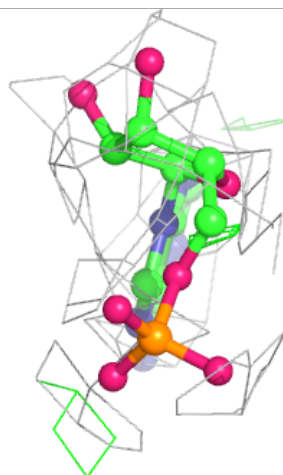
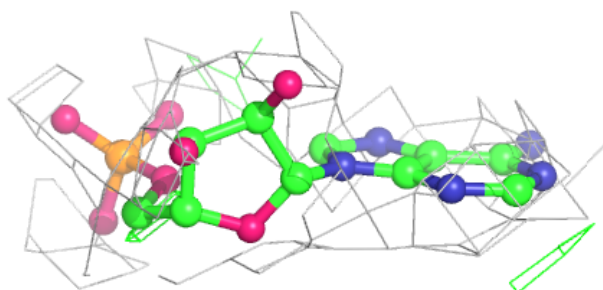
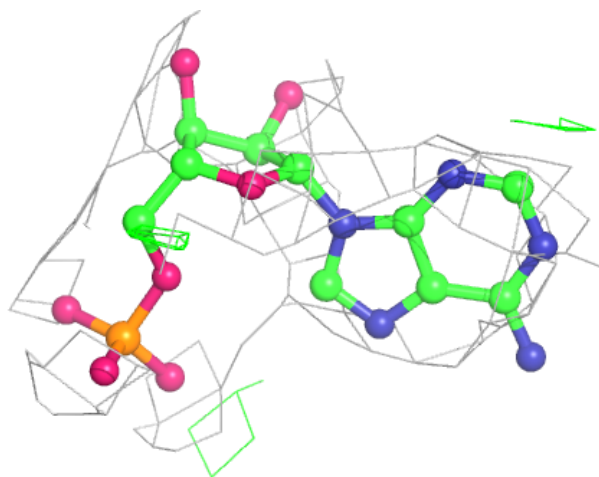
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	CG7	A	602	34/34	0.84	0.32	136,136,137,137	0
7	AMP	C	400	23/23	0.84	0.31	134,134,134,135	0
7	AMP	C	401	23/23	0.85	0.25	143,143,143,143	0
5	STU	A	601	35/35	0.92	0.33	88,88,89,90	0

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.



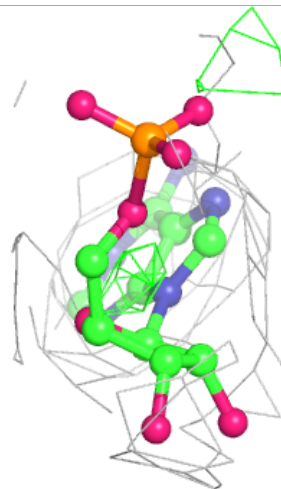
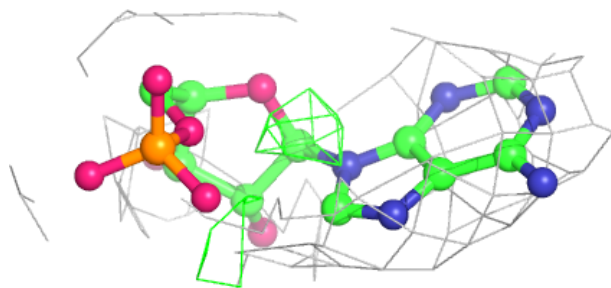
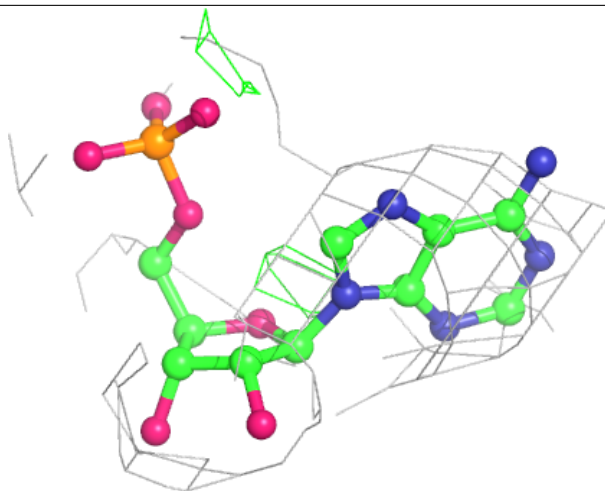
Electron density around AMP C 400:

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



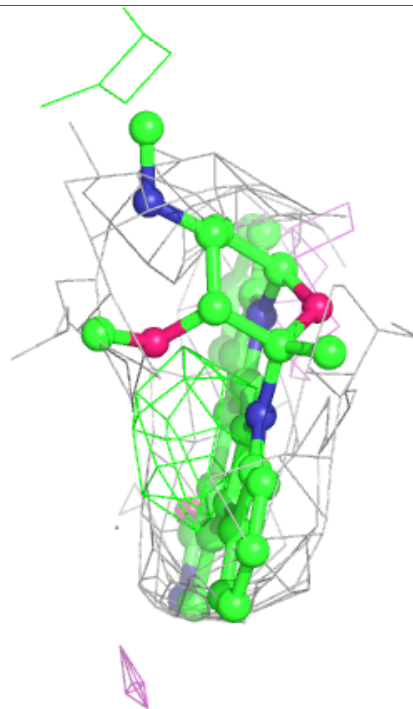
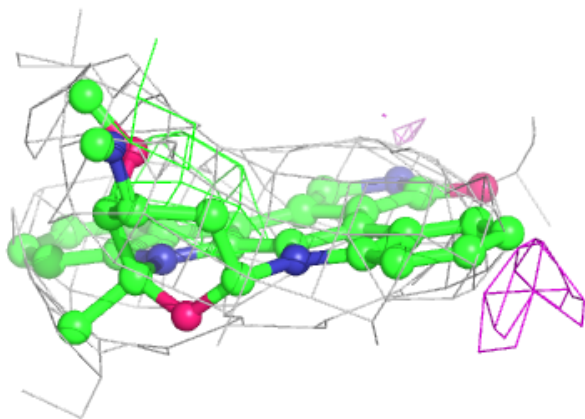
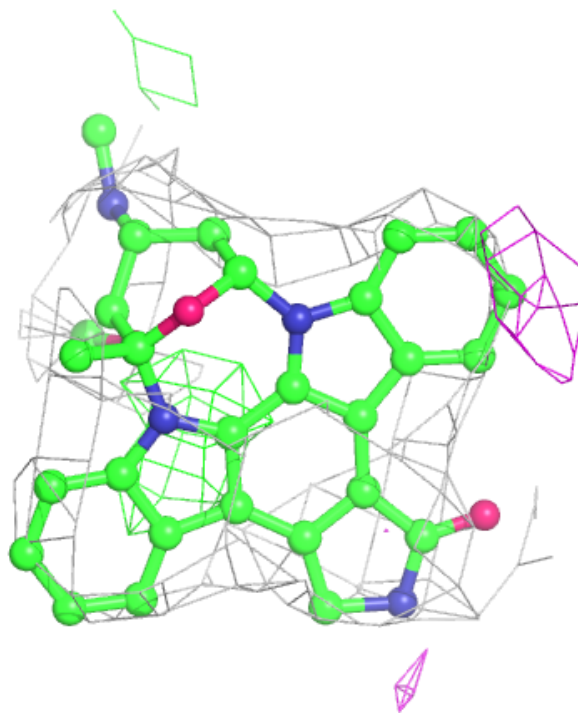
Electron density around AMP C 401:

$2mF_o-DF_c$ (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.