



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2022 – 01:08 am BST

PDB ID : 7Q1J
Title : Hybrid form of uridine phosphorylase from E. coli and Salmonella typhimurium
in the presence PEG
Authors : Safonova, T.; Polyakov, K.
Deposited on : 2021-10-20
Resolution : 1.71 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.27
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

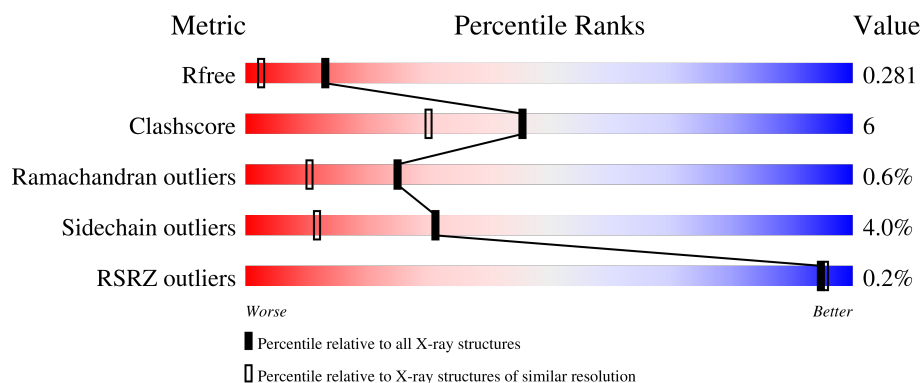
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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	AAA	250	
1	BBB	250	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4086 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 Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	250	Total	C	N	O	S	0	0	0
			1883	1180	329	363	11			
1	BBB	250	Total	C	N	O	S	0	3	0
			1893	1186	332	364	11			

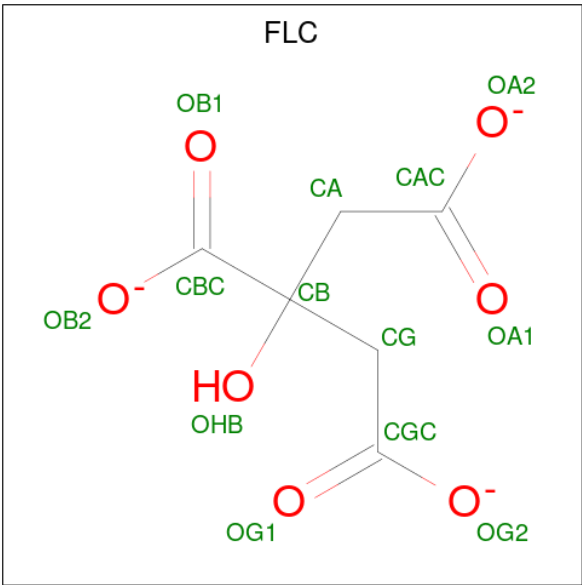
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	17	GLN	THR	conflict	UNP E6BNQ3
AAA	26	GLU	ASP	conflict	UNP E6BNQ3
BBB	17	GLN	THR	conflict	UNP E6BNQ3
BBB	26	GLU	ASP	conflict	UNP E6BNQ3

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	1	Total	K	0	0
			1	1		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	C	O	0	0
			13	6	7		
3	BBB	1	Total	C	O	0	0
			13	6	7		

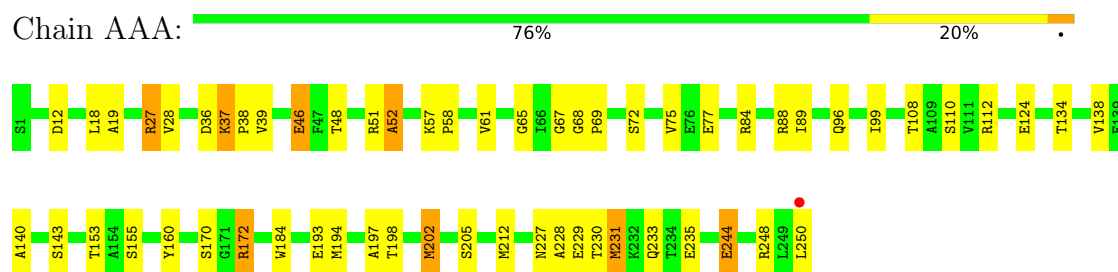
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	137	Total	O	0	0
			137	137		
4	BBB	146	Total	O	0	0
			146	146		

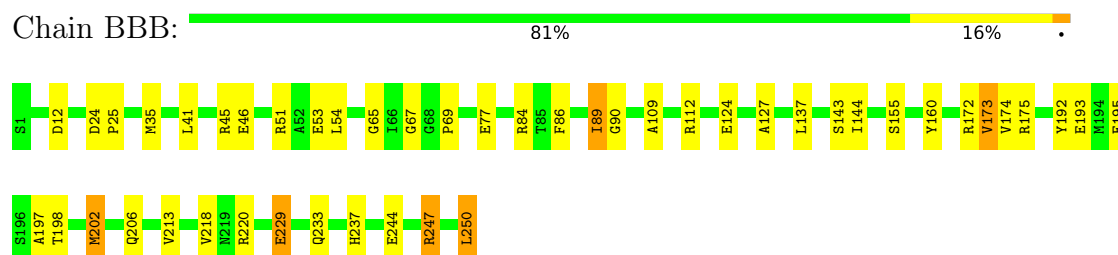
3 Residue-property plots [i](#)

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: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	150.59Å 150.59Å 46.29Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.71 33.74 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.00-1.71) 99.5 (33.74-1.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.71Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.204 , 0.281 0.204 , 0.281	Depositor DCC
R_{free} test set	2149 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.574	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.029 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4086	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, FLC

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	AAA	0.90	3/1915 (0.2%)	1.32	15/2598 (0.6%)
1	BBB	0.95	3/1939 (0.2%)	1.32	10/2630 (0.4%)
All	All	0.93	6/3854 (0.2%)	1.32	25/5228 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	BBB	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	124	GLU	CD-OE2	10.64	1.37	1.25
1	AAA	124	GLU	CD-OE1	9.30	1.35	1.25
1	BBB	77	GLU	CD-OE1	8.20	1.34	1.25
1	BBB	195	GLU	CD-OE1	-7.76	1.17	1.25
1	AAA	124	GLU	CD-OE2	5.34	1.31	1.25
1	AAA	46	GLU	CD-OE2	5.29	1.31	1.25

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	84	ARG	CG-CD-NE	-8.18	94.62	111.80
1	BBB	53	GLU	CB-CA-C	7.35	125.09	110.40
1	BBB	84	ARG	CG-CD-NE	-6.90	97.31	111.80
1	BBB	220	ARG	NE-CZ-NH1	-6.85	116.88	120.30
1	BBB	175	ARG	CG-CD-NE	6.51	125.46	111.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	202	MET	CG-SD-CE	6.09	109.95	100.20
1	AAA	27	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	AAA	248	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	AAA	75	VAL	CA-CB-CG1	5.92	119.79	110.90
1	BBB	45	ARG	CB-CA-C	5.83	122.05	110.40
1	AAA	12	ASP	CB-CA-C	-5.81	98.78	110.40
1	AAA	52	ALA	N-CA-CB	5.80	118.22	110.10
1	AAA	194	MET	CG-SD-CE	-5.70	91.08	100.20
1	AAA	77	GLU	CB-CA-C	5.56	121.52	110.40
1	BBB	173	VAL	CA-CB-CG1	5.43	119.05	110.90
1	AAA	108	THR	CA-CB-OG1	-5.41	97.64	109.00
1	AAA	248	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	BBB	112	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	AAA	48	THR	CA-CB-OG1	-5.24	97.99	109.00
1	AAA	112	ARG	CG-CD-NE	5.22	122.76	111.80
1	BBB	86	PHE	CB-CG-CD2	-5.22	117.15	120.80
1	AAA	172	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	AAA	202	MET	CG-SD-CE	5.15	108.44	100.20
1	AAA	184	TRP	C-N-CA	-5.14	108.85	121.70
1	BBB	192	TYR	CA-CB-CG	5.09	123.08	113.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BBB	173	VAL	Mainchain
1	BBB	174	VAL	Mainchain

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	AAA	1883	0	1890	27	0
1	BBB	1893	0	1905	27	0
2	AAA	1	0	0	0	0
3	AAA	13	0	5	0	0
3	BBB	13	0	5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AAA	137	0	0	0	0
4	BBB	146	0	0	7	0
All	All	4086	0	3805	49	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (49) 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:AAA:28:VAL:HG13	1:AAA:61:VAL:HG12	1.51	0.92
1:BBB:229:GLU:HB3	4:BBB:402:HOH:O	1.71	0.90
1:BBB:172[B]:ARG:NH1	4:BBB:401:HOH:O	2.14	0.80
1:BBB:155:SER:HB3	1:BBB:197:ALA:HB2	1.68	0.74
1:BBB:172[A]:ARG:NE	4:BBB:401:HOH:O	2.19	0.73
1:AAA:205:SER:O	1:BBB:172[A]:ARG:NH1	2.21	0.69
1:BBB:12:ASP:HB3	1:BBB:41:LEU:HD13	1.75	0.68
1:AAA:46:GLU:HB3	1:BBB:46:GLU:HB3	1.77	0.66
1:AAA:88:ARG:HB3	1:AAA:212:MET:HG3	1.82	0.62
1:BBB:89:ILE:HD13	1:BBB:90:GLY:N	2.15	0.61
1:AAA:96:GLN:HB2	1:AAA:99:ILE:HD12	1.81	0.61
1:AAA:27:ARG:HD3	1:AAA:235:GLU:OE2	2.02	0.59
1:AAA:37:LYS:N	1:AAA:38:PRO:CD	2.65	0.59
1:BBB:137:LEU:HD22	1:BBB:213:VAL:HB	1.85	0.59
1:AAA:198:THR:O	1:AAA:202:MET:HG2	2.04	0.56
1:BBB:172[A]:ARG:CZ	4:BBB:401:HOH:O	2.52	0.56
1:BBB:233:GLN:NE2	4:BBB:402:HOH:O	2.15	0.53
1:AAA:155:SER:HB3	1:AAA:197:ALA:HB2	1.89	0.53
1:AAA:67:GLY:HA3	1:BBB:69:PRO:HB2	1.90	0.53
1:BBB:172[A]:ARG:NH2	4:BBB:401:HOH:O	2.42	0.52
1:BBB:198:THR:O	1:BBB:202:MET:HG2	2.10	0.51
1:AAA:170:SER:HB3	1:BBB:206:GLN:HE21	1.75	0.49
1:BBB:244:GLU:OE2	1:BBB:247:ARG:NH1	2.43	0.49
1:AAA:39:VAL:HG11	1:AAA:51:ARG:NH2	2.27	0.49
1:AAA:69:PRO:HB2	1:BBB:67:GLY:HA3	1.96	0.48
1:AAA:72:SER:HA	1:AAA:202:MET:SD	2.54	0.47
1:BBB:89:ILE:HD13	1:BBB:89:ILE:C	2.35	0.47
1:AAA:37:LYS:N	1:AAA:38:PRO:HD2	2.30	0.47
1:AAA:228:ALA:HA	1:AAA:231:MET:HE3	1.96	0.47
1:AAA:36:ASP:O	1:AAA:37:LYS:HB2	2.16	0.45
1:BBB:12:ASP:O	1:BBB:51:ARG:HD3	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:51:ARG:HG2	1:AAA:52:ALA:N	2.31	0.45
1:BBB:35:MET:HG2	1:BBB:54:LEU:HD13	1.98	0.45
1:BBB:202:MET:HE3	1:BBB:202:MET:HB2	1.89	0.44
1:AAA:250:LEU:HD23	1:AAA:250:LEU:HA	1.78	0.44
1:BBB:109:ALA:HA	1:BBB:127:ALA:O	2.18	0.44
1:AAA:233:GLN:HE21	1:AAA:233:GLN:HB2	1.40	0.44
1:AAA:68:GLY:HA3	1:AAA:198:THR:OG1	2.18	0.44
1:AAA:140:ALA:HB1	1:AAA:244:GLU:HB3	1.98	0.44
1:AAA:134:THR:O	1:AAA:138:VAL:HG23	2.18	0.43
1:AAA:46:GLU:HG3	1:AAA:65:GLY:HA3	1.98	0.43
1:BBB:172[B]:ARG:CZ	4:BBB:401:HOH:O	2.60	0.43
1:BBB:250:LEU:HD12	1:BBB:250:LEU:HA	1.89	0.43
1:BBB:24:ASP:OD1	1:BBB:25:PRO:HD2	2.19	0.42
1:AAA:110:SER:HA	1:AAA:153:THR:O	2.20	0.41
1:AAA:57:LYS:HA	1:AAA:58:PRO:HD3	1.92	0.41
1:BBB:46:GLU:HG3	1:BBB:65:GLY:HA3	2.02	0.41
1:AAA:18:LEU:HD23	1:AAA:19:ALA:N	2.35	0.41
1:BBB:144:ILE:HD12	1:BBB:237:HIS:CD2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	248/250 (99%)	236 (95%)	10 (4%)	2 (1%)	19	6
1	BBB	251/250 (100%)	245 (98%)	5 (2%)	1 (0%)	34	18
All	All	499/500 (100%)	481 (96%)	15 (3%)	3 (1%)	25	10

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	160	TYR
1	BBB	160	TYR
1	AAA	37	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	201/201 (100%)	192 (96%)	9 (4%)	27	9
1	BBB	204/201 (102%)	196 (96%)	8 (4%)	32	12
All	All	405/402 (101%)	388 (96%)	17 (4%)	31	11

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	89	ILE
1	AAA	143	SER
1	AAA	172	ARG
1	AAA	193	GLU
1	AAA	227	ASN
1	AAA	229	GLU
1	AAA	230	THR
1	AAA	231	MET
1	AAA	244	GLU
1	BBB	89	ILE
1	BBB	143	SER
1	BBB	193	GLU
1	BBB	218[A]	VAL
1	BBB	218[B]	VAL
1	BBB	229	GLU
1	BBB	247	ARG
1	BBB	250	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
3	FLC	AAA	302	-	3,12,12	0.24	0	3,17,17	1.45	0
3	FLC	BBB	301	-	3,12,12	0.36	0	3,17,17	1.01	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
3	FLC	AAA	302	-	-	1/6/16/16	-
3	FLC	BBB	301	-	-	3/6/16/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

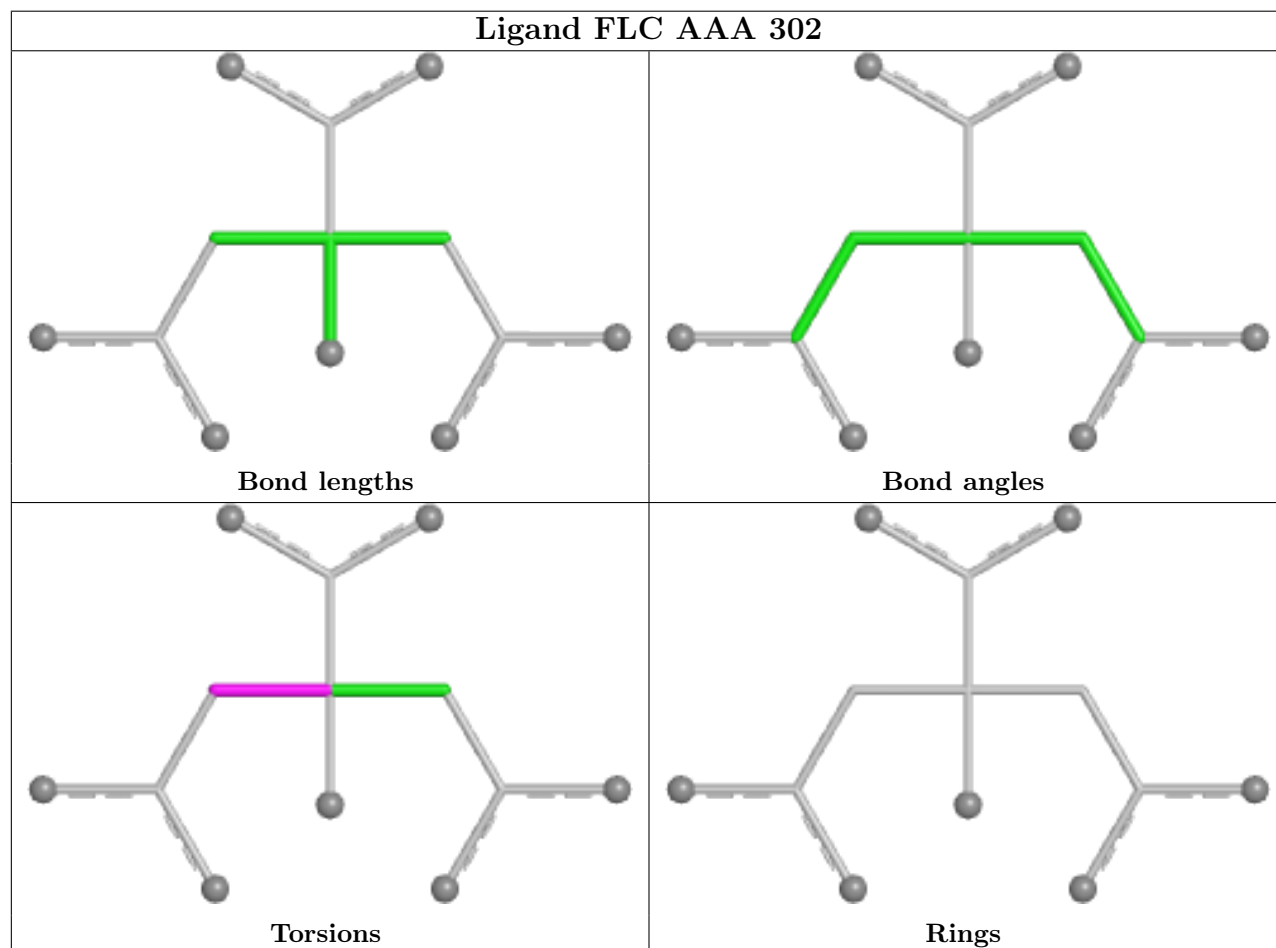
All (4) torsion outliers are listed below:

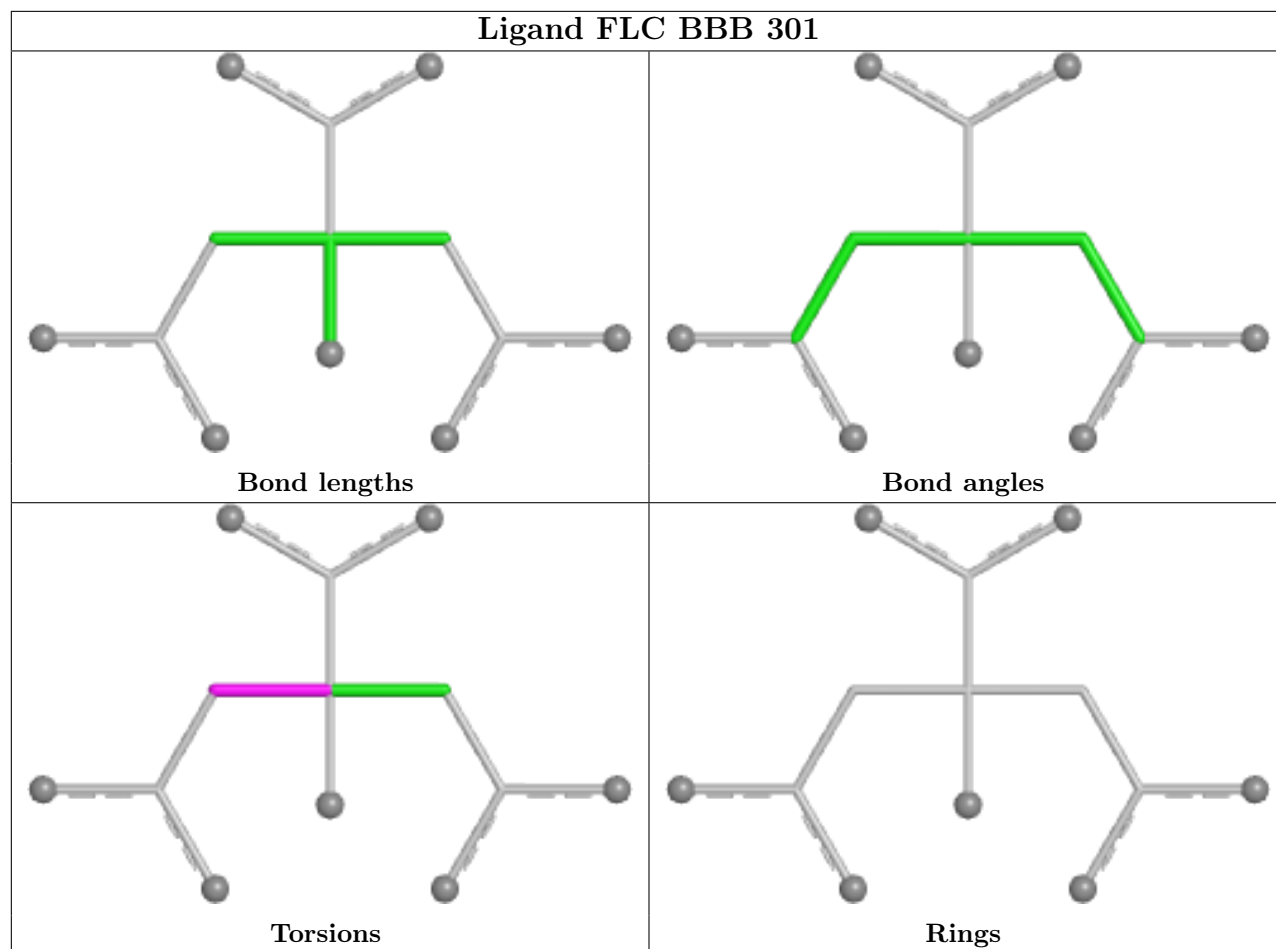
Mol	Chain	Res	Type	Atoms
3	BBB	301	FLC	CAC-CA-CB-CBC
3	BBB	301	FLC	CAC-CA-CB-CG
3	BBB	301	FLC	CAC-CA-CB-OHB
3	AAA	302	FLC	CAC-CA-CB-CG

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	AAA	250/250 (100%)	-0.18	1 (0%) 92 93	15, 24, 43, 54	0
1	BBB	250/250 (100%)	-0.11	0 100 100	14, 24, 40, 62	0
All	All	500/500 (100%)	-0.15	1 (0%) 95 95	14, 24, 42, 62	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	250	LEU	2.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

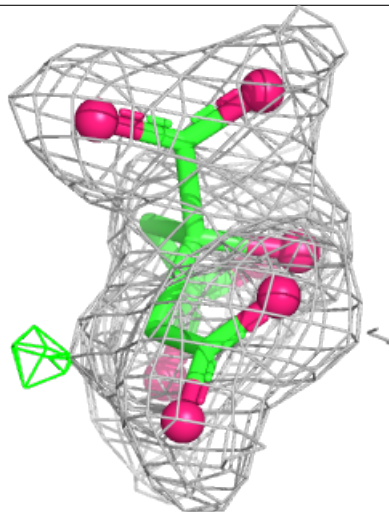
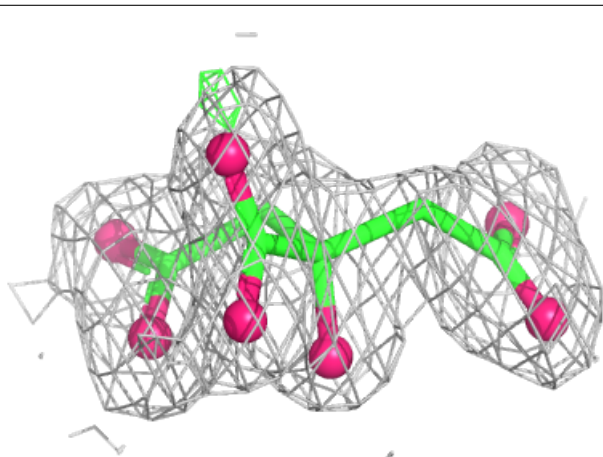
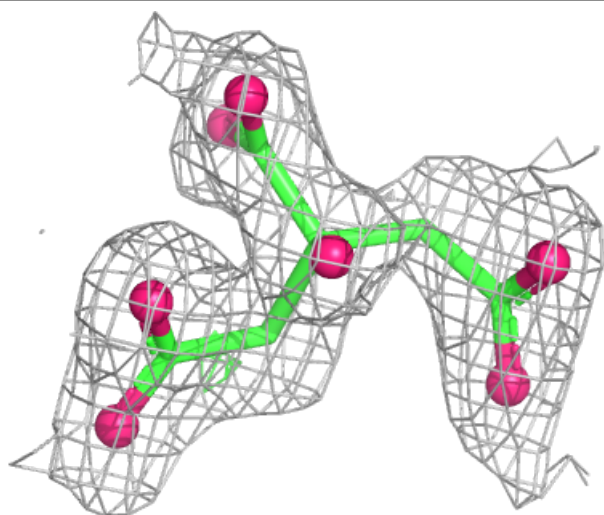
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FLC	AAA	302	13/13	0.88	0.10	30,35,38,38	0
3	FLC	BBB	301	13/13	0.92	0.09	29,35,45,47	0
2	K	AAA	301	1/1	1.00	0.09	23,23,23,23	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.

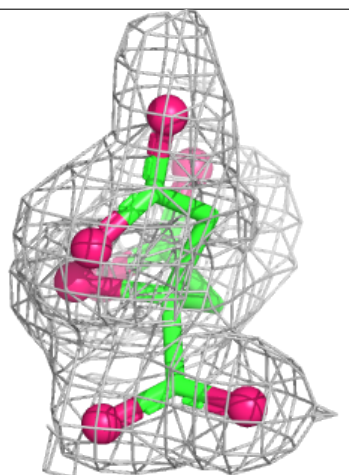
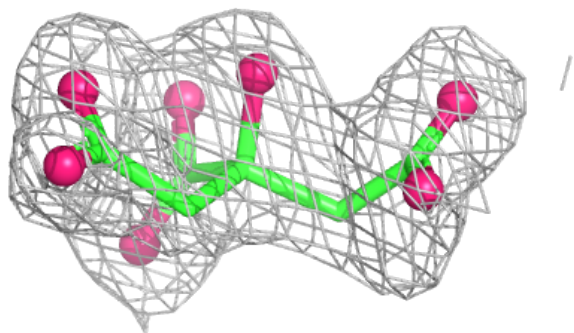
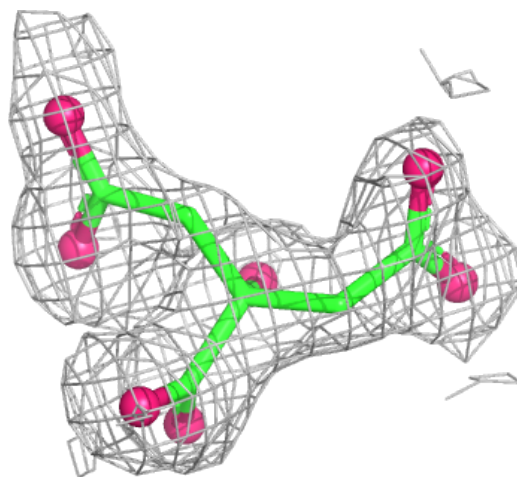
Electron density around FLC AAA 302:

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



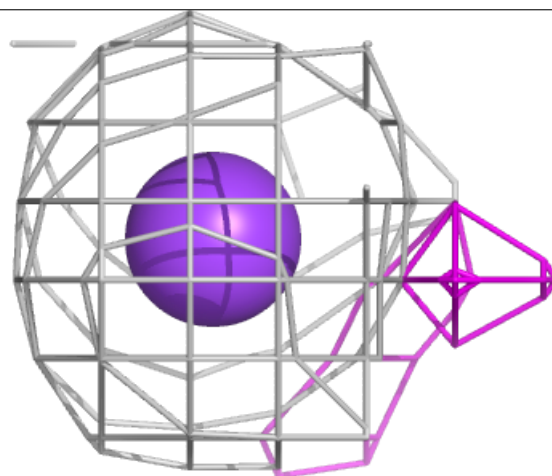
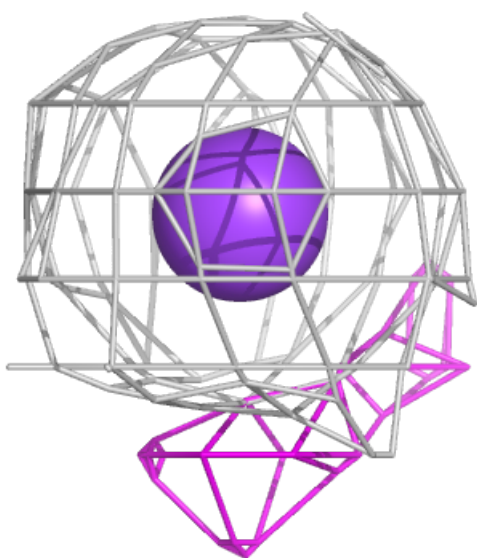
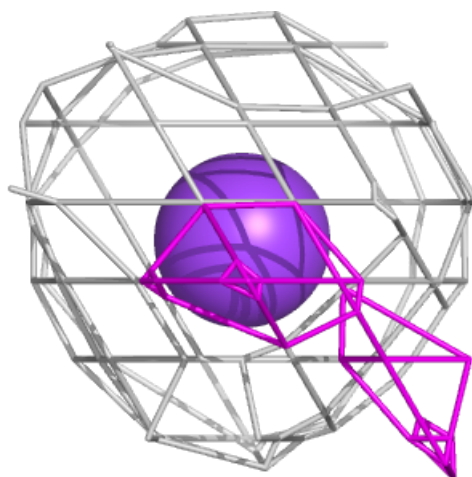
Electron density around FLC BBB 301:

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



Electron density around K AAA 301:

$2mF_o-DF_c$ (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.