



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 3, 2025 – 09:06 am GMT

PDB ID : 9GUK
Title : Crystal structure of transcription factor NtcA from *Synechococcus elongatus* in complex with its transcriptional co- activator PipX and its target DNA (Crystal I)
Authors : Forcada-Nadal, A.; Llacer, J.L.; Rubio, V.
Deposited on : 2024-09-19
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 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	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41

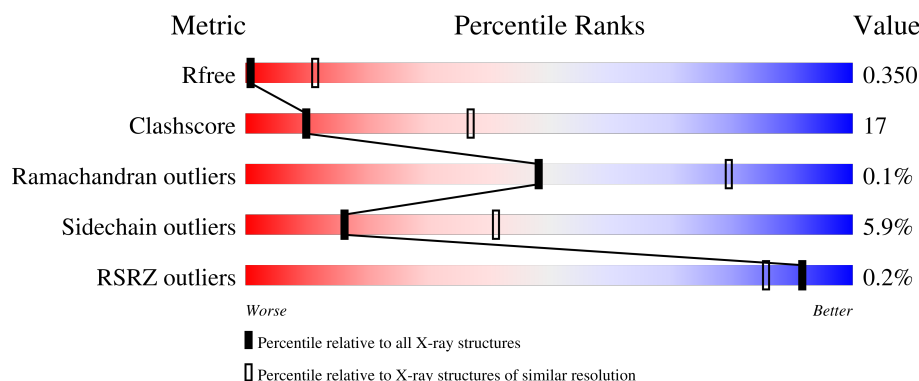
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




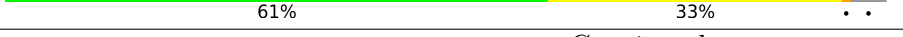
The reported resolution of this entry is 3.80 Å.

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}	164625	1025 (3.98-3.62)
Clashscore	180529	1005 (3.96-3.64)
Ramachandran outliers	177936	1044 (3.98-3.62)
Sidechain outliers	177891	1039 (3.98-3.62)
RSRZ outliers	164620	1025 (3.98-3.62)

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	222	
1	B	222	
1	D	222	
1	F	222	

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Mol	Chain	Length	Quality of chain
2	C	31	<div><div></div><div>48%48%</div><div></div></div>
2	G	31	<div><div></div><div>45%52%</div><div></div></div>
2	I	31	<div><div></div><div>42%55%</div><div></div></div>
2	K	31	<div><div></div><div>61%35%</div><div></div></div>
3	E	89	<div><div></div><div>66%24%6%</div><div></div></div>
3	H	89	<div><div></div><div>69%26%</div><div></div></div>
3	J	89	<div><div></div><div>%72%19%6%</div><div></div></div>
3	L	89	<div><div></div><div>%69%21%6%</div><div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12043 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 Global nitrogen regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	213	Total	C	N	O	S	0	0	0
			1669	1072	288	302	7			
1	F	213	Total	C	N	O	S	0	0	0
			1681	1082	290	302	7			
1	A	212	Total	C	N	O	S	0	0	0
			1664	1071	286	300	7			
1	B	213	Total	C	N	O	S	0	0	0
			1681	1082	290	302	7			

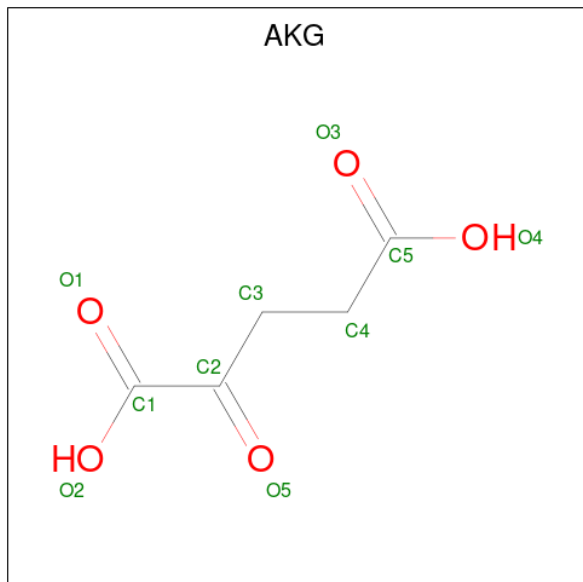
- Molecule 2 is a DNA chain called DNA (30-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	30	Total	C	N	O	P	0	0	0
			615	297	108	180	30			
2	I	30	Total	C	N	O	P	0	0	0
			615	297	108	180	30			
2	C	30	Total	C	N	O	P	0	0	0
			615	297	108	180	30			
2	K	30	Total	C	N	O	P	0	0	0
			615	297	108	180	30			

- Molecule 3 is a protein called PipX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	J	84	Total	C	N	O	S	0	0	0
			707	454	128	123	2			
3	H	86	Total	C	N	O	S	0	0	0
			720	463	130	125	2			
3	L	85	Total	C	N	O	S	0	0	0
			712	457	129	124	2			
3	E	85	Total	C	N	O	S	0	0	0
			709	457	126	124	2			

- Molecule 4 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: $C_5H_6O_5$) (labeled as "Ligand of Interest" by depositor).

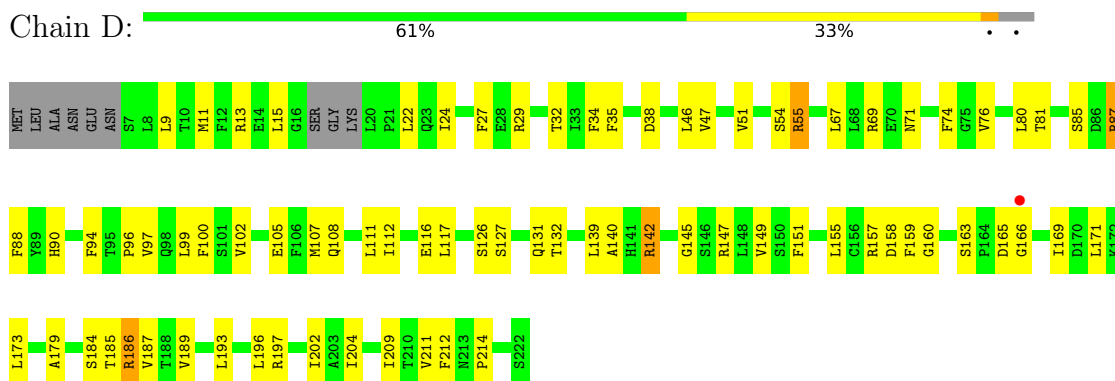


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			10	5	5		
4	F	1	Total	C	O	0	0
			10	5	5		
4	A	1	Total	C	O	0	0
			10	5	5		
4	B	1	Total	C	O	0	0
			10	5	5		

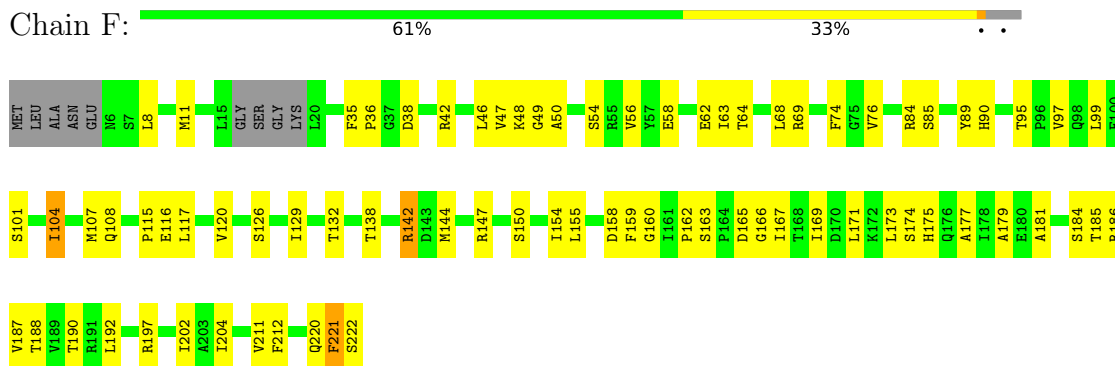
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

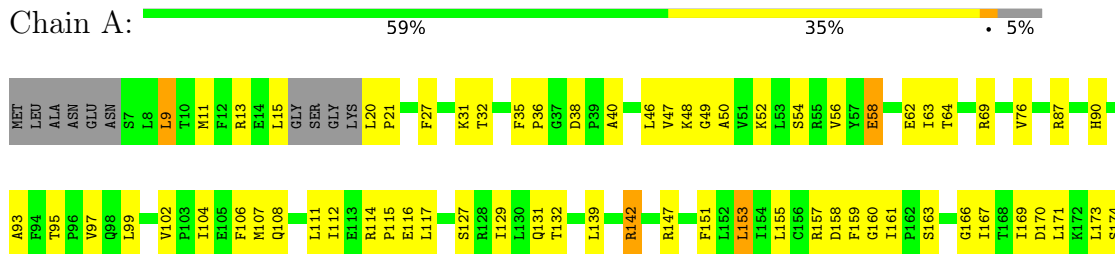
- Molecule 1: Global nitrogen regulator



- Molecule 1: Global nitrogen regulator



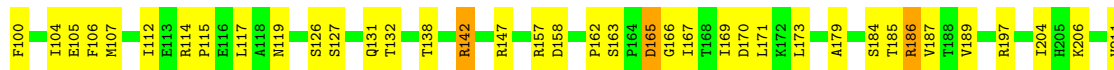
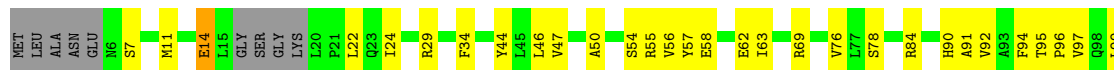
- Molecule 1: Global nitrogen regulator





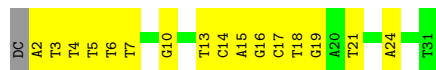
- Molecule 1: Global nitrogen regulator

Chain B: 63% 31% . .



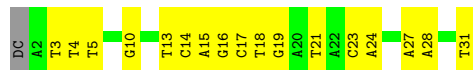
- Molecule 2: DNA (30-MER)

Chain G: 45% 52% .



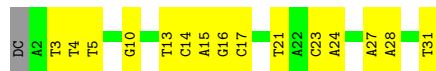
- Molecule 2: DNA (30-MER)

Chain I: 42% 55% .



- Molecule 2: DNA (30-MER)

Chain C: 48% 48% .



- Molecule 2: DNA (30-MER)

Chain K: 61% 35% .



- Molecule 3: PipX

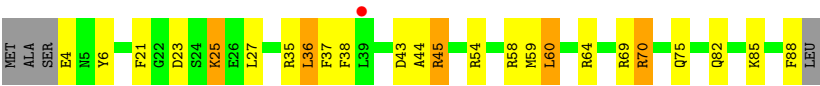
Chain J: % 72% 19% 6% . .



● Molecule 3: PipX



● Molecule 3: PipX



● Molecule 3: PipX



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.26Å 68.18Å 126.25Å 90.00° 115.07° 90.00°	Depositor
Resolution (Å)	64.14 – 3.80 64.14 – 3.80	Depositor EDS
% Data completeness (in resolution range)	91.6 (64.14-3.80) 91.6 (64.14-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 3.77Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.315 , 0.354 0.308 , 0.350	Depositor DCC
R_{free} test set	888 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	69.6	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	0.084 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12043	wwPDB-VP
Average B, all atoms (Å ²)	71.0	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 77.50 % 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 8.4072e-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: AKG

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	0.58	0/1691	0.74	0/2285
1	B	0.54	0/1708	0.70	0/2305
1	D	0.56	0/1696	0.72	0/2291
1	F	0.59	0/1708	0.74	0/2305
2	C	0.59	0/689	0.89	0/1061
2	G	0.56	0/689	0.88	0/1061
2	I	0.60	0/689	0.86	0/1061
2	K	0.56	0/689	0.90	0/1061
3	E	0.58	0/723	0.72	0/972
3	H	0.51	0/735	0.71	0/989
3	J	0.58	0/721	0.76	0/968
3	L	0.53	0/727	0.73	0/978
All	All	0.57	0/12465	0.77	0/17337

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	D	0	1
3	E	0	1
3	H	0	1
3	J	0	1
3	L	0	2
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	87	ARG	Sidechain
3	H	66	ARG	Sidechain
3	J	70	ARG	Sidechain
3	L	64	ARG	Sidechain
3	L	70	ARG	Sidechain

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	1664	0	1723	78	0
1	B	1681	0	1753	65	0
1	D	1669	0	1723	99	0
1	F	1681	0	1753	78	0
2	C	615	0	343	17	0
2	G	615	0	343	16	0
2	I	615	0	343	15	0
2	K	615	0	343	11	0
3	E	709	0	692	14	0
3	H	720	0	706	16	0
3	J	707	0	692	13	0
3	L	712	0	695	16	0
4	A	10	0	4	0	0
4	B	10	0	4	0	0
4	D	10	0	4	1	0
4	F	10	0	4	2	0
All	All	12043	0	11125	396	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 396 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:D:171:LEU:CD1	1:D:173:LEU:HG	1.63	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:171:LEU:HD11	1:D:173:LEU:CD1	1.68	1.22
1:B:11:MET:HB3	1:B:117:LEU:HD13	1.18	1.15
1:D:46:LEU:CD1	1:D:97:VAL:CG2	2.25	1.14
1:B:78:SER:HB2	1:B:104:ILE:HG21	1.21	1.12

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	208/222 (94%)	201 (97%)	7 (3%)	0	100	100
1	B	209/222 (94%)	200 (96%)	9 (4%)	0	100	100
1	D	209/222 (94%)	203 (97%)	6 (3%)	0	100	100
1	F	209/222 (94%)	201 (96%)	8 (4%)	0	100	100
3	E	81/89 (91%)	77 (95%)	4 (5%)	0	100	100
3	H	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
3	J	80/89 (90%)	78 (98%)	2 (2%)	0	100	100
3	L	83/89 (93%)	78 (94%)	4 (5%)	1 (1%)	11	40
All	All	1163/1244 (94%)	1120 (96%)	42 (4%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	23	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	184/194 (95%)	176 (96%)	8 (4%)	25	49
1	B	187/194 (96%)	176 (94%)	11 (6%)	16	41
1	D	184/194 (95%)	177 (96%)	7 (4%)	28	52
1	F	187/194 (96%)	182 (97%)	5 (3%)	40	60
3	E	73/78 (94%)	62 (85%)	11 (15%)	2	14
3	H	74/78 (95%)	68 (92%)	6 (8%)	9	32
3	J	73/78 (94%)	70 (96%)	3 (4%)	26	50
3	L	73/78 (94%)	63 (86%)	10 (14%)	3	17
All	All	1035/1088 (95%)	974 (94%)	61 (6%)	16	41

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	186	ARG
3	E	67	GLN
1	B	119	ASN
3	E	66	ARG
3	E	76	GLU

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

Mol	Chain	Res	Type
1	D	108	GLN
1	F	119	ASN
1	F	123	GLN

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 oligosaccharides in this entry.

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	$\# Z > 2$
4	AKG	F	301	-	9,9,9	2.14	1 (11%)	11,11,11	2.06	3 (27%)
4	AKG	B	501	-	9,9,9	1.94	2 (22%)	11,11,11	1.48	2 (18%)
4	AKG	D	301	-	9,9,9	2.14	2 (22%)	11,11,11	1.47	2 (18%)
4	AKG	A	500	-	9,9,9	1.48	2 (22%)	11,11,11	1.67	2 (18%)

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	AKG	F	301	-	-	0/9/9/9	-
4	AKG	B	501	-	-	0/9/9/9	-
4	AKG	D	301	-	-	1/9/9/9	-
4	AKG	A	500	-	-	0/9/9/9	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	301	AKG	C2-C1	-5.85	1.45	1.53
4	D	301	AKG	C2-C1	-5.06	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	AKG	C2-C1	-4.20	1.48	1.53
4	A	500	AKG	C2-C1	-2.71	1.50	1.53
4	D	301	AKG	O4-C5	-2.41	1.22	1.30

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	301	AKG	O1-C1-C2	-4.33	115.93	121.72
4	F	301	AKG	C3-C2-C1	3.52	122.50	115.97
4	A	500	AKG	C3-C2-C1	2.94	121.44	115.97
4	B	501	AKG	C3-C2-C1	2.73	121.05	115.97
4	D	301	AKG	C3-C2-C1	2.64	120.86	115.97

There are no chirality outliers.

All (1) torsion outliers are listed below:

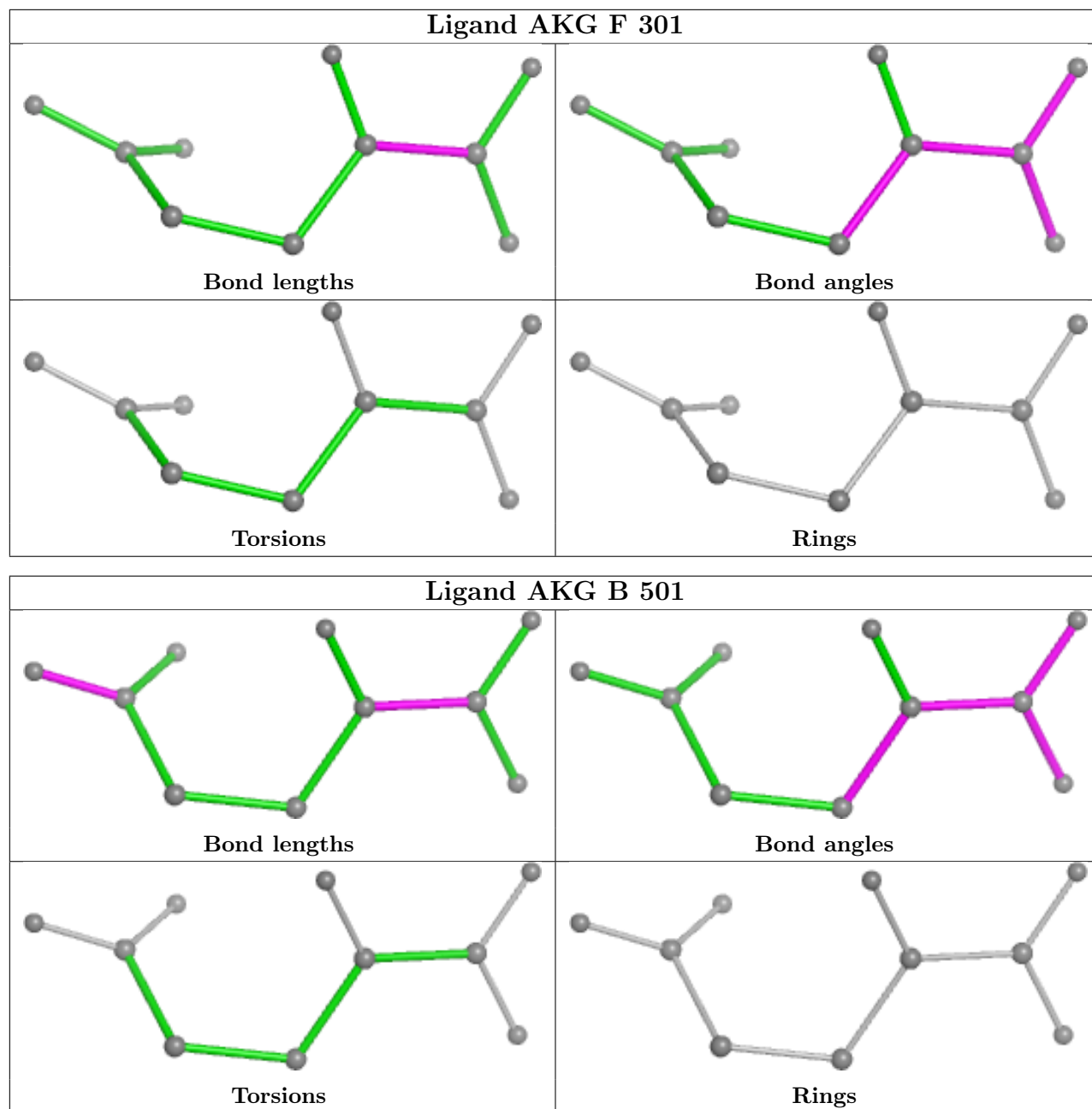
Mol	Chain	Res	Type	Atoms
4	D	301	AKG	C2-C3-C4-C5

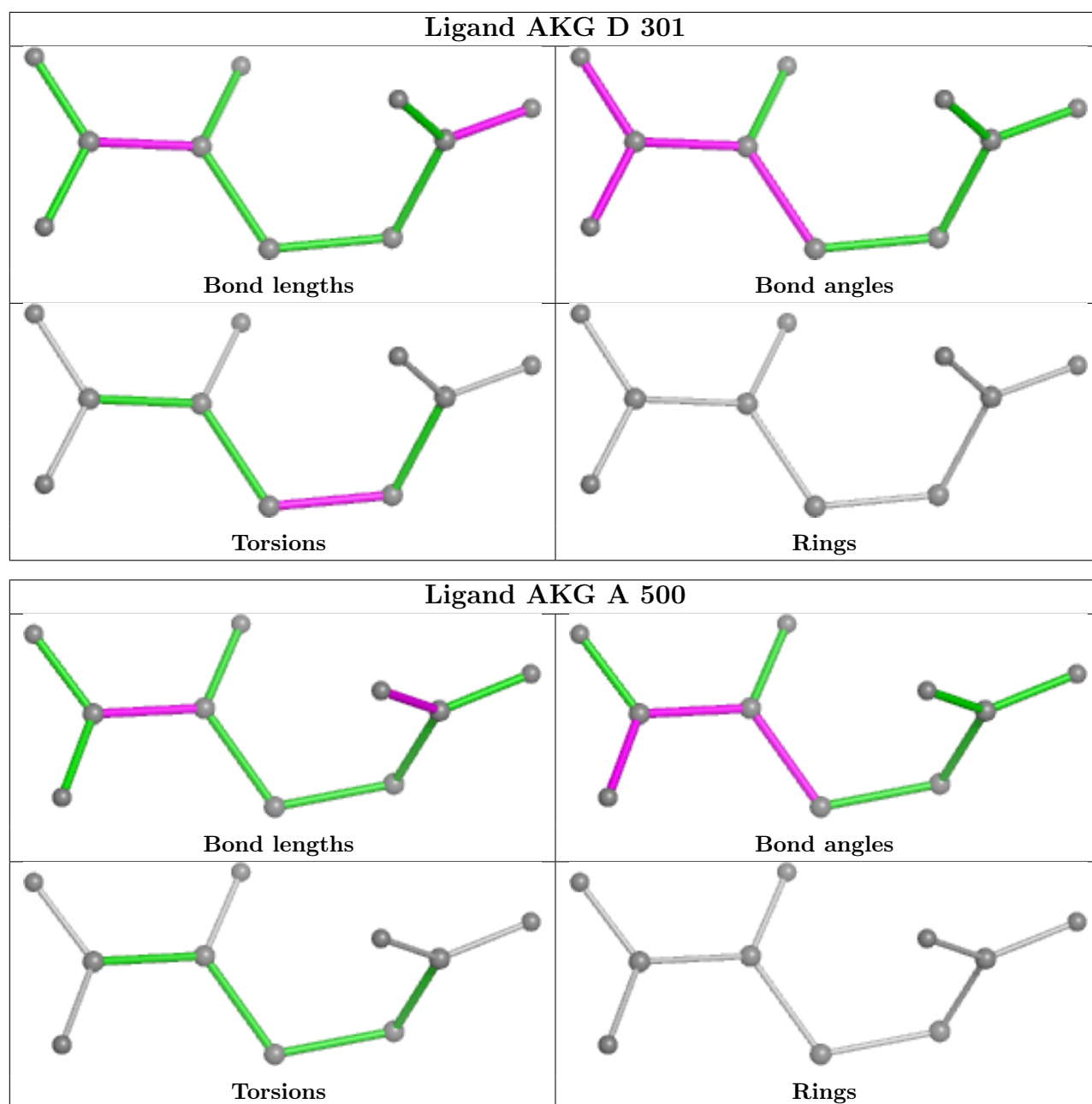
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	301	AKG	2	0
4	D	301	AKG	1	0

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





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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	212/222 (95%)	-0.59	0	100	100	44, 63, 95, 105	0
1	B	213/222 (95%)	-0.60	0	100	100	45, 68, 93, 129	0
1	D	213/222 (95%)	-0.54	1 (0%)	87	75	46, 68, 95, 117	0
1	F	213/222 (95%)	-0.61	0	100	100	42, 62, 95, 103	0
2	C	30/31 (96%)	-0.82	0	100	100	64, 79, 93, 104	0
2	G	30/31 (96%)	-0.77	0	100	100	59, 74, 95, 103	0
2	I	30/31 (96%)	-0.79	0	100	100	63, 80, 93, 102	0
2	K	30/31 (96%)	-0.70	0	100	100	62, 82, 105, 115	0
3	E	85/89 (95%)	-0.60	0	100	100	48, 70, 104, 114	0
3	H	86/89 (96%)	-0.63	0	100	100	53, 72, 104, 119	0
3	J	84/89 (94%)	-0.45	1 (1%)	76	60	49, 75, 95, 121	0
3	L	85/89 (95%)	-0.55	1 (1%)	76	60	46, 70, 98, 112	0
All	All	1311/1368 (95%)	-0.60	3 (0%)	92	86	42, 68, 97, 129	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	39	LEU	2.3
1	D	166	GLY	2.2
3	J	22	GLY	2.2

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

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

6.3 Carbohydrates [i](#)

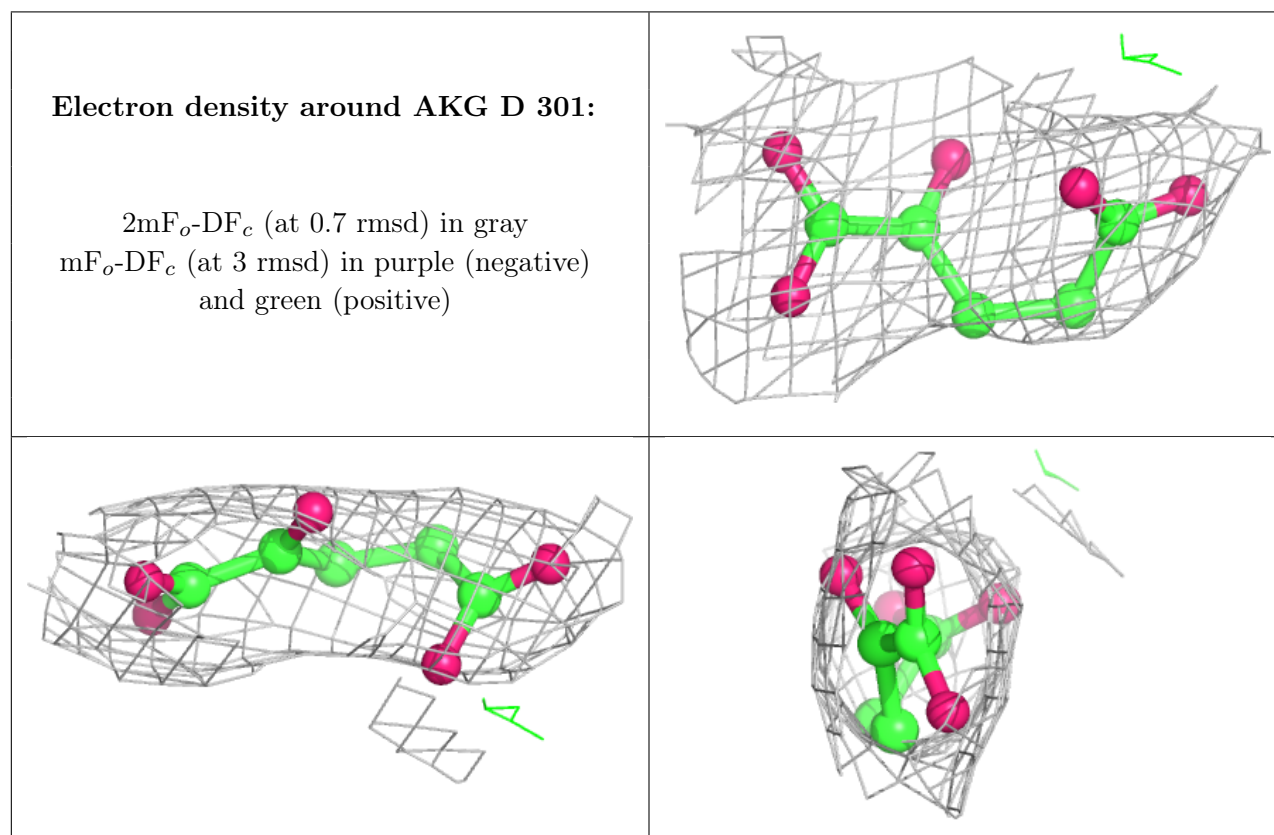
There are no monosaccharides in this entry.

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.

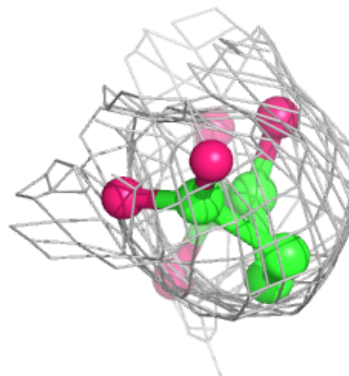
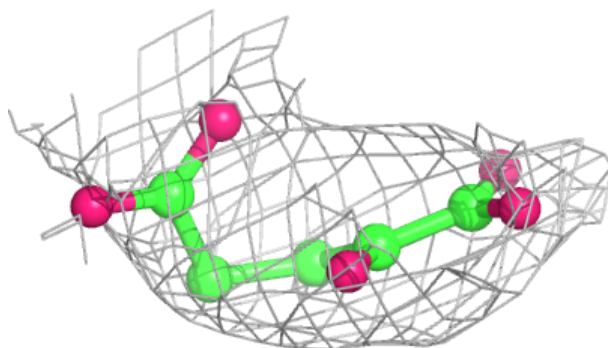
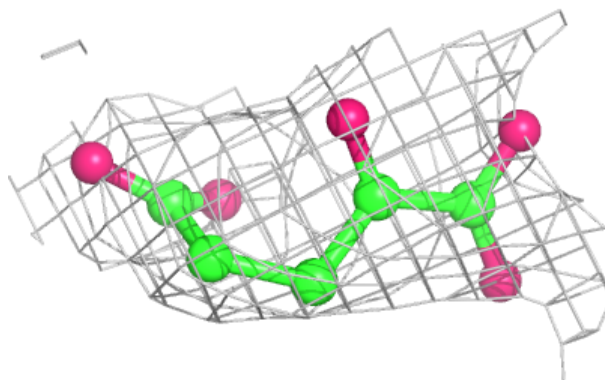
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	AKG	D	301	10/10	0.96	0.07	44,50,56,58	0
4	AKG	F	301	10/10	0.96	0.11	48,54,62,63	0
4	AKG	A	500	10/10	0.96	0.11	51,60,63,64	0
4	AKG	B	501	10/10	0.97	0.07	42,51,59,60	0

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.

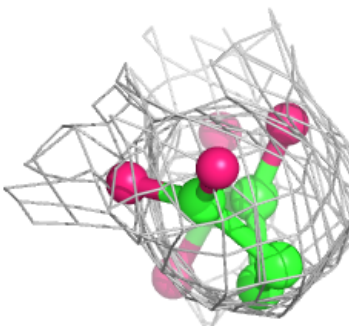
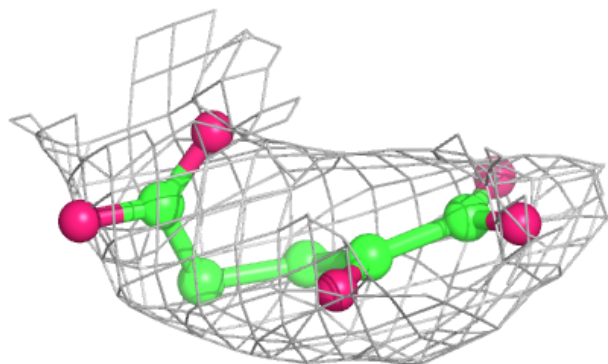
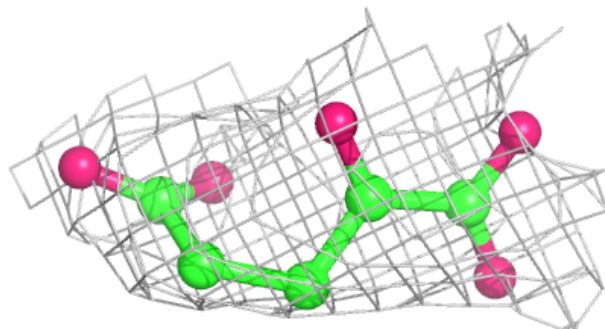


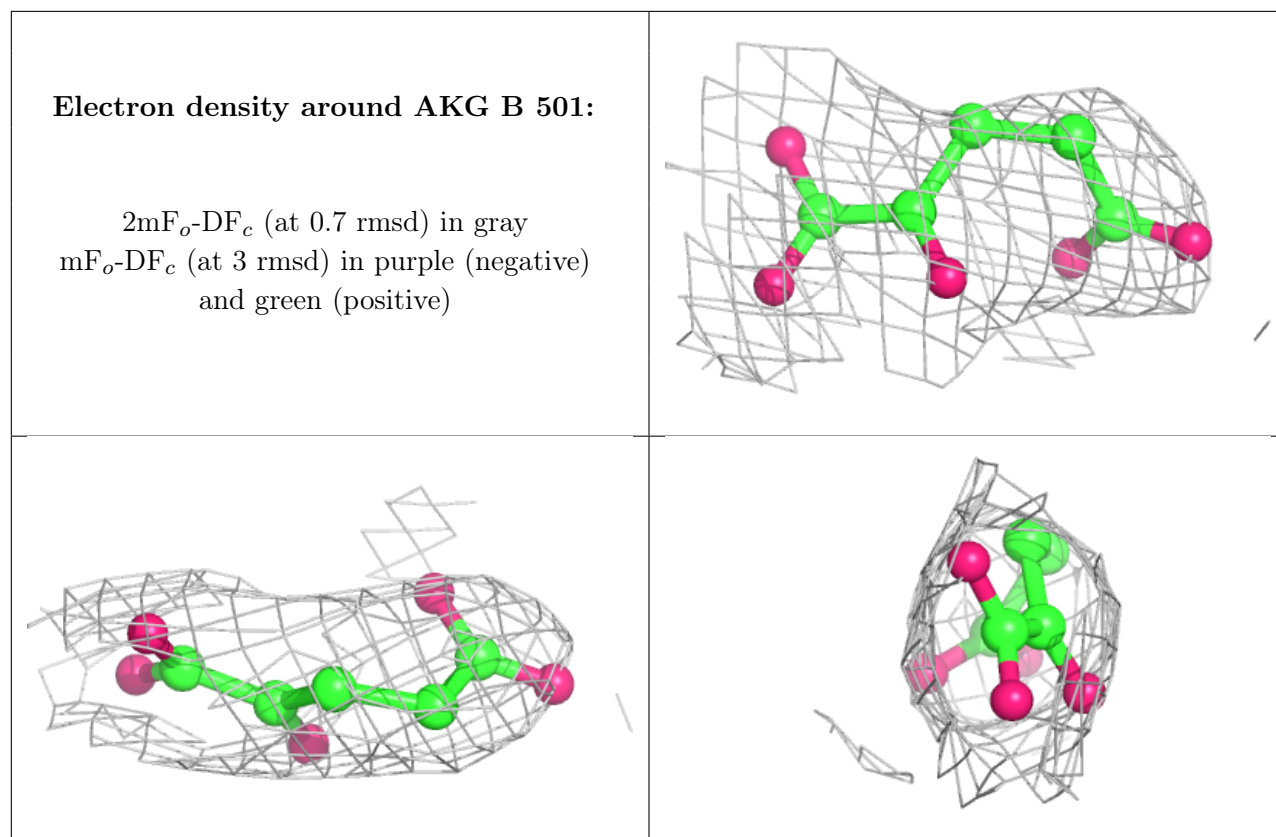
Electron density around AKG F 301:

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

**Electron density around AKG A 500:**

$2mF_o-DF_c$ (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.