wwPDB X-ray Structure Validation Summary Report (i)

Jan 20, 2024 – 12:53 pm GMT

PDB ID	:	7PDB
Title	:	Crystal structure of Lymnaea stagnalis Acetylcholine-binding protein (Ls-AChBP) Q55R/M114V double mutant complexed with Flupyradifurone
Authors	:	Montgomery, M.G.
Deposited on	:	2021-08-05
Resolution	:	2.33 Å(reported)

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

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

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

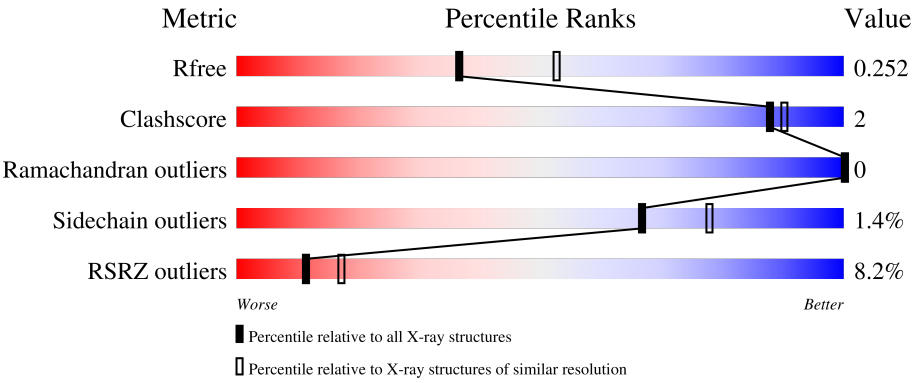
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.33 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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

Mol	Chain	Length	Quality of chain
1	AaA	210	11% 94% 6%
1	BaB	210	6% 93%
1	CaC	210	12% 93% 6%
1	DaD	210	4% 93% 6%
1	EaE	210	6% 93% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8091 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 Acetylcholine-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AaA	198	Total	C	N	O	S	0	0	0
			1584	995	273	312	4			
1	BaB	201	Total	C	N	O	S	0	0	0
			1605	1006	279	316	4			
1	CaC	197	Total	C	N	O	S	0	0	0
			1577	991	272	310	4			
1	DaD	198	Total	C	N	O	S	0	0	0
			1584	995	273	312	4			
1	EaE	200	Total	C	N	O	S	0	1	0
			1607	1008	281	314	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AaA	1	ALA	-	expression tag	UNP P58154
AaA	55	ARG	GLN	engineered mutation	UNP P58154
AaA	66	ASP	ASN	engineered mutation	UNP P58154
AaA	114	VAL	MET	engineered mutation	UNP P58154
BaB	1	ALA	-	expression tag	UNP P58154
BaB	55	ARG	GLN	engineered mutation	UNP P58154
BaB	66	ASP	ASN	engineered mutation	UNP P58154
BaB	114	VAL	MET	engineered mutation	UNP P58154
CaC	1	ALA	-	expression tag	UNP P58154
CaC	55	ARG	GLN	engineered mutation	UNP P58154
CaC	66	ASP	ASN	engineered mutation	UNP P58154
CaC	114	VAL	MET	engineered mutation	UNP P58154
DaD	1	ALA	-	expression tag	UNP P58154
DaD	55	ARG	GLN	engineered mutation	UNP P58154
DaD	66	ASP	ASN	engineered mutation	UNP P58154
DaD	114	VAL	MET	engineered mutation	UNP P58154
EaE	1	ALA	-	expression tag	UNP P58154
EaE	55	ARG	GLN	engineered mutation	UNP P58154
EaE	66	ASP	ASN	engineered mutation	UNP P58154

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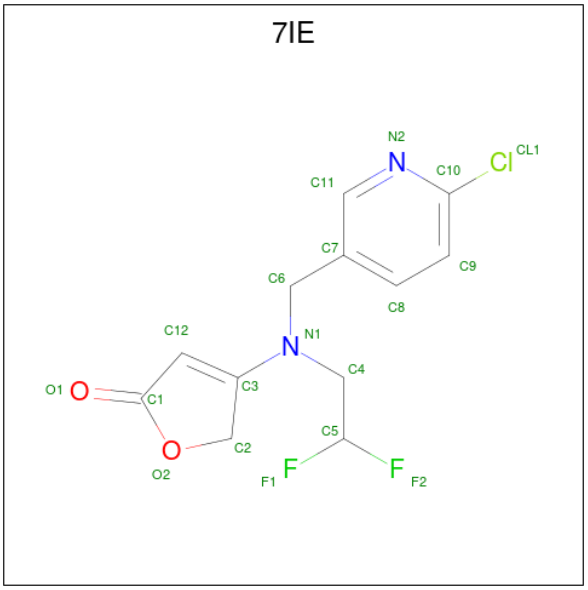
Chain	Residue	Modelled	Actual	Comment	Reference
EaE	114	VAL	MET	engineered mutation	UNP P58154

- Molecule 2 is Flupyradifurone (three-letter code: 7IE) (formula: $C_{12}H_{11}ClF_2N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AaA	1	Total	C	Cl	F	N	O	0	0
			19	12	1	2	2	2		
2	BaB	1	Total	C	Cl	F	N	O	0	0
			19	12	1	2	2	2		
2	CaC	1	Total	C	Cl	F	N	O	0	0
			19	12	1	2	2	2		
2	DaD	1	Total	C	Cl	F	N	O	0	0
			19	12	1	2	2	2		
2	EaE	1	Total	C	Cl	F	N	O	0	0
			19	12	1	2	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AaA	7	Total	O	0	0
			7	7		
3	BaB	12	Total	O	0	0
			12	12		
3	CaC	4	Total	O	0	0
			4	4		

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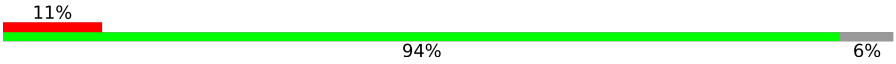
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	DaD	7	Total O 7 7	0	0
3	EaE	9	Total O 9 9	0	0

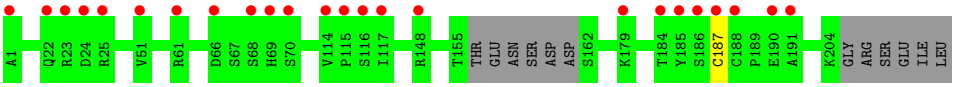
3 Residue-property plots (i)

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: Acetylcholine-binding protein

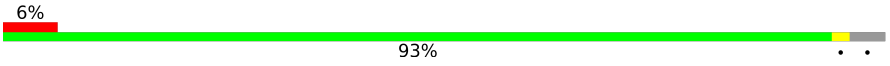
Chain AaA:

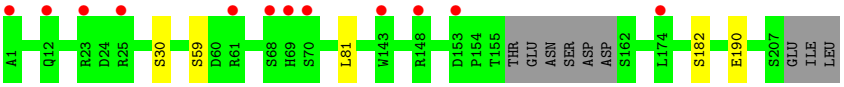




- Molecule 1: Acetylcholine-binding protein

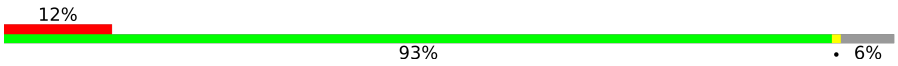
Chain BaB:

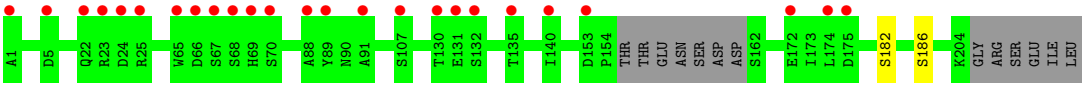




- Molecule 1: Acetylcholine-binding protein

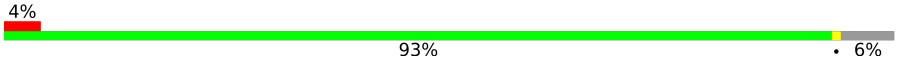
Chain CaC:

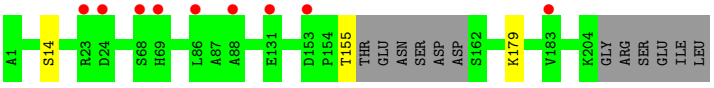




- Molecule 1: Acetylcholine-binding protein

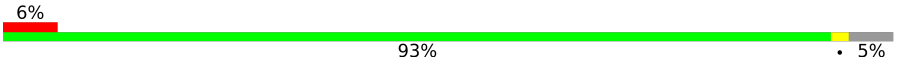
Chain DaD:

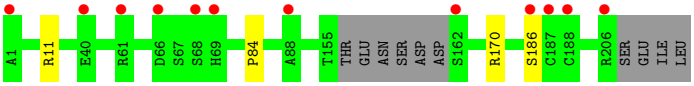




- Molecule 1: Acetylcholine-binding protein

Chain EaE:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	73.69Å 73.69Å 348.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.12 – 2.33 31.12 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.8 (31.12-2.33) 99.8 (31.12-2.33)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.19 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.224 , 0.256 0.227 , 0.252	Depositor DCC
R_{free} test set	2204 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	45.4	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 26.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.095 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8091	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 7IE

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	0.76	0/1619	0.92	1/2209 (0.0%)
1	BaB	0.78	0/1640	0.92	0/2236
1	CaC	0.78	0/1612	0.89	0/2199
1	DaD	0.80	0/1619	0.90	0/2209
1	EaE	0.78	0/1645	0.91	1/2242 (0.0%)
All	All	0.78	0/8135	0.91	2/11095 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AaA	187	CYS	CB-CA-C	-7.32	95.77	110.40
1	EaE	170	ARG	CG-CD-NE	5.54	123.42	111.80

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	AaA	1584	0	1542	0	0
1	BaB	1605	0	1563	0	0
1	CaC	1577	0	1535	0	0
1	DaD	1584	0	1542	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EaE	1607	0	1573	0	0
2	AaA	19	0	0	0	0
2	BaB	19	0	0	0	0
2	CaC	19	0	0	0	0
2	DaD	19	0	0	0	0
2	EaE	19	0	0	0	0
3	AaA	7	0	0	0	0
3	BaB	12	0	0	0	0
3	CaC	4	0	0	0	0
3	DaD	7	0	0	0	0
3	EaE	9	0	0	0	0
All	All	8091	0	7755	0	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 2.

There are no clashes within the asymmetric unit.

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	194/210 (92%)	193 (100%)	1 (0%)	0	100	100
1	BaB	197/210 (94%)	195 (99%)	2 (1%)	0	100	100
1	CaC	193/210 (92%)	192 (100%)	1 (0%)	0	100	100
1	DaD	194/210 (92%)	193 (100%)	1 (0%)	0	100	100
1	EaE	197/210 (94%)	196 (100%)	1 (0%)	0	100	100
All	All	975/1050 (93%)	969 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	AaA	184/195 (94%)	184 (100%)	0	100	100
1	BaB	186/195 (95%)	181 (97%)	5 (3%)	44	55
1	CaC	183/195 (94%)	181 (99%)	2 (1%)	73	83
1	DaD	184/195 (94%)	181 (98%)	3 (2%)	62	74
1	EaE	186/195 (95%)	183 (98%)	3 (2%)	62	74
All	All	923/975 (95%)	910 (99%)	13 (1%)	67	78

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DaD	14	SER
1	DaD	155	THR
1	EaE	186	SER
1	EaE	11	ARG
1	EaE	84	PRO

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\| > 2$
2	7IE	AaA	301	-	19,20,20	0.70	0	19,27,27	0.54	0
2	7IE	DaD	301	-	19,20,20	0.93	0	19,27,27	0.69	0
2	7IE	CaC	301	-	19,20,20	0.83	1 (5%)	19,27,27	0.82	0
2	7IE	EaE	301	-	19,20,20	0.98	0	19,27,27	0.80	1 (5%)
2	7IE	BaB	301	-	19,20,20	0.97	0	19,27,27	0.74	1 (5%)

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	7IE	AaA	301	-	-	0/10/21/21	0/2/2/2
2	7IE	DaD	301	-	-	0/10/21/21	0/2/2/2
2	7IE	CaC	301	-	-	1/10/21/21	0/2/2/2
2	7IE	EaE	301	-	-	0/10/21/21	0/2/2/2
2	7IE	BaB	301	-	-	0/10/21/21	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CaC	301	7IE	C11-C7	2.03	1.43	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	EaE	301	7IE	C5-C4-N1	-2.19	109.71	112.48
2	BaB	301	7IE	F1-C5-F2	2.06	110.57	105.53

There are no chirality outliers.

All (1) torsion outliers are listed below:

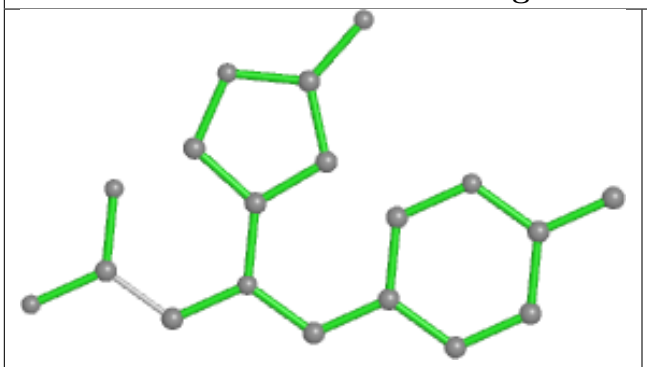
Mol	Chain	Res	Type	Atoms
2	CaC	301	7IE	N1-C4-C5-F2

There are no ring outliers.

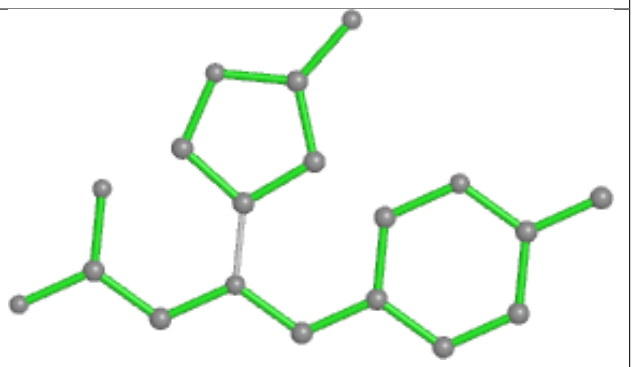
No monomer is involved in short contacts.

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

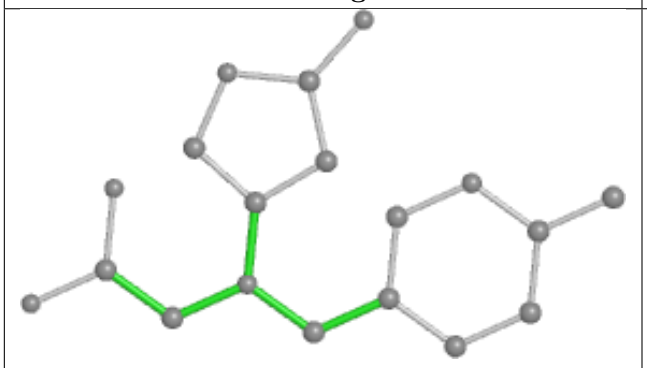
Ligand 7IE AaA 301



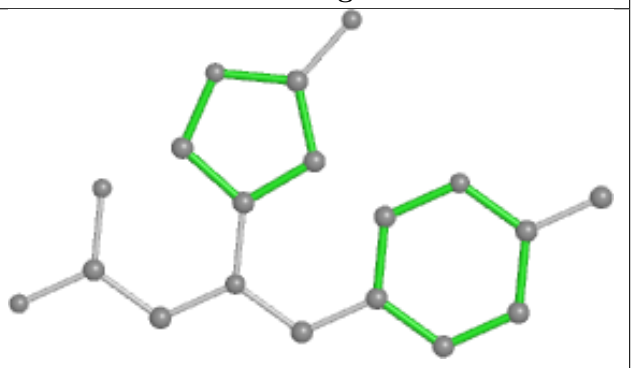
Bond lengths



Bond angles

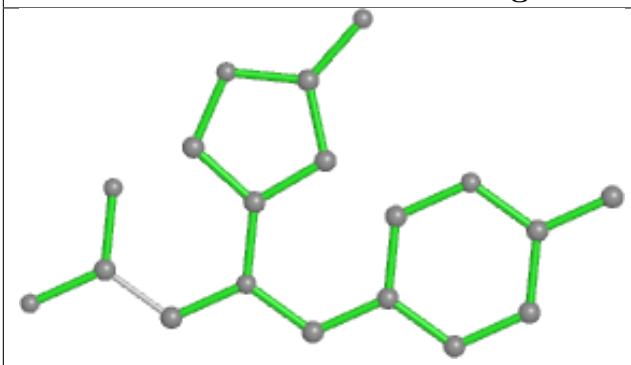


Torsions

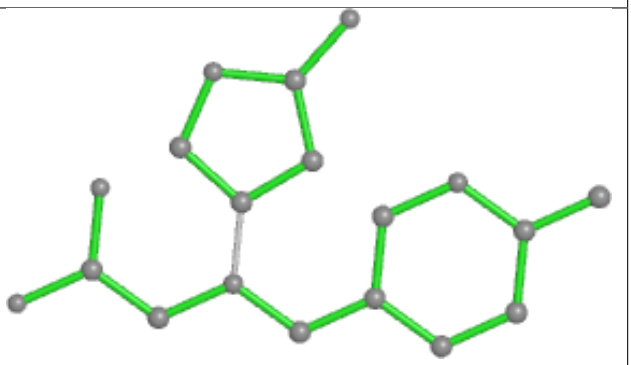


Rings

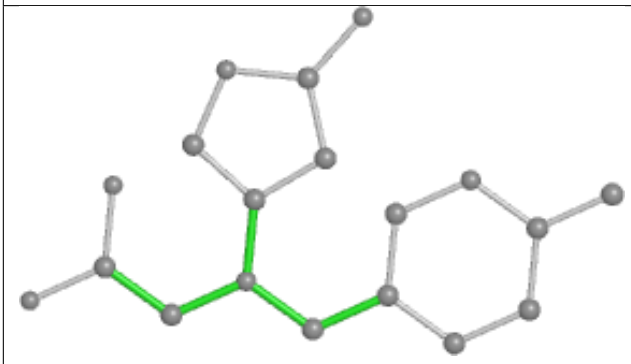
Ligand 7IE DaD 301



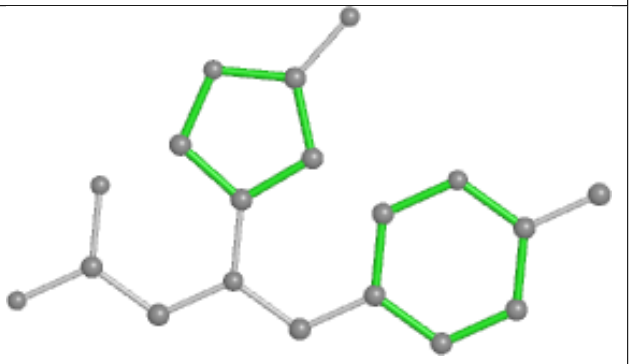
Bond lengths



Bond angles

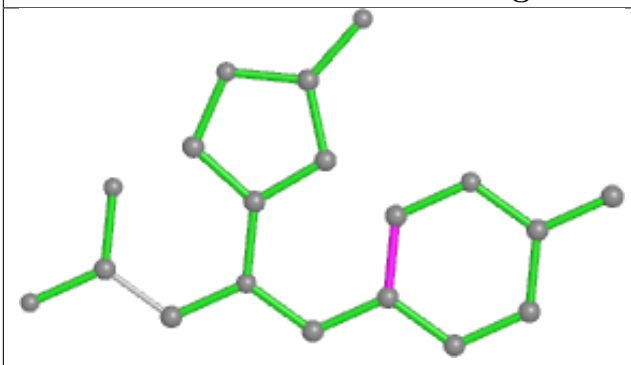


Torsions

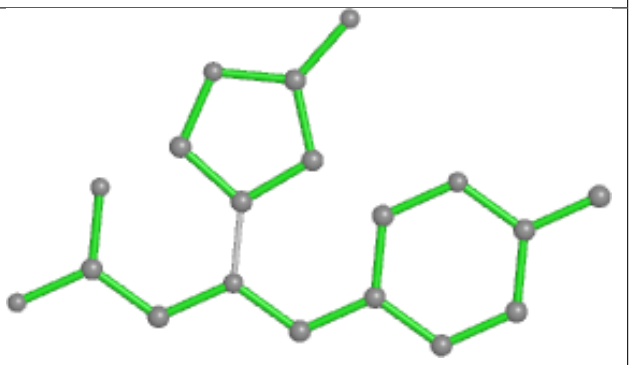


Rings

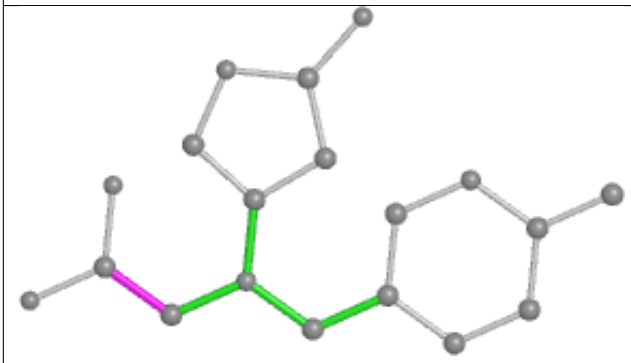
Ligand 7IE CaC 301



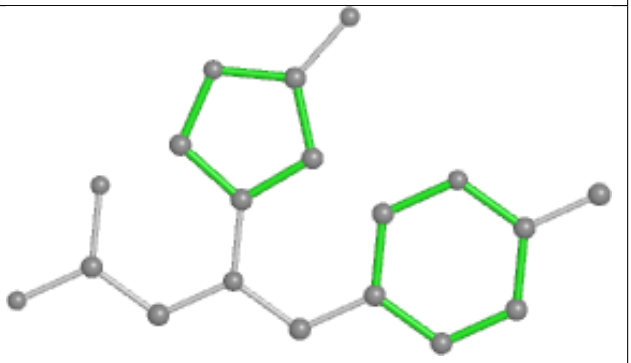
Bond lengths



Bond angles

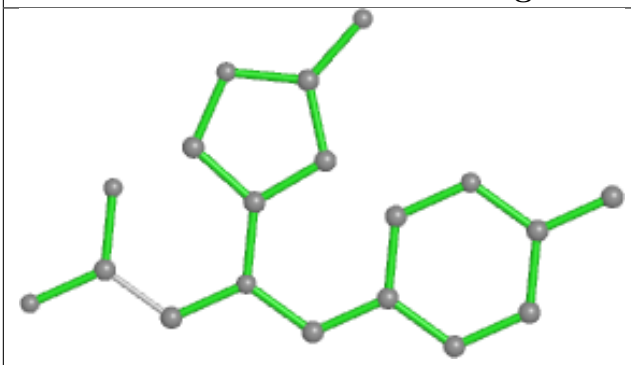


Torsions

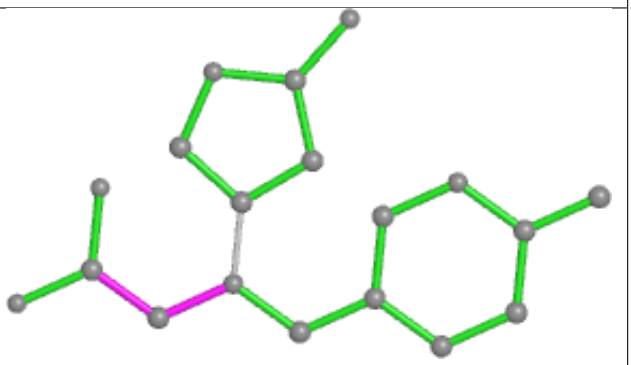


Rings

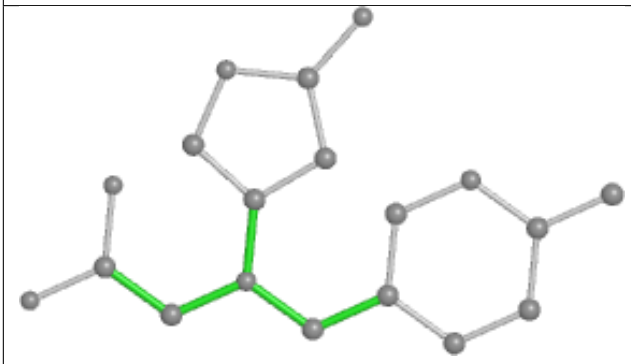
Ligand 7IE EaE 301



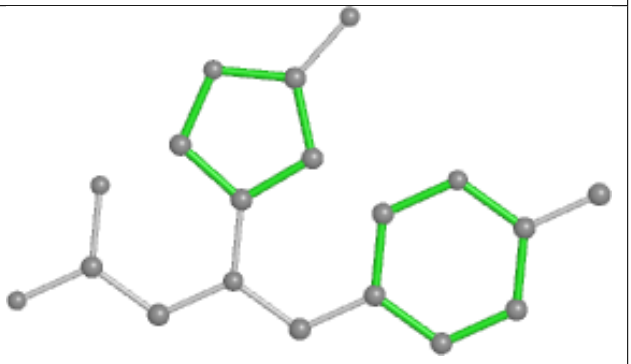
Bond lengths



Bond angles

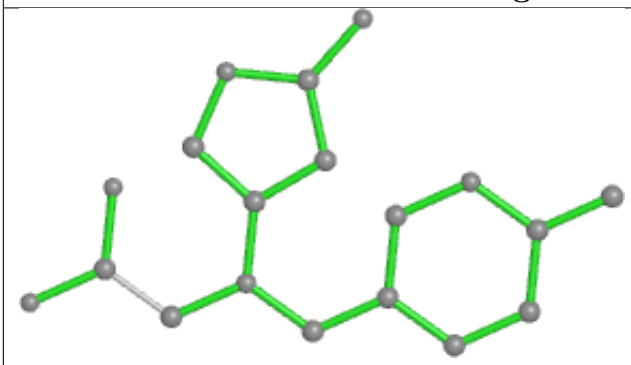


Torsions

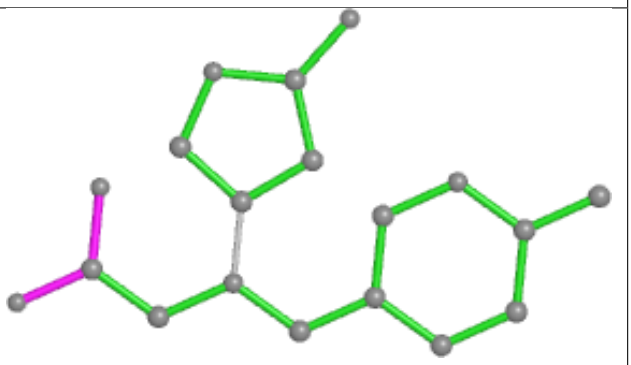


Rings

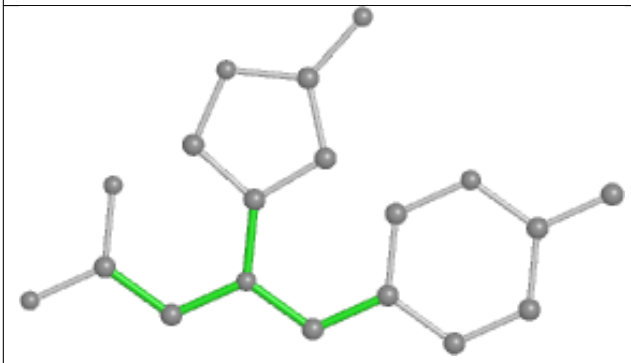
Ligand 7IE BaB 301



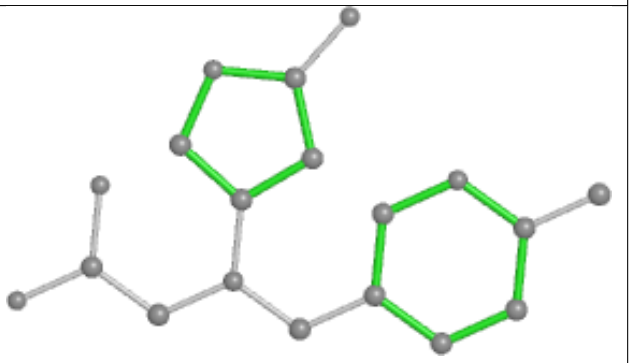
Bond lengths



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

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, 95^{th} 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	198/210 (94%)	0.53	24 (12%) 4 7	20, 29, 63, 84	0
1	BaB	201/210 (95%)	0.40	12 (5%) 21 30	18, 34, 60, 81	0
1	CaC	197/210 (93%)	0.75	25 (12%) 3 6	23, 35, 59, 87	0
1	DaD	198/210 (94%)	0.44	9 (4%) 33 44	19, 31, 57, 78	0
1	EaE	200/210 (95%)	0.35	12 (6%) 21 30	15, 24, 50, 70	0
All	All	994/1050 (94%)	0.49	82 (8%) 11 17	15, 31, 59, 87	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	DaD	69	HIS	6.9
1	CaC	67	SER	5.8
1	EaE	69	HIS	5.7
1	BaB	68	SER	5.6
1	CaC	1	ALA	5.6

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

There are no monosaccharides in this entry.

6.4 Ligands

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,

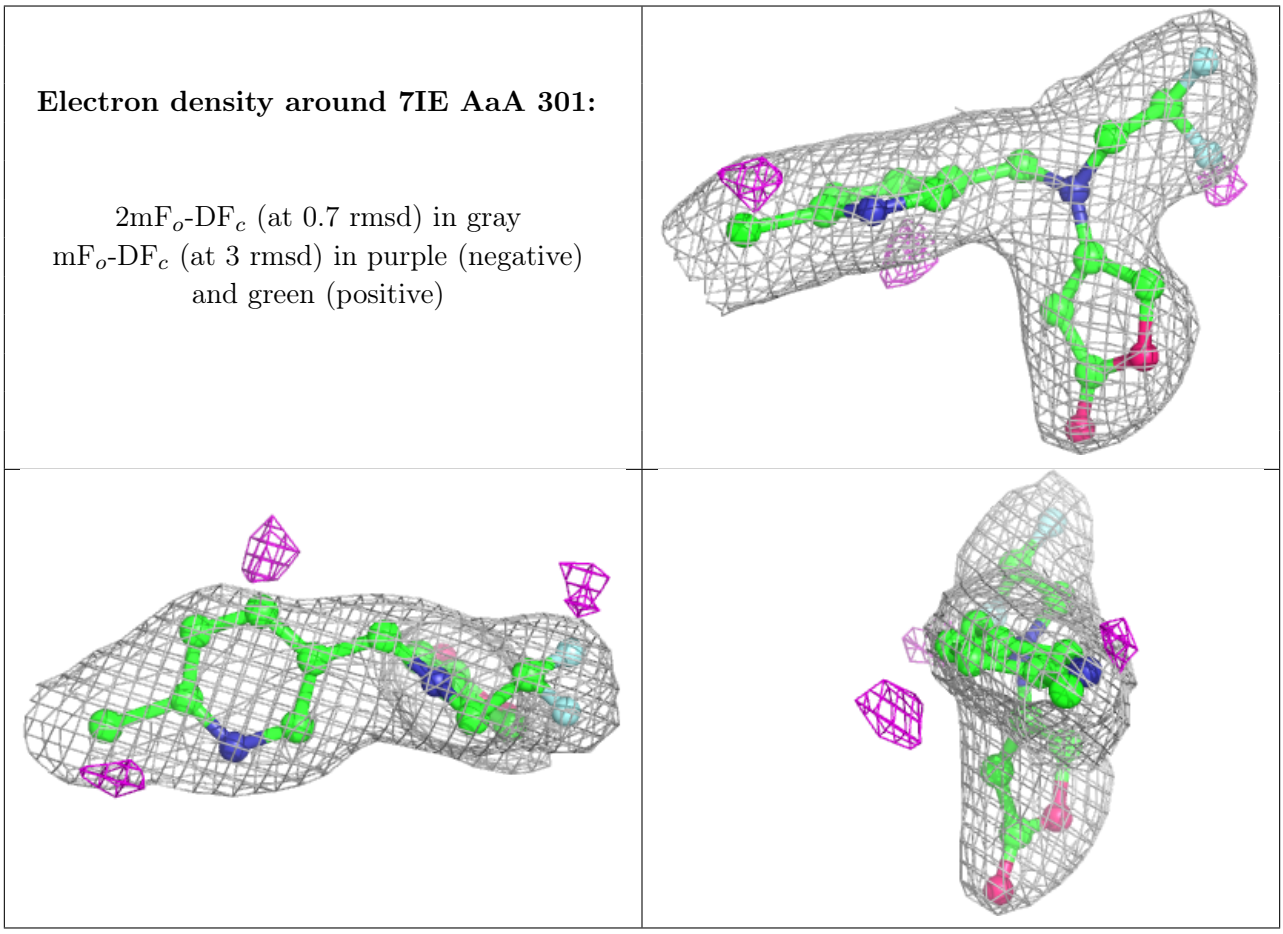
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	7IE	AaA	301	19/19	0.89	0.15	27,32,35,40	0
2	7IE	BaB	301	19/19	0.93	0.16	27,29,34,36	0
2	7IE	DaD	301	19/19	0.94	0.16	19,22,32,36	0
2	7IE	EaE	301	19/19	0.94	0.17	24,28,34,35	0
2	7IE	CaC	301	19/19	0.96	0.12	20,28,32,36	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.

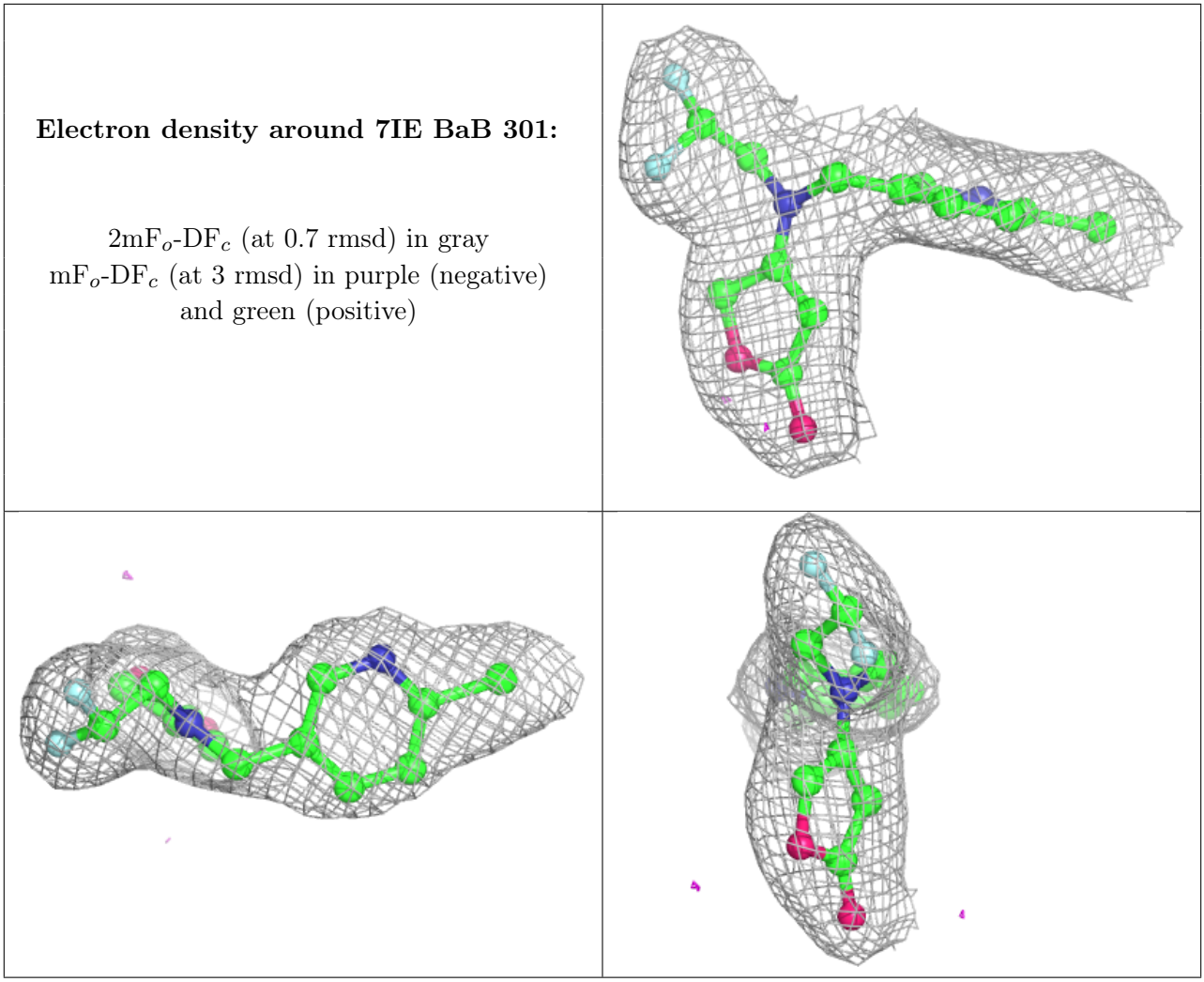
Electron density around 7IE AaA 301:

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



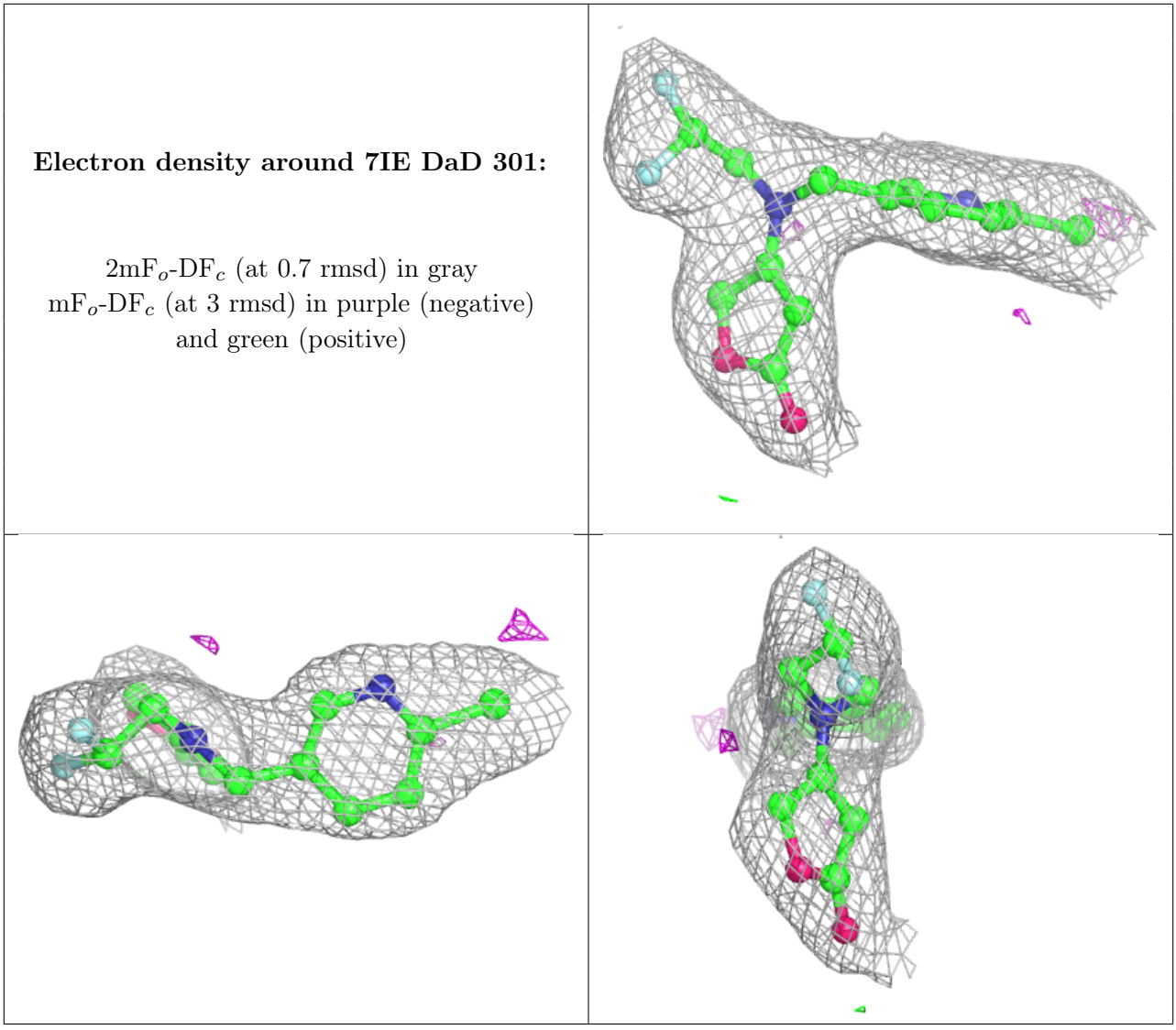
Electron density around 7IE BaB 301:

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



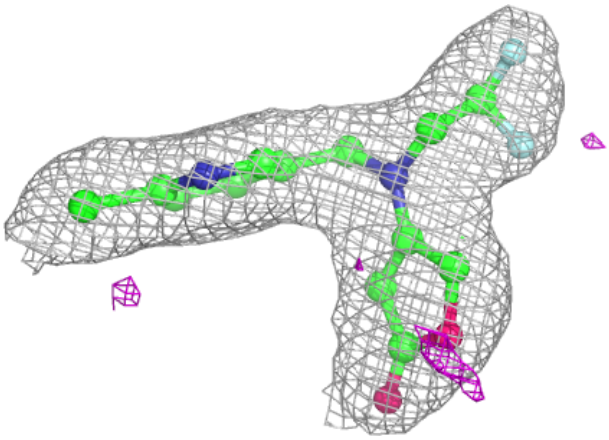
Electron density around 7IE DaD 301:

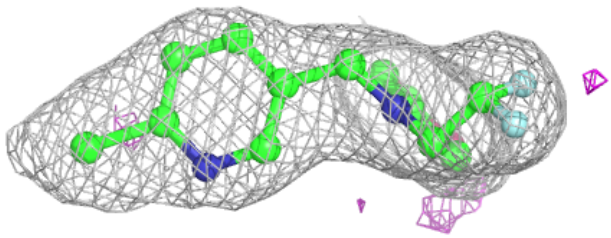
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

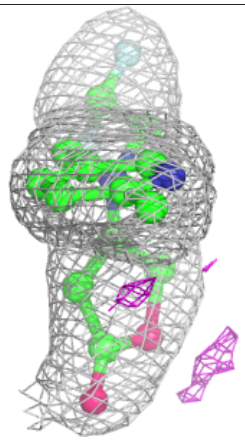


Electron density around 7IE EaE 301:

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

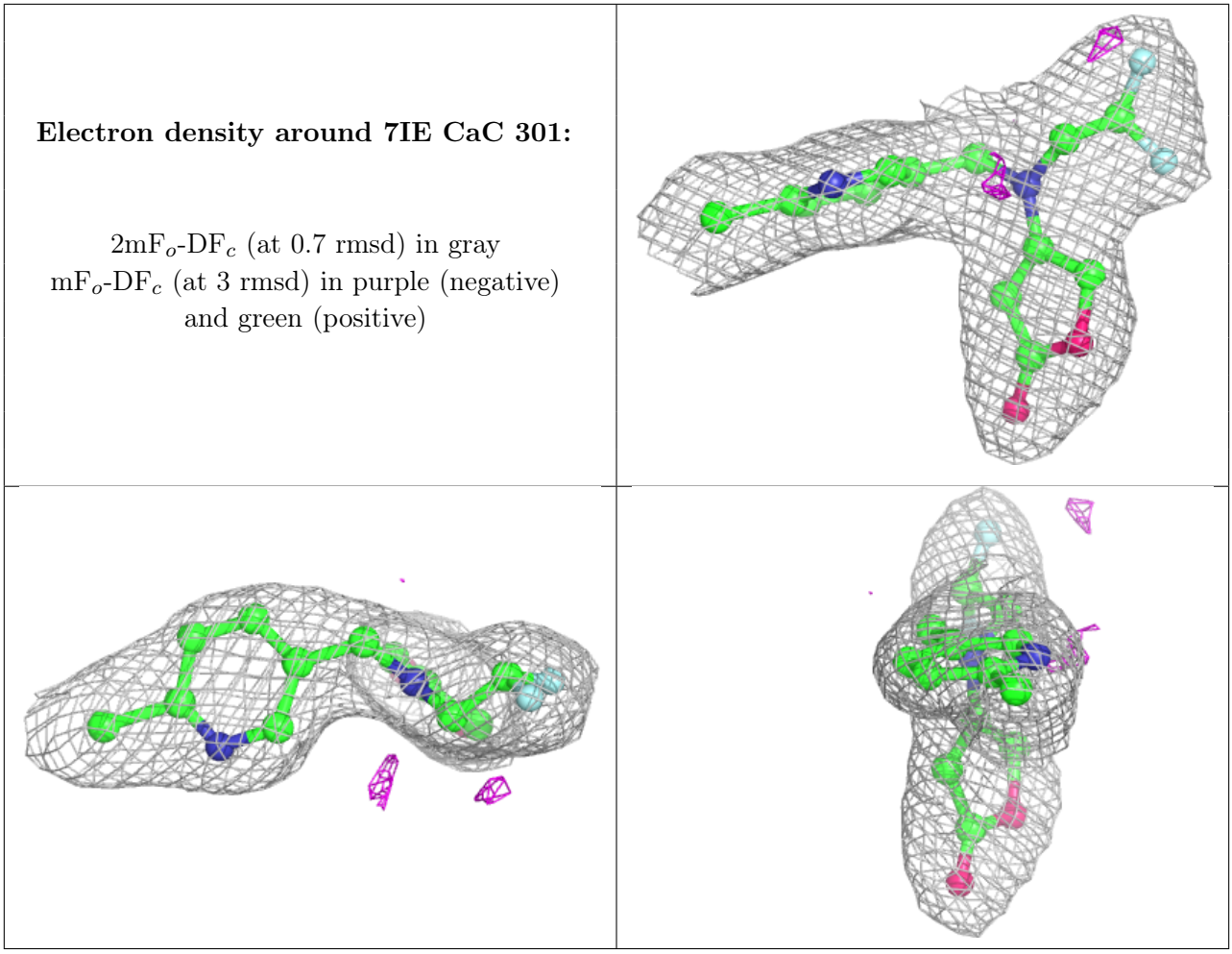






Electron density around 7IE CaC 301:

$2mF_o$-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.