



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 20, 2024 – 06:36 pm GMT

PDB ID : 7NLV
Title : WILDTYPE CORE-STREPTAVIDIN WITH a conjugated BIOTINYLATED
PYRROLIDINE II
Authors : Nodling, A.R.; Santi, N.; Tsai, Y.H.; Rizkallah, P.; Luk, L.Y.P.; Jin, Y.
Deposited on : 2021-02-22
Resolution : 1.29 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 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 : 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

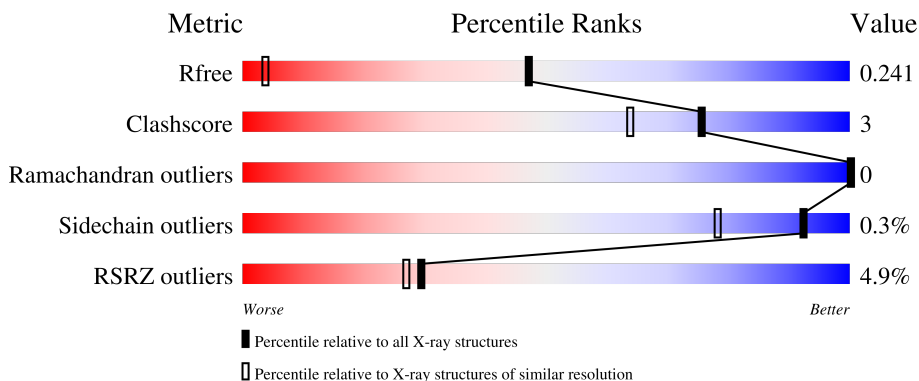
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.29 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	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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	128	
1	BBB	128	
1	CCC	128	
1	DDD	128	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3956 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.

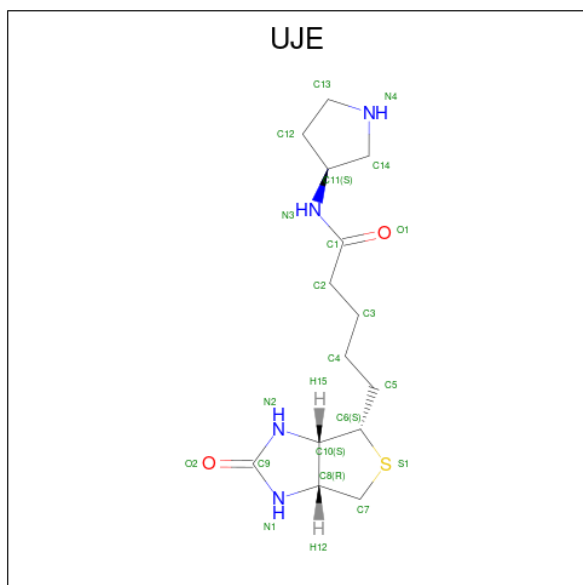
- Molecule 1 is a protein called Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	AAA	117	882	550	153	179	0	1	0
1	BBB	118	916	575	157	184	0	4	0
1	CCC	120	912	570	158	184	0	2	0
1	DDD	118	882	551	153	178	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	12	MET	-	initiating methionine	UNP P22629
BBB	12	MET	-	initiating methionine	UNP P22629
CCC	12	MET	-	initiating methionine	UNP P22629
DDD	12	MET	-	initiating methionine	UNP P22629

- Molecule 2 is 5-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1*H*-thieno[3,4-*d*]imidazol-4-yl)-*N*-((*S*)-pyrrolidin-3-yl)pentanamide (three-letter code: UJE) (formula: C₁₄H₂₄N₄O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	AAA	1	21	14	4	2	1	0	0
2	BBB	1	21	14	4	2	1	0	0
2	CCC	1	21	14	4	2	1	0	0
2	DDD	1	21	14	4	2	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	AAA	72	72	72	0	0
3	BBB	59	59	59	0	0
3	CCC	70	70	70	0	0
3	DDD	79	79	79	0	0

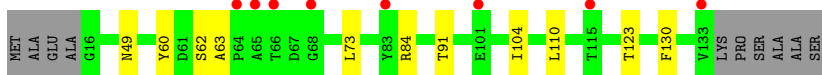
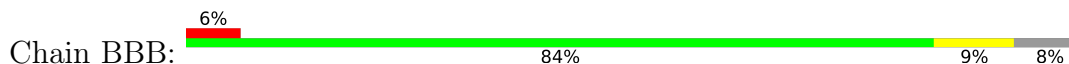
3 Residue-property plots [i](#)

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.

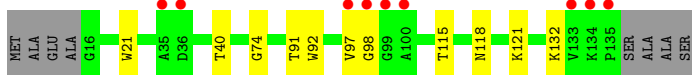
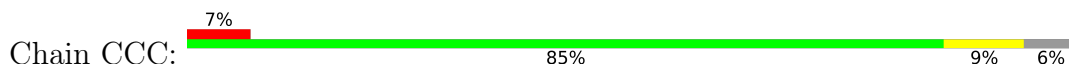
- Molecule 1: Streptavidin



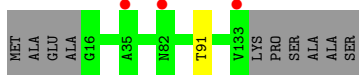
- Molecule 1: Streptavidin



- Molecule 1: Streptavidin



- Molecule 1: Streptavidin



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.32Å 97.60Å 50.90Å 90.00° 110.26° 90.00°	Depositor
Resolution (Å)	46.27 – 1.29 46.27 – 1.29	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.27-1.29) 85.0 (46.27-1.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.29Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.207 , 0.247 0.212 , 0.241	Depositor DCC
R_{free} test set	5406 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtrriage
Anisotropy	0.302	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.136 for l,-k,h	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3956	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% 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: UJE

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	0.71	0/904	0.90	0/1238
1	BBB	0.70	0/940	0.86	0/1288
1	CCC	0.73	0/935	0.87	0/1281
1	DDD	0.69	0/904	0.88	0/1238
All	All	0.71	0/3683	0.88	0/5045

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	AAA	882	0	820	5	0
1	BBB	916	0	853	9	0
1	CCC	912	0	855	11	0
1	DDD	882	0	823	1	0
2	AAA	21	0	0	0	0
2	BBB	21	0	0	0	0
2	CCC	21	0	0	0	0
2	DDD	21	0	0	0	0
3	AAA	72	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BBB	59	0	0	0	0
3	CCC	70	0	0	1	0
3	DDD	79	0	0	0	0
All	All	3956	0	3351	22	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (22) 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:CCC:118:ASN:HB3	1:CCC:121:LYS:NZ	2.17	0.60
1:AAA:91:THR:HB	1:BBB:91:THR:HB	1.85	0.57
1:CCC:97:VAL:HG22	1:CCC:98:GLY:N	2.20	0.56
1:CCC:91:THR:HB	1:DDD:91:THR:HB	1.93	0.51
1:CCC:118:ASN:HB3	1:CCC:121:LYS:HZ3	1.79	0.47
1:BBB:73:LEU:C	1:BBB:73:LEU:HD12	2.35	0.47
1:AAA:80:LYS:HE2	1:BBB:63:ALA:HB3	1.96	0.46
1:BBB:60:TYR:CE2	1:BBB:62:SER:HA	2.50	0.46
1:CCC:21:TRP:CZ2	1:CCC:132:LYS:HE2	2.51	0.46
1:CCC:115:THR:OG1	1:CCC:118:ASN:ND2	2.48	0.45
1:AAA:30:ILE:O	1:AAA:41:GLY:HA3	2.16	0.45
1:CCC:40[B]:THR:HG22	3:CCC:327:HOH:O	2.16	0.44
1:CCC:118:ASN:CB	1:CCC:121:LYS:NZ	2.81	0.44
1:CCC:74:GLY:HA2	1:CCC:92:TRP:O	2.18	0.43
1:BBB:49:ASN:OD1	1:BBB:84:ARG:HD3	2.19	0.43
1:AAA:80:LYS:CE	1:BBB:63:ALA:HB3	2.49	0.42
1:CCC:118:ASN:CG	1:CCC:121:LYS:HZ1	2.23	0.42
1:BBB:110[A]:LEU:C	1:BBB:110[A]:LEU:HD23	2.40	0.41
1:CCC:97:VAL:HG22	1:CCC:98:GLY:H	1.85	0.41
1:BBB:110[A]:LEU:O	1:BBB:123:THR:HA	2.22	0.40
1:BBB:104:ILE:HB	1:BBB:130:PHE:HB2	2.03	0.40
1:AAA:74:GLY:HA2	1:AAA:92:TRP:O	2.21	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	116/128 (91%)	113 (97%)	3 (3%)	0	100	100
1	BBB	120/128 (94%)	118 (98%)	2 (2%)	0	100	100
1	CCC	120/128 (94%)	117 (98%)	3 (2%)	0	100	100
1	DDD	116/128 (91%)	113 (97%)	3 (3%)	0	100	100
All	All	472/512 (92%)	461 (98%)	11 (2%)	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	87/93 (94%)	86 (99%)	1 (1%)	73	45
1	BBB	91/93 (98%)	91 (100%)	0	100	100
1	CCC	91/93 (98%)	91 (100%)	0	100	100
1	DDD	87/93 (94%)	87 (100%)	0	100	100
All	All	356/372 (96%)	355 (100%)	1 (0%)	92	78

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	131	THR

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](#)

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
2	UJE	DDD	201	-	22,23,23	0.38	0	28,31,31	0.95	1 (3%)
2	UJE	CCC	201	-	22,23,23	0.48	0	28,31,31	0.83	0
2	UJE	BBB	201	-	22,23,23	0.62	0	28,31,31	0.60	0
2	UJE	AAA	201	-	22,23,23	0.57	0	28,31,31	0.75	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UJE	DDD	201	-	-	0/11/39/39	0/3/3/3
2	UJE	CCC	201	-	-	0/11/39/39	0/3/3/3
2	UJE	BBB	201	-	-	1/11/39/39	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UJE	AAA	201	-	-	0/11/39/39	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	DDD	201	UJE	C7-S1-C6	-2.19	85.39	89.89

There are no chirality outliers.

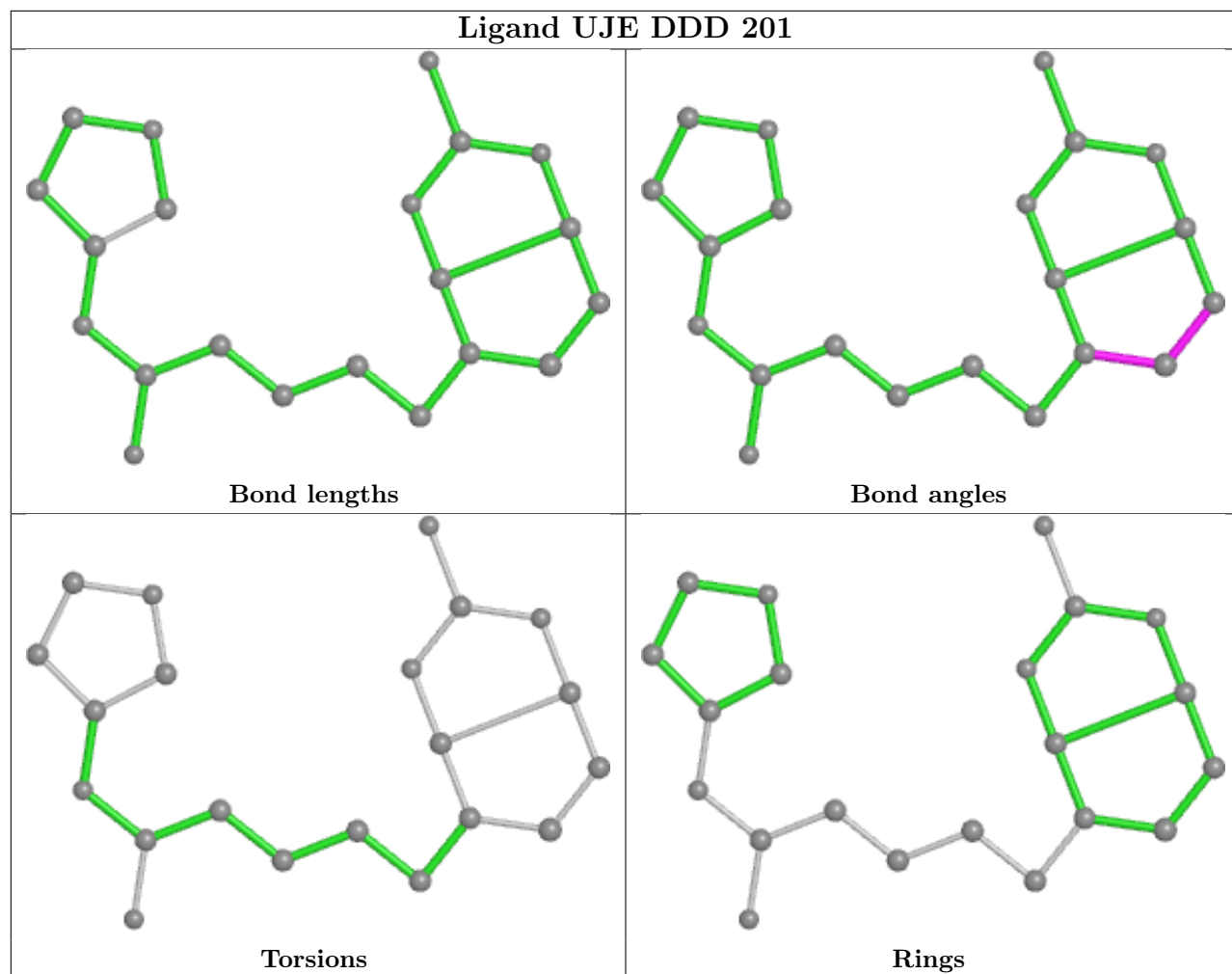
All (1) torsion outliers are listed below:

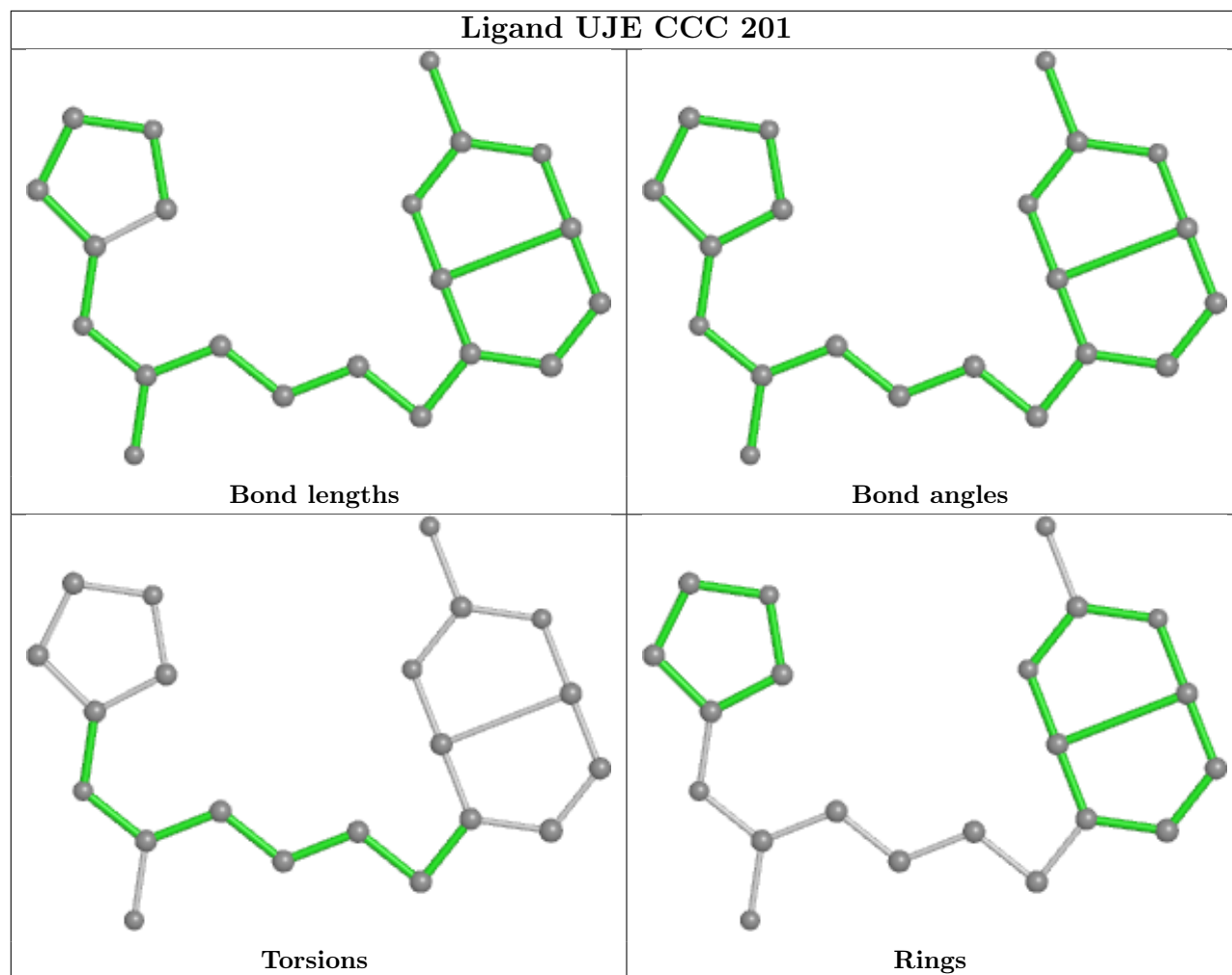
Mol	Chain	Res	Type	Atoms
2	BBB	201	UJE	C12-C11-N3-C1

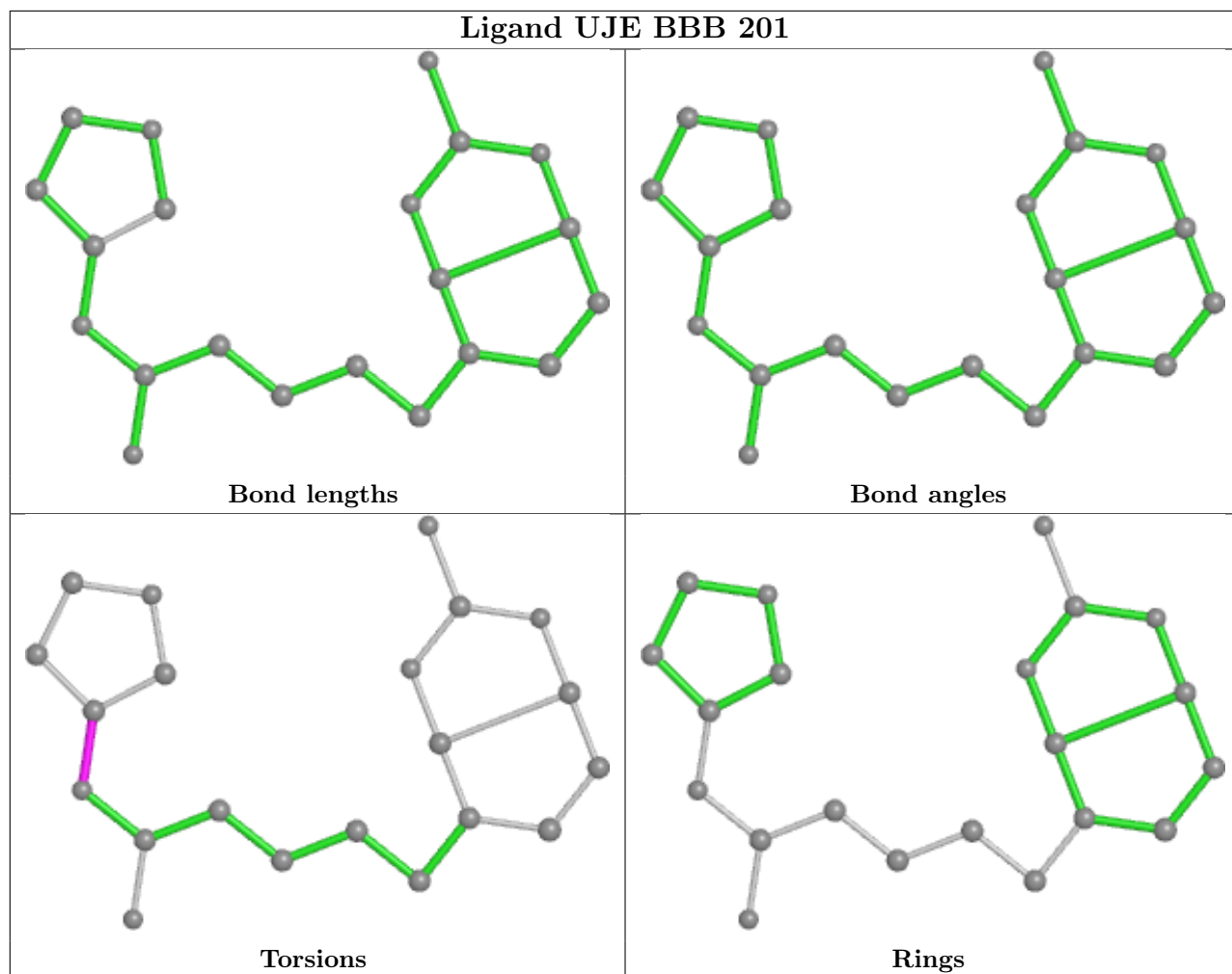
There are no ring outliers.

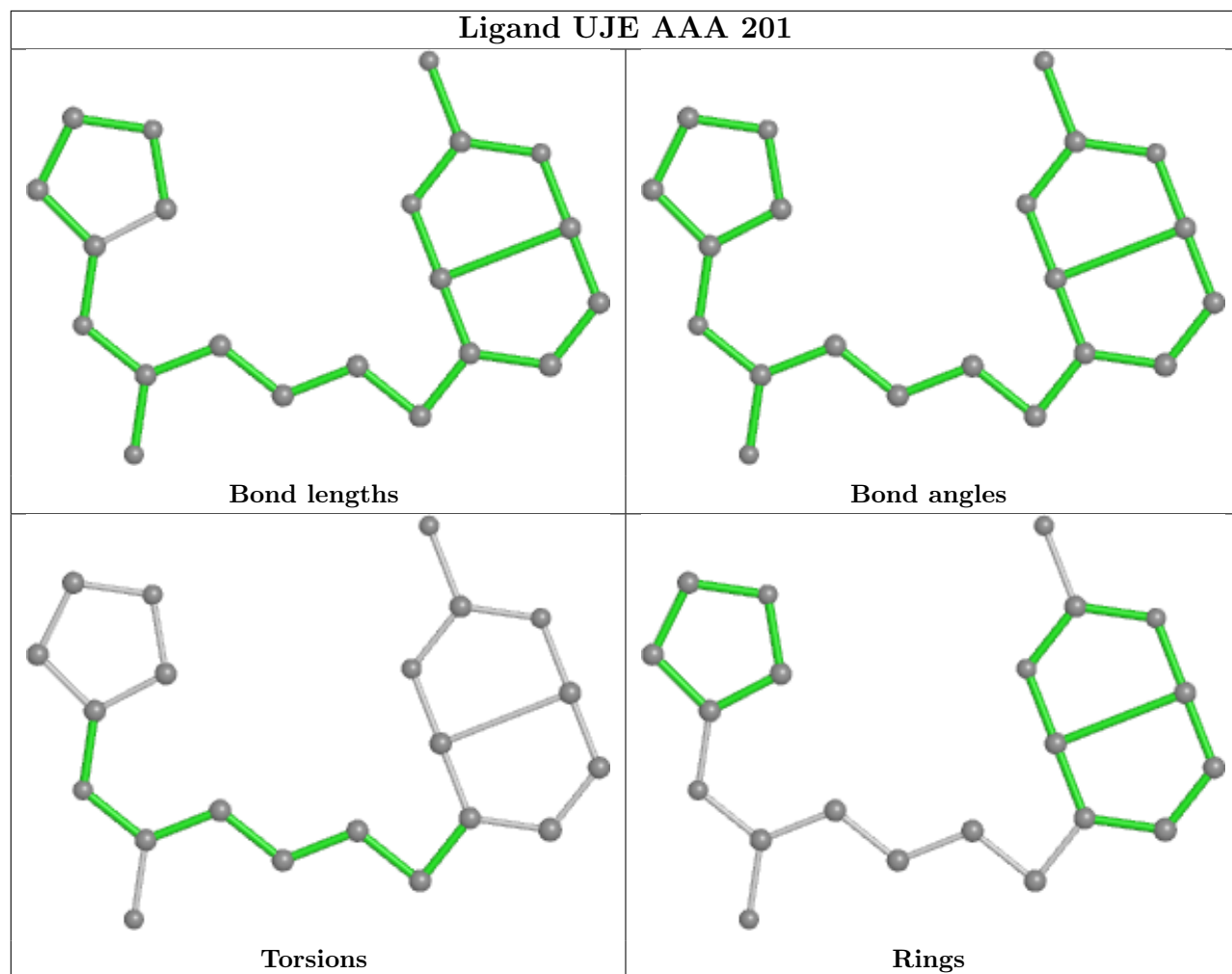
No monomer is involved in short contacts.

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

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	AAA	117/128 (91%)	0.27	3 (2%) 56 54	16, 22, 35, 44	2 (1%)
1	BBB	118/128 (92%)	0.61	8 (6%) 17 14	17, 26, 38, 44	3 (2%)
1	CCC	120/128 (93%)	0.60	9 (7%) 14 11	16, 22, 41, 63	6 (5%)
1	DDD	118/128 (92%)	0.35	3 (2%) 57 56	16, 23, 36, 44	2 (1%)
All	All	473/512 (92%)	0.46	23 (4%) 29 27	16, 23, 39, 63	13 (2%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CCC	98	GLY	15.5
1	CCC	100	ALA	11.0
1	CCC	135	PRO	5.4
1	CCC	99	GLY	4.6
1	BBB	83[A]	TYR	4.5
1	DDD	133	VAL	4.5
1	BBB	66	THR	4.3
1	AAA	99	GLY	3.8
1	CCC	134	LYS	3.6
1	BBB	65	ALA	3.3
1	AAA	66	THR	2.8
1	BBB	68	GLY	2.8
1	CCC	133	VAL	2.5
1	CCC	97	VAL	2.5
1	AAA	22	TYR	2.4
1	DDD	35	ALA	2.4
1	BBB	133	VAL	2.2
1	BBB	115	THR	2.2
1	BBB	101	GLU	2.1
1	CCC	35	ALA	2.1
1	BBB	64[A]	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	DDD	82	ASN	2.0
1	CCC	36	ASP	2.0

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](#)

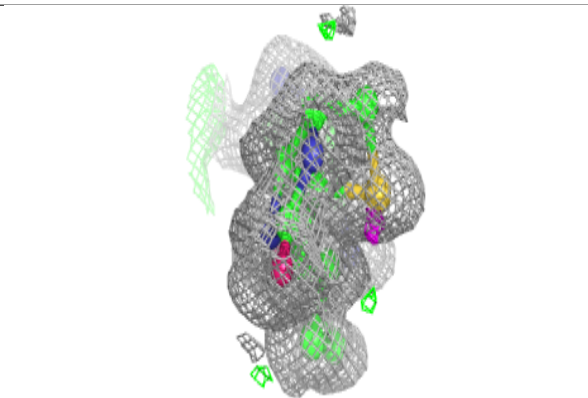
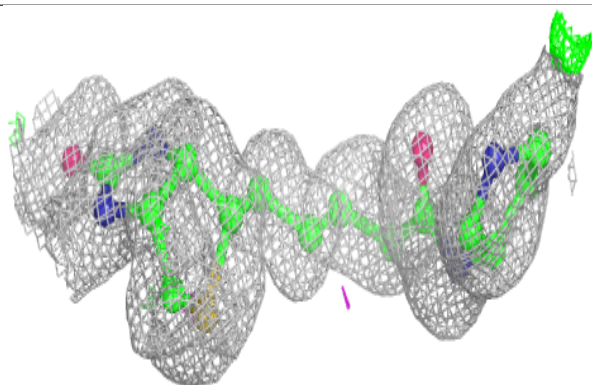
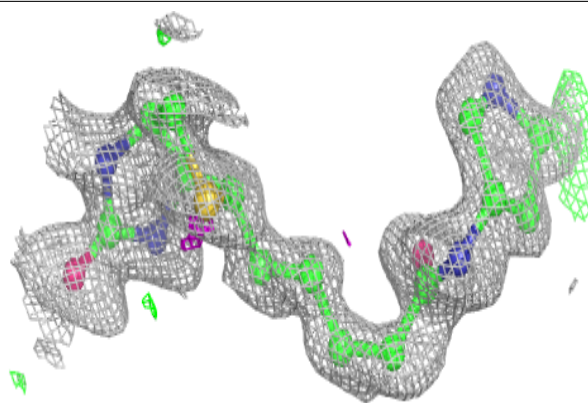
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	UJE	BBB	201	21/21	0.97	0.09	17,20,28,31	0
2	UJE	AAA	201	21/21	0.98	0.09	15,18,30,32	0
2	UJE	CCC	201	21/21	0.98	0.10	16,18,30,32	0
2	UJE	DDD	201	21/21	0.98	0.09	18,20,34,37	0

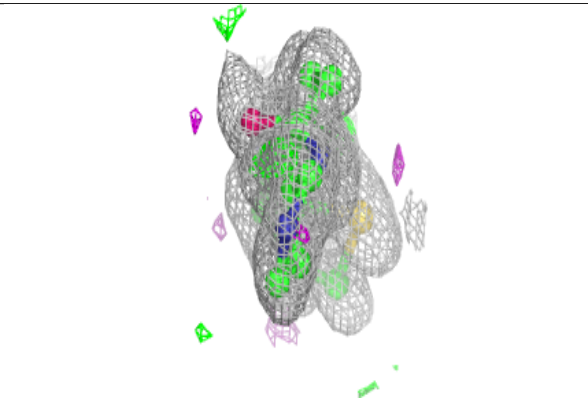
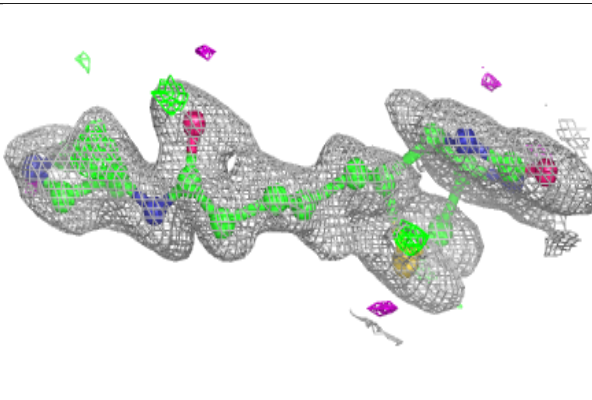
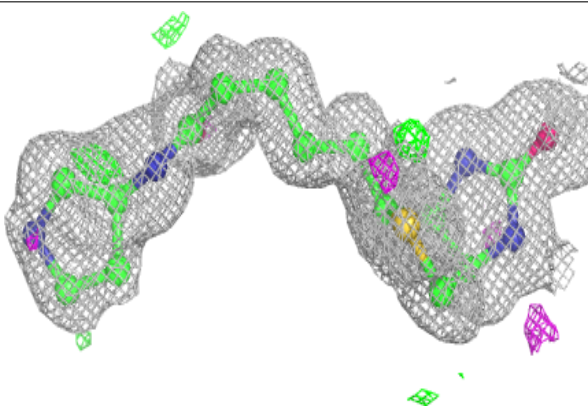
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around UJE BBB 201:

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

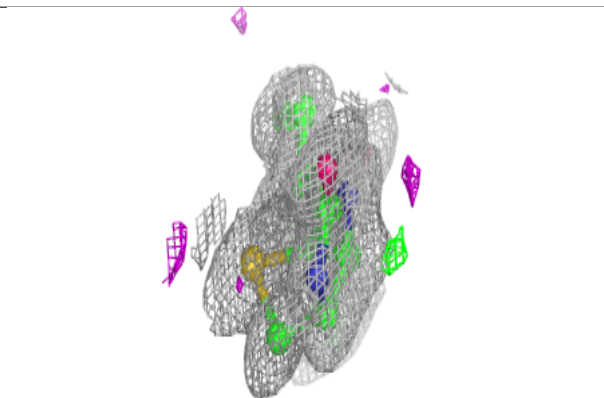
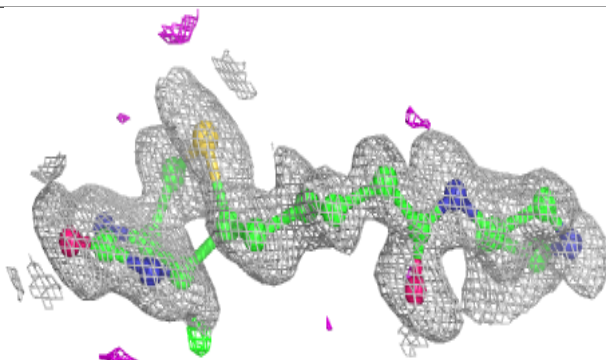
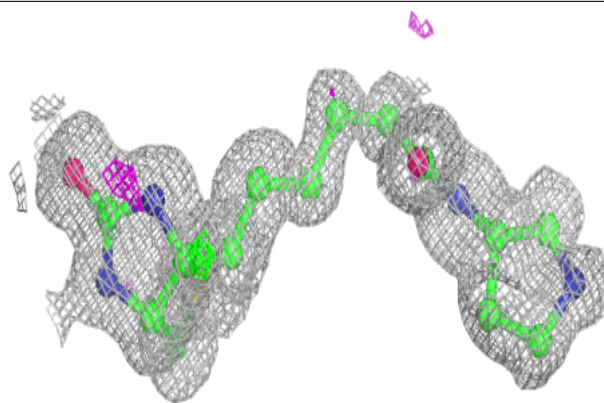
**Electron density around UJE AAA 201:**

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

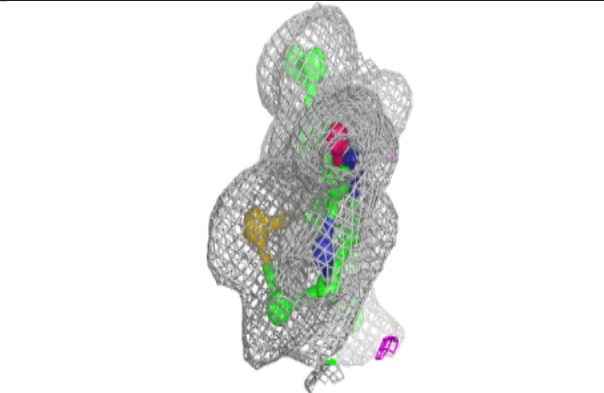
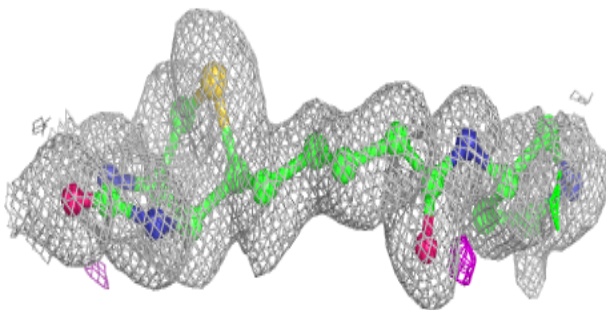
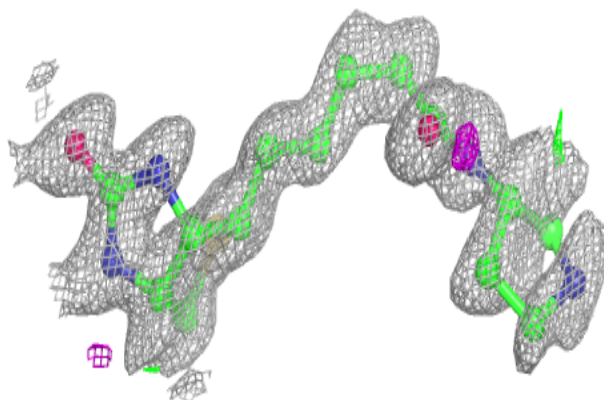


Electron density around UJE CCC 201:

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

**Electron density around UJE DDD 201:**

$2mF_o-DF_c$ (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.