wwPDB X-ray Structure Validation Summary Report (i)

Sep 3, 2023 – 08:20 PM EDT

PDB ID	:	3RZ3
Title	:	Human Cdc34 E2 in complex with CC0651 inhibitor
Authors	:	Ceccarelli, D.F.; Webb, D.R.; Sicheri, F.
Deposited on	:	2011-05-11
Resolution	:	2.30 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:

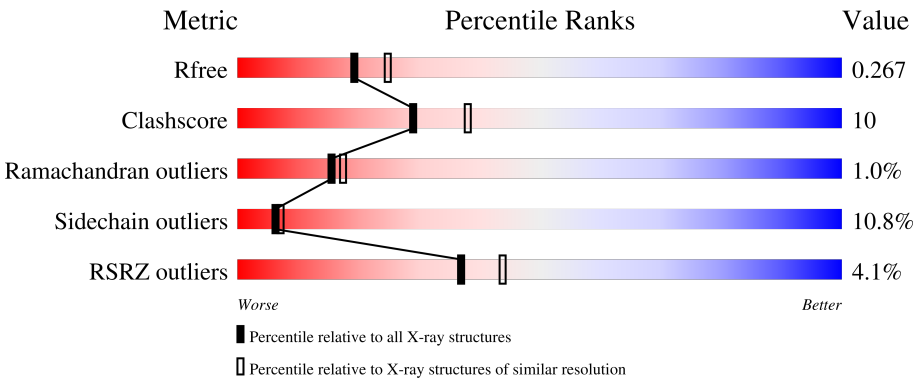
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	183	2%, 66%, 17%, 5%, 10%
1	B	183	3%, 71%, 16%, 10%
1	C	183	4%, 66%, 15%, 15%
1	D	183	5%, 62%, 14%, 20%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5042 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.

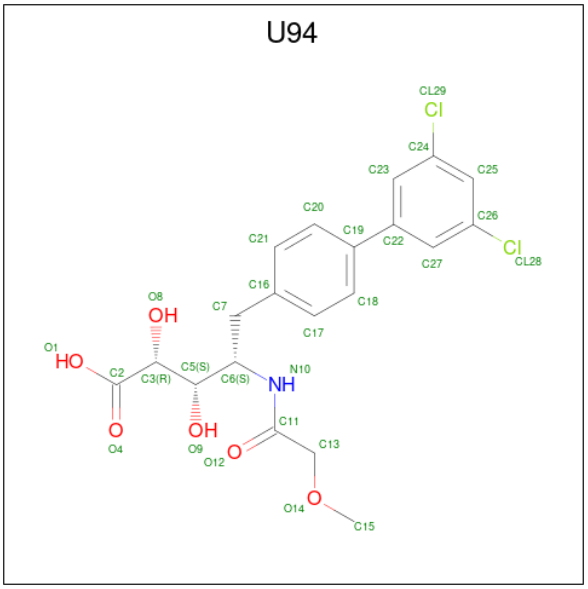
- Molecule 1 is a protein called Ubiquitin-conjugating enzyme E2 R1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	164	1257	812	205	237	3	0	0	0
1	B	164	1285	833	210	239	3	0	0	0
1	C	156	1195	777	200	215	3	0	0	0
1	D	146	1116	725	188	200	3	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	expression tag	UNP P49427
A	3	ALA	-	expression tag	UNP P49427
A	4	MET	-	expression tag	UNP P49427
A	5	GLY	-	expression tag	UNP P49427
A	6	SER	-	expression tag	UNP P49427
B	2	GLY	-	expression tag	UNP P49427
B	3	ALA	-	expression tag	UNP P49427
B	4	MET	-	expression tag	UNP P49427
B	5	GLY	-	expression tag	UNP P49427
B	6	SER	-	expression tag	UNP P49427
C	2	GLY	-	expression tag	UNP P49427
C	3	ALA	-	expression tag	UNP P49427
C	4	MET	-	expression tag	UNP P49427
C	5	GLY	-	expression tag	UNP P49427
C	6	SER	-	expression tag	UNP P49427
D	2	GLY	-	expression tag	UNP P49427
D	3	ALA	-	expression tag	UNP P49427
D	4	MET	-	expression tag	UNP P49427
D	5	GLY	-	expression tag	UNP P49427
D	6	SER	-	expression tag	UNP P49427

- Molecule 2 is 4,5-dideoxy-5-(3',5'-dichlorobiphenyl-4-yl)-4-[(methoxyacetyl)amino]-L-arabinonic acid (three-letter code: U94) (formula: $C_{20}H_{21}Cl_2NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	29	20	2	1	6	0	0
			Total	C	Cl	N	O		
2	B	1	29	20	2	1	6	0	0
			Total	C	Cl	N	O		
2	C	1	29	20	2	1	6	0	0
			Total	C	Cl	N	O		
2	D	1	29	20	2	1	6	0	0

- Molecule 3 is water.

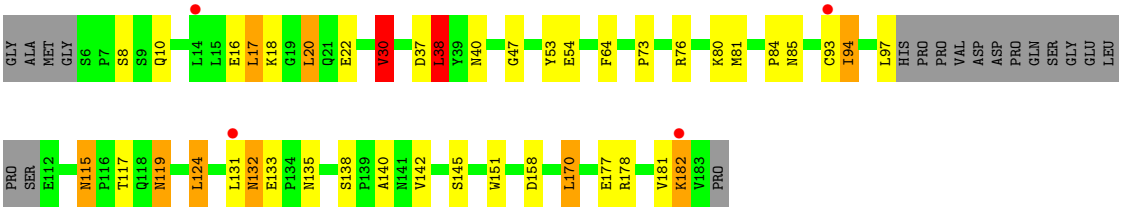
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	21	21	21	0	0
			Total	O		
3	B	21	21	21	0	0
			Total	O		
3	C	17	17	17	0	0
			Total	O		
3	D	14	14	14	0	0

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.

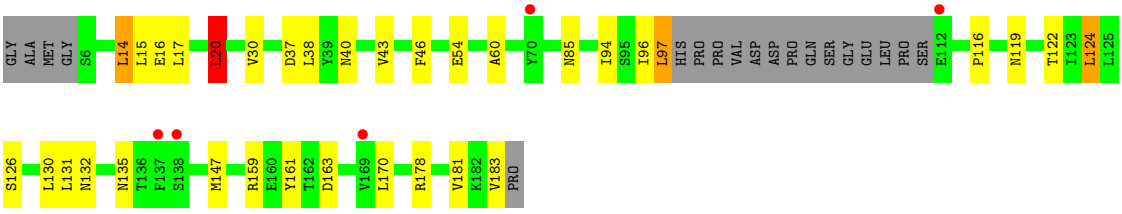
• Molecule 1: Ubiquitin-conjugating enzyme E2 R1

Chain A:



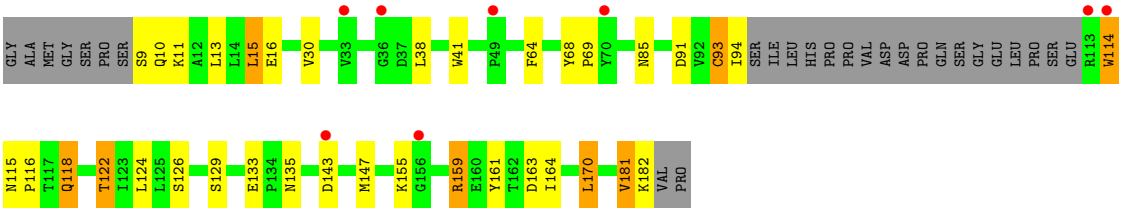
• Molecule 1: Ubiquitin-conjugating enzyme E2 R1

Chain B:



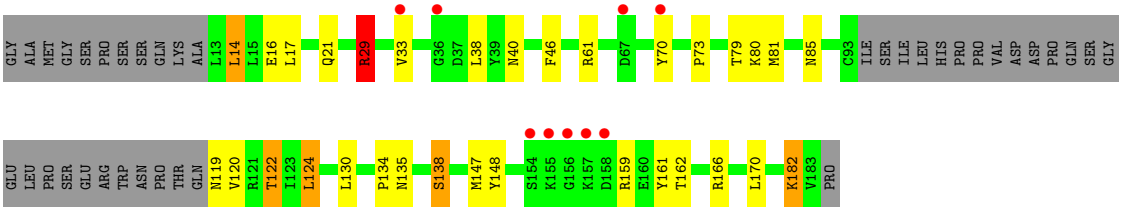
• Molecule 1: Ubiquitin-conjugating enzyme E2 R1

Chain C:



• Molecule 1: Ubiquitin-conjugating enzyme E2 R1

Chain D:


GLY
ALA
MET
GLY
SER
PRO
SER
SER
GLN
LYS
ALA
L13
L14
L15
E16
L17
Q21
R29
V33
G36
D37
L38
Y39
N40
F46
R61
D67
Y70
P73
T79
K80
M81
N85
C93
ILE
SER
ILE
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HIS
PRO
PRO
VAL
ASP
ASP
PRO
GLN
SER
GLY

GLU
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ARG
TRP
ASN
PRO
THR
GLN
N119
V120
R121
T122
I123
L124
L130
P134
N135
S138
M147
Y148
S154
K155
G156
K157
D158
R159
E160
Y161
T162
R166
L170
K182
V183
PRO

4 Data and refinement statistics (i)

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	121.80Å 139.53Å 216.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.30 24.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	84.2 (25.00-2.30) 84.2 (24.96-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.221 , 0.258 0.232 , 0.267	Depositor DCC
R_{free} test set	1744 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	41.5	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5042	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: U94

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	1.20	3/1291 (0.2%)	1.19	13/1771 (0.7%)
1	B	1.12	1/1320 (0.1%)	1.05	6/1804 (0.3%)
1	C	0.98	1/1229 (0.1%)	0.88	2/1684 (0.1%)
1	D	0.97	1/1147 (0.1%)	0.92	2/1570 (0.1%)
All	All	1.08	6/4987 (0.1%)	1.02	23/6829 (0.3%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	93	CYS	CB-SG	9.78	1.98	1.82
1	A	115	ASN	CB-CG	-7.25	1.34	1.51
1	A	80	LYS	CA-CB	6.37	1.68	1.53
1	A	142	VAL	CA-CB	5.41	1.66	1.54
1	B	54	GLU	CD-OE1	5.14	1.31	1.25

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	178	ARG	NE-CZ-NH1	10.46	125.53	120.30
1	A	178	ARG	NE-CZ-NH2	-9.01	115.80	120.30
1	A	76	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	A	178	ARG	NE-CZ-NH1	8.04	124.32	120.30
1	D	29	ARG	NE-CZ-NH1	7.96	124.28	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1257	0	1170	25	0
1	B	1285	0	1226	23	0
1	C	1195	0	1117	26	0
1	D	1116	0	1039	16	0
2	A	29	0	20	2	0
2	B	29	0	20	0	0
2	C	29	0	20	2	0
2	D	29	0	20	3	0
3	A	21	0	0	0	0
3	B	21	0	0	0	0
3	C	17	0	0	1	0
3	D	14	0	0	2	0
All	All	5042	0	4632	92	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 10.

The worst 5 of 92 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:B:159:ARG:NH1	1:B:163:ASP:OD1	1.89	1.06
1:B:183:VAL:HG12	1:B:183:VAL:O	1.59	1.01
2:A:1:U94:H5	3:C:186:HOH:O	1.65	0.93
1:C:85:ASN:HD21	1:C:135:ASN:H	1.18	0.89
1:A:16:GLU:OE2	1:A:119:ASN:HB2	1.71	0.89

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	160/183 (87%)	155 (97%)	4 (2%)	1 (1%)	25	31
1	B	160/183 (87%)	158 (99%)	2 (1%)	0	100	100
1	C	152/183 (83%)	147 (97%)	2 (1%)	3 (2%)	7	6
1	D	142/183 (78%)	135 (95%)	5 (4%)	2 (1%)	11	11
All	All	614/732 (84%)	595 (97%)	13 (2%)	6 (1%)	15	17

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	LYS
1	C	93	CYS
1	D	33	VAL
1	C	181	VAL
1	C	155	LYS

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	129/162 (80%)	115 (89%)	14 (11%)	6	7
1	B	135/162 (83%)	122 (90%)	13 (10%)	8	10
1	C	119/162 (74%)	105 (88%)	14 (12%)	5	5
1	D	110/162 (68%)	98 (89%)	12 (11%)	6	7
All	All	493/648 (76%)	440 (89%)	53 (11%)	6	7

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	15	LEU
1	C	124	LEU
1	D	138	SER

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Mol	Chain	Res	Type
1	C	91	ASP
1	C	115	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	85	ASN
1	C	115	ASN
1	D	85	ASN
1	C	118	GLN
1	A	132	ASN

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	U94	B	1	-	29,30,30	1.95	3 (10%)	35,41,41	2.18	11 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	U94	D	1	-	29,30,30	1.11	2 (6%)	35,41,41	1.46	7 (20%)
2	U94	A	1	-	29,30,30	1.49	2 (6%)	35,41,41	2.19	11 (31%)
2	U94	C	1	-	29,30,30	1.19	4 (13%)	35,41,41	1.95	9 (25%)

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	U94	B	1	-	-	14/23/27/27	0/2/2/2
2	U94	D	1	-	-	14/23/27/27	0/2/2/2
2	U94	A	1	-	-	13/23/27/27	0/2/2/2
2	U94	C	1	-	-	9/23/27/27	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	U94	C3-C2	8.09	1.63	1.52
2	A	1	U94	C3-C2	5.42	1.60	1.52
2	B	1	U94	C5-C6	2.93	1.58	1.53
2	C	1	U94	C3-C2	2.92	1.56	1.52
2	D	1	U94	O8-C3	2.43	1.47	1.42

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	U94	C5-C3-C2	7.66	118.95	109.32
2	A	1	U94	C7-C6-N10	-5.43	102.16	110.07
2	C	1	U94	C7-C6-C5	5.11	121.64	111.11
2	A	1	U94	C15-O14-C13	-5.10	93.29	112.83
2	A	1	U94	C5-C3-C2	4.62	115.12	109.32

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	U94	O1-C2-C3-O8
2	A	1	U94	O4-C2-C3-O8
2	A	1	U94	C2-C3-C5-O9

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Mol	Chain	Res	Type	Atoms
2	A	1	U94	O8-C3-C5-C6
2	A	1	U94	O8-C3-C5-O9

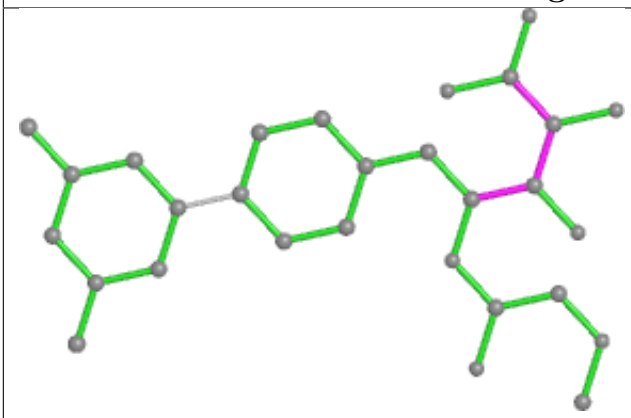
There are no ring outliers.

3 monomers are involved in 7 short contacts:

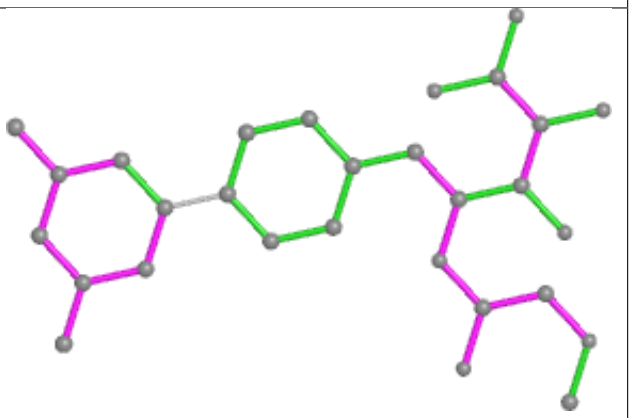
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	U94	3	0
2	A	1	U94	2	0
2	C	1	U94	2	0

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 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.

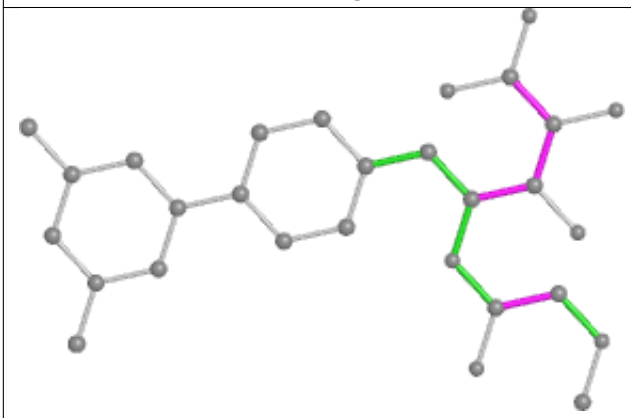
Ligand U94 B 1



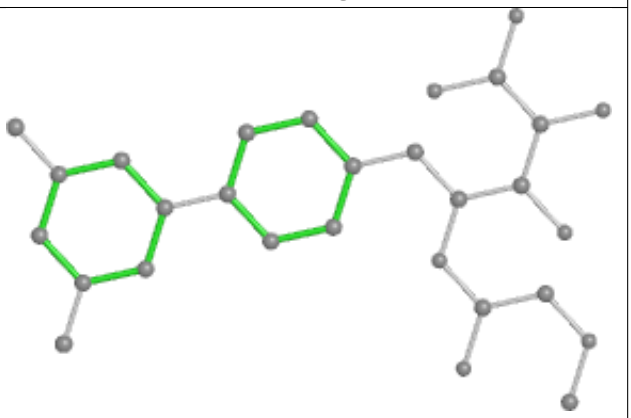
Bond lengths



Bond angles

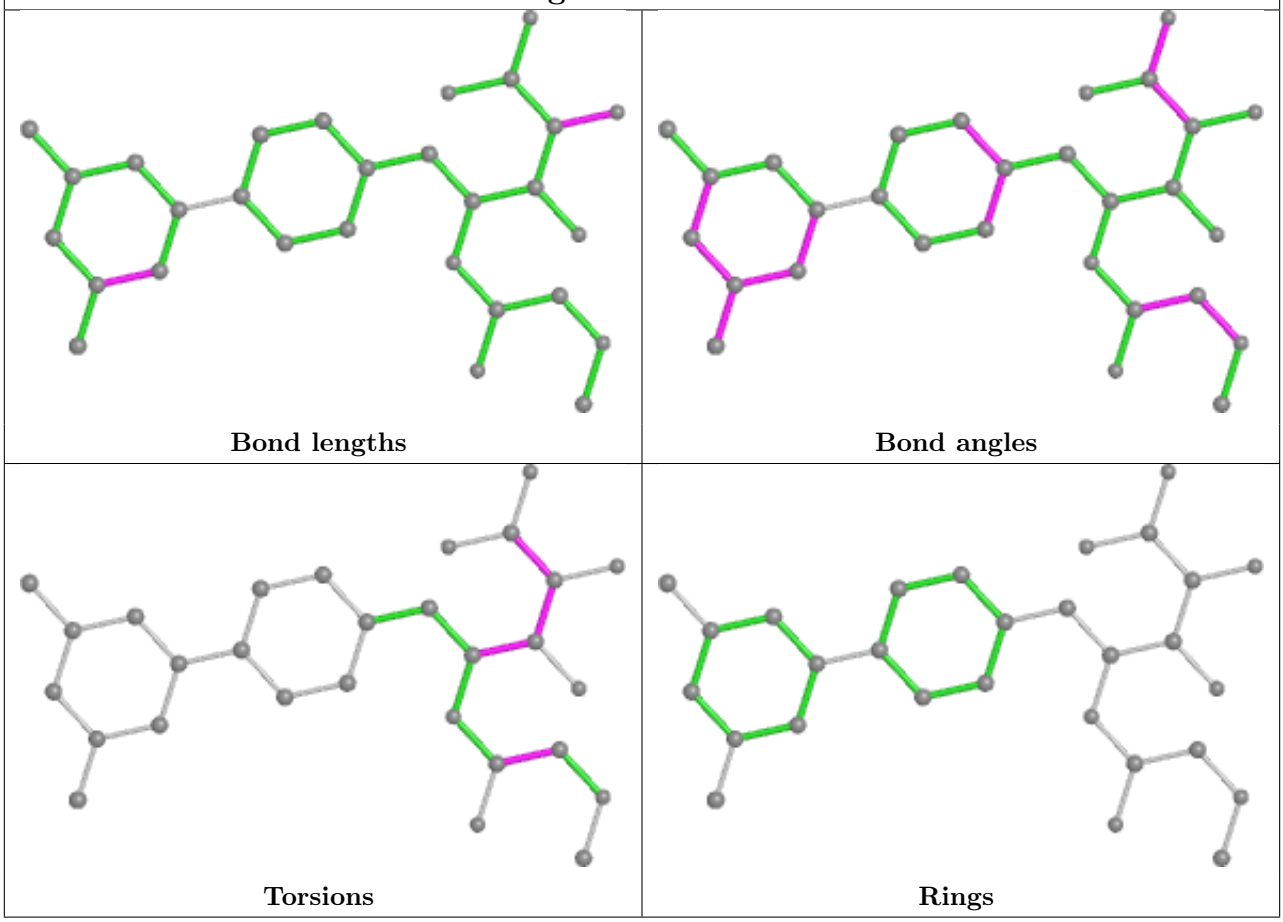


Torsions

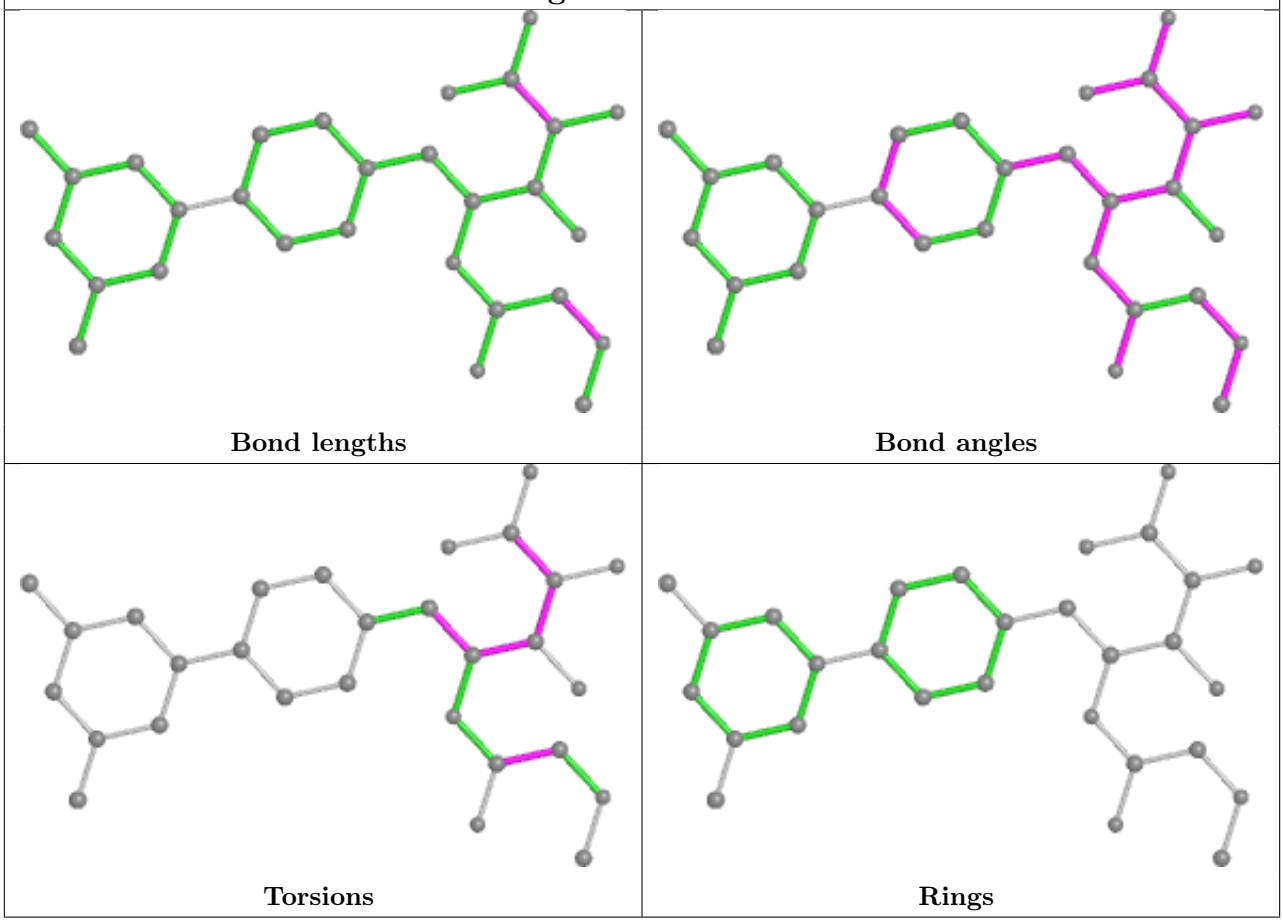


Rings

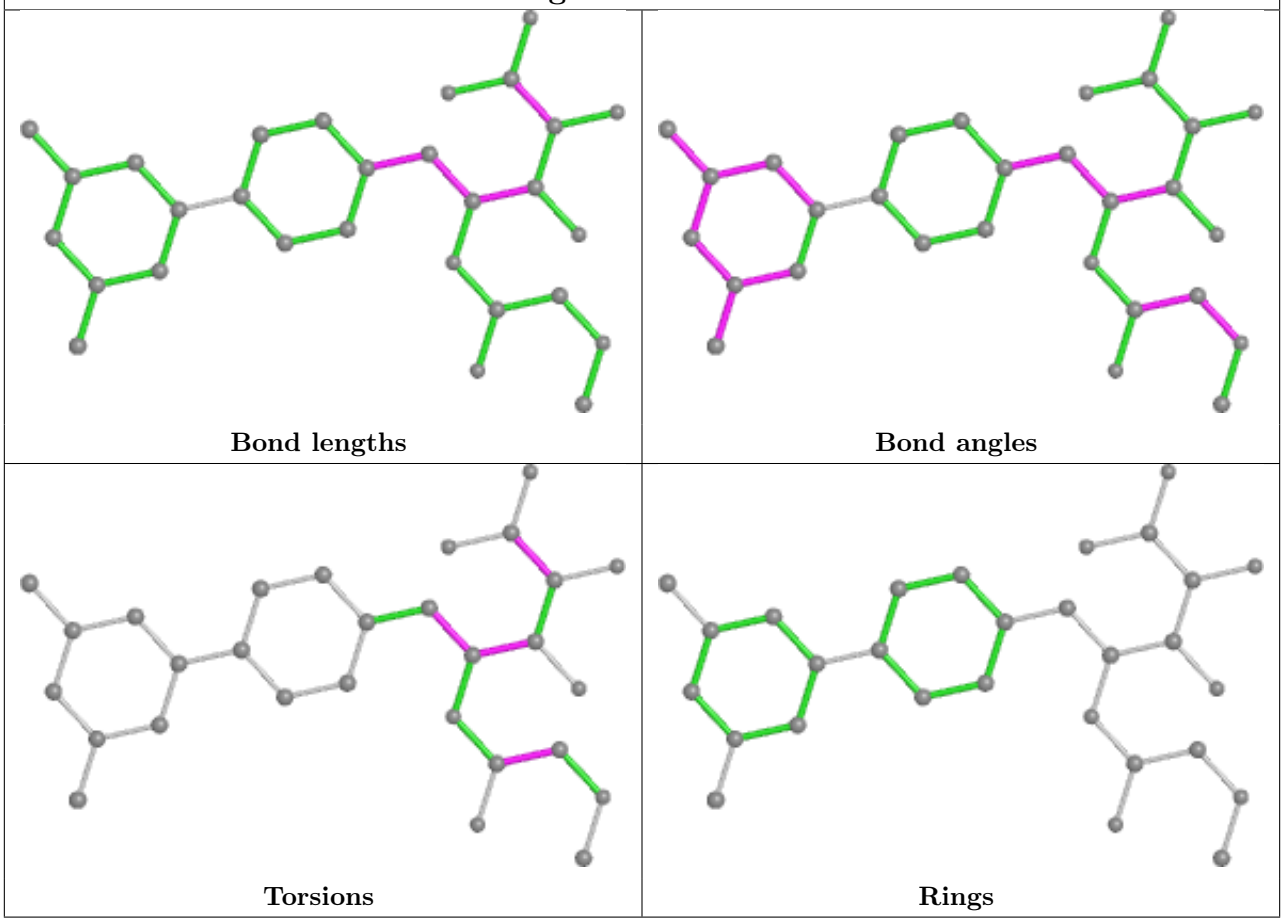
Ligand U94 D 1



Ligand U94 A 1



Ligand U94 C 1



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	164/183 (89%)	0.18	4 (2%)	59	66	25, 31, 54, 64	0
1	B	164/183 (89%)	0.26	5 (3%)	50	57	26, 36, 59, 73	0
1	C	156/183 (85%)	0.26	8 (5%)	28	35	28, 44, 68, 84	0
1	D	146/183 (79%)	0.36	9 (6%)	20	26	28, 45, 72, 90	0
All	All	630/732 (86%)	0.26	26 (4%)	37	44	25, 39, 64, 90	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	156	GLY	5.9
1	D	36	GLY	4.0
1	B	137	PHE	3.7
1	D	157	LYS	3.7
1	C	114	TRP	3.3

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)

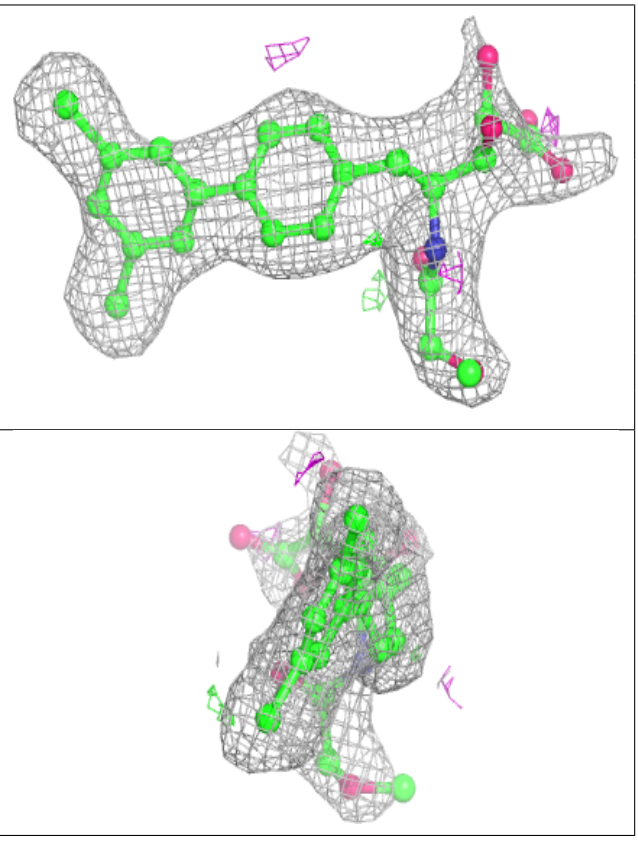
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	U94	D	1	29/29	0.79	0.21	62,68,86,89	0
2	U94	C	1	29/29	0.81	0.21	53,63,78,78	0
2	U94	A	1	29/29	0.85	0.21	49,54,73,74	0
2	U94	B	1	29/29	0.90	0.20	47,50,64,67	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.

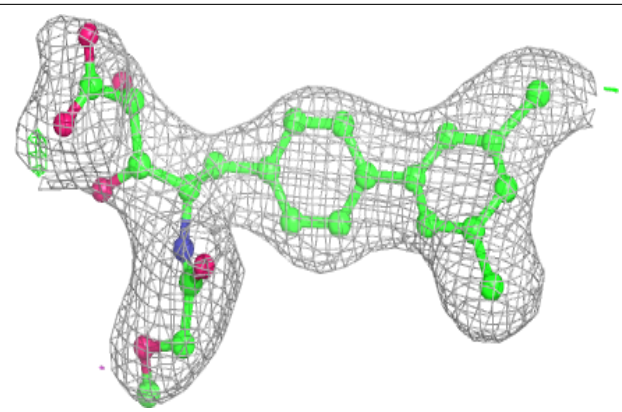
Electron density around U94 D 1:

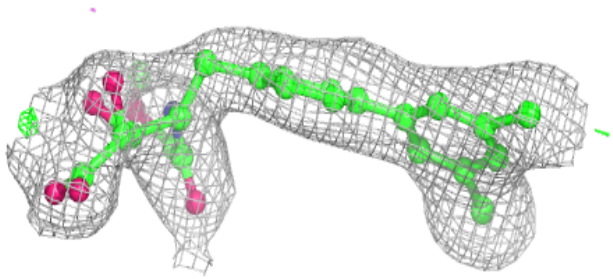
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

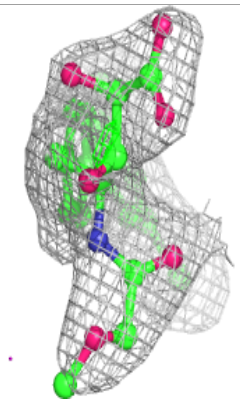


Electron density around U94 C 1:

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

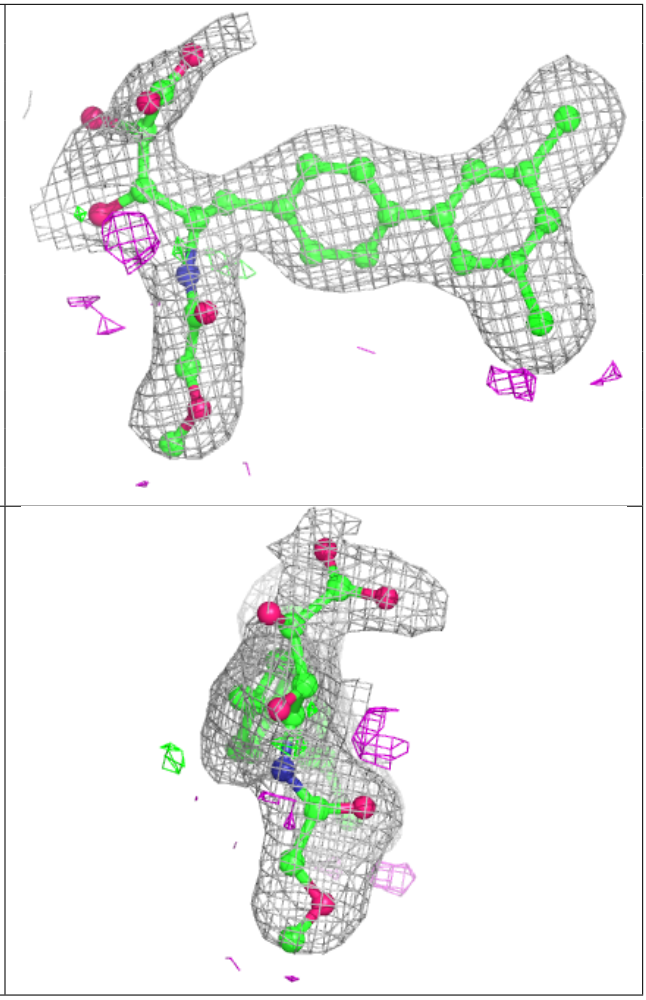






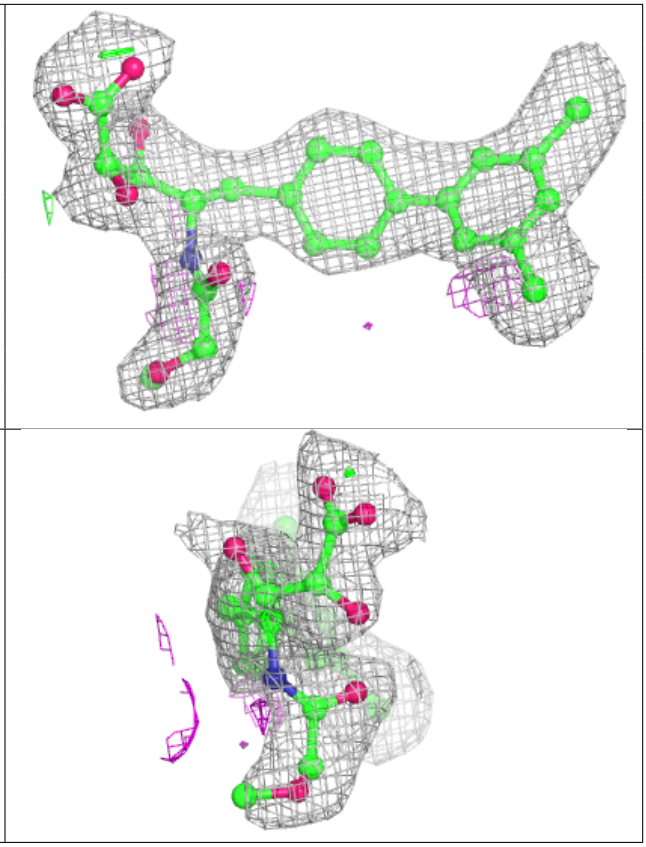
Electron density around U94 A 1:

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



Electron density around U94 B 1:

$2mF_o$-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.