

Full wwPDB X-ray Structure Validation Report (i)

May 28, 2020 - 12:42 am BST

:	4NV5
:	C50A mutant of Synechococcus VKOR, C2 crystal form (dehydrated)
:	Liu, S.; Cheng, W.; Fowle Grider, R.; Shen, G.; Li, W.
	2013-12-04
:	2.79 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

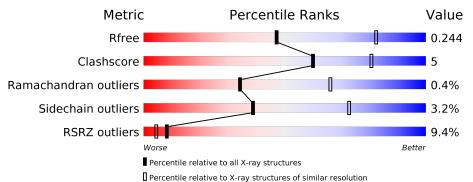
MolProbity	:	4.02b-467
e e e e e e e e e e e e e e e e e e e	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.79 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	3140(2.80-2.80)
Clashscore	141614	3569(2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	А	291	8%	8%	• 11%
1	В	291	9%	10%	10%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3995 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	259	Total	С	Ν	0	\mathbf{S}	0	0	0
	A	209	1956	1282	319	342	13	0	0	0
1	D	262	Total	С	Ν	Ο	S	0	0	0
	D	202	1973	1296	319	345	13	0	0	U

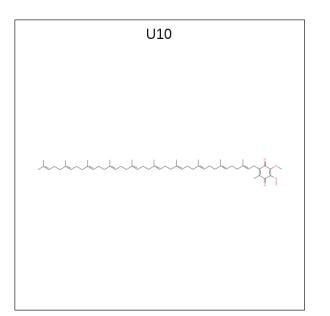
• Molecule 1 is a protein called VKORC1/thioredoxin domain protein.

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	ALA	CYS	ENGINEERED MUTATION	UNP Q2JJF6
A	284	LEU	-	EXPRESSION TAG	UNP Q2JJF6
A	285	GLU	-	EXPRESSION TAG	UNP Q2JJF6
A	286	HIS	-	EXPRESSION TAG	UNP Q2JJF6
A	287	HIS	-	EXPRESSION TAG	UNP Q2JJF6
A	288	HIS	-	EXPRESSION TAG	UNP Q2JJF6
A	289	HIS	-	EXPRESSION TAG	UNP Q2JJF6
A	290	HIS	-	EXPRESSION TAG	UNP Q2JJF6
A	291	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	50	ALA	CYS	ENGINEERED MUTATION	UNP Q2JJF6
В	284	LEU	-	EXPRESSION TAG	UNP Q2JJF6
В	285	GLU	-	EXPRESSION TAG	UNP Q2JJF6
В	286	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	287	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	288	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	289	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	290	HIS	-	EXPRESSION TAG	UNP Q2JJF6
В	291	HIS	_	EXPRESSION TAG	UNP Q2JJF6

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



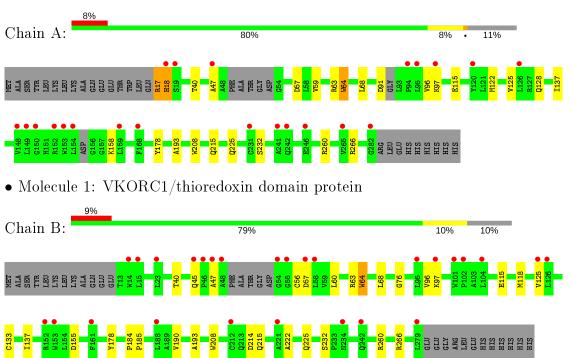


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total C O 33 29 4	0	0
2	В	1	Total C O 33 29 4	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: VKORC1/thioredoxin domain protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	140.84Å 118.82Å 68.03Å	Deneiten
a, b, c, α , β , γ	90.00° 89.85° 90.00°	Depositor
Resolution (Å)	37.80 - 2.79	Depositor
Resolution (A)	37.74 - 2.79	EDS
% Data completeness	99.1 (37.80-2.79)	Depositor
(in resolution range)	99.2 (37.74 - 2.79)	EDS
R _{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.91 (at 2.81 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
D D	0.232 , 0.245	Depositor
R, R_{free}	0.231 , 0.244	DCC
R _{free} test set	2743 reflections (9.96%)	wwPDB-VP
Wilson B-factor $(Å^2)$	73.3	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.30 , 31.5	EDS
L-test for twinning ²	$< L >=0.41, < L^2>=0.24$	Xtriage
Estimated twinning fraction	0.297 for -h,-k,l	Xtriage
Percented twinning fraction	0.664 for H, K, L	Depositor
Reported twinning fraction	0.336 for h,-k,-l	Depositor
Outliers	0 of 27546 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3995	wwPDB-VP
Average B, all atoms $(Å^2)$	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.41% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: U10 $\,$

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	
	Cham	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.28	0/2006	0.47	0/2741
1	В	0.29	0/2026	0.47	0/2775
All	All	0.29	0/4032	0.47	0/5516

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	А	1956	0	1976	15	1
1	В	1973	0	1990	19	0
2	А	33	0	39	3	0
2	В	33	0	39	5	0
All	All	3995	0	4044	37	1

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 5.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:B:215:GLN:HE22	1:B:266:ARG:H	1.28	0.80
1:A:215:GLN:HE22	1:A:266:ARG:H	1.30	0.79
1:A:63:ARG:O	1:A:64:TRP:HB2	1.95	0.66
1:B:63:ARG:O	1:B:64:TRP:HB2	1.97	0.63
1:A:59:VAL:HG13	2:A:501:U10:H3M3	1.81	0.63
1:A:215:GLN:NE2	1:A:266:ARG:H	1.97	0.62
1:B:215:GLN:NE2	1:B:266:ARG:H	1.99	0.60
1:B:60:LEU:HD23	2:B:501:U10:H4M3	1.83	0.60
1:B:115:GLU:HG3	1:B:137:ILE:HG12	1.84	0.58
1:B:118:MET:HB3	2:B:501:U10:H1M3	1.85	0.57
1:A:63:ARG:O	1:A:64:TRP:CB	2.55	0.54
1:B:63:ARG:O	1:B:64:TRP:CB	2.56	0.54
1:A:115:GLU:HG3	1:A:137:ILE:HG12	1.89	0.54
1:A:17:ARG:HG2	1:A:18:HIS:N	2.23	0.54
1:A:64:TRP:HA	1:A:178:TYR:CE1	2.43	0.53
1:A:40:THR:HG21	1:A:47:ALA:HB2	1.90	0.53
1:A:193:ALA:HB1	1:A:225:GLN:HB2	1.91	0.50
1:B:40:THR:HG23	1:B:45:GLN:O	2.12	0.50
1:B:193:ALA:HB1	1:B:225:GLN:HB2	1.94	0.48
1:A:208:TRP:CZ3	1:A:232:SER:HB2	2.48	0.48
1:A:115:GLU:HG2	1:A:137:ILE:HA	1.96	0.47
1:B:133:CYS:HB3	2:B:501:U10:H1M2	1.98	0.46
1:B:64:TRP:HA	1:B:178:TYR:CE1	2.50	0.46
1:B:76:GLY:HA3	2:B:501:U10:H112	1.98	0.46
1:B:208:TRP:CZ3	1:B:232:SER:HB2	2.50	0.46
1:B:40:THR:HG21	1:B:47:ALA:HB2	1.99	0.45
2:B:501:U10:H72	2:B:501:U10:H1M1	1.77	0.43
1:A:91:ASP:HB2	1:A:97:LYS:HB2	2.01	0.43
1:B:115:GLU:HG2	1:B:137:ILE:HA	2.00	0.43
1:A:122:MET:HB3	1:A:128:GLN:O	2.19	0.43
1:B:96:VAL:HG23	1:B:97:LYS:H	1.84	0.42
1:B:190:VAL:HG22	1:B:222:ALA:HB2	2.02	0.42
1:B:56:CYS:HB3	1:B:60:LEU:HD12	2.01	0.42
2:A:501:U10:H1M1	2:A:501:U10:H103	2.02	0.41
2:A:501:U10:C4M	2:A:501:U10:O3	2.67	0.41
1:B:184:PRO:HA	1:B:185:PRO:HD3	1.91	0.41
1:A:96:VAL:HG23	1:A:97:LYS:H	1.86	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:GLN:NE2	1:A:225:GLN:NE2[2_554]	2.17	0.03

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	Perce	ntiles
1	А	251/291~(86%)	246~(98%)	4 (2%)	1 (0%)	34	66
1	В	258/291~(89%)	252~(98%)	5(2%)	1 (0%)	34	66
All	All	509/582~(88%)	498~(98%)	9(2%)	2(0%)	34	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	64	TRP
1	В	64	TRP

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	А	201/229~(88%)	194~(96%)	7 (4%)	36 70
1	В	202/229~(88%)	196~(97%)	6 (3%)	41 75
All	All	403/458~(88%)	390~(97%)	13 (3%)	39 73

All (13) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	17	ARG
1	А	18	HIS
1	А	57	ASP
1	А	68	LEU
1	А	125	VAL
1	А	158	LYS
1	А	260	ARG
1	В	57	ASP
1	В	68	LEU
1	В	125	VAL
1	В	155	ASP
1	В	214	ASP
1	В	260	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	45	GLN
1	А	215	GLN
1	В	45	GLN
1	В	215	GLN
1	В	242	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.



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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	Tune	Chain	Res Link		Bo	ond leng	\mathbf{ths}	В	ond ang	les
IVIOI	Type	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	U10	А	501	-	$33,\!33,\!63$	1.65	2 (6%)	$40,\!43,\!79$	1.30	8 (20%)
2	U10	В	501	-	$33,\!33,\!63$	1.59	2 (6%)	40,43,79	1.33	5 (12%)

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	U10	А	501	-	-	7/27/51/87	0/1/1/1
2	U10	В	501	-	-	4/27/51/87	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	А	501	U10	C6-C1	8.33	1.50	1.35
2	В	501	U10	C6-C1	7.88	1.49	1.35
2	А	501	U10	C4-C3	3.27	1.49	1.36
2	В	501	U10	C4-C3	3.18	1.49	1.36

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	501	U10	C15-C14-C16	3.05	120.40	115.27
2	В	501	U10	C20-C19-C21	2.93	120.21	115.27
2	В	501	U10	C1M-C1-C6	-2.77	119.87	124.40
2	А	501	U10	C20-C19-C21	2.45	119.39	115.27
2	В	501	U10	C7-C8-C9	-2.39	122.82	126.79
2	В	501	U10	C15-C14-C16	2.33	119.19	115.27
2	А	501	U10	C10-C9-C11	2.25	119.06	115.27
2	А	501	U10	C7-C8-C9	-2.19	123.15	126.79
2	В	501	U10	C10-C9-C11	2.16	118.91	115.27
2	А	501	U10	C26-C24-C25	2.14	119.33	114.60

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Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	501	U10	C17-C18-C19	-2.08	122.66	127.66
2	А	501	U10	C4M-O4-C4	2.04	123.71	116.47
2	А	501	U10	C12-C13-C14	-2.01	122.82	127.66

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There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	501	U10	C14-C16-C17-C18
2	В	501	U10	C19-C21-C22-C23
2	А	501	U10	C15-C14-C16-C17
2	А	501	U10	C13-C14-C16-C17
2	В	501	U10	C12-C11-C9-C8
2	В	501	U10	C12-C11-C9-C10
2	А	501	U10	C9-C11-C12-C13
2	А	501	U10	C5-C4-O4-C4M
2	А	501	U10	C12-C11-C9-C10
2	В	501	U10	C15-C14-C16-C17
2	А	501	U10	С12-С11-С9-С8

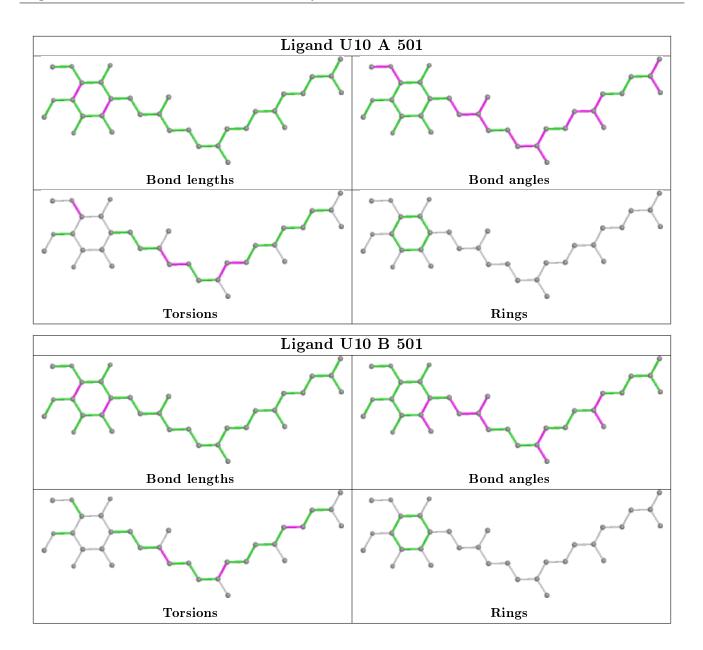
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	501	U10	3	0
2	В	501	U10	5	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.





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, 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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	259/291~(89%)	0.85	22 (8%) 10 5	54, 70, 103, 120	0
1	В	262/291~(90%)	0.94	27 (10%) 6 3	63, 78, 114, 132	0
All	All	521/582~(89%)	0.90	49 (9%) 8 4	54, 75, 109, 132	0

All (49) RSRZ outliers are listed below:

Mol	Chain	in Res Type		RSRZ	
1	В	54	GLY	9.0	
1	А	154	LEU	8.2	
1	А	242	GLN	6.2	
1	В	45	GLN	6.2	
1	В	48	ALA	5.9	
1	В	46	PRO	5.9	
1	В	14	TRP	4.5	
1	А	153	TRP	4.4	
1	А	265	VAL	4.3	
1	А	246	GLU	4.3	
1	А	282	GLY	4.3	
1	А	152	ARG	4.2	
1	А	94	PRO	4.1	
1	А	159	LEU	4.1	
1	В	15	LEU	4.1	
1	А	47	ALA	3.9	
1	В	279	LEU	3.9	
1	В	55	GLY	3.6	
1	В	95	LEU	3.4	
1	В	153	TRP	3.3	
1	В	221	ALA	3.3	
1	А	95	LEU	3.3	
1	В	152	ARG	3.2	
1	В	188	LEU	2.9	

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Mol	Chain	Res	Type	RSRZ
1	В	242	GLN	2.9
1	В	58	LEU	2.8
1	В	125	VAL	2.8
1	В	57	ASP	2.8
1	В	104	LEU	2.7
1	В	234	ASN	2.7
1	А	120	TYR	2.7
1	А	148	VAL	2.6
1	В	97	LYS	2.5
1	В	47	ALA	2.4
1	А	19	SER	2.4
1	А	241	ALA	2.3
1	А	126	LEU	2.3
1	А	149	LEU	2.2
1	В	23	LEU	2.2
1	В	212	CYS	2.2
1	В	126	LEU	2.2
1	А	150	GLY	2.1
1	В	101	TRP	2.1
1	А	168	PHE	2.1
1	А	97	LYS	2.1
1	А	231	CYS	2.1
1	А	18	HIS	2.1
1	В	102	PRO	2.1
1	В	161	PHE	2.0

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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 carbohydrates in this entry.

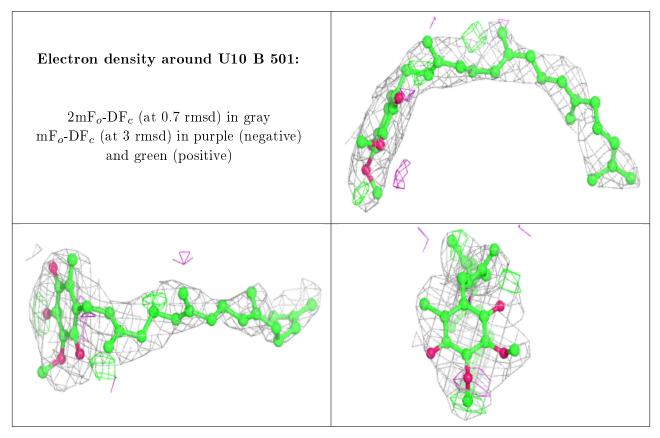
6.4 Ligands (i)

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, 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.

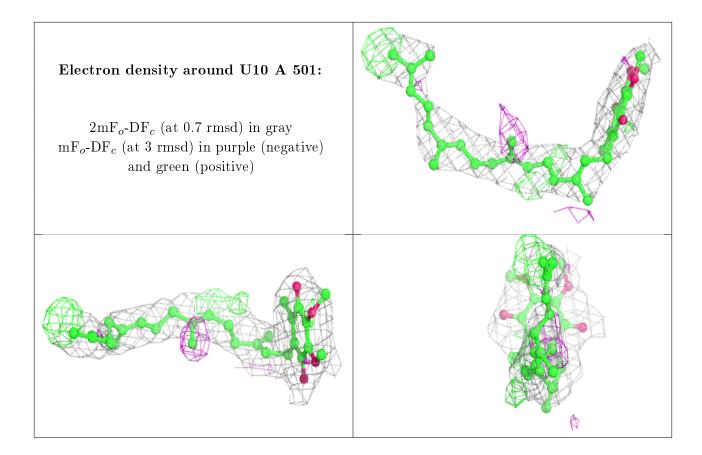


Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B} ext{-factors}({f A}^2)$	$Q{<}0.9$
2	U10	В	501	33/63	0.83	0.44	$73,\!80,\!85,\!86$	0
2	U10	А	501	33/63	0.87	0.38	$62,\!65,\!70,\!71$	0

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.







6.5 Other polymers (i)

There are no such residues in this entry.

