

Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 02:45 PM JST

:	6JEZ
:	Covalent labeling of rVDR-LBD by turn-on fluorescent probe mediated by
	conjugate addition and cyclization
:	Kojima, H.; Yamamoto, K.; Itoh, T.
:	2019-02-07
:	2.30 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

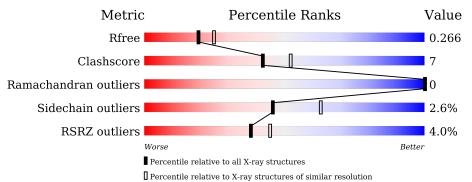
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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: $X\text{-}RAY \, DIFFRACTION$

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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
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 chair	n	
1	А	271	3%	77%	11%	11%
2	С	13	23%	38%	8%	15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EJO	А	502	-	-	Х	Х



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Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2111 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 Vitamin D3 receptor, Vitamin D3 receptor.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	240	Total 1917	C 1219	N 326	0 361	S 11	0	1	0

Chain Modelled Residue Actual Comment Reference UNP P13053 А 106 GLY _ expression tag SER А 107 expression tag UNP P13053 _ Α 108 HIS UNP P13053 expression tag -А 109MET expression tag <u>UNP</u> P13053 _ А 110GLY UNP P13053 _ expression tag А SER expression tag UNP P13053 111 _ А 112PRO expression tag UNP P13053 _ А 113ASN expression tag UNP P13053 _ А 114 SER expression tag UNP P13053 _ А PRO UNP P13053 115expression tag -А 211GLY linker UNP P13053 _ А 212 SER UNP P13053 linker _

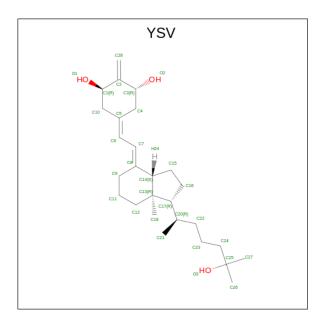
There are 12 discrepancies between the modelled and reference sequences:

• Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	С	11	Total 87	$\begin{array}{c} \mathrm{C} \\ 56 \end{array}$	N 16	O 13	${ m S} { m 2}$	0	0	0

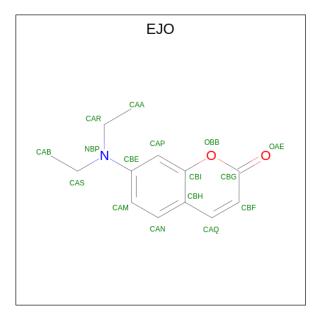
• Molecule 3 is (1R,3R)-5-(2-((1R,3aS,7aR,E)-1-((R)-6-hydroxy-6-methylheptan-2-yl)-7a-met hyloctahydro-4H-inden-4-ylidene)ethylidene)-2- methylenecyclohexane-1,3-diol (three-letter code: YSV) (formula: $C_{27}H_{44}O_3$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	Δ	1	Total	С	0	0	0
5	Π	1	30	27	3	0	0

• Molecule 4 is 7-(diethylamino)chromen-2-one (three-letter code: EJO) (formula: $C_{13}H_{15}NO_2$).



Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
4	А	1	Total 16	C 13	N 1	O 2	0	0

• Molecule 5 is water.



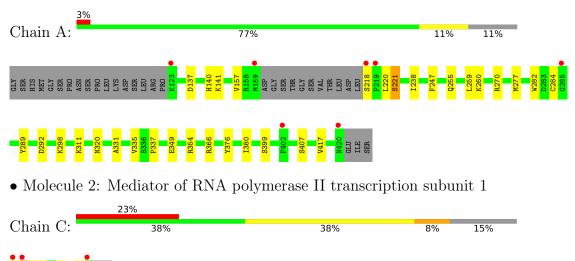
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	58	Total O 58 58	0	0
5	С	3	Total O 3 3	0	0



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: Vitamin D3 receptor, Vitamin D3 receptor





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	153.93Å 43.39Å 42.00Å	Depositor
a, b, c, α , β , γ	90.00° 95.30° 90.00°	Depositor
Resolution (Å)	29.18 - 2.30	Depositor
Resolution (A)	29.18 - 2.30	EDS
% Data completeness	98.7 (29.18-2.30)	Depositor
(in resolution range)	98.8 (29.18-2.30)	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$11.27 (at 2.31 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
D D.	0.202 , 0.256	Depositor
R, R_{free}	0.208 , 0.266	DCC
R_{free} test set	592 reflections $(4.80%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	28.1	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36 , 36.8	EDS
L-test for twinning ²	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2111	wwPDB-VP
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.22% 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: YSV, EJO

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).

Mal	Mol Chain		nd lengths	Bond angles		
NIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.75	1/1960~(0.1%)	0.81	4/2654~(0.2%)	
2	С	0.69	0/88	0.75	0/117	
All	All	0.75	1/2048~(0.0%)	0.81	4/2771~(0.1%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	282	TRP	CB-CG	-5.10	1.41	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
1	А	270	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	А	366	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	А	292	ASP	CB-CG-OD1	5.35	123.12	118.30
1	А	354	ARG	NE-CZ-NH1	5.12	122.86	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	А	1917	0	1915	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	С	87	0	91	9	0
3	А	30	0	0	0	0
4	А	16	0	0	7	0
5	А	58	0	0	0	0
5	С	3	0	0	0	0
All	All	2111	0	2006	28	0

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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 7.

All (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A. 1		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:140:HIS:CB	4:A:502:EJO:CAN	2.23	1.15
1:A:140:HIS:HB3	4:A:502:EJO:CAN	1.82	1.06
1:A:140:HIS:HB2	4:A:502:EJO:CAN	1.97	0.90
2:C:625:LYS:O	2:C:626:ASN:ND2	2.18	0.77
1:A:260:LYS:HE3	2:C:627:HIS:CE1	2.28	0.68
1:A:260:LYS:CE	2:C:627:HIS:CE1	2.82	0.63
1:A:376:TYR:CZ	1:A:380:ILE:HD11	2.34	0.62
1:A:260:LYS:HE3	2:C:627:HIS:HE1	1.65	0.61
1:A:140:HIS:CG	4:A:502:EJO:CAN	2.85	0.60
1:A:247:PHE:CE2	1:A:255:GLN:HG2	2.40	0.57
1:A:331:ALA:O	1:A:335:VAL:HG12	2.08	0.52
1:A:284:CYS:HB2	1:A:289:TYR:O	2.12	0.50
1:A:137:ASP:O	1:A:141:LYS:HG2	2.12	0.49
1:A:417:VAL:HG22	2:C:630:LEU:HD22	1.95	0.48
2:C:625:LYS:C	2:C:626:ASN:HD22	2.19	0.46
1:A:337:PRO:HG3	1:A:349:GLU:HA	1.97	0.46
1:A:141:LYS:HD3	4:A:502:EJO:CAR	2.47	0.45
1:A:137:ASP:OD1	4:A:502:EJO:CAP	2.65	0.44
1:A:260:LYS:CE	2:C:627:HIS:HE1	2.23	0.44
1:A:137:ASP:OD1	4:A:502:EJO:CBI	2.65	0.44
1:A:218:SER:HB2	1:A:221:SER:OG	2.18	0.43
1:A:238:ILE:HG12	1:A:259:LEU:HD13	2.00	0.43
2:C:627:HIS:N	2:C:628:PRO:HD3	2.33	0.43
1:A:220:LEU:HA	1:A:298:LYS:O	2.20	0.42
1:A:259:LEU:CD1	2:C:634:LEU:HD21	2.50	0.41
1:A:157:VAL:O	1:A:221:SER:HB3	2.21	0.41
1:A:311:LYS:HD3	1:A:311:LYS:HA	1.75	0.40
1:A:376:TYR:CE1	1:A:380:ILE:HD11	2.56	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	Perce	ntiles
1	А	237/271 (88%)	233~(98%)	4 (2%)	0	100	100
2	С	9/13~(69%)	9 (100%)	0	0	100	100
All	All	246/284~(87%)	242 (98%)	4 (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 side chain 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	218/247~(88%)	213~(98%)	5(2%)	50 67
2	С	10/13~(77%)	9 (90%)	1 (10%)	7 9
All	All	228/260~(88%)	222~(97%)	6 (3%)	46 63

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	221	SER
1	А	277	MET
1	А	320	ASN
1	А	399	SER
1	А	407	SER

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Mol	Chain	Res	Type
2	С	626	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	255	GLN
1	А	272	ASN
2	С	626	ASN
2	С	627	HIS

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)

2 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	Chain	Chain	Chain	Chain	Chain	Dec	Link	Bo	ond leng	$_{\rm ths}$	B	ond ang	gles
NIOI	Type	Chain	Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2					
3	YSV	А	501	-	30,32,32	0.81	1 (3%)	40,48,48	1.57	10 (25%)					
4	EJO	А	502	-	17,17,17	1.51	4 (23%)	23,23,23	1.59	4 (17%)					



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.

Ν	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	3	YSV	А	501	-	-	4/16/60/60	0/3/3/3
	4	EJO	А	502	-	-	7/8/8/8	0/2/2/2

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	А	502	EJO	CBH-CBI	3.63	1.48	1.41
4	А	502	EJO	CBF-CAQ	2.88	1.39	1.34
3	А	501	YSV	C13-C14	-2.85	1.51	1.56
4	А	502	EJO	CBH-CAQ	-2.45	1.39	1.44
4	А	502	EJO	CBF-CBG	-2.11	1.39	1.44

All (5) bond length outliers are listed below:

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	А	501	YSV	C6-C7-C8	-4.36	119.62	126.20
4	А	502	EJO	OBB-CBI-CAP	3.75	121.42	115.79
4	А	502	EJO	OAE-CBG-CBF	-3.57	119.37	126.00
3	А	501	YSV	C9-C8-C7	-3.38	121.42	125.26
3	А	501	YSV	C11-C12-C13	-3.16	109.24	113.17
3	А	501	YSV	C16-C17-C20	2.96	116.73	112.15
3	А	501	YSV	C7-C6-C5	-2.76	123.06	127.30
4	А	502	EJO	OBB-CBG-CBF	2.68	121.21	117.12
3	А	501	YSV	C13-C14-C8	-2.66	108.81	113.13
3	А	501	YSV	C22-C20-C17	2.41	115.25	110.28
4	А	502	EJO	OBB-CBG-OAE	2.34	119.42	116.44
3	А	501	YSV	C21-C20-C17	-2.29	109.42	112.92
3	А	501	YSV	C13-C17-C20	-2.16	116.10	119.49
3	А	501	YSV	C4-C5-C6	-2.05	119.03	123.44

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	501	YSV	C13-C17-C20-C22
3	А	501	YSV	C16-C17-C20-C21
3	А	501	YSV	C13-C17-C20-C21

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Mol	Chain	\mathbf{Res}	Type	Atoms
4	А	502	EJO	CAB-CAS-NBP-CBE
4	А	502	EJO	CAB-CAS-NBP-CAR
4	А	502	EJO	CAP-CBE-NBP-CAR
4	А	502	EJO	CAM-CBE-NBP-CAS
4	А	502	EJO	CAM-CBE-NBP-CAR
4	А	502	EJO	CAP-CBE-NBP-CAS
3	А	501	YSV	C16-C17-C20-C22
4	А	502	EJO	CAA-CAR-NBP-CBE

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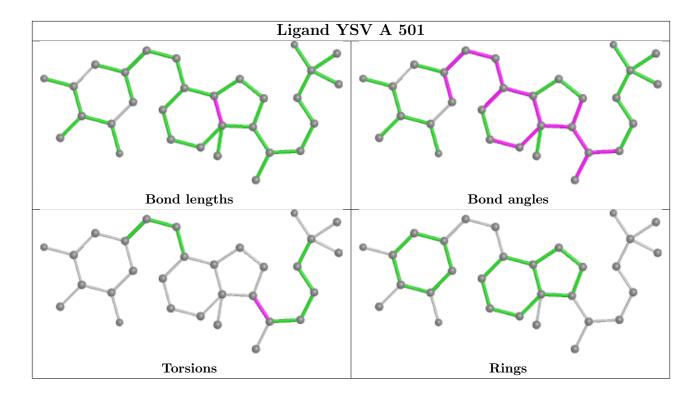
There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	502	EJO	7	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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	240/271~(88%)	0.29	7 (2%) 51 58	16, 31, 50, 73	0
2	С	11/13~(84%)	1.23	3 (27%) 0 0	38, 44, 65, 76	0
All	All	251/284~(88%)	0.33	10 (3%) 38 45	16, 31, 52, 76	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	218	SER	8.9
1	А	420	ASN	5.7
1	А	159	MET	5.7
1	А	402	PHE	4.8
2	С	625	LYS	4.4
1	А	285	GLY	3.6
1	А	219	PRO	3.2
2	С	626	ASN	3.1
2	С	635	LYS	2.8
1	А	123	LYS	2.3

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.

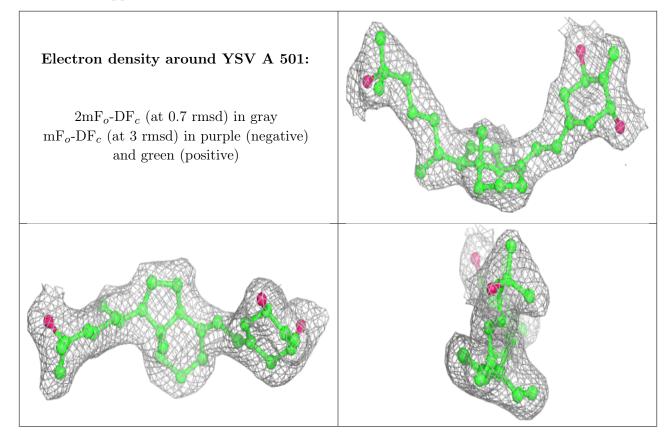


6.4 Ligands (i)

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, 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
4	EJO	А	502	16/16	0.65	0.66	$50,\!52,\!57,\!61$	16
3	YSV	А	501	30/30	0.95	0.21	20,21,29,31	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.

