

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 25, 2022 – 12:10 PM EDT

PDB ID : 7FL5

Title: PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment

P04H07 from the F2X-Universal Library

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Deposited on : 2022-08-26

Resolution : 1.89 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 as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.31.2

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

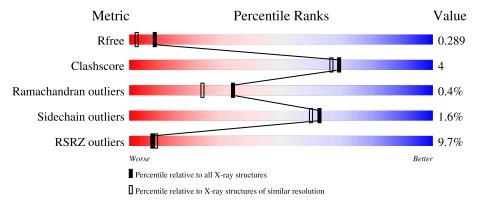
Validation Pipeline (wwPDB-VP) : 2.31.2

## 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 1.89 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	258	7%	12%	8%
2	В	308	11% 85%	12	2% • •



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9208 atoms, of which 4539 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	237	Total 4068	C 1287	H 2060	N 336	O 373	S 12	0	21	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
A	1833	GLY	-	expression tag	UNP P33334	
A	1834	ALA	-	expression tag	UNP P33334	
A	1835	MET	-	expression tag	UNP P33334	

• Molecule 2 is a protein called A1 cistron-splicing factor AAR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	В	300	Total 5044	C 1654	H 2464	N 421	O 485	S 20	0	17	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-3	GLY	=	expression tag	UNP P32357
В	-2	ALA	-	expression tag	UNP P32357
В	-1	MET	-	expression tag	UNP P32357
В	0	ALA	-	expression tag	UNP P32357
В	166	SER	LEU	$\operatorname{conflict}$	UNP P32357
В	167	SER	LYS	$\operatorname{conflict}$	UNP P32357
В	?	-	LEU	deletion	UNP P32357
В	?	-	GLN	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357
В	?	-	ALA	deletion	UNP P32357
В	?	-	GLY	deletion	UNP P32357
В	?	-	SER	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357

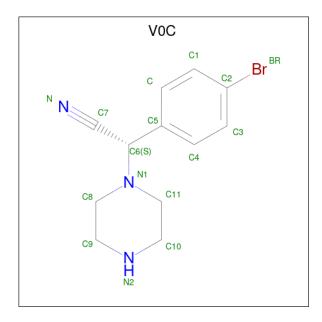
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Chain	Residue	Modelled	Actual	Comment	Reference
В	?	-	MET	deletion	UNP P32357
В	?	-	GLU	deletion	UNP P32357
В	?	-	ALA	deletion	UNP P32357
В	?	-	LYS	deletion	UNP P32357
В	?	-	ASN	deletion	UNP P32357
В	?	-	GLU	deletion	UNP P32357
В	170	SER	ASP	conflict	UNP P32357

 $\bullet$  Molecule 3 is (2S)-(4-bromophenyl) (piperazin-1-yl)acetonitrile (three-letter code: V0C) (formula:  $C_{12}H_{14}BrN_3).$ 



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	В	1	Total				N	0	0
			31	T	12	15	3		

• Molecule 4 is water.

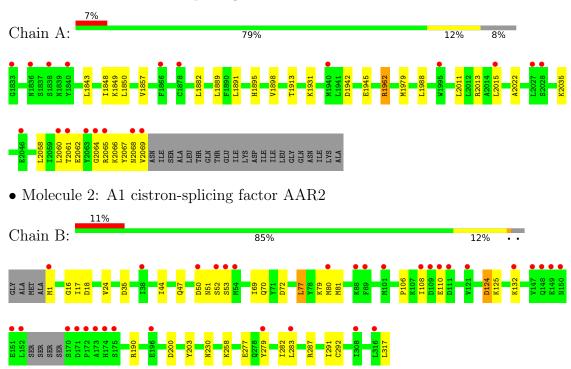
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	34	Total O 34 34	0	0
4	В	31	Total O 31 31	0	0



# 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: Pre-mRNA-splicing factor 8





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	89.67Å 81.67Å 92.93Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 108.43° 90.00°	Depositor
Resolution (Å)	42.54 - 1.89	Depositor
rtesolution (A)	44.67 - 1.89	EDS
% Data completeness	99.4 (42.54-1.89)	Depositor
(in resolution range)	99.5 (44.67-1.89)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.96 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D.D.	0.243 , 0.283	Depositor
$R, R_{free}$	0.257 , $0.289$	DCC
$R_{free}$ test set	2100 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.4	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39, 49.3	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.50, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9208	wwPDB-VP
Average B, all atoms $(Å^2)$	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: V0C

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		nd lengths	Bond angles		
Moi Chair		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.69	$2/2149 \ (0.1\%)$	0.84	8/2911 (0.3%)	
2	В	0.77	$4/2739 \ (0.1\%)$	0.83	4/3699 (0.1%)	
All	All	0.73	6/4888 (0.1%)	0.83	$12/6610 \ (0.2\%)$	

#### All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
2	В	230[A]	ASN	C-O	6.05	1.34	1.23
2	В	230[B]	ASN	C-O	6.05	1.34	1.23
2	В	292	CYS	CB-SG	-5.86	1.72	1.81
1	A	1945	GLU	CG-CD	5.55	1.60	1.51
1	A	1889	LEU	CG-CD1	5.25	1.71	1.51
2	В	24	VAL	CB-CG2	5.01	1.63	1.52

All (12) bond angle outliers are listed below:

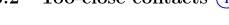
Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	200	ASP	CB-CG-OD1	8.19	125.67	118.30
1	A	1889	LEU	CB-CG-CD1	-7.66	97.98	111.00
1	A	1882	LEU	CB-CG-CD2	-6.32	100.25	111.00
1	A	1889	LEU	CB-CG-CD2	6.28	121.68	111.00
2	В	200	ASP	CB-CG-OD2	-6.28	112.65	118.30
1	A	1942	ASP	CB-CG-OD1	5.75	123.47	118.30
2	В	72	ASP	CB-CG-OD2	-5.68	113.19	118.30
1	A	2011	LEU	CB-CG-CD1	-5.57	101.53	111.00
1	A	1942	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	A	1850	LEU	CB-CG-CD2	-5.24	102.09	111.00
1	A	1891	LEU	CB-CG-CD2	5.04	119.57	111.00
2	В	18	ASP	CB-CG-OD1	-5.04	113.77	118.30



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	2008	2060	1974	13	0
2	В	2580	2464	2398	19	0
3	В	16	15	0	1	0
4	A	34	0	0	0	0
4	В	31	0	0	2	0
All	All	4669	4539	4372	34	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 4.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.08	0.87
2:B:1:MET:N	4:B:501:HOH:O	2.11	0.82
1:A:2062:GLU:OE1	1:A:2065:ARG:NH1	2.31	0.64
2:B:258:LYS:HD2	2:B:258:LYS:H	1.67	0.59
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.51	0.57
1:A:2064:GLY:O	1:A:2068:ASN:N	2.37	0.55
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.88	0.55
1:A:2058:LEU:C	1:A:2058:LEU:HD23	2.29	0.53
2:B:50:ASP:OD1	2:B:51:ASN:N	2.42	0.53
1:A:1895:HIS:O	1:A:1898[A]:VAL:HG22	2.10	0.51
1:A:2069:VAL:HG12	1:A:2069:VAL:O	2.10	0.51
3:B:401:V0C:C11	3:B:401:V0C:C	2.87	0.51
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.95	0.48
2:B:279:TYR:HB3	2:B:283:LEU:HD12	1.96	0.47
2:B:110:GLU:HG2	2:B:110:GLU:O	2.16	0.45
2:B:108:ILE:HD13	2:B:108:ILE:N	2.31	0.45
1:A:2015:LEU:HD23	1:A:2022:ALA:HB3	1.99	0.45
1:A:2061:THR:O	1:A:2064:GLY:N	2.48	0.45

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Atom-1	Atom-2	Interatomic	Clash
7100111 1	1100111 2	distance (Å)	overlap (Å)
2:B:47:GLN:NE2	2:B:52:SER:O	2.49	0.44
2:B:124:ASP:OD2	2:B:125:LYS:HD3	2.18	0.43
2:B:287:ARG:O	2:B:291:ILE:HD13	2.19	0.43
2:B:69:ILE:HD13	2:B:80:MET:HA	2.01	0.43
1:A:1857:VAL:HG21	1:A:1913:THR:OG1	2.20	0.42
2:B:17:ILE:HD12	2:B:44[B]:ILE:HG13	2.02	0.42
2:B:70:GLN:HB3	2:B:81:MET:HE1	2.01	0.42
2:B:51:ASN:HD21	2:B:53:SER:HB2	1.85	0.42
2:B:190:ARG:HG3	2:B:203[B]:TYR:CE2	2.55	0.41
2:B:17:ILE:CD1	2:B:44[B]:ILE:HG13	2.51	0.41
1:A:2035:LYS:HA	1:A:2035:LYS:HD3	1.93	0.40
2:B:277:GLU:H	2:B:277:GLU:CD	2.25	0.40
1:A:2066:LYS:HD2	1:A:2067:TYR:CE1	2.56	0.40
2:B:1:MET:HB3	2:B:35:ASP:HA	2.04	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	entiles
1	A	258/258 (100%)	249 (96%)	9 (4%)	0	100	100
2	В	315/308 (102%)	304 (96%)	9 (3%)	2 (1%)	25	15
All	All	573/566 (101%)	553 (96%)	18 (3%)	2 (0%)	34	31

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	132	LYS
2	В	106	PRO



#### 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	Perce	ntiles
1	A	237/233 (102%)	231 (98%)	6 (2%)	47	41
2	В	294/284 (104%)	290 (99%)	4 (1%)	67	65
All	All	531/517 (103%)	521 (98%)	10 (2%)	62	53

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1962	ARG
1	A	1979[A]	MET
1	A	1979[B]	MET
1	A	1979[C]	MET
1	A	1988	LEU
1	A	2060	LEU
2	В	77	LEU
2	В	124	ASP
2	В	282	ILE
2	В	317	LEU

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)

1 ligand is 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	Bo	ond leng	$ ag{ths}$	В	ond ang	les
IVIOI	Type	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	V0C	В	401	-	16,17,17	0.29	0	20,22,22	0.55	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
3	V0C	В	401	-	-	3/8/18/18	1/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	401	V0C	C7-C6-N1-C8
3	В	401	V0C	C7-C6-N1-C11
3	В	401	V0C	C4-C5-C6-C7

All (1) ring outliers are listed below:

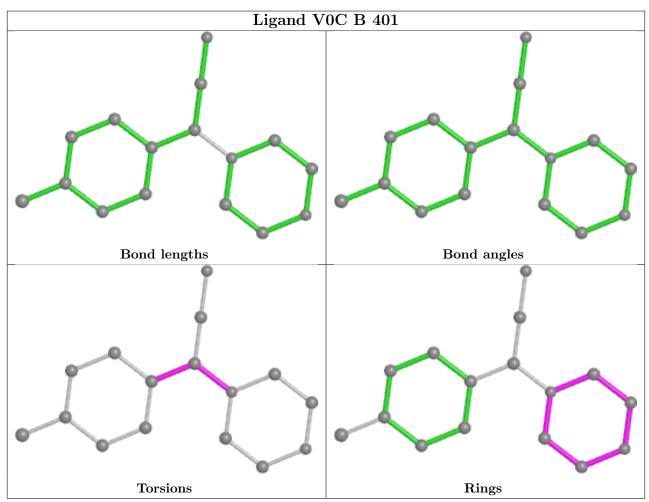
Mol	Chain	Res	Type	Atoms
3	В	401	V0C	C10-C11-C8-C9-N1-N2

1 monomer is involved in 1 short contact:

$\mathbf{Mol}$	Chain	$\operatorname{Res}$	Type	Clashes	Symm-Clashes
3	В	401	V0C	1	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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	$237/258 \ (91\%)$	0.82	19 (8%) 12 13	37, 60, 102, 153	0
2	В	300/308~(97%)	0.99	33 (11%) 5 6	39, 64, 106, 172	0
All	All	537/566~(94%)	0.91	52 (9%) 7 9	37, 63, 105, 172	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
2	В	53	SER	7.9	
2	В	1	MET	7.5	
2	В	172	PRO	7.5	
1	A	1833	GLY	6.5	
2	В	173	ALA	5.9	
1	A	2064	GLY	5.5	
2	В	52	SER	5.3	
1	A	2069	VAL	5.2	
2	В	174	HIS	5.0	
2	В	150	ASN	4.9	
1	1 A		SER	4.8	
1			TYR	4.5	
1	1 A		ASN	4.3	
1	1 A		SER	4.2	
2	В	171	ASP	4.2	
1	A	1878	CYS	4.0	
2	В	170	SER	3.9	
2	2 B		ASP	3.8	
1	1 A		THR	3.8	
2	2 B		MET	3.6	
1	A	1836	ASN	3.4	
2	В	108	ILE	3.2	
1	1 A		LEU	3.1	
1	A	2027	LEU	3.0	

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Mol	Chain	Res	Type	RSRZ
1	1 A		ARG	3.0
2	В	109 ASP		2.9
2	В	121	VAL	2.9
1	A	1866	PHE	2.9
2	В	279	TYR	2.7
2	В	110	GLU	2.7
2	В	148	GLN	2.7
1	A	1840	TYR	2.6
1	A	2046	GLU	2.6
2	В	151	GLU	2.6
2	В	80	MET	2.5
2	В	316	LEU	2.5
2	В	50	ASP	2.4
1	A	1940	MET	2.4
2	В	147	VAL	2.4
2	В	175	SER	2.4
1	A	1995	TRP	2.4
2	В	89	PHE	2.3
2	В	88	LYS	2.2
2	В	54[A]	MET	2.2
2	В	308	ILE	2.2
2	В	149	GLU	2.2
2	В	38	ILE	2.1
2	В	152 LEU		2.1
2	В	196	GLU	2.1
1	A	2015	LEU	2.1
2	В	283	LEU	2.0
2	В	132	LYS	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)

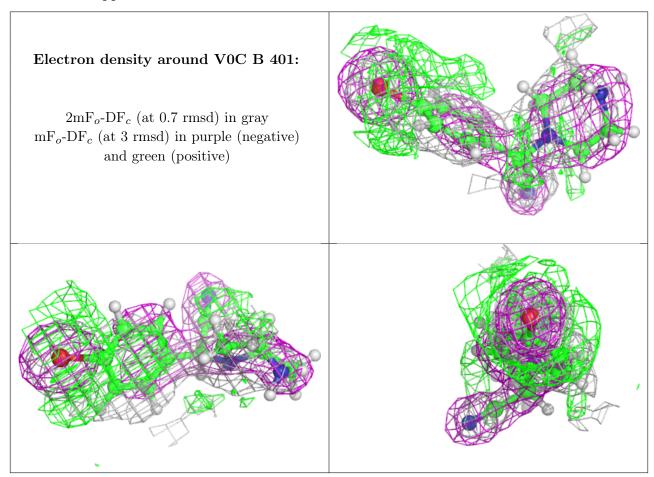
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



median,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	V0C	В	401	16/16	0.94	0.41	30,30,30,30	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.

