

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

May 26, 2020 – 08:01 am BST

PDB ID : 4GTV

Title: Engineered RabGGTase in complex with BMS analogue 13

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R.S.

Deposited on : 2012-08-29

Resolution : 1.95 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

Mogul: 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

CCP4 : 7.0.044 (Gargrove)

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

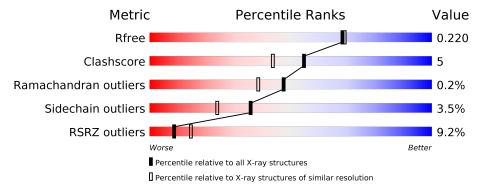
Validation Pipeline (wwPDB-VP) : 2.11

# 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 1.95 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
$R_{free}$	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	A	330	13%	7% • 7%
2	В	330	85%	12% ••



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5458 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 Geranylgeranyl transferase type-2 subunit alpha.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	307	Total	С	N	О	S	0	7	0
_	Λ	551	2498	1599	423	462	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled Actual		Comment	Reference	
A	238	ALA	_	LINKER	UNP Q08602	
A	239	GLY	-	LINKER	UNP Q08602	
A	240	SER	_	LINKER	UNP Q08602	
A	241	GLY	-	LINKER	UNP Q08602	

• Molecule 2 is a protein called Geranylgeranyl transferase type-2 subunit beta.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
2	В	324	Total 2533	C 1621	N 420	O 471	S 21	0	4	0

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

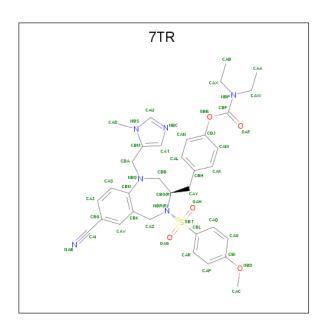
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total Zn 1 1	0	0

• Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Ca 1 1	0	0

• Molecule 5 is  $4-(\{(3R)-7-cyano-4-[(4-methoxyphenyl)sulfonyl]-1-[(1-methyl-1H-imidazol-5-yl)methyl]-2,3,4,5-tetrahydro-1H-1,4-benzodiazepin-3-yl}methyl)phenyl diethylcarbamate (three-letter code: 7TR) (formula: <math>C_{34}H_{38}N_6O_5S$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	D	1	Total	С	N	О	S	0	0
5	Б	1	46	34	6	5	1	0	0

### • Molecule 6 is water.

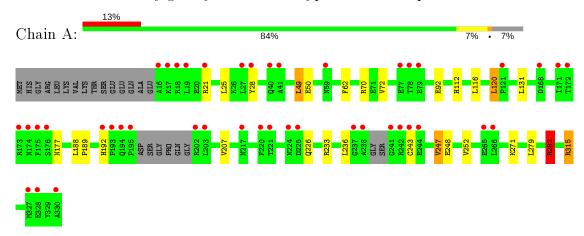
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	${f AltConf}$
6	A	157	Total O 157 157	0	0
6	В	222	Total O 222 222	0	0



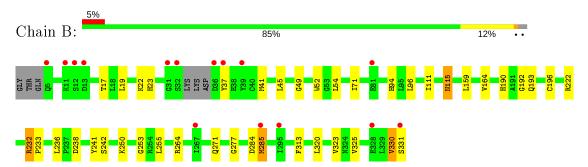
# 3 Residue-property plots (i)

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: Geranylgeranyl transferase type-2 subunit alpha



• Molecule 2: Geranylgeranyl transferase type-2 subunit beta





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	66.62Å 90.74Å 115.54Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 - 1.95	Depositor
resolution (A)	19.95 - 1.95	EDS
% Data completeness	98.7 (19.99-1.95)	Depositor
(in resolution range)	98.7 (19.95-1.95)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$< I/\sigma(I) > 1$	4.63 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
P. P.	0.168 , 0.211	Depositor
$R, R_{free}$	0.178 , $0.220$	DCC
$R_{free}$ test set	2565 reflections $(5.02\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.0	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38, 57.3	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5458	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.29% 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: ZN, CA, 7TR

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.44	0/2578	0.54	3/3501 (0.1%)	
2	В	0.47	0/2604	0.59	$2/3532 \ (0.1\%)$	
All	All	0.46	0/5182	0.57	5/7033 (0.1%)	

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	315	ARG	NE-CZ-NH2	-6.58	117.01	120.30
2	В	232	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	315	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	A	282	ARG	NE-CZ-NH2	-5.68	117.46	120.30
2	В	232	ARG	NE-CZ-NH1	5.04	122.82	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	2498	0	2436	20	0
2	В	2533	0	2480	33	0
3	В	1	0	0	0	0
4	В	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
5	В	46	0	38	0	0
6	A	157	0	0	11	0
6	В	222	0	0	7	0
All	All	5458	0	4954	52	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 5.

All (52) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1       Atom-2         2:B:323:VAL:HG23       2:B:325:VAL:HG12         1:A:131:LEU:HD21       6:A:448:HOH:O         2:B:94:HIS:HD2       2:B:96:LEU:H         2:B:323:VAL:CG2       2:B:325:VAL:HG12	1.74 1.33 2 2.24	0.94 0.86 0.74
1:A:131:LEU:HD21 6:A:448:HOH:O 2:B:94:HIS:HD2 2:B:96:LEU:H	1.74 1.33 2 2.24	0.86 0.74
2:B:94:HIS:HD2 2:B:96:LEU:H	1.33 2 2.24	0.74
	2 2.24	
2:B:323:VAL:CG2 2:B:325:VAL:HG12		
		0.65
2:B:190:HIS:HD2 2:B:192:GLY:H	1.45	0.64
2:B:23:HIS:HD1 2:B:277:GLY:H	1.43	0.63
1:A:131:LEU:CD2 6:A:448:HOH:O	2.40	0.62
1:A:226:GLN:NE2 6:A:411:HOH:O	2.34	0.61
2:B:264:ARG:NE 6:B:720:HOH:O	2.36	0.57
2:B:17:THR:HG22 6:B:637:HOH:O	2.03	0.57
2:B:37:TYR:O 2:B:41:MET:HG2	2.05	0.55
2:B:54:LEU:HD11 2:B:71:ILE:HD13	1.88	0.55
2:B:19:LEU:H 2:B:271:GLN:HE22	2 1.55	0.55
1:A:131:LEU:HD11 6:A:448:HOH:O	2.06	0.55
2:B:94:HIS:HE1 6:B:514:HOH:O	1.93	0.52
1:A:315:ARG:HD2 6:A:515:HOH:O	2.10	0.51
2:B:115:ASN:C 2:B:115:ASN:HD22	2 2.13	0.51
2:B:320:LEU:HD22 2:B:325:VAL:HG13	3 1.93	0.51
2:B:285:MET:HA 2:B:285:MET:CE	2.43	0.49
1:A:92:GLU:OE2 1:A:112:HIS:HE1	1.95	0.48
2:B:284:ASP:OD1 6:B:659:HOH:O	2.20	0.48
2:B:238:ASP:HB3 2:B:241:TYR:CD2	2.48	0.48
1:A:70:ARG:HH11 1:A:112:HIS:HD2	1.62	0.48
2:B:330:VAL:O 2:B:330:VAL:HG12	2 2.14	0.47
2:B:232:ARG:HD3 6:B:628:HOH:O	2.15	0.47
1:A:233:ARG:HG3 1:A:279:LEU:HD13	3 1.97	0.46
2:B:164:VAL:HG23 6:B:547:HOH:O	2.14	0.46
2:B:190:HIS:HD2 2:B:192:GLY:N	2.13	0.46
2:B:94:HIS:CD2 2:B:96:LEU:H	2.22	0.46
1:A:131:LEU:CD1 6:A:448:HOH:O	2.64	0.46

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A 4 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \; ({\rm \AA})$	$overlap(\AA)$
1:A:226:GLN:NE2	6:A:434:HOH:O	2.39	0.45
2:B:190:HIS:CD2	2:B:192:GLY:H	2.28	0.45
2:B:250:LYS:HD3	2:B:255:LEU:HD22	1.99	0.45
2:B:253:GLY:HA3	2:B:330:VAL:O	2.16	0.45
1:A:188:LEU:HB2	1:A:189:PRO:HD3	1.98	0.44
2:B:323:VAL:HG23	2:B:325:VAL:CG1	2.32	0.44
1:A:116:LEU:O	1:A:120:LEU:HD13	2.18	0.44
2:B:45:LEU:C	2:B:45:LEU:HD12	2.39	0.43
2:B:325:VAL:HG13	2:B:325:VAL:O	2.18	0.43
2:B:49:GLY:HA2	2:B:52:TRP:CE3	2.54	0.43
1:A:247:VAL:HG13	6:A:501:HOH:O	2.18	0.43
1:A:282:ARG:HD2	6:A:405:HOH:O	2.18	0.43
1:A:177:ASN:ND2	6:A:428:HOH:O	2.51	0.43
2:B:232:ARG:HB2	2:B:233:PRO:CD	2.49	0.43
2:B:313:PHE:HB2	2:B:320:LEU:HD11	2.00	0.43
1:A:282:ARG:CD	6:A:405:HOH:O	2.67	0.42
1:A:248:GLU:O	1:A:252:VAL:HG23	2.20	0.42
2:B:193:GLN:HA	2:B:196[B]:CYS:SG	2.60	0.42
1:A:49:LEU:HD13	1:A:72:VAL:HG11	2.02	0.41
1:A:192:HIS:CE1	1:A:207:VAL:HG21	2.55	0.41
1:A:28[B]:TYR:CE1	2:B:41:MET:HE3	2.56	0.41
2:B:242:SER:CB	6:B:701:HOH:O	2.68	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	308/330 (93%)	303 (98%)	5 (2%)	0	100	100
2	В	324/330 (98%)	321 (99%)	2 (1%)	1 (0%)	41	30
All	All	632/660 (96%)	624 (99%)	7 (1%)	1 (0%)	47	38



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
2	В	330	VAL	

#### 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	$269/292 \ (92\%)$	258 (96%)	11 (4%)	30 18		
2	В	278/283 (98%)	270 (97%)	8 (3%)	42 31		
All	All	547/575 (95%)	528 (96%)	19 (4%)	36 24		

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Α	21	ARG
1	A	25	LEU
1	Α	49	LEU
1	A	50	GLU
1	A	62	PHE
1	A	120	LEU
1	A	236	LEU
1	A	243	CYS
1	A	247	VAL
1	Α	271	LYS
1	Α	282	ARG
2	В	22	LYS
2	В	111	ILE
2	В	115	ASN
2	В	159	LEU
2	В	222	ARG
2	В	236	LEU
2	В	285	MET
2	В	331	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:



Mol	Chain	Res	Type
1	Α	33	GLN
1	A	54	GLN
1	A	112	HIS
1	A	177	ASN
1	A	216	GLN
1	A	217	ASN
1	A	226	GLN
1	A	264	GLN
2	В	94	HIS
2	В	115	ASN
2	В	176	ASN
2	В	190	HIS
2	В	271	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)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	ths	В	ond ang	gles
MIOI	туре	Chain	res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	7TR	В	403	3	44,50,50	1.81	5 (11%)	60,71,71	1.86	10 (16%)



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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
5	7TR	В	403	3	-	3/36/52/52	0/4/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
5	В	403	7TR	OAG-SBT	5.95	1.50	1.43
5	В	403	7TR	OAH-SBT	5.84	1.50	1.43
5	В	403	7TR	CBN-NBQ	-5.82	1.33	1.43
5	В	403	7TR	SBT-NBR	4.02	1.69	1.63
5	В	403	7TR	CBA-CBM	2.02	1.54	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
5	В	403	7TR	OBE-CBF-NBP	7.45	117.99	110.75
5	В	403	7TR	OAH-SBT-OAG	-7.10	108.02	119.52
5	В	403	7TR	CAZ-CBK-CAV	-4.68	113.16	119.17
5	В	403	7TR	NBC-CAU-NBS	-3.84	106.56	112.26
5	В	403	7TR	CAY-CBO-NBR	-2.98	107.87	112.61
5	В	403	7TR	CAZ-CBK-CBN	2.89	126.81	122.40
5	В	403	7TR	CBL-SBT-NBR	2.77	112.29	107.36
5	В	403	7TR	CAC-OBD-CBI	-2.67	111.73	117.51
5	В	403	7TR	CBB-NBQ-CBN	2.22	121.95	116.90
5	В	403	7TR	OBE-CBF-OAF	-2.12	119.66	123.74

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	В	403	7TR	CAP-CBI-OBD-CAC
5	В	403	7TR	CAO-CBI-OBD-CAC
5	В	403	7TR	OAF-CBF-OBE-CBJ

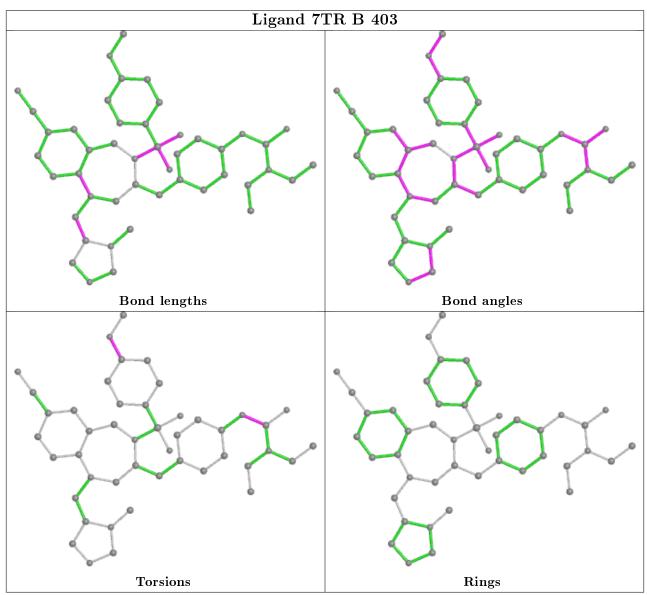
There are no ring outliers.

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 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB( m \AA^2)$	Q<0.9
1	A	307/330 (93%)	0.76	43 (14%) 2 4	19, 37, 63, 94	0
2	В	$324/330 \ (98\%)$	0.13	15 (4%) 32 42	17, 27, 46, 77	0
All	All	631/660 (95%)	0.44	58 (9%) 9 14	17, 31, 58, 94	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	238	ALA	8.4
1	A	241	GLY	8.0
1	A	16	ALA	7.6
2	В	331	SER	7.3
1	A	243	CYS	7.3
1	A	18	ARG	6.8
1	A	194	GLN	6.5
1	A	193	PRO	6.0
1	A	19	LEU	6.0
1	A	330	ALA	5.8
1	A	242	ARG	5.4
1	A	327	MET	5.0
2	В	36	ASP	4.8
1	A	17	LYS	4.6
1	A	41	ALA	4.6
1	A	244	GLU	4.6
1	A	176	SER	4.5
1	A	27	LEU	4.2
1	A	237	GLY	4.0
1	A	40	GLN	3.9
1	A	195	PRO	3.8
2	В	12	SER	3.6
1	A	172	THR	3.5
1	A	21	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
2	В	5	GLN	3.4
2	В	32	SER	3.4
1	A	175	PHE	3.4
1	A	28[A]	TYR	3.3
2	В	37	TYR	3.2
2	В	81	GLU	3.2
1	A	173	ARG	3.1
1	A	121	PRO	3.1
2	В	285	MET	3.1
1	A	168	ASP	3.1
2	В	13	ASP	3.1
1	A	171	ILE	3.1
2	В	11	LYS	3.0
1	A	192	HIS	3.0
1	A	79	GLU	2.8
1	A	221	THR	2.7
1	A	202	ARG	2.7
2	В	267	ILE	2.5
1	A	59	ASN	2.3
1	A	174	ASN	2.3
2	В	31	GLY	2.3
1	A	78	THR	2.3
1	A	203	LEU	2.3
1	A	225	ASP	2.3
1	A	265	GLU	2.2
1	A	266	LEU	2.2
2	В	328	GLU	2.2
1	A	77	GLU	2.2
1	A	224	ASN	2.1
1	A	328	GLU	2.1
2	В	295	ILE	2.1
2	В	39	TYR	2.1
1	A	217	ASN	2.1
1	A	220	PHE	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)

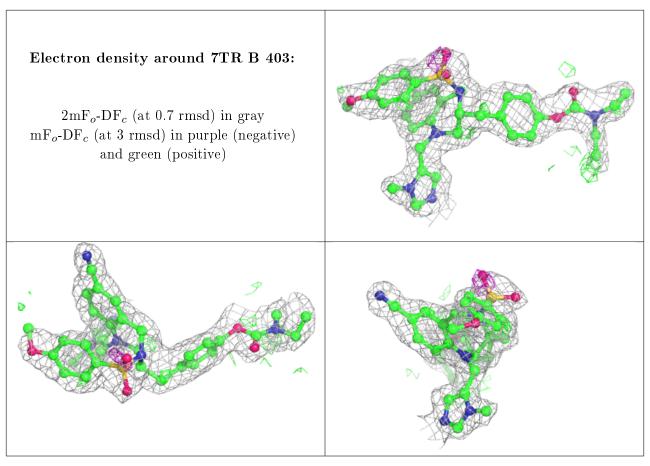
There are no carbohydrates in this entry.

### 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	$\operatorname{B-factors}( \mathrm{\AA}^2 )$	Q<0.9
5	7TR	В	403	46/46	0.88	0.14	38,55,64,72	0
4	CA	В	402	1/1	0.99	0.05	28,28,28,28	0
3	ZN	В	401	1/1	1.00	0.04	26,26,26,26	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.

