

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

Sep 6, 2023 – 07:56 PM EDT

PDB ID : 4GZL

Title: Crystal structure of RAC1 Q61L mutant

Authors: Ha, B.H.; Boggon, T.J.

Deposited on : 2012-09-06

Resolution : 2.00 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 : 2.35

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)

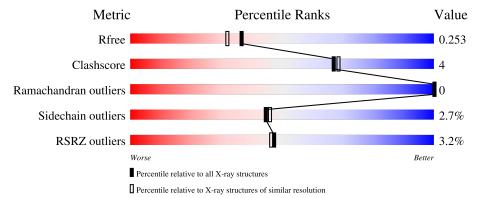
Validation Pipeline (wwPDB-VP) : 2.35

## 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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	204	73%	11%		15%		
1	В	204	74%	10%		15%		



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2982 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 Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	173	Total 1377			O 256	S 7	0	5	0
1	В	174	Total 1379			O 256	S 7	0	4	0

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	expression tag	UNP P63000
A	-25	GLY	-	expression tag	UNP P63000
A	-24	SER	-	- expression tag	
A	-23	SER	-	expression tag	UNP P63000
A	-22	HIS	-	expression tag	UNP P63000
A	-21	HIS	-	expression tag	UNP P63000
A	-20	HIS	-	expression tag	UNP P63000
A	-19	HIS	-	expression tag	UNP P63000
A	-18	HIS	-	expression tag	UNP P63000
A	-17	HIS	-	expression tag	UNP P63000
A	-16	SER	-	expression tag	UNP P63000
A	-15	SER	-	expression tag	UNP P63000
A	-14	GLY	-	expression tag	UNP P63000
A	-13	LEU	-	expression tag	UNP P63000
A	-12	VAL	-	expression tag	UNP P63000
A	-11	PRO	-	expression tag	UNP P63000
A	-10	ARG	-	expression tag	UNP P63000
A	-9	GLY	-	expression tag	UNP P63000
A	-8	SER	-	expression tag	UNP P63000
A	-7	HIS	-	expression tag	UNP P63000
A	-6	MET	-	expression tag	UNP P63000
A	-5	GLU	-	expression tag	UNP P63000
A	-4	ASN	-	expression tag	UNP P63000
A	-3	LEU	-	expression tag	UNP P63000
A	-2	TYR	-	expression tag	UNP P63000

Continued on next page...

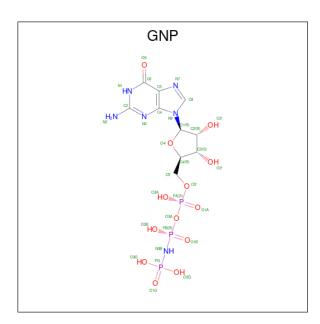


 $Continued\ from\ previous\ page...$ 

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	PHE	-	expression tag	UNP P63000
A	0	GLN	_	expression tag	UNP P63000
A	1	GLY	-	expression tag	UNP P63000
A	61	LEU	GLN	engineered mutation	UNP P63000
В	-26	MET	-	expression tag	UNP P63000
В	-25	GLY	-	expression tag	UNP P63000
В	-24	SER	-	expression tag	UNP P63000
В	-23	SER	-	expression tag	UNP P63000
В	-22	HIS	-	expression tag	UNP P63000
В	-21	HIS	-	expression tag	UNP P63000
В	-20	HIS	-	expression tag	UNP P63000
В	-19	HIS	-	expression tag	UNP P63000
В	-18	HIS	-	expression tag	UNP P63000
В	-17	HIS	-	expression tag	UNP P63000
В	-16	SER	-	expression tag	UNP P63000
В	-15	SER	-	expression tag	UNP P63000
В	-14	GLY	-	expression tag	UNP P63000
В	-13	LEU	-	expression tag	UNP P63000
В	-12	VAL	-	expression tag	UNP P63000
В	-11	PRO	-	expression tag	UNP P63000
В	-10	ARG	_	expression tag	UNP P63000
В	-9	GLY	-	expression tag	UNP P63000
В	-8	SER	-	expression tag	UNP P63000
В	-7	HIS	-	expression tag	UNP P63000
В	-6	MET	-	expression tag	UNP P63000
В	-5	GLU	-	expression tag	UNP P63000
В	-4	ASN	-	expression tag	UNP P63000
В	-3	LEU	-	expression tag	UNP P63000
В	-2	TYR	-	expression tag	UNP P63000
В	-1	PHE	-	expression tag	UNP P63000
В	0	GLN	-	expression tag	UNP P63000
В	1	GLY	-	expression tag	UNP P63000
В	61	LEU	GLN	engineered mutation	UNP P63000

• Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ).





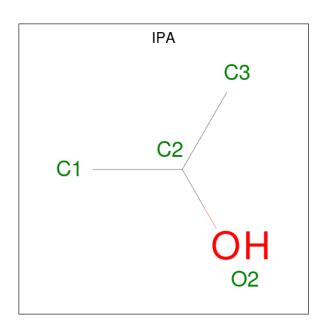
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	2 A	1	Total	С	N	О	Р	0	0
2		1	32	10	6	13	3	U	
9	D	1	Total	С	N	О	Р	0	0
2	2   B	1	32	10	6	13	3	U	U

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	В	1	Total Mg 1 1	0	0

 $\bullet$  Molecule 4 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula:  $\mathrm{C_3H_8O}).$ 





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 3	O 1	0	0

#### • Molecule 5 is water.

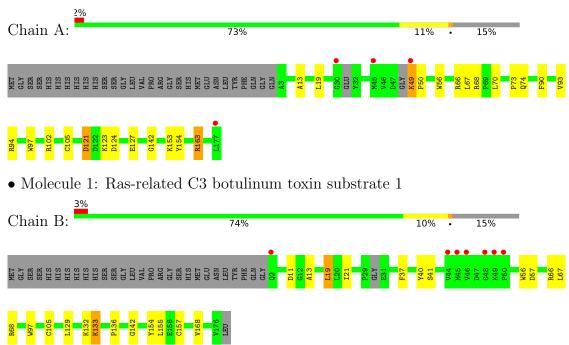
$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	80	Total O 80 80	0	0
5	В	76	Total O 76 76	0	0



# 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: Ras-related C3 botulinum toxin substrate 1





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	49.83Å 72.94Å 91.60Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	50.00 - 2.00	Depositor
resolution (A)	45.80 - 2.00	EDS
% Data completeness	99.6 (50.00-2.00)	Depositor
(in resolution range)	99.6 (45.80-2.00)	EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$< I/\sigma(I) > 1$	2.83 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
P.P.	0.186 , 0.250	Depositor
$R, R_{free}$	0.189 , $0.253$	DCC
$R_{free}$ test set	1194 reflections $(5.16\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.9	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.37, 51.4	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.53, < L^2> = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2982	wwPDB-VP
Average B, all atoms $(Å^2)$	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 45.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2533e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<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: MG, IPA, GNP

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	Chain	Bo	nd lengths	Bond angles		
Mol Chain		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.96	2/1420 (0.1%)	1.28	8/1930 (0.4%)	
1	В	0.95	2/1420 (0.1%)	0.94	4/1932~(0.2%)	
All	All	0.95	4/2840 (0.1%)	1.12	$12/3862 \ (0.3\%)$	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	В	97	TRP	CD2-CE2	8.86	1.51	1.41
1	A	56	TRP	CD2-CE2	6.98	1.49	1.41
1	A	97	TRP	CD2-CE2	6.78	1.49	1.41
1	В	56	TRP	CD2-CE2	5.46	1.48	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	102	ARG	NE-CZ-NH2	-25.75	107.43	120.30
1	A	102	ARG	NE-CZ-NH1	24.08	132.34	120.30
1	A	102	ARG	CD-NE-CZ	9.67	137.13	123.60
1	В	68	ARG	NE-CZ-NH2	-8.62	115.99	120.30
1	В	68	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	A	121	ASP	CB-CG-OD2	5.92	123.63	118.30
1	A	163	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	A	121	ASP	CB-CG-OD1	-5.35	113.48	118.30
1	A	94	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	В	11	ASP	CB-CG-OD1	5.19	122.97	118.30
1	A	68	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	В	57	ASP	CB-CG-OD1	5.11	122.89	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	1377	0	1409	13	0
1	В	1379	0	1410	11	0
2	A	32	0	13	1	0
2	В	32	0	13	1	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	4	0	8	2	0
5	A	80	0	0	2	0
5	В	76	0	0	2	0
All	All	2982	0	2853	22	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 (22) 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:A:66:ARG:NH1	1:B:37:PHE:O	1.89	1.06
1:A:163:ARG:HH11	4:A:203:IPA:H13	1.13	1.05
1:A:163:ARG:NH1	4:A:203:IPA:H13	1.88	0.87
1:B:105:CYS:SG	5:B:1150:HOH:O	2.37	0.83
1:B:13:ALA:H	2:B:1000:GNP:HNB3	1.45	0.64
1:A:13:ALA:H	2:A:201:GNP:HNB3	1.46	0.62
1:A:67:LEU:HD13	1:B:67:LEU:HD13	1.83	0.60
1:A:105:CYS:SG	5:A:322:HOH:O	2.25	0.54
1:B:132:LYS:O	1:B:133:LYS:HG2	2.10	0.52
1:B:66:ARG:HG3	5:B:1130:HOH:O	2.09	0.51
1:A:142:GLY:HA3	1:A:154:TYR:CZ	2.47	0.50
1:B:155:LEU:HD13	1:B:168:VAL:HA	1.97	0.47
1:B:19:LEU:HD12	1:B:157:CYS:SG	2.56	0.46
1:A:67:LEU:HD23	1:A:70:LEU:CD1	2.46	0.45
1:A:49:LYS:HD2	1:A:50:PRO:HD3	2.00	0.43
1:B:21[B]:ILE:HD11	1:B:40:TYR:CZ	2.55	0.41
1:A:73:PRO:O	1:A:74:GLN:CB	2.69	0.41
1:A:127[B]:GLU:HA	1:A:127[B]:GLU:OE1	2.19	0.41

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance } ( ext{Å}) \end{array}$	Clash overlap (Å)	
1:A:121:ASP:HB2	5:A:306:HOH:O	2.20	0.41	
1:A:90:PHE:O	1:A:93:VAL:HB	2.21	0.41	
1:B:129:LEU:HD12	1:B:136:PRO:HG3	2.04	0.40	
1:B:142:GLY:HA3	1:B:154:TYR:CZ	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	Favoured Allowed		iers   Percentil	
1	A	172/204 (84%)	169 (98%)	3 (2%)	0	100	100
1	В	174/204~(85%)	170 (98%)	4 (2%)	0	100	100
All	All	346/408 (85%)	339 (98%)	7 (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 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	155/176 (88%)	150 (97%)	5 (3%)	39 38		
1	В	155/176 (88%)	152 (98%)	3 (2%)	57 61		
All	All	310/352 (88%)	302 (97%)	8 (3%)	44 48		



A 11	(0)	• 1	• . 1			. 1 1 .		1. / 1	1 1
$A\Pi$	(8)	residues	with	$\mathbf{a}$	non-rotameric	sidechain	are	listed	below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	49	LYS
1	A	123	LYS
1	A	124	ASP
1	A	153	LYS
1	В	19	LEU
1	В	41	SER
1	В	133	LYS

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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	Bond lengths			Bond angles		
						Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
	2	GNP	A	201	3	29,34,34	2.41	8 (27%)	33,54,54	2.35	12 (36%)



Mol	Type	Chain	Res	Link	Bond lengths			В	ond ang	gles
MIOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GNP	В	1000	3	29,34,34	1.97	8 (27%)	33,54,54	2.38	12 (36%)
4	IPA	A	203	-	3,3,3	0.70	0	3,3,3	0.31	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
2	GNP	A	201	3	-	5/14/38/38	0/3/3/3
2	GNP	В	1000	3	-	5/14/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	A	201	GNP	PG-O1G	8.61	1.59	1.46
2	В	1000	GNP	PB-O1B	5.58	1.55	1.46
2	A	201	GNP	PG-O3G	-4.20	1.45	1.56
2	A	201	GNP	PB-N3B	4.10	1.74	1.63
2	A	201	GNP	PG-N3B	3.99	1.73	1.63
2	A	201	GNP	PB-O1B	3.73	1.52	1.46
2	В	1000	GNP	PG-N3B	3.59	1.72	1.63
2	В	1000	GNP	C5-C4	3.36	1.49	1.40
2	В	1000	GNP	C5-C6	3.36	1.47	1.41
2	A	201	GNP	C5-C6	2.95	1.46	1.41
2	В	1000	GNP	PB-O2B	-2.94	1.48	1.56
2	A	201	GNP	O4'-C1'	2.86	1.45	1.41
2	В	1000	GNP	PB-N3B	2.81	1.70	1.63
2	A	201	GNP	C2-N2	2.24	1.38	1.33
2	В	1000	GNP	PG-O3G	2.17	1.62	1.56
2	В	1000	GNP	C2-N1	2.11	1.39	1.35

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
2	A	201	GNP	C2-N3-C4	5.84	122.03	115.36
2	В	1000	GNP	C2-N3-C4	5.06	121.14	115.36
2	A	201	GNP	N3-C2-N1	-4.63	121.05	127.22
2	A	201	GNP	C4-C5-C6	-4.51	116.49	120.80
2	A	201	GNP	O2G-PG-O3G	4.42	119.41	107.64
2	В	1000	GNP	C3'-C2'-C1'	4.24	107.36	100.98

Continued on next page...



 $Continued\ from\ previous\ page...$ 

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1000	GNP	O3'-C3'-C4'	-4.09	99.23	111.05
2	В	1000	GNP	C5-C6-N1	-3.82	118.21	123.43
2	В	1000	GNP	C2-N1-C6	3.78	121.93	115.93
2	В	1000	GNP	C4-C5-C6	-3.78	117.19	120.80
2	В	1000	GNP	N3-C2-N1	-3.72	122.26	127.22
2	A	201	GNP	N2-C2-N1	3.66	122.95	117.25
2	A	201	GNP	C2-N1-C6	3.52	121.52	115.93
2	В	1000	GNP	N2-C2-N1	3.49	122.69	117.25
2	В	1000	GNP	C4-C5-N7	-3.29	105.97	109.40
2	A	201	GNP	C5-C6-N1	-3.09	119.20	123.43
2	A	201	GNP	O1B-PB-N3B	-2.93	107.45	111.77
2	В	1000	GNP	PB-O3A-PA	-2.82	122.67	132.62
2	В	1000	GNP	O3'-C3'-C2'	-2.81	102.73	111.82
2	A	201	GNP	O2G-PG-O1G	-2.56	107.01	113.45
2	A	201	GNP	O1G-PG-N3B	-2.50	108.10	111.77
2	A	201	GNP	O3'-C3'-C2'	-2.44	103.94	111.82
2	В	1000	GNP	O1G-PG-N3B	-2.26	108.44	111.77
2	A	201	GNP	C3'-C2'-C1'	2.06	104.07	100.98

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	GNP	PB-N3B-PG-O1G
2	A	201	GNP	PG-N3B-PB-O1B
2	A	201	GNP	PA-O3A-PB-O1B
2	A	201	GNP	PA-O3A-PB-O2B
2	В	1000	GNP	PB-N3B-PG-O1G
2	В	1000	GNP	PG-N3B-PB-O1B
2	В	1000	GNP	PA-O3A-PB-O1B
2	В	1000	GNP	PA-O3A-PB-O2B
2	A	201	GNP	C5'-O5'-PA-O3A
2	В	1000	GNP	C5'-O5'-PA-O1A

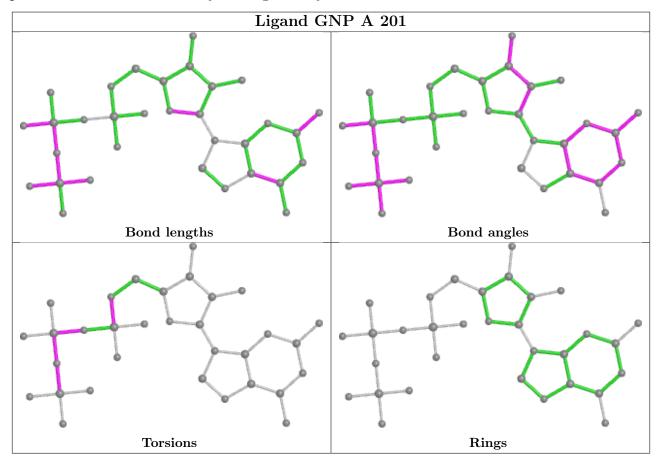
There are no ring outliers.

3 monomers are involved in 4 short contacts:

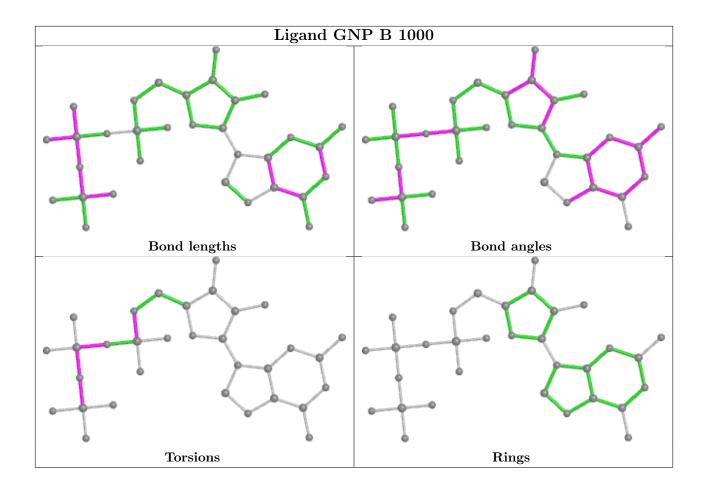
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	GNP	1	0
2	В	1000	GNP	1	0
4	A	203	IPA	2	0



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.







# 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	173/204 (84%)	-0.19	4 (2%) 60 59	20, 31, 66, 84	0
1	В	174/204~(85%)	-0.23	7 (4%) 38 37	20, 31, 67, 95	0
All	All	347/408 (85%)	-0.21	11 (3%) 47 46	20, 31, 66, 95	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	48	GLY	3.7
1	A	30	GLY	3.5
1	A	177	LEU	3.2
1	В	2	GLN	3.1
1	В	44	VAL	2.9
1	В	50	PRO	2.7
1	В	45	MET	2.6
1	A	49	LYS	2.5
1	A	45	MET	2.5
1	В	49	LYS	2.4
1	В	46	VAL	2.4

### 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.

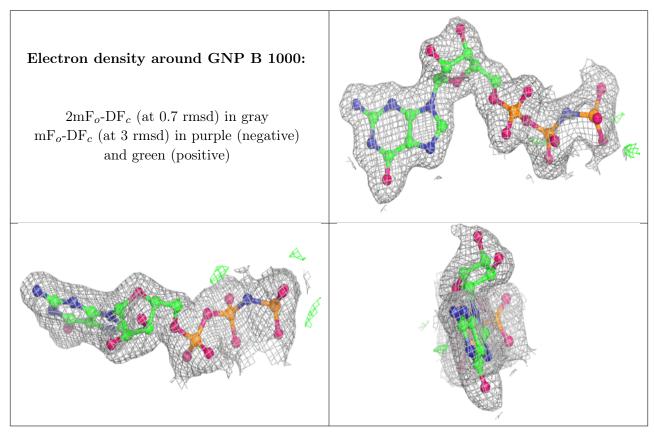


### 6.4 Ligands (i)

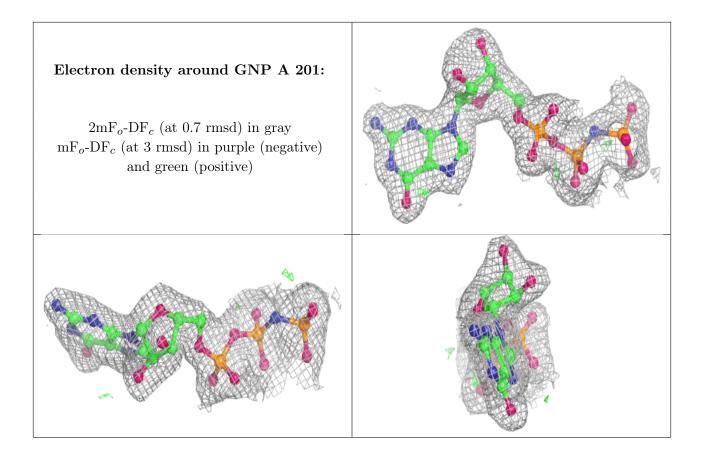
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	MG	В	1001	1/1	0.97	0.06	29,29,29,29	0
2	GNP	В	1000	32/32	0.98	0.09	24,27,34,42	0
2	GNP	A	201	32/32	0.98	0.09	26,30,35,42	0
4	IPA	A	203	4/4	0.98	0.13	21,30,37,39	0
3	MG	A	202	1/1	0.99	0.02	28,28,28,28	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.

