

Full wwPDB X-ray Structure Validation Report (i)

Nov 17, 2020 – 02:06 PM GMT

PDB ID : 6ZRN

Title: Crystal structure of the RLIP 76 Ral binding domain mutant (E427S/L429M

/Q433L/K440R) in complex with RalB-GMPPNP

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Deposited on : 2020-07-13

Resolution : 1.48 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 : 2.14.6

 $buster\text{-report} \quad : \quad 1.1.7 \ (2018)$

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)

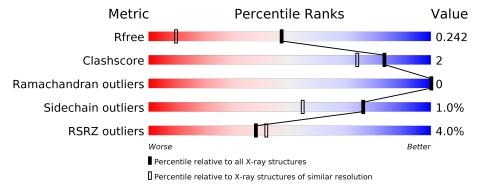
Validation Pipeline (wwPDB-VP) : 2.14.6

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 1.48 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	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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	185	86%	8% 6%
1	В	185	88%	5% • 6%
2	С	59	80% 7%	14%
2	D	59	88%	8% •



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4047 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 protein Ral-B.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Α	173		otal C		О	S	0	0	0
	7.1	110	1388	877	232	275	4		0	
1	D	173	Total	С	N	Ο	S	0	4	0
	D	Б 173	1421	897	240	280	4	U	4	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	LEU	GLN	engineered mutation	UNP P11234
В	72	LEU	GLN	engineered mutation	UNP P11234

• Molecule 2 is a protein called RalA-binding protein 1.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace			
9	С	51	Total	С	N	О	S	0 1	1	0
		91	436	271	87	77	1		1	
2	D	57	Total	С	N	О	S	0	2	0
2	ש	D 57	480	299	94	86	1	U		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	388	GLY	-	expression tag	UNP Q15311
С	389	PRO	_	expression tag	UNP Q15311
С	390	LEU	-	expression tag	UNP Q15311
С	391	GLY	-	expression tag	UNP Q15311
С	392	SER	-	expression tag	UNP Q15311
С	411	SER	CYS	engineered mutation	UNP Q15311
С	427	SER	GLU	engineered mutation	UNP Q15311
С	429	MET	LEU	engineered mutation	UNP Q15311
С	433	LEU	GLN	engineered mutation	UNP Q15311
С	440	ARG	LYS	engineered mutation	UNP Q15311



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Chain	Residue	Modelled	Actual	Actual Comment	
D	388	GLY	_	expression tag	UNP Q15311
D	389	PRO	-	expression tag	UNP Q15311
D	390	LEU	_	expression tag	UNP Q15311
D	391	GLY	-	expression tag	UNP Q15311
D	392	SER	-	expression tag	UNP Q15311
D	411	SER	CYS	engineered mutation	UNP Q15311
D	427	SER	GLU	engineered mutation	UNP Q15311
D	429	MET	LEU	engineered mutation	UNP Q15311
D	433	LEU	GLN	engineered mutation	UNP Q15311
D	440	ARG	LYS	engineered mutation	UNP Q15311

• Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	
9	Λ	1	Total	С	Ν	О	Р	0	0	
3	А	1	32	10	6	13	3	0		
9	В	D	1	Total	С	N	О	Р	0	0
3		$\mathbf{B} \mid \mathbf{I} \mid$	32	10	6	13	3	U	U	

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

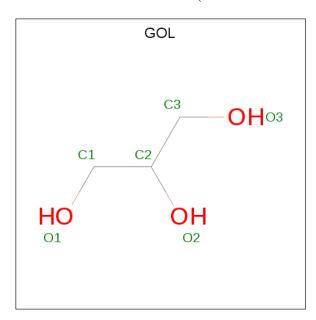
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Mg 1 1	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	С	1	Total C O 6 3 3	0	0

• Molecule 6 is water.

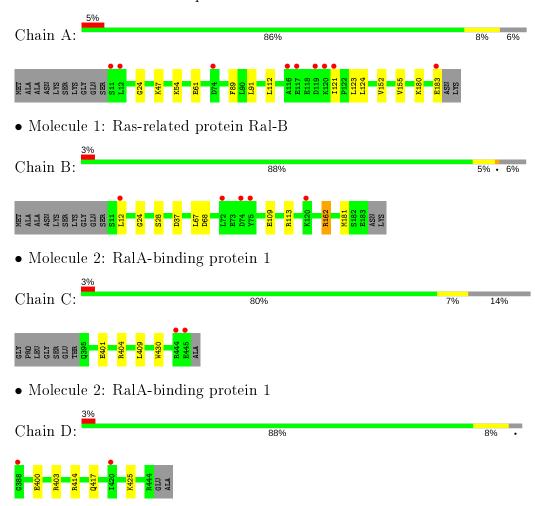
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	85	Total O 85 85	0	0
			Total O		
6	6 B	91	91 91	0	0
6	С	43	Total O	0	0
_	_		43 43	-	_
6	D	25	Total O	0	0
			25 25		



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 protein Ral-B





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	47.20Å 77.52Å 65.77Å	Donogiton
a, b, c, α , β , γ	90.00° 90.07° 90.00°	Depositor
Resolution (Å)	50.15 - 1.48	Depositor
Resolution (A)	65.77 - 1.48	EDS
% Data completeness	99.9 (50.15-1.48)	Depositor
(in resolution range)	99.9 (65.77-1.48)	EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.62 (at 1.48Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
D D.	0.209 , 0.238	Depositor
R, R_{free}	0.213 , 0.242	DCC
R_{free} test set	3868 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 45.0	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.008 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4047	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.45% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: GOL, GNP, MG

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		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.33	0/1409	0.52	0/1895	
1	В	0.42	0/1442	0.57	0/1938	
2	С	0.33	0/439	0.46	0/582	
2	D	0.28	0/484	0.41	0/644	
All	All	0.36	0/3774	0.52	0/5059	

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	A	1388	0	1371	8	0
1	В	1421	0	1407	6	0
2	С	436	0	461	3	0
2	D	480	0	507	2	0
3	A	32	0	13	1	0
3	В	32	0	13	1	0
4	A	1	0	0	0	0
4	В	1	0	0	0	0
5	A	6	0	8	0	0



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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes	
5	С	6	0	8	1	0	
6	A	85	0	0	0	0	
6	В	91	0	0	0	0	
6	С	43	0	0	0	0	
6	D	25	0	0	0	0	
All	All	4047	0	3788	18	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 2.

All (18) 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:B:37:ASP:OD1	1:B:162[A]:ARG:NH1	2.34	0.60
2:D:400:GLU:OE2	2:D:403:ARG:NH2	2.39	0.55
1:A:112:LEU:HD23	1:A:121:ILE:HD12	1.90	0.53
1:A:89:PHE:HB2	1:A:123:LEU:HD23	1.90	0.53
1:A:123:LEU:HD12	1:A:152:VAL:HG11	1.91	0.52
2:D:414:ARG:O	2:D:417:GLN:HG2	2.11	0.50
1:A:180:LYS:O	1:A:183:GLU:HG2	2.12	0.50
1:A:91:LEU:HB2	1:A:123:LEU:HD21	1.97	0.47
1:A:124:LEU:HD21	1:A:155:VAL:HG23	1.96	0.47
1:A:24:GLY:H	3:A:201:GNP:HNB3	1.61	0.47
1:B:109:GLU:O	1:B:113:ARG:HG3	2.15	0.46
1:B:24:GLY:H	3:B:201:GNP:HNB3	1.64	0.45
2:C:409:LEU:HD23	5:C:501:GOL:H32	2.00	0.44
1:B:67:LEU:HD12	2:C:430:TRP:CE2	2.54	0.43
2:C:401:GLU:OE2	2:C:404:ARG:NH1	2.52	0.42
1:B:12:LEU:HD21	1:B:181:MET:HG3	2.02	0.42
1:B:28:SER:OG	1:B:68:ASP:OD2	2.38	0.41
1:A:47:LYS:HE2	1:A:47:LYS:HB2	1.87	0.41

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 r	number	of	residues	for	which	the	backbone	conformation	was
analysed, and the total numb	er of	residues								

Mol	Chain	Analysed Favoured Allowed		Allowed	Outliers	Perce	\mathbf{ntiles}
1	A	171/185 (92%)	164 (96%)	7 (4%)	0	100	100
1	В	175/185~(95%)	170 (97%)	5 (3%)	0	100	100
2	С	50/59~(85%)	49 (98%)	1 (2%)	0	100	100
2	D	$57/59 \; (97\%)$	56 (98%)	1 (2%)	0	100	100
All	All	453/488 (93%)	439 (97%)	14 (3%)	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	${f Analysed}$	Rotameric	Outliers	Percentiles		
1	A	150/159~(94%)	148 (99%)	2 (1%)	69 42		
1	В	$154/159 \ (97\%)$	152 (99%)	2 (1%)	69 42		
2	С	47/51 (92%)	47 (100%)	0	100 100		
2	D	$52/51 \; (102\%)$	51 (98%)	1 (2%)	57 26		
All	All	$403/420 \ (96\%)$	398 (99%)	5 (1%)	76 46		

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	LYS
1	A	61	GLU
1	В	162[A]	ARG
1	В	162[B]	ARG
2	D	425	LYS

Some 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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	Tuna	Chain	Res	Res Link	Bond lengths			Bond angles		
MIOI	Type	e Chain Res Li	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
3	GNP	A	201	4	28,34,34	2.19	8 (28%)	30,54,54	1.83	5 (16%)
3	GNP	В	201	4	28,34,34	2.43	10 (35%)	30,54,54	1.75	4 (13%)
5	GOL	С	501	-	5,5,5	0.87	0	5,5,5	1.08	0
5	GOL	A	203	_	5,5,5	0.78	0	5,5,5	0.94	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	${f Res}$	Link	Chirals	${f Torsions}$	Rings
3	GNP	A	201	4	-	5/17/38/38	0/3/3/3
3	GNP	В	201	4	-	4/17/38/38	0/3/3/3
5	GOL	С	501	-	-	2/4/4/4	-
5	GOL	A	203	_	-	4/4/4/4	-



All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
3	В	201	GNP	C4-N9	-7.92	1.37	1.47
3	A	201	GNP	C4-N9	-7.21	1.38	1.47
3	В	201	GNP	C5-C6	-5.00	1.44	1.52
3	A	201	GNP	C5-C6	-4.60	1.44	1.52
3	В	201	GNP	PG-01G	3.99	1.52	1.46
3	В	201	GNP	C6-N1	3.79	1.39	1.33
3	A	201	GNP	C6-N1	3.70	1.39	1.33
3	A	201	GNP	PB-O2B	-3.02	1.48	1.56
3	A	201	GNP	PB-O1B	2.91	1.50	1.46
3	В	201	GNP	PB-O2B	-2.70	1.49	1.56
3	В	201	GNP	PG-N3B	2.62	1.70	1.63
3	В	201	GNP	PB-O1B	2.55	1.50	1.46
3	В	201	GNP	PG-O2G	-2.51	1.50	1.56
3	В	201	GNP	C5-C4	-2.41	1.38	1.53
3	A	201	GNP	C5-C4	-2.40	1.38	1.53
3	В	201	GNP	C8-N9	-2.37	1.37	1.45
3	A	201	GNP	C8-N9	-2.25	1.37	1.45
3	A	201	GNP	PG-N3B	2.20	1.69	1.63

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
3	A	201	GNP	C4-C5-N7	5.97	110.37	102.46
3	В	201	GNP	C4-C5-N7	5.96	110.36	102.46
3	В	201	GNP	C5-C6-N1	-5.16	111.82	118.19
3	A	201	GNP	C5-C6-N1	-4.90	112.14	118.19
3	A	201	GNP	O6-C6-C5	3.62	127.25	119.86
3	В	201	GNP	O6-C6-C5	3.40	126.79	119.86
3	В	201	GNP	O1G-PG-N3B	-2.88	107.53	111.77
3	A	201	GNP	O1G-PG-N3B	-2.18	108.56	111.77
3	A	201	GNP	O3G-PG-O2G	2.15	113.37	107.64

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	201	GNP	PG-N3B-PB-O1B
3	В	201	GNP	PA-O3A-PB-O1B
3	В	201	GNP	PA-O3A-PB-O2B
3	В	201	GNP	C2'-C1'-N9-C4
3	A	201	GNP	PB-N3B-PG-O1G



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Mol	Chain	Res	Type	Atoms
3	A	201	GNP	PG-N3B-PB-O1B
3	A	201	GNP	PA-O3A-PB-O1B
3	A	201	GNP	PA-O3A-PB-O2B
3	A	201	GNP	C2'-C1'-N9-C4
5	A	203	GOL	O1-C1-C2-C3
5	A	203	GOL	C1-C2-C3-O3
5	A	203	GOL	O2-C2-C3-O3
5	A	203	GOL	O1-C1-C2-O2
5	С	501	GOL	O1-C1-C2-O2
5	С	501	GOL	O1-C1-C2-C3

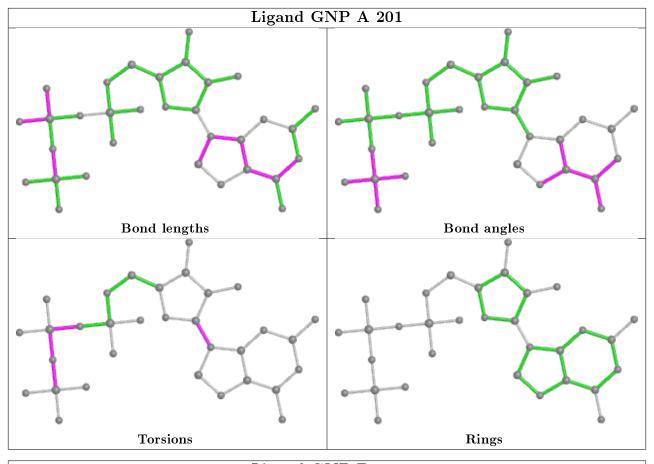
There are no ring outliers.

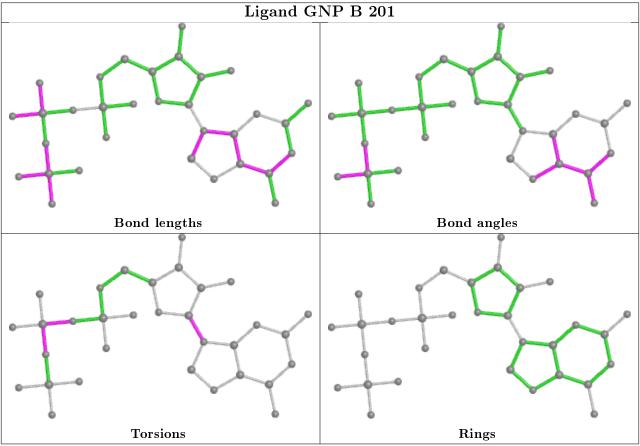
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	GNP	1	0
3	В	201	GNP	1	0
5	С	501	GOL	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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	173/185 (93%)	0.23	9 (5%) 27 29	16, 27, 53, 78	0
1	В	173/185 (93%)	0.21	5 (2%) 51 56	15, 26, 48, 59	0
2	С	51/59 (86%)	0.20	2 (3%) 39 43	16, 26, 38, 60	0
2	D	57/59 (96%)	0.46	2 (3%) 44 48	21, 33, 48, 59	0
All	All	454/488 (93%)	0.25	18 (3%) 38 42	15, 28, 50, 78	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	119	ASP	5.3
1	A	183	GLU	4.6
1	В	74	ASP	4.4
1	A	12	LEU	3.5
1	В	12	LEU	3.5
1	A	117	GLU	3.3
1	A	74	ASP	2.7
1	A	120	LYS	2.7
1	В	72	LEU	2.5
2	С	444	ARG	2.4
1	В	120	LYS	2.3
1	В	75	TYR	2.3
1	A	11	SER	2.2
1	A	116	ALA	2.1
2	D	388	GLY	2.1
1	A	121	ILE	2.1
2	D	420	ILE	2.1
2	С	445	GLU	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.

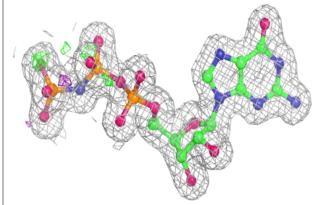
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
5	GOL	A	203	6/6	0.90	0.22	26,37,38,55	0
5	GOL	С	501	6/6	0.91	0.23	28,36,39,47	0
3	GNP	A	201	32/32	0.98	0.09	15,19,23,26	0
3	GNP	В	201	32/32	0.98	0.09	12,17,22,23	0
4	MG	В	202	1/1	0.99	0.06	16,16,16,16	0
4	MG	A	202	1/1	1.00	0.07	16,16,16,16	0

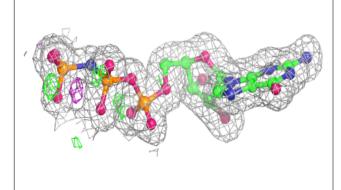
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

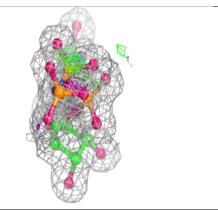


Electron density around GNP A 201:

 $2 \mathrm{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

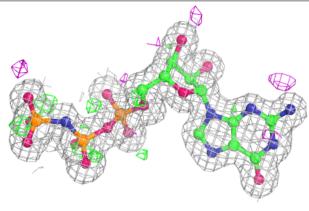


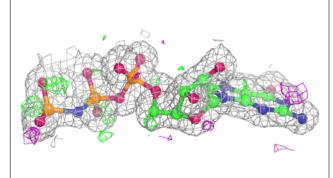


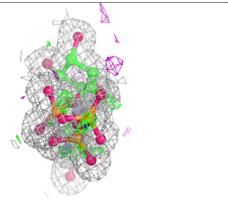


Electron density around GNP B 201:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

