



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:45 PM GMT

PDB ID : 4DCN  
Title : Crystal Structure Analysis of the Arfaptin2 BAR domain in Complex with ARL1  
Authors : Nakamura, K.; Xie, Y.; Kawasaki, M.; Kato, R.; Wakatsuki, S.  
Deposited on : 2012-01-18  
Resolution : 3.01 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

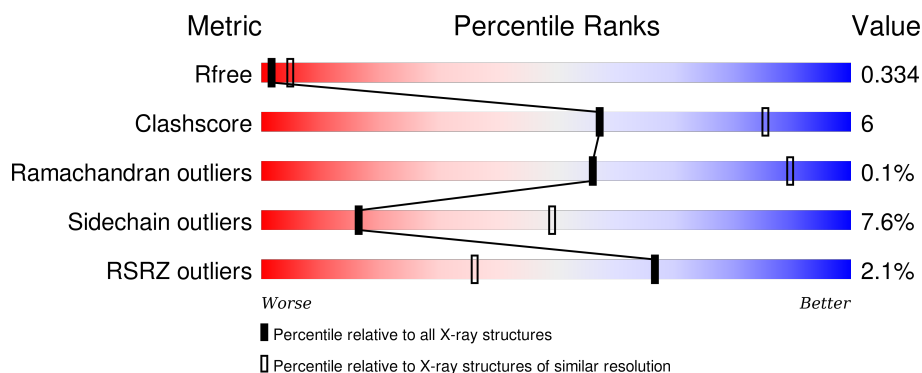
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.01 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1773 (3.04-3.00)
Clashscore	102246	2117 (3.04-3.00)
Ramachandran outliers	100387	2050 (3.04-3.00)
Sidechain outliers	100360	2053 (3.04-3.00)
RSRZ outliers	91569	1788 (3.04-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . 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	166	<div> <div>3%</div> <div>83%</div> <div>16%</div> <div>..</div> </div>
1	B	166	<div> <div>78%</div> <div>21%</div> <div>..</div> </div>
2	C	198	<div> <div>3%</div> <div>79%</div> <div>16%</div> <div>..</div> </div>
2	D	198	<div> <div>3%</div> <div>75%</div> <div>22%</div> <div>..</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5805 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 ADP-ribosylation factor-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1307	832	217	250	8			
1	B	165	Total	C	N	O	S	0	0	0
			1307	832	217	250	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	LEU	GLN	ENGINEERED MUTATION	UNP P40616
B	71	LEU	GLN	ENGINEERED MUTATION	UNP P40616

- Molecule 2 is a protein called Arfaptin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	193	Total	C	N	O	S	0	0	0
			1546	977	267	298	4			
2	D	196	Total	C	N	O	S	0	0	0
			1575	994	274	303	4			

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

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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	B	1	Total	C	N	O	P	0	0
			32	10	6	13	3		


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	O	0	0
			2	2		
5	B	2	Total	O	0	0
			2	2		

### 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 errors 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.

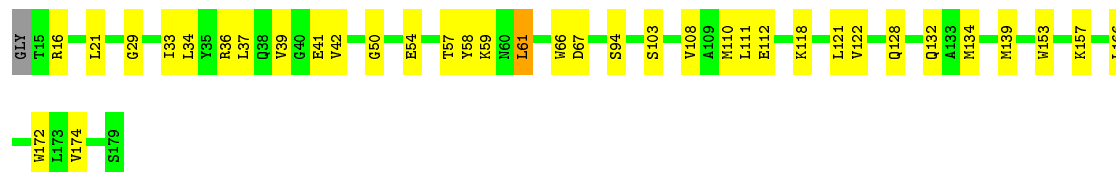
- Molecule 1: ADP-ribosylation factor-like protein 1

Chain A: 




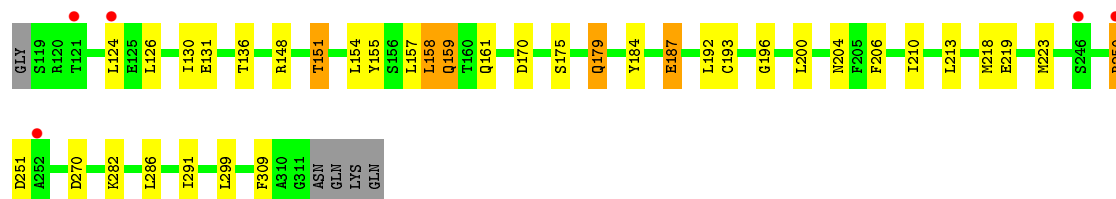
- Molecule 1: ADP-ribosylation factor-like protein 1

Chain B: 




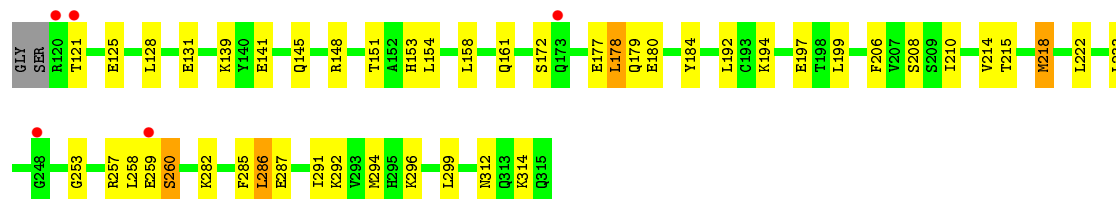
- Molecule 2: Arfaptin-2

Chain C: 



- Molecule 2: Arfaptin-2

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.76Å 111.12Å 119.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.01 43.33 – 3.01	Depositor EDS
% Data completeness (in resolution range)	96.7 (50.00-3.01) 96.7 (43.33-3.01)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.66 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.264 , 0.333 0.264 , 0.334	Depositor DCC
$R_{free}$ test set	834 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.2	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 16567 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	5805	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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: 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	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.38	0/1327	0.51	0/1794
1	B	0.39	0/1327	0.57	0/1794
2	C	0.37	0/1568	0.52	0/2110
2	D	0.38	0/1597	0.53	0/2148
All	All	0.38	0/5819	0.53	0/7846

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	1307	0	1331	14	0
1	B	1307	0	1330	22	0
2	C	1546	0	1557	18	0
2	D	1575	0	1587	21	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	32	0	13	0	0
4	B	32	0	13	0	0
5	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	2	0	0	0	0
All	All	5805	0	5831	70	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 6.

All (70) 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:B:94:SER:HA	1:B:139:MET:CE	2.02	0.90
2:C:161:GLN:HB3	2:C:193:CYS:SG	2.19	0.82
1:A:23:LEU:HD21	1:A:68:LEU:HD12	1.67	0.75
1:A:51:PHE:HB3	1:A:68:LEU:HD23	1.68	0.73
2:D:121:THR:O	2:D:125:GLU:HB2	1.90	0.71
2:C:213:LEU:O	2:C:218:MET:HG3	1.90	0.71
1:B:36:ARG:HG2	1:B:166:LEU:HD13	1.73	0.70
2:D:141:GLU:O	2:D:145:GLN:HG2	1.90	0.70
1:B:94:SER:HA	1:B:139:MET:HE3	1.73	0.69
1:B:94:SER:HA	1:B:139:MET:HE1	1.75	0.68
1:B:108:VAL:O	1:B:112:GLU:HG3	1.95	0.67
2:D:292:LYS:HG2	2:D:296:LYS:HE3	1.77	0.67
2:D:287:GLU:O	2:D:291:ILE:HG12	1.96	0.66
1:B:29:GLY:O	1:B:33:ILE:HG12	1.97	0.65
2:C:219:GLU:O	2:C:223:MET:HG2	1.97	0.64
2:C:161:GLN:CB	2:C:193:CYS:SG	2.87	0.62
1:A:69:GLY:HA3	1:A:74:ILE:HD11	1.84	0.59
2:D:282:LYS:O	2:D:286:LEU:HB2	2.02	0.59
1:B:61:LEU:HD12	1:B:174:VAL:HG13	1.85	0.58
2:C:151:THR:HG21	2:C:204:ASN:OD1	2.04	0.57
2:C:250:ARG:HB3	2:C:250:ARG:HH11	1.70	0.56
1:B:134:MET:CE	1:B:139:MET:HG2	2.35	0.56
1:B:128:GLN:HG3	1:B:157:LYS:HB3	1.90	0.54
1:B:36:ARG:HG2	1:B:166:LEU:CD1	2.38	0.53
1:A:145:LEU:HD23	1:A:153:TRP:CE3	2.43	0.53
2:D:148:ARG:O	2:D:151:THR:HG22	2.08	0.53
1:B:21:LEU:HD23	1:B:66:TRP:HB2	1.90	0.53
2:C:155:TYR:HD1	2:C:200:LEU:HD21	1.75	0.51
1:A:69:GLY:CA	1:A:74:ILE:HD11	2.42	0.49
1:B:134:MET:HE2	1:B:139:MET:HG2	1.93	0.49
1:A:75:ARG:N	1:A:76:PRO:HD2	2.28	0.49
1:A:122:VAL:HG21	1:A:173:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:170:ASP:OD2	2:D:139:LYS:NZ	2.39	0.48
1:B:39:VAL:HG23	1:B:41:GLU:HB2	1.95	0.48
1:B:110:MET:HG3	1:B:111:LEU:N	2.28	0.48
2:C:126:LEU:O	2:C:130:ILE:HG12	2.14	0.48
2:D:172:SER:O	2:D:179:GLN:HG3	2.14	0.48
2:C:157:LEU:HD12	2:D:153:HIS:HB3	1.96	0.48
2:C:184:TYR:HA	2:C:187:GLU:HG2	1.95	0.48
1:A:61:LEU:HD12	1:A:174:VAL:HG13	1.97	0.47
2:D:154:LEU:HD11	2:D:199:LEU:HD23	1.97	0.47
1:A:23:LEU:HD22	1:A:78:TRP:CD2	2.50	0.47
1:B:50:GLY:HA2	2:D:285:PHE:CE1	2.51	0.46
2:D:218:MET:CE	2:D:286:LEU:HD21	2.45	0.46
2:D:257:ARG:HA	2:D:260:SER:HB2	1.97	0.46
2:D:206:PHE:O	2:D:210:ILE:HG12	2.16	0.45
2:C:309:PHE:HE2	2:D:312:ASN:HD22	1.63	0.45
2:C:159:GLN:HE21	2:C:159:GLN:HB2	1.59	0.45
2:C:206:PHE:O	2:C:210:ILE:HG12	2.17	0.45
2:D:141:GLU:HG3	2:D:214:VAL:HG11	1.99	0.45
2:C:282:LYS:O	2:C:286:LEU:HB2	2.18	0.44
2:D:161:GLN:NE2	2:D:192:LEU:HD23	2.32	0.44
2:C:158:LEU:HD11	2:C:196:GLY:HA3	2.00	0.43
2:C:291:ILE:HG23	2:D:178:LEU:HD11	1.99	0.43
1:A:33:ILE:HG13	1:A:160:ALA:HB2	1.99	0.43
1:B:58:TYR:HE2	1:B:59:LYS:HZ3	1.66	0.43
1:B:121:LEU:O	1:B:153:TRP:HA	2.18	0.43
1:A:64:GLN:HG2	1:A:66:TRP:HE1	1.84	0.43
2:D:131:GLU:OE2	2:D:131:GLU:HA	2.18	0.43
1:B:33:ILE:O	1:B:37:LEU:HG	2.19	0.42
1:B:134:MET:HE1	1:B:139:MET:HG2	2.02	0.42
1:A:82:TYR:HE2	1:A:113:GLU:HG3	1.85	0.41
1:B:36:ARG:NH1	1:B:42:VAL:HG23	2.36	0.41
2:D:194:LYS:O	2:D:197:GLU:HB3	2.21	0.41
2:D:215:THR:O	2:D:215:THR:HG22	2.20	0.41
1:A:100:ILE:HD11	1:A:143:LEU:HG	2.03	0.41
1:B:122:VAL:HG22	1:B:172:TRP:CZ3	2.56	0.41
1:B:34:LEU:HD11	1:B:54:GLU:HB2	2.02	0.41
2:C:179:GLN:HE21	2:C:179:GLN:HB2	1.74	0.41
1:A:145:LEU:N	1:A:146:PRO:CD	2.84	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	Percentiles	
1	A	163/166 (98%)	156 (96%)	7 (4%)	0	100	100
1	B	163/166 (98%)	155 (95%)	8 (5%)	0	100	100
2	C	191/198 (96%)	181 (95%)	10 (5%)	0	100	100
2	D	194/198 (98%)	186 (96%)	7 (4%)	1 (0%)	34	75
All	All	711/728 (98%)	678 (95%)	32 (4%)	1 (0%)	56	90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	253	GLY

### 5.3.2 Protein sidechains

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	144/144 (100%)	137 (95%)	7 (5%)	31	69
1	B	144/144 (100%)	137 (95%)	7 (5%)	31	69
2	C	165/169 (98%)	149 (90%)	16 (10%)	10	36
2	D	168/169 (99%)	151 (90%)	17 (10%)	9	33
All	All	621/626 (99%)	574 (92%)	47 (8%)	16	49

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	THR
1	A	44	THR
1	A	46	ILE
1	A	61	LEU
1	A	100	ILE
1	A	117	ARG
1	A	149	LYS
1	B	16	ARG
1	B	57	THR
1	B	61	LEU
1	B	67	ASP
1	B	103	SER
1	B	118	LYS
1	B	132	GLN
2	C	124	LEU
2	C	131	GLU
2	C	136	THR
2	C	148	ARG
2	C	151	THR
2	C	154	LEU
2	C	158	LEU
2	C	159	GLN
2	C	175	SER
2	C	179	GLN
2	C	187	GLU
2	C	192	LEU
2	C	250	ARG
2	C	251	ASP
2	C	270	ASP
2	C	299	LEU
2	D	128	LEU
2	D	158	LEU
2	D	177	GLU
2	D	178	LEU
2	D	180	GLU
2	D	184	TYR
2	D	208	SER
2	D	218	MET
2	D	222	LEU
2	D	233	LEU
2	D	258	LEU
2	D	259	GLU
2	D	260	SER

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Mol	Chain	Res	Type
2	D	286	LEU
2	D	294	MET
2	D	299	LEU
2	D	314	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	B	52	ASN
1	B	128	GLN
1	B	154	GLN
2	C	153	HIS
2	C	159	GLN
2	C	179	GLN
2	C	211	ASN
2	C	302	HIS
2	D	153	HIS
2	D	189	GLN
2	D	268	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z  > 2$
4	GNP	A	202	3	28,34,34	1.75	5 (17%)	33,54,54	2.25	7 (21%)
4	GNP	B	202	3	28,34,34	1.84	5 (17%)	33,54,54	2.26	7 (21%)

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
4	GNP	A	202	3	-	0/12/38/38	0/3/3/3
4	GNP	B	202	3	-	2/12/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	202	GNP	PB-O3A	-4.74	1.53	1.59
4	A	202	GNP	PB-O3A	-4.11	1.54	1.59
4	B	202	GNP	PB-O2B	-3.05	1.48	1.56
4	A	202	GNP	PB-O2B	-2.98	1.48	1.56
4	B	202	GNP	C8-N7	-2.20	1.30	1.34
4	A	202	GNP	PB-O1B	2.12	1.48	1.46
4	B	202	GNP	C6-N1	3.70	1.40	1.33
4	A	202	GNP	C6-N1	3.72	1.40	1.33
4	A	202	GNP	PG-O1G	4.17	1.50	1.46
4	B	202	GNP	PG-O1G	4.28	1.51	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	202	GNP	C5-C6-N1	-8.34	112.19	123.59
4	A	202	GNP	C5-C6-N1	-8.17	112.42	123.59
4	B	202	GNP	O3G-PG-O1G	-3.95	102.98	113.49
4	A	202	GNP	O3G-PG-O1G	-3.50	104.18	113.49
4	A	202	GNP	N3-C2-N1	-2.49	123.66	127.44
4	B	202	GNP	PA-O3A-PB	-2.30	124.96	132.67
4	A	202	GNP	PA-O3A-PB	-2.25	125.14	132.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	202	GNP	N3-C2-N1	-2.15	124.17	127.44
4	A	202	GNP	O3G-PG-O2G	2.30	114.39	107.58
4	B	202	GNP	O3G-PG-O2G	2.32	114.45	107.58
4	B	202	GNP	O2B-PB-O1B	3.25	116.78	110.00
4	A	202	GNP	O2B-PB-O1B	3.64	117.59	110.00
4	B	202	GNP	C6-N1-C2	5.89	124.11	115.94
4	A	202	GNP	C6-N1-C2	6.22	124.57	115.94

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	202	GNP	O1G-PG-N3B-PB
4	B	202	GNP	O1B-PB-N3B-PG

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	165/166 (99%)	0.37	5 (3%) 54 24	52, 69, 86, 87	0
1	B	165/166 (99%)	-0.33	0 100 100	25, 33, 44, 49	0
2	C	193/198 (97%)	0.15	5 (2%) 59 29	37, 50, 78, 85	0
2	D	196/198 (98%)	0.18	5 (2%) 59 29	29, 49, 73, 81	0
All	All	719/728 (98%)	0.10	15 (2%) 67 36	25, 49, 82, 87	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	ASN	3.8
2	D	121	THR	3.3
1	A	150	ASP	3.2
1	A	149	LYS	2.8
2	D	120	ARG	2.7
2	C	246	SER	2.5
1	A	147	ALA	2.5
2	D	173	GLN	2.4
2	D	248	GLY	2.4
2	C	124	LEU	2.4
2	C	121	THR	2.2
1	A	41	GLU	2.2
2	C	250	ARG	2.2
2	D	259	GLU	2.1
2	C	252	ALA	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GNP	A	202	32/32	0.92	0.15	-1.41	60,70,72,73	0
4	GNP	B	202	32/32	0.98	0.15	-1.81	21,25,30,30	0
3	MG	B	201	1/1	0.98	0.07	-5.70	16,16,16,16	0
3	MG	A	201	1/1	0.90	0.09	-	23,23,23,23	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.