



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:49 AM GMT

PDB ID : 3DZG  
Title : Crystal structure of human CD38 extracellular domain, ara-F-ribose-5'-phosphate/nicotinamide complex  
Authors : Liu, Q.; Kriksunov, I.A.; Jiang, H.; Graeff, R.; Lin, H.; Lee, H.C.; Hao, Q.  
Deposited on : 2008-07-29  
Resolution : 1.65 Å (reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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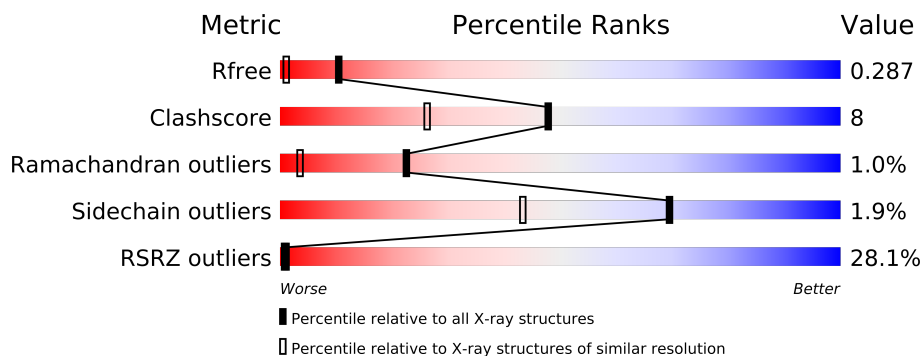
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.65 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))
$R_{free}$	66092	1404 (1.68-1.64)
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)
RSRZ outliers	66119	1404 (1.68-1.64)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	262	
1	B	262	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4612 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

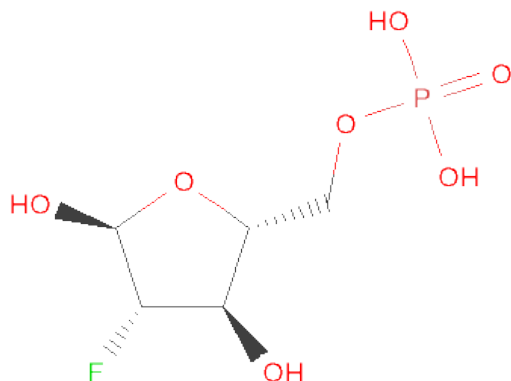
- Molecule 1 is a protein called ADP-ribosyl cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2050	1290	358	386	16			
1	B	252	Total	C	N	O	S	0	0	0
			2050	1290	358	386	16			

There are 22 discrepancies between the modelled and reference sequences:

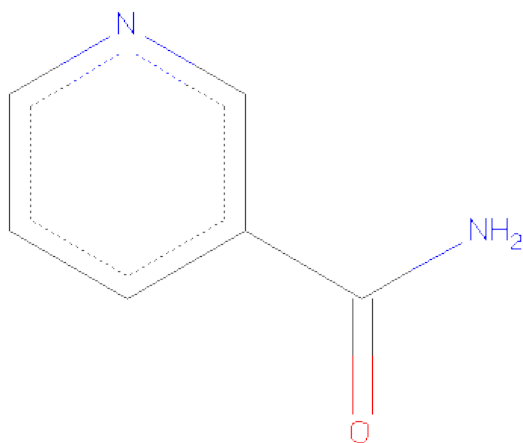
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LYS	-	EXPRESSION TAG	UNP P28907
A	40	ARG	-	EXPRESSION TAG	UNP P28907
A	41	GLU	-	EXPRESSION TAG	UNP P28907
A	42	ALA	-	EXPRESSION TAG	UNP P28907
A	43	GLU	-	EXPRESSION TAG	UNP P28907
A	44	ALA	-	EXPRESSION TAG	UNP P28907
A	49	THR	GLN	ENGINEERED	UNP P28907
A	100	ASP	ASN	ENGINEERED	UNP P28907
A	164	ASP	ASN	ENGINEERED	UNP P28907
A	209	ASP	ASN	ENGINEERED	UNP P28907
A	219	ASP	ASN	ENGINEERED	UNP P28907
B	39	LYS	-	EXPRESSION TAG	UNP P28907
B	40	ARG	-	EXPRESSION TAG	UNP P28907
B	41	GLU	-	EXPRESSION TAG	UNP P28907
B	42	ALA	-	EXPRESSION TAG	UNP P28907
B	43	GLU	-	EXPRESSION TAG	UNP P28907
B	44	ALA	-	EXPRESSION TAG	UNP P28907
B	49	THR	GLN	ENGINEERED	UNP P28907
B	100	ASP	ASN	ENGINEERED	UNP P28907
B	164	ASP	ASN	ENGINEERED	UNP P28907
B	209	ASP	ASN	ENGINEERED	UNP P28907
B	219	ASP	ASN	ENGINEERED	UNP P28907

- Molecule 2 is 1,4-ANHYDRO-2-DEOXY-2-FLUORO-5-O-PHOSPHONO-D-ARABINITOL (three-letter code: RF5) (formula: C<sub>5</sub>H<sub>10</sub>FO<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	O	P	0	0
			13	5	1	6	1		
2	B	1	Total	C	F	O	P	0	0
			13	5	1	6	1		

- Molecule 3 is NICOTINAMIDE (three-letter code: NCA) (formula:  $C_6H_6N_2O$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	6	2	1		
3	B	1	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 4 is water.

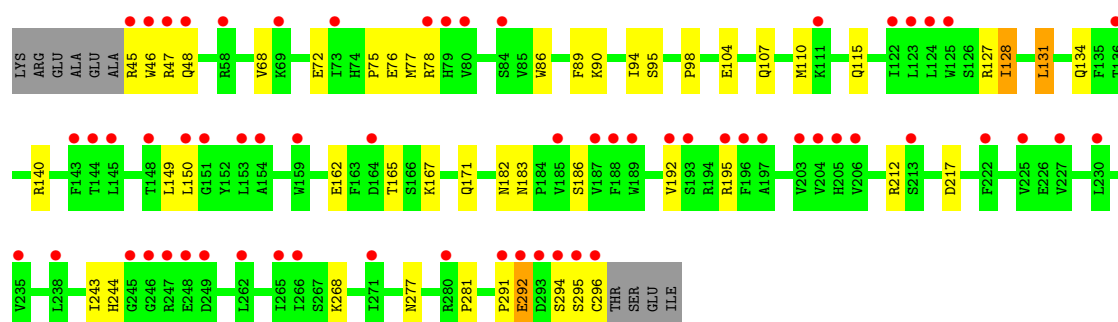
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	236	Total 236	O 236	0	0
4	B	232	Total 232	O 232	0	0

### 3 Residue-property plots

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.

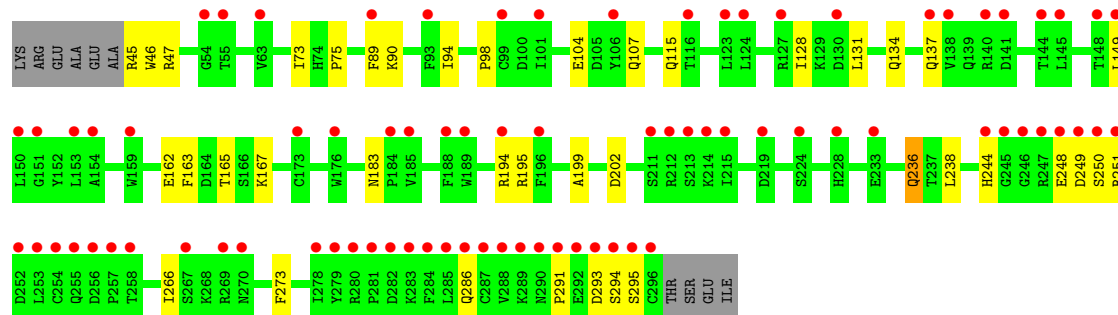
#### • Molecule 1: ADP-ribosyl cyclase 1

Chain A: 



#### • Molecule 1: ADP-ribosyl cyclase 1

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.69Å 52.81Å 65.38Å 106.06° 91.95° 95.12°	Depositor
Resolution (Å)	20.00 – 1.65 30.12 – 1.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.65) 95.9 (30.12-1.65)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.12 (at 1.64Å)	Xtriage
Refinement program	REFMAC 5.3.0021	Depositor
R, $R_{free}$	0.174 , 0.211 0.262 , 0.287	Depositor DCC
$R_{free}$ test set	3136 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 55.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 61986 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4612	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NCA, RF5

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	0.72	3/2101 (0.1%)	0.77	2/2846 (0.1%)
1	B	0.59	0/2101	0.67	0/2846
All	All	0.66	3/4202 (0.1%)	0.72	2/5692 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	72	GLU	CD-OE2	13.79	1.40	1.25
1	A	68	VAL	CA-CB	5.68	1.66	1.54
1	A	72	GLU	CD-OE1	5.51	1.31	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	VAL	CA-CB-CG1	-7.06	100.31	110.90
1	A	131	LEU	CB-CG-CD2	5.37	120.13	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2050	0	1976	32	0
1	B	2050	0	1976	34	0
2	A	13	0	0	0	0
2	B	13	0	0	0	0
3	A	9	0	6	0	0
3	B	9	0	6	0	0
4	A	236	0	0	6	0
4	B	232	0	0	10	0
All	All	4612	0	3964	64	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (64) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:194:ARG:HD2	4:B:541:HOH:O	1.67	0.94
1:B:115:GLN:HE22	1:B:149:LEU:H	1.18	0.92
1:A:115:GLN:HE22	1:A:149:LEU:H	1.18	0.90
1:A:165:THR:HG23	1:A:167:LYS:H	1.36	0.88
1:B:165:THR:HG23	1:B:167:LYS:H	1.35	0.87
1:B:266:ILE:HD11	1:B:273:PHE:HB2	1.60	0.82
1:B:202:ASP:HB3	4:B:503:HOH:O	1.80	0.80
1:A:75:PRO:HA	1:A:78:ARG:HG3	1.67	0.77
1:A:195:ARG:HD3	4:A:531:HOH:O	1.84	0.75
1:B:90:LYS:HG3	1:B:94:ILE:HG13	1.70	0.73
1:B:236:GLN:NE2	4:B:630:HOH:O	2.27	0.68
1:A:127:ARG:NH1	1:A:217:ASP:OD2	2.21	0.67
1:A:294:SER:O	1:A:296:CYS:N	2.28	0.67
1:B:266:ILE:HD11	1:B:273:PHE:CB	2.25	0.65
1:A:183:ASN:ND2	1:A:186:SER:H	1.95	0.65
1:A:268:LYS:HD3	1:B:163:PHE:CE1	2.32	0.65
1:A:140:ARG:NH2	4:A:431:HOH:O	2.29	0.64
1:B:162:GLU:HB2	1:B:165:THR:HG22	1.79	0.64
1:A:162:GLU:HB2	1:A:165:THR:HG22	1.80	0.63
1:A:182:ASN:HB2	4:A:413:HOH:O	1.99	0.62
1:A:86:TRP:CE2	1:A:90:LYS:HG3	2.35	0.61
1:A:110:MET:HE1	1:A:150:LEU:HD13	1.82	0.61
1:B:137:GLN:HG2	4:B:627:HOH:O	2.02	0.60
1:A:127:ARG:HB3	1:A:212:ARG:HE	1.66	0.60
1:A:268:LYS:HD3	1:B:163:PHE:HE1	1.66	0.58
1:B:115:GLN:NE2	1:B:149:LEU:H	1.96	0.57
1:B:104:GLU:HA	1:B:107:GLN:HG2	1.88	0.56
1:A:46:TRP:HE1	1:A:47:ARG:NH2	2.04	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:244:HIS:HD2	1:B:250:SER:HB3	1.70	0.55
1:A:48:GLN:NE2	1:A:171:GLN:HB3	2.22	0.55
1:B:195:ARG:HB2	4:B:528:HOH:O	2.07	0.54
1:B:45:ARG:HG3	1:B:46:TRP:N	2.23	0.54
1:A:78:ARG:NH1	4:A:395:HOH:O	2.41	0.53
1:B:194:ARG:NH1	4:B:634:HOH:O	2.41	0.53
1:B:195:ARG:HG3	4:B:527:HOH:O	2.09	0.52
1:B:293:ASP:CG	1:B:294:SER:H	2.13	0.52
1:B:244:HIS:CD2	1:B:250:SER:HB3	2.44	0.52
1:B:47:ARG:NH2	4:B:639:HOH:O	2.41	0.52
1:B:266:ILE:HD11	1:B:273:PHE:CA	2.40	0.52
1:A:244:HIS:HE1	1:A:277:ASN:OD1	1.94	0.50
1:A:183:ASN:HD21	1:A:186:SER:H	1.58	0.49
1:A:243:ILE:HG23	1:A:281:PRO:HG3	1.95	0.49
1:B:90:LYS:CG	1:B:94:ILE:HG13	2.39	0.49
1:B:238:LEU:HB3	1:B:266:ILE:HD13	1.95	0.47
1:A:134:GLN:CD	4:A:444:HOH:O	2.53	0.47
1:A:76:GLU:HG2	1:A:77:MET:HG2	1.97	0.46
1:B:98:PRO:O	1:B:183:ASN:HA	2.15	0.46
1:B:45:ARG:HG3	1:B:47:ARG:H	1.81	0.46
1:B:195:ARG:HD3	4:B:528:HOH:O	2.14	0.46
1:B:248:GLU:HG3	1:B:249:ASP:H	1.81	0.45
1:A:115:GLN:NE2	1:A:149:LEU:H	1.99	0.45
1:A:98:PRO:O	1:A:183:ASN:HA	2.18	0.44
1:B:134:GLN:O	1:B:137:GLN:HB2	2.18	0.43
1:A:104:GLU:HA	1:A:107:GLN:HG2	2.00	0.43
1:A:291:PRO:O	1:A:292:GLU:HB3	2.18	0.43
1:B:199:ALA:HB3	4:B:591:HOH:O	2.19	0.42
1:B:162:GLU:HB2	1:B:165:THR:CG2	2.47	0.42
1:A:94:ILE:O	1:A:95:SER:HB2	2.20	0.42
1:A:128:ILE:HG13	4:A:418:HOH:O	2.19	0.42
1:A:243:ILE:CG2	1:A:281:PRO:HG3	2.49	0.41
1:B:73:ILE:O	1:B:75:PRO:HD3	2.21	0.41
1:B:47:ARG:HH11	1:B:47:ARG:HG2	1.85	0.41
1:A:110:MET:HE1	1:A:192:VAL:HG12	2.02	0.41
1:A:78:ARG:HB2	1:A:78:ARG:HE	1.70	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	250/262 (95%)	240 (96%)	8 (3%)	2 (1%)	27	6
1	B	250/262 (95%)	239 (96%)	8 (3%)	3 (1%)	19	2
All	All	500/524 (95%)	479 (96%)	16 (3%)	5 (1%)	22	3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	295	SER
1	B	291	PRO
1	B	295	SER
1	A	128	ILE
1	B	128	ILE

### 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	233/241 (97%)	229 (98%)	4 (2%)	73	48
1	B	233/241 (97%)	228 (98%)	5 (2%)	66	37
All	All	466/482 (97%)	457 (98%)	9 (2%)	69	43

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ARG
1	A	89	PHE
1	A	131	LEU
1	A	292	GLU

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Mol	Chain	Res	Type
1	B	89	PHE
1	B	131	LEU
1	B	236	GLN
1	B	251	ARG
1	B	286	GLN

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	48	GLN
1	A	115	GLN
1	A	134	GLN
1	A	139	GLN
1	A	183	ASN
1	A	244	HIS
1	B	115	GLN
1	B	134	GLN
1	B	229	ASN
1	B	244	HIS
1	B	270	ASN
1	B	286	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

4 ligands are 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	RF5	A	301	1	0,0,14	0.00	-	0,0,21	0.00	-
3	NCA	A	302	-	9,9,9	0.52	0	11,11,11	2.04	4 (36%)
2	RF5	B	301	1	0,0,14	0.00	-	0,0,21	0.00	-
3	NCA	B	302	-	9,9,9	0.40	0	11,11,11	1.67	4 (36%)

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	RF5	A	301	1	-	0/0/0/22	0/0/0/1
3	NCA	A	302	-	-	0/4/4/4	0/1/1/1
2	RF5	B	301	1	-	0/0/0/22	0/0/0/1
3	NCA	B	302	-	-	0/4/4/4	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	NCA	C3-C2-N1	-3.37	118.59	123.51
3	A	302	NCA	O7-C7-C3	-3.33	115.82	119.58
3	B	302	NCA	C3-C2-N1	-2.85	119.35	123.51
3	A	302	NCA	C6-N1-C2	2.78	121.84	116.85
3	B	302	NCA	C6-N1-C2	2.71	121.71	116.85
3	A	302	NCA	C4-C3-C2	2.69	120.94	117.64
3	B	302	NCA	C3-C7-N7	2.51	120.62	117.77
3	B	302	NCA	O7-C7-C3	-2.28	117.00	119.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	252/262 (96%)	1.39	63 (25%) 1 1	24, 30, 39, 48	0
1	B	252/262 (96%)	1.64	80 (31%) 1 0	26, 31, 39, 43	0
All	All	504/524 (96%)	1.52	143 (28%) 1 1	24, 30, 39, 48	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	246	GLY	9.9
1	A	293	ASP	9.5
1	A	249	ASP	8.8
1	B	247	ARG	8.5
1	B	249	ASP	8.1
1	B	291	PRO	7.4
1	A	246	GLY	7.4
1	B	213	SER	7.3
1	B	295	SER	7.2
1	A	294	SER	7.2
1	B	248	GLU	6.7
1	B	245	GLY	6.7
1	A	248	GLU	6.6
1	B	290	ASN	6.4
1	B	292	GLU	6.4
1	A	292	GLU	6.3
1	B	294	SER	5.6
1	B	296	CYS	5.5
1	A	47	ARG	5.4
1	A	124	LEU	5.3
1	A	145	LEU	5.2
1	B	293	ASP	5.2
1	B	287	CYS	5.2
1	B	286	GLN	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	247	ARG	5.0
1	A	213	SER	4.9
1	B	159	TRP	4.9
1	B	282	ASP	4.7
1	B	153	LEU	4.6
1	B	127	ARG	4.6
1	B	280	ARG	4.5
1	A	230	LEU	4.3
1	A	123	LEU	4.3
1	B	189	TRP	4.3
1	B	285	LEU	4.2
1	B	284	PHE	4.2
1	A	238	LEU	4.1
1	B	250	SER	4.0
1	A	46	TRP	3.9
1	A	204	VAL	3.9
1	B	150	LEU	3.8
1	B	211	SER	3.8
1	B	185	VAL	3.8
1	A	189	TRP	3.7
1	A	295	SER	3.7
1	A	222	PHE	3.7
1	A	164	ASP	3.7
1	A	192	VAL	3.7
1	A	196	PHE	3.6
1	B	141	ASP	3.5
1	A	296	CYS	3.5
1	B	188	PHE	3.5
1	B	116	THR	3.5
1	B	228	HIS	3.5
1	B	145	LEU	3.5
1	A	206	VAL	3.4
1	A	188	PHE	3.4
1	B	124	LEU	3.4
1	B	151	GLY	3.4
1	A	227	VAL	3.4
1	A	45	ARG	3.3
1	B	289	LYS	3.3
1	A	225	VAL	3.3
1	B	123	LEU	3.3
1	A	185	VAL	3.2
1	A	235	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	244	HIS	3.1
1	A	197	ALA	3.1
1	A	266	ILE	3.1
1	B	215	ILE	3.1
1	B	176	TRP	3.1
1	A	79	HIS	3.0
1	A	125	TRP	3.0
1	B	212	ARG	3.0
1	A	73	ILE	3.0
1	B	269	ARG	3.0
1	B	89	PHE	3.0
1	A	271	ILE	3.0
1	B	196	PHE	2.9
1	A	48	GLN	2.9
1	A	159	TRP	2.9
1	A	150	LEU	2.9
1	A	193	SER	2.9
1	A	291	PRO	2.9
1	B	184	PRO	2.9
1	A	144	THR	2.8
1	A	148	THR	2.8
1	A	122	ILE	2.8
1	B	251	ARG	2.8
1	B	138	VAL	2.8
1	A	84	SER	2.7
1	B	279	TYR	2.7
1	B	137	GLN	2.7
1	B	255	GLN	2.6
1	A	143	PHE	2.6
1	B	219	ASP	2.6
1	A	187	VAL	2.6
1	A	262	LEU	2.6
1	A	245	GLY	2.6
1	B	252	ASP	2.6
1	B	253	LEU	2.5
1	B	257	PRO	2.5
1	B	214	LYS	2.5
1	B	154	ALA	2.5
1	B	283	LYS	2.5
1	A	80	VAL	2.4
1	B	93	PHE	2.4
1	A	203	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	69	LYS	2.4
1	A	205	HIS	2.4
1	B	224	SER	2.4
1	A	111	LYS	2.3
1	A	136	THR	2.3
1	B	99	CYS	2.3
1	B	148	THR	2.3
1	B	149	LEU	2.3
1	B	144	THR	2.3
1	B	173	CYS	2.3
1	A	154	ALA	2.3
1	A	78	ARG	2.3
1	B	281	PRO	2.3
1	B	106	TYR	2.3
1	A	195	ARG	2.3
1	B	140	ARG	2.3
1	B	288	VAL	2.3
1	A	265	ILE	2.2
1	A	153	LEU	2.2
1	B	267	SER	2.2
1	B	254	CYS	2.2
1	B	258	THR	2.2
1	A	151	GLY	2.2
1	B	278	ILE	2.2
1	B	233	GLU	2.2
1	B	54	GLY	2.2
1	B	256	ASP	2.1
1	A	58	ARG	2.1
1	A	280	ARG	2.1
1	B	55	THR	2.1
1	B	63	VAL	2.1
1	B	130	ASP	2.1
1	B	194	ARG	2.0
1	B	101	ILE	2.0
1	B	270	ASN	2.0

## 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

There are no carbohydrates in this entry.

### 6.4 Ligands

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	RF5	B	301	13/14	0.08	-1.15	22,26,30,33	0
3	NCA	B	302	9/9	0.11	-1.38	19,24,25,26	0
3	NCA	A	302	9/9	0.10	-1.78	19,23,25,26	0
2	RF5	A	301	13/14	0.07	-2.59	14,18,19,21	0

### 6.5 Other polymers

There are no such residues in this entry.