



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:39 PM GMT

PDB ID : 4CZM  
Title : C. crescentus MreB, monomeric, AMPPNP  
Authors : Lowe, J.; van den Ent, F.  
Deposited on : 2014-04-19  
Resolution : 2.20 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

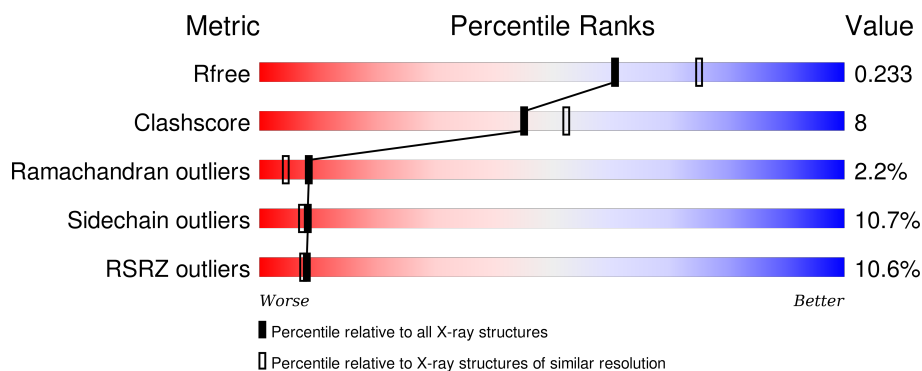
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	348	<div> <div>10%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>• • •</div> </div> </div>
1	B	348	<div> <div>10%</div> <div> <div></div> <div>69%</div> <div>24%</div> <div>• •</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10221 atoms, of which 5156 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 ROD SHAPE-DETERMINING PROTEIN MREB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	336	Total	C	H	N	O	S	0	0	0
			5045	1542	2566	451	471	15			
1	B	336	Total	C	H	N	O	S	0	0	0
			5045	1542	2566	451	471	15			

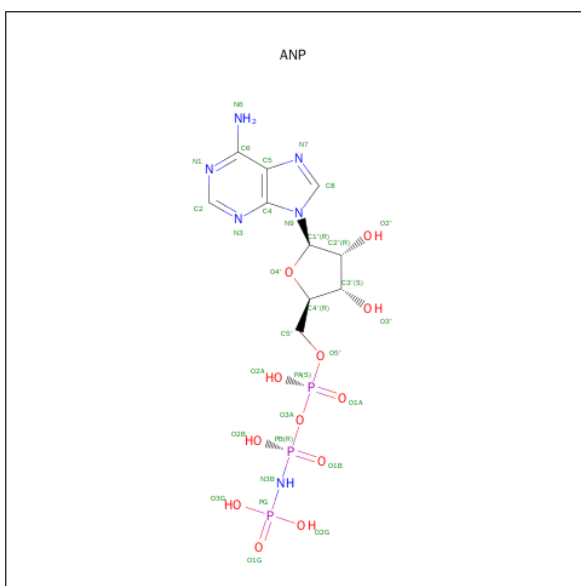
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	EXPRESSION TAG	UNP B8H609
A	348	GLY	-	EXPRESSION TAG	UNP B8H609
A	349	SER	-	EXPRESSION TAG	UNP B8H609
A	350	HIS	-	EXPRESSION TAG	UNP B8H609
A	351	HIS	-	EXPRESSION TAG	UNP B8H609
A	352	HIS	-	EXPRESSION TAG	UNP B8H609
A	353	HIS	-	EXPRESSION TAG	UNP B8H609
A	354	HIS	-	EXPRESSION TAG	UNP B8H609
A	355	HIS	-	EXPRESSION TAG	UNP B8H609
A	102	SER	PHE	ENGINEERED MUTATION	UNP B8H609
A	103	GLY	VAL	ENGINEERED MUTATION	UNP B8H609
A	283	ASP	SER	ENGINEERED MUTATION	UNP B8H609
B	8	MET	-	EXPRESSION TAG	UNP B8H609
B	348	GLY	-	EXPRESSION TAG	UNP B8H609
B	349	SER	-	EXPRESSION TAG	UNP B8H609
B	350	HIS	-	EXPRESSION TAG	UNP B8H609
B	351	HIS	-	EXPRESSION TAG	UNP B8H609
B	352	HIS	-	EXPRESSION TAG	UNP B8H609
B	353	HIS	-	EXPRESSION TAG	UNP B8H609
B	354	HIS	-	EXPRESSION TAG	UNP B8H609
B	355	HIS	-	EXPRESSION TAG	UNP B8H609
B	102	SER	PHE	ENGINEERED MUTATION	UNP B8H609
B	103	GLY	VAL	ENGINEERED MUTATION	UNP B8H609
B	283	ASP	SER	ENGINEERED MUTATION	UNP B8H609

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			43	10	12	6	12	3		
3	B	1	Total	C	H	N	O	P	0	0
			43	10	12	6	12	3		

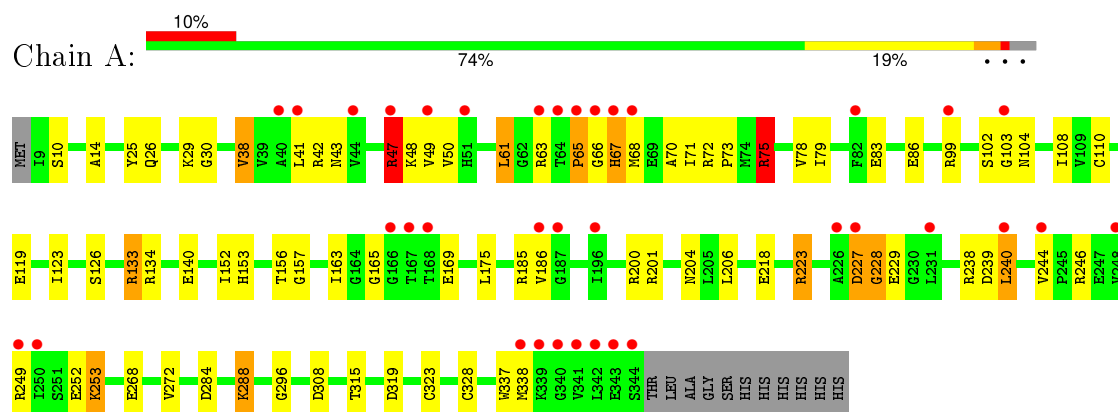
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		
4	B	16	Total	O	0	0
			16	16		

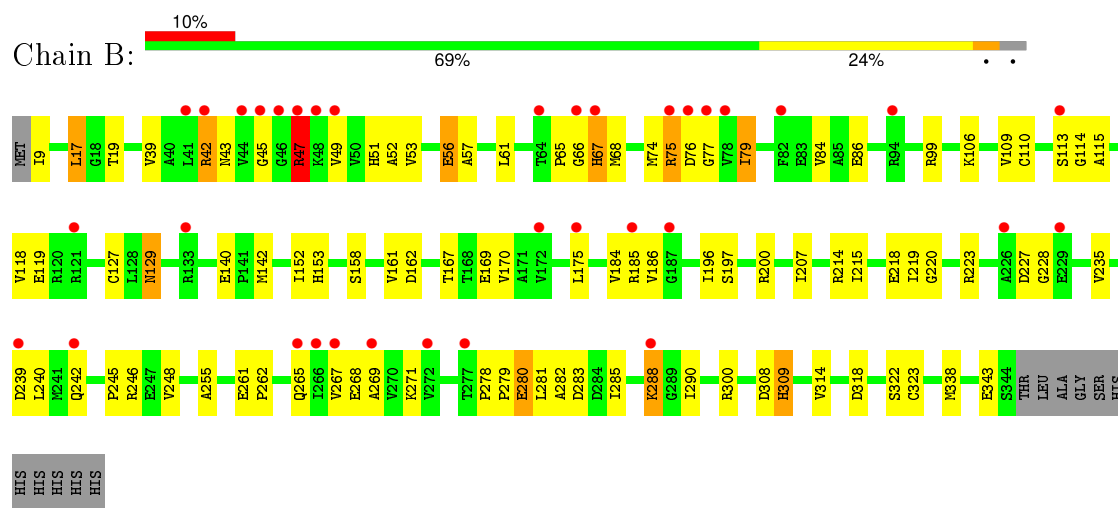
### 3 Residue-property plots [i](#)

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: ROD SHAPE-DETERMINING PROTEIN MREB



#### • Molecule 1: ROD SHAPE-DETERMINING PROTEIN MREB



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.79 Å 67.79 Å 320.56 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.14 – 2.20 43.74 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (41.14-2.20) 100.0 (43.74-2.20)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 2.20 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.209 , 0.277 0.237 , 0.233	Depositor DCC
$R_{free}$ test set	1973 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	61.9	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 54.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 39333 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10221	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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

### 5.1 Standard geometry

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

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	0.85	2/2510 (0.1%)	0.92	4/3392 (0.1%)
1	B	0.88	3/2510 (0.1%)	0.92	2/3392 (0.1%)
All	All	0.86	5/5020 (0.1%)	0.92	6/6784 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	323	CYS	CB-SG	-8.26	1.68	1.82
1	A	323	CYS	CB-SG	-5.77	1.72	1.81
1	A	186	VAL	CB-CG1	-5.57	1.41	1.52
1	B	322	SER	CB-OG	-5.39	1.35	1.42
1	B	162	ASP	CB-CG	5.10	1.62	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	47	ARG	NE-CZ-NH1	8.81	124.70	120.30
1	A	38	VAL	CB-CA-C	-7.25	97.62	111.40
1	B	162	ASP	CB-CG-OD1	6.23	123.90	118.30
1	B	17	LEU	CA-CB-CG	5.39	127.69	115.30
1	A	47	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	A	75	ARG	NE-CZ-NH1	5.28	122.94	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-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 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	2479	2566	2558	42	1
1	B	2479	2566	2558	40	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	12	13	1	0
3	B	31	12	13	0	0
4	A	27	0	0	1	0
4	B	16	0	0	1	0
All	All	5065	5156	5142	79	3

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 8.

All (79) 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:201:ARG:NH1	1:B:119:GLU:OE2	2.03	0.90
1:A:67:HIS:ND1	4:A:2010:HOH:O	2.27	0.68
1:A:65:PRO:O	1:A:67:HIS:N	2.34	0.60
1:A:239:ASP:OD1	1:A:246:ARG:NH2	2.34	0.60
1:B:227:ASP:OD1	1:B:228:GLY:N	2.36	0.58
1:B:269:ALA:O	4:B:2012:HOH:O	2.17	0.58
1:B:219:ILE:HD13	1:B:255:ALA:HB2	1.85	0.57
1:B:86:GLU:OE1	1:B:129:ASN:ND2	2.38	0.56
1:A:201:ARG:NH2	1:B:114:GLY:O	2.35	0.56
1:B:184:VAL:HG12	1:B:186:VAL:HG12	1.88	0.56
1:B:52:ALA:HB1	1:B:56:GLU:HG2	1.87	0.55
1:B:110:CYS:SG	1:B:140:GLU:HG2	2.45	0.55
1:A:119:GLU:O	1:A:123:ILE:HG12	2.06	0.55
1:A:43:ASN:HB3	1:A:48:LYS:HD3	1.92	0.52
1:A:200:ARG:HG3	1:A:240:LEU:CD1	2.40	0.52
1:B:113:SER:C	1:B:115:ALA:H	2.14	0.50
1:A:14:ALA:HB1	1:A:328:CYS:HB3	1.93	0.50
1:A:104:ASN:O	1:A:133:ARG:CZ	2.59	0.50
1:B:308:ASP:OD1	1:B:308:ASP:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:ARG:HH11	1:A:47:ARG:HG3	1.76	0.49
1:B:19:THR:HA	1:B:74:MET:HB2	1.95	0.49
1:A:163:ILE:HG22	1:A:296:GLY:HA3	1.94	0.49
1:B:215:ILE:HG23	1:B:219:ILE:HD11	1.96	0.48
1:A:104:ASN:O	1:A:133:ARG:HG2	2.13	0.48
1:B:109:VAL:HG21	1:B:127:CYS:SG	2.54	0.48
1:B:281:LEU:O	1:B:285:ILE:N	2.41	0.47
1:A:47:ARG:HH11	1:A:47:ARG:CG	2.27	0.47
1:B:279:PRO:O	1:B:283:ASP:N	2.42	0.47
1:A:223:ARG:NH2	1:A:308:ASP:OD2	2.48	0.47
1:B:262:PRO:HA	1:B:265:GLN:HG3	1.97	0.47
1:A:79:ILE:HD12	1:A:79:ILE:N	2.30	0.47
1:A:204:ASN:OD1	1:A:240:LEU:HB3	2.16	0.46
1:A:41:LEU:HD23	1:A:50:VAL:HA	1.96	0.46
1:B:75:ARG:O	1:B:77:GLY:N	2.49	0.46
1:A:61:LEU:HD12	1:A:70:ALA:HB2	1.98	0.46
1:B:279:PRO:HA	1:B:282:ALA:HB3	1.98	0.45
1:A:133:ARG:HD2	1:A:134:ARG:HH21	1.80	0.45
1:A:204:ASN:HB2	1:B:118:VAL:CG1	2.47	0.45
1:B:42:ARG:HD2	1:B:51:HIS:CE1	2.52	0.45
1:A:110:CYS:SG	1:A:140:GLU:HG2	2.56	0.45
1:B:220:GLY:O	1:B:300:ARG:HD2	2.17	0.44
1:A:26:GLN:HB3	1:A:29:LYS:HB2	1.99	0.44
1:B:39:VAL:HG11	1:B:84:VAL:CG1	2.48	0.44
1:A:25:TYR:CE2	1:A:30:GLY:HA2	2.53	0.44
1:B:39:VAL:HG11	1:B:84:VAL:HG11	2.00	0.44
1:B:278:PRO:HB2	1:B:280:GLU:HG3	2.00	0.43
1:B:219:ILE:CD1	1:B:255:ALA:HB2	2.46	0.43
1:A:268:GLU:O	1:A:272:VAL:HG23	2.17	0.43
1:B:142:MET:SD	1:B:152:ILE:HD13	2.58	0.43
1:B:290:ILE:HD12	1:B:314:VAL:HG22	2.00	0.43
1:A:104:ASN:O	1:A:133:ARG:NE	2.53	0.42
1:B:39:VAL:HG23	1:B:53:VAL:HG22	1.99	0.42
1:A:157:GLY:O	1:A:288:LYS:NZ	2.52	0.42
1:B:239:ASP:OD1	1:B:246:ARG:NE	2.52	0.42
1:A:228:GLY:O	1:A:253:LYS:HG3	2.19	0.42
1:A:156:THR:HG23	1:A:284:ASP:HB3	2.01	0.42
1:B:267:VAL:CG1	1:B:309:HIS:HB2	2.49	0.42
1:B:158:SER:OG	1:B:288:LYS:NZ	2.50	0.42
1:A:163:ILE:CG2	1:A:296:GLY:HA3	2.49	0.42
1:A:103:GLY:O	1:A:104:ASN:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:CYS:SG	1:B:140:GLU:HA	2.60	0.41
1:A:71:ILE:O	1:A:73:PRO:HD3	2.20	0.41
1:A:108:ILE:HG13	1:A:338:MET:HE3	2.01	0.41
1:B:153:HIS:HB3	1:B:338:MET:CE	2.51	0.41
1:B:79:ILE:O	1:B:79:ILE:HG12	2.20	0.41
1:B:47:ARG:NH2	1:B:49:VAL:HG11	2.35	0.41
1:A:41:LEU:HD13	1:A:48:LYS:HB3	2.03	0.41
1:A:229:GLU:HA	1:A:253:LYS:HB2	2.02	0.41
1:A:75:ARG:HG2	1:A:75:ARG:HH11	1.86	0.41
1:B:223:ARG:O	1:B:223:ARG:HG3	2.21	0.41
1:A:108:ILE:HD11	1:A:338:MET:HG3	2.02	0.41
1:A:152:ILE:HD11	1:A:153:HIS:CE1	2.56	0.41
1:A:165:GLY:H	3:A:1346:ANP:HNB1	1.69	0.40
1:B:196:ILE:HA	1:B:207:ILE:HD11	2.02	0.40
1:A:227:ASP:CG	1:A:228:GLY:N	2.72	0.40
1:B:161:VAL:HG13	1:B:170:VAL:HG22	2.03	0.40
1:A:86:GLU:HG2	1:A:126:SER:OG	2.21	0.40
1:A:75:ARG:CG	1:A:75:ARG:HH11	2.35	0.40
1:B:57:ALA:O	1:B:61:LEU:HD12	2.21	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:GLU:O	1:B:300:ARG:NH2[7_375]	2.05	0.15
1:A:42:ARG:NH1	1:A:252:GLU:OE2[6_485]	2.18	0.02
1:B:214:ARG:NH2	1:B:318:ASP:O[7_375]	2.19	0.01

## 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	334/348 (96%)	312 (93%)	17 (5%)	5 (2%)	13	9
1	B	334/348 (96%)	296 (89%)	28 (8%)	10 (3%)	5	2
All	All	668/696 (96%)	608 (91%)	45 (7%)	15 (2%)	8	4

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	GLY
1	A	227	ASP
1	B	65	PRO
1	B	76	ASP
1	A	65	PRO
1	A	102	SER
1	B	66	GLY
1	B	185	ARG
1	B	242	GLN
1	B	45	GLY
1	B	47	ARG
1	B	67	HIS
1	B	268	GLU
1	A	228	GLY
1	B	245	PRO

### 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	261/271 (96%)	232 (89%)	29 (11%)	8	6
1	B	261/271 (96%)	234 (90%)	27 (10%)	9	8
All	All	522/542 (96%)	466 (89%)	56 (11%)	8	7

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER

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Mol	Chain	Res	Type
1	A	38	VAL
1	A	47	ARG
1	A	49	VAL
1	A	61	LEU
1	A	63	ARG
1	A	67	HIS
1	A	68	MET
1	A	72	ARG
1	A	75	ARG
1	A	78	VAL
1	A	83	GLU
1	A	99	ARG
1	A	133	ARG
1	A	169	GLU
1	A	175	LEU
1	A	185	ARG
1	A	206	LEU
1	A	218	GLU
1	A	223	ARG
1	A	238	ARG
1	A	240	LEU
1	A	244	VAL
1	A	249	ARG
1	A	253	LYS
1	A	288	LYS
1	A	315	THR
1	A	319	ASP
1	A	337	TRP
1	B	9	ILE
1	B	17	LEU
1	B	42	ARG
1	B	43	ASN
1	B	47	ARG
1	B	56	GLU
1	B	67	HIS
1	B	68	MET
1	B	75	ARG
1	B	79	ILE
1	B	99	ARG
1	B	106	LYS
1	B	129	ASN
1	B	167	THR

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Mol	Chain	Res	Type
1	B	169	GLU
1	B	175	LEU
1	B	197	SER
1	B	200	ARG
1	B	235	VAL
1	B	240	LEU
1	B	248	VAL
1	B	261	GLU
1	B	271	LYS
1	B	280	GLU
1	B	288	LYS
1	B	309	HIS
1	B	343	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	HIS
1	A	203	HIS
1	A	334	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
3	ANP	A	1346	2	27,33,33	1.05	3 (11%)	30,52,52	1.44	5 (16%)
3	ANP	B	1346	2	27,33,33	1.62	4 (14%)	30,52,52	1.88	7 (23%)

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
3	ANP	A	1346	2	-	0/12/38/38	0/3/3/3
3	ANP	B	1346	2	-	0/12/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1346	ANP	PB-O3A	-6.06	1.51	1.59
3	B	1346	ANP	PA-O5'	-2.17	1.49	1.59
3	B	1346	ANP	PG-O3G	-2.15	1.50	1.56
3	A	1346	ANP	PG-N3B	2.07	1.68	1.63
3	A	1346	ANP	PB-N3B	2.22	1.69	1.63
3	A	1346	ANP	PG-O1G	2.61	1.49	1.46
3	B	1346	ANP	PB-O1B	3.12	1.49	1.46

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1346	ANP	O1B-PB-N3B	-5.75	103.08	111.90
3	A	1346	ANP	O1B-PB-N3B	-3.71	106.20	111.90
3	B	1346	ANP	C4'-O4'-C1'	-3.48	105.89	109.72
3	A	1346	ANP	O3G-PG-O1G	-2.83	105.98	113.49
3	A	1346	ANP	O2G-PG-O1G	-2.56	106.69	113.49
3	B	1346	ANP	O5'-PA-O1A	-2.50	99.91	109.62
3	B	1346	ANP	O2G-PG-O1G	-2.34	107.28	113.49
3	B	1346	ANP	O3'-C3'-C2'	-2.18	104.73	111.83
3	A	1346	ANP	O2B-PB-O1B	2.12	114.42	110.00
3	A	1346	ANP	O2A-PA-O1A	2.52	126.20	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1346	ANP	O2B-PB-O3A	2.71	117.38	105.09
3	B	1346	ANP	O1G-PG-N3B	3.52	117.29	111.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1346	ANP	1	0

## 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	336/348 (96%)	0.63	36 (10%) 8 7	45, 70, 113, 146	0
1	B	336/348 (96%)	0.62	35 (10%) 8 8	46, 75, 112, 152	0
All	All	672/696 (96%)	0.63	71 (10%) 8 7	45, 72, 113, 152	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	67	HIS	6.9
1	A	63	ARG	6.1
1	A	65	PRO	5.6
1	B	45	GLY	5.5
1	B	64	THR	5.1
1	B	78	VAL	5.0
1	A	49	VAL	4.7
1	B	67	HIS	4.5
1	A	68	MET	4.2
1	A	343	GLU	4.1
1	A	64	THR	4.0
1	A	339	LYS	3.9
1	A	226	ALA	3.7
1	A	249	ARG	3.7
1	A	338	MET	3.6
1	A	341	VAL	3.5
1	B	133	ARG	3.4
1	A	244	VAL	3.3
1	A	231	LEU	3.3
1	B	66	GLY	3.3
1	A	103	GLY	3.3
1	A	47	ARG	3.3
1	B	77	GLY	3.2
1	B	226	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	250	ILE	3.0
1	A	66	GLY	3.0
1	A	166	GLY	3.0
1	A	40	ALA	3.0
1	B	113	SER	3.0
1	A	51	HIS	3.0
1	B	41	LEU	3.0
1	B	46	GLY	2.9
1	B	277	THR	2.9
1	A	99	ARG	2.8
1	B	76	ASP	2.7
1	A	44	VAL	2.7
1	B	121	ARG	2.7
1	B	48	LYS	2.7
1	B	269	ALA	2.6
1	B	265	GLN	2.5
1	B	242	GLN	2.5
1	A	340	GLY	2.5
1	A	342	LEU	2.5
1	A	240	LEU	2.5
1	A	344	SER	2.4
1	B	82	PHE	2.4
1	B	47	ARG	2.4
1	B	288	LYS	2.4
1	B	75	ARG	2.4
1	B	187	GLY	2.4
1	B	267	VAL	2.3
1	B	272	VAL	2.3
1	B	42	ARG	2.3
1	A	196	ILE	2.2
1	B	185	ARG	2.2
1	B	266	ILE	2.2
1	B	94	ARG	2.2
1	B	172	VAL	2.2
1	A	82	PHE	2.2
1	B	175	LEU	2.2
1	A	186	VAL	2.1
1	A	227	ASP	2.1
1	B	49	VAL	2.1
1	A	167	THR	2.1
1	A	187	GLY	2.1
1	A	248	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	44	VAL	2.1
1	A	41	LEU	2.0
1	B	239	ASP	2.0
1	B	229	GLU	2.0
1	A	168	THR	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. 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(Å <sup>2</sup> )	Q<0.9
3	ANP	B	1346	31/31	0.99	0.21	0.82	40,50,59,71	0
3	ANP	A	1346	31/31	0.98	0.21	0.43	42,57,73,78	0
2	MG	B	1345	1/1	0.99	0.17	0.21	46,46,46,46	0
2	MG	A	1345	1/1	0.91	0.18	0.06	49,49,49,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.