



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 05:57 AM GMT

PDB ID : 1ZBH
Title : 3'-end specific recognition of histone mRNA stem-loop by 3'-exonuclease
Authors : Cheng, Y.; Patel, D.J.
Deposited on : 2005-04-08
Resolution : 3.00 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

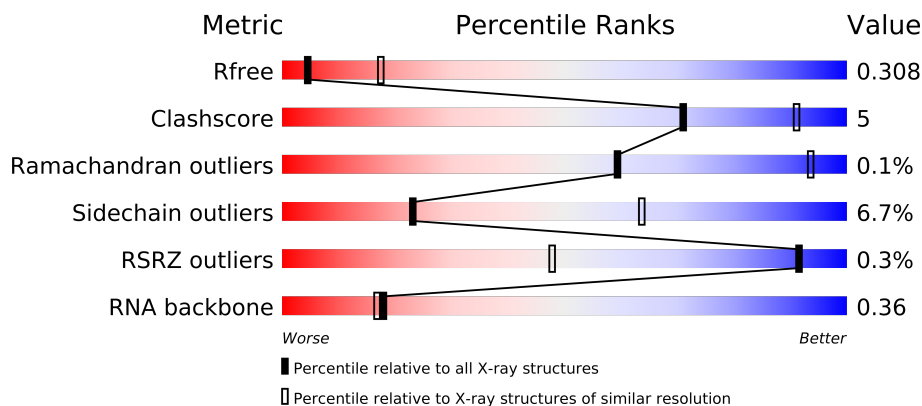
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)
RNA backbone	1838	1070 (3.50-2.50)

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. 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	E	20	
1	F	20	
2	A	299	
2	B	299	
2	C	299	
2	D	299	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9138 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 RNA chain called 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*C P*AP*GP*AP*GP*CP*CP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	16	Total	C	N	O	P	0	0	0
			333	150	55	113	15			
1	E	16	Total	C	N	O	P	0	0	0
			333	150	55	113	15			

- Molecule 2 is a protein called 3'-5' exonuclease ERI1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	289	Total	C	N	O	S	0	0	0
			2354	1503	395	439	17			
2	B	225	Total	C	N	O	S	0	0	0
			1823	1164	302	343	14			
2	C	225	Total	C	N	O	S	0	0	0
			1823	1164	302	343	14			
2	D	289	Total	C	N	O	S	0	0	0
			2354	1503	395	439	17			

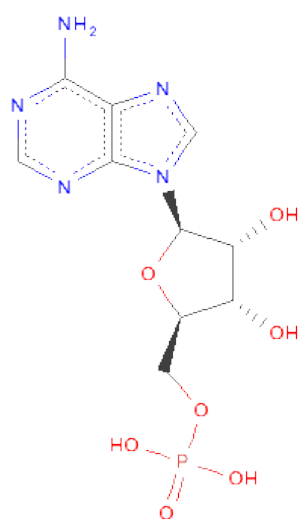
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	213	LEU	TRP	ENGINEERED	UNP Q8IV48
A	293	ASN	HIS	ENGINEERED	UNP Q8IV48
B	213	LEU	TRP	ENGINEERED	UNP Q8IV48
B	293	ASN	HIS	ENGINEERED	UNP Q8IV48
C	213	LEU	TRP	ENGINEERED	UNP Q8IV48
C	293	ASN	HIS	ENGINEERED	UNP Q8IV48
D	213	LEU	TRP	ENGINEERED	UNP Q8IV48
D	293	ASN	HIS	ENGINEERED	UNP Q8IV48

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Mg 2 2	0	0
3	A	2	Total Mg 2 2	0	0
3	D	2	Total Mg 2 2	0	0
3	C	2	Total Mg 2 2	0	0

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 23 10 5 7 1	0	0
4	B	1	Total C N O P 23 10 5 7 1	0	0
4	C	1	Total C N O P 23 10 5 7 1	0	0
4	D	1	Total C N O P 23 10 5 7 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	8	Total O 8 8	0	0
5	B	5	Total O 5 5	0	0

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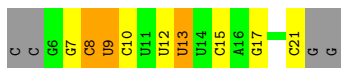
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total 2	O 2	0	0
5	D	2	Total 2	O 2	0	0
5	F	1	Total 1	O 1	0	0

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.

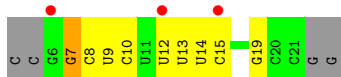
- Molecule 1: 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*CP*AP*GP*AP*GP*CP*CP*GP*G)-3'

Chain F: 



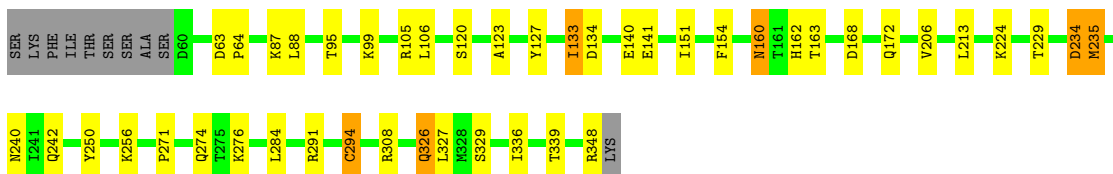
- Molecule 1: 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*CP*AP*GP*AP*GP*CP*CP*GP*G)-3'

Chain E: 



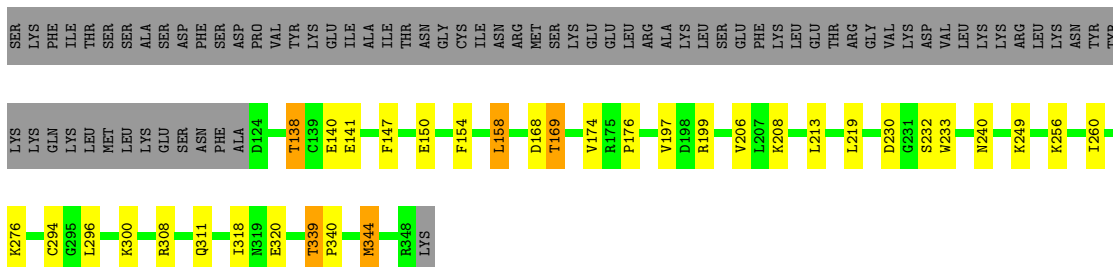
- Molecule 2: 3'-5' exonuclease ERI1

Chain A: 



- Molecule 2: 3'-5' exonuclease ERI1

Chain B: 



- Molecule 2: 3'-5' exonuclease ERI1

Chain C: 

SER	LYS	LYS	PHE	ILE	THR	SER	SER	ALA	SER	ASP	PHE	SER	ASP	PRO	VAL	TYR	LYS	GLU	ILE	ALA	ILE	THR	ASN	GLY	CYS	ILE	ARG	ASN	ARG	MET	SER	LYS	GLU	GLU	LEU	SER	GLU	PHE	LYS	LEU	GLU	THR	ARG	GLY	VAL	LYS	ASP	VAL	LEU	LYS	LYS	ARG	LEU	LYS	ASN	TYR	TYR
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LYS	LYS	GLN	LYS	LEU	MET	LEU	LYS	GLU	SER	ASN	PHE	ALA	D124	C131	N143	F154	L158	Q172	Y173	V174	V206	L207	K208	K209	K217	L227	L228	T229	D230	Q244	I260	R261	K262	L284	R308	R317	I316	N319	Q326	I336	M344	R348
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LYS

- Molecule 2: 3'-5' exonuclease ERI1

Chain D:

SER	LYS	PHE	ILE	THR	SER	SER	ALA	SER	D80	F81	S82	Y86	I89	L84	K87	L88	E94	L106	K107	M116	L117	K118	D124	S125	Y126	Y127	D134	F154	P155	V156	V157	L158	L159	N160	T161	H162	T163	I166	E167	D168	T169	Q181	F203	P204	V210
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I211	D212	I213	K217	D230	D234	M235	S236	M240	K256	M259	I260	L284	I305	R308	M319	E320	K321	M322	V330	S331	L334	P335	I336	M344	R348	LYS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.39Å 195.15Å 87.97Å 90.00° 92.13° 90.00°	Depositor
Resolution (Å)	19.92 – 3.00 19.91 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (19.92-3.00) 95.8 (19.91-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.98Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.209 , 0.260 0.273 , 0.308	Depositor DCC
R_{free} test set	3223 reflections (9.96%)	DCC
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 3.7	EDS
Estimated twinning fraction	0.056 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 33770 reflections	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	9138	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: AMP, 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	E	0.66	0/370	1.27	3/574 (0.5%)
1	F	0.65	0/370	1.32	3/574 (0.5%)
2	A	0.33	0/2402	0.49	0/3235
2	B	0.33	0/1864	0.49	0/2521
2	C	0.33	0/1864	0.48	0/2521
2	D	0.35	0/2402	0.49	0/3235
All	All	0.37	0/9272	0.61	6/12660 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	7	G	O3'-P-O5'	-11.54	82.08	104.00
1	E	7	G	O3'-P-O5'	-11.16	82.80	104.00
1	F	7	G	OP1-P-O3'	-9.85	83.52	105.20
1	E	7	G	OP1-P-O3'	-8.45	86.60	105.20
1	E	7	G	OP2-P-O3'	-8.43	86.65	105.20

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	E	333	0	173	0	0
1	F	333	0	173	3	0
2	A	2354	0	2381	21	0
2	B	1823	0	1817	13	0
2	C	1823	0	1817	17	0
2	D	2354	0	2381	31	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	23	0	12	0	0
4	B	23	0	12	0	0
4	C	23	0	12	0	0
4	D	23	0	12	0	0
5	A	8	0	0	0	0
5	B	5	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
5	F	1	0	0	0	0
All	All	9138	0	8790	81	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 5.

The worst 5 of 81 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:317:ARG:HH11	2:C:317:ARG:HG3	1.18	1.03
2:D:259:ASN:H	2:D:319:ASN:HD21	1.13	0.93
2:D:127:TYR:O	2:D:161:THR:HG21	1.82	0.80
2:D:160:ASN:ND2	2:D:163:THR:H	1.81	0.78
2:C:317:ARG:NH1	2:C:317:ARG:HG3	1.97	0.72

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	
2	A	287/299 (96%)	276 (96%)	10 (4%)	1 (0%)	50	90
2	B	223/299 (75%)	218 (98%)	5 (2%)	0	100	100
2	C	223/299 (75%)	217 (97%)	6 (3%)	0	100	100
2	D	287/299 (96%)	277 (96%)	10 (4%)	0	100	100
All	All	1020/1196 (85%)	988 (97%)	31 (3%)	1 (0%)	59	93

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	99	LYS

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	
2	A	267/276 (97%)	247 (92%)	20 (8%)	19	57
2	B	208/276 (75%)	191 (92%)	17 (8%)	17	52
2	C	208/276 (75%)	201 (97%)	7 (3%)	49	88
2	D	267/276 (97%)	247 (92%)	20 (8%)	19	57
All	All	950/1104 (86%)	886 (93%)	64 (7%)	23	64

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	233	TRP
2	B	339	THR
2	D	240	ASN
2	B	240	ASN
2	B	276	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	172	GLN

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Mol	Chain	Res	Type
2	C	205	GLN
2	D	240	ASN
2	B	343	GLN
2	C	143	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	15/20 (75%)	8 (53%)	1 (6%)
1	F	15/20 (75%)	6 (40%)	0
All	All	30/40 (75%)	14 (46%)	1 (3%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	F	8	C
1	F	9	U
1	F	12	U
1	F	13	U
1	F	15	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	14	U

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 ⓘ

Of 12 ligands modelled in this entry, 8 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	AMP	A	1002	3	25,25,25	1.12	2 (8%)	38,38,38	1.89	9 (23%)
4	AMP	B	2002	3	25,25,25	1.10	2 (8%)	38,38,38	1.98	8 (21%)
4	AMP	C	3002	3	25,25,25	1.11	2 (8%)	38,38,38	1.96	8 (21%)
4	AMP	D	4002	3	25,25,25	1.12	2 (8%)	38,38,38	1.88	9 (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
4	AMP	A	1002	3	-	0/10/26/26	0/1/3/3
4	AMP	B	2002	3	-	0/10/26/26	0/1/3/3
4	AMP	C	3002	3	-	0/10/26/26	0/1/3/3
4	AMP	D	4002	3	-	0/10/26/26	0/1/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4002	AMP	C5-C4	3.34	1.48	1.40
4	A	1002	AMP	C5-C4	3.25	1.47	1.40
4	C	3002	AMP	C5-C4	3.12	1.47	1.40
4	B	2002	AMP	C5-C4	3.12	1.47	1.40
4	C	3002	AMP	C4-N9	-2.60	1.34	1.37

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2002	AMP	N3-C2-N1	-6.62	123.17	128.71
4	A	1002	AMP	N3-C2-N1	-6.50	123.28	128.71
4	C	3002	AMP	N3-C2-N1	-6.47	123.30	128.71
4	D	4002	AMP	N3-C2-N1	-6.32	123.42	128.71
4	B	2002	AMP	N3-C4-N9	5.49	135.35	125.43

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, 95th 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 ²)	Q<0.9
1	E	16/20 (80%)	1.07	3 (18%) 2 1	49, 49, 50, 51	0
1	F	16/20 (80%)	0.15	0 100 100	49, 50, 50, 51	0
2	A	289/299 (96%)	0.10	0 100 100	46, 50, 54, 68	0
2	B	225/299 (75%)	-0.06	0 100 100	45, 49, 53, 55	0
2	C	225/299 (75%)	-0.03	0 100 100	45, 49, 53, 54	0
2	D	289/299 (96%)	-0.01	0 100 100	46, 50, 54, 69	0
All	All	1060/1236 (85%)	0.02	3 (0%) 91 48	45, 50, 53, 69	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	6	G	3.0
1	E	15	C	2.4
1	E	12	U	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 ⓘ

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, 95th 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 ²)	Q<0.9
3	MG	D	4001	1/1	0.18	-0.57	50,50,50,50	0
4	AMP	C	3002	23/23	0.20	-0.72	34,35,36,36	0
4	AMP	D	4002	23/23	0.20	-0.78	49,50,52,52	0
4	AMP	B	2002	23/23	0.17	-1.07	30,32,34,34	0
3	MG	C	3001	1/1	0.17	-1.22	10,10,10,10	0
3	MG	B	2000	1/1	0.19	-1.41	20,20,20,20	0
4	AMP	A	1002	23/23	0.17	-1.64	46,47,47,48	0
3	MG	B	2001	1/1	0.13	-2.25	17,17,17,17	0
3	MG	A	1001	1/1	0.11	-2.72	28,28,28,28	0
3	MG	C	3000	1/1	0.18	-2.84	14,14,14,14	0
3	MG	D	4000	1/1	0.12	-6.30	38,38,38,38	0
3	MG	A	1000	1/1	0.10	-21.89	21,21,21,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.