



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 30, 2024 – 10:03 PM EST

PDB ID : 1JJ2  
Title : Fully Refined Crystal Structure of the Haloarcula marismortui Large Ribosomal Subunit at 2.4 Angstrom Resolution  
Authors : Klein, D.J.; Schmeing, T.M.; Moore, P.B.; Steitz, T.A.  
Deposited on : 2001-07-03  
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

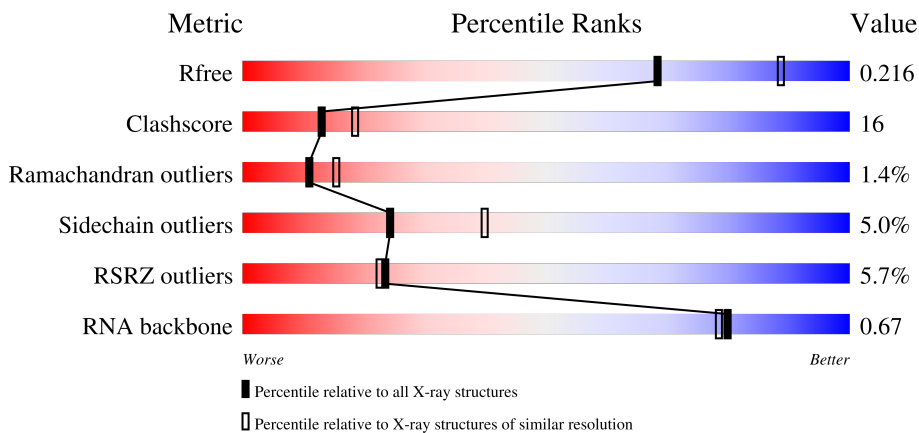
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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.



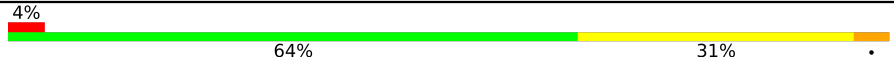
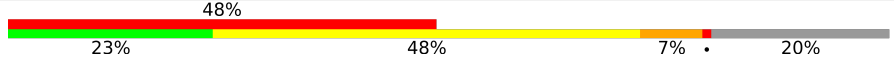
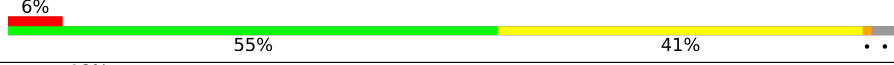


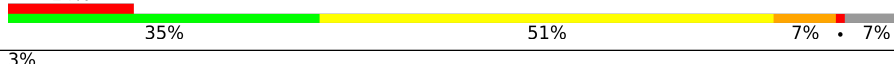
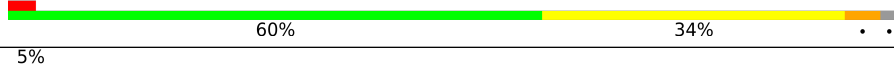

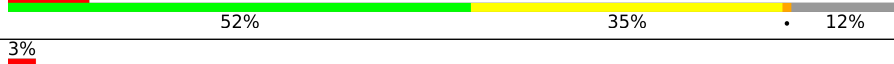
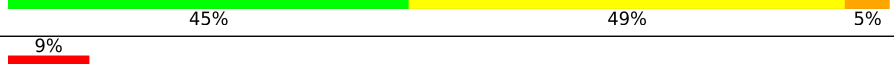

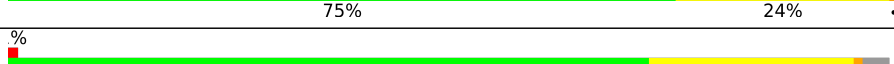
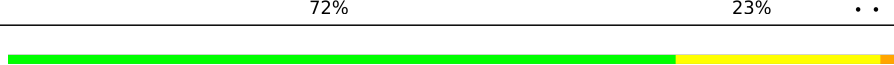
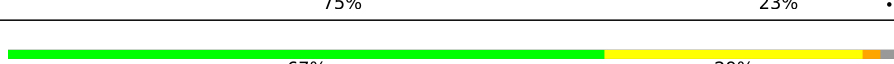

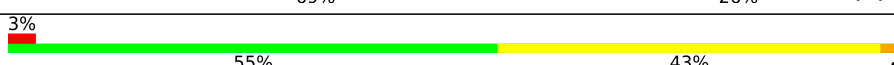
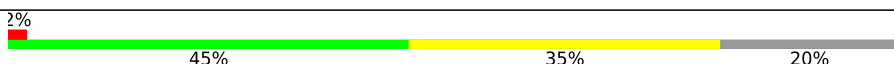
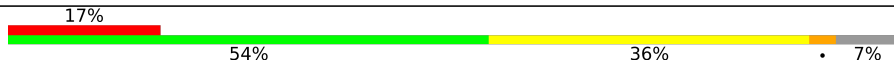
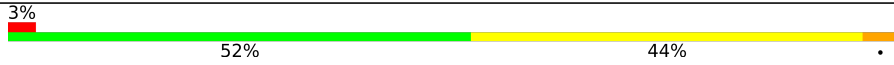

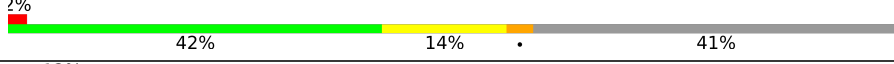

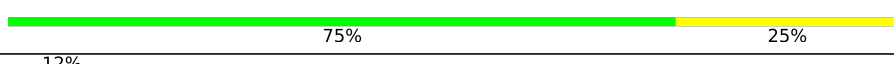


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)
RNA backbone	3102	1174 (2.80-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . 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	0	2922	 2% 65% 24% 5% • 6%
2	9	122	 5% 56% 32% 9% •
3	A	239	 8% 62% 31% 6% •
4	B	337	 4% 53% 41% 5%

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	176	
7	E	177	
8	F	119	
9	G	348	
10	H	167	
11	I	145	
12	J	132	
13	K	164	
14	L	194	
15	M	186	
16	N	115	
17	O	148	
18	P	95	
19	Q	154	
20	R	84	
21	S	119	
22	T	66	
23	U	70	
24	V	154	
25	W	91	
26	X	240	
27	Y	73	
28	Z	56	
29	1	48	

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Mol	Chain	Length	Quality of chain
30	2	92	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	NA	0	8370	-	-	-	X
33	NA	Q	8386	-	-	-	X

## 2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 98543 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 RNA chain called 23S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	0	2754	59017	26346	10878	19048	2745	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	conflict	GB 3377779

- Molecule 2 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	9	122	2600	1160	472	847	121	0	0	0

- Molecule 3 is a protein called RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	237	1754	1072	352	325	5	0	0	0

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	B	337	2624	1616	493	510	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP P20279
B	310	ARG	PHE	conflict	UNP P20279

- Molecule 5 is a protein called RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	C	246	1858	1131	344	382	1	0	0	0

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	D	140	1094	685	195	210	4	0	0	0

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	E	172	1357	840	224	289	4	0	0	0

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	F	119	885	552	141	191	1	0	0	0

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	G	29	240	149	39	51	1	0	0	0

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	H	156	1215	766	233	212	4	0	0	0

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	I	142	1119	696	199	221	3	0	0	0

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	J	132	993	609	189	191	4	0	0	0

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	K	145	1114	668	222	224		0	0	0

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	L	194	1605	988	346	266	5	0	0	0

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
15	M	186	1444	895	262	285	2	0	0	0

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L18E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
16	N	115	864	529	161	174	0	0	0

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L19E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
17	O	143	1133	680	230	223	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	71	LYS	TYR	conflict	UNP P14119

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L21E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
18	P	95	734	450	141	143	0	0	0

- Molecule 19 is a protein called RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
19	Q	150	1149	713	209	223	4	0	0	0

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
20	R	81	641	389	111	138	3	0	0	0

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
21	S	119	949	568	180	201	0	0	0

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L24E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
22	T	53	410	244	75	86	5	0	0	0

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
23	U	65	499	304	94	100	1	0	0	0

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
24	V	154	1195	737	209	243	6	0	0	0

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L31E.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
25	W	82	654	402	129	122	1	0	0	0

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L32E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
26	X	142	1130	686	228	216		0	0	0

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
27	Y	73	563	359	111	86	7	0	0	0

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
28	Z	56	430	258	86	82	4	0	0	0

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
29	1	46	393	238	86	68	1	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	ARG	deletion	UNP P22452

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
30	2	92	755	458	153	137	7	0	0	0

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
31	0	109	Total Mg 109 109	0	0
31	9	1	Total Mg 1 1	0	0
31	A	2	Total Mg 2 2	0	0
31	B	1	Total Mg 1 1	0	0
31	J	1	Total Mg 1 1	0	0
31	S	1	Total Mg 1 1	0	0
31	X	1	Total Mg 1 1	0	0
31	2	1	Total Mg 1 1	0	0

- Molecule 32 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	0	2	Total K 2 2	0	0

- Molecule 33 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	72	Total Na 72 72	0	0
33	9	2	Total Na 2 2	0	0
33	A	1	Total Na 1 1	0	0
33	C	1	Total Na 1 1	0	0
33	H	2	Total Na 2 2	0	0
33	I	1	Total Na 1 1	0	0
33	K	1	Total Na 1 1	0	0
33	L	1	Total Na 1 1	0	0
33	P	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	Q	2	Total 2	Na 2	0	0
33	R	1	Total 1	Na 1	0	0
33	S	1	Total 1	Na 1	0	0

- Molecule 34 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	10	Total 10	Cl 10	0	0
34	A	1	Total 1	Cl 1	0	0
34	B	1	Total 1	Cl 1	0	0
34	I	3	Total 3	Cl 3	0	0
34	K	1	Total 1	Cl 1	0	0
34	L	1	Total 1	Cl 1	0	0
34	M	1	Total 1	Cl 1	0	0
34	N	1	Total 1	Cl 1	0	0
34	Q	1	Total 1	Cl 1	0	0
34	X	1	Total 1	Cl 1	0	0
34	2	1	Total 1	Cl 1	0	0

- Molecule 35 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	N	1	Total 1	Cd 1	0	0
35	T	1	Total 1	Cd 1	0	0
35	Y	1	Total 1	Cd 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	Z	1	Total 1	Cd 1	0	0
35	2	1	Total 1	Cd 1	0	0

- Molecule 36 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	5938	Total 5938	O 5938	0	0
36	9	135	Total 135	O 135	0	0
36	A	126	Total 126	O 126	0	0
36	B	150	Total 150	O 150	0	0
36	C	172	Total 172	O 172	0	0
36	D	53	Total 53	O 53	0	0
36	E	46	Total 46	O 46	0	0
36	F	28	Total 28	O 28	0	0
36	G	21	Total 21	O 21	0	0
36	H	74	Total 74	O 74	0	0
36	I	56	Total 56	O 56	0	0
36	J	62	Total 62	O 62	0	0
36	K	80	Total 80	O 80	0	0
36	L	127	Total 127	O 127	0	0
36	M	70	Total 70	O 70	0	0
36	N	43	Total 43	O 43	0	0
36	O	68	Total 68	O 68	0	0

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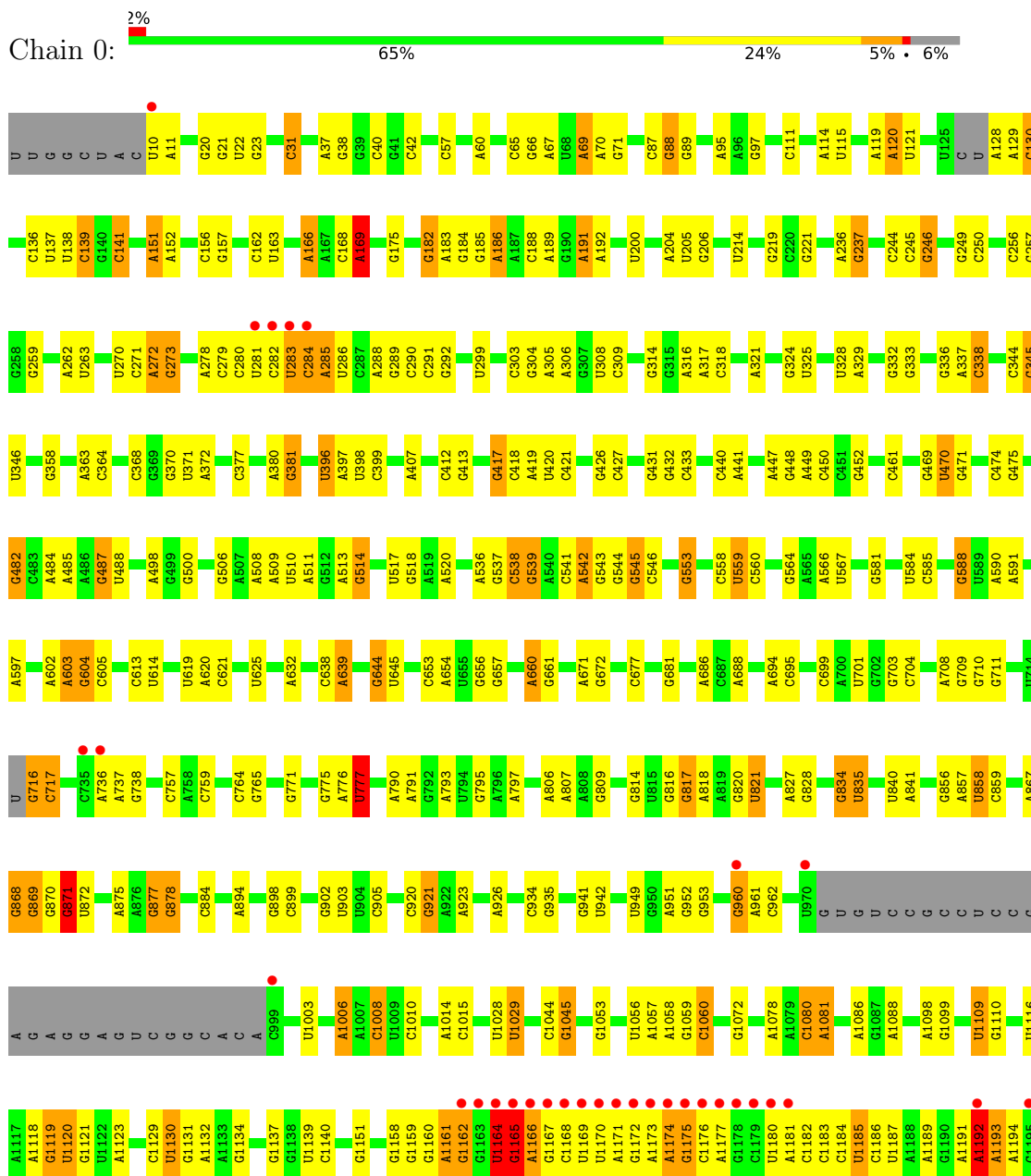
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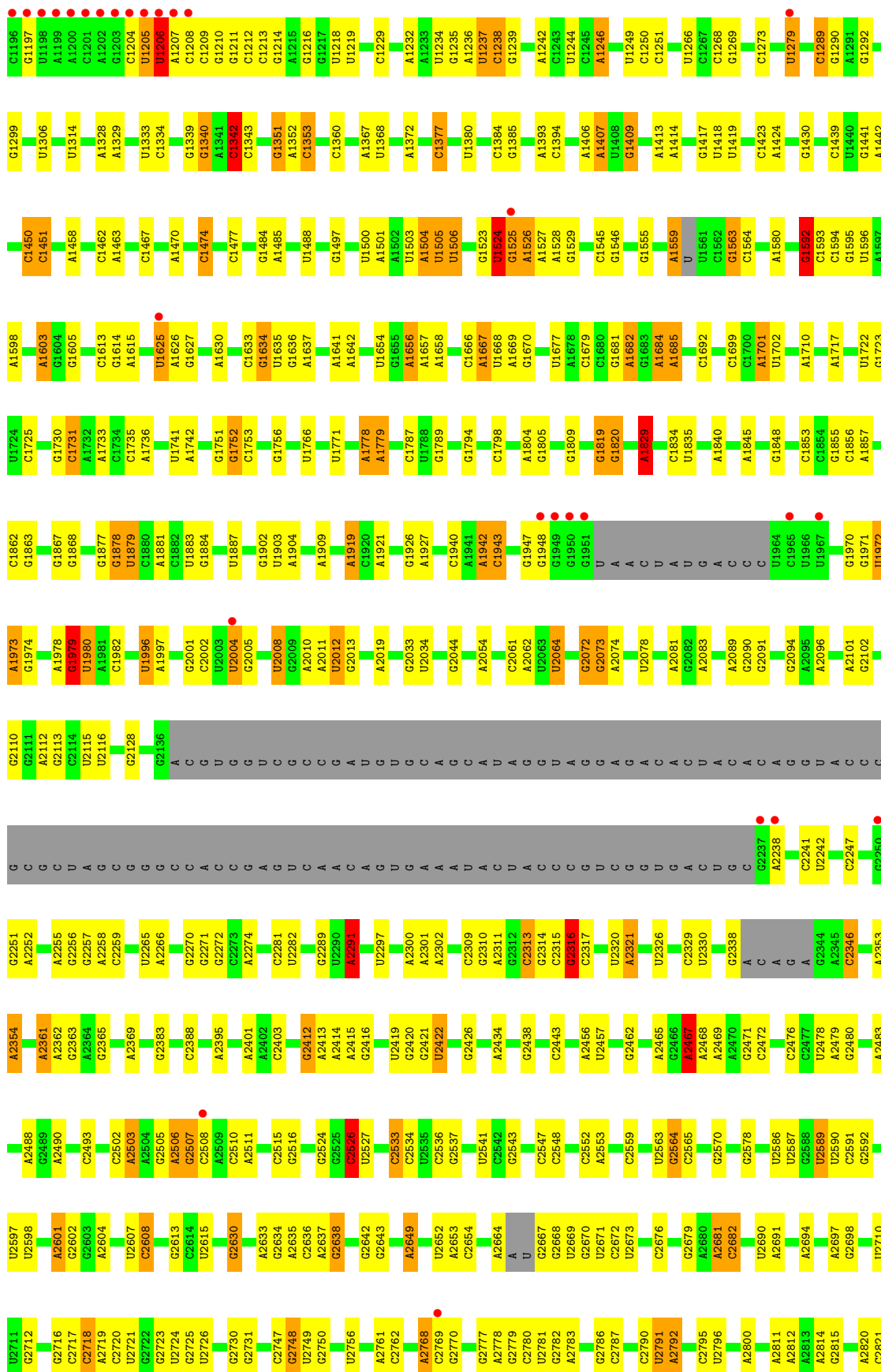
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36	Q	81	Total 81	O 81	0	0
36	R	32	Total 32	O 32	0	0
36	S	39	Total 39	O 39	0	0
36	T	25	Total 25	O 25	0	0
36	U	15	Total 15	O 15	0	0
36	V	67	Total 67	O 67	0	0
36	W	29	Total 29	O 29	0	0
36	X	99	Total 99	O 99	0	0
36	Y	39	Total 39	O 39	0	0
36	Z	53	Total 53	O 53	0	0
36	1	40	Total 40	O 40	0	0
36	2	72	Total 72	O 72	0	0

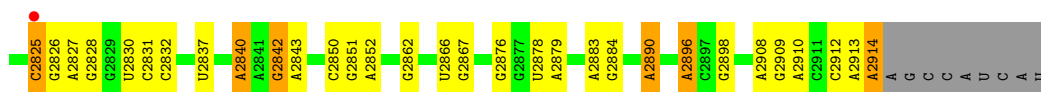
### 3 Residue-property plots

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.

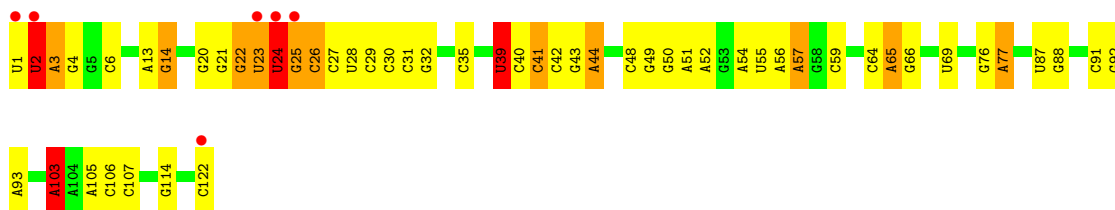
- Molecule 1: 23S RRNA



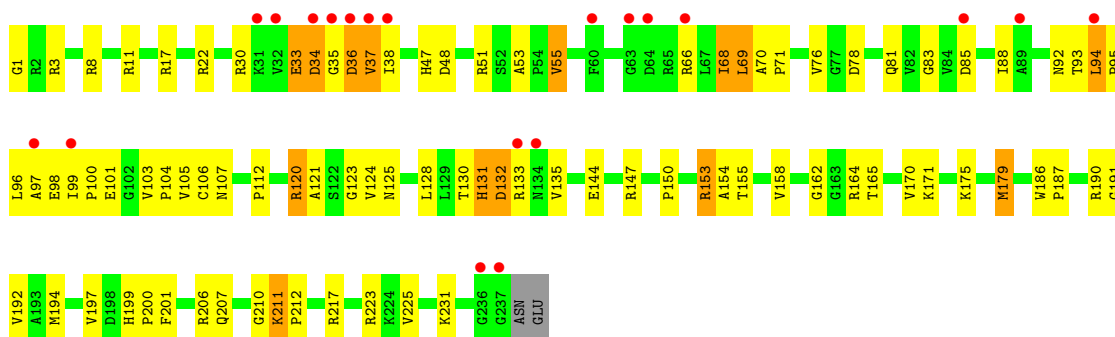




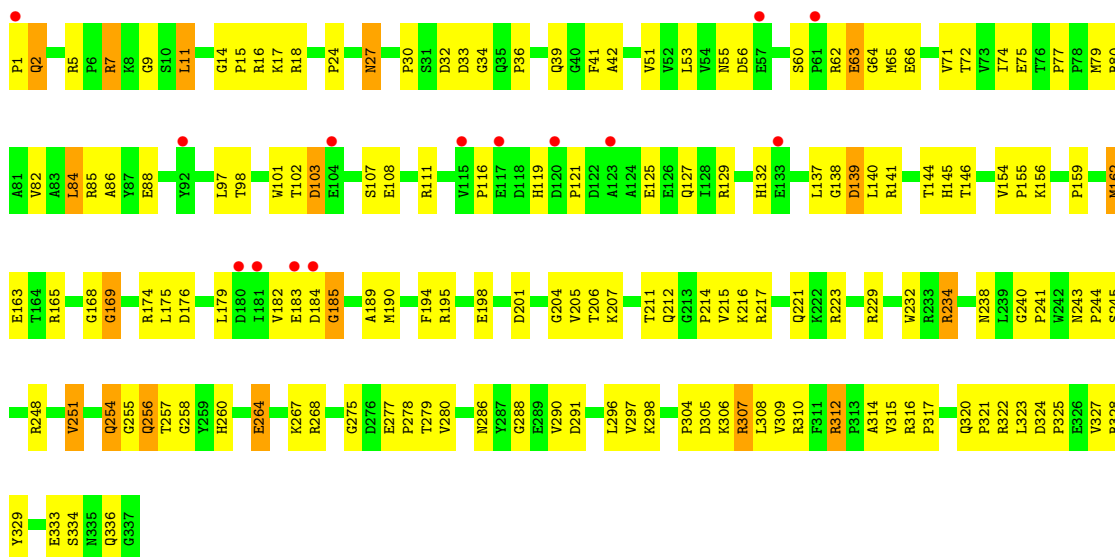
• Molecule 2: 5S RRNA



• Molecule 3: RIBOSOMAL PROTEIN L2

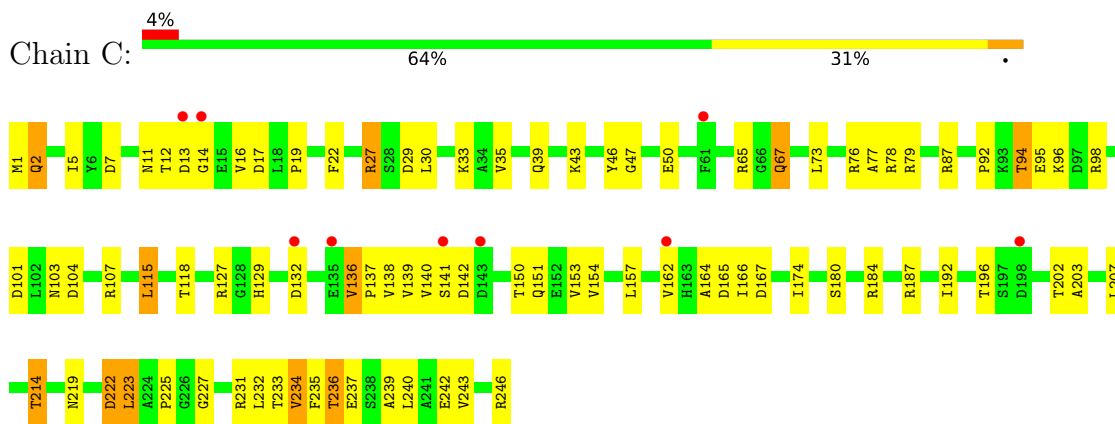


• Molecule 4: RIBOSOMAL PROTEIN L3

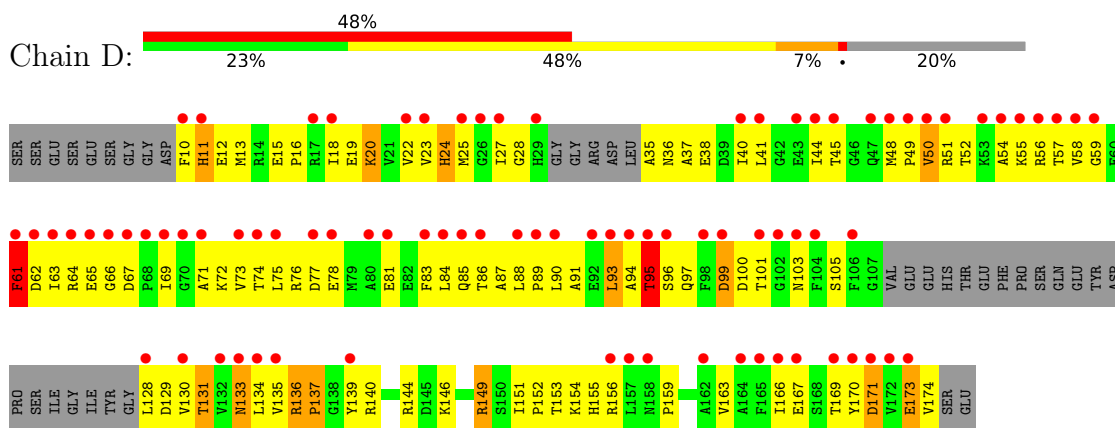


• Molecule 5: RIBOSOMAL PROTEIN L4

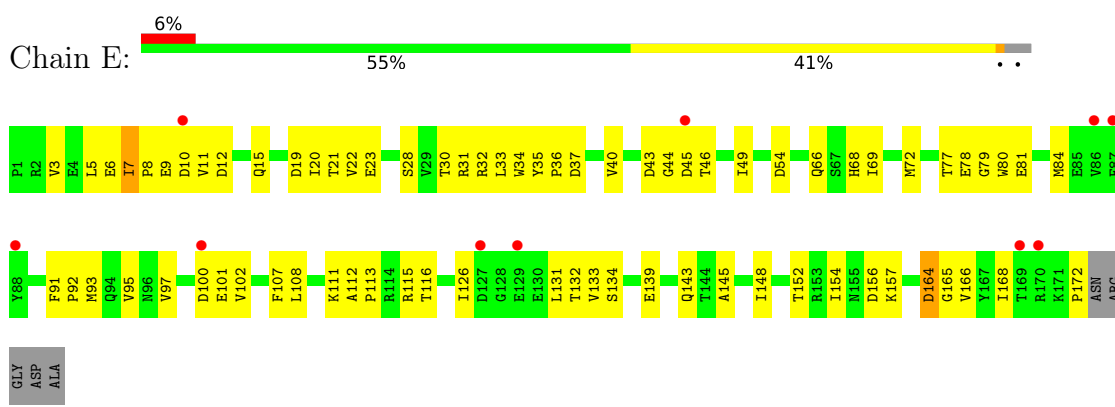




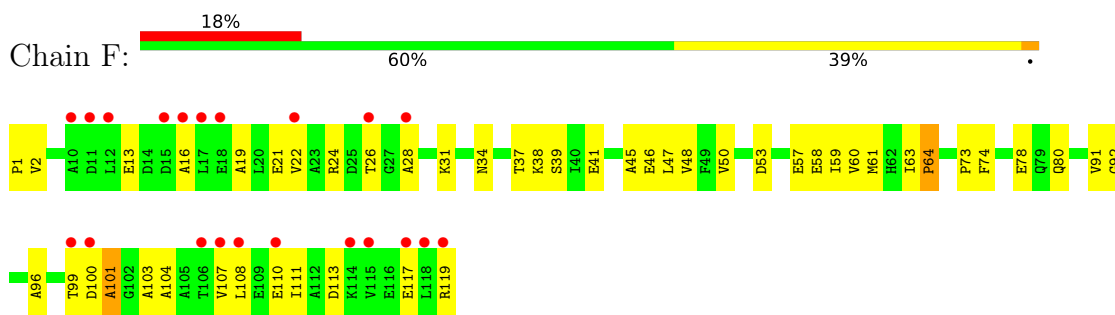
• Molecule 6: RIBOSOMAL PROTEIN L5



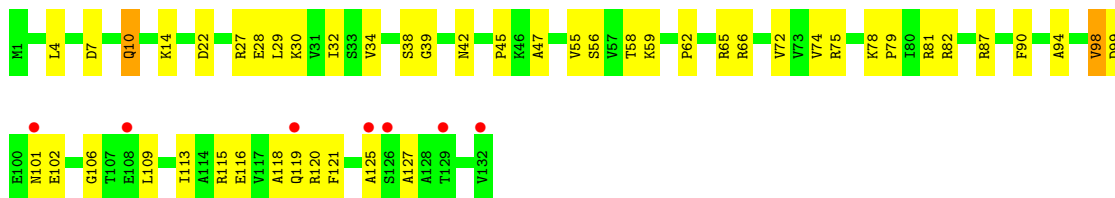
• Molecule 7: RIBOSOMAL PROTEIN L6



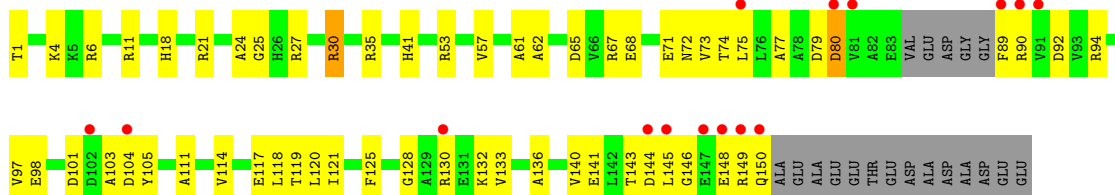
• Molecule 8: RIBOSOMAL PROTEIN L7AE



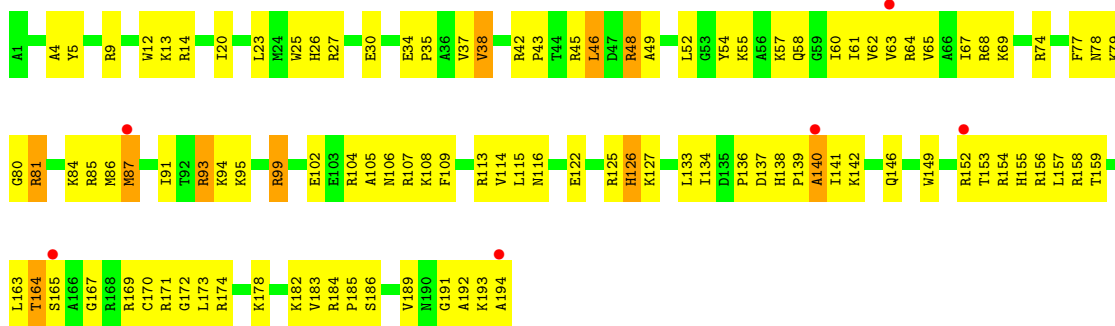




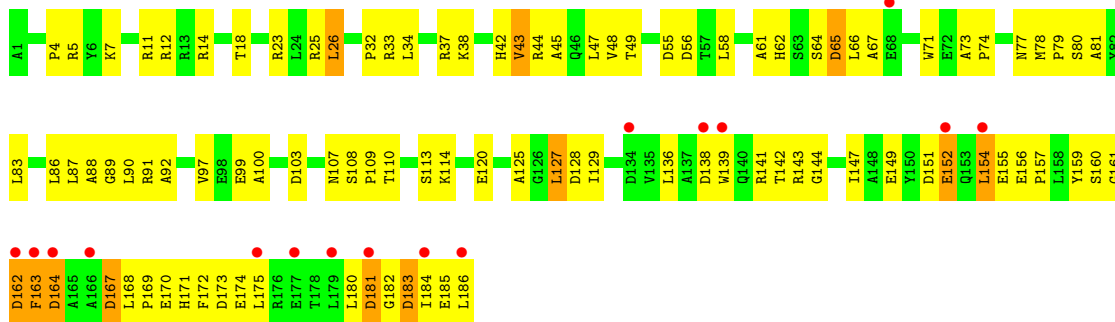
- Molecule 13: RIBOSOMAL PROTEIN L15



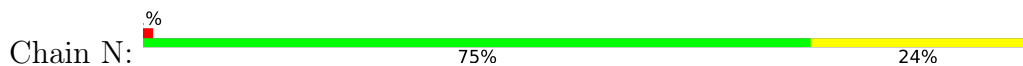
- Molecule 14: RIBOSOMAL PROTEIN L15E

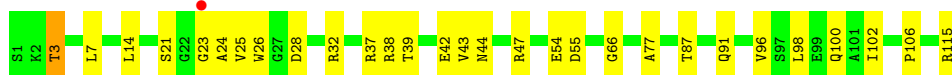


- Molecule 15: RIBOSOMAL PROTEIN L18

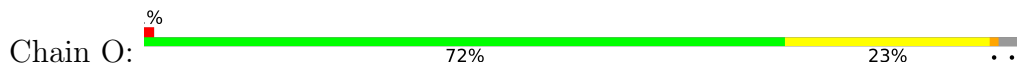


- Molecule 16: RIBOSOMAL PROTEIN L18E





- Molecule 17: RIBOSOMAL PROTEIN L19E



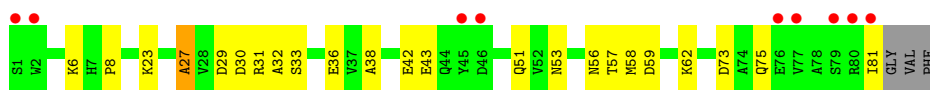
- Molecule 18: RIBOSOMAL PROTEIN L21E



- Molecule 19: RIBOSOMAL PROTEIN L22



- Molecule 20: RIBOSOMAL PROTEIN L23



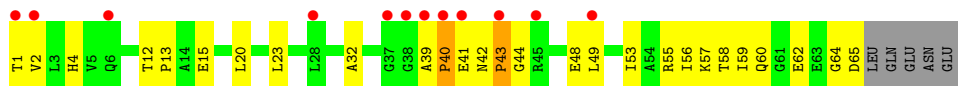
- Molecule 21: RIBOSOMAL PROTEIN L24



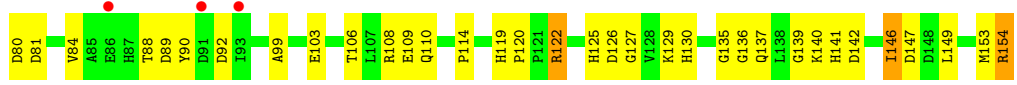
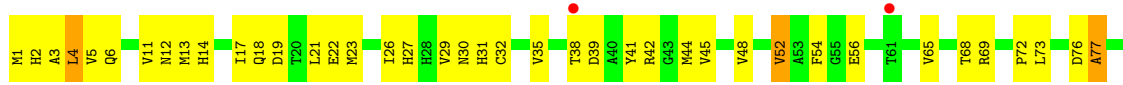
- Molecule 22: RIBOSOMAL PROTEIN L24E



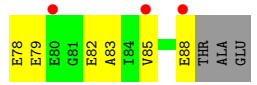
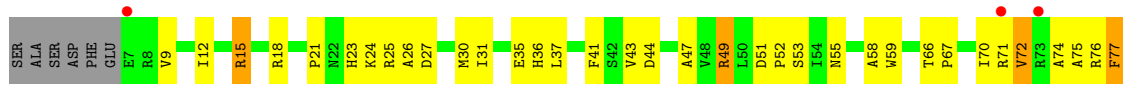
• Molecule 23: RIBOSOMAL PROTEIN L29



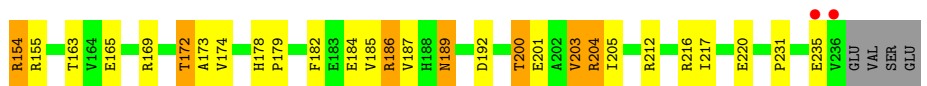
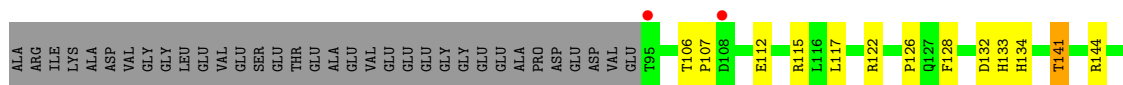
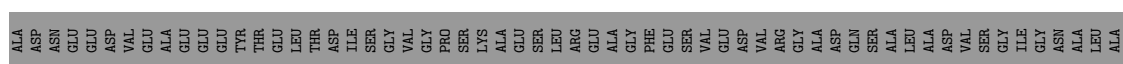
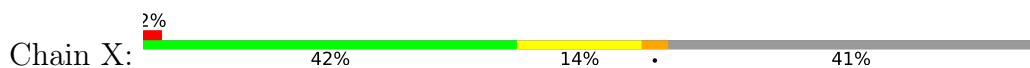
• Molecule 24: RIBOSOMAL PROTEIN L30



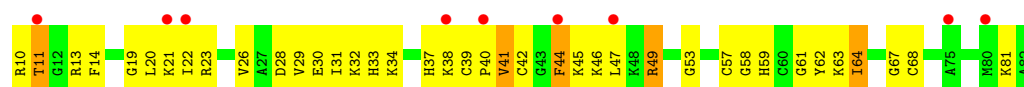
• Molecule 25: RIBOSOMAL PROTEIN L31E



• Molecule 26: RIBOSOMAL PROTEIN L32E



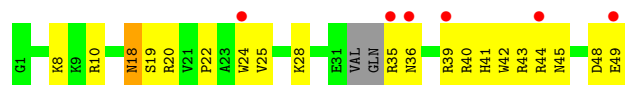
• Molecule 27: RIBOSOMAL PROTEIN L37Ae



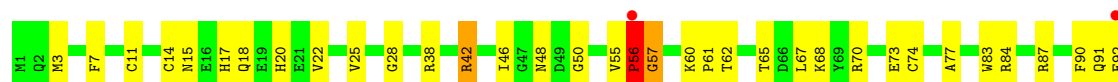
- Molecule 28: RIBOSOMAL PROTEIN L37E



- Molecule 29: RIBOSOMAL PROTEIN L39E



- Molecule 30: RIBOSOMAL PROTEIN L44E



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	211.66Å 299.67Å 573.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 85.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	90.2 (15.00-2.40) 90.6 (85.48-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 2.40Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.189 , 0.222 0.183 , 0.216	Depositor DCC
$R_{free}$ test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.9	Xtrriage
Anisotropy	0.263	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	98543	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.50% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: NA, K, MG, CL, CD

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	0	0.38	3/66076 (0.0%)	0.71	32/103052 (0.0%)
2	9	0.44	3/2905 (0.1%)	0.85	11/4528 (0.2%)
3	A	0.34	0/1787	0.66	0/2409
4	B	0.34	0/2689	0.64	0/3652
5	C	0.39	0/1883	0.67	0/2551
6	D	0.31	0/1111	0.59	0/1498
7	E	0.31	0/1382	0.57	0/1880
8	F	0.33	0/896	0.56	0/1219
9	G	0.25	0/241	0.47	0/324
10	H	0.38	0/1246	0.74	1/1686 (0.1%)
11	I	0.33	0/1135	0.61	0/1530
12	J	0.33	0/1003	0.65	0/1351
13	K	0.34	0/1126	0.68	0/1504
14	L	0.41	0/1633	0.71	1/2180 (0.0%)
15	M	0.29	0/1473	0.64	0/1999
16	N	0.32	0/873	0.61	1/1181 (0.1%)
17	O	0.33	0/1143	0.54	0/1521
18	P	0.35	0/748	0.68	0/1005
19	Q	0.35	0/1172	0.67	0/1578
20	R	0.32	0/648	0.59	1/875 (0.1%)
21	S	0.31	0/957	0.63	0/1289
22	T	0.32	0/417	0.58	0/562
23	U	0.29	0/502	0.54	0/675
24	V	0.33	0/1218	0.62	0/1655
25	W	0.32	0/664	0.60	0/895
26	X	0.34	0/1146	0.63	0/1536
27	Y	0.37	0/575	0.69	0/763
28	Z	0.42	0/437	0.67	0/578
29	1	0.34	0/398	0.54	0/527
30	2	0.38	0/771	0.62	0/1024
All	All	0.37	6/98255 (0.0%)	0.70	47/147027 (0.0%)



Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	1	62
2	9	0	2
All	All	1	64

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	9	3	A	C2'-O2'	-7.92	1.31	1.41
1	0	1206	U	P-OP2	6.22	1.59	1.49
2	9	3	A	O5'-C5'	6.21	1.54	1.44
1	0	1206	U	C3'-O3'	-5.28	1.34	1.42
1	0	1205	U	C3'-O3'	-5.23	1.34	1.42

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1165	G	O5'-P-OP1	-22.95	83.17	110.70
1	0	1164	U	OP1-P-O3'	-20.79	59.47	105.20
1	0	1165	G	O5'-P-OP2	-15.10	92.11	105.70
2	9	3	A	OP1-P-O3'	-13.36	75.82	105.20
1	0	1164	U	OP2-P-O3'	-13.28	75.98	105.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1563	G	C3'

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	182	G	Sidechain
1	0	191	A	Sidechain
1	0	22	U	Sidechain
1	0	221	G	Sidechain
1	0	246	G	Sidechain

## 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	0	59017	0	29807	760	0
2	9	2600	0	1326	78	0
3	A	1754	0	1763	109	0
4	B	2624	0	2533	176	0
5	C	1858	0	1816	105	0
6	D	1094	0	1085	130	0
7	E	1357	0	1266	79	0
8	F	885	0	854	59	0
9	G	240	0	231	18	0
10	H	1215	0	1215	150	0
11	I	1119	0	1098	62	0
12	J	993	0	1027	56	0
13	K	1114	0	1072	55	0
14	L	1605	0	1676	141	0
15	M	1444	0	1401	119	0
16	N	864	0	873	31	0
17	O	1133	0	1127	38	0
18	P	734	0	728	18	0
19	Q	1149	0	1122	49	0
20	R	641	0	605	21	0
21	S	949	0	923	52	0
22	T	410	0	364	31	0
23	U	499	0	511	28	0
24	V	1195	0	1137	91	0
25	W	654	0	653	44	0
26	X	1130	0	1133	52	0
27	Y	563	0	597	53	0
28	Z	430	0	426	22	0
29	1	393	0	406	32	0
30	2	755	0	728	36	0
31	0	109	0	0	0	0
31	2	1	0	0	0	0
31	9	1	0	0	0	0
31	A	2	0	0	0	0
31	B	1	0	0	0	0
31	J	1	0	0	0	0
31	S	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	X	1	0	0	0	0
32	0	2	0	0	0	0
33	0	72	0	0	0	0
33	9	2	0	0	0	0
33	A	1	0	0	0	0
33	C	1	0	0	0	0
33	H	2	0	0	0	0
33	I	1	0	0	0	0
33	K	1	0	0	0	0
33	L	1	0	0	0	0
33	P	1	0	0	0	0
33	Q	2	0	0	0	0
33	R	1	0	0	0	0
33	S	1	0	0	0	0
34	0	10	0	0	0	0
34	2	1	0	0	0	0
34	A	1	0	0	0	0
34	B	1	0	0	0	0
34	I	3	0	0	1	0
34	K	1	0	0	0	0
34	L	1	0	0	1	0
34	M	1	0	0	0	0
34	N	1	0	0	0	0
34	Q	1	0	0	0	0
34	X	1	0	0	0	0
35	2	1	0	0	0	0
35	N	1	0	0	0	0
35	T	1	0	0	0	0
35	Y	1	0	0	0	0
35	Z	1	0	0	0	0
36	0	5938	0	0	173	0
36	1	40	0	0	6	0
36	2	72	0	0	10	0
36	9	135	0	0	14	0
36	A	126	0	0	20	0
36	B	150	0	0	30	0
36	C	172	0	0	30	0
36	D	53	0	0	18	0
36	E	46	0	0	12	0
36	F	28	0	0	7	0
36	G	21	0	0	4	0
36	H	74	0	0	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	I	56	0	0	5	0
36	J	62	0	0	13	0
36	K	80	0	0	17	0
36	L	127	0	0	19	0
36	M	70	0	0	16	0
36	N	43	0	0	6	0
36	O	68	0	0	1	0
36	P	53	0	0	1	0
36	Q	81	0	0	9	0
36	R	32	0	0	5	0
36	S	39	0	0	5	0
36	T	25	0	0	6	0
36	U	15	0	0	4	0
36	V	67	0	0	10	0
36	W	29	0	0	3	0
36	X	99	0	0	15	0
36	Y	39	0	0	12	0
36	Z	53	0	0	1	0
All	All	98543	0	59503	2453	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 16.

The worst 5 of 2453 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)
1:0:1160:G:H5'	1:0:1161:A:H5'	1.26	1.14
10:H:86:ARG:NH1	10:H:133:ILE:HG13	1.62	1.12
5:C:5:ILE:HD11	5:C:16:VAL:HG23	1.35	1.07
25:W:37:LEU:HD13	25:W:85:VAL:HG21	1.29	1.06
1:0:960:G:H4'	36:0:6956:HOH:O	1.54	1.06

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 number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	235/239 (98%)	216 (92%)	14 (6%)	5 (2%)	7	8
4	B	335/337 (99%)	314 (94%)	14 (4%)	7 (2%)	7	8
5	C	244/246 (99%)	226 (93%)	18 (7%)	0	100	100
6	D	134/176 (76%)	97 (72%)	28 (21%)	9 (7%)	1	0
7	E	170/177 (96%)	161 (95%)	8 (5%)	1 (1%)	25	36
8	F	117/119 (98%)	106 (91%)	9 (8%)	2 (2%)	9	11
9	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
10	H	152/167 (91%)	135 (89%)	12 (8%)	5 (3%)	4	3
11	I	140/145 (97%)	130 (93%)	7 (5%)	3 (2%)	7	8
12	J	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	19	29
13	K	141/164 (86%)	121 (86%)	19 (14%)	1 (1%)	22	32
14	L	192/194 (99%)	181 (94%)	10 (5%)	1 (0%)	29	41
15	M	184/186 (99%)	167 (91%)	10 (5%)	7 (4%)	3	2
16	N	113/115 (98%)	109 (96%)	4 (4%)	0	100	100
17	O	141/148 (95%)	138 (98%)	3 (2%)	0	100	100
18	P	93/95 (98%)	89 (96%)	4 (4%)	0	100	100
19	Q	148/154 (96%)	143 (97%)	4 (3%)	1 (1%)	22	32
20	R	79/84 (94%)	75 (95%)	4 (5%)	0	100	100
21	S	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
22	T	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
23	U	63/70 (90%)	58 (92%)	3 (5%)	2 (3%)	4	3
24	V	152/154 (99%)	147 (97%)	4 (3%)	1 (1%)	22	32
25	W	80/91 (88%)	70 (88%)	8 (10%)	2 (2%)	5	6
26	X	140/240 (58%)	140 (100%)	0	0	100	100
27	Y	71/73 (97%)	64 (90%)	5 (7%)	2 (3%)	5	4
28	Z	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
29	1	42/48 (88%)	42 (100%)	0	0	100	100
30	2	90/92 (98%)	86 (96%)	2 (2%)	2 (2%)	6	7
All	All	3633/4235 (86%)	3372 (93%)	209 (6%)	52 (1%)	11	15

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	139	ASP
6	D	93	LEU
6	D	95	THR
6	D	137	PRO
6	D	173	GLU

### 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	Analysed	Rotameric	Outliers	Percentiles	
3	A	179/181 (99%)	166 (93%)	13 (7%)	14	22
4	B	282/282 (100%)	264 (94%)	18 (6%)	17	28
5	C	193/193 (100%)	179 (93%)	14 (7%)	14	22
6	D	117/147 (80%)	106 (91%)	11 (9%)	8	13
7	E	152/155 (98%)	148 (97%)	4 (3%)	46	66
8	F	92/92 (100%)	91 (99%)	1 (1%)	73	87
9	G	27/283 (10%)	27 (100%)	0	100	100
10	H	122/122 (100%)	109 (89%)	13 (11%)	6	9
11	I	118/121 (98%)	109 (92%)	9 (8%)	13	20
12	J	106/106 (100%)	103 (97%)	3 (3%)	43	63
13	K	112/126 (89%)	108 (96%)	4 (4%)	35	54
14	L	166/166 (100%)	157 (95%)	9 (5%)	22	36
15	M	149/149 (100%)	143 (96%)	6 (4%)	31	49
16	N	93/93 (100%)	91 (98%)	2 (2%)	52	71
17	O	113/116 (97%)	111 (98%)	2 (2%)	59	76
18	P	79/79 (100%)	75 (95%)	4 (5%)	24	39
19	Q	117/121 (97%)	114 (97%)	3 (3%)	46	66
20	R	71/73 (97%)	71 (100%)	0	100	100
21	S	105/105 (100%)	101 (96%)	4 (4%)	33	51
22	T	44/52 (85%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	51/56 (91%)	50 (98%)	1 (2%)	55	74
24	V	130/130 (100%)	122 (94%)	8 (6%)	18	29
25	W	66/73 (90%)	62 (94%)	4 (6%)	18	30
26	X	120/195 (62%)	110 (92%)	10 (8%)	11	17
27	Y	56/56 (100%)	52 (93%)	4 (7%)	14	23
28	Z	46/46 (100%)	46 (100%)	0	100	100
29	1	42/44 (96%)	41 (98%)	1 (2%)	49	68
30	2	79/79 (100%)	76 (96%)	3 (4%)	33	51
All	All	3027/3441 (88%)	2876 (95%)	151 (5%)	24	40

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	Q	82	GLU
27	Y	11	THR
21	S	96	VAL
25	W	27	ASP
30	2	56	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
19	Q	113	HIS
25	W	23	HIS
19	Q	122	GLN
24	V	27	HIS
26	X	189	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2747/2922 (94%)	239 (8%)	35 (1%)
2	9	121/122 (99%)	16 (13%)	5 (4%)
All	All	2868/3044 (94%)	255 (8%)	40 (1%)

5 of 255 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	11	A
1	0	31	C
1	0	60	A
1	0	67	A
1	0	69	A

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	2526	C
2	9	2	U
1	0	2536	C
1	0	2726	U
2	9	24	U

#### 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 232 ligands modelled in this entry, 232 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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

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<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	0	2754/2922 (94%)	-0.39	61 (2%) 62 60	17, 36, 79, 126	0
2	9	122/122 (100%)	-0.36	6 (4%) 29 28	31, 54, 78, 136	0
3	A	237/239 (99%)	0.38	20 (8%) 11 10	19, 38, 71, 92	0
4	B	337/337 (100%)	0.37	14 (4%) 36 35	21, 45, 71, 82	0
5	C	246/246 (100%)	0.31	9 (3%) 41 41	15, 35, 58, 70	0
6	D	140/176 (79%)	2.56	84 (60%) 0 0	43, 86, 105, 108	0
7	E	172/177 (97%)	0.59	10 (5%) 23 22	37, 59, 77, 81	0
8	F	119/119 (100%)	0.90	21 (17%) 1 1	37, 58, 83, 88	0
9	G	29/348 (8%)	2.56	21 (72%) 0 0	64, 79, 86, 91	0
10	H	156/167 (93%)	0.70	23 (14%) 2 2	30, 47, 75, 79	0
11	I	142/145 (97%)	0.24	5 (3%) 44 43	29, 42, 63, 84	0
12	J	132/132 (100%)	0.16	7 (5%) 26 25	27, 42, 61, 71	0
13	K	145/164 (88%)	0.70	15 (10%) 6 6	18, 54, 90, 102	0
14	L	194/194 (100%)	0.12	6 (3%) 49 47	19, 32, 50, 62	0
15	M	186/186 (100%)	0.60	16 (8%) 10 9	31, 50, 91, 103	0
16	N	115/115 (100%)	-0.03	1 (0%) 84 82	27, 44, 60, 69	0
17	O	143/148 (96%)	0.14	1 (0%) 87 86	30, 44, 56, 64	0
18	P	95/95 (100%)	0.08	0 100 100	25, 34, 50, 60	0
19	Q	150/154 (97%)	-0.04	0 100 100	23, 36, 54, 63	0
20	R	81/84 (96%)	0.46	9 (11%) 5 4	31, 46, 68, 72	0
21	S	119/119 (100%)	0.40	4 (3%) 45 44	28, 45, 69, 81	0
22	T	53/66 (80%)	0.34	1 (1%) 66 64	33, 47, 63, 71	0
23	U	65/70 (92%)	1.62	12 (18%) 1 1	39, 59, 97, 101	0
24	V	154/154 (100%)	0.33	5 (3%) 47 46	27, 40, 57, 65	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	W	82/91 (90%)	0.45	6 (7%) 15 13	35, 48, 73, 91	0
26	X	142/240 (59%)	-0.01	4 (2%) 53 51	22, 35, 59, 74	0
27	Y	73/73 (100%)	0.57	9 (12%) 4 3	36, 49, 63, 77	0
28	Z	56/56 (100%)	0.21	0 100 100	17, 24, 32, 35	0
29	1	46/48 (95%)	0.51	6 (13%) 3 3	27, 49, 77, 86	0
30	2	92/92 (100%)	0.19	2 (2%) 62 60	23, 44, 59, 72	0
All	All	6577/7279 (90%)	0.10	378 (5%) 23 22	15, 41, 80, 136	0

The worst 5 of 378 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
23	U	1	THR	13.9
6	D	63	ILE	10.0
23	U	39	ALA	8.7
6	D	57	THR	7.6
2	9	1	U	6.7

## 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
31	MG	0	8087	1/1	0.62	0.28	72,72,72,72	0
33	NA	Q	8386	1/1	0.62	0.44	74,74,74,74	0
31	MG	0	8050	1/1	0.75	0.13	56,56,56,56	0
33	NA	0	8371	1/1	0.76	0.35	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
33	NA	0	8370	1/1	0.77	0.44	61,61,61,61	0
31	MG	0	8103	1/1	0.78	0.23	54,54,54,54	0
33	NA	0	8329	1/1	0.80	0.14	48,48,48,48	0
31	MG	0	8072	1/1	0.81	0.08	47,47,47,47	0
31	MG	9	8095	1/1	0.81	0.15	69,69,69,69	0
33	NA	0	8384	1/1	0.82	0.14	52,52,52,52	0
31	MG	0	8102	1/1	0.83	0.11	51,51,51,51	0
31	MG	0	8049	1/1	0.84	0.12	56,56,56,56	0
31	MG	0	8070	1/1	0.84	0.15	40,40,40,40	0
33	NA	C	8304	1/1	0.85	0.17	30,30,30,30	0
33	NA	H	8322	1/1	0.86	0.25	52,52,52,52	0
31	MG	0	8113	1/1	0.86	0.13	36,36,36,36	0
31	MG	0	8047	1/1	0.87	0.10	54,54,54,54	0
33	NA	0	8307	1/1	0.88	0.13	42,42,42,42	0
31	MG	0	8076	1/1	0.88	0.04	46,46,46,46	0
33	NA	0	8363	1/1	0.88	0.32	52,52,52,52	0
31	MG	0	8101	1/1	0.89	0.30	48,48,48,48	0
33	NA	9	8383	1/1	0.89	0.21	43,43,43,43	0
31	MG	0	8034	1/1	0.89	0.09	31,31,31,31	0
33	NA	0	8308	1/1	0.89	0.18	42,42,42,42	0
33	NA	0	8311	1/1	0.89	0.15	48,48,48,48	0
33	NA	9	8351	1/1	0.90	0.12	42,42,42,42	0
31	MG	0	8043	1/1	0.90	0.07	33,33,33,33	0
33	NA	0	8340	1/1	0.90	0.26	47,47,47,47	0
33	NA	0	8373	1/1	0.90	0.12	43,43,43,43	0
31	MG	0	8090	1/1	0.90	0.31	53,53,53,53	0
33	NA	0	8358	1/1	0.91	0.35	74,74,74,74	0
31	MG	0	8067	1/1	0.91	0.14	34,34,34,34	0
31	MG	0	8089	1/1	0.91	0.06	51,51,51,51	0
31	MG	B	8055	1/1	0.91	0.07	40,40,40,40	0
31	MG	0	8062	1/1	0.91	0.08	41,41,41,41	0
33	NA	0	8376	1/1	0.91	0.28	39,39,39,39	0
31	MG	0	8094	1/1	0.92	0.09	59,59,59,59	0
31	MG	0	8077	1/1	0.92	0.14	23,23,23,23	0
31	MG	0	8117	1/1	0.92	0.17	36,36,36,36	0
33	NA	0	8385	1/1	0.92	0.40	48,48,48,48	0
31	MG	0	8022	1/1	0.92	0.12	32,32,32,32	0
33	NA	0	8369	1/1	0.92	0.22	40,40,40,40	0
33	NA	0	8318	1/1	0.92	0.25	49,49,49,49	0
33	NA	0	8327	1/1	0.92	0.27	38,38,38,38	0
33	NA	0	8372	1/1	0.92	0.43	54,54,54,54	0
33	NA	0	8356	1/1	0.93	0.20	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
33	NA	0	8314	1/1	0.93	0.32	40,40,40,40	0
33	NA	0	8360	1/1	0.93	0.21	41,41,41,41	0
33	NA	0	8361	1/1	0.93	0.23	38,38,38,38	0
33	NA	0	8302	1/1	0.93	0.24	44,44,44,44	0
31	MG	0	8085	1/1	0.93	0.07	35,35,35,35	0
33	NA	A	8345	1/1	0.93	0.09	46,46,46,46	0
31	MG	0	8099	1/1	0.93	0.24	44,44,44,44	0
31	MG	0	8014	1/1	0.93	0.09	25,25,25,25	0
33	NA	0	8350	1/1	0.93	0.35	36,36,36,36	0
33	NA	R	8312	1/1	0.93	0.09	26,26,26,26	0
34	CL	I	8521	1/1	0.93	0.17	47,47,47,47	0
31	MG	0	8093	1/1	0.94	0.12	35,35,35,35	0
31	MG	0	8051	1/1	0.94	0.09	56,56,56,56	0
33	NA	0	8362	1/1	0.94	0.34	51,51,51,51	0
31	MG	0	8016	1/1	0.94	0.09	32,32,32,32	0
33	NA	0	8368	1/1	0.94	0.14	48,48,48,48	0
33	NA	0	8310	1/1	0.94	0.11	27,27,27,27	0
31	MG	0	8064	1/1	0.94	0.14	26,26,26,26	0
33	NA	0	8313	1/1	0.94	0.09	48,48,48,48	0
31	MG	0	8080	1/1	0.94	0.07	41,41,41,41	0
31	MG	0	8082	1/1	0.94	0.17	56,56,56,56	0
33	NA	0	8321	1/1	0.94	0.25	40,40,40,40	0
33	NA	0	8377	1/1	0.94	0.23	50,50,50,50	0
33	NA	0	8382	1/1	0.94	0.10	64,64,64,64	0
33	NA	0	8325	1/1	0.94	0.23	47,47,47,47	0
31	MG	0	8104	1/1	0.94	0.13	45,45,45,45	0
31	MG	0	8006	1/1	0.94	0.07	27,27,27,27	0
33	NA	0	8333	1/1	0.94	0.09	23,23,23,23	0
31	MG	0	8068	1/1	0.94	0.04	44,44,44,44	0
33	NA	0	8341	1/1	0.94	0.11	37,37,37,37	0
31	MG	0	8046	1/1	0.94	0.05	38,38,38,38	0
31	MG	0	8071	1/1	0.94	0.04	62,62,62,62	0
33	NA	0	8357	1/1	0.94	0.08	39,39,39,39	0
31	MG	J	8069	1/1	0.94	0.12	46,46,46,46	0
31	MG	0	8066	1/1	0.95	0.49	85,85,85,85	0
33	NA	0	8315	1/1	0.95	0.17	30,30,30,30	0
31	MG	0	8012	1/1	0.95	0.14	32,32,32,32	0
32	K	0	8201	1/1	0.95	0.14	62,62,62,62	0
33	NA	0	8324	1/1	0.95	0.13	48,48,48,48	0
31	MG	0	8045	1/1	0.95	0.07	51,51,51,51	0
33	NA	0	8326	1/1	0.95	0.21	37,37,37,37	0
31	MG	0	8106	1/1	0.95	0.13	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
33	NA	0	8365	1/1	0.95	0.18	28,28,28,28	0
31	MG	0	8098	1/1	0.95	0.07	27,27,27,27	0
31	MG	0	8115	1/1	0.95	0.07	36,36,36,36	0
33	NA	P	8348	1/1	0.95	0.07	32,32,32,32	0
33	NA	0	8334	1/1	0.95	0.09	33,33,33,33	0
31	MG	0	8013	1/1	0.95	0.15	22,22,22,22	0
31	MG	0	8079	1/1	0.95	0.16	19,19,19,19	0
33	NA	0	8317	1/1	0.96	0.10	27,27,27,27	0
31	MG	0	8002	1/1	0.96	0.08	26,26,26,26	0
33	NA	0	8342	1/1	0.96	0.22	33,33,33,33	0
33	NA	0	8349	1/1	0.96	0.18	37,37,37,37	0
33	NA	0	8374	1/1	0.96	0.20	44,44,44,44	0
33	NA	0	8319	1/1	0.96	0.13	29,29,29,29	0
33	NA	0	8355	1/1	0.96	0.38	47,47,47,47	0
31	MG	0	8097	1/1	0.96	0.07	30,30,30,30	0
31	MG	0	8107	1/1	0.96	0.03	30,30,30,30	0
31	MG	0	8028	1/1	0.96	0.06	25,25,25,25	0
33	NA	0	8359	1/1	0.96	0.26	39,39,39,39	0
31	MG	0	8059	1/1	0.96	0.07	25,25,25,25	0
31	MG	0	8100	1/1	0.96	0.06	64,64,64,64	0
31	MG	0	8081	1/1	0.96	0.11	39,39,39,39	0
31	MG	0	8091	1/1	0.96	0.10	41,41,41,41	0
31	MG	0	8032	1/1	0.96	0.07	23,23,23,23	0
33	NA	Q	8337	1/1	0.96	0.07	33,33,33,33	0
33	NA	0	8366	1/1	0.96	0.26	54,54,54,54	0
33	NA	0	8335	1/1	0.96	0.18	31,31,31,31	0
34	CL	I	8502	1/1	0.96	0.11	53,53,53,53	0
33	NA	0	8336	1/1	0.96	0.06	37,37,37,37	0
34	CL	X	8520	1/1	0.96	0.13	38,38,38,38	0
31	MG	0	8020	1/1	0.97	0.09	24,24,24,24	0
33	NA	0	8316	1/1	0.97	0.22	35,35,35,35	0
31	MG	0	8074	1/1	0.97	0.06	36,36,36,36	0
33	NA	0	8364	1/1	0.97	0.25	38,38,38,38	0
31	MG	0	8010	1/1	0.97	0.17	24,24,24,24	0
31	MG	0	8023	1/1	0.97	0.14	30,30,30,30	0
33	NA	0	8367	1/1	0.97	0.26	45,45,45,45	0
31	MG	0	8026	1/1	0.97	0.15	26,26,26,26	0
31	MG	0	8011	1/1	0.97	0.10	23,23,23,23	0
31	MG	0	8108	1/1	0.97	0.07	62,62,62,62	0
31	MG	0	8031	1/1	0.97	0.12	24,24,24,24	0
31	MG	0	8114	1/1	0.97	0.09	35,35,35,35	0
31	MG	0	8009	1/1	0.97	0.14	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
33	NA	0	8330	1/1	0.97	0.07	39,39,39,39	0
33	NA	0	8332	1/1	0.97	0.12	33,33,33,33	0
31	MG	0	8058	1/1	0.97	0.06	27,27,27,27	0
33	NA	0	8378	1/1	0.97	0.17	39,39,39,39	0
33	NA	0	8379	1/1	0.97	0.45	48,48,48,48	0
31	MG	0	8033	1/1	0.97	0.09	20,20,20,20	0
31	MG	A	8065	1/1	0.97	0.07	24,24,24,24	0
31	MG	A	8105	1/1	0.97	0.16	27,27,27,27	0
31	MG	0	8061	1/1	0.97	0.13	32,32,32,32	0
31	MG	0	8018	1/1	0.97	0.06	27,27,27,27	0
31	MG	0	8063	1/1	0.97	0.12	62,62,62,62	0
33	NA	0	8344	1/1	0.97	0.11	24,24,24,24	0
33	NA	0	8301	1/1	0.97	0.09	33,33,33,33	0
33	NA	K	8380	1/1	0.97	0.26	42,42,42,42	0
33	NA	L	8347	1/1	0.97	0.14	18,18,18,18	0
31	MG	0	8036	1/1	0.97	0.08	35,35,35,35	0
31	MG	0	8037	1/1	0.97	0.07	35,35,35,35	0
31	MG	0	8096	1/1	0.97	0.10	37,37,37,37	0
31	MG	0	8039	1/1	0.97	0.07	32,32,32,32	0
33	NA	S	8343	1/1	0.97	0.06	29,29,29,29	0
34	CL	0	8517	1/1	0.97	0.09	50,50,50,50	0
34	CL	0	8522	1/1	0.97	0.15	44,44,44,44	0
31	MG	0	8040	1/1	0.97	0.12	38,38,38,38	0
31	MG	0	8041	1/1	0.97	0.10	33,33,33,33	0
34	CL	N	8508	1/1	0.97	0.07	52,52,52,52	0
34	CL	Q	8506	1/1	0.97	0.12	40,40,40,40	0
31	MG	0	8042	1/1	0.97	0.10	29,29,29,29	0
31	MG	0	8054	1/1	0.98	0.16	18,18,18,18	0
33	NA	0	8331	1/1	0.98	0.27	39,39,39,39	0
31	MG	S	8073	1/1	0.98	0.06	39,39,39,39	0
31	MG	X	8109	1/1	0.98	0.08	25,25,25,25	0
31	MG	2	8078	1/1	0.98	0.10	39,39,39,39	0
31	MG	0	8075	1/1	0.98	0.06	28,28,28,28	0
31	MG	0	8056	1/1	0.98	0.04	31,31,31,31	0
33	NA	0	8339	1/1	0.98	0.19	20,20,20,20	0
31	MG	0	8057	1/1	0.98	0.12	35,35,35,35	0
33	NA	0	8381	1/1	0.98	0.12	41,41,41,41	0
33	NA	0	8303	1/1	0.98	0.17	32,32,32,32	0
33	NA	0	8305	1/1	0.98	0.22	32,32,32,32	0
33	NA	0	8306	1/1	0.98	0.13	28,28,28,28	0
31	MG	0	8003	1/1	0.98	0.11	21,21,21,21	0
31	MG	0	8025	1/1	0.98	0.10	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
33	NA	0	8352	1/1	0.98	0.12	40,40,40,40	0
33	NA	0	8354	1/1	0.98	0.16	25,25,25,25	0
31	MG	0	8001	1/1	0.98	0.11	25,25,25,25	0
33	NA	I	8346	1/1	0.98	0.09	34,34,34,34	0
31	MG	0	8044	1/1	0.98	0.09	32,32,32,32	0
31	MG	0	8083	1/1	0.98	0.07	30,30,30,30	0
31	MG	0	8084	1/1	0.98	0.07	39,39,39,39	0
31	MG	0	8035	1/1	0.98	0.07	36,36,36,36	0
31	MG	0	8112	1/1	0.98	0.10	23,23,23,23	0
31	MG	0	8027	1/1	0.98	0.06	37,37,37,37	0
31	MG	0	8007	1/1	0.98	0.17	21,21,21,21	0
34	CL	0	8503	1/1	0.98	0.17	40,40,40,40	0
34	CL	0	8505	1/1	0.98	0.11	41,41,41,41	0
34	CL	0	8511	1/1	0.98	0.10	37,37,37,37	0
34	CL	0	8514	1/1	0.98	0.20	36,36,36,36	0
31	MG	0	8048	1/1	0.98	0.08	39,39,39,39	0
31	MG	0	8116	1/1	0.98	0.10	42,42,42,42	0
34	CL	A	8509	1/1	0.98	0.12	50,50,50,50	0
34	CL	I	8501	1/1	0.98	0.09	44,44,44,44	0
31	MG	0	8038	1/1	0.98	0.13	22,22,22,22	0
31	MG	0	8092	1/1	0.98	0.10	66,66,66,66	0
34	CL	K	8510	1/1	0.98	0.08	36,36,36,36	0
34	CL	L	8518	1/1	0.98	0.15	32,32,32,32	0
31	MG	0	8029	1/1	0.98	0.09	35,35,35,35	0
31	MG	0	8015	1/1	0.98	0.18	26,26,26,26	0
31	MG	0	8052	1/1	0.98	0.06	45,45,45,45	0
34	CL	2	8504	1/1	0.98	0.06	45,45,45,45	0
35	CD	N	8405	1/1	0.98	0.08	71,71,71,71	0
33	NA	0	8328	1/1	0.99	0.12	28,28,28,28	0
31	MG	0	8030	1/1	0.99	0.07	22,22,22,22	0
33	NA	0	8375	1/1	0.99	0.21	39,39,39,39	0
31	MG	0	8024	1/1	0.99	0.15	22,22,22,22	0
31	MG	0	8110	1/1	0.99	0.10	24,24,24,24	0
31	MG	0	8111	1/1	0.99	0.11	32,32,32,32	0
31	MG	0	8053	1/1	0.99	0.07	28,28,28,28	0
34	CL	0	8512	1/1	0.99	0.11	34,34,34,34	0
34	CL	0	8513	1/1	0.99	0.10	44,44,44,44	0
31	MG	0	8086	1/1	0.99	0.09	33,33,33,33	0
34	CL	0	8515	1/1	0.99	0.11	48,48,48,48	0
34	CL	0	8516	1/1	0.99	0.14	42,42,42,42	0
32	K	0	8202	1/1	0.99	0.08	37,37,37,37	0
31	MG	0	8019	1/1	0.99	0.05	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
33	NA	0	8338	1/1	0.99	0.06	36,36,36,36	0
34	CL	B	8519	1/1	0.99	0.14	33,33,33,33	0
31	MG	0	8088	1/1	0.99	0.09	20,20,20,20	0
33	NA	0	8320	1/1	0.99	0.30	38,38,38,38	0
31	MG	0	8004	1/1	0.99	0.13	21,21,21,21	0
33	NA	0	8323	1/1	0.99	0.13	31,31,31,31	0
33	NA	H	8309	1/1	0.99	0.10	28,28,28,28	0
34	CL	M	8507	1/1	0.99	0.08	45,45,45,45	0
31	MG	0	8021	1/1	0.99	0.09	24,24,24,24	0
31	MG	0	8005	1/1	0.99	0.12	24,24,24,24	0
31	MG	0	8008	1/1	0.99	0.10	22,22,22,22	0
31	MG	0	8060	1/1	0.99	0.21	31,31,31,31	0
33	NA	0	8353	1/1	0.99	0.14	18,18,18,18	0
35	CD	T	8401	1/1	0.99	0.10	49,49,49,49	0
35	CD	Y	8403	1/1	0.99	0.14	49,49,49,49	0
35	CD	Z	8402	1/1	0.99	0.04	37,37,37,37	0
35	CD	2	8404	1/1	0.99	0.09	47,47,47,47	0
31	MG	0	8017	1/1	1.00	0.13	12,12,12,12	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.