



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:56 PM UTC

PDB ID : 1YJW / pdb_00001yjl
Title : Crystal Structure Of Quinupristin Bound To The G2099A Mutant 50S Ribosomal Subunit Of Haloarcula Marismortui
Authors : Tu, D.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2005-01-15
Resolution : 2.90 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

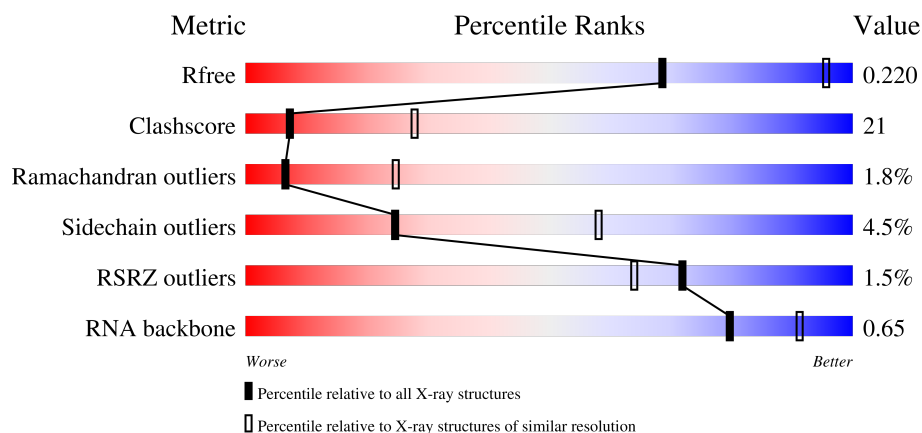
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)
RNA backbone	3983	1120 (3.10-2.70)

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 ≥ 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	53% 36% 5% • 6%
2	1	57	60% 39% •
3	2	50	4% 42% 50% 8%
4	3	92	55% 42% •

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Mol	Chain	Length	Quality of chain
5	4	8	
6	9	122	
7	A	240	
8	B	338	
9	C	246	
10	D	177	
11	E	178	
12	F	120	
13	G	348	
14	H	177	
15	I	162	
16	J	145	
17	K	132	
18	L	165	
19	M	195	
20	N	187	
21	O	116	
22	P	149	
23	Q	96	
24	R	155	
25	S	85	
26	T	120	
27	U	66	
28	V	71	
29	W	154	

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Mol	Chain	Length	Quality of chain
30	X	92	
31	Y	241	
32	Z	83	

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
36	CL	O	3189	-	-	X	-
36	CL	N	201	-	-	X	-

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99111 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 RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59020	26349	10873	19053	2745			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	2099	A	G	conflict	GB 55229667

- Molecule 2 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 3 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 4 is a protein called 50S ribosomal protein L44e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 5 is a protein called QUINUPRISTIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4	8	Total	C	N	O	S	0	0	0
			73	53	9	10	1			

- Molecule 6 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	LEU	GLN	conflict	UNP P12735

- Molecule 10 is a protein called 50S ribosomal protein L5.

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

- Molecule 11 is a protein called 50S ribosomal protein L6.

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

- Molecule 12 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 13 is a protein called 50S ribosomal protein L10.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	248	ASP	ALA	conflict	UNP P15825

- Molecule 14 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 15 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	conflict	UNP P22450

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	L	145	Total	C	N	O	0	0	0
			1118	670	222	226			

- Molecule 19 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	M	194	Total	C	N	O	S	0	0	0
			1558	942	332	283	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	conflict	UNP P60618

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 21 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	O	115	Total	C	N	O	0	0	0
			865	529	161	175			

- Molecule 22 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

- Molecule 23 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	Q	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 24 is a protein called 50S ribosomal protein L22.

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

- Molecule 25 is a protein called 50S ribosomal protein L23.

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

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	T	119	Total	C	N	O	S	0	0	0
			950	568	180	202				

- Molecule 27 is a protein called 50S ribosomal protein L24e.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 30 is a protein called 50S ribosomal protein L31e.

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

- Molecule 31 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
31	Y	142	Total	C	N	O	0	0	0
			1130	686	228	216			

- Molecule 32 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	-	expression tag	UNP P60619

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	109	Total	Mg	0	0
			109	109		
33	3	1	Total	Mg	0	0
			1	1		
33	4	1	Total	Mg	0	0
			1	1		
33	9	1	Total	Mg	0	0
			1	1		
33	A	1	Total	Mg	0	0
			1	1		
33	B	1	Total	Mg	0	0
			1	1		
33	K	1	Total	Mg	0	0
			1	1		
33	T	1	Total	Mg	0	0
			1	1		
33	Y	1	Total	Mg	0	0
			1	1		

- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	2	Total	K	0	0
			2	2		

- Molecule 35 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	0	74	Total Na 74 74	0	0
35	9	2	Total Na 2 2	0	0
35	A	1	Total Na 1 1	0	0
35	C	1	Total Na 1 1	0	0
35	H	1	Total Na 1 1	0	0
35	J	1	Total Na 1 1	0	0
35	L	1	Total Na 1 1	0	0
35	M	1	Total Na 1 1	0	0
35	Q	1	Total Na 1 1	0	0
35	R	2	Total Na 2 2	0	0
35	S	1	Total Na 1 1	0	0

- Molecule 36 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	0	10	Total Cl 10 10	0	0
36	3	1	Total Cl 1 1	0	0
36	A	1	Total Cl 1 1	0	0
36	B	1	Total Cl 1 1	0	0
36	J	3	Total Cl 3 3	0	0
36	L	1	Total Cl 1 1	0	0
36	M	1	Total Cl 1 1	0	0
36	N	1	Total Cl 1 1	0	0
36	O	1	Total Cl 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	R	1	Total 1	Cl 1	0	0
36	Y	1	Total 1	Cl 1	0	0

- Molecule 37 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	1	1	Total 1	Cd 1	0	0
37	3	1	Total 1	Cd 1	0	0
37	O	1	Total 1	Cd 1	0	0
37	U	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	0	5842	Total 5842	O 5842	0	0
38	1	60	Total 60	O 60	0	0
38	2	49	Total 49	O 49	0	0
38	3	69	Total 69	O 69	0	0
38	4	2	Total 2	O 2	0	0
38	9	143	Total 143	O 143	0	0
38	A	123	Total 123	O 123	0	0
38	B	146	Total 146	O 146	0	0
38	C	185	Total 185	O 185	0	0
38	D	49	Total 49	O 49	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	E	42	Total 42	O 42	0	0
38	F	26	Total 26	O 26	0	0
38	G	20	Total 20	O 20	0	0
38	H	69	Total 69	O 69	0	0
38	I	9	Total 9	O 9	0	0
38	J	55	Total 55	O 55	0	0
38	K	59	Total 59	O 59	0	0
38	L	82	Total 82	O 82	0	0
38	M	129	Total 129	O 129	0	0
38	N	60	Total 60	O 60	0	0
38	O	42	Total 42	O 42	0	0
38	P	72	Total 72	O 72	0	0
38	Q	48	Total 48	O 48	0	0
38	R	85	Total 85	O 85	0	0
38	S	30	Total 30	O 30	0	0
38	T	39	Total 39	O 39	0	0
38	U	29	Total 29	O 29	0	0
38	V	13	Total 13	O 13	0	0
38	W	69	Total 69	O 69	0	0
38	X	26	Total 26	O 26	0	0
38	Y	101	Total 101	O 101	0	0

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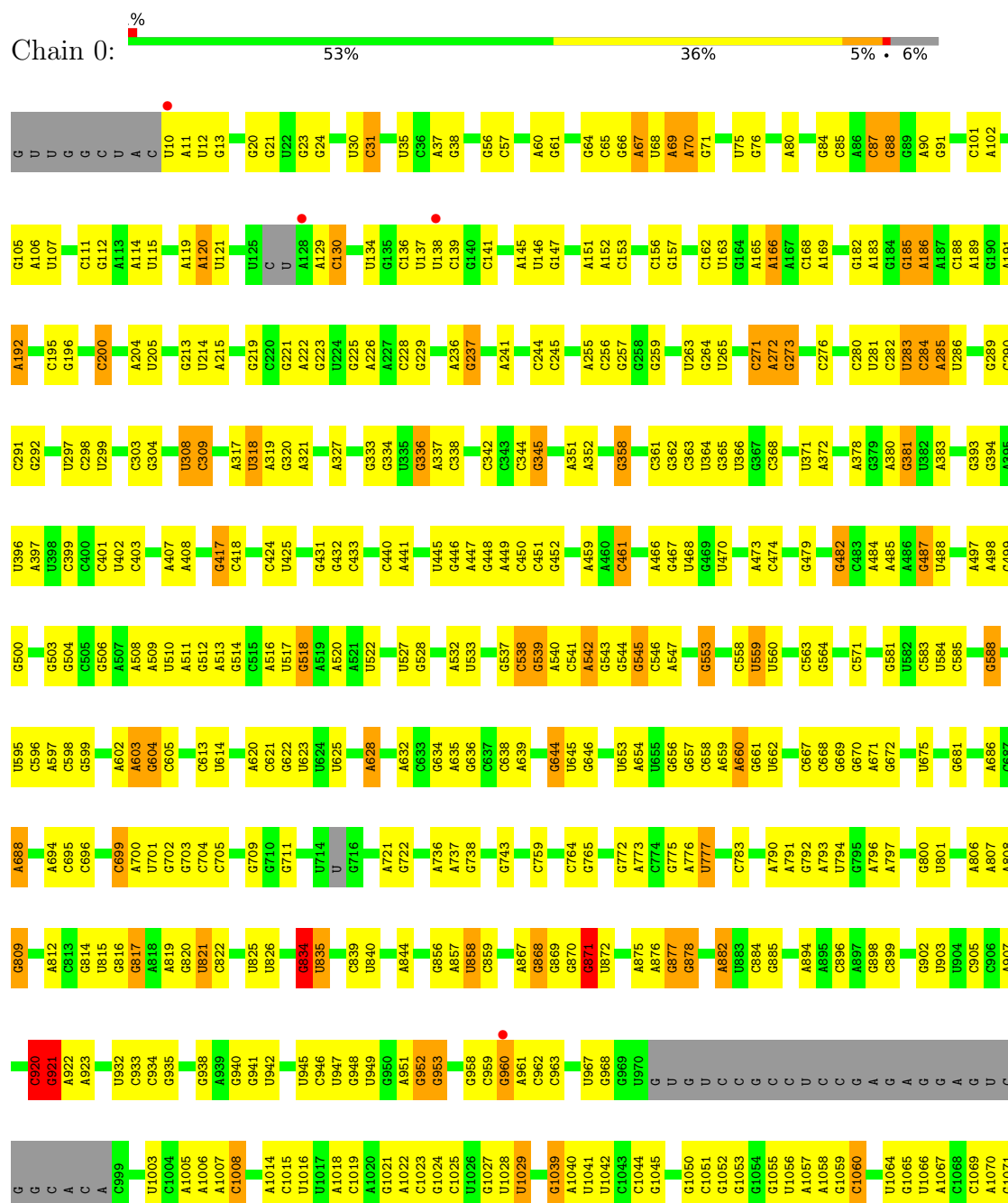
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	Z	37	Total	O	0	0
			37	37		

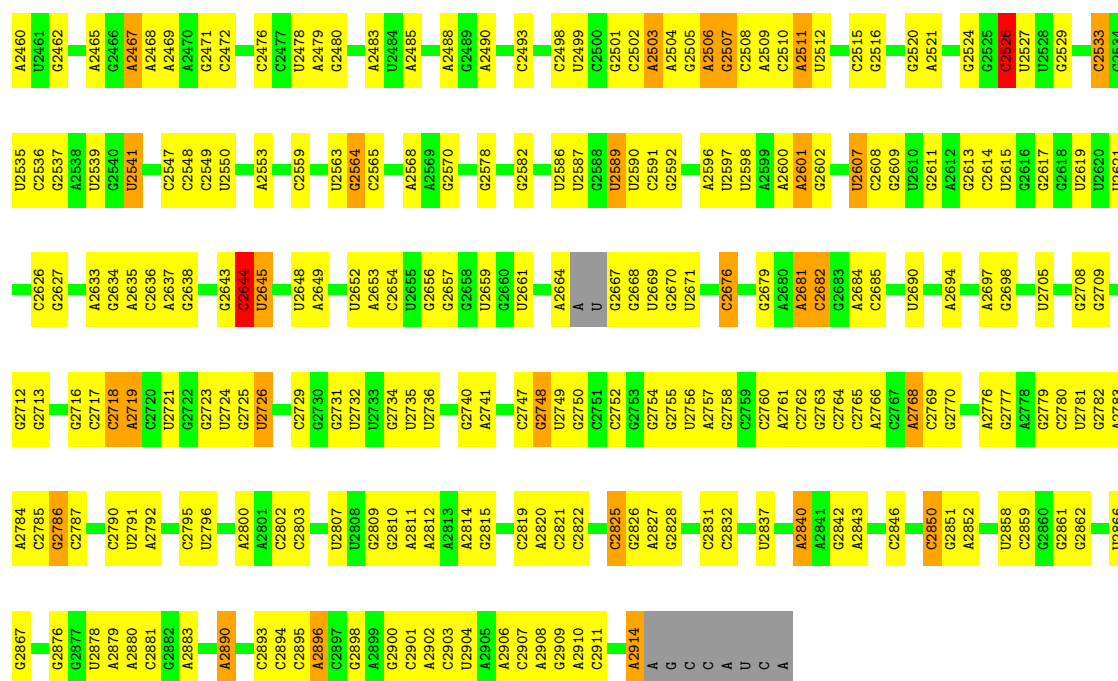
3 Residue-property plots

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 RIBOSOMAL RNA

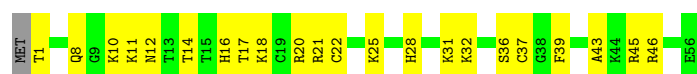


G2365	G2272	C	G	U2034	C1940	G1824	C1734	U1635	C1534	G1438	A1352	C1243	G1171	G1072
A2369	C2273	C	G	C2035	C1940	U1825	C1735	G1636	G1535	C1439	A1352	U1244	G1172	A1073
A2370	A2274	A	U	C2036	A1941	C1826	A1736	C1637	C1536	U1440	C1353	C1245	A1173	G1074
A2371	G2275	G	C	C2037	A1942	C	C	U1638	C1537	U1441	A1354	A1246	G1174	A1081
A2372	U2276	A	C	A2038	C1943	A1829	U1741	A1641	G1543	U1446	A1355	C1250	G1175	A1086
U2373	U2277	C	C	A2039	C1946	C1830	A1742	A1642	U1544	U1446	A1358	C1251	G1176	G1087
U2377	C2281	A	G	C2040	G1947	C1834	G1743	C1643	C1545	U1446	U1359	G1260	G1177	A1088
U2378	U2282	C	G	G2044	G1948	U1835	G1744	C1643	C1545	C1460	C1360	A1261	G1178	G1087
G2379	A	A	U	A	G1949	U1838	U1748	A1653	U1559	C1461	G1363	A1261	G1179	A1088
A2380	A2291	G	U	G2050	G1950	U1839	U1749	A1654	U	C1462	G1363	A1261	G1179	A1088
A2382	G2293	U	U	G2053	G1951	A1839	G1750	G1655	C1556	U1461	U1266	A1266	A1097	A1097
G2383	A	G	C	A2054	C	A1840	G1751	A1656	C1557	C1462	C1366	U1267	A1181	A1098
U2384	A	A	C	A2055	A	C1841	G1752	A1657	G1558	U1470	C1268	C1268	C1182	A1099
G2385	A2301	A	G	U2064	C	A1845	A1754	A1658	C1564	A1471	G1269	A1269	C1184	C1102
G2386	A2302	U	C	C2065	U	G1849	A1755	G1660	G1572	A1471	G1273	C1273	U1109	U1109
U2387	A2303	A	A	A	U	C1853	U1761	C1665	A1571	U1472	G1277	A1277	G1110	G1110
C2388	C	C	U	G	G	C1854	C1762	A1667	A1572	C1474	C1377	G1277	U1111	U1111
C2389	A	A	G	G2072	A	C1855	C1763	U1668	C1574	C1477	G1378	U1278	G1112	G1112
C2392	C	C	G	A2074	C	C1856	U1766	G1669	A1580	U1478	U1380	U1279	A1191	U1116
A2401	G2312	C	U	A2081	C	G1862	A1767	A1670	A1580	G1479	G1386	A1287	A1192	A1117
A2402	C2313	G	G	U1964	U1964	C1863	C1768	C1674	C1584	C1483	G1387	U1288	A1193	A1118
C2411	C2315	U	G	C1965	C1965	G1863	C1769	U1677	C1585	G1484	G1391	G1290	U1120	A1119
A2412	G2316	C	G	U1966	U1966	G1868	U1770	A1678	U1587	U1488	A1392	A1291	G1121	U1121
A2413	C2317	G	G	C1967	C1967	C1872	C1772	C1679	G1589	G1490	A1393	U1293	A1122	A1122
A2414	U2320	U	C	A1969	A1969	G1873	C1773	G1682	G1596	U1500	C1394	G1295	A1123	A1123
A2415	A2321	G	U	G1970	G1970	U1874	G1773	A1682	A1597	A1493	G1398	U1295	C1129	C1129
U2419	C	C	U	G1971	G1971	C1877	A1778	A1683	U1598	A1493	G1399	U1205	U1130	U1130
G2420	U2325	U	U	A1972	A1972	G1878	A1779	A1684	C1594	A1494	C1400	U1206	G1131	G1131
G2421	C2326	G	C	G1974	G1974	U1879	A1783	A1685	G1595	A1496	U1304	A1207	A1132	A1132
U2422	C	C	A	C1975	C1975	C1882	U1784	C1692	U1596	G1497	U1306	C1209	G1137	G1137
G2423	U2329	A	G	U1977	U1977	U1884	G1785	A1701	A1597	U1500	A1406	G1210	G1138	G1138
A2424	U2330	G	G	A1978	A1978	G1884	C1786	U1702	A1598	A1500	U1408	G1211	U1139	U1139
G2425	C2241	C	U	G1979	G1979	U1884	C1787	U1702	U1599	A1501	G1409	C1212	C1140	C1140
G2426	C2243	A	U	U1980	U1980	U1903	C1789	A1710	G1600	A1502	U1413	G1213	A1150	A1150
C2431	C2248	C	C	U1986	U1986	A1904	C1790	A1711	A1603	A1504	A1414	G1214	A1151	A1151
A2433	G2251	C	C	A1987	A1987	U1905	U1791	A1712	G1604	U1505	G1415	G1216	G1154	G1154
A2434	A2252	A	G	G2000	G2000	A1909	A1797	C1714	G1614	C1513	G1417	G1217	G1155	G1155
U2435	G2253	C	G	C2001	C2001	A1910	C1799	C1715	A1615	C1514	U1418	G1226	C1156	C1156
U2441	A2254	A	C	U2003	U2003	A1919	A1804	A1717	A1616	A1515	C1420	A1328	C1157	C1157
G2442	G2255	C	C	U2004	U2004	G1925	G1805	G1718	G1617	U1516	C1421	G1331	G1158	G1158
C2443	G2257	U	U	G2005	G2005	G1926	G1806	G1719	G1618	C1517	U1422	C1332	G1159	G1159
U2444	U2265	G	G	U2008	U2008	G1927	C1810	U1722	C1620	U1518	C1423	U1333	G1160	G1160
G2445	A2266	C	C	G2009	G2009	C1928	A1811	G1723	A1624	U1524	A1427	C1334	A1161	A1161
G2446	C2267	G	G	A2011	A2011	G1929	C1812	U1724	U1625	G1525	G1430	C1335	G1162	G1162
G2453	C2268	C	C	C2013	C2013	A1930	G1819	C1725	A1626	A1527	U1434	U1340	U1164	U1164
C2454	G2269	C	C	C	C	A1931	G1820	G1730	G1627	A1528	A1434	G1340	A1236	A1236
A2455	G2270	A	A	U2032	U2032	C1935	A1821	C1731	G1633	G1529	C1435	C1343	U1237	G1165
G2456	G2271	C	C	G2033	G2033	C1936	G1823	A1733	G1634	A1533	A1437	A1348	G1167	G1167



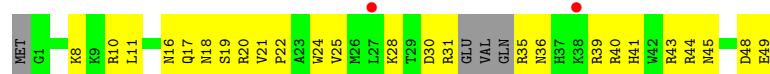
• Molecule 2: 50S ribosomal protein L37e

Chain 1: 60% 39%



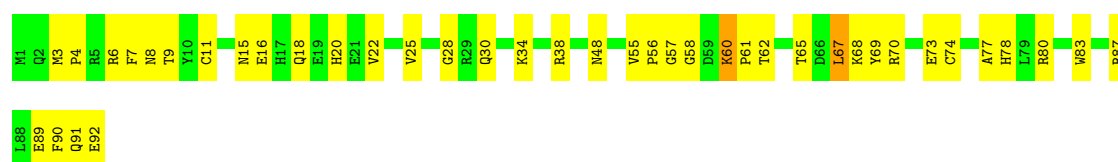
• Molecule 3: 50S ribosomal protein L39e

Chain 2: 4% 42% 50% 8%



• Molecule 4: 50S ribosomal protein L44e

Chain 3: 55% 42%

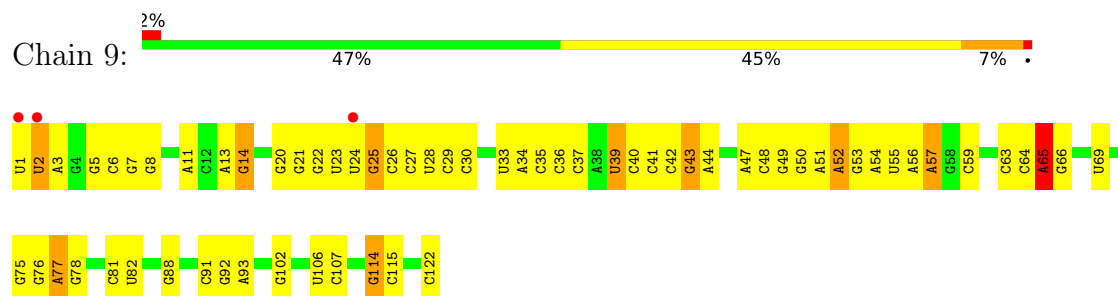


• Molecule 5: QUINUPRISTIN

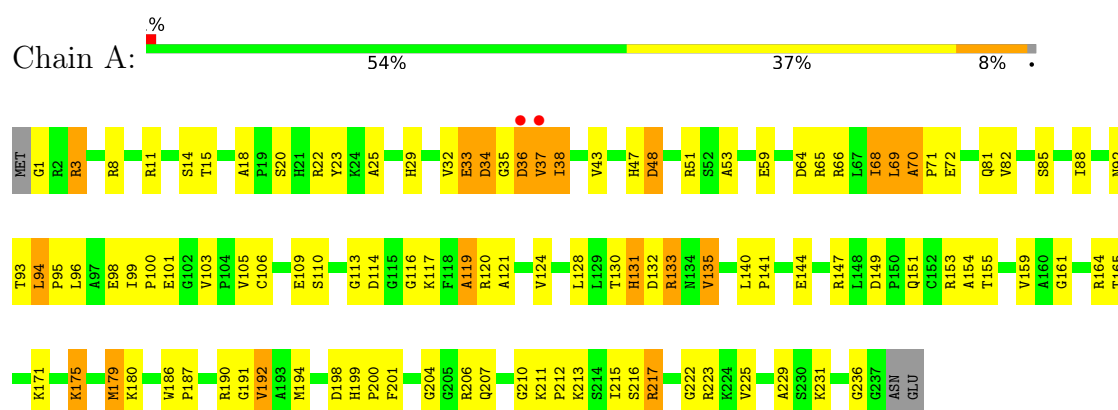
Chain 4: 38% 62%



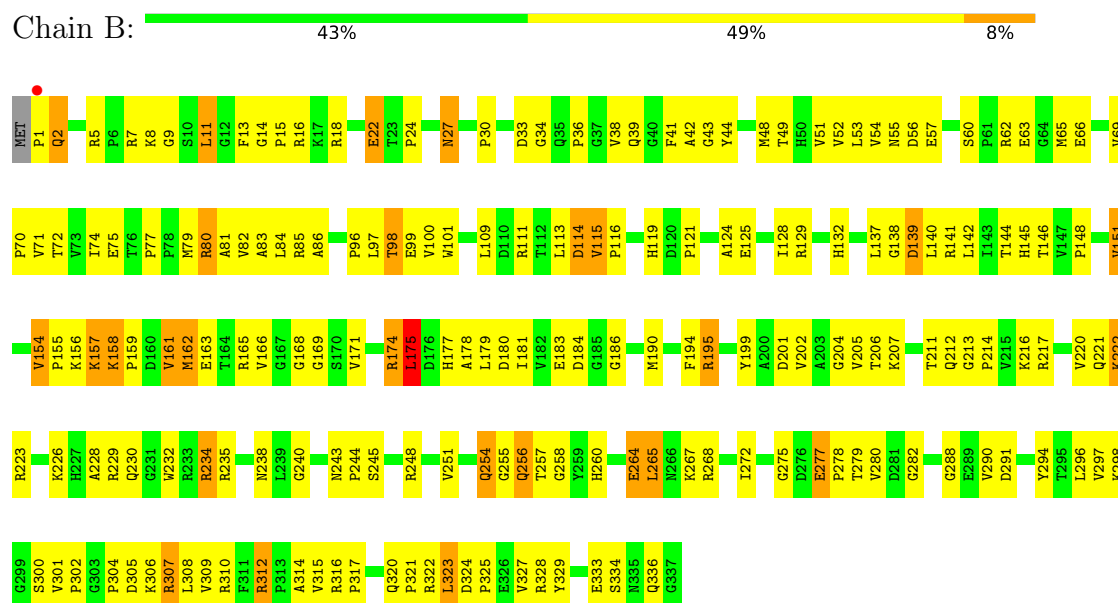
- Molecule 6: 5S RIBOSOMAL RNA



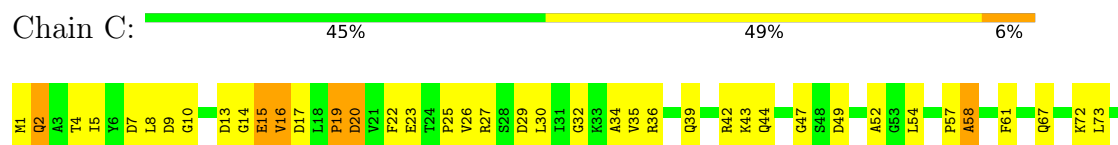
- Molecule 7: 50S ribosomal protein L2

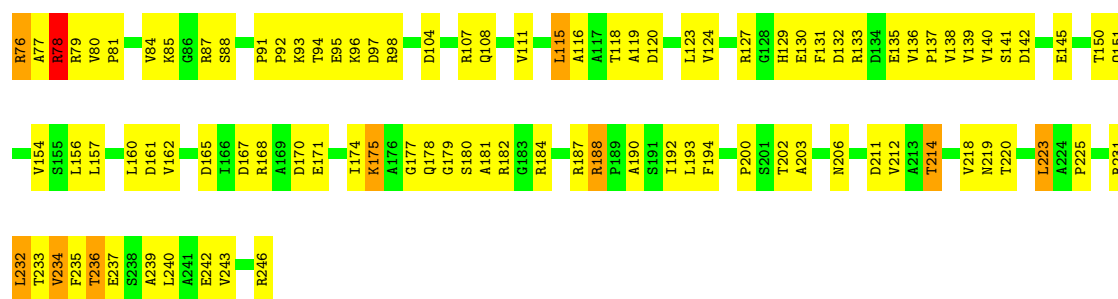


- Molecule 8: 50S ribosomal protein L3

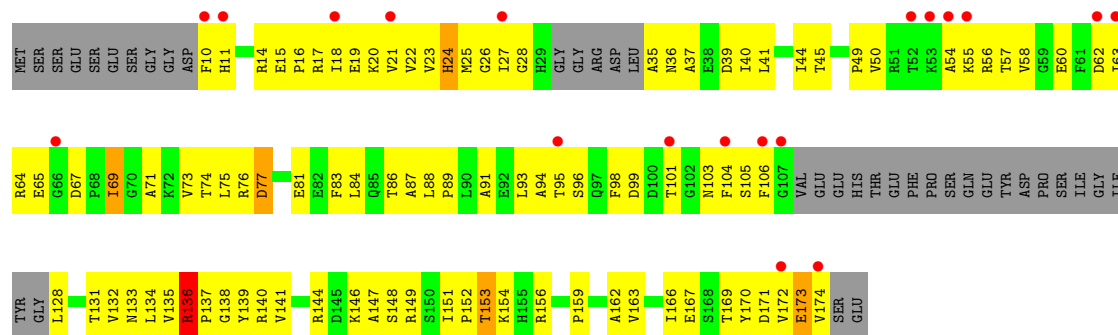


- Molecule 9: 50S ribosomal protein L4

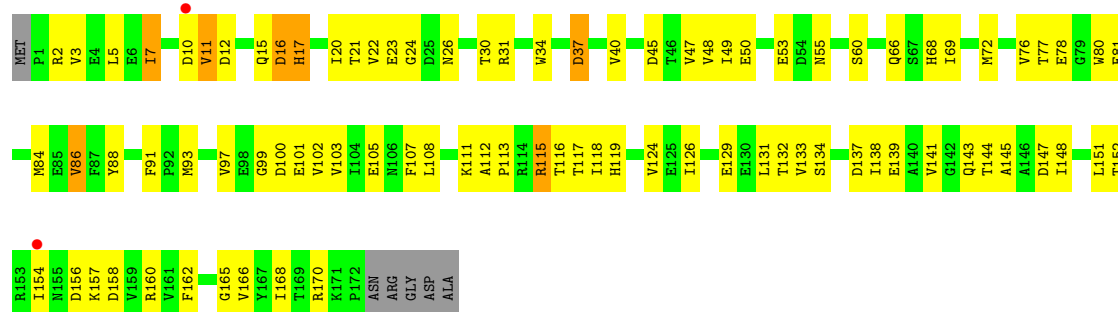




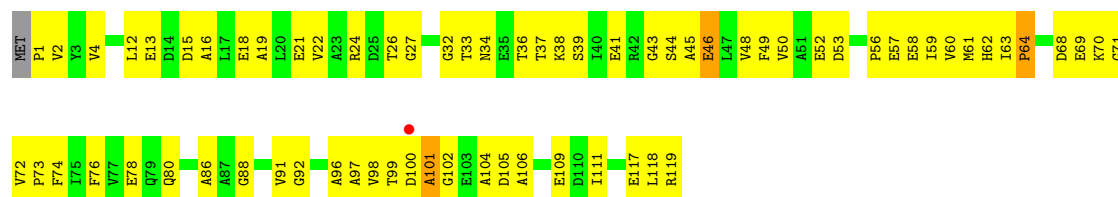
• Molecule 10: 50S ribosomal protein L5



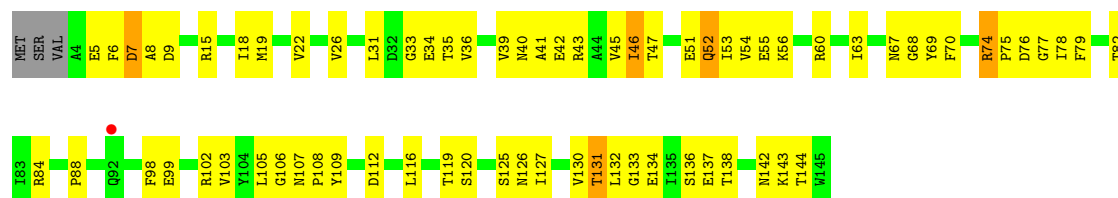
• Molecule 11: 50S ribosomal protein L6



• Molecule 12: 50S ribosomal protein L7Ae

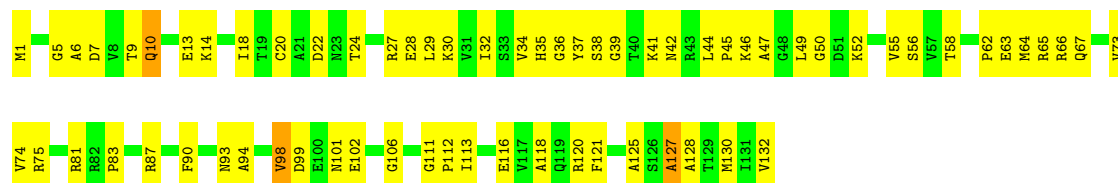


• Molecule 13: 50S ribosomal protein L10



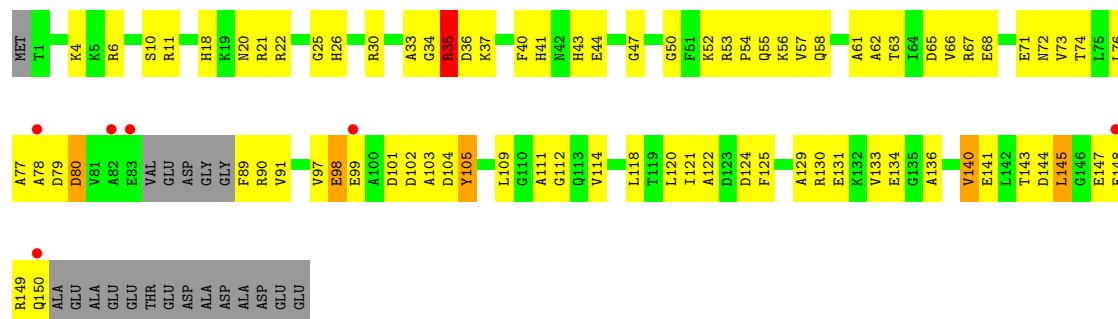
• Molecule 17: 50S ribosomal protein L14

Chain K: 49% 48%



• Molecule 18: 50S ribosomal protein L15

Chain L: 4% 39% 45% 12%



• Molecule 19: 50S ribosomal protein L15e

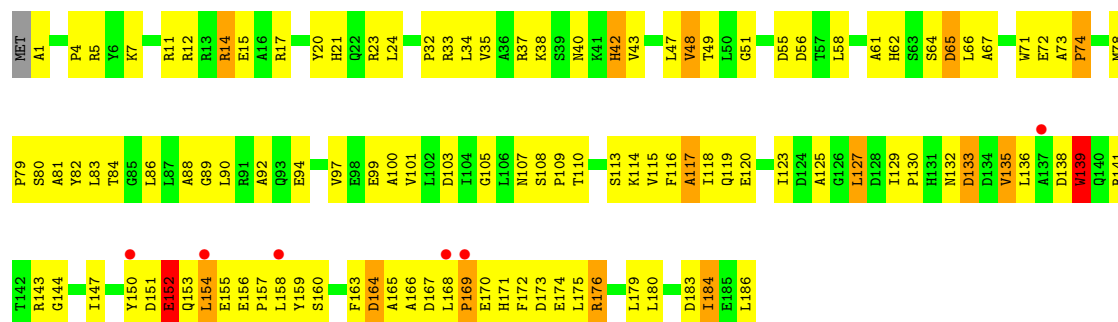
Chain M: 60% 37%



• Molecule 20: 50S ribosomal protein L18

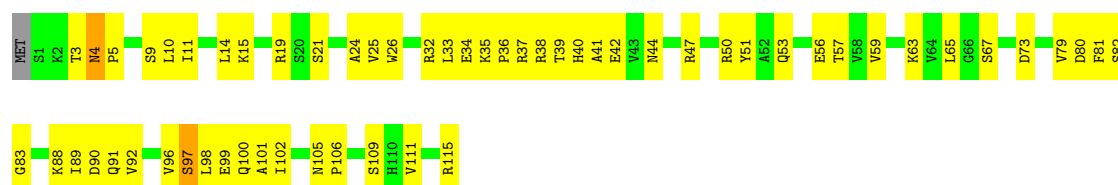
Chain N: 3% 38% 53% 7%

Chain N: 3% 38% 53% 7%



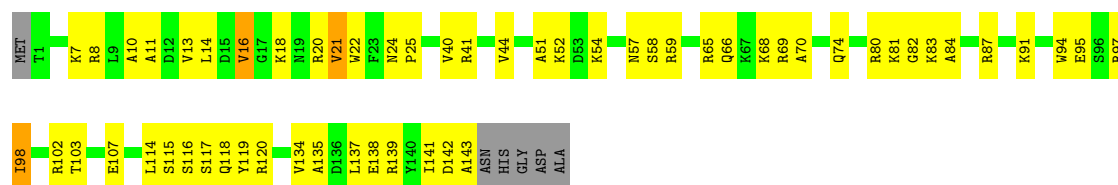
• Molecule 21: 50S ribosomal protein L18e

Chain O: 49% 48% ..



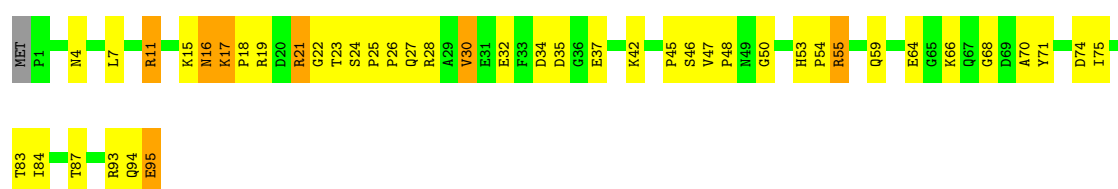
• Molecule 22: 50S ribosomal protein L19e

Chain P: 58% 36% ..



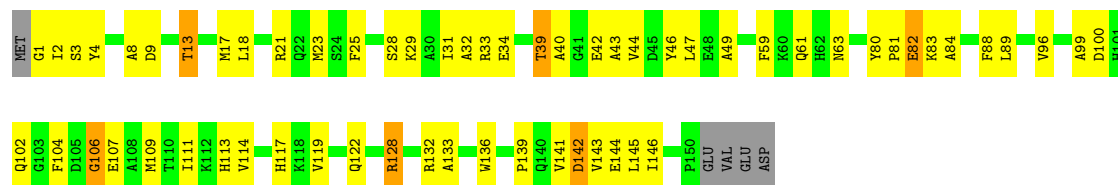
• Molecule 23: 50S ribosomal protein L21e

Chain Q: 53% 39% 7% .



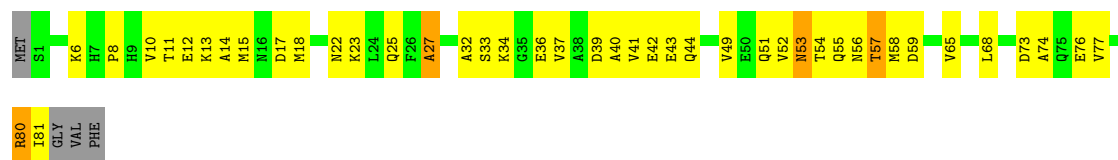
• Molecule 24: 50S ribosomal protein L22

Chain R: 57% 35% ..



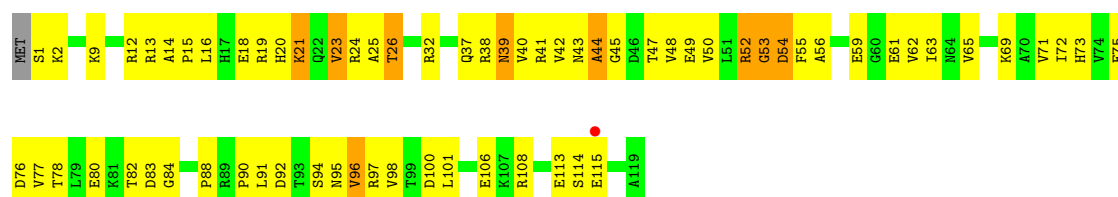
- Molecule 25: 50S ribosomal protein L23

Chain S: 



- Molecule 26: 50S ribosomal protein L24

Chain T: 



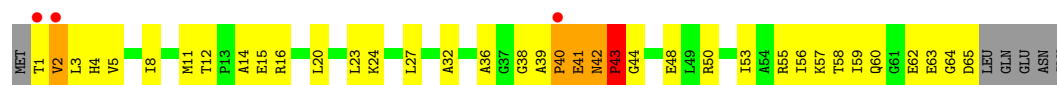
- Molecule 27: 50S ribosomal protein L24e

Chain U: 



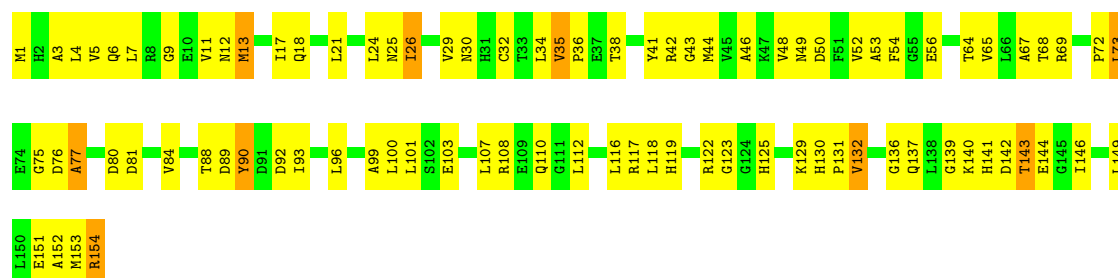
- Molecule 28: 50S ribosomal protein L29

Chain V: 

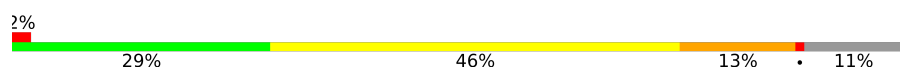


- Molecule 29: 50S ribosomal protein L30

Chain W: 



- Molecule 30: 50S ribosomal protein L31e

Chain X: 

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.69Å 299.78Å 573.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 2.90 29.98 – 2.90	Depositor EDS
% Data completeness (in resolution range)	83.8 (29.98-2.90) 83.7 (29.98-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.91Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.171 , 0.223 0.171 , 0.220	Depositor DCC
R_{free} test set	3279 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 68.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99111	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 2.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MHW, K, DBB, 1MA, MG, MHU, CL, OMU, CD, 004, UR3, PSU, NA, MHV, OMG, MHT

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	0/65957	0.60	22/102867 (0.0%)
2	1	0.44	0/438	0.93	1/578 (0.2%)
3	2	0.41	0/401	0.82	1/529 (0.2%)
4	3	0.42	0/771	0.86	2/1024 (0.2%)
5	4	1.72	0/13	1.80	0/15
6	9	0.37	0/2904	0.60	2/4526 (0.0%)
7	A	0.43	0/1786	1.02	11/2408 (0.5%)
8	B	0.42	0/2690	1.03	20/3652 (0.5%)
9	C	0.47	0/1884	1.01	9/2551 (0.4%)
10	D	0.37	0/1111	0.89	3/1498 (0.2%)
11	E	0.41	0/1382	0.89	2/1880 (0.1%)
12	F	0.40	0/901	0.89	2/1224 (0.2%)
13	G	0.37	0/241	0.80	0/324
14	H	0.41	0/1302	0.96	5/1743 (0.3%)
15	I	0.38	0/526	0.96	2/716 (0.3%)
16	J	0.43	0/1136	0.94	3/1530 (0.2%)
17	K	0.43	0/1001	1.00	3/1347 (0.2%)
18	L	0.39	0/1130	0.94	3/1509 (0.2%)
19	M	0.42	0/1582	0.89	2/2117 (0.1%)
20	N	0.39	0/1474	1.07	12/1999 (0.6%)
21	O	0.43	0/874	0.94	3/1181 (0.3%)
22	P	0.42	0/1147	0.88	1/1528 (0.1%)
23	Q	0.45	0/749	1.01	5/1005 (0.5%)
24	R	0.46	0/1172	0.96	5/1578 (0.3%)
25	S	0.41	0/648	0.87	2/875 (0.2%)
26	T	0.41	0/958	0.94	3/1289 (0.2%)
27	U	0.40	0/417	0.97	3/562 (0.5%)
28	V	0.38	0/502	0.99	2/675 (0.3%)
29	W	0.50	0/1219	0.99	5/1655 (0.3%)
30	X	0.43	0/664	0.99	2/895 (0.2%)
31	Y	0.44	0/1146	0.94	3/1536 (0.2%)
32	Z	0.41	0/589	0.97	1/787 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.39	0/98715	0.72	140/147603 (0.1%)

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	0	20
6	9	0	1
29	W	0	1
All	All	0	22

There are no bond length outliers.

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	N	135	VAL	N-CA-C	-10.39	103.02	113.10
7	A	222	GLY	N-CA-C	-8.49	104.38	114.48
26	T	54	ASP	N-CA-C	-8.11	102.83	112.89
8	B	213	GLY	CA-C-N	8.09	127.38	118.97
8	B	213	GLY	C-N-CA	8.09	127.38	118.97

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	792	G	Sidechain
1	0	817	G	Sidechain
1	0	867	A	Sidechain

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	0	59020	0	29811	1132	0
2	1	431	0	426	29	0
3	2	396	0	413	33	0
4	3	755	0	728	39	0
5	4	73	0	64	1	0
6	9	2599	0	1325	72	0
7	A	1753	0	1766	124	0
8	B	2625	0	2533	208	0
9	C	1859	0	1816	147	0
10	D	1094	0	1085	116	0
11	E	1357	0	1266	87	0
12	F	890	0	843	63	0
13	G	240	0	231	19	0
14	H	1282	0	1292	96	0
15	I	519	0	500	65	0
16	J	1120	0	1098	78	0
17	K	992	0	1031	79	0
18	L	1118	0	1076	92	0
19	M	1558	0	1566	86	0
20	N	1445	0	1401	150	0
21	O	865	0	873	54	0
22	P	1136	0	1123	59	0
23	Q	735	0	729	45	0
24	R	1149	0	1122	67	0
25	S	641	0	605	40	0
26	T	950	0	923	73	0
27	U	410	0	364	36	0
28	V	499	0	511	45	0
29	W	1196	0	1137	120	0
30	X	654	0	653	63	0
31	Y	1130	0	1133	73	0
32	Z	578	0	539	29	0
33	0	109	0	0	0	0
33	3	1	0	0	0	0
33	4	1	0	0	0	0
33	9	1	0	0	0	0
33	A	1	0	0	0	0
33	B	1	0	0	0	0
33	K	1	0	0	0	0
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	2	0	0	0	0
35	0	74	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	9	2	0	0	0	0
35	A	1	0	0	0	0
35	C	1	0	0	0	0
35	H	1	0	0	0	0
35	J	1	0	0	0	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0
36	0	10	0	0	2	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	2	0
36	L	1	0	0	0	0
36	M	1	0	0	0	0
36	N	1	0	0	2	0
36	O	1	0	0	0	0
36	R	1	0	0	0	0
36	Y	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5842	0	0	196	0
38	1	60	0	0	8	0
38	2	49	0	0	6	0
38	3	69	0	0	12	0
38	4	2	0	0	0	0
38	9	143	0	0	9	0
38	A	123	0	0	20	0
38	B	146	0	0	19	0
38	C	185	0	0	37	0
38	D	49	0	0	22	0
38	E	42	0	0	12	0
38	F	26	0	0	5	0
38	G	20	0	0	2	0
38	H	69	0	0	16	0
38	I	9	0	0	4	0
38	J	55	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	K	59	0	0	10	0
38	L	82	0	0	22	0
38	M	129	0	0	12	0
38	N	60	0	0	11	0
38	O	42	0	0	7	0
38	P	72	0	0	5	0
38	Q	48	0	0	6	0
38	R	85	0	0	7	0
38	S	30	0	0	5	0
38	T	39	0	0	9	0
38	U	29	0	0	3	0
38	V	13	0	0	3	0
38	W	69	0	0	12	0
38	X	26	0	0	6	0
38	Y	101	0	0	16	0
38	Z	37	0	0	2	0
All	All	99111	0	59983	3112	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 21.

The worst 5 of 3112 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)
6:9:6:C:H5''	20:N:37:ARG:NH1	1.59	1.16
1:0:156:C:H5''	19:M:171:ARG:HD3	1.25	1.15
6:9:6:C:H5''	20:N:37:ARG:HH12	0.97	1.14
29:W:5:VAL:HG11	29:W:153:MET:HE1	1.30	1.10
1:0:1160:G:H5'	1:0:1161:A:H5'	1.26	1.07

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	
2	1	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
3	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
4	3	90/92 (98%)	82 (91%)	7 (8%)	1 (1%)	11	36
5	4	2/8 (25%)	2 (100%)	0	0	100	100
7	A	235/240 (98%)	203 (86%)	28 (12%)	4 (2%)	7	26
8	B	335/338 (99%)	294 (88%)	36 (11%)	5 (2%)	8	28
9	C	244/246 (99%)	218 (89%)	21 (9%)	5 (2%)	6	22
10	D	134/177 (76%)	92 (69%)	39 (29%)	3 (2%)	5	20
11	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	21	51
12	F	117/120 (98%)	100 (86%)	12 (10%)	5 (4%)	2	8
13	G	25/348 (7%)	23 (92%)	1 (4%)	1 (4%)	2	9
14	H	156/177 (88%)	139 (89%)	14 (9%)	3 (2%)	6	23
15	I	68/162 (42%)	50 (74%)	16 (24%)	2 (3%)	3	15
16	J	140/145 (97%)	127 (91%)	10 (7%)	3 (2%)	5	21
17	K	130/132 (98%)	120 (92%)	10 (8%)	0	100	100
18	L	141/165 (86%)	113 (80%)	24 (17%)	4 (3%)	4	15
19	M	192/195 (98%)	175 (91%)	17 (9%)	0	100	100
20	N	184/187 (98%)	154 (84%)	21 (11%)	9 (5%)	1	6
21	O	113/116 (97%)	100 (88%)	12 (11%)	1 (1%)	14	41
22	P	141/149 (95%)	127 (90%)	14 (10%)	0	100	100
23	Q	93/96 (97%)	83 (89%)	9 (10%)	1 (1%)	11	36
24	R	148/155 (96%)	133 (90%)	14 (10%)	1 (1%)	18	48
25	S	79/85 (93%)	68 (86%)	11 (14%)	0	100	100
26	T	117/120 (98%)	104 (89%)	10 (8%)	3 (3%)	4	17
27	U	51/66 (77%)	46 (90%)	5 (10%)	0	100	100
28	V	63/71 (89%)	53 (84%)	6 (10%)	4 (6%)	1	3
29	W	152/154 (99%)	138 (91%)	13 (9%)	1 (1%)	18	48
30	X	80/92 (87%)	66 (82%)	9 (11%)	5 (6%)	1	3
31	Y	140/241 (58%)	133 (95%)	7 (5%)	0	100	100
32	Z	71/83 (86%)	54 (76%)	14 (20%)	3 (4%)	2	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	3707/4445 (83%)	3245 (88%)	397 (11%)	65 (2%)	6	25

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	34	ASP
7	A	37	VAL
8	B	184	ASP
9	C	8	LEU
10	D	173	GLU

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	1	46/47 (98%)	45 (98%)	1 (2%)	45	77
3	2	42/46 (91%)	42 (100%)	0	100	100
4	3	79/79 (100%)	79 (100%)	0	100	100
5	4	2/2 (100%)	2 (100%)	0	100	100
7	A	179/182 (98%)	169 (94%)	10 (6%)	19	50
8	B	282/283 (100%)	264 (94%)	18 (6%)	16	44
9	C	193/193 (100%)	179 (93%)	14 (7%)	13	38
10	D	117/148 (79%)	112 (96%)	5 (4%)	26	60
11	E	152/156 (97%)	146 (96%)	6 (4%)	28	63
12	F	93/94 (99%)	91 (98%)	2 (2%)	45	77
13	G	27/283 (10%)	27 (100%)	0	100	100
14	H	134/145 (92%)	128 (96%)	6 (4%)	24	58
15	I	58/130 (45%)	58 (100%)	0	100	100
16	J	118/121 (98%)	111 (94%)	7 (6%)	18	48
17	K	106/106 (100%)	104 (98%)	2 (2%)	50	79
18	L	113/127 (89%)	109 (96%)	4 (4%)	32	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	M	158/159 (99%)	151 (96%)	7 (4%)	25	59
20	N	149/150 (99%)	144 (97%)	5 (3%)	32	66
21	O	93/94 (99%)	90 (97%)	3 (3%)	34	68
22	P	113/117 (97%)	108 (96%)	5 (4%)	25	59
23	Q	79/80 (99%)	73 (92%)	6 (8%)	12	36
24	R	117/122 (96%)	113 (97%)	4 (3%)	32	66
25	S	71/74 (96%)	68 (96%)	3 (4%)	26	60
26	T	105/106 (99%)	98 (93%)	7 (7%)	15	43
27	U	44/52 (85%)	44 (100%)	0	100	100
28	V	51/57 (90%)	50 (98%)	1 (2%)	48	78
29	W	130/130 (100%)	123 (95%)	7 (5%)	20	51
30	X	66/74 (89%)	58 (88%)	8 (12%)	5	16
31	Y	120/196 (61%)	115 (96%)	5 (4%)	26	60
32	Z	60/68 (88%)	57 (95%)	3 (5%)	22	53
All	All	3097/3621 (86%)	2958 (96%)	139 (4%)	24	58

5 of 139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	V	43	PRO
29	W	73	LEU
30	X	85	VAL
11	E	7	ILE
10	D	153	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
19	M	24	GLN
22	P	118	GLN
31	Y	129	ASN
19	M	58	GLN
20	N	107	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	247 (8%)	23 (0%)
6	9	121/122 (99%)	16 (13%)	1 (0%)
All	All	2866/3044 (94%)	263 (9%)	24 (0%)

5 of 263 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1856	C
1	0	2467	A
1	0	2313	C
1	0	2526	C
1	0	871	G

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

10 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	0	2621	1	18,21,22	1.52	2 (11%)	21,30,33	1.36	3 (14%)
1	1MA	0	628	35,1	21,25,26	0.75	1 (4%)	30,37,40	0.75	1 (3%)
1	UR3	0	2619	1	19,22,23	0.46	0	26,32,35	0.69	1 (3%)
5	MHU	4	5	5	14,15,16	3.04	10 (71%)	18,19,21	1.72	5 (27%)
5	DBB	4	3	5	4,5,6	1.09	0	1,5,7	0.09	0
5	MHW	4	1	33,5	9,9,10	2.77	4 (44%)	10,11,13	1.70	3 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MHV	4	6	5	7,9,10	2.07	2 (28%)	8,11,13	1.57	2 (25%)
1	OMG	0	2588	1	23,26,27	0.29	0	32,38,41	0.36	0
1	OMU	0	2587	35,1	19,22,23	0.22	0	25,31,34	0.43	0
5	004	4	7	5	9,10,11	3.17	4 (44%)	9,12,14	1.83	3 (33%)

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
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	35,1	-	2/7/25/26	0/3/3/3
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2
5	MHU	4	5	5	-	0/9/12/14	0/1/1/1
5	DBB	4	3	5	-	0/3/4/6	-
5	MHW	4	1	33,5	-	0/2/2/4	0/1/1/1
5	MHV	4	6	5	-	0/1/12/14	0/1/1/1
1	OMG	0	2588	1	-	0/9/27/28	0/3/3/3
1	OMU	0	2587	35,1	-	0/9/27/28	0/2/2/2
5	004	4	7	5	-	0/4/6/8	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	4	7	004	CB-CA	7.46	1.60	1.52
5	4	1	MHW	CA-N	5.39	1.42	1.35
1	0	2621	PSU	C2-N1	4.84	1.43	1.36
5	4	5	MHU	CA-N	4.64	1.55	1.47
5	4	6	MHV	CB-CG	4.49	1.57	1.50

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	4	7	004	CG2-CB-CA	3.97	126.81	120.64
5	4	1	MHW	CB-CA-C	3.80	122.91	120.09
5	4	5	MHU	CB-CA-N	3.75	116.00	110.48
1	0	2621	PSU	C6-C5-C4	3.36	120.44	118.17
5	4	5	MHU	O-C-CA	-3.24	116.43	124.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	628	1MA	C2'-C1'-N9-C8
1	0	628	1MA	C2'-C1'-N9-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	628	1MA	1	0
1	0	2587	OMU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	0	2749/2922 (94%)	-0.60	22 (0%) 82 77	18, 42, 85, 147	0
2	1	56/57 (98%)	-0.73	0 100 100	23, 28, 34, 41	0
3	2	46/50 (92%)	0.16	2 (4%) 40 31	24, 56, 82, 96	0
4	3	92/92 (100%)	-0.20	0 100 100	30, 48, 61, 79	0
5	4	2/8 (25%)	0.16	0 100 100	49, 49, 49, 54	0
6	9	122/122 (100%)	-0.13	3 (2%) 58 48	36, 57, 84, 148	0
7	A	237/240 (98%)	-0.18	2 (0%) 82 77	21, 44, 80, 100	0
8	B	337/338 (99%)	-0.14	1 (0%) 90 87	23, 50, 76, 86	0
9	C	246/246 (100%)	-0.30	0 100 100	19, 39, 62, 72	0
10	D	140/177 (79%)	0.99	19 (13%) 7 5	47, 94, 117, 125	0
11	E	172/178 (96%)	0.10	2 (1%) 76 69	41, 61, 83, 88	0
12	F	119/120 (99%)	0.17	1 (0%) 82 77	41, 63, 88, 104	0
13	G	29/348 (8%)	0.64	2 (6%) 23 18	71, 87, 95, 96	0
14	H	160/177 (90%)	0.08	2 (1%) 75 67	36, 52, 88, 105	0
15	I	70/162 (43%)	1.69	22 (31%) 1 1	108, 118, 136, 138	0
16	J	142/145 (97%)	-0.20	1 (0%) 84 79	34, 46, 66, 86	0
17	K	132/132 (100%)	-0.25	0 100 100	26, 46, 65, 75	0
18	L	145/165 (87%)	0.13	6 (4%) 41 33	22, 60, 100, 114	0
19	M	194/195 (99%)	-0.44	0 100 100	25, 36, 52, 59	0
20	N	186/187 (99%)	0.20	6 (3%) 50 41	34, 58, 100, 110	0
21	O	115/116 (99%)	-0.17	0 100 100	33, 47, 66, 71	0
22	P	143/149 (95%)	-0.19	0 100 100	33, 49, 61, 73	0
23	Q	95/96 (98%)	-0.36	0 100 100	28, 39, 54, 66	0
24	R	150/155 (96%)	-0.51	0 100 100	28, 40, 58, 67	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	S	81/85 (95%)	-0.21	0 100 100	37, 52, 71, 79	0
26	T	119/120 (99%)	-0.05	1 (0%) 82 77	35, 51, 80, 94	0
27	U	53/66 (80%)	-0.17	0 100 100	39, 51, 67, 78	0
28	V	65/71 (91%)	0.38	3 (4%) 37 29	46, 66, 105, 112	0
29	W	154/154 (100%)	-0.29	0 100 100	27, 42, 59, 71	0
30	X	82/92 (89%)	-0.03	2 (2%) 59 50	38, 55, 76, 96	0
31	Y	142/241 (58%)	-0.33	1 (0%) 84 79	24, 40, 62, 81	0
32	Z	73/83 (87%)	0.16	2 (2%) 56 47	39, 53, 69, 87	0
All	All	6648/7489 (88%)	-0.29	100 (1%) 72 64	18, 46, 91, 148	0

The worst 5 of 100 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
15	I	128	THR	4.8
28	V	1	THR	4.7
32	Z	82	SER	4.7
14	H	174	LEU	4.4
14	H	171	GLY	4.2

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

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, 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MHV	4	6	9/10	0.85	0.12	53,55,59,59	0
5	DBB	4	3	6/7	0.88	0.14	51,51,52,53	0
5	MHW	4	1	9/10	0.93	0.11	46,47,49,50	0
5	MHU	4	5	15/16	0.94	0.12	56,59,62,63	0
5	004	4	7	10/11	0.95	0.10	45,48,49,51	0
1	PSU	0	2621	20/21	0.97	0.07	33,35,37,38	0
1	OMU	0	2587	21/22	0.97	0.07	29,32,37,38	0
1	OMG	0	2588	24/25	0.97	0.07	28,31,34,35	0
1	1MA	0	628	23/24	0.98	0.07	25,28,31,32	0
1	UR3	0	2619	21/22	0.98	0.06	30,35,39,42	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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. 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	3183	1/1	0.53	0.27	81,81,81,81	0
35	NA	0	3137	1/1	0.62	0.25	81,81,81,81	0
35	NA	0	3173	1/1	0.76	0.24	53,53,53,53	0
35	NA	0	3175	1/1	0.77	0.14	54,54,54,54	0
33	MG	0	3087	1/1	0.80	0.23	75,75,75,75	0
35	NA	0	3140	1/1	0.83	0.09	47,47,47,47	0
33	MG	0	3050	1/1	0.83	0.09	72,72,72,72	0
33	MG	0	3089	1/1	0.85	0.12	47,47,47,47	0
35	NA	R	202	1/1	0.85	0.44	75,75,75,75	0
35	NA	0	3122	1/1	0.86	0.08	47,47,47,47	0
33	MG	0	3082	1/1	0.86	0.11	46,46,46,46	0
35	NA	9	203	1/1	0.86	0.31	85,85,85,85	0
35	NA	0	3174	1/1	0.86	0.20	75,75,75,75	0
33	MG	0	3105	1/1	0.87	0.18	47,47,47,47	0
33	MG	0	3063	1/1	0.87	0.14	37,37,37,37	0
35	NA	0	3182	1/1	0.88	0.09	40,40,40,40	0
36	CL	0	3192	1/1	0.88	0.17	88,88,88,88	0
35	NA	0	3120	1/1	0.89	0.15	36,36,36,36	0
35	NA	L	201	1/1	0.89	0.30	61,61,61,61	0
35	NA	0	3176	1/1	0.89	0.19	60,60,60,60	0
35	NA	9	202	1/1	0.89	0.19	31,31,31,31	0
35	NA	0	3179	1/1	0.90	0.31	64,64,64,64	0
33	MG	0	3049	1/1	0.90	0.15	58,58,58,58	0
33	MG	0	3064	1/1	0.91	0.10	96,96,96,96	0
35	NA	0	3138	1/1	0.91	0.05	41,41,41,41	0
35	NA	0	3125	1/1	0.91	0.11	39,39,39,39	0
35	NA	0	3166	1/1	0.91	0.08	35,35,35,35	0
35	NA	0	3168	1/1	0.92	0.06	40,40,40,40	0
35	NA	0	3170	1/1	0.92	0.25	72,72,72,72	0
35	NA	0	3118	1/1	0.92	0.06	39,39,39,39	0
35	NA	0	3157	1/1	0.92	0.16	71,71,71,71	0
35	NA	0	3160	1/1	0.92	0.27	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	R	201	1/1	0.92	0.07	33,33,33,33	0
35	NA	0	3165	1/1	0.92	0.25	60,60,60,60	0
35	NA	0	3121	1/1	0.92	0.10	50,50,50,50	0
33	MG	0	3046	1/1	0.93	0.07	52,52,52,52	0
35	NA	Q	101	1/1	0.93	0.07	33,33,33,33	0
35	NA	0	3159	1/1	0.93	0.18	49,49,49,49	0
33	MG	0	3047	1/1	0.93	0.09	62,62,62,62	0
33	MG	0	3041	1/1	0.93	0.09	38,38,38,38	0
35	NA	0	3142	1/1	0.94	0.08	26,26,26,26	0
35	NA	0	3147	1/1	0.94	0.10	44,44,44,44	0
33	MG	0	3098	1/1	0.94	0.07	48,48,48,48	0
35	NA	0	3181	1/1	0.94	0.09	46,46,46,46	0
33	MG	0	3088	1/1	0.94	0.07	48,48,48,48	0
33	MG	K	201	1/1	0.94	0.05	46,46,46,46	0
35	NA	0	3161	1/1	0.94	0.12	54,54,54,54	0
33	MG	T	201	1/1	0.94	0.05	45,45,45,45	0
35	NA	0	3132	1/1	0.94	0.10	39,39,39,39	0
34	K	0	3110	1/1	0.94	0.23	86,86,86,86	0
33	MG	0	3045	1/1	0.94	0.06	58,58,58,58	0
35	NA	0	3119	1/1	0.94	0.08	40,40,40,40	0
36	CL	0	3187	1/1	0.94	0.10	57,57,57,57	0
35	NA	0	3141	1/1	0.94	0.11	37,37,37,37	0
36	CL	J	203	1/1	0.94	0.07	63,63,63,63	0
33	MG	0	3081	1/1	0.95	0.06	41,41,41,41	0
35	NA	0	3143	1/1	0.95	0.11	47,47,47,47	0
33	MG	0	3107	1/1	0.95	0.06	49,49,49,49	0
35	NA	0	3148	1/1	0.95	0.04	29,29,29,29	0
35	NA	0	3151	1/1	0.95	0.06	30,30,30,30	0
35	NA	0	3154	1/1	0.95	0.12	40,40,40,40	0
33	MG	0	3068	1/1	0.95	0.07	59,59,59,59	0
35	NA	0	3184	1/1	0.95	0.08	45,45,45,45	0
33	MG	0	3092	1/1	0.95	0.10	42,42,42,42	0
35	NA	0	3130	1/1	0.95	0.18	61,61,61,61	0
35	NA	C	301	1/1	0.95	0.05	32,32,32,32	0
33	MG	0	3094	1/1	0.95	0.14	73,73,73,73	0
35	NA	0	3134	1/1	0.95	0.15	72,72,72,72	0
34	K	0	3111	1/1	0.95	0.13	62,62,62,62	0
35	NA	0	3167	1/1	0.95	0.24	43,43,43,43	0
35	NA	0	3117	1/1	0.95	0.07	56,56,56,56	0
33	MG	0	3097	1/1	0.95	0.16	79,79,79,79	0
36	CL	0	3193	1/1	0.95	0.06	56,56,56,56	0
36	CL	0	3195	1/1	0.95	0.12	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	CL	J	202	1/1	0.95	0.07	55,55,55,55	0
33	MG	0	3077	1/1	0.95	0.14	58,58,58,58	0
36	CL	J	204	1/1	0.95	0.08	57,57,57,57	0
36	CL	L	202	1/1	0.95	0.09	46,46,46,46	0
36	CL	N	201	1/1	0.95	0.08	57,57,57,57	0
33	MG	0	3083	1/1	0.96	0.06	25,25,25,25	0
33	MG	0	3101	1/1	0.96	0.09	73,73,73,73	0
35	NA	0	3150	1/1	0.96	0.05	42,42,42,42	0
35	NA	0	3114	1/1	0.96	0.19	50,50,50,50	0
35	NA	0	3115	1/1	0.96	0.06	29,29,29,29	0
35	NA	S	101	1/1	0.96	0.05	10,10,10,10	0
33	MG	0	3090	1/1	0.96	0.04	41,41,41,41	0
33	MG	0	3106	1/1	0.96	0.06	42,42,42,42	0
33	MG	0	3085	1/1	0.96	0.07	41,41,41,41	0
36	CL	0	3194	1/1	0.96	0.06	58,58,58,58	0
33	MG	9	201	1/1	0.96	0.04	53,53,53,53	0
36	CL	3	103	1/1	0.96	0.05	53,53,53,53	0
35	NA	0	3164	1/1	0.96	0.15	75,75,75,75	0
33	MG	0	3043	1/1	0.96	0.09	35,35,35,35	0
35	NA	0	3185	1/1	0.96	0.19	38,38,38,38	0
33	MG	0	3056	1/1	0.96	0.06	42,42,42,42	0
35	NA	0	3146	1/1	0.96	0.03	26,26,26,26	0
36	CL	O	202	1/1	0.96	0.09	74,74,74,74	0
35	NA	0	3139	1/1	0.97	0.13	62,62,62,62	0
35	NA	0	3163	1/1	0.97	0.08	44,44,44,44	0
35	NA	A	302	1/1	0.97	0.10	38,38,38,38	0
33	MG	0	3084	1/1	0.97	0.07	49,49,49,49	0
35	NA	H	201	1/1	0.97	0.09	38,38,38,38	0
35	NA	J	201	1/1	0.97	0.04	61,61,61,61	0
33	MG	0	3065	1/1	0.97	0.04	38,38,38,38	0
33	MG	0	3066	1/1	0.97	0.04	34,34,34,34	0
35	NA	0	3112	1/1	0.97	0.04	21,21,21,21	0
35	NA	0	3144	1/1	0.97	0.04	44,44,44,44	0
35	NA	0	3113	1/1	0.97	0.05	44,44,44,44	0
36	CL	0	3186	1/1	0.97	0.07	43,43,43,43	0
35	NA	0	3172	1/1	0.97	0.19	58,58,58,58	0
36	CL	0	3188	1/1	0.97	0.08	57,57,57,57	0
36	CL	0	3189	1/1	0.97	0.07	39,39,39,39	0
36	CL	0	3190	1/1	0.97	0.07	46,46,46,46	0
35	NA	0	3127	1/1	0.97	0.06	26,26,26,26	0
33	MG	0	3067	1/1	0.97	0.05	41,41,41,41	0
33	MG	0	3108	1/1	0.97	0.06	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	3116	1/1	0.97	0.19	33,33,33,33	0
35	NA	0	3135	1/1	0.97	0.10	60,60,60,60	0
35	NA	0	3180	1/1	0.97	0.18	45,45,45,45	0
35	NA	0	3156	1/1	0.97	0.12	55,55,55,55	0
35	NA	0	3136	1/1	0.97	0.13	50,50,50,50	0
35	NA	0	3158	1/1	0.97	0.25	43,43,43,43	0
33	MG	0	3039	1/1	0.97	0.08	33,33,33,33	0
33	MG	0	3099	1/1	0.97	0.06	53,53,53,53	0
36	CL	R	203	1/1	0.97	0.08	43,43,43,43	0
36	CL	Y	302	1/1	0.97	0.08	30,30,30,30	0
35	NA	0	3152	1/1	0.98	0.14	34,34,34,34	0
35	NA	0	3153	1/1	0.98	0.08	43,43,43,43	0
35	NA	0	3124	1/1	0.98	0.06	48,48,48,48	0
35	NA	0	3155	1/1	0.98	0.08	39,39,39,39	0
33	MG	0	3048	1/1	0.98	0.04	48,48,48,48	0
35	NA	0	3126	1/1	0.98	0.05	28,28,28,28	0
33	MG	0	3034	1/1	0.98	0.05	29,29,29,29	0
35	NA	0	3129	1/1	0.98	0.05	25,25,25,25	0
35	NA	M	201	1/1	0.98	0.04	30,30,30,30	0
33	MG	0	3109	1/1	0.98	0.06	20,20,20,20	0
35	NA	0	3131	1/1	0.98	0.09	39,39,39,39	0
35	NA	0	3162	1/1	0.98	0.15	49,49,49,49	0
33	MG	0	3001	1/1	0.98	0.06	30,30,30,30	0
33	MG	0	3053	1/1	0.98	0.07	48,48,48,48	0
33	MG	0	3055	1/1	0.98	0.03	40,40,40,40	0
33	MG	0	3071	1/1	0.98	0.04	55,55,55,55	0
33	MG	0	3093	1/1	0.98	0.06	45,45,45,45	0
33	MG	0	3076	1/1	0.98	0.06	50,50,50,50	0
35	NA	0	3169	1/1	0.98	0.04	35,35,35,35	0
33	MG	0	3095	1/1	0.98	0.05	49,49,49,49	0
33	MG	0	3012	1/1	0.98	0.07	25,25,25,25	0
33	MG	0	3080	1/1	0.98	0.03	65,65,65,65	0
33	MG	0	3059	1/1	0.98	0.07	44,44,44,44	0
36	CL	A	303	1/1	0.98	0.09	58,58,58,58	0
36	CL	B	402	1/1	0.98	0.09	40,40,40,40	0
33	MG	0	3060	1/1	0.98	0.03	27,27,27,27	0
33	MG	0	3102	1/1	0.98	0.03	23,23,23,23	0
33	MG	0	3103	1/1	0.98	0.05	60,60,60,60	0
33	MG	0	3104	1/1	0.98	0.05	40,40,40,40	0
33	MG	0	3061	1/1	0.98	0.04	52,52,52,52	0
35	NA	0	3149	1/1	0.98	0.03	35,35,35,35	0
33	MG	0	3042	1/1	0.98	0.06	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	3123	1/1	0.98	0.04	27,27,27,27	0
37	CD	O	201	1/1	0.98	0.04	70,70,70,70	0
33	MG	Y	301	1/1	0.99	0.04	34,34,34,34	0
33	MG	0	3027	1/1	0.99	0.05	40,40,40,40	0
35	NA	0	3145	1/1	0.99	0.04	55,55,55,55	0
33	MG	0	3051	1/1	0.99	0.04	58,58,58,58	0
33	MG	0	3052	1/1	0.99	0.03	35,35,35,35	0
33	MG	0	3086	1/1	0.99	0.04	41,41,41,41	0
33	MG	0	3028	1/1	0.99	0.03	39,39,39,39	0
33	MG	0	3054	1/1	0.99	0.03	24,24,24,24	0
33	MG	0	3029	1/1	0.99	0.03	33,33,33,33	0
33	MG	0	3030	1/1	0.99	0.02	31,31,31,31	0
33	MG	0	3091	1/1	0.99	0.04	26,26,26,26	0
33	MG	0	3031	1/1	0.99	0.03	28,28,28,28	0
33	MG	0	3033	1/1	0.99	0.02	31,31,31,31	0
33	MG	0	3010	1/1	0.99	0.03	24,24,24,24	0
33	MG	0	3035	1/1	0.99	0.02	50,50,50,50	0
33	MG	0	3096	1/1	0.99	0.04	49,49,49,49	0
33	MG	0	3037	1/1	0.99	0.03	44,44,44,44	0
33	MG	0	3002	1/1	0.99	0.08	26,26,26,26	0
33	MG	0	3040	1/1	0.99	0.05	70,70,70,70	0
33	MG	0	3014	1/1	0.99	0.05	31,31,31,31	0
35	NA	0	3128	1/1	0.99	0.03	22,22,22,22	0
33	MG	0	3015	1/1	0.99	0.03	38,38,38,38	0
36	CL	0	3191	1/1	0.99	0.05	51,51,51,51	0
33	MG	0	3069	1/1	0.99	0.04	56,56,56,56	0
33	MG	0	3016	1/1	0.99	0.03	23,23,23,23	0
33	MG	0	3072	1/1	0.99	0.02	47,47,47,47	0
35	NA	0	3133	1/1	0.99	0.05	50,50,50,50	0
33	MG	0	3075	1/1	0.99	0.04	38,38,38,38	0
33	MG	0	3017	1/1	0.99	0.05	26,26,26,26	0
35	NA	0	3171	1/1	0.99	0.12	65,65,65,65	0
33	MG	0	3018	1/1	0.99	0.02	34,34,34,34	0
33	MG	0	3079	1/1	0.99	0.07	42,42,42,42	0
33	MG	0	3021	1/1	0.99	0.04	32,32,32,32	0
33	MG	A	301	1/1	0.99	0.03	44,44,44,44	0
36	CL	M	202	1/1	0.99	0.04	31,31,31,31	0
33	MG	B	401	1/1	0.99	0.04	32,32,32,32	0
35	NA	0	3177	1/1	0.99	0.08	58,58,58,58	0
35	NA	0	3178	1/1	0.99	0.04	29,29,29,29	0
33	MG	0	3024	1/1	0.99	0.04	12,12,12,12	0
37	CD	1	101	1/1	0.99	0.03	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	CD	3	102	1/1	0.99	0.03	55,55,55,55	0
33	MG	0	3025	1/1	0.99	0.03	42,42,42,42	0
33	MG	0	3013	1/1	1.00	0.03	37,37,37,37	0
33	MG	0	3005	1/1	1.00	0.01	27,27,27,27	0
33	MG	0	3006	1/1	1.00	0.03	46,46,46,46	0
33	MG	0	3007	1/1	1.00	0.03	12,12,12,12	0
33	MG	0	3070	1/1	1.00	0.02	25,25,25,25	0
33	MG	0	3008	1/1	1.00	0.03	33,33,33,33	0
33	MG	0	3032	1/1	1.00	0.05	40,40,40,40	0
33	MG	0	3073	1/1	1.00	0.02	28,28,28,28	0
33	MG	0	3074	1/1	1.00	0.02	20,20,20,20	0
33	MG	0	3100	1/1	1.00	0.02	35,35,35,35	0
33	MG	0	3009	1/1	1.00	0.03	22,22,22,22	0
33	MG	0	3019	1/1	1.00	0.02	23,23,23,23	0
33	MG	0	3020	1/1	1.00	0.02	22,22,22,22	0
33	MG	0	3078	1/1	1.00	0.04	22,22,22,22	0
33	MG	0	3036	1/1	1.00	0.04	32,32,32,32	0
33	MG	0	3003	1/1	1.00	0.02	31,31,31,31	0
33	MG	0	3038	1/1	1.00	0.02	28,28,28,28	0
33	MG	0	3057	1/1	1.00	0.04	32,32,32,32	0
33	MG	0	3058	1/1	1.00	0.04	27,27,27,27	0
33	MG	3	101	1/1	1.00	0.05	40,40,40,40	0
33	MG	4	102	1/1	1.00	0.03	46,46,46,46	0
33	MG	0	3022	1/1	1.00	0.02	36,36,36,36	0
33	MG	0	3023	1/1	1.00	0.01	34,34,34,34	0
33	MG	0	3011	1/1	1.00	0.02	21,21,21,21	0
33	MG	0	3062	1/1	1.00	0.01	51,51,51,51	0
33	MG	0	3004	1/1	1.00	0.02	27,27,27,27	0
33	MG	0	3026	1/1	1.00	0.01	19,19,19,19	0
33	MG	0	3044	1/1	1.00	0.06	37,37,37,37	0
37	CD	U	8701	1/1	1.00	0.02	60,60,60,60	0
37	CD	Z	101	1/1	1.00	0.03	59,59,59,59	0

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

There are no such residues in this entry.