



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:06 AM UTC

PDB ID : 2OTL / pdb_00002otl
Title : Girodazole bound to the large subunit of Haloarcula marismortui
Authors : Blaha, G.; Schroeder, S.J.; Tirado-Rives, J.
Deposited on : 2007-02-08
Resolution : 2.70 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

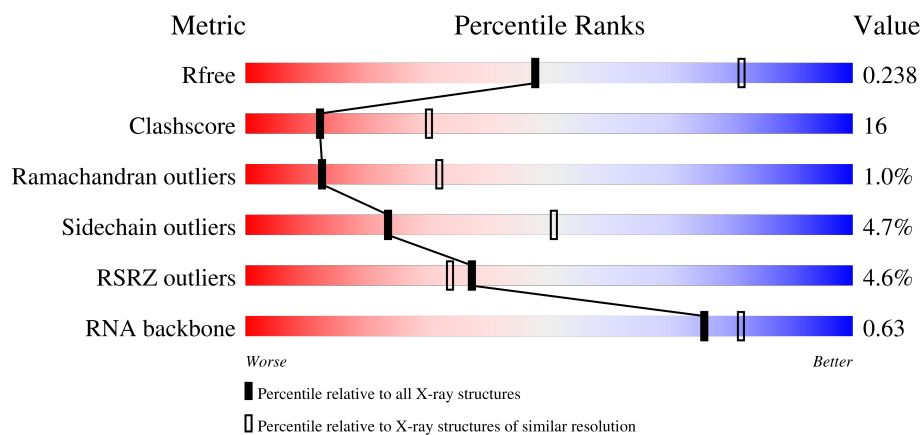
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



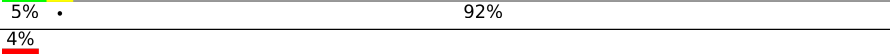
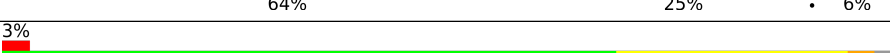
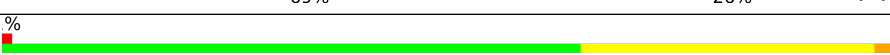
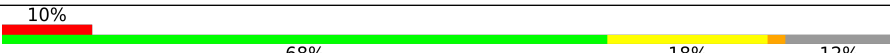
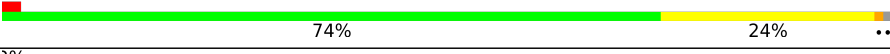
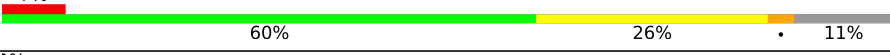
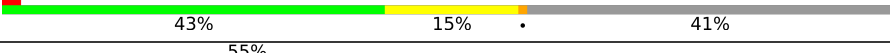
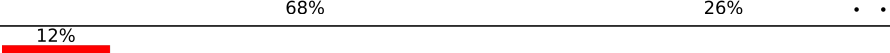
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	2% 49% 39% 6% 6%
2	9	122	4% 43% 43% 12%
3	A	239	4% 67% 28%
4	B	337	0% 58% 36% 5%

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	171	
11	J	145	
12	K	132	
13	L	165	
14	M	194	
15	N	187	
16	O	116	
17	P	149	
18	Q	96	
19	R	155	
20	S	85	
21	T	120	
22	U	66	
23	V	71	
24	W	154	
25	X	92	
26	Y	241	
27	Z	73	
28	1	57	
29	2	50	

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Mol	Chain	Length	Quality of chain
30	3	92	% 72% 25% .
31	I	162	22% 24% 17% .. 57%

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	0	8713	-	-	X	-
36	CL	J	8701	-	-	X	-
36	CL	M	8718	-	-	X	-

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99016 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
			59021	26350	10878	19048	2745			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	conflict	GB 3377779
0	628	1MA	A	modified residue	GB 3377779
0	2587	OMU	U	modified residue	GB 3377779
0	2588	OMG	G	modified residue	GB 3377779
0	2619	UR3	U	modified residue	GB 3377779
0	2621	PSU	U	modified residue	GB 3377779

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

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

- Molecule 3 is a protein called 50S ribosomal protein L2P.

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

- Molecule 4 is a protein called 50S ribosomal protein L3P.

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

- Molecule 5 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	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 6 is a protein called 50S ribosomal protein L5P.

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

- Molecule 7 is a protein called 50S ribosomal protein L6P.

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

- Molecule 8 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 9 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	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 10 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	160	Total	C	N	O	S	0	0	0
			1266	785	237	238	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	164	ASP	-	insertion	UNP P60617
H	165	SER	-	insertion	UNP P60617
H	166	SER	-	insertion	UNP P60617
H	167	PRO	-	insertion	UNP P60617
H	168	ALA	-	insertion	UNP P60617
H	169	GLY	-	insertion	UNP P60617
H	170	ASN	-	insertion	UNP P60617
H	171	ALA	-	insertion	UNP P60617

- Molecule 11 is a protein called 50S ribosomal protein L13P.

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

- Molecule 12 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	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 13 is a protein called 50S ribosomal protein L15P.

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

- Molecule 14 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	M	194	Total	C	N	O	S	0	0	0
			1560	943	332	284	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	conflict	UNP P60618
M	194	ALA	-	insertion	UNP P60618

- Molecule 15 is a protein called 50S ribosomal protein L18P.

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

- Molecule 16 is a protein called 50S ribosomal protein L18e.

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

- Molecule 17 is a protein called 50S ribosomal protein L19e.

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

- Molecule 18 is a protein called 50S ribosomal protein L21e.

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

- Molecule 19 is a protein called 50S ribosomal protein L22P.

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

- Molecule 20 is a protein called 50S ribosomal protein L23P.

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

- Molecule 21 is a protein called 50S ribosomal protein L24P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24e.

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

- Molecule 23 is a protein called 50S ribosomal protein L29P.

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

- Molecule 24 is a protein called 50S ribosomal protein L30P.

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

- Molecule 25 is a protein called 50S ribosomal protein L31e.

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

- Molecule 26 is a protein called 50S ribosomal protein L32e.

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

- Molecule 27 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Z	73	Total	C	N	O	S			
			579	346	116	112	5	0	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 28 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	1	56	Total	C	N	O	S	0	0	0
			430	258	86	82	4			

- Molecule 29 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

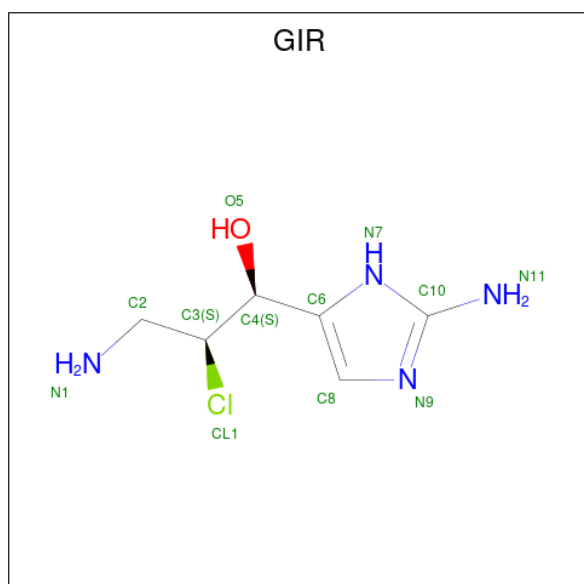
- Molecule 30 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is a protein called 50S ribosomal protein L11P.

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

- Molecule 32 is GIRODAZOLE (CCD ID: GIR) (formula: C₆H₁₁ClN₄O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
32	0	1	Total	C	Cl	N	O	0	0
			12	6	1	4	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	107	Total	Mg	0	0
			107	107		
33	9	1	Total	Mg	0	0
			1	1		
33	A	2	Total	Mg	0	0
			2	2		
33	B	2	Total	Mg	0	0
			2	2		
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		
33	3	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	71	Total	Na	0	0
			71	71		
35	9	2	Total	Na	0	0
			2	2		
35	A	1	Total	Na	0	0
			1	1		
35	C	1	Total	Na	0	0
			1	1		
35	H	2	Total	Na	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	J	1	Total 1	Na 1	0	0
35	L	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0
35	Q	1	Total 1	Na 1	0	0
35	R	3	Total 3	Na 3	0	0
35	S	1	Total 1	Na 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	9	Total 9	Cl 9	0	0
36	A	1	Total 1	Cl 1	0	0
36	B	1	Total 1	Cl 1	0	0
36	J	3	Total 3	Cl 3	0	0
36	L	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0
36	N	1	Total 1	Cl 1	0	0
36	O	1	Total 1	Cl 1	0	0
36	Q	1	Total 1	Cl 1	0	0
36	R	1	Total 1	Cl 1	0	0
36	Y	1	Total 1	Cl 1	0	0
36	3	1	Total 1	Cl 1	0	0

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

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

- Molecule 38 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
38	0	5893	Total O 5893 5893	0	0
38	9	145	Total O 145 145	0	0
38	A	118	Total O 118 118	0	0
38	B	147	Total O 147 147	0	0
38	C	163	Total O 163 163	0	0
38	D	48	Total O 48 48	0	0
38	E	46	Total O 46 46	0	0
38	F	23	Total O 23 23	0	0
38	G	19	Total O 19 19	0	0
38	H	69	Total O 69 69	0	0
38	J	58	Total O 58 58	0	0
38	K	58	Total O 58 58	0	0
38	L	81	Total O 81 81	0	0
38	M	115	Total O 115 115	0	0
38	N	58	Total O 58 58	0	0

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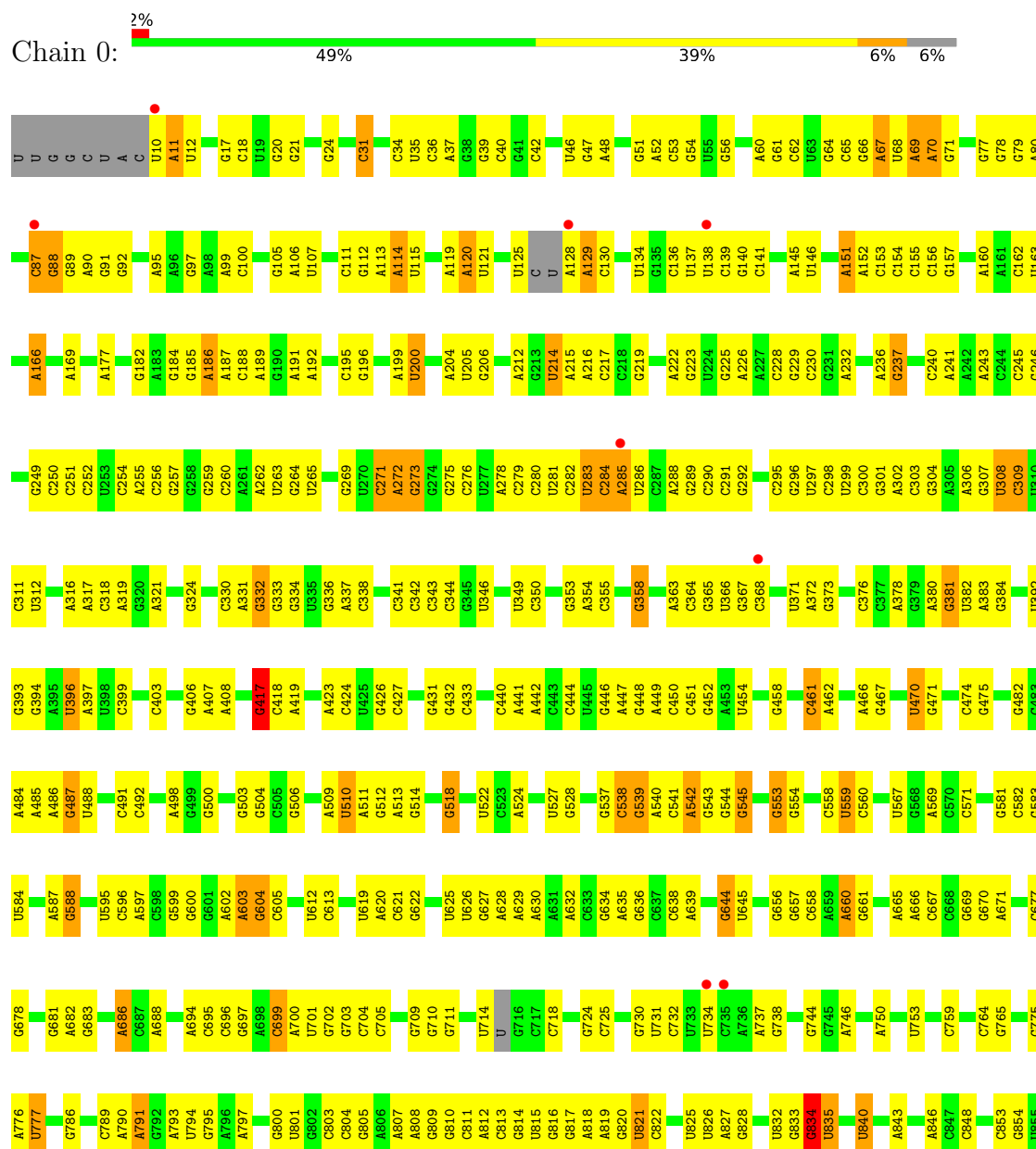
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	O	44	Total 44	O 44	0	0
38	P	61	Total 61	O 61	0	0
38	Q	55	Total 55	O 55	0	0
38	R	81	Total 81	O 81	0	0
38	S	37	Total 37	O 37	0	0
38	T	39	Total 39	O 39	0	0
38	U	28	Total 28	O 28	0	0
38	V	11	Total 11	O 11	0	0
38	W	70	Total 70	O 70	0	0
38	X	26	Total 26	O 26	0	0
38	Y	99	Total 99	O 99	0	0
38	Z	32	Total 32	O 32	0	0
38	1	56	Total 56	O 56	0	0
38	2	40	Total 40	O 40	0	0
38	3	66	Total 66	O 66	0	0
38	I	4	Total 4	O 4	0	0

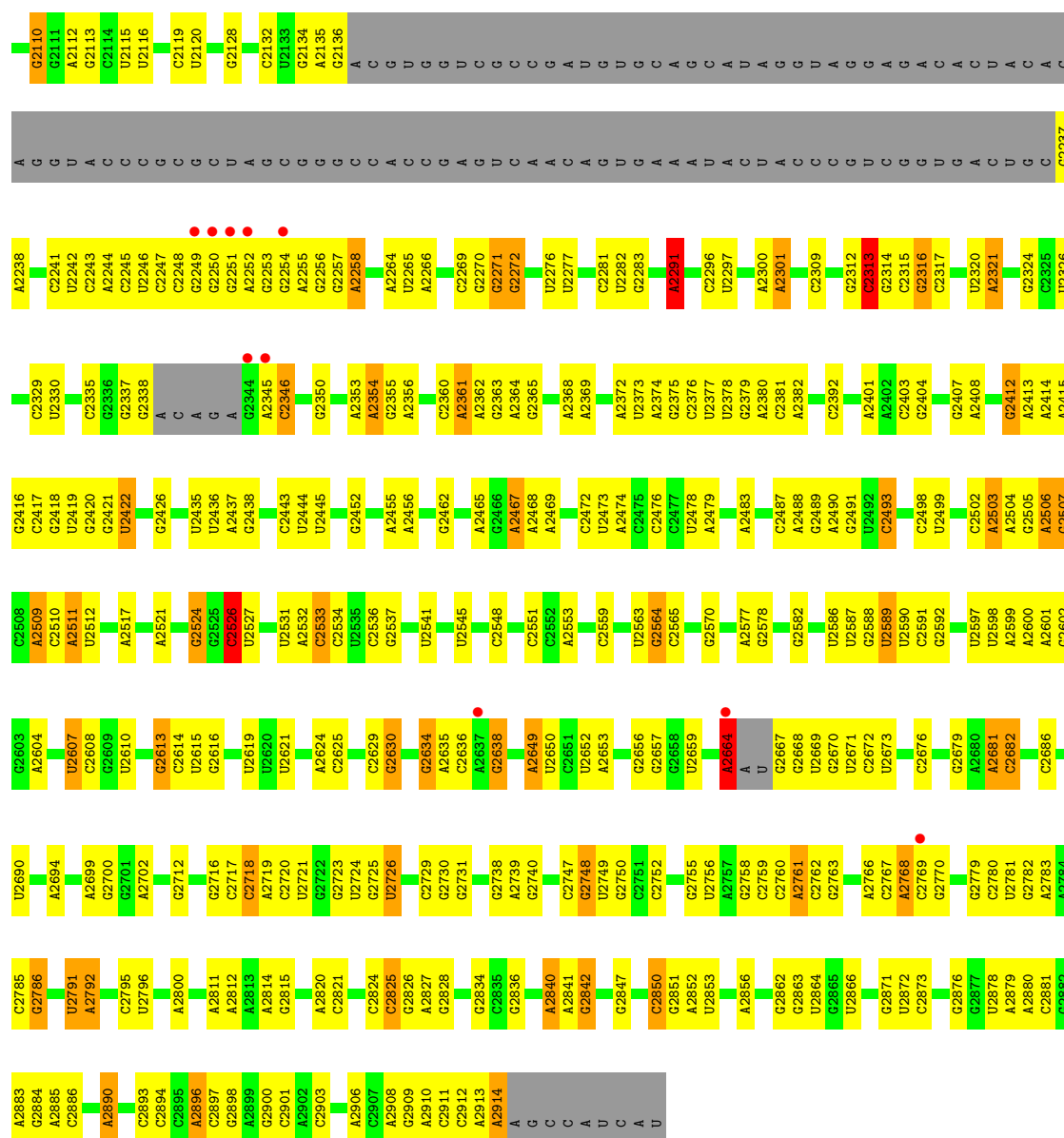
3 Residue-property plots [i](#)

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.

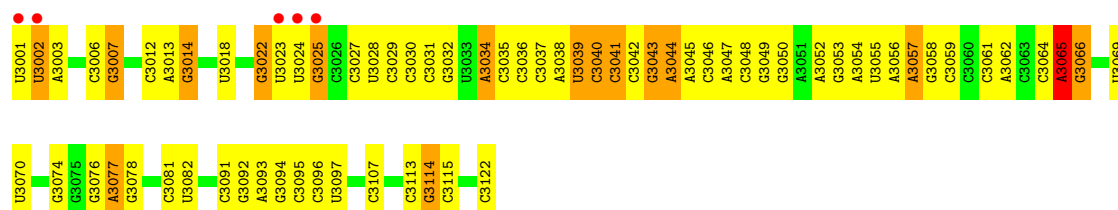
• Molecule 1: 23S ribosomal RNA



A1997	G953	G126	G160	C129	G195	A1567	U1654	G1745	C1916	A1997	A2054	C2071	G856
G2000	U954	G127	A1161	A1230	A1414	G1568	G1655	A1746	G1917	A1829	G2044	G2072	A857
G2001	A955	U1028	G1163	A1231	G1415	U1569	A1656	A1747	U1918	C1834	G2045	G2073	U858
C2002	G958	U1029	U1164	A1232	G1416	A1572	A1657	G1752	C1920	U1835	G2046	A2074	C859
U2003	C959	A1032	U1165	U1234	U1417	A1573	A1658	G1753	C1920	U1836			U860
U2004	U960	A1032	A1166	G1235	U1418	C1574	G1659	C1759	A1921	A1836			A861
G2005	C961	U1032	A1167	G1236	U1419	U1503	G1660	C1759	A1922	A1836			U862
U2008	A962	C1044	G1168	U1237	C1420	A1504	A1661	A1759	G1925	A1840			G868
G2009	C963	G1045	U1169	A1237	C1421	U1505	C1662	G1765	G1926	C1841			G869
A2010	G968	U1052	U1170	G1238	U1422	U1506	A1663	A1766	A1927	A1842			G870
A2011	G969	G1053	U1171	G1239	U1423	C1507	G1664	G1767	C1928	U1845			G871
U2012	U970	G1054	A1171	G1240	U1424	C1508	C1665	G1768	G1929	A1846			U872
G2013	G	G1055	G1172	G1241	A1425	G1509	A1667	C1769	A1931	A1847			G873
U2016	U	U1056	A1173	A1241	C1426	G1512	U1668	U1770	G1936	G1848			A874
U2028	G	U1057	U1174	A1242	A1427	C1513	U1587	U1771	C1937	U1849			A875
C2029	U	U1058	G1175	C1243	G1432	C1514	A1669	G1773	U1937	U1850			A876
G2033	C	U1059	A1177	C1244	U1433	C1515	U1671	G1774	C1938	U1851			U877
U2034	U	G1060	U1180	A1247	U1434	C1516	G1672	G1777	U1939	C1853			G878
G2039	C	U1066	A1181	A1252	U1435	U1517	U1677	G1778	C1940	C1854			U883
G2044	G	A1067	A1182	C1253	C1436	G1520	A1678	A1778	G2033	G1855			C884
G2045	A	A1067	C1183	C1254	U1440	G1521	U1679	A1779	A1941	G1856			G885
G2046	C	G1072	C1184	C1254	G1441	C1522	G1680	G1780	A1942	A1857			A886
A2039	C	A1078	U1185	G1262	U1442	G1523	A1681	G1781	C1944	G1857			G887
G2044	G	A1079	C1186	U1266	G1443	U1524	G1683	G1782	G1945	G1862			U888
G2045	A	U1079	U1187	U1267	G1444	U1525	A1678	A1783	C1946	G1863			A894
G2046	C	A1081	U1188	C1268	G1445	A1526	A1685	G1784	G2045	G1855			G895
A2054	C	A1086	U1189	G1269	U1446	A1527	G1686	G1785	G1947	G1856			G898
U2063	G	A1087	A1191	G1273	U1447	A1528	C1687	U1788	G1951	G1873			G902
U2064	G	A1088	A1192	C1273	C1450	G1529	C1692	G1789	U	U1874			C905
C2065	U	C1102	A1193	A1278	C1451	A1533	A1701	C1790	A	G1877			A907
C2066	C	U1109	U1195	A1280	G1452	G1534	U1702	U1791	C	U1878			A912
G2071	G	G1110	G1197	U1285	U1454	G1535	U1702	G1795	U	C1880			C920
G2072	C	G1116	U1198	U1288	G1455	C1537	A1710	A1796	U	A1881			G921
G2073	A	U1117	A1199	G1289	U1456	U1538	A1711	A1797	G	C1882			A922
A2074	C	A1118	C1201	G1290	A1463	U1539	A1712	C1798	C	U1883			A923
A2081	C	G1119	U1202	A1294	U1471	G1543	A1713	C1803	C	A1885			G924
G2082	U1001	U1120	U1203	U1288	U1473	U1544	A1717	G1804	U1964	A1886			
A2083	C1004	U130	U1205	G1299	U1475	C1545	U1722	G1805		C1889			
C2088	A1005	G131	A1207	G1311	C1474	C1553	G1723	G1806	G1970	U1890			
G2090	A1006	A132	C1208	G1312	C1477	U1554	U1724	G1809	G1971	C1894			
G2091	C1008	U135	C1209	A1307	U1478	G1555	C1725	C1810	U1972	C1895			
G2092	U1009	G136	G1210	A1308	A1479	G1556	G1730	A1811	A1973	A1895			
A2096	C1010	U137	G1211	U1306	U1479	G1557	C1731	G1812	G1974	G1896			
A2101	A1013	G138	C1212	U1307	G1484	C1558	A1732	C1818	G1975	U1897			
G2102	A1014	U139	G1213	A1307	A1485	U1559	A1733	G1819	G1976	G1902			
A2103	C1015	U140	G1214	A1307	U1485	U	C1734	G1820	U1977	A1903			
C2104	U1016	C140	A1215	A1307	G1489	U1561	C1735	G1821	A1978	A1904			
C2105	C156	C156	G1216	G1315	G1490	C1562	U1741	A1821	G1979	U1980			
C2106	G157	C157	G1217	G1316	G1491	G1563	U1742	G1823	U1992	U1980			
	G159	G159	U1218	A1321	A1492	C1564	G1743	C1824	U1992	A1904			
			U1219	G1322	A1493	C1565	G1744	C1826	U1996	A1904			

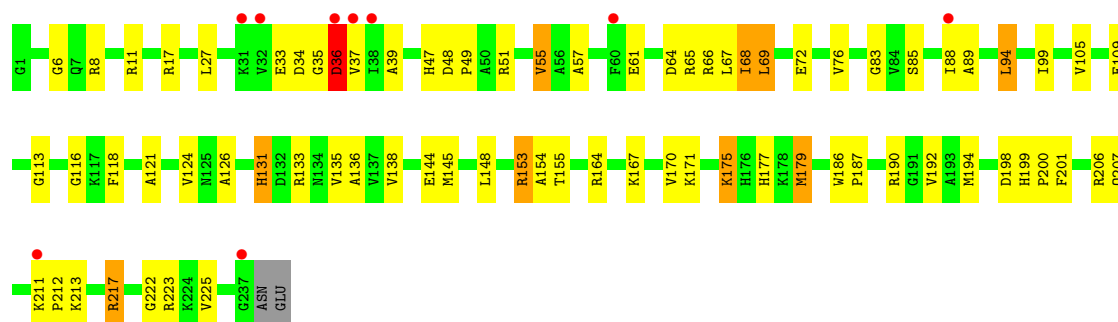


• Molecule 2: 5S ribosomal RNA

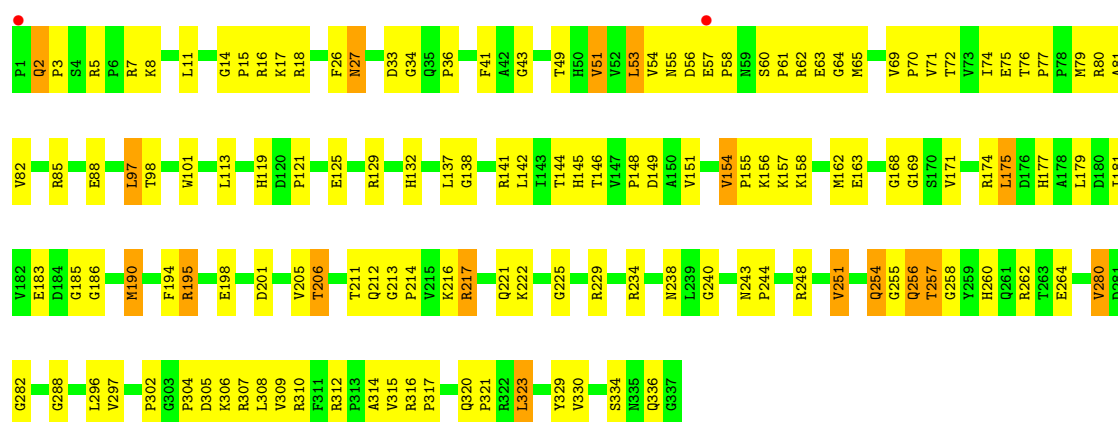


• Molecule 3: 50S ribosomal protein L2P

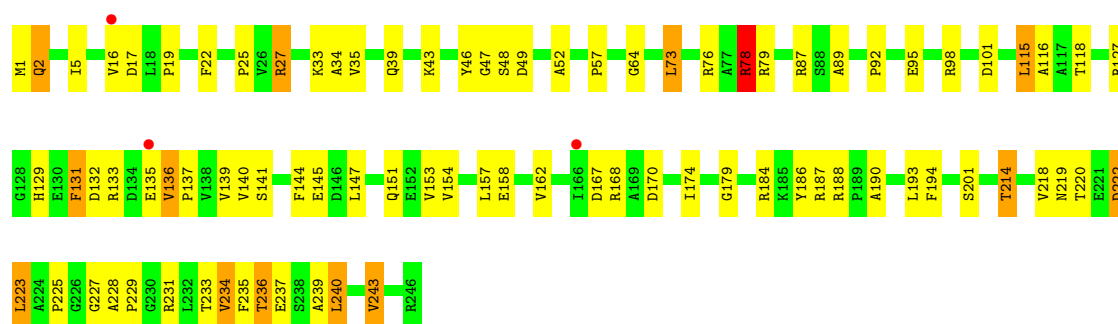




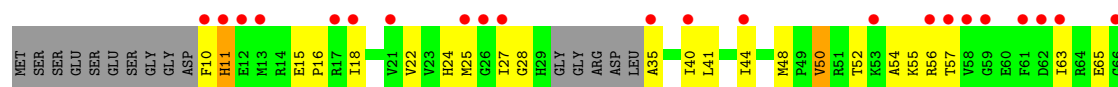
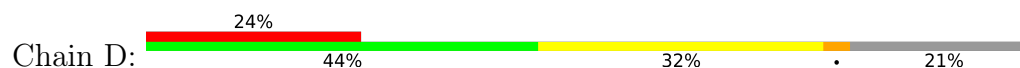
• Molecule 4: 50S ribosomal protein L3P

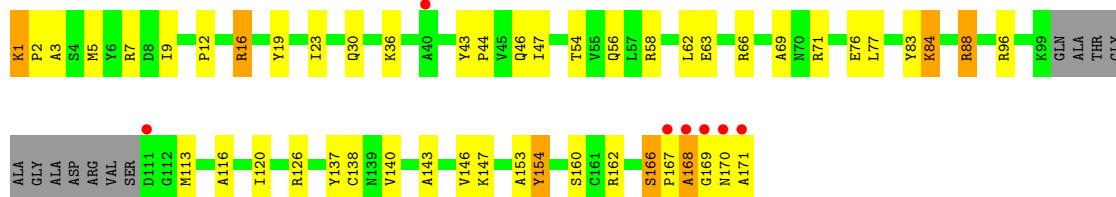


• Molecule 5: 50S ribosomal protein L4P

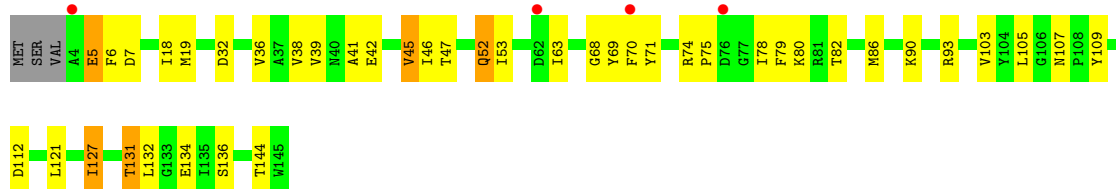


• Molecule 6: 50S ribosomal protein L5P

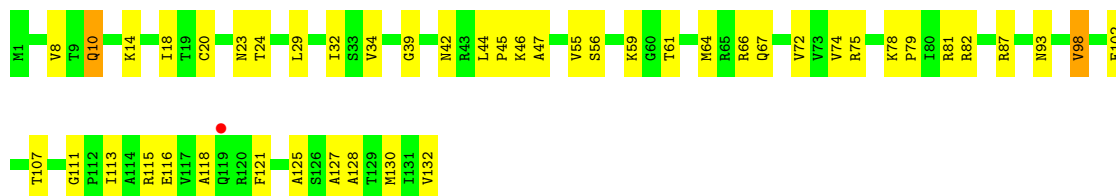




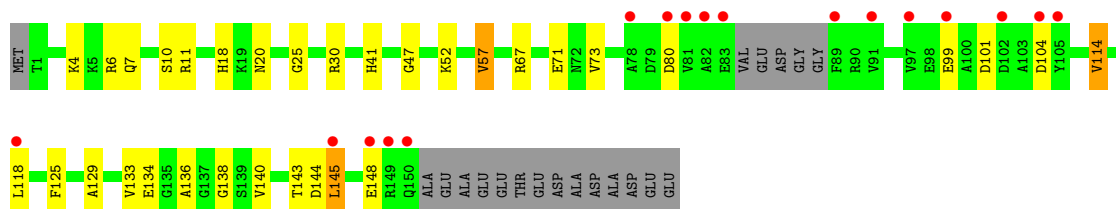
• Molecule 11: 50S ribosomal protein L13P



• Molecule 12: 50S ribosomal protein L14P



• Molecule 13: 50S ribosomal protein L15P

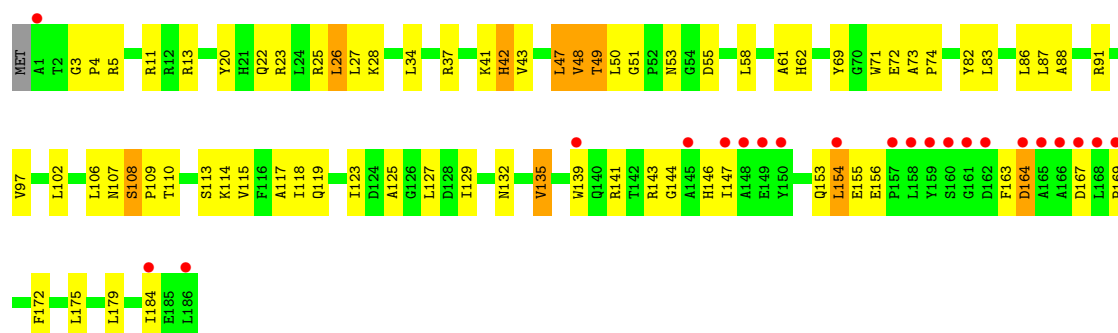


• Molecule 14: 50S ribosomal protein L15e

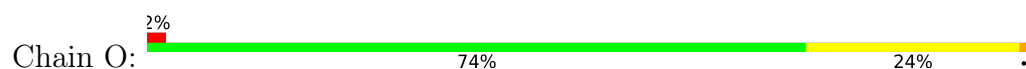




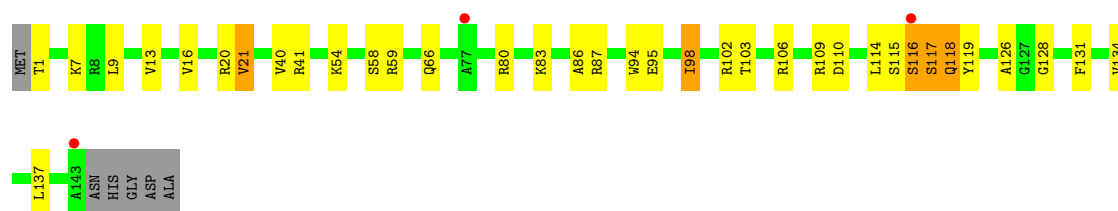
• Molecule 15: 50S ribosomal protein L18P



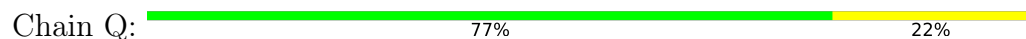
• Molecule 16: 50S ribosomal protein L18e



• Molecule 17: 50S ribosomal protein L19e



• Molecule 18: 50S ribosomal protein L21e



• Molecule 19: 50S ribosomal protein L22P





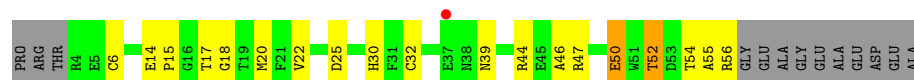
- Molecule 20: 50S ribosomal protein L23P



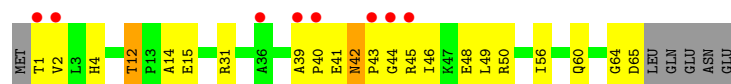
- Molecule 21: 50S ribosomal protein L24P



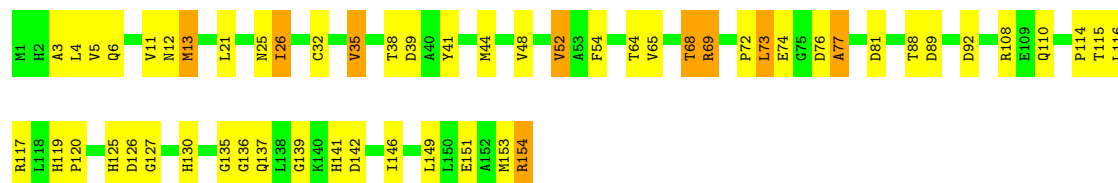
- Molecule 22: 50S ribosomal protein L24e



- Molecule 23: 50S ribosomal protein L29P



- Molecule 24: 50S ribosomal protein L30P

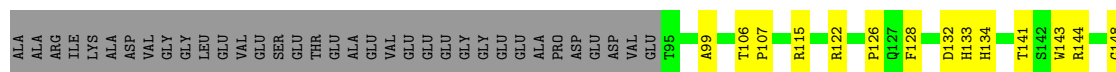
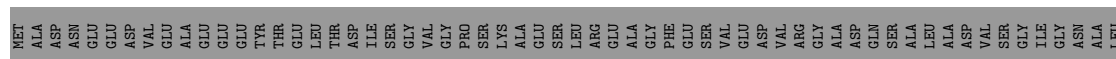
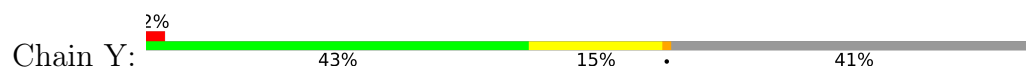


- Molecule 25: 50S ribosomal protein L31e

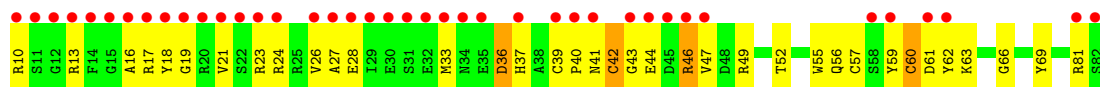




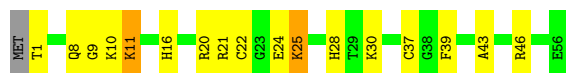
• Molecule 26: 50S ribosomal protein L32e



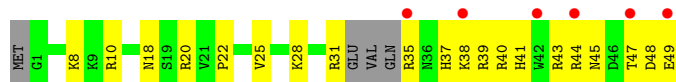
• Molecule 27: 50S ribosomal protein L37Ae



• Molecule 28: 50S ribosomal protein L37e



• Molecule 29: 50S ribosomal protein L39e

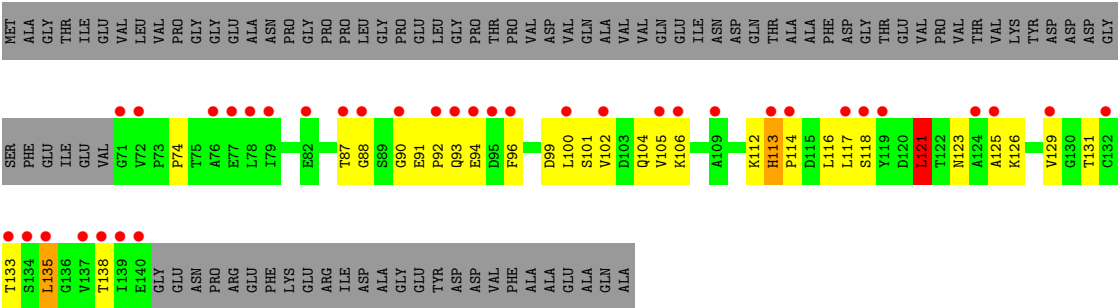


• Molecule 30: 50S ribosomal protein L44E



• Molecule 31: 50S ribosomal protein L11P





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.08Å 300.60Å 575.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.36 – 2.70 49.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.36-2.70) 90.6 (49.36-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.204 , 0.248 0.196 , 0.238	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99016	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage'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.*

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: OMG, PSU, NA, CL, K, MG, GIR, 1MA, OMU, CD, UR3

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	0.40	0/65959	0.62	18/102870 (0.0%)
2	9	0.38	0/2905	0.59	2/4528 (0.0%)
3	A	0.44	0/1786	1.01	7/2408 (0.3%)
4	B	0.43	0/2690	1.02	14/3652 (0.4%)
5	C	0.48	0/1884	1.03	8/2551 (0.3%)
6	D	0.40	0/1111	0.96	7/1498 (0.5%)
7	E	0.41	0/1382	0.87	2/1880 (0.1%)
8	F	0.44	0/901	0.97	2/1224 (0.2%)
9	G	0.35	0/241	0.83	0/324
10	H	0.42	0/1287	0.98	6/1725 (0.3%)
11	J	0.46	0/1136	0.98	6/1530 (0.4%)
12	K	0.44	0/1001	1.05	6/1347 (0.4%)
13	L	0.43	0/1130	1.00	6/1509 (0.4%)
14	M	0.43	0/1584	0.95	3/2119 (0.1%)
15	N	0.40	0/1474	1.05	14/1999 (0.7%)
16	O	0.45	0/874	0.91	2/1181 (0.2%)
17	P	0.41	0/1147	0.86	1/1528 (0.1%)
18	Q	0.44	0/749	1.05	4/1005 (0.4%)
19	R	0.49	0/1172	0.96	4/1578 (0.3%)
20	S	0.38	0/648	0.91	2/875 (0.2%)
21	T	0.41	0/958	0.98	4/1289 (0.3%)
22	U	0.45	0/417	0.87	1/562 (0.2%)
23	V	0.40	0/502	1.00	2/675 (0.3%)
24	W	0.53	1/1219 (0.1%)	0.98	4/1655 (0.2%)
25	X	0.47	0/664	1.04	5/895 (0.6%)
26	Y	0.46	0/1146	0.95	2/1536 (0.1%)
27	Z	0.60	0/590	1.01	2/787 (0.3%)
28	1	0.45	0/437	0.94	2/578 (0.3%)
29	2	0.47	0/401	0.77	0/529
30	3	0.45	0/771	0.87	5/1024 (0.5%)
31	I	0.41	0/526	0.97	2/716 (0.3%)
All	All	0.41	1/98692 (0.0%)	0.73	143/147577 (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	52

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	W	13	MET	SD-CE	-6.17	1.64	1.79

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1979	G	C2'-C3'-O3'	9.87	124.31	109.50
21	T	52	ARG	N-CA-C	8.61	124.63	113.18
18	Q	17	LYS	N-CA-C	-8.00	99.67	109.83
17	P	118	GLN	N-CA-C	-7.87	102.01	111.69
3	A	222	GLY	N-CA-C	-7.83	105.16	114.48

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	214	U	Sidechain
1	0	332	G	Sidechain
1	0	396	U	Sidechain
1	0	417	G	Sidechain
1	0	48	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	59021	0	29810	1368	0
2	9	2600	0	1326	96	0
3	A	1753	0	1766	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	2625	0	2533	111	0
5	C	1859	0	1816	71	0
6	D	1094	0	1085	48	0
7	E	1357	0	1266	39	0
8	F	890	0	843	36	0
9	G	240	0	231	9	0
10	H	1266	0	1268	44	0
11	J	1120	0	1098	42	0
12	K	992	0	1031	40	0
13	L	1118	0	1076	25	0
14	M	1560	0	1568	57	0
15	N	1445	0	1401	63	0
16	O	865	0	873	22	0
17	P	1136	0	1123	35	0
18	Q	735	0	729	13	0
19	R	1149	0	1122	42	0
20	S	641	0	605	12	0
21	T	950	0	923	38	0
22	U	410	0	364	17	0
23	V	499	0	511	20	0
24	W	1196	0	1137	55	0
25	X	654	0	653	22	0
26	Y	1130	0	1133	38	0
27	Z	579	0	540	46	0
28	1	430	0	426	20	0
29	2	396	0	413	26	0
30	3	755	0	729	28	0
31	I	519	0	500	27	0
32	0	12	0	10	0	0
33	0	107	0	0	0	0
33	3	1	0	0	0	0
33	9	1	0	0	0	0
33	A	2	0	0	0	0
33	B	2	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	71	0	0	0	0
35	9	2	0	0	0	0
35	A	1	0	0	0	0
35	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	H	2	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	3	0	0	0	0
35	S	1	0	0	0	0
36	O	9	0	0	4	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	4	0
36	L	1	0	0	0	0
36	M	1	0	0	2	0
36	N	1	0	0	1	0
36	O	1	0	0	0	0
36	Q	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	O	5893	0	0	184	0
38	1	56	0	0	1	0
38	2	40	0	0	3	0
38	3	66	0	0	5	0
38	9	145	0	0	9	0
38	A	118	0	0	10	0
38	B	147	0	0	14	0
38	C	163	0	0	14	0
38	D	48	0	0	8	0
38	E	46	0	0	4	0
38	F	23	0	0	3	0
38	G	19	0	0	0	0
38	H	69	0	0	6	0
38	I	4	0	0	1	0
38	J	58	0	0	4	0
38	K	58	0	0	3	0
38	L	81	0	0	8	0
38	M	115	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	58	0	0	5	0
38	O	44	0	0	7	0
38	P	61	0	0	1	0
38	Q	55	0	0	4	0
38	R	81	0	0	4	0
38	S	37	0	0	0	0
38	T	39	0	0	3	0
38	U	28	0	0	2	0
38	V	11	0	0	3	0
38	W	70	0	0	5	0
38	X	26	0	0	2	0
38	Y	99	0	0	10	0
38	Z	32	0	0	5	0
All	All	99016	0	59909	2329	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 2329 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)
10:H:46:GLN:HB3	10:H:167:PRO:HD2	1.29	1.15
1:0:871:G:H5'	1:0:871:G:H8	1.06	1.12
1:0:656:G:H5'	16:O:3:THR:HG22	1.16	1.12
2:9:3056:A:H2'	2:9:3057:A:H5''	1.31	1.10
1:0:1559:A:H1'	38:0:5862:HOH:O	1.50	1.09

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	235/239 (98%)	209 (89%)	23 (10%)	3 (1%)	9	25
4	B	335/337 (99%)	305 (91%)	24 (7%)	6 (2%)	6	18
5	C	244/246 (99%)	228 (93%)	15 (6%)	1 (0%)	30	54
6	D	134/177 (76%)	107 (80%)	23 (17%)	4 (3%)	3	8
7	E	170/178 (96%)	163 (96%)	7 (4%)	0	100	100
8	F	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	35
9	G	25/348 (7%)	25 (100%)	0	0	100	100
10	H	156/171 (91%)	143 (92%)	9 (6%)	4 (3%)	4	11
11	J	140/145 (97%)	128 (91%)	11 (8%)	1 (1%)	18	41
12	K	130/132 (98%)	122 (94%)	8 (6%)	0	100	100
13	L	141/165 (86%)	127 (90%)	14 (10%)	0	100	100
14	M	192/194 (99%)	178 (93%)	13 (7%)	1 (0%)	24	48
15	N	184/187 (98%)	168 (91%)	13 (7%)	3 (2%)	7	20
16	O	113/116 (97%)	109 (96%)	4 (4%)	0	100	100
17	P	141/149 (95%)	136 (96%)	3 (2%)	2 (1%)	9	23
18	Q	93/96 (97%)	87 (94%)	5 (5%)	1 (1%)	11	29
19	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	18	41
20	S	79/85 (93%)	76 (96%)	2 (2%)	1 (1%)	9	25
21	T	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
22	U	51/66 (77%)	49 (96%)	2 (4%)	0	100	100
23	V	63/71 (89%)	59 (94%)	3 (5%)	1 (2%)	7	20
24	W	152/154 (99%)	146 (96%)	4 (3%)	2 (1%)	9	25
25	X	80/92 (87%)	74 (92%)	4 (5%)	2 (2%)	4	11
26	Y	140/241 (58%)	140 (100%)	0	0	100	100
27	Z	71/73 (97%)	58 (82%)	9 (13%)	4 (6%)	1	2
28	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
29	2	42/50 (84%)	42 (100%)	0	0	100	100
30	3	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
31	I	68/162 (42%)	65 (96%)	3 (4%)	0	100	100
All	All	3705/4418 (84%)	3435 (93%)	232 (6%)	38 (1%)	12	32

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	137	PRO
6	D	173	GLU
8	F	101	ALA
10	H	166	SER
10	H	168	ALA

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	
3	A	179/181 (99%)	168 (94%)	11 (6%)	17	40
4	B	282/282 (100%)	263 (93%)	19 (7%)	15	36
5	C	193/193 (100%)	173 (90%)	20 (10%)	7	17
6	D	117/148 (79%)	112 (96%)	5 (4%)	26	54
7	E	152/156 (97%)	147 (97%)	5 (3%)	33	63
8	F	93/94 (99%)	90 (97%)	3 (3%)	34	64
9	G	27/283 (10%)	26 (96%)	1 (4%)	30	59
10	H	132/138 (96%)	126 (96%)	6 (4%)	24	52
11	J	118/121 (98%)	110 (93%)	8 (7%)	14	35
12	K	106/106 (100%)	104 (98%)	2 (2%)	50	77
13	L	113/127 (89%)	109 (96%)	4 (4%)	32	61
14	M	158/158 (100%)	151 (96%)	7 (4%)	25	53
15	N	149/150 (99%)	142 (95%)	7 (5%)	23	51
16	O	93/94 (99%)	89 (96%)	4 (4%)	26	54
17	P	113/117 (97%)	109 (96%)	4 (4%)	32	61
18	Q	79/80 (99%)	78 (99%)	1 (1%)	61	83
19	R	117/122 (96%)	112 (96%)	5 (4%)	26	54
20	S	71/74 (96%)	68 (96%)	3 (4%)	26	55
21	T	105/106 (99%)	101 (96%)	4 (4%)	29	58
22	U	44/52 (85%)	42 (96%)	2 (4%)	24	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
23	V	51/57 (90%)	50 (98%)	1 (2%)	48 76
24	W	130/130 (100%)	123 (95%)	7 (5%)	20 45
25	X	66/74 (89%)	62 (94%)	4 (6%)	17 40
26	Y	120/196 (61%)	115 (96%)	5 (4%)	26 55
27	Z	60/60 (100%)	58 (97%)	2 (3%)	33 63
28	1	46/47 (98%)	45 (98%)	1 (2%)	45 74
29	2	42/46 (91%)	41 (98%)	1 (2%)	43 72
30	3	79/79 (100%)	77 (98%)	2 (2%)	42 71
31	I	58/130 (45%)	56 (97%)	2 (3%)	32 62
All	All	3093/3601 (86%)	2947 (95%)	146 (5%)	23 51

5 of 146 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	T	26	THR
30	3	14	CYS
22	U	52	THR
25	X	66	THR
5	C	240	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
19	R	113	HIS
24	W	27	HIS
19	R	122	GLN
21	T	73	HIS
24	W	125	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2746/2922 (93%)	242 (8%)	35 (1%)
2	9	121/122 (99%)	18 (14%)	1 (0%)
All	All	2867/3044 (94%)	260 (9%)	36 (1%)

5 of 260 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 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	2467	A
2	9	3065	A
1	0	2536	C
1	0	2761	A
1	0	1120	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

5 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	1MA	0	628	35,1	21,25,26	0.72	1 (4%)	30,37,40	0.71	1 (3%)
1	OMU	0	2587	1	19,22,23	0.32	0	25,31,34	0.43	0
1	PSU	0	2621	1	18,21,22	1.56	2 (11%)	21,30,33	1.40	3 (14%)
1	OMG	0	2588	1	23,26,27	0.29	0	32,38,41	0.37	0
1	UR3	0	2619	1	19,22,23	0.45	0	26,32,35	0.71	1 (3%)

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	1MA	0	628	35,1	-	2/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	0	2587	1	-	0/9/27/28	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	OMG	0	2588	1	-	0/9/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C2-N1	5.33	1.43	1.36
1	0	628	1MA	C6-N6	2.45	1.33	1.28
1	0	2621	PSU	C6-C5	2.26	1.37	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C6-C5-C4	3.77	120.72	118.17
1	0	2621	PSU	C6-N1-C2	-3.03	119.88	122.69
1	0	2621	PSU	O2-C2-N1	3.00	125.88	122.79
1	0	628	1MA	N1-C2-N3	2.82	129.34	126.00
1	0	2619	UR3	C4-N3-C2	2.79	126.82	124.58

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 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0
1	0	2588	OMG	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 231 ligands modelled in this entry, 230 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
32	GIR	0	9000	-	8,12,12	1.26	0	8,16,16	2.26	2 (25%)

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
32	GIR	0	9000	-	-	0/8/10/10	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
32	0	9000	GIR	C6-C8-N9	-4.24	107.00	111.46
32	0	9000	GIR	C8-C6-N7	3.82	110.56	105.61

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

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.31	53 (1%) 66 63	24, 49, 93, 153	0
2	9	122/122 (100%)	0.18	5 (4%) 41 37	38, 64, 91, 149	0
3	A	237/239 (99%)	0.31	9 (3%) 44 40	30, 58, 99, 119	0
4	B	337/337 (100%)	0.19	2 (0%) 85 85	28, 56, 84, 95	0
5	C	246/246 (100%)	0.14	3 (1%) 76 75	25, 49, 74, 80	0
6	D	140/177 (79%)	1.54	43 (30%) 1 1	61, 105, 127, 136	0
7	E	172/178 (96%)	0.52	10 (5%) 29 25	46, 68, 87, 93	0
8	F	119/120 (99%)	0.81	7 (5%) 28 25	53, 78, 99, 117	0
9	G	29/348 (8%)	1.44	8 (27%) 1 1	77, 94, 105, 107	0
10	H	160/171 (93%)	0.26	7 (4%) 39 35	40, 58, 92, 100	0
11	J	142/145 (97%)	0.14	4 (2%) 55 51	35, 50, 74, 90	0
12	K	132/132 (100%)	0.25	1 (0%) 82 81	36, 54, 77, 87	0
13	L	145/165 (87%)	0.72	17 (11%) 9 7	29, 71, 118, 130	0
14	M	194/194 (100%)	-0.01	3 (1%) 72 70	35, 47, 63, 73	0
15	N	186/187 (99%)	0.79	22 (11%) 9 7	41, 68, 115, 120	0
16	O	115/116 (99%)	0.39	2 (1%) 69 67	41, 57, 75, 80	0
17	P	143/149 (95%)	0.34	3 (2%) 63 61	43, 59, 78, 83	0
18	Q	95/96 (98%)	-0.07	0 100 100	37, 48, 62, 78	0
19	R	150/155 (96%)	-0.13	0 100 100	33, 47, 66, 74	0
20	S	81/85 (95%)	0.28	2 (2%) 58 55	47, 67, 87, 94	0
21	T	119/120 (99%)	0.34	2 (1%) 69 67	41, 61, 88, 108	0
22	U	53/66 (80%)	0.36	1 (1%) 66 63	44, 61, 77, 83	0
23	V	65/71 (91%)	1.12	8 (12%) 8 7	60, 84, 118, 121	0
24	W	154/154 (100%)	-0.01	0 100 100	34, 49, 66, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	X	82/92 (89%)	0.46	6 (7%) 21 18	45, 61, 87, 102	0
26	Y	142/241 (58%)	0.01	4 (2%) 55 51	28, 47, 71, 92	0
27	Z	73/73 (100%)	2.20	40 (54%) 0 0	61, 98, 111, 115	0
28	1	56/57 (98%)	-0.44	0 100 100	29, 37, 43, 50	0
29	2	46/50 (92%)	0.72	6 (13%) 7 6	39, 68, 101, 114	0
30	3	92/92 (100%)	0.29	1 (1%) 78 76	40, 62, 75, 83	0
31	I	70/162 (43%)	2.24	36 (51%) 0 0	105, 124, 141, 141	0
All	All	6646/7462 (89%)	0.11	305 (4%) 37 34	24, 55, 105, 153	0

The worst 5 of 305 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
31	I	133	THR	7.5
27	Z	26	VAL	7.3
23	V	1	THR	7.2
6	D	10	PHE	6.0
14	M	194	ALA	5.4

6.2 Non-standard residues in protein, DNA, RNA chains [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, 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
1	UR3	0	2619	21/22	0.97	0.06	36,39,42,48	0
1	OMU	0	2587	21/22	0.98	0.06	34,36,37,39	0
1	OMG	0	2588	24/25	0.98	0.06	33,36,38,39	0
1	1MA	0	628	23/24	0.98	0.06	28,32,33,35	0
1	PSU	0	2621	20/21	0.98	0.05	28,30,33,34	0

6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
33	MG	0	8049	1/1	0.67	0.24	92,92,92,92	0
35	NA	0	8566	1/1	0.67	0.26	66,66,66,66	0
35	NA	0	8568	1/1	0.68	0.24	71,71,71,71	0
33	MG	9	8095	1/1	0.71	0.15	76,76,76,76	0
35	NA	9	8551	1/1	0.73	0.25	50,50,50,50	0
35	NA	0	8524	1/1	0.76	0.31	62,62,62,62	0
35	NA	0	8529	1/1	0.78	0.17	77,77,77,77	0
35	NA	R	8586	1/1	0.80	0.63	95,95,95,95	0
35	NA	0	8577	1/1	0.81	0.27	71,71,71,71	0
35	NA	0	8540	1/1	0.82	0.13	58,58,58,58	0
33	MG	0	8087	1/1	0.83	0.13	66,66,66,66	0
35	NA	0	8582	1/1	0.83	0.23	79,79,79,79	0
35	NA	0	8584	1/1	0.84	0.12	62,62,62,62	0
33	MG	0	8090	1/1	0.84	0.26	69,69,69,69	0
35	NA	9	8583	1/1	0.84	0.18	65,65,65,65	0
35	NA	0	8526	1/1	0.84	0.14	58,58,58,58	0
35	NA	0	8571	1/1	0.86	0.34	65,65,65,65	0
35	NA	0	8508	1/1	0.86	0.16	56,56,56,56	0
35	NA	0	8585	1/1	0.86	0.28	51,51,51,51	0
33	MG	0	8114	1/1	0.87	0.17	67,67,67,67	0
35	NA	0	8563	1/1	0.87	0.18	57,57,57,57	0
33	MG	0	8094	1/1	0.88	0.17	77,77,77,77	0
35	NA	0	8533	1/1	0.88	0.15	39,39,39,39	0
35	NA	0	8503	1/1	0.89	0.17	47,47,47,47	0
35	NA	0	8564	1/1	0.89	0.13	53,53,53,53	0
35	NA	0	8570	1/1	0.90	0.38	69,69,69,69	0
32	GIR	0	9000	12/12	0.90	0.15	23,40,50,53	0
35	NA	0	8557	1/1	0.90	0.16	61,61,61,61	0
35	NA	0	8579	1/1	0.90	0.17	64,64,64,64	0
35	NA	0	8534	1/1	0.90	0.17	45,45,45,45	0
35	NA	S	8512	1/1	0.90	0.07	43,43,43,43	0
35	NA	0	8552	1/1	0.91	0.16	62,62,62,62	0
35	NA	0	8556	1/1	0.91	0.15	49,49,49,49	0
35	NA	0	8505	1/1	0.91	0.11	33,33,33,33	0
33	MG	0	8044	1/1	0.91	0.08	46,46,46,46	0
35	NA	0	8521	1/1	0.91	0.18	61,61,61,61	0
35	NA	0	8541	1/1	0.91	0.10	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8560	1/1	0.92	0.20	51,51,51,51	0
35	NA	0	8562	1/1	0.92	0.16	60,60,60,60	0
33	MG	0	8043	1/1	0.92	0.09	48,48,48,48	0
33	MG	0	8101	1/1	0.92	0.12	69,69,69,69	0
33	MG	0	8103	1/1	0.92	0.14	82,82,82,82	0
35	NA	0	8567	1/1	0.92	0.17	59,59,59,59	0
33	MG	0	8070	1/1	0.92	0.12	50,50,50,50	0
35	NA	R	8537	1/1	0.92	0.09	48,48,48,48	0
35	NA	0	8532	1/1	0.92	0.15	49,49,49,49	0
35	NA	0	8510	1/1	0.92	0.08	36,36,36,36	0
36	CL	3	8704	1/1	0.92	0.12	71,71,71,71	0
33	MG	0	8046	1/1	0.93	0.10	53,53,53,53	0
35	NA	0	8572	1/1	0.93	0.15	54,54,54,54	0
35	NA	0	8574	1/1	0.93	0.16	66,66,66,66	0
35	NA	C	8504	1/1	0.93	0.06	49,49,49,49	0
33	MG	T	8073	1/1	0.93	0.07	71,71,71,71	0
33	MG	0	8041	1/1	0.93	0.13	56,56,56,56	0
33	MG	0	8096	1/1	0.93	0.06	52,52,52,52	0
36	CL	0	8722	1/1	0.93	0.27	81,81,81,81	0
36	CL	A	8709	1/1	0.93	0.15	77,77,77,77	0
35	NA	0	8555	1/1	0.93	0.16	57,57,57,57	0
35	NA	0	8535	1/1	0.94	0.14	56,56,56,56	0
33	MG	0	8100	1/1	0.94	0.14	66,66,66,66	0
33	MG	0	8092	1/1	0.94	0.12	89,89,89,89	0
35	NA	0	8565	1/1	0.94	0.21	40,40,40,40	0
35	NA	0	8542	1/1	0.94	0.12	47,47,47,47	0
33	MG	0	8102	1/1	0.94	0.10	73,73,73,73	0
33	MG	0	8023	1/1	0.94	0.12	41,41,41,41	0
35	NA	M	8547	1/1	0.94	0.11	34,34,34,34	0
35	NA	0	8569	1/1	0.94	0.15	74,74,74,74	0
35	NA	R	8538	1/1	0.94	0.05	60,60,60,60	0
33	MG	0	8082	1/1	0.94	0.11	63,63,63,63	0
33	MG	0	8116	1/1	0.94	0.06	58,58,58,58	0
36	CL	0	8705	1/1	0.94	0.12	67,67,67,67	0
36	CL	0	8715	1/1	0.94	0.15	86,86,86,86	0
35	NA	0	8559	1/1	0.94	0.22	49,49,49,49	0
35	NA	0	8511	1/1	0.94	0.09	50,50,50,50	0
36	CL	J	8701	1/1	0.94	0.13	66,66,66,66	0
35	NA	0	8561	1/1	0.94	0.08	56,56,56,56	0
35	NA	0	8502	1/1	0.95	0.08	51,51,51,51	0
33	MG	0	8053	1/1	0.95	0.06	45,45,45,45	0
33	MG	0	8063	1/1	0.95	0.07	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8506	1/1	0.95	0.16	48,48,48,48	0
33	MG	0	8047	1/1	0.95	0.15	74,74,74,74	0
35	NA	0	8539	1/1	0.95	0.04	30,30,30,30	0
35	NA	A	8545	1/1	0.95	0.08	62,62,62,62	0
33	MG	0	8039	1/1	0.95	0.09	52,52,52,52	0
35	NA	H	8509	1/1	0.95	0.08	39,39,39,39	0
35	NA	J	8546	1/1	0.95	0.06	53,53,53,53	0
33	MG	0	8085	1/1	0.95	0.06	54,54,54,54	0
35	NA	0	8513	1/1	0.95	0.05	62,62,62,62	0
35	NA	0	8550	1/1	0.95	0.09	45,45,45,45	0
33	MG	A	8066	1/1	0.95	0.07	72,72,72,72	0
35	NA	0	8523	1/1	0.95	0.13	43,43,43,43	0
33	MG	B	8055	1/1	0.95	0.05	48,48,48,48	0
36	CL	0	8713	1/1	0.95	0.09	65,65,65,65	0
35	NA	0	8573	1/1	0.95	0.07	69,69,69,69	0
33	MG	0	8050	1/1	0.95	0.05	59,59,59,59	0
35	NA	0	8575	1/1	0.95	0.23	61,61,61,61	0
35	NA	0	8527	1/1	0.95	0.07	44,44,44,44	0
36	CL	J	8702	1/1	0.95	0.07	57,57,57,57	0
35	NA	0	8578	1/1	0.95	0.23	51,51,51,51	0
33	MG	0	8113	1/1	0.96	0.05	53,53,53,53	0
35	NA	0	8530	1/1	0.96	0.07	50,50,50,50	0
34	K	0	8401	1/1	0.96	0.18	85,85,85,85	0
35	NA	0	8558	1/1	0.96	0.23	82,82,82,82	0
33	MG	0	8088	1/1	0.96	0.04	38,38,38,38	0
35	NA	0	8514	1/1	0.96	0.14	38,38,38,38	0
35	NA	0	8516	1/1	0.96	0.09	54,54,54,54	0
35	NA	0	8536	1/1	0.96	0.06	55,55,55,55	0
35	NA	0	8520	1/1	0.96	0.04	34,34,34,34	0
35	NA	0	8581	1/1	0.96	0.06	48,48,48,48	0
33	MG	0	8057	1/1	0.96	0.07	45,45,45,45	0
36	CL	0	8717	1/1	0.96	0.06	65,65,65,65	0
33	MG	0	8051	1/1	0.96	0.09	59,59,59,59	0
33	MG	0	8104	1/1	0.96	0.07	65,65,65,65	0
35	NA	0	8507	1/1	0.96	0.11	59,59,59,59	0
33	MG	0	8112	1/1	0.96	0.09	42,42,42,42	0
36	CL	L	8710	1/1	0.96	0.09	60,60,60,60	0
36	CL	N	8707	1/1	0.96	0.06	66,66,66,66	0
36	CL	O	8708	1/1	0.96	0.12	73,73,73,73	0
35	NA	0	8553	1/1	0.96	0.06	30,30,30,30	0
33	MG	0	8097	1/1	0.97	0.06	34,34,34,34	0
35	NA	0	8543	1/1	0.97	0.08	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8544	1/1	0.97	0.04	28,28,28,28	0
35	NA	0	8549	1/1	0.97	0.10	51,51,51,51	0
33	MG	0	8042	1/1	0.97	0.07	38,38,38,38	0
35	NA	0	8531	1/1	0.97	0.07	50,50,50,50	0
36	CL	0	8714	1/1	0.97	0.06	54,54,54,54	0
35	NA	0	8518	1/1	0.97	0.10	42,42,42,42	0
36	CL	0	8716	1/1	0.97	0.14	56,56,56,56	0
33	MG	0	8072	1/1	0.97	0.05	63,63,63,63	0
33	MG	0	8075	1/1	0.97	0.04	44,44,44,44	0
33	MG	0	8076	1/1	0.97	0.05	55,55,55,55	0
33	MG	0	8093	1/1	0.97	0.05	56,56,56,56	0
35	NA	0	8525	1/1	0.97	0.06	56,56,56,56	0
35	NA	H	8522	1/1	0.97	0.26	67,67,67,67	0
33	MG	0	8045	1/1	0.97	0.09	53,53,53,53	0
33	MG	0	8064	1/1	0.97	0.09	30,30,30,30	0
36	CL	Y	8720	1/1	0.97	0.06	46,46,46,46	0
35	NA	Q	8548	1/1	0.97	0.04	42,42,42,42	0
37	CD	O	8605	1/1	0.97	0.06	93,93,93,93	0
35	NA	0	8515	1/1	0.98	0.08	42,42,42,42	0
35	NA	L	8580	1/1	0.98	0.09	57,57,57,57	0
33	MG	0	8117	1/1	0.98	0.03	32,32,32,32	0
35	NA	0	8517	1/1	0.98	0.06	51,51,51,51	0
33	MG	0	8062	1/1	0.98	0.05	54,54,54,54	0
33	MG	0	8098	1/1	0.98	0.08	40,40,40,40	0
33	MG	0	8048	1/1	0.98	0.06	54,54,54,54	0
33	MG	0	8052	1/1	0.98	0.04	54,54,54,54	0
36	CL	0	8703	1/1	0.98	0.07	58,58,58,58	0
33	MG	Y	8109	1/1	0.98	0.06	37,37,37,37	0
36	CL	0	8712	1/1	0.98	0.06	49,49,49,49	0
33	MG	0	8067	1/1	0.98	0.06	52,52,52,52	0
35	NA	0	8576	1/1	0.98	0.09	46,46,46,46	0
35	NA	0	8554	1/1	0.98	0.14	40,40,40,40	0
35	NA	0	8501	1/1	0.98	0.11	32,32,32,32	0
33	MG	0	8089	1/1	0.98	0.06	74,74,74,74	0
35	NA	0	8528	1/1	0.98	0.14	42,42,42,42	0
33	MG	0	8014	1/1	0.98	0.04	32,32,32,32	0
36	CL	B	8719	1/1	0.98	0.06	51,51,51,51	0
33	MG	0	8106	1/1	0.98	0.03	65,65,65,65	0
33	MG	0	8108	1/1	0.98	0.11	70,70,70,70	0
36	CL	J	8721	1/1	0.98	0.05	58,58,58,58	0
33	MG	0	8110	1/1	0.98	0.04	27,27,27,27	0
33	MG	0	8024	1/1	0.98	0.04	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8059	1/1	0.98	0.05	43,43,43,43	0
33	MG	0	8061	1/1	0.98	0.04	41,41,41,41	0
33	MG	0	8115	1/1	0.98	0.04	52,52,52,52	0
33	MG	0	8081	1/1	0.98	0.05	49,49,49,49	0
33	MG	0	8022	1/1	0.99	0.03	38,38,38,38	0
33	MG	0	8071	1/1	0.99	0.03	69,69,69,69	0
33	MG	0	8011	1/1	0.99	0.07	27,27,27,27	0
33	MG	0	8074	1/1	0.99	0.02	36,36,36,36	0
33	MG	0	8012	1/1	0.99	0.04	39,39,39,39	0
33	MG	0	8025	1/1	0.99	0.02	37,37,37,37	0
33	MG	0	8111	1/1	0.99	0.03	42,42,42,42	0
33	MG	0	8079	1/1	0.99	0.03	37,37,37,37	0
33	MG	0	8080	1/1	0.99	0.06	45,45,45,45	0
33	MG	0	8027	1/1	0.99	0.03	44,44,44,44	0
33	MG	0	8029	1/1	0.99	0.03	35,35,35,35	0
33	MG	0	8084	1/1	0.99	0.04	47,47,47,47	0
33	MG	0	8031	1/1	0.99	0.03	34,34,34,34	0
33	MG	0	8086	1/1	0.99	0.04	52,52,52,52	0
33	MG	0	8033	1/1	0.99	0.02	31,31,31,31	0
33	MG	0	8035	1/1	0.99	0.03	46,46,46,46	0
33	MG	B	8056	1/1	0.99	0.03	55,55,55,55	0
33	MG	K	8069	1/1	0.99	0.03	58,58,58,58	0
33	MG	0	8037	1/1	0.99	0.02	43,43,43,43	0
33	MG	0	8058	1/1	0.99	0.04	39,39,39,39	0
33	MG	3	8078	1/1	0.99	0.04	43,43,43,43	0
33	MG	0	8091	1/1	0.99	0.04	51,51,51,51	0
34	K	0	8402	1/1	0.99	0.18	57,57,57,57	0
33	MG	0	8006	1/1	0.99	0.03	33,33,33,33	0
33	MG	0	8060	1/1	0.99	0.07	40,40,40,40	0
33	MG	0	8040	1/1	0.99	0.03	60,60,60,60	0
33	MG	0	8015	1/1	0.99	0.03	35,35,35,35	0
36	CL	M	8718	1/1	0.99	0.05	47,47,47,47	0
33	MG	0	8016	1/1	0.99	0.04	40,40,40,40	0
33	MG	0	8018	1/1	0.99	0.06	50,50,50,50	0
36	CL	Q	8711	1/1	0.99	0.07	55,55,55,55	0
36	CL	R	8706	1/1	0.99	0.04	46,46,46,46	0
33	MG	0	8099	1/1	0.99	0.04	45,45,45,45	0
33	MG	0	8021	1/1	0.99	0.03	30,30,30,30	0
33	MG	0	8068	1/1	0.99	0.04	61,61,61,61	0
37	CD	Z	8603	1/1	0.99	0.03	98,98,98,98	0
37	CD	1	8602	1/1	0.99	0.05	63,63,63,63	0
37	CD	3	8604	1/1	0.99	0.02	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8007	1/1	1.00	0.02	22,22,22,22	0
33	MG	0	8038	1/1	1.00	0.02	34,34,34,34	0
33	MG	0	8019	1/1	1.00	0.04	35,35,35,35	0
33	MG	0	8020	1/1	1.00	0.02	33,33,33,33	0
33	MG	A	8065	1/1	1.00	0.03	41,41,41,41	0
33	MG	0	8008	1/1	1.00	0.03	37,37,37,37	0
33	MG	0	8009	1/1	1.00	0.01	35,35,35,35	0
33	MG	0	8010	1/1	1.00	0.02	33,33,33,33	0
33	MG	0	8002	1/1	1.00	0.04	34,34,34,34	0
33	MG	0	8003	1/1	1.00	0.03	35,35,35,35	0
33	MG	0	8026	1/1	1.00	0.03	26,26,26,26	0
33	MG	0	8013	1/1	1.00	0.02	38,38,38,38	0
33	MG	0	8028	1/1	1.00	0.02	38,38,38,38	0
33	MG	0	8004	1/1	1.00	0.04	29,29,29,29	0
33	MG	0	8077	1/1	1.00	0.02	33,33,33,33	0
33	MG	0	8030	1/1	1.00	0.02	25,25,25,25	0
33	MG	0	8005	1/1	1.00	0.02	33,33,33,33	0
33	MG	0	8032	1/1	1.00	0.07	28,28,28,28	0
33	MG	0	8107	1/1	1.00	0.02	36,36,36,36	0
33	MG	0	8001	1/1	1.00	0.01	36,36,36,36	0
33	MG	0	8083	1/1	1.00	0.01	43,43,43,43	0
33	MG	0	8054	1/1	1.00	0.02	37,37,37,37	0
37	CD	U	8601	1/1	1.00	0.02	62,62,62,62	0
33	MG	0	8034	1/1	1.00	0.02	33,33,33,33	0
33	MG	0	8017	1/1	1.00	0.01	26,26,26,26	0
33	MG	0	8036	1/1	1.00	0.03	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.