



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:24 PM BST

PDB ID : 3J7O  
EMDB ID: : EMD-2649  
Title : Structure of the mammalian 60S ribosomal subunit  
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.  
Deposited on : 2014-08-01  
Resolution : 3.50 Å(reported)  
Based on PDB ID : 3J3B, 3J3F

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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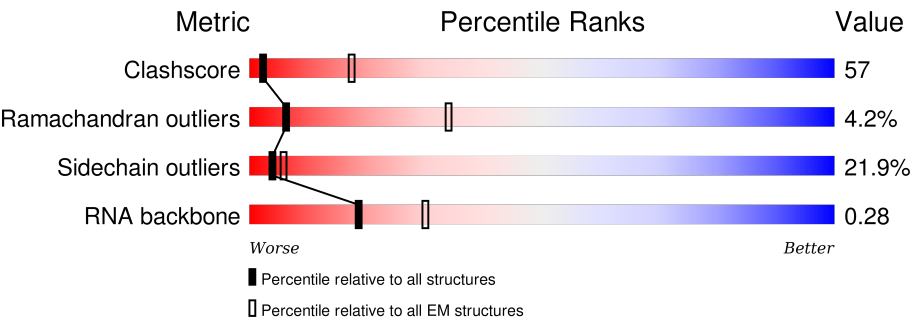
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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.



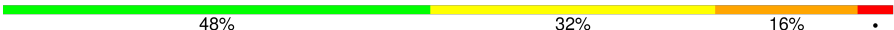





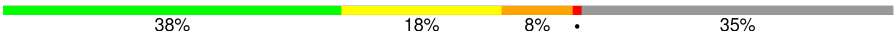





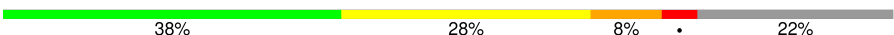












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	5	3664	8% 44% 35% 12%
2	7	120	18% 56% 21% 5%
3	8	156	7% 53% 26% 13%
4	A	257	50% 27% 12% 6% 5%
5	B	394	48% 34% 14% 5%
6	C	367	55% 31% 11% .
7	D	297	46% 35% 12% 5% .
8	E	236	47% 27% 19% 6%













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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	 78%15%5% ..
35	g	117	 77%19% ..
36	h	123	 80%12%6% ..
37	i	105	 76%17% ..
38	j	86	 73%21%6%
39	k	70	 71%27% ..
40	l	51	 76%18% ..
41	m	128	 31%8% ..59%
42	n	25	 72%20%8%
43	o	106	 69%23%6% ..
44	p	91	 82%15% ..
45	r	125	 74%22% ..

## 2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 136815 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called Ribosomal protein eL27.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 39 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	8	4	Total	Mg	0
			4	4	
46	7	5	Total	Mg	0
			5	5	
46	P	1	Total	Mg	0
			1	1	
46	V	1	Total	Mg	0
			1	1	
46	5	119	Total	Mg	0
			119	119	

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	o	1	Total	Zn	0
			1	1	
47	j	1	Total	Zn	0
			1	1	

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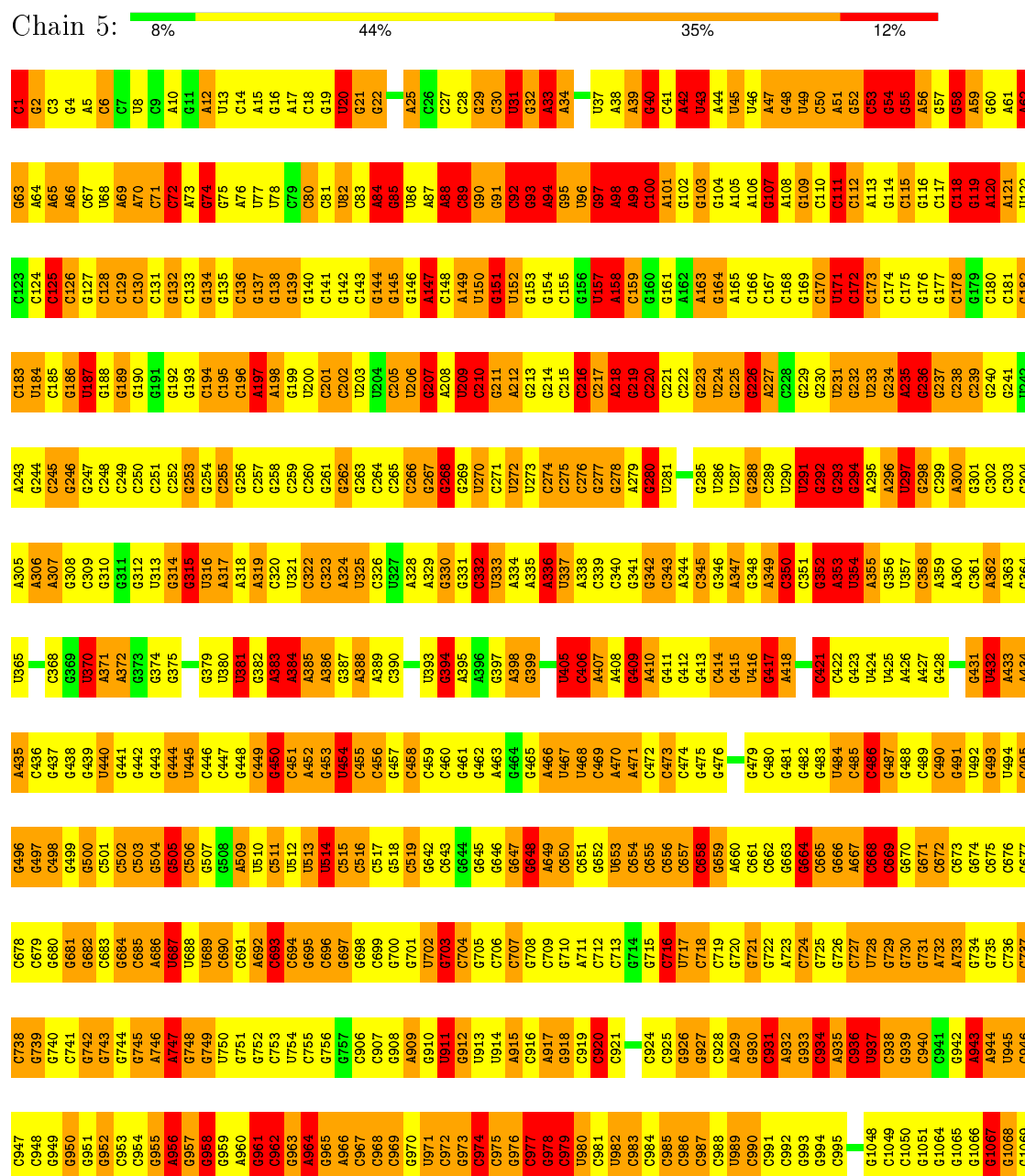
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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
47	m	1	1	1	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: 28S ribosomal RNA



U2080	A2017	A1956	G1895	U1834	U1773	U1693	G1571	C1507	C1446	C1386	A1326	G1265	G1196	G1070
C2081	C2018	U1959	A1896	G1835	C1774	C1694	U1572	A1508	C1447	A1387	C1327	G1266	C1197	C1071
G2082	C2019	U1959	A1897	G1836	A1776	U1695	U1573	G1509	C1448	A1388	G1328	G1267	C1197	C1072
C2084	U2020	A1960	A1898	A1837	A1775	C1696	G1574	G1510	U1449	U1389	G1329	G1268	G1199	G1073
G2085	G2021	G1961	G1899	A1838	C1777	A1697	U1575	U1511	G1450	A1390	A1330	G1269	G1200	G1074
G2086	G2022	A1962	C1900	U1839	C1778	C1698	U1576	G1512	G1451	G1391	C1331	A1270	U1201	G1075
C2087	G2023	G1963	C1901	G1840	U1779	U1699	G1577	U1513	A1452	A1392	C1332	G1271	C1202	G1076
G2088	G2024	A1964	G1902	C	A1780	C1718	U1578	U1514	G1453	G1393	A1333	G1272	G1203	C1077
A2025	A2025	G1965	G1903	G1842	U1781	A1719	U1579	A1515	G1454	G1394	A1334	G1273	C1204	A1078
G2089	G2026	G1966	G1904	A1843	U1782	C1720	C1580	G1516	G1455	U1395	G1335	A1274	G1205	C1079
U2027	U2027	A1967	U1905	G1844	C1783	G1721	C1581	G1517	C1456	G1396	G1336	G1275	C1206	C1080
C2091	C2091	G1968	U1906	U1845	U1784	A1722	U1582	A1518	G1457	A1397	A1337	C1276	C1207	C1081
G2092	G2092	A1907	G1907	G1846	U1785	C1723	U1583	A1519	C1458	A1398	G1338	G1277	G1208	C1082
A2093	A2093	A1970	A1908	C1847	A1786	G1724	U1584	C1520	A1459	G1399	U1339	C1278	U1209	U1083
G2094	G2034	G1971	G1909	C1848	U1787	U1725	C1585	G1521	C1460	A1340	C1340	A1279	C1210	C1084
A2095	C2035	G1972	G1910	A1849	A1788	U1726	U1586	G1522	C1401	U1341	U1341	C1280	C1211	C1085
G2096	G2036	G1973	A1850	C1850	C1789	U1727	U1587	A1523	C1402	A1342	A1342	G1281	G1212	C1086
U2097	C2037	U1974	G1912	G1851	U1790	U1728	U1588	A1524	C1403	A1343	A1343	G1282	G1213	A1087
G2098	U2038	G1975	C1913	U1852	U1791	A1729	C1589	A1525	G1465	G1404	C1344	G1283	C1214	C1088
G2099	G2039	G1976	G1853	G	U1794	U1730	U1590	A1526	G1466	C1405	C1345	G1284	C1215	G1089
A2100	A2040	U1977	G1854	G1854	A1795	G1733	U1591	U1528	C1467	A1406	A1346	G1285	C1216	G1090
C2101	A2041	A1978	G1855	G1855	U1796	G1734	C1594	G1529	C1468	C1407	C1347	G1286	C1217	C1091
G2102	A2042	C1978	C1856	C1856	U1797	A1735	G1595	G1530	C1469	G1408	U1348	G1287	G1218	C1092
G2103	A2043	U1980	G1919	C1857	G1797	U1736	U1596	A1534	G1470	C1409	G1349	G1288	G1219	C1093
G2104	U2044	G1981	C1920	A1858	G1798	A1743	U1597	C1535	U1471	U1410	C1350	G1289	G1220	G1094
A2105	G2045	G1982	C1921	C1859	G1799	U1744	C1603	U1542	C1472	C1411	G1351	G1290	G1221	A1095
G2106	G2046	A1983	G1922	U1860	U1800	G1739	C1604	U1543	C1473	G1412	C1352	G1291	A1222	C1096
C2107	A2047	A1984	A1923	A1861	A1801	C1740	U1598	U1538	C1474	C1413	G1353	C1292	G1232	C1097
G2108	U2048	G1979	U1918	C1856	U1796	G1741	A1600	G1545	C1481	G1420	G1360	G1293	G1233	G1098
G2109	G2049	U1986	G1925	C1857	A1803	A1742	A1601	C1540	G1475	G1421	G1361	G1294	G1234	C1099
C2110	G2050	C1987	C1926	G1865	A1804	A1743	C1603	C1541	C1477	G1416	G1362	G1295	G1235	U1100
G2111	G2051	U1988	U1927	U1866	A1805	U1744	G1602	U1542	C1478	C1417	C1367	G1296	C1236	G1167
C2112	G2052	G1989	C1928	A1867	G1806	G1745	U1604	U1543	C1479	C1418	G1368	U1297	C1237	G1168
G2113	C2053	A1990	A1929	C1869	C1807	U1746	C1666	G1544	G1480	G1419	G1359	C1298	A1238	G1169
G2114	U2054	A1991	U1930	A1868	A1808	U1747	C1667	G1545	C1482	G1420	G1360	G1299	C1239	G1170
G2115	G2055	U1992	C1931	C1870	C1809	U1748	A1669	G1546	G1483	G1421	G1361	G1300	G1240	G1171
C2116	G2056	C1993	A1932	A1871	G1810	A1749	C1670	A1547	C1483	G1422	G1362	C1301	G1241	C1172
G2117	A2057	C1994	G1933	G1872	G1811	G1750	C1610	G1548	G1484	U1423	C1363	U1302	G1242	G1173
G2118	G2058	G1995	A1934	A1873	C1812	A1751	C1611	G1549	C1485	G1424	U1364	A1303	C1243	G1174
C2119	C2059	C1996	C1935	A1874	U1813	G1752	G1612	G1550	C1486	G1425	G1365	C1304	G1244	A1175
G2120	G2060	U1997	G1936	C1875	G1814	G1753	A1613	C1551	G1487	G1426	G1366	C1305	G1245	C1176
C2121	U2061	A1998	C1937	U1876	G1815	U1754	C1614	G1552	G1488	A1427	C1367	C1306	G1246	U1177
G2122	C2062	A1999	G1938	G1877	C1816	C1755	C1615	A1553	G1489	U1428	A1368	A1307	U1247	G1178
C2123	G2063	G2000	A1939	G1878	U1817	U1756	U1616	A1554	G1490	C1429	C1369	C1308	U1247	U1179
G2124	G2064	G2001	G1940	C1879	G1818	U1757	U1617	G1555	A1491	C1430	G1370	C1309	C1249	C1180
C2125	G2065	A2002	A1942	G1880	G1819	G1758	G1618	C1556	G1492	C1431	A1371	C1310	C1250	C1181
G2126	C2066	G2003	C1943	C1881	C1820	G1759	A1679	C1557	G1493	G1432	A1372	G1311	C1251	C1182
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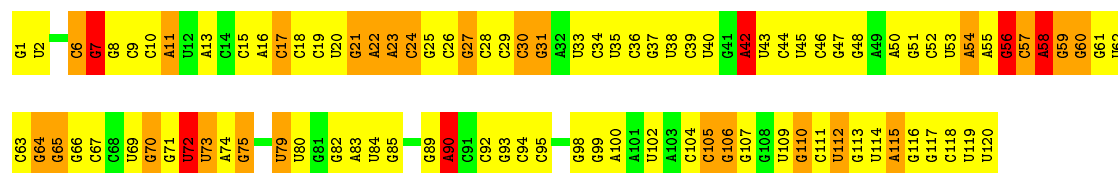
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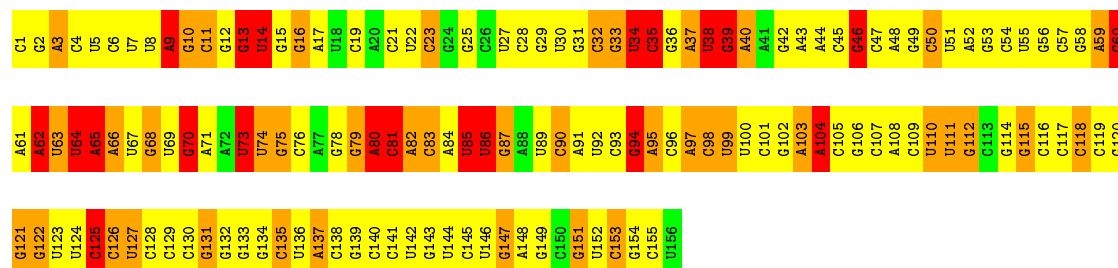
- Molecule 2: 5S ribosomal RNA

Chain 7: 



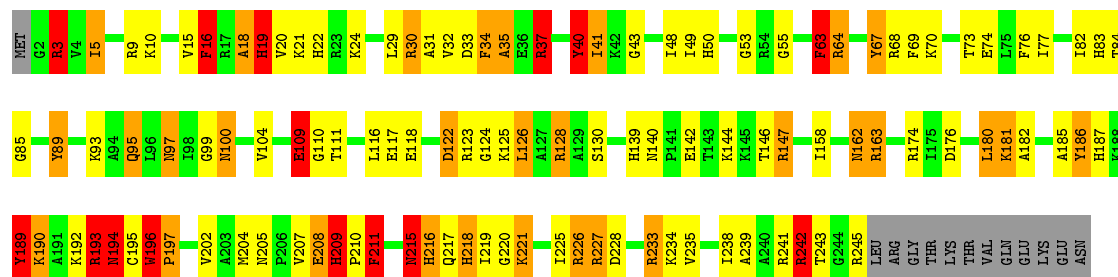
- Molecule 3: 5.8S ribosomal RNA

Chain 8: 

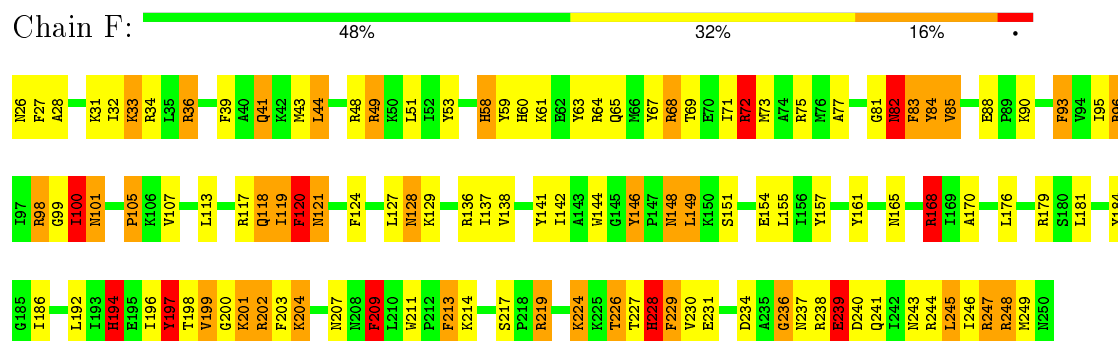


- Molecule 4: Ribosomal protein uL2

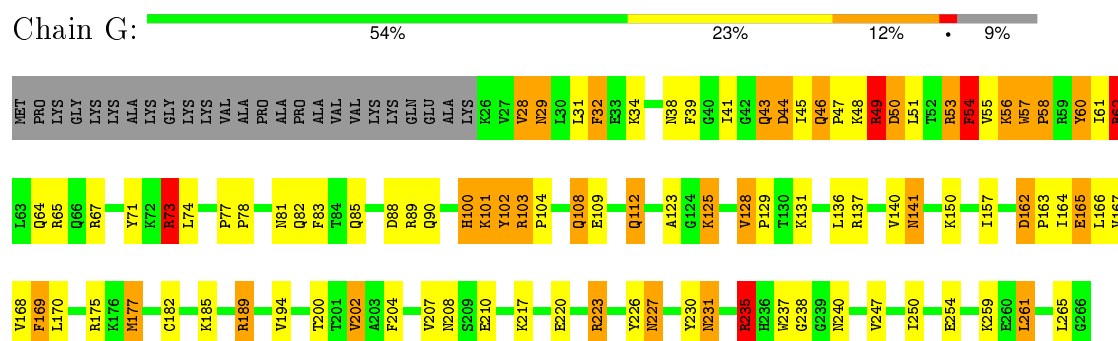
Chain A: 



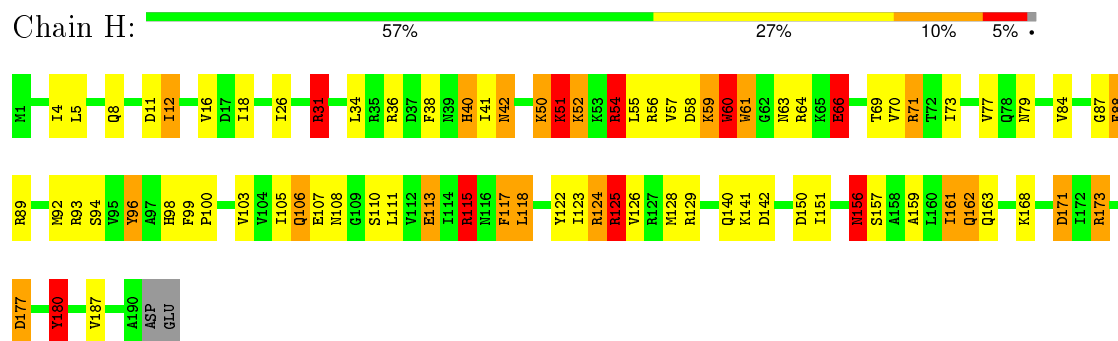




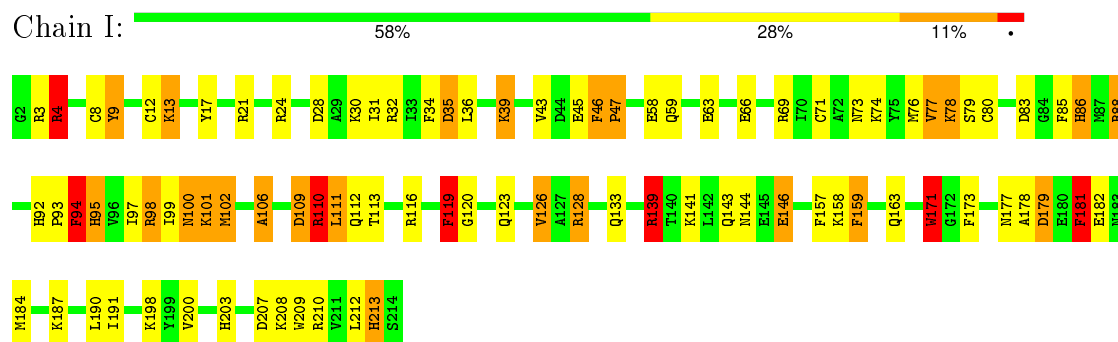
- Molecule 10: Ribosomal protein eL8



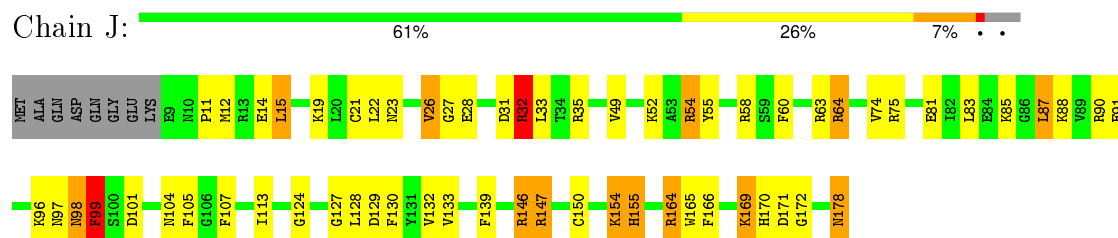
- Molecule 11: Ribosomal protein uL6



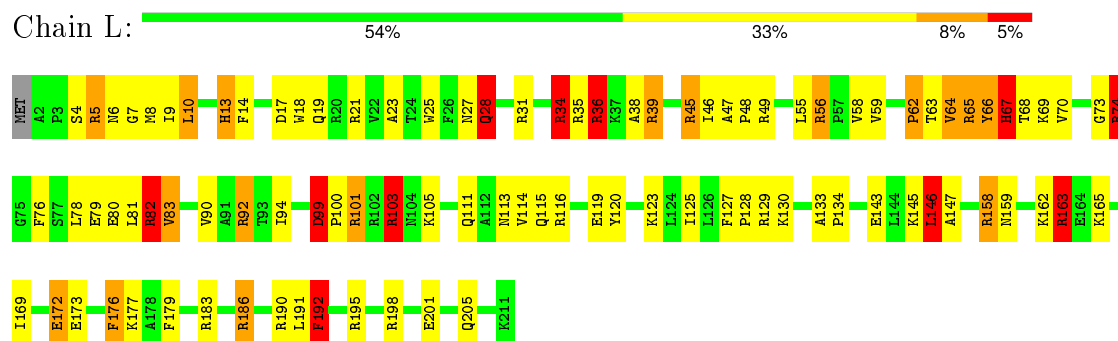
- Molecule 12: Ribosomal protein uL16



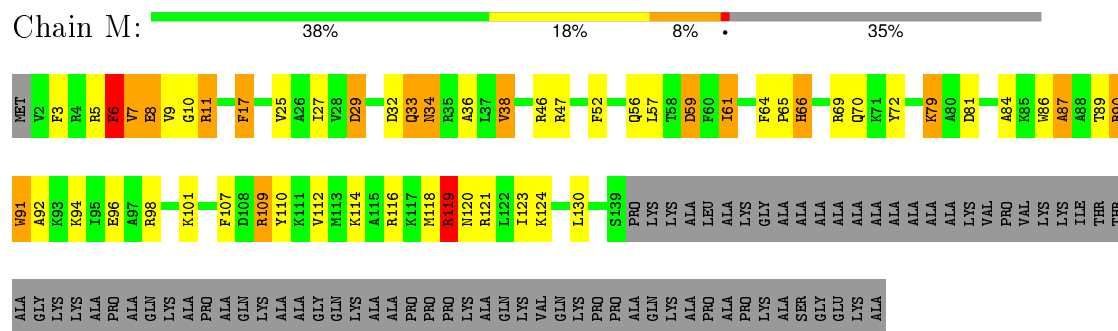
- Molecule 13: Ribosomal protein uL5



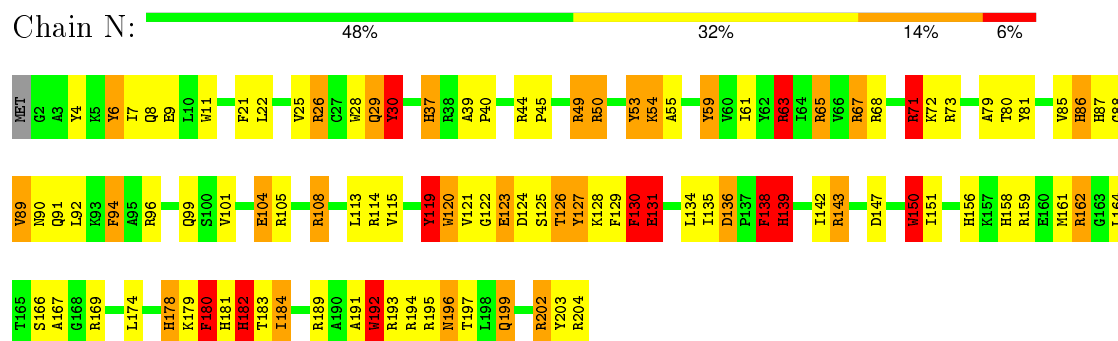
• Molecule 14: Ribosomal protein eL13



• Molecule 15: Ribosomal protein eL14

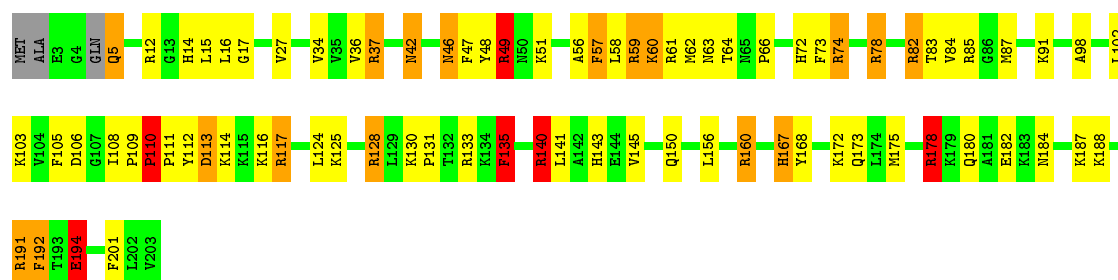


• Molecule 16: Ribosomal protein eL15



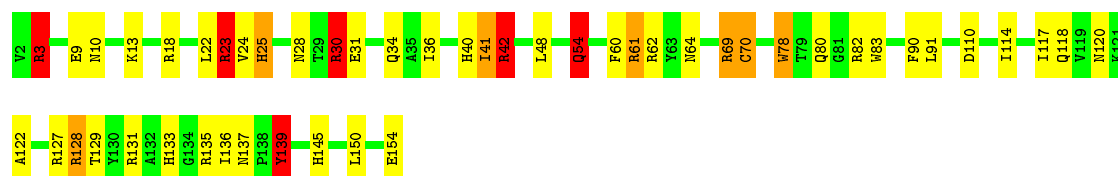
• Molecule 17: Ribosomal protein uL13





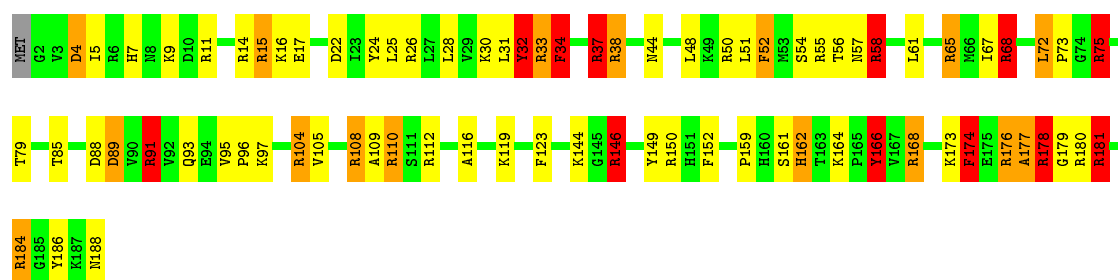
• Molecule 18: Ribosomal protein uL22

Chain P: 68% 24% 5% .



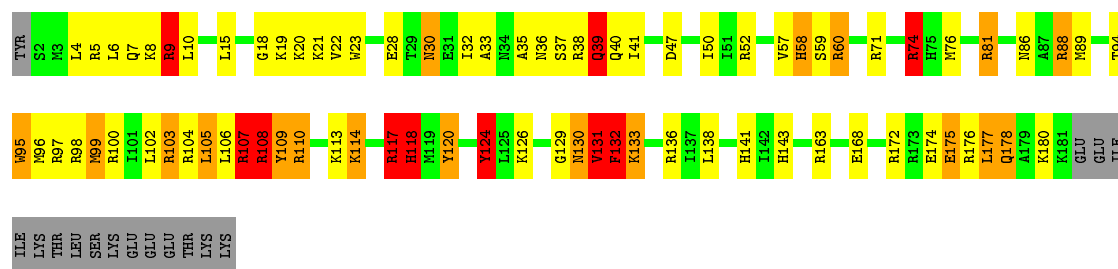
• Molecule 19: Ribosomal protein eL18

Chain Q: 58% 27% 9% 6% .



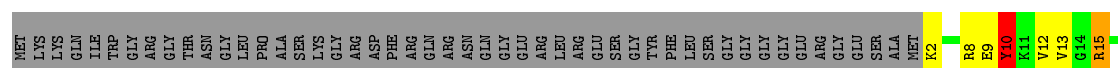
• Molecule 20: Ribosomal protein eL19

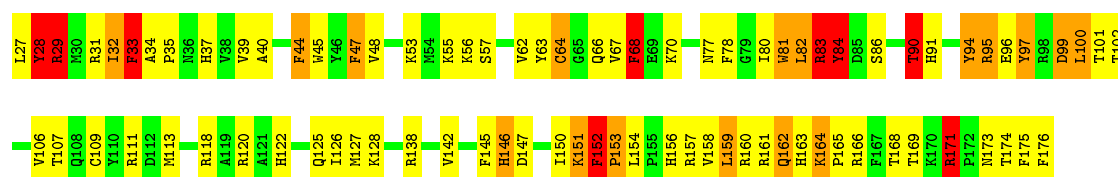
Chain R: 51% 27% 9% 5% 8%



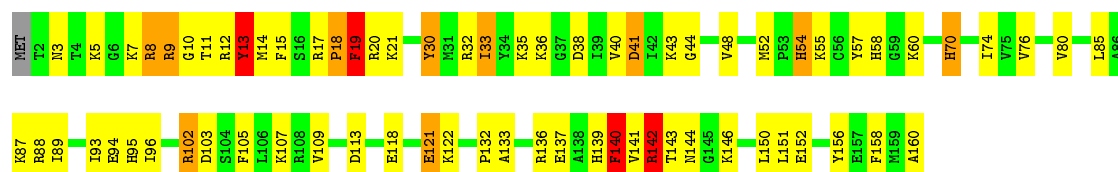
• Molecule 21: Ribosomal protein eL20

Chain S: 38% 28% 8% . 22%

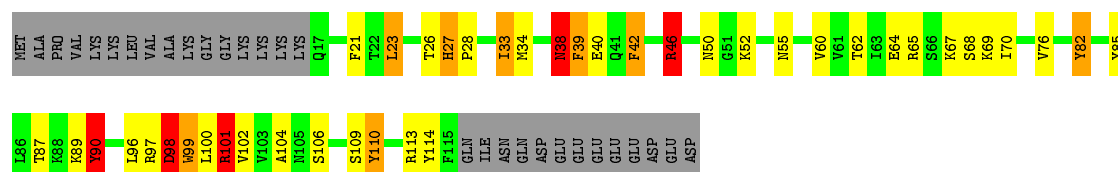




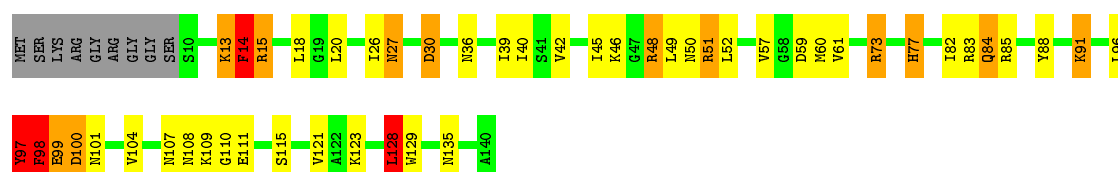
• Molecule 22: Ribosomal protein eL21



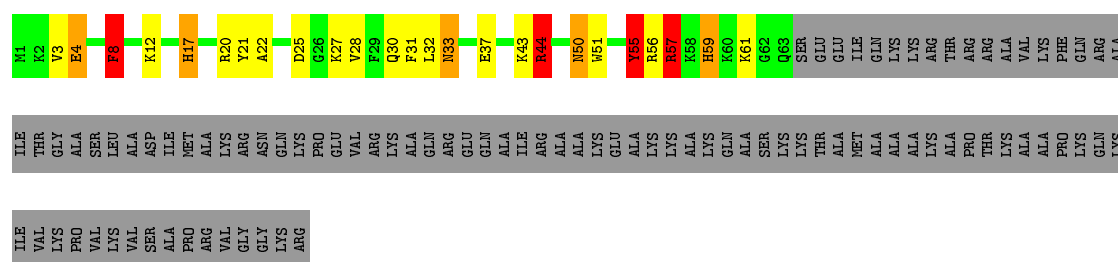
• Molecule 23: Ribosomal protein eL22



• Molecule 24: Ribosomal protein uL14



• Molecule 25: Ribosomal protein eL24



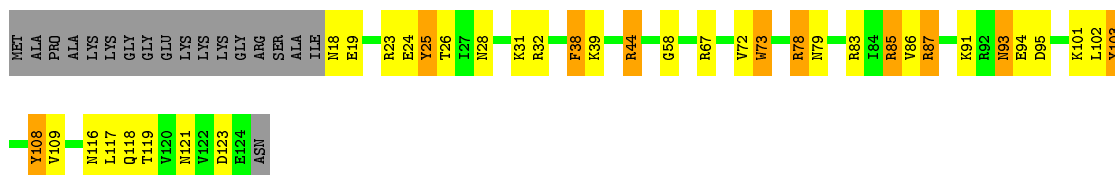
• Molecule 26: Ribosomal protein uL23





GLU  
LYS

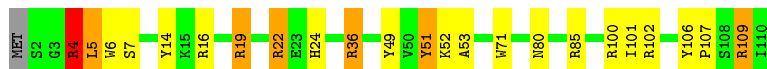
- Molecule 32: Ribosomal protein eL31

Chain d:  56% 22% 8% 14%


- Molecule 33: Ribosomal protein eL32

Chain e:  68% 23% 5% 5%


- Molecule 34: Ribosomal protein eL33

Chain f:  78% 15% 5% 2%

- Molecule 35: Ribosomal protein eL34

Chain g:  77% 19% 4% 2%

- Molecule 36: Ribosomal protein uL29

Chain h:  80% 12% 6% 2%

- Molecule 37: Ribosomal protein eL36

Chain i:  76% 17% 7% 2%



- Molecule 38: Ribosomal protein eL37

Chain j:  73% 21% 6%



- Molecule 39: Ribosomal protein eL38

Chain k:  71% 27% 2%



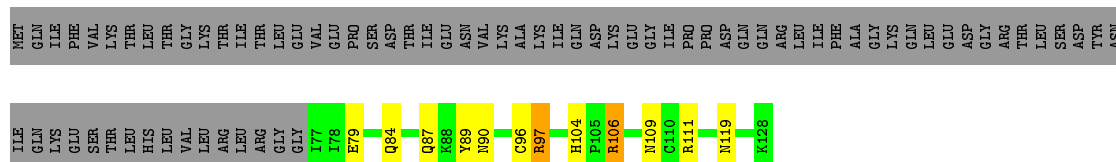
- Molecule 40: Ribosomal protein eL39

Chain l:  76% 18% 6%



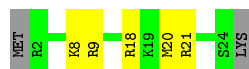
- Molecule 41: Ribosomal protein eL40

Chain m:  31% 8% 59%



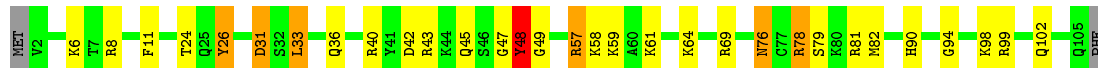
- Molecule 42: Ribosomal protein eL41

Chain n:  72% 20% 8%




- Molecule 43: Ribosomal protein eL42

Chain o:  69% 23% 6% 2%



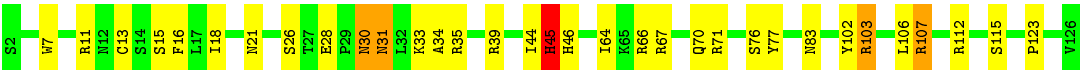
- Molecule 44: Ribosomal protein eL43

Chain p:  82% 15% 3%



● Molecule 45: Ribosomal protein eL28

Chain r:  74% 22% . .



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	80019	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	5	0.64	80/87792 (0.1%)	1.13	737/136945 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	11/1849 (0.6%)
14	L	0.70	2/1734 (0.1%)	1.12	15/2318 (0.6%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
2	7	0.53	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	20/2002 (1.0%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.71	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	19/1504 (1.3%)
28	Z	0.63	0/1130	1.11	11/1507 (0.7%)
29	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
3	8	0.68	3/3701 (0.1%)	1.19	42/5766 (0.7%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
33	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.22	14/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	k	0.59	0/575	0.97	1/761 (0.1%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	l	0.70	0/454	1.14	4/599 (0.7%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.49	0/223	1.01	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
5	B	0.81	8/3214 (0.2%)	1.16	25/4308 (0.6%)
6	C	0.73	3/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	28/3252 (0.9%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	26/2539 (1.0%)
All	All	0.68	164/147634 (0.1%)	1.15	1311/218352 (0.6%)

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	5	1	155
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5
2	7	0	2
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	8	0	11
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
4	A	0	6
43	o	0	6
44	p	0	1
45	r	0	5
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
All	All	1	335

The worst 5 of 164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	41.50	2.10	1.61
10	G	109	GLU	CD-OE2	16.18	1.43	1.25
11	H	66	GLU	CD-OE1	15.80	1.43	1.25
34	f	6	TRP	CB-CG	-15.72	1.22	1.50
30	b	16	TRP	CB-CG	-13.53	1.25	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	60	G	N9-C1'-C2'	16.18	135.03	114.00
38	j	11	ARG	NE-CZ-NH2	-13.77	113.42	120.30
19	Q	37	ARG	NE-CZ-NH2	12.86	126.73	120.30
1	5	92	C	N1-C1'-C2'	-12.64	97.57	114.00
12	I	139	ARG	CG-CD-NE	12.31	137.66	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 335 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	78486	0	39661	10164	0
2	7	2558	0	1296	303	0
3	8	3314	0	1683	486	0
4	A	1868	0	1959	155	0
5	B	3147	0	3280	217	0
6	C	2919	0	3100	159	0
7	D	2380	0	2412	172	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	172	0
10	G	1934	0	2086	106	0
11	H	1518	0	1601	84	0
12	I	1713	0	1752	88	0
13	J	1359	0	1390	62	0
14	L	1703	0	1818	75	0
15	M	1131	0	1209	69	0
16	N	1701	0	1749	115	0
17	O	1651	0	1786	88	0
18	P	1242	0	1269	55	0
19	Q	1506	0	1623	73	0
20	R	1508	0	1664	94	0
21	S	1454	0	1496	117	0
22	T	1298	0	1366	74	0
23	U	808	0	831	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	V	979	0	1039	51	0
25	W	528	0	541	53	0
26	X	976	0	1053	37	0
27	Y	1115	0	1205	61	0
28	Z	1107	0	1182	49	0
29	a	1163	0	1211	0	0
30	b	610	0	650	0	0
31	c	732	0	769	0	0
32	d	888	0	930	0	0
33	e	1053	0	1147	0	0
34	f	876	0	912	0	0
35	g	906	0	1002	0	0
36	h	1015	0	1149	0	0
37	i	832	0	917	0	0
38	j	706	0	743	0	0
39	k	569	0	637	0	0
40	l	444	0	483	0	0
41	m	429	0	466	0	0
42	n	222	0	264	0	0
43	o	851	0	922	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	5	119	0	0	0	0
46	7	5	0	0	0	0
46	8	4	0	0	0	0
46	P	1	0	0	0	0
46	V	1	0	0	0	0
47	j	1	0	0	0	0
47	m	1	0	0	0	0
47	o	1	0	0	0	0
All	All	136815	0	98126	12485	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 57.

The worst 5 of 12485 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:100:C:C5	1:5:101:A:C8	2.00	1.49
1:5:1266:G:N2	1:5:2111:G:N3	1.67	1.41
1:5:1174:G:N2	1:5:1175:A:N7	1.67	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2361:G:O6	18:P:25:HIS:CD2	1.74	1.38
1:5:4283:G:C2	1:5:4284:C:C6	2.13	1.37

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 PDB entries followed by that with respect to all EM entries.

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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	4	36
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	13
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	3	33
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	15
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	5
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	30
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	6	42
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	9	50
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	2	21
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	3	28
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	2	25
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	13	56
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	42
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	13	56
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	15	60
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	44
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	49
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	10	51
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	9	50
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	8	48
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	12	55
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	54
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	30
28	Z	133/136 (98%)	113 (85%)	16 (12%)	4 (3%)	5	42
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	24
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	24
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	31
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	35
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	24	70
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	29
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	11	53
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	7	46
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	51
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	3	28
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	15
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	32
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	22
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	63
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	3	27
All	All	6371/7060 (90%)	5341 (84%)	764 (12%)	266 (4%)	6	32

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	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 PDB entries followed by that with respect to all EM entries.

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	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	4
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	8
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	7
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	3
8	E	209/209 (100%)	158 (76%)	51 (24%)	1	5
9	F	194/194 (100%)	145 (75%)	49 (25%)	1	4
10	G	206/226 (91%)	158 (77%)	48 (23%)	1	5
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	4
12	I	180/180 (100%)	136 (76%)	44 (24%)	1	5
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	9
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	5
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	12
16	N	171/172 (99%)	129 (75%)	42 (25%)	1	5
17	O	172/174 (99%)	146 (85%)	26 (15%)	3	21
18	P	134/134 (100%)	112 (84%)	22 (16%)	3	17
19	Q	163/164 (99%)	132 (81%)	31 (19%)	2	10
20	R	159/175 (91%)	120 (76%)	39 (24%)	1	5
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	6
22	T	139/140 (99%)	112 (81%)	27 (19%)	2	10
23	U	89/114 (78%)	67 (75%)	22 (25%)	1	5
24	V	101/107 (94%)	77 (76%)	24 (24%)	1	5
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	5
26	X	107/133 (80%)	89 (83%)	18 (17%)	2	15
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	6
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	9
29	a	119/120 (99%)	102 (86%)	17 (14%)	4	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	3
31	c	79/97 (81%)	60 (76%)	19 (24%)	1	5
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	7
34	f	88/89 (99%)	73 (83%)	15 (17%)	2	15
35	g	98/100 (98%)	79 (81%)	19 (19%)	2	10
36	h	109/110 (99%)	92 (84%)	17 (16%)	3	20
37	i	86/89 (97%)	71 (83%)	15 (17%)	2	14
38	j	73/73 (100%)	60 (82%)	13 (18%)	2	13
39	k	64/65 (98%)	52 (81%)	12 (19%)	2	11
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	15
41	m	48/116 (41%)	36 (75%)	12 (25%)	1	4
42	n	22/24 (92%)	17 (77%)	5 (23%)	1	6
43	o	92/94 (98%)	70 (76%)	22 (24%)	1	5
44	p	74/74 (100%)	61 (82%)	13 (18%)	2	13
45	r	109/109 (100%)	86 (79%)	23 (21%)	1	8
All	All	5536/6001 (92%)	4323 (78%)	1213 (22%)	4	7

5 of 1213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	L	162	LYS
19	Q	65	ARG
39	k	27	LYS
15	M	38	VAL
16	N	195	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 176 such sidechains are listed below:

Mol	Chain	Res	Type
15	M	48	GLN
18	P	145	HIS
43	o	21	HIS
16	N	8	GLN
17	O	96	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3664 (99%)	1612 (44%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3921/3940 (99%)	1704 (43%)	660 (16%)

5 of 1704 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2116	C
1	5	2576	G
1	5	4938	A
1	5	2250	C
1	5	2361	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 133 ligands modelled in this entry, 133 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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.