



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:58 AM UTC

PDB ID : 1YJ9 / pdb_00001yj9
Title : Crystal Structure Of The Mutant 50S Ribosomal Subunit Of Haloarcula Marismortui Containing a three residue deletion in L22
Authors : Tu, D.; Blaha, G.; Moore, P.B.; Steitz, T.A.
Deposited on : 2005-01-13
Resolution : 2.80 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

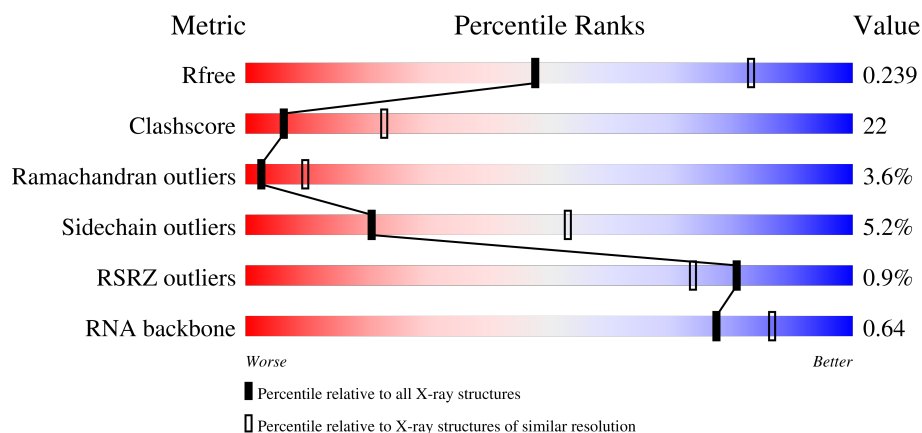
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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.



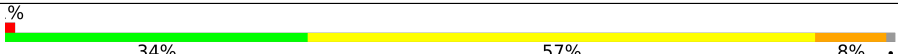
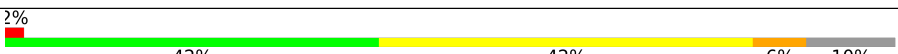
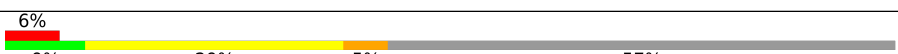
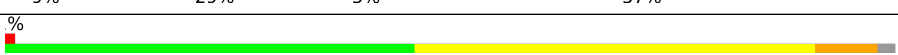
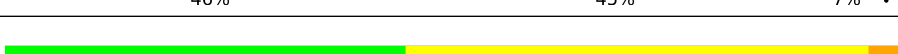
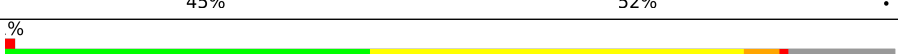
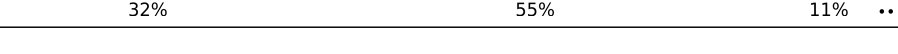
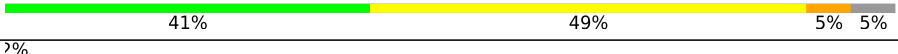
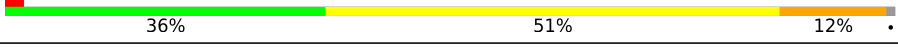
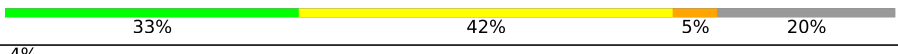
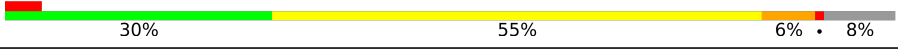
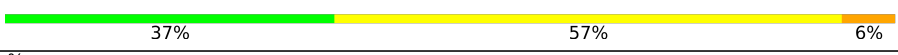
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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	50% 38% 6% 6%
2	9	122	2% 39% 52% 9% .
3	A	240	% 47% 42% 10% .
4	B	338	41% 49% 8% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	177	
11	I	162	
12	J	145	
13	K	132	
14	L	165	
15	M	195	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	152	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	2	50	
31	3	92	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	NA	R	8586	-	-	-	X
35	CL	J	8801	-	-	X	-
35	CL	J	8802	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 99031 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	1	0
			59041	26358	10875	19062	2746			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	modified residue	GB 55229667
0	2587	OMU	U	modified residue	GB 55229667
0	2588	OMG	G	modified residue	GB 55229667
0	2619	UR3	U	modified residue	GB 55229667
0	2621	PSU	U	modified residue	GB 55229667

- 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
			2599	1160	471	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 L4E.

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

- 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 ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

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

- 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
			1282	798	240	238	6			

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L11P.

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

- Molecule 12 is a protein called 50S ribosomal protein L13P.

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

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	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 14 is a protein called 50S ribosomal protein L15P.

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

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	conflict	GB 55231501

- Molecule 16 is a protein called 50S ribosomal protein L18P.

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

- Molecule 17 is a protein called 50S ribosomal protein L18e.

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

- Molecule 18 is a protein called 50S ribosomal protein L19E.

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

- Molecule 19 is a protein called 50S ribosomal protein L21e.

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

- Molecule 20 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	147	Total	C	N	O	S	0	0	0
			1123	699	204	216	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	?	-	GLN	deletion	UNP P10970
R	?	-	GLN	deletion	UNP P10970
R	?	-	GLY	deletion	UNP P10970

- Molecule 21 is a protein called 50S ribosomal protein L23P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24P.

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

- Molecule 23 is a protein called 50S ribosomal protein L24E.

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

- Molecule 24 is a protein called 50S ribosomal protein L29P.

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

- Molecule 25 is a protein called 50S ribosomal protein L30P.

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

- Molecule 26 is a protein called 50S ribosomal protein L31e.

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

- Molecule 27 is a protein called 50S ribosomal protein L32E.

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

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	conflict	GB 55231162

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	49	Total	C	N	O	S	0	0	0
			421	254	93	73	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	107	Total	Mg	0	0
			107	107		
32	9	1	Total	Mg	0	0
			1	1		
32	A	2	Total	Mg	0	0
			2	2		
32	B	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	2	Total	K	0	0
			2	2		

- Molecule 34 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	74	Total	Na	0	0
			74	74		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	9	2	Total 2	Na 2	0	0
34	A	1	Total 1	Na 1	0	0
34	C	1	Total 1	Na 1	0	0
34	J	1	Total 1	Na 1	0	0
34	L	1	Total 1	Na 1	0	0
34	M	1	Total 1	Na 1	0	0
34	Q	1	Total 1	Na 1	0	0
34	R	2	Total 2	Na 2	0	0
34	S	1	Total 1	Na 1	0	0
34	T	1	Total 1	Na 1	0	0

- Molecule 35 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	9	Total 9	Cl 9	0	0
35	A	1	Total 1	Cl 1	0	0
35	B	1	Total 1	Cl 1	0	0
35	J	3	Total 3	Cl 3	0	0
35	L	1	Total 1	Cl 1	0	0
35	M	1	Total 1	Cl 1	0	0
35	N	1	Total 1	Cl 1	0	0
35	O	1	Total 1	Cl 1	0	0
35	Q	1	Total 1	Cl 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	R	1	Total 1	Cl 1	0	0
35	Y	1	Total 1	Cl 1	0	0
35	3	1	Total 1	Cl 1	0	0

- Molecule 36 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	O	1	Total 1	Cd 1	0	0
36	U	1	Total 1	Cd 1	0	0
36	Z	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	3	1	Total 1	Cd 1	0	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	5866	Total 5866	O 5866	0	0
37	9	143	Total 143	O 143	0	0
37	A	119	Total 119	O 119	0	0
37	B	148	Total 148	O 148	0	0
37	C	180	Total 180	O 180	0	0
37	D	46	Total 46	O 46	0	0
37	E	45	Total 45	O 45	0	0
37	F	27	Total 27	O 27	0	0
37	G	19	Total 19	O 19	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	H	69	Total 69	O 69	0	0
37	I	9	Total 9	O 9	0	0
37	J	57	Total 57	O 57	0	0
37	K	54	Total 54	O 54	0	0
37	L	84	Total 84	O 84	0	0
37	M	130	Total 130	O 130	0	0
37	N	64	Total 64	O 64	0	0
37	O	45	Total 45	O 45	0	0
37	P	64	Total 64	O 64	0	0
37	Q	53	Total 53	O 53	0	0
37	R	58	Total 58	O 58	0	0
37	S	34	Total 34	O 34	0	0
37	T	32	Total 32	O 32	0	0
37	U	26	Total 26	O 26	0	0
37	V	14	Total 14	O 14	0	0
37	W	72	Total 72	O 72	0	0
37	X	24	Total 24	O 24	0	0
37	Y	104	Total 104	O 104	0	0
37	Z	34	Total 34	O 34	0	0
37	1	63	Total 63	O 63	0	0
37	2	32	Total 32	O 32	0	0

Continued on next page...

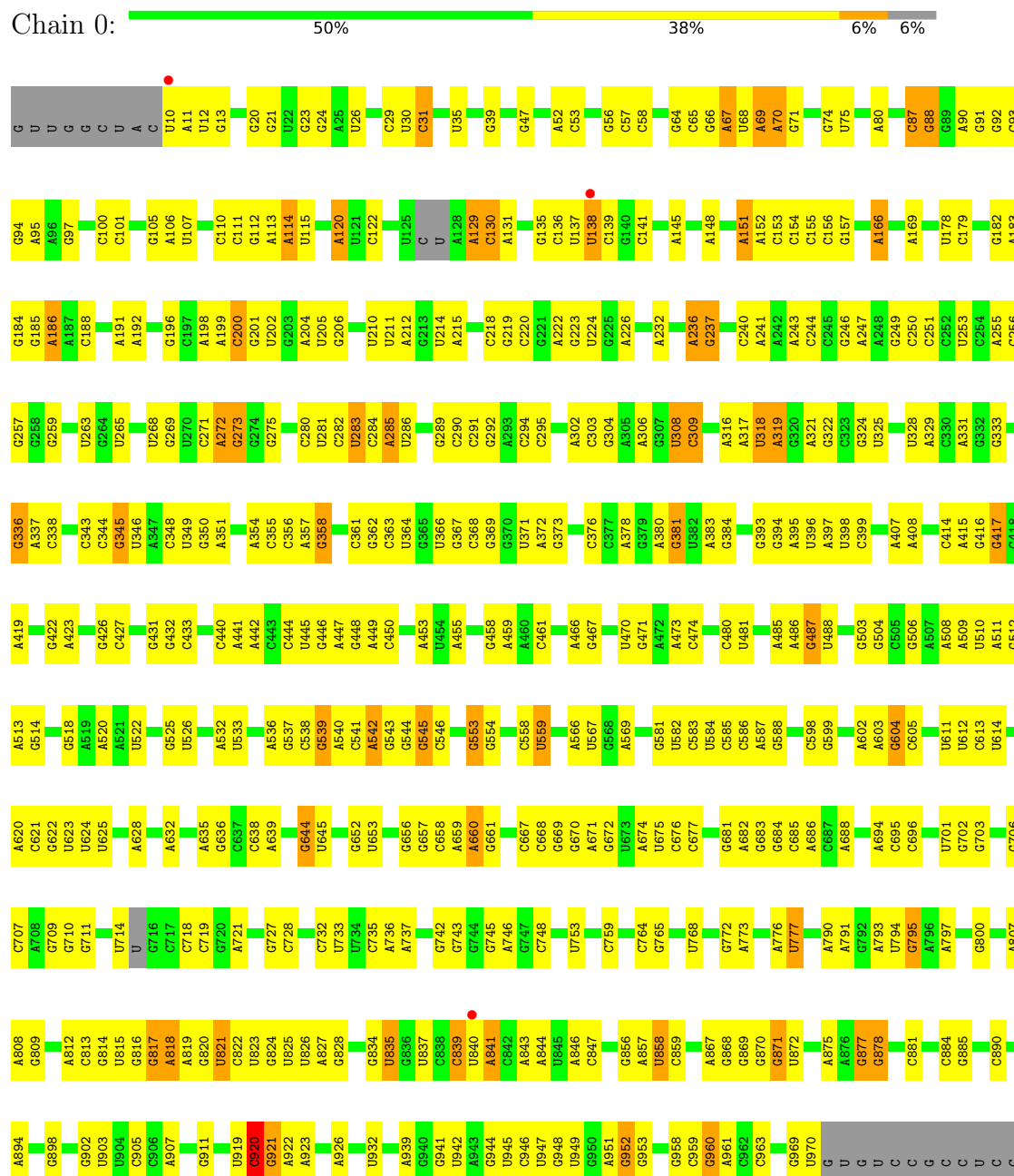
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	3	69	Total	O	0	0
			69	69		

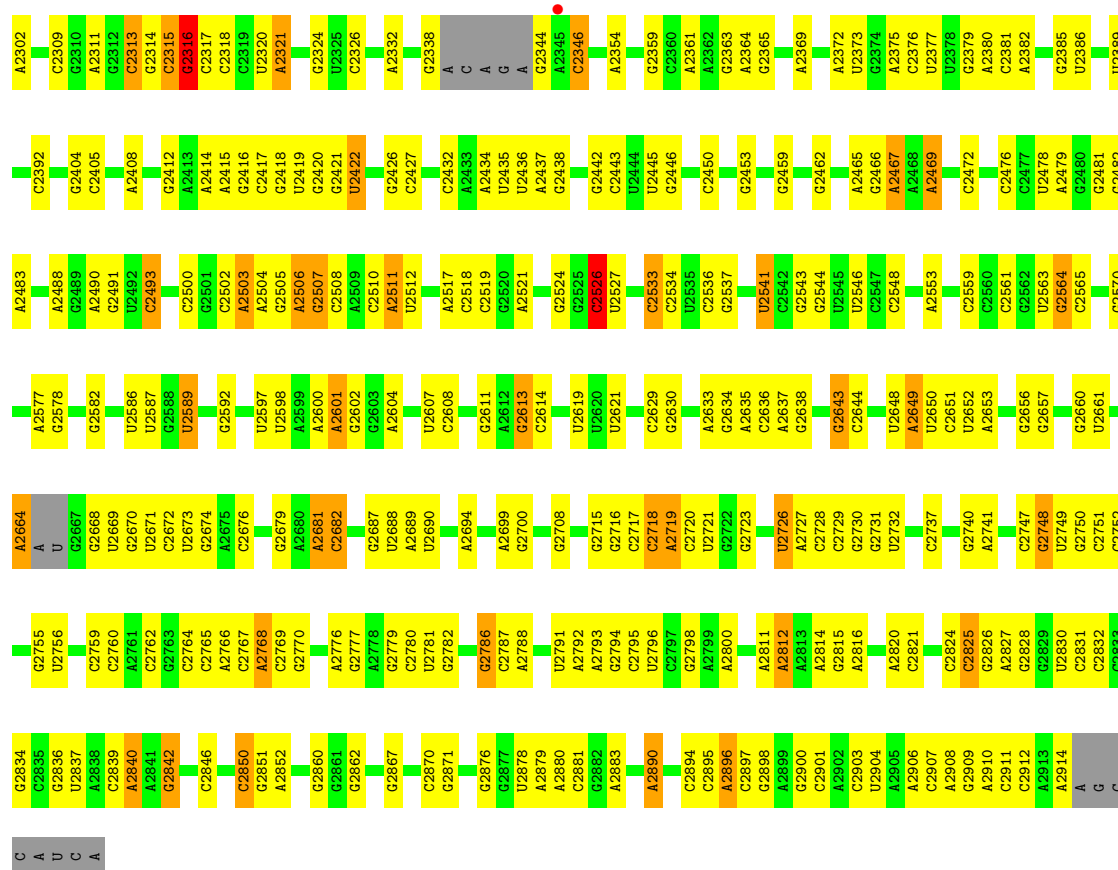
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

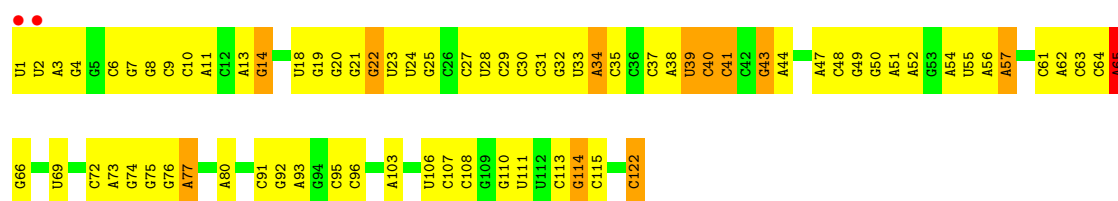
• Molecule 1: 23S Ribosomal RNA



U	G2080	G1974	C1894	A1815	C1735	G1634	U1544	U1457	G1351	C1243	A1166	A1067	G
A	A2081	A1978	C1904	C1816	U1741	U1635	C1545	U1461	A1352	U1244	G1167	A1070	A
C	C2084	G1979	A1904	U1817	A1742	G1636	G1546	C1462	C1353	C1245	C1168	G1071	A
C	A2085	U1980	U1905	G1819	G1743	A1637	A1547	U1463	C1360	A1246	A1171	G1072	A
G	C	G	G	G1820	G1743	A1641	C1549	U1463	C1361	C1250	G1172		G
G	A2089	U1996	A1909	A1821	A1746	A1642	G1552	G1468	U1362	C1251	A1173	A1078	A
C	G2090	A1997	A1910	G1823	A1747	C1643	C1553	C1469	C1366	C1254	A1174	A1079	G
G	G2091	G	G	G1824	G1751	U1645	C1554	A1470	C1366	C1254	G1175	C1080	U
U	G2094	G2000	C1916	U1825	G1752	G1649	G1555	C1472	G1370	A1261	C1176	A1081	C
U	A2095	C2002	U1918	G1826	A1755	U1653	G1556	U1473	U1371	A1261	A1177		G
A	A2096	U2003	C1920	G1827	G1756	A1654	C1557	C1474	A1372	U1266	A1086		G
C	C	U2004	A1921	A1829	U1758	U1655	G1558	C1477	C1377	C1267	G1087		C
U	A2101	G2005	A1922	C1830	U1759	A1656	U	C1477	C1378	C1268	A1088		A
U	G2102	C2006	A1923	C1830	U1758	A1656	A1559	U1488	A1379	G1269	U1091		C
C	C	A2007	G1923	A1834	A1759	A1657	U1561	C1483	G1378	C1273	A1092		A
G	C2105	U2008	A1924	C1834	G1760	A1657	C1562	G1484	A1379	U1185	A1097		C999
A	C2106	A	G1925	U1835	U1761	A1658	C1562	A1485	U1388	C1273	A1097		G1000
G	U2107	G	G1926	U1836	U1762	A1659	G1568	A1486	G1389	U1276	C1187		U1001
G	A2108	U2012	A1927	U1838	C1763	U1660	U1569	U1487	A1390	C1277	A1188		A1006
U	U2109	G2013	A1839	U1839	U1766	A1661	U1577	U1488	G1391	A1278	A1189		A1007
A	G2110	G2014	A1930	A1840	A1767	C1662	A1572	U1493	A1392	U1279	G1190		G1008
C	G2111	U2015	A1931	C1841	U1767	C1662	A1573	A1493	A1393	U1116	A1191		A1012
C	C	U2016	G1932	U1845	C1768	C1666	A1573	A1494	C1394	U1285	A1192		A1013
C	U2115	U2028	A1933	U1846	U1770	A1667	G1576	A1496	C1395	U1285	A1193		A1014
G	U2116	C2029	A1934	A1847	C1771	U1668	U1577	C1495	C1396	C1289	A1194		U1015
G	G2121	U1937	G1848	C1853	C1772	C1679	A1580	G1497	G1397	G1290	G1195		U1016
C	U2032	G1938	U1937	C1854	G1773	C1679	A1580	U1500	A1399	U1297	C1196		
U	G2128	U2033	U1939	G1849	G1774	A1682	U1587	U1503	C1400	U1298	G1197		A1020
A	A2251	U2034	G1940	U1850	U1778	G1683	G1588	A1504	A1407	C1299	A1200		C1127
G	C2132	C2035	A1941	C1852	A1778	A1684	G1589	U1505	U1407	C1129	C1201		G1023
C	U2133	C2036	C1942	C1853	C1779	A1685	G1592	U1506	A1414	U1304	A1202		G1024
G	G2134	C2036	C1943	C1854	U1779	C1686	G1593	C1507	G1415	C1305	G1131		C1025
G	A2135	A2039	C1943	C1855	G1782	C1687	C1593	C1507	G1415	C1305	U1205		U1026
C	G2136	C	G1947	C1856	A1783	C1688	C1594	C1508	U1419	G1311	U1206		U1027
A	C	G2044	G1951	A1857	U1784	A1691	C1594	C1508	U1419	G1311	U1206		U1028
C	C	C	G1951	A1858	U1784	A1691	C1594	C1508	U1419	G1311	U1206		U1029
A	G	C2047	U	A1859	C1787	C1692	A1597	C1513	U1422	C1312	A1207		C1137
C	U	A	A	U1860	U1788	C1692	A1597	C1513	U1422	C1312	C1208		G1138
C	G	A	A	C1861	G1789	A1701	U1599	A1515	C1423	G1315	C1209		U1139
C	U	C	C	C1862	C1790	U1702	U1599	U1516	C1426	G1316	G1213		G1145
U	G	G	U	G1863	U1791	G1703	G1600	C1517	A1427	G1319	A1215		C1043
G	A	G	U	C1864	U1791	G1703	G1601	A1518	C1428	U1149	G1216		C1044
A	C	U	A	C1864	G1794	A1711	C1602	U1523	U1429	A1150	G1217		G1045
C	C	U	G	G1868	G1794	A1711	A1603	G1523	G1430	G1329	U1218		C1051
C	C	U2063	A	C	C1798	A1712	G1604	U1524	G1329	A1151	G1151		G1052
A	G	U2064	C	C	C1798	A1717	G1605	G1525	A1330	G1330	G1221		G1053
C	A	A2067	C	C1872	C1803	A1717	C1613	A1526	C1439	A1154	A1154		G1054
A	U	G2068	C	U1874	A1804	U1722	G1613	A1527	U1440	G1155	C1156		G1055
G	U	C2068	A	A1875	G1805	U1722	C1614	A1528	G1441	C1229	C1157		U1056
U	U	U	C	C1876	G1806	U1724	G1529	G1529	A1442	C1334	G1157		A1057
U	U	U	C	C1876	G1806	U1724	G1529	G1529	A1442	C1334	C1157		A1057
G	G	C2071	U	G1877	U1807	C1725	C1617	G1535	U1446	U1234	G1159		A1058
A	C	G2072	U	U1878	G1808	C1725	A1624	C1536	G1340	G1235	G1159		A1058
A	C	G2073	A	U1879	G1809	G1730	A1624	C1536	G1340	A1237	G1160		A1059
A	C	A2074	U	A1968	C1810	C1731	A1626	C1538	C1450	G1162	C1060		C1060
U	C	U2074	U	G1971	A1811	A1732	U1539	U1539	C1451	G1239	G1163		U1064
C	U	U2078	A	U1972	G1883	A1732	A1632	G1540	C1451	G1239	G1163		U1064
C	A	C2079	A	A1972	G1884	C1734	A1632	G1540	C1451	G1239	G1163		U1065



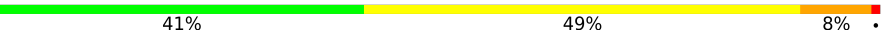
• Molecule 2: 5S Ribosomal RNA

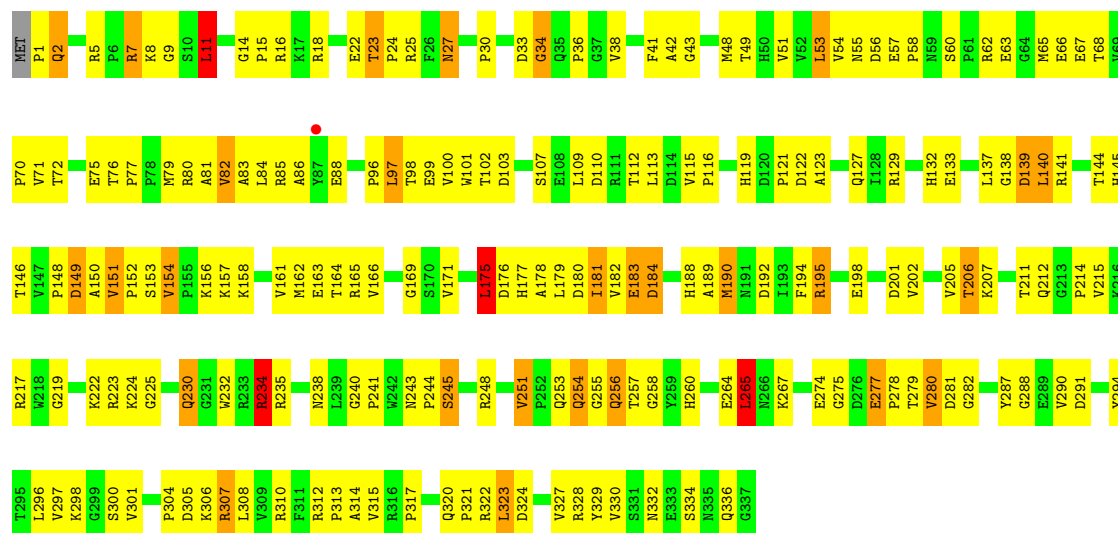


• Molecule 3: 50S ribosomal protein L2P



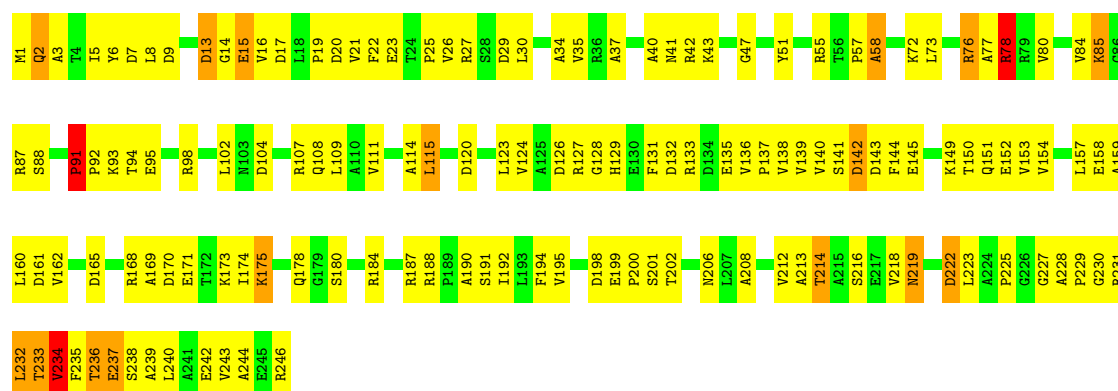
• Molecule 4: 50S ribosomal protein L3P

Chain B:  41% 49% 8% .



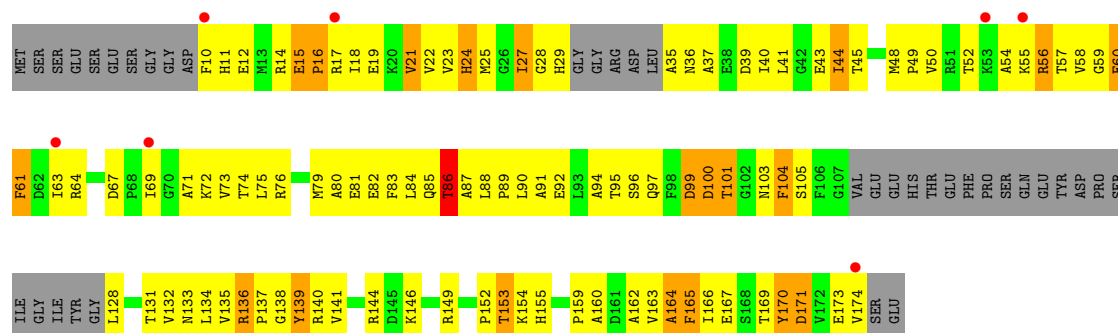
• Molecule 5: 50S ribosomal protein L4E

Chain C:  41% 51% 7% .

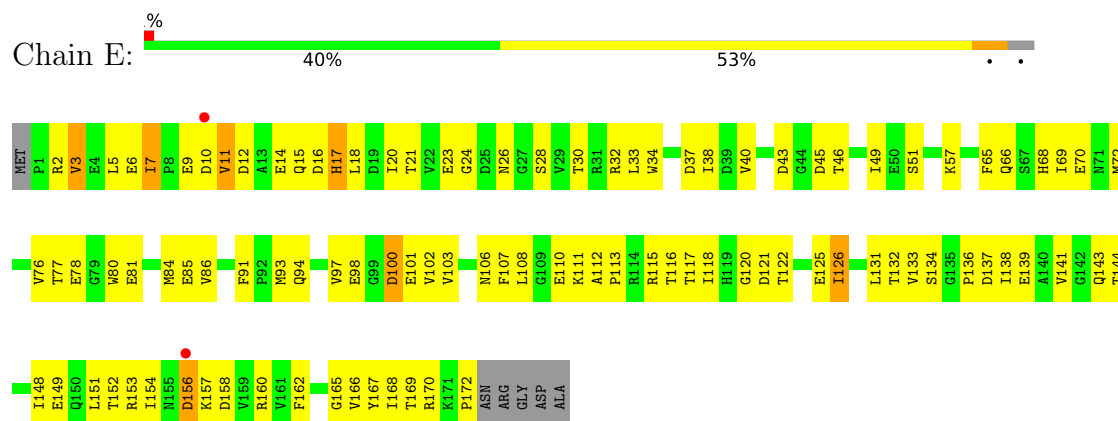


• Molecule 6: 50S ribosomal protein L5P

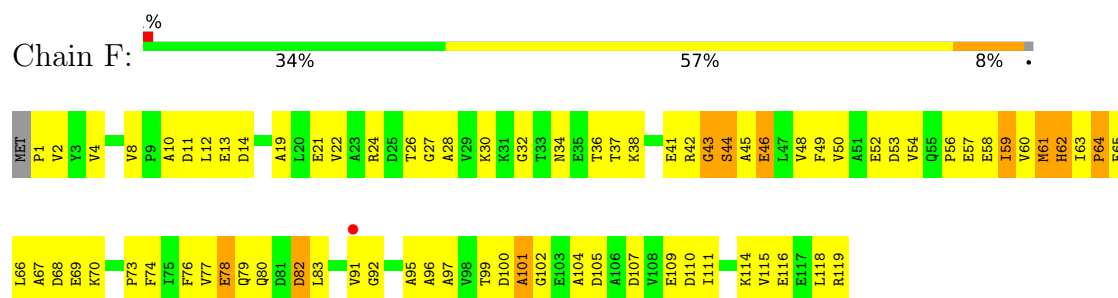
Chain D:  4% 20% 47% 11% 21% .



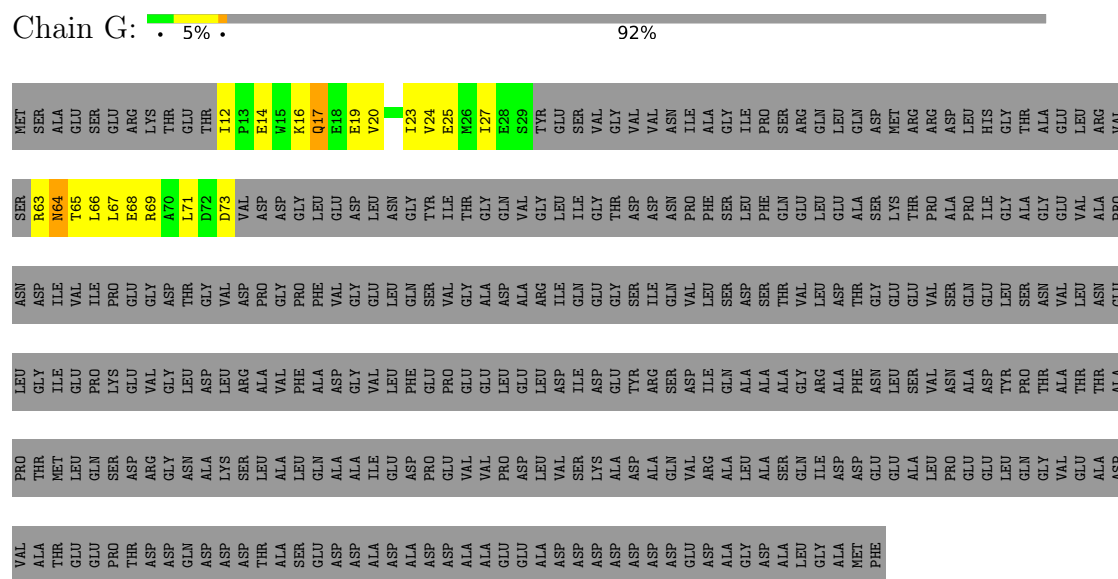
- Molecule 7: 50S ribosomal protein L6P



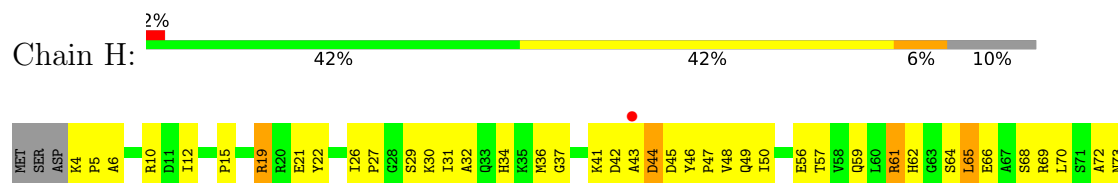
- Molecule 8: 50S ribosomal protein L7AE

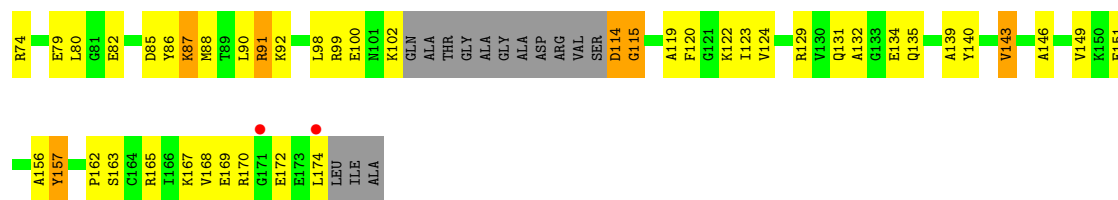


- Molecule 9: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG

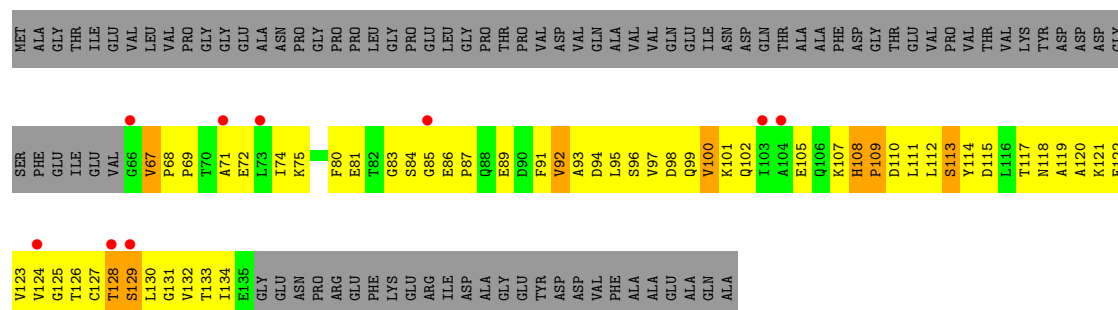
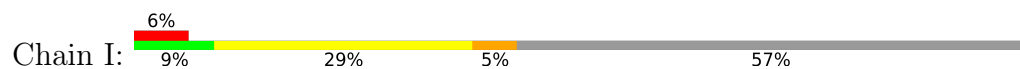


- Molecule 10: 50S RIBOSOMAL PROTEIN L10E

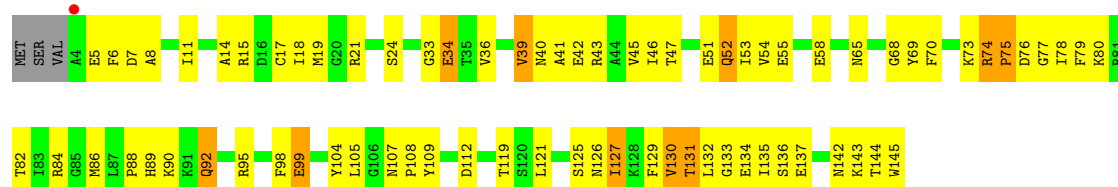




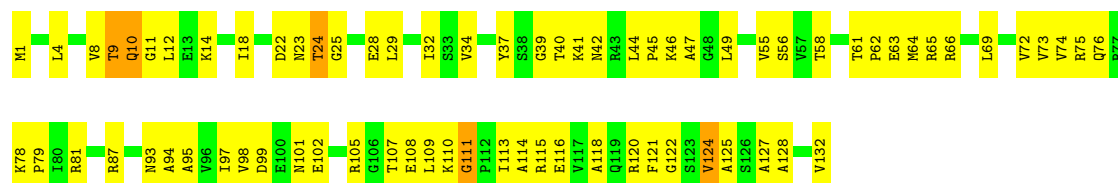
• Molecule 11: 50S RIBOSOMAL PROTEIN L11P



• Molecule 12: 50S ribosomal protein L13P

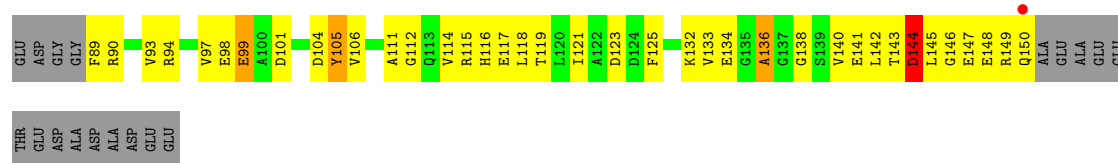


• Molecule 13: 50S ribosomal protein L14P

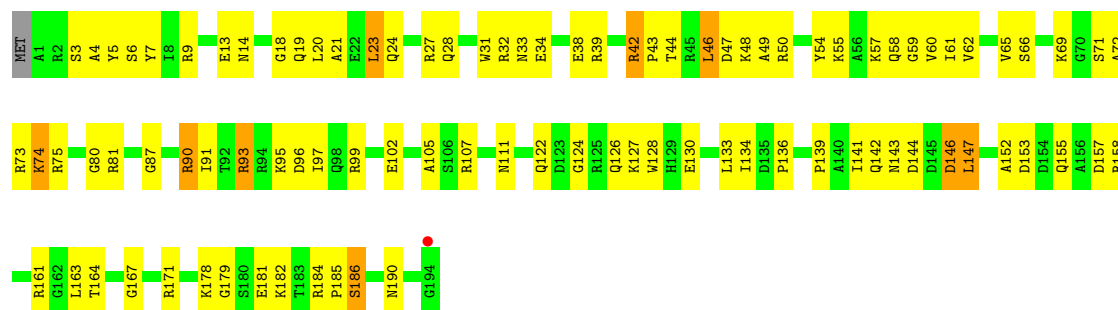


• Molecule 14: 50S ribosomal protein L15P

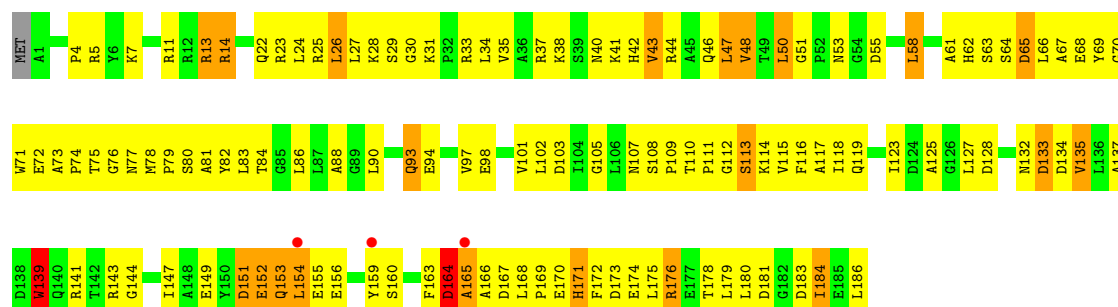




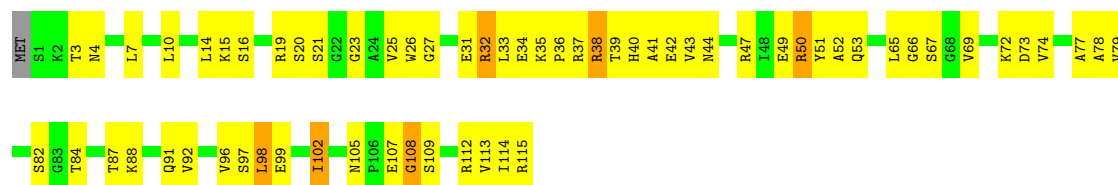
• Molecule 15: 50S Ribosomal Protein L15E



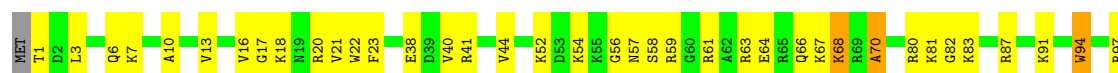
• Molecule 16: 50S ribosomal protein L18P



• Molecule 17: 50S ribosomal protein L18e



• Molecule 18: 50S ribosomal protein L19E





- Molecule 19: 50S ribosomal protein L21e



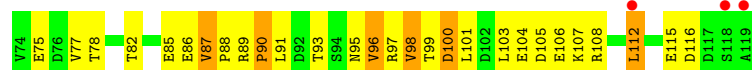
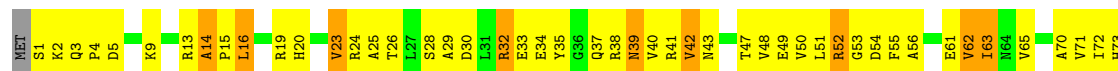
- Molecule 20: 50S ribosomal protein L22P



- Molecule 21: 50S ribosomal protein L23P

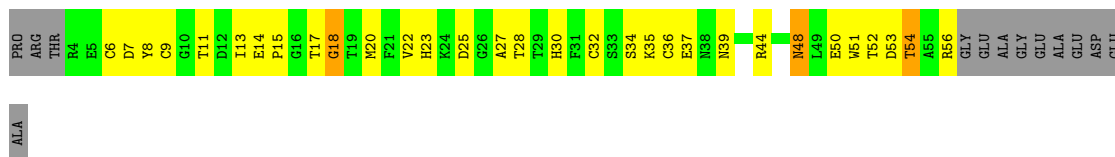


- Molecule 22: 50S ribosomal protein L24P

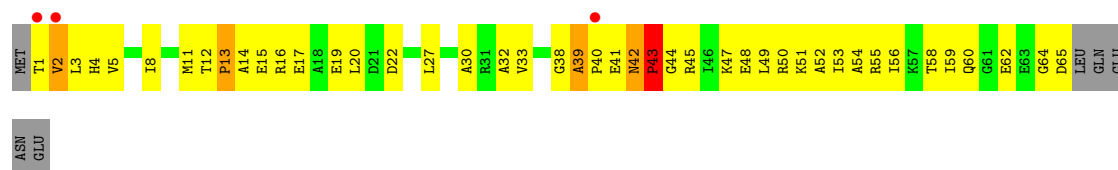


- Molecule 23: 50S ribosomal protein L24E

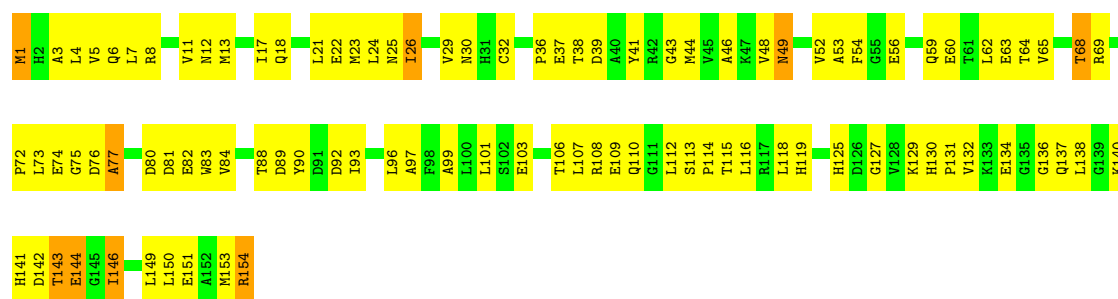
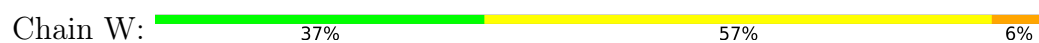




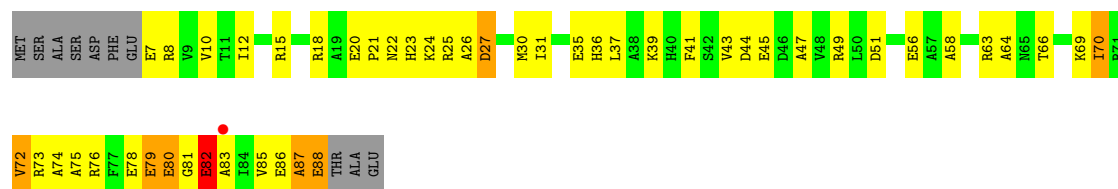
- Molecule 24: 50S ribosomal protein L29P



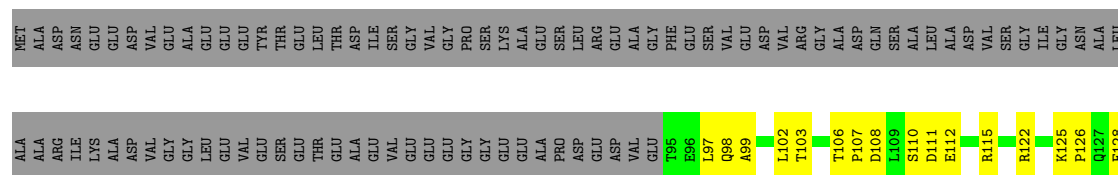
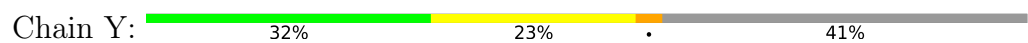
- Molecule 25: 50S ribosomal protein L30P

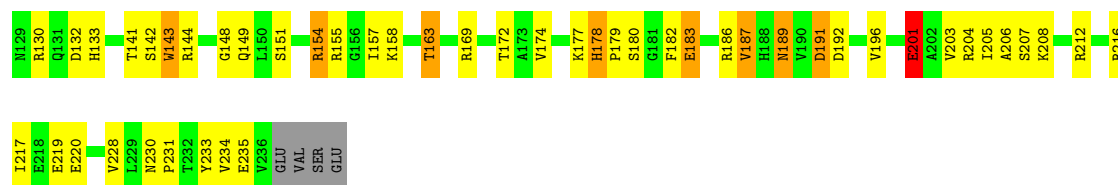


- Molecule 26: 50S ribosomal protein L31e

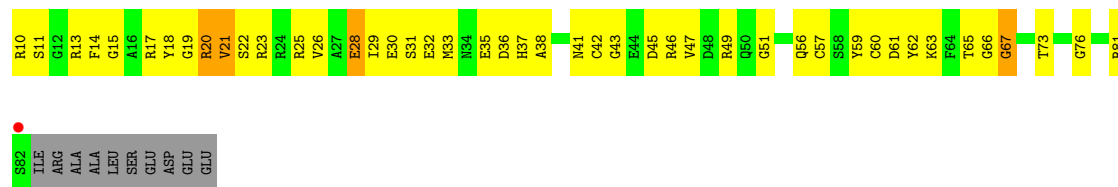


- Molecule 27: 50S ribosomal protein L32E

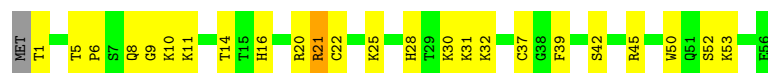




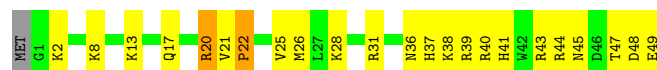
- Molecule 28: 50S ribosomal protein L37Ae



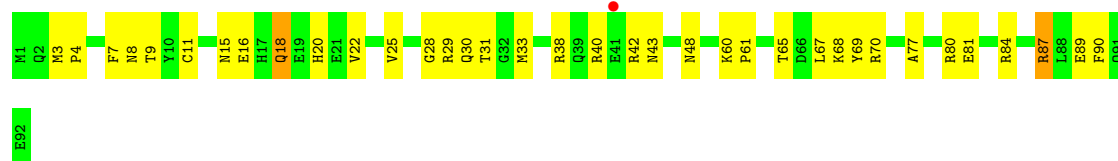
- Molecule 29: 50S ribosomal protein L37e



- Molecule 30: 50S ribosomal protein L39e



- Molecule 31: 50S ribosomal protein L44E



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 300.75Å 575.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.94 – 2.80 29.94 – 2.80	Depositor EDS
% Data completeness (in resolution range)	89.3 (29.94-2.80) 89.3 (29.94-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.184 , 0.242 0.183 , 0.239	Depositor DCC
R_{free} test set	3987 reflections (0.99%)	wwPDB-VP
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	99031	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% 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: CL, PSU, NA, UR3, OMG, OMU, MG, 1MA, CD, K

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	0/65980	0.62	18/102903 (0.0%)
2	9	0.39	0/2904	0.62	3/4526 (0.1%)
3	A	0.45	0/1786	1.03	12/2408 (0.5%)
4	B	0.46	0/2690	1.07	19/3652 (0.5%)
5	C	0.49	0/1884	1.04	10/2551 (0.4%)
6	D	0.39	0/1111	0.92	7/1498 (0.5%)
7	E	0.42	0/1382	0.90	1/1880 (0.1%)
8	F	0.39	0/901	0.96	3/1224 (0.2%)
9	G	0.36	0/241	0.90	1/324 (0.3%)
10	H	0.47	0/1302	1.04	8/1743 (0.5%)
11	I	0.40	0/526	0.95	3/716 (0.4%)
12	J	0.49	0/1136	0.95	4/1530 (0.3%)
13	K	0.46	0/1001	1.05	6/1347 (0.4%)
14	L	0.41	0/1130	1.00	5/1509 (0.3%)
15	M	0.45	0/1582	0.96	5/2117 (0.2%)
16	N	0.40	0/1474	1.10	12/1999 (0.6%)
17	O	0.46	0/874	0.97	3/1181 (0.3%)
18	P	0.43	0/1147	0.88	4/1528 (0.3%)
19	Q	0.51	0/749	1.15	6/1005 (0.6%)
20	R	0.52	0/1146	0.97	2/1544 (0.1%)
21	S	0.40	0/648	0.90	4/875 (0.5%)
22	T	0.43	0/958	1.02	11/1289 (0.9%)
23	U	0.41	0/417	0.95	2/562 (0.4%)
24	V	0.38	0/502	1.02	2/675 (0.3%)
25	W	0.51	0/1219	1.02	5/1655 (0.3%)
26	X	0.48	0/664	1.05	3/895 (0.3%)
27	Y	0.47	0/1146	0.99	6/1536 (0.4%)
28	Z	0.42	0/589	0.92	0/787
29	1	0.47	0/438	0.95	1/578 (0.2%)
30	2	0.50	0/427	0.89	0/566
31	3	0.45	0/771	0.86	1/1024 (0.1%)
All	All	0.42	0/98725	0.74	167/147627 (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	46
2	9	0	1
All	All	0	47

There are no bond length outliers.

The worst 5 of 167 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
16	N	153	GLN	N-CA-C	-10.07	101.63	113.21
18	P	118	GLN	N-CA-C	-9.66	100.71	111.14
19	Q	17	LYS	N-CA-C	-8.91	98.89	109.93
4	B	323	LEU	N-CA-C	8.68	122.16	110.35
16	N	135	VAL	N-CA-C	-8.41	104.97	113.47

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	148	A	Sidechain
1	0	26	U	Sidechain
1	0	333	G	Sidechain
1	0	398	U	Sidechain
1	0	458	G	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	59041	0	29817	1167	0
2	9	2599	0	1325	86	0
3	A	1753	0	1766	152	0
4	B	2625	0	2533	211	0
5	C	1859	0	1816	164	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	1094	0	1085	144	0
7	E	1357	0	1266	91	0
8	F	890	0	843	83	0
9	G	240	0	231	24	0
10	H	1282	0	1292	97	0
11	I	519	0	500	63	0
12	J	1120	0	1098	86	0
13	K	992	0	1031	83	0
14	L	1118	0	1076	87	0
15	M	1558	0	1566	100	0
16	N	1445	0	1401	156	0
17	O	865	0	873	65	0
18	P	1136	0	1123	72	0
19	Q	735	0	729	38	0
20	R	1123	0	1099	77	0
21	S	641	0	605	40	0
22	T	950	0	923	101	0
23	U	410	0	364	34	0
24	V	499	0	511	48	0
25	W	1196	0	1137	134	0
26	X	654	0	653	57	0
27	Y	1130	0	1133	67	0
28	Z	578	0	539	43	0
29	1	431	0	426	35	0
30	2	421	0	437	36	0
31	3	755	0	728	32	0
32	0	107	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	2	0	0	0	0
34	0	74	0	0	0	0
34	9	2	0	0	0	0
34	A	1	0	0	0	0
34	C	1	0	0	0	0
34	J	1	0	0	0	0
34	L	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	2	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
35	0	9	0	0	1	0
35	3	1	0	0	0	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	J	3	0	0	4	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	N	1	0	0	1	0
35	O	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	1	1	0	0	0	0
36	3	1	0	0	0	0
36	O	1	0	0	0	0
36	U	1	0	0	0	0
36	Z	1	0	0	0	0
37	0	5866	0	0	247	0
37	1	63	0	0	8	0
37	2	32	0	0	3	0
37	3	69	0	0	8	0
37	9	143	0	0	12	0
37	A	119	0	0	23	0
37	B	148	0	0	31	0
37	C	180	0	0	34	0
37	D	46	0	0	18	0
37	E	45	0	0	11	0
37	F	27	0	0	8	0
37	G	19	0	0	2	0
37	H	69	0	0	12	0
37	I	9	0	0	5	0
37	J	57	0	0	8	0
37	K	54	0	0	10	0
37	L	84	0	0	17	0
37	M	130	0	0	11	0
37	N	64	0	0	22	0
37	O	45	0	0	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	P	64	0	0	10	0
37	Q	53	0	0	7	0
37	R	58	0	0	5	0
37	S	34	0	0	3	0
37	T	32	0	0	9	0
37	U	26	0	0	3	0
37	V	14	0	0	5	0
37	W	72	0	0	12	0
37	X	24	0	0	5	0
37	Y	104	0	0	15	0
37	Z	34	0	0	3	0
All	All	99031	0	59926	3351	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 22.

The worst 5 of 3351 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)
5:C:127:ARG:NH2	5:C:225:PRO:HG2	1.66	1.09
6:D:25:MET:HE2	6:D:41:LEU:HG	1.35	1.09
5:C:236:THR:HG22	5:C:239:ALA:H	0.95	1.08
1:O:1160:G:H5'	1:O:1161:A:H5'	1.13	1.07
4:B:264:GLU:HG2	4:B:267:LYS:HE2	1.36	1.04

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	235/240 (98%)	191 (81%)	31 (13%)	13 (6%)	1 4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	335/338 (99%)	291 (87%)	35 (10%)	9 (3%)	4	15
5	C	244/246 (99%)	201 (82%)	32 (13%)	11 (4%)	2	7
6	D	134/177 (76%)	85 (63%)	31 (23%)	18 (13%)	0	0
7	E	170/178 (96%)	150 (88%)	15 (9%)	5 (3%)	3	13
8	F	117/120 (98%)	93 (80%)	17 (14%)	7 (6%)	1	3
9	G	25/348 (7%)	23 (92%)	2 (8%)	0	100	100
10	H	156/177 (88%)	134 (86%)	17 (11%)	5 (3%)	3	11
11	I	68/162 (42%)	49 (72%)	14 (21%)	5 (7%)	1	2
12	J	140/145 (97%)	121 (86%)	14 (10%)	5 (4%)	2	10
13	K	130/132 (98%)	111 (85%)	17 (13%)	2 (2%)	8	28
14	L	141/165 (86%)	114 (81%)	25 (18%)	2 (1%)	9	30
15	M	192/195 (98%)	169 (88%)	20 (10%)	3 (2%)	7	27
16	N	184/187 (98%)	149 (81%)	23 (12%)	12 (6%)	1	3
17	O	113/116 (97%)	102 (90%)	8 (7%)	3 (3%)	4	15
18	P	141/149 (95%)	125 (89%)	12 (8%)	4 (3%)	4	14
19	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	5	19
20	R	145/152 (95%)	122 (84%)	18 (12%)	5 (3%)	3	11
21	S	79/85 (93%)	69 (87%)	9 (11%)	1 (1%)	9	31
22	T	117/120 (98%)	92 (79%)	19 (16%)	6 (5%)	1	5
23	U	51/66 (77%)	43 (84%)	7 (14%)	1 (2%)	6	21
24	V	63/71 (89%)	50 (79%)	9 (14%)	4 (6%)	1	3
25	W	152/154 (99%)	136 (90%)	14 (9%)	2 (1%)	9	31
26	X	80/92 (87%)	69 (86%)	8 (10%)	3 (4%)	2	9
27	Y	140/241 (58%)	138 (99%)	2 (1%)	0	100	100
28	Z	71/83 (86%)	56 (79%)	10 (14%)	5 (7%)	1	2
29	1	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
30	2	47/50 (94%)	44 (94%)	1 (2%)	2 (4%)	2	7
31	3	90/92 (98%)	84 (93%)	6 (7%)	0	100	100
All	All	3707/4434 (84%)	3148 (85%)	424 (11%)	135 (4%)	2	10

5 of 135 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	34	ASP
4	B	34	GLY
4	B	139	ASP
4	B	206	THR
5	C	8	LEU

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	179/182 (98%)	170 (95%)	9 (5%)	22	54
4	B	282/283 (100%)	258 (92%)	24 (8%)	10	31
5	C	193/193 (100%)	180 (93%)	13 (7%)	15	42
6	D	117/148 (79%)	110 (94%)	7 (6%)	17	47
7	E	152/156 (97%)	145 (95%)	7 (5%)	24	58
8	F	93/94 (99%)	90 (97%)	3 (3%)	34	70
9	G	27/283 (10%)	25 (93%)	2 (7%)	13	37
10	H	134/145 (92%)	128 (96%)	6 (4%)	24	58
11	I	58/130 (45%)	56 (97%)	2 (3%)	32	68
12	J	118/121 (98%)	110 (93%)	8 (7%)	14	42
13	K	106/106 (100%)	105 (99%)	1 (1%)	70	89
14	L	113/127 (89%)	109 (96%)	4 (4%)	32	67
15	M	158/159 (99%)	153 (97%)	5 (3%)	34	70
16	N	149/150 (99%)	140 (94%)	9 (6%)	17	47
17	O	93/94 (99%)	87 (94%)	6 (6%)	15	43
18	P	113/117 (97%)	108 (96%)	5 (4%)	25	59
19	Q	79/80 (99%)	77 (98%)	2 (2%)	42	76
20	R	114/120 (95%)	110 (96%)	4 (4%)	32	67
21	S	71/74 (96%)	67 (94%)	4 (6%)	19	50
22	T	105/106 (99%)	98 (93%)	7 (7%)	15	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	44/52 (85%)	40 (91%)	4 (9%)	9	28
24	V	51/57 (90%)	49 (96%)	2 (4%)	28	64
25	W	130/130 (100%)	125 (96%)	5 (4%)	29	64
26	X	66/74 (89%)	60 (91%)	6 (9%)	9	28
27	Y	120/196 (61%)	111 (92%)	9 (8%)	12	37
28	Z	60/68 (88%)	59 (98%)	1 (2%)	53	83
29	1	46/47 (98%)	45 (98%)	1 (2%)	45	78
30	2	45/46 (98%)	44 (98%)	1 (2%)	45	78
31	3	79/79 (100%)	76 (96%)	3 (4%)	29	64
All	All	3095/3617 (86%)	2935 (95%)	160 (5%)	21	53

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	R	109	MET
26	X	82	GLU
21	S	71	ASP
23	U	48	ASN
27	Y	191	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
15	M	170	ASN
31	3	48	ASN
19	Q	40	HIS
31	3	43	ASN
27	Y	149	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2744/2922 (93%)	250 (9%)	26 (0%)
2	9	121/122 (99%)	17 (14%)	1 (0%)
All	All	2865/3044 (94%)	267 (9%)	27 (0%)

5 of 267 RNA backbone outliers are listed below:

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

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1450	C
1	0	1979	G
1	0	2718	C
1	0	1942	A
1	0	2011	A

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	PSU	0	2621	1	18,21,22	1.60	2 (11%)	21,30,33	1.26	3 (14%)
1	UR3	0	2619	1	19,22,23	0.36	0	26,32,35	0.70	1 (3%)
1	OMG	0	2588	1	23,26,27	0.30	0	32,38,41	0.44	0
1	1MA	0	628	1	21,25,26	0.73	1 (4%)	30,37,40	0.77	1 (3%)
1	OMU	0	2587	1	19,22,23	0.36	0	25,31,34	0.42	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2
1	OMG	0	2588	1	-	1/9/27/28	0/3/3/3
1	1MA	0	628	1	-	2/7/25/26	0/3/3/3
1	OMU	0	2587	1	-	0/9/27/28	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	5.37	1.43	1.36
1	0	2621	PSU	C6-C5	3.25	1.38	1.35
1	0	628	1MA	C6-N6	2.55	1.34	1.28

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C6-C5-C4	2.93	120.15	118.17
1	0	2621	PSU	O2-C2-N1	2.90	125.78	122.79
1	0	2621	PSU	C6-N1-C2	-2.86	120.04	122.69
1	0	628	1MA	N1-C2-N3	2.83	129.36	126.00
1	0	2619	UR3	C4-N3-C2	2.76	126.80	124.58

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	2588	OMG	C3'-C2'-O2'-CM2
1	0	628	1MA	C2'-C1'-N9-C4
1	0	628	1MA	C2'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 231 ligands modelled in this entry, 231 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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.60	11 (0%) 88 84	29, 55, 100, 157	1 (0%)
2	9	122/122 (100%)	-0.35	2 (1%) 70 61	44, 68, 95, 159	0
3	A	237/240 (98%)	-0.14	3 (1%) 75 66	34, 62, 95, 116	0
4	B	337/338 (99%)	-0.17	1 (0%) 90 86	32, 64, 90, 97	0
5	C	246/246 (100%)	-0.22	0 100 100	29, 58, 81, 90	0
6	D	140/177 (79%)	0.68	7 (5%) 34 26	62, 107, 129, 138	0
7	E	172/178 (96%)	0.04	2 (1%) 76 68	52, 75, 97, 101	0
8	F	119/120 (99%)	0.16	1 (0%) 82 75	65, 84, 105, 117	0
9	G	29/348 (8%)	0.51	0 100 100	76, 98, 106, 107	0
10	H	160/177 (90%)	-0.12	3 (1%) 66 57	40, 61, 96, 107	0
11	I	70/162 (43%)	1.12	9 (12%) 7 6	112, 126, 144, 147	0
12	J	142/145 (97%)	-0.16	1 (0%) 84 77	43, 58, 82, 95	0
13	K	132/132 (100%)	-0.07	0 100 100	40, 61, 84, 89	0
14	L	145/165 (87%)	0.09	2 (1%) 73 64	29, 75, 115, 126	0
15	M	194/195 (99%)	-0.33	1 (0%) 87 82	40, 55, 69, 79	0
16	N	186/187 (99%)	0.14	3 (1%) 70 61	46, 71, 115, 125	0
17	O	115/116 (99%)	-0.13	0 100 100	47, 65, 81, 83	0
18	P	143/149 (95%)	-0.09	0 100 100	44, 66, 80, 86	0
19	Q	95/96 (98%)	-0.37	0 100 100	39, 51, 64, 79	0
20	R	147/152 (96%)	-0.13	5 (3%) 48 39	41, 56, 114, 128	0
21	S	81/85 (95%)	-0.15	0 100 100	52, 72, 88, 95	0
22	T	119/120 (99%)	-0.04	3 (2%) 58 48	51, 69, 94, 111	0
23	U	53/66 (80%)	-0.12	0 100 100	51, 64, 79, 85	0
24	V	65/71 (91%)	0.34	3 (4%) 37 29	63, 85, 118, 122	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.41	0 100 100	41, 56, 76, 85	0
26	X	82/92 (89%)	-0.06	1 (1%) 76 68	49, 66, 87, 101	0
27	Y	142/241 (58%)	-0.39	0 100 100	31, 53, 79, 95	0
28	Z	73/83 (87%)	0.23	1 (1%) 73 64	53, 69, 86, 102	0
29	1	56/57 (98%)	-0.72	0 100 100	35, 43, 49, 58	0
30	2	49/50 (98%)	0.09	0 100 100	40, 66, 94, 104	0
31	3	92/92 (100%)	-0.16	1 (1%) 78 70	42, 63, 76, 91	0
All	All	6646/7478 (88%)	-0.29	60 (0%) 81 74	29, 61, 106, 159	1 (0%)

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	9	1	U	5.1
1	0	840[A]	U	4.8
10	H	174	LEU	4.7
10	H	171	GLY	4.0
1	0	1175	G	3.7

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	OMU	0	2587	21/22	0.97	0.07	39,42,43,46	0
1	OMG	0	2588	24/25	0.98	0.06	40,42,44,44	0
1	UR3	0	2619	21/22	0.98	0.04	40,42,43,46	0
1	PSU	0	2621	20/21	0.98	0.05	40,41,43,44	0
1	1MA	0	628	23/24	0.99	0.05	32,37,39,39	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
34	NA	R	8586	1/1	0.70	0.41	81,81,81,81	0
32	MG	0	8038	1/1	0.74	0.15	38,38,38,38	0
34	NA	0	8568	1/1	0.75	0.33	84,84,84,84	0
34	NA	0	8569	1/1	0.81	0.18	66,66,66,66	0
32	MG	0	8050	1/1	0.85	0.08	97,97,97,97	0
32	MG	0	8104	1/1	0.86	0.13	61,61,61,61	0
34	NA	0	8513	1/1	0.86	0.07	72,72,72,72	0
34	NA	0	8567	1/1	0.86	0.24	70,70,70,70	0
32	MG	0	8049	1/1	0.86	0.12	70,70,70,70	0
32	MG	0	8014	1/1	0.86	0.07	20,20,20,20	0
34	NA	0	8582	1/1	0.86	0.19	78,78,78,78	0
32	MG	0	8087	1/1	0.86	0.10	81,81,81,81	0
35	CL	0	8815	1/1	0.86	0.28	112,112,112,112	0
34	NA	0	8507	1/1	0.87	0.10	61,61,61,61	0
32	MG	0	8043	1/1	0.87	0.09	62,62,62,62	0
34	NA	0	8571	1/1	0.87	0.25	61,61,61,61	0
34	NA	0	8526	1/1	0.87	0.31	78,78,78,78	0
34	NA	9	8551	1/1	0.87	0.24	46,46,46,46	0
34	NA	9	8583	1/1	0.87	0.11	71,71,71,71	0
34	NA	0	8566	1/1	0.87	0.08	68,68,68,68	0
32	MG	2	8076	1/1	0.87	0.10	69,69,69,69	0
34	NA	0	8527	1/1	0.88	0.22	69,69,69,69	0
34	NA	0	8557	1/1	0.88	0.10	65,65,65,65	0
34	NA	0	8584	1/1	0.89	0.12	70,70,70,70	0
34	NA	0	8585	1/1	0.89	0.27	60,60,60,60	0
34	NA	0	8528	1/1	0.89	0.17	61,61,61,61	0
32	MG	0	8041	1/1	0.89	0.15	59,59,59,59	0
34	NA	0	8572	1/1	0.89	0.19	69,69,69,69	0
34	NA	0	8563	1/1	0.89	0.15	51,51,51,51	0
34	NA	0	8524	1/1	0.90	0.14	68,68,68,68	0
32	MG	0	8031	1/1	0.90	0.09	34,34,34,34	0
34	NA	0	8533	1/1	0.90	0.17	49,49,49,49	0
34	NA	R	8537	1/1	0.90	0.08	51,51,51,51	0
34	NA	0	8541	1/1	0.90	0.08	53,53,53,53	0
34	NA	0	8556	1/1	0.90	0.15	58,58,58,58	0
35	CL	A	8809	1/1	0.90	0.14	82,82,82,82	0
34	NA	0	8529	1/1	0.91	0.14	79,79,79,79	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	NA	0	8564	1/1	0.91	0.10	40,40,40,40	0
32	MG	0	8092	1/1	0.91	0.13	80,80,80,80	0
34	NA	0	8540	1/1	0.91	0.08	40,40,40,40	0
32	MG	0	8114	1/1	0.91	0.09	47,47,47,47	0
34	NA	0	8552	1/1	0.91	0.22	62,62,62,62	0
32	MG	0	8115	1/1	0.91	0.05	70,70,70,70	0
34	NA	S	8512	1/1	0.91	0.05	48,48,48,48	0
34	NA	0	8516	1/1	0.91	0.07	61,61,61,61	0
34	NA	0	8573	1/1	0.91	0.09	73,73,73,73	0
32	MG	T	8073	1/1	0.92	0.05	68,68,68,68	0
34	NA	0	8532	1/1	0.92	0.21	47,47,47,47	0
34	NA	0	8560	1/1	0.92	0.24	61,61,61,61	0
34	NA	0	8508	1/1	0.92	0.14	73,73,73,73	0
34	NA	0	8574	1/1	0.92	0.19	63,63,63,63	0
35	CL	B	8819	1/1	0.92	0.18	74,74,74,74	0
35	CL	J	8802	1/1	0.92	0.07	75,75,75,75	0
35	CL	N	8807	1/1	0.92	0.09	74,74,74,74	0
35	CL	O	8808	1/1	0.92	0.16	99,99,99,99	0
35	CL	Y	8820	1/1	0.92	0.12	55,55,55,55	0
34	NA	0	8530	1/1	0.93	0.07	72,72,72,72	0
35	CL	0	8805	1/1	0.93	0.08	77,77,77,77	0
32	MG	0	8089	1/1	0.93	0.07	69,69,69,69	0
32	MG	0	8099	1/1	0.93	0.06	62,62,62,62	0
34	NA	0	8505	1/1	0.93	0.07	49,49,49,49	0
34	NA	A	8545	1/1	0.93	0.07	46,46,46,46	0
34	NA	C	8504	1/1	0.93	0.04	48,48,48,48	0
34	NA	0	8579	1/1	0.93	0.15	62,62,62,62	0
32	MG	0	8100	1/1	0.93	0.12	66,66,66,66	0
35	CL	3	8804	1/1	0.93	0.09	74,74,74,74	0
32	MG	0	8103	1/1	0.94	0.12	67,67,67,67	0
32	MG	0	8093	1/1	0.94	0.14	50,50,50,50	0
32	MG	0	8105	1/1	0.94	0.16	63,63,63,63	0
34	NA	0	8577	1/1	0.94	0.16	72,72,72,72	0
32	MG	0	8094	1/1	0.94	0.10	67,67,67,67	0
32	MG	0	8097	1/1	0.94	0.08	51,51,51,51	0
34	NA	0	8534	1/1	0.94	0.10	55,55,55,55	0
35	CL	J	8801	1/1	0.94	0.06	67,67,67,67	0
32	MG	9	8095	1/1	0.94	0.06	54,54,54,54	0
32	MG	0	8046	1/1	0.94	0.08	55,55,55,55	0
34	NA	0	8550	1/1	0.94	0.14	56,56,56,56	0
35	CL	R	8806	1/1	0.94	0.10	63,63,63,63	0
34	NA	0	8570	1/1	0.94	0.21	66,66,66,66	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8042	1/1	0.94	0.06	55,55,55,55	0
36	CD	3	8704	1/1	0.94	0.06	72,72,72,72	0
35	CL	0	8817	1/1	0.95	0.08	74,74,74,74	0
35	CL	0	8822	1/1	0.95	0.11	79,79,79,79	0
34	NA	0	8520	1/1	0.95	0.06	33,33,33,33	0
32	MG	0	8051	1/1	0.95	0.09	67,67,67,67	0
32	MG	0	8107	1/1	0.95	0.10	65,65,65,65	0
32	MG	0	8082	1/1	0.95	0.13	76,76,76,76	0
34	NA	0	8559	1/1	0.95	0.13	66,66,66,66	0
34	NA	0	8514	1/1	0.95	0.14	39,39,39,39	0
34	NA	T	8543	1/1	0.95	0.10	43,43,43,43	0
34	NA	0	8562	1/1	0.95	0.17	81,81,81,81	0
32	MG	0	8045	1/1	0.95	0.07	59,59,59,59	0
35	CL	0	8816	1/1	0.95	0.16	79,79,79,79	0
32	MG	0	8057	1/1	0.96	0.13	67,67,67,67	0
34	NA	0	8517	1/1	0.96	0.06	52,52,52,52	0
32	MG	0	8088	1/1	0.96	0.07	34,34,34,34	0
34	NA	0	8561	1/1	0.96	0.11	50,50,50,50	0
34	NA	L	8580	1/1	0.96	0.15	72,72,72,72	0
34	NA	M	8547	1/1	0.96	0.09	45,45,45,45	0
34	NA	0	8523	1/1	0.96	0.12	37,37,37,37	0
32	MG	0	8062	1/1	0.96	0.06	65,65,65,65	0
32	MG	K	8069	1/1	0.96	0.04	62,62,62,62	0
34	NA	0	8565	1/1	0.96	0.10	49,49,49,49	0
32	MG	0	8101	1/1	0.96	0.06	70,70,70,70	0
35	CL	0	8814	1/1	0.96	0.10	71,71,71,71	0
32	MG	Y	8108	1/1	0.96	0.06	48,48,48,48	0
32	MG	0	8102	1/1	0.96	0.06	71,71,71,71	0
33	K	0	8401	1/1	0.96	0.28	91,91,91,91	0
33	K	0	8402	1/1	0.96	0.10	69,69,69,69	0
32	MG	0	8063	1/1	0.96	0.12	73,73,73,73	0
34	NA	0	8506	1/1	0.96	0.19	51,51,51,51	0
32	MG	0	8075	1/1	0.96	0.07	54,54,54,54	0
32	MG	0	8040	1/1	0.96	0.05	57,57,57,57	0
35	CL	L	8810	1/1	0.96	0.08	73,73,73,73	0
34	NA	0	8575	1/1	0.96	0.10	58,58,58,58	0
34	NA	0	8544	1/1	0.96	0.04	33,33,33,33	0
32	MG	0	8096	1/1	0.96	0.03	53,53,53,53	0
32	MG	0	8112	1/1	0.96	0.06	64,64,64,64	0
34	NA	0	8555	1/1	0.96	0.12	67,67,67,67	0
34	NA	0	8515	1/1	0.96	0.12	65,65,65,65	0
32	MG	0	8044	1/1	0.97	0.11	51,51,51,51	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
34	NA	0	8509	1/1	0.97	0.10	37,37,37,37	0
34	NA	Q	8548	1/1	0.97	0.07	49,49,49,49	0
34	NA	0	8510	1/1	0.97	0.12	40,40,40,40	0
34	NA	0	8511	1/1	0.97	0.04	43,43,43,43	0
32	MG	0	8047	1/1	0.97	0.05	59,59,59,59	0
32	MG	0	8048	1/1	0.97	0.05	62,62,62,62	0
35	CL	0	8803	1/1	0.97	0.08	80,80,80,80	0
34	NA	0	8536	1/1	0.97	0.05	52,52,52,52	0
35	CL	0	8812	1/1	0.97	0.10	65,65,65,65	0
35	CL	0	8813	1/1	0.97	0.08	67,67,67,67	0
34	NA	0	8538	1/1	0.97	0.06	61,61,61,61	0
32	MG	0	8098	1/1	0.97	0.06	30,30,30,30	0
32	MG	0	8064	1/1	0.97	0.08	43,43,43,43	0
32	MG	0	8091	1/1	0.97	0.06	53,53,53,53	0
34	NA	0	8518	1/1	0.97	0.04	32,32,32,32	0
34	NA	0	8519	1/1	0.97	0.04	34,34,34,34	0
34	NA	0	8554	1/1	0.97	0.08	38,38,38,38	0
34	NA	0	8578	1/1	0.97	0.14	77,77,77,77	0
34	NA	0	8502	1/1	0.97	0.06	49,49,49,49	0
34	NA	0	8522	1/1	0.97	0.22	68,68,68,68	0
34	NA	0	8503	1/1	0.97	0.25	70,70,70,70	0
34	NA	0	8558	1/1	0.97	0.21	107,107,107,107	0
35	CL	Q	8811	1/1	0.97	0.09	72,72,72,72	0
32	MG	0	8071	1/1	0.97	0.06	80,80,80,80	0
34	NA	0	8525	1/1	0.97	0.06	50,50,50,50	0
32	MG	0	8052	1/1	0.97	0.05	44,44,44,44	0
32	MG	A	8066	1/1	0.97	0.05	88,88,88,88	0
32	MG	0	8109	1/1	0.98	0.08	33,33,33,33	0
32	MG	0	8111	1/1	0.98	0.04	48,48,48,48	0
32	MG	0	8070	1/1	0.98	0.06	54,54,54,54	0
34	NA	0	8576	1/1	0.98	0.06	51,51,51,51	0
34	NA	0	8501	1/1	0.98	0.03	29,29,29,29	0
34	NA	0	8531	1/1	0.98	0.07	55,55,55,55	0
32	MG	0	8113	1/1	0.98	0.07	49,49,49,49	0
34	NA	0	8581	1/1	0.98	0.06	52,52,52,52	0
32	MG	0	8024	1/1	0.98	0.05	45,45,45,45	0
32	MG	0	8061	1/1	0.98	0.04	36,36,36,36	0
34	NA	0	8535	1/1	0.98	0.21	73,73,73,73	0
32	MG	0	8081	1/1	0.98	0.07	74,74,74,74	0
34	NA	0	8521	1/1	0.98	0.10	73,73,73,73	0
34	NA	0	8539	1/1	0.98	0.03	26,26,26,26	0
35	CL	J	8821	1/1	0.98	0.07	54,54,54,54	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	A	8065	1/1	0.98	0.05	43,43,43,43	0
35	CL	M	8818	1/1	0.98	0.05	60,60,60,60	0
34	NA	J	8546	1/1	0.98	0.04	48,48,48,48	0
32	MG	0	8025	1/1	0.98	0.03	58,58,58,58	0
34	NA	0	8542	1/1	0.98	0.12	51,51,51,51	0
32	MG	0	8084	1/1	0.98	0.06	54,54,54,54	0
32	MG	0	8027	1/1	0.98	0.04	63,63,63,63	0
32	MG	0	8053	1/1	0.98	0.10	47,47,47,47	0
36	CD	O	8705	1/1	0.98	0.04	98,98,98,98	0
34	NA	0	8553	1/1	0.98	0.04	36,36,36,36	0
32	MG	0	8003	1/1	0.99	0.04	47,47,47,47	0
32	MG	0	8034	1/1	0.99	0.03	36,36,36,36	0
32	MG	3	8078	1/1	0.99	0.04	43,43,43,43	0
32	MG	0	8036	1/1	0.99	0.03	44,44,44,44	0
32	MG	0	8067	1/1	0.99	0.04	54,54,54,54	0
32	MG	0	8068	1/1	0.99	0.03	70,70,70,70	0
32	MG	0	8037	1/1	0.99	0.04	51,51,51,51	0
32	MG	0	8015	1/1	0.99	0.02	41,41,41,41	0
32	MG	0	8072	1/1	0.99	0.03	61,61,61,61	0
32	MG	0	8074	1/1	0.99	0.02	40,40,40,40	0
32	MG	0	8039	1/1	0.99	0.10	44,44,44,44	0
32	MG	0	8080	1/1	0.99	0.04	47,47,47,47	0
32	MG	0	8106	1/1	0.99	0.03	38,38,38,38	0
32	MG	0	8016	1/1	0.99	0.02	48,48,48,48	0
32	MG	0	8018	1/1	0.99	0.04	50,50,50,50	0
32	MG	0	8110	1/1	0.99	0.03	59,59,59,59	0
32	MG	0	8005	1/1	0.99	0.03	45,45,45,45	0
34	NA	0	8549	1/1	0.99	0.06	54,54,54,54	0
32	MG	0	8085	1/1	0.99	0.04	62,62,62,62	0
32	MG	0	8086	1/1	0.99	0.04	46,46,46,46	0
32	MG	0	8056	1/1	0.99	0.04	49,49,49,49	0
32	MG	0	8012	1/1	0.99	0.02	33,33,33,33	0
32	MG	0	8116	1/1	0.99	0.06	39,39,39,39	0
32	MG	0	8058	1/1	0.99	0.05	46,46,46,46	0
32	MG	0	8090	1/1	0.99	0.03	59,59,59,59	0
32	MG	0	8059	1/1	0.99	0.03	44,44,44,44	0
32	MG	B	8055	1/1	0.99	0.06	46,46,46,46	0
32	MG	0	8060	1/1	0.99	0.03	50,50,50,50	0
36	CD	Z	8703	1/1	0.99	0.02	71,71,71,71	0
32	MG	0	8013	1/1	0.99	0.03	54,54,54,54	0
32	MG	0	8011	1/1	1.00	0.04	32,32,32,32	0
32	MG	0	8028	1/1	1.00	0.03	48,48,48,48	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MG	0	8083	1/1	1.00	0.06	52,52,52,52	0
32	MG	0	8029	1/1	1.00	0.02	55,55,55,55	0
32	MG	0	8030	1/1	1.00	0.02	34,34,34,34	0
32	MG	0	8001	1/1	1.00	0.02	33,33,33,33	0
32	MG	0	8054	1/1	1.00	0.02	43,43,43,43	0
32	MG	0	8032	1/1	1.00	0.03	32,32,32,32	0
32	MG	0	8033	1/1	1.00	0.02	37,37,37,37	0
32	MG	0	8004	1/1	1.00	0.02	43,43,43,43	0
32	MG	0	8035	1/1	1.00	0.02	58,58,58,58	0
32	MG	0	8002	1/1	1.00	0.04	35,35,35,35	0
32	MG	0	8006	1/1	1.00	0.01	37,37,37,37	0
32	MG	0	8007	1/1	1.00	0.03	29,29,29,29	0
32	MG	0	8017	1/1	1.00	0.04	33,33,33,33	0
32	MG	0	8008	1/1	1.00	0.02	35,35,35,35	0
32	MG	0	8019	1/1	1.00	0.02	39,39,39,39	0
32	MG	0	8020	1/1	1.00	0.03	31,31,31,31	0
32	MG	0	8021	1/1	1.00	0.01	31,31,31,31	0
32	MG	0	8022	1/1	1.00	0.02	42,42,42,42	0
32	MG	0	8023	1/1	1.00	0.02	42,42,42,42	0
32	MG	0	8009	1/1	1.00	0.04	36,36,36,36	0
32	MG	0	8010	1/1	1.00	0.02	45,45,45,45	0
32	MG	0	8077	1/1	1.00	0.03	32,32,32,32	0
36	CD	U	8701	1/1	1.00	0.01	76,76,76,76	0
32	MG	0	8079	1/1	1.00	0.02	43,43,43,43	0
36	CD	1	8702	1/1	1.00	0.04	68,68,68,68	0
32	MG	0	8026	1/1	1.00	0.01	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.