



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:03 PM BST

PDB ID : 3J3V
EMDB ID: : EMD-5642
Title : Atomic model of the immature 50S subunit from Bacillus subtilis (state I-a)
Authors : Li, N.; Guo, Q.; Zhang, Y.; Yuan, Y.; Ma, C.; Lei, J.; Gao, N.
Deposited on : 2013-04-28
Resolution : 13.30 Å (reported)
Based on PDB ID : 2J01, 2AW4

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
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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

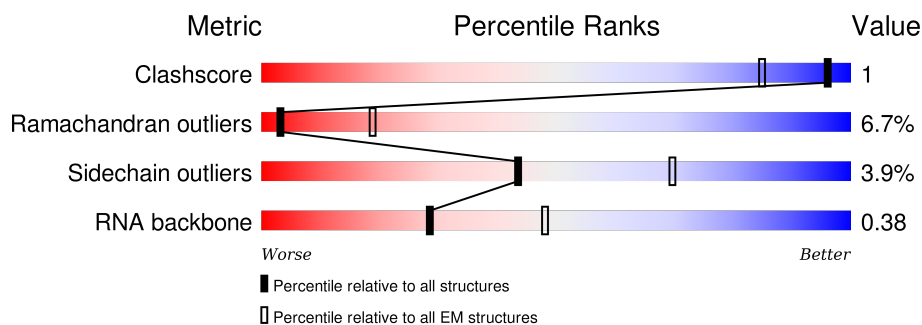
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.30 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.









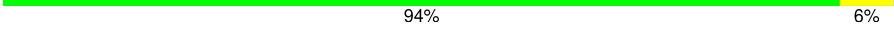


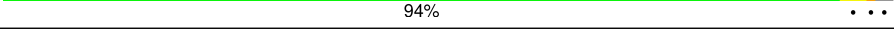

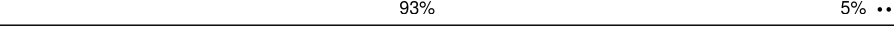

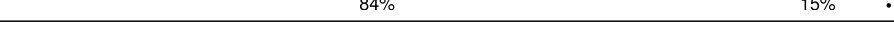


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 ≥ 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	0	59	86% 7% 7%
2	2	44	93% 7%
3	5	232	44% 7% 48%
4	6	141	94% 6%
5	A	2927	53% 36% 9% .
6	B	119	66% 25% 8% .
7	C	277	90% 9% .
8	D	209	89% 9% ..

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Mol	Chain	Length	Quality of chain
9	E	207	 86% 12% •
10	F	179	 86% 13% •
11	G	179	 87% • 9%
12	J	145	 86% 11% ••
13	K	122	 93% 7%
14	L	146	 85% 12% •
15	N	120	 94% 6%
16	O	120	 83% 15% •
17	P	115	 73% 20% • •
18	Q	119	 94% • • •
19	R	102	 88% 11% •
20	S	113	 93% 5% ••
21	T	95	 86% 12% •
22	U	103	 84% 15% •
23	X	66	 85% 8% 8%
24	Y	59	 92% • 5%

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 86157 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	55	Total	C	N	O	S	0	0
			433	267	87	72	7		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	44	Total	C	N	O	S	0	0
			368	222	89	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	120	Total	C	N	O	S	0	0
			910	576	156	176	2		

- Molecule 4 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	141	Total	C	N	O	S	0	0
			1044	657	184	196	7		

- Molecule 5 is a RNA chain called ribosome RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2884	Total	C	N	O	P	0	0
			61914	27625	11428	19979	2882		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	119	Total	C	N	O	P	0	0
			2542	1135	462	827	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	277	Total	C	N	O	S	0	0
			2129	1323	419	380	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	206	Total	C	N	O	S	0	0
			1568	984	289	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	206	Total	C	N	O	S	0	0
			1567	983	290	292	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	179	Total	C	N	O	S	0	0
			1413	898	246	261	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	163	Total	C	N	O	S	0	0
			1246	776	226	242	2		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	143	Total	C	N	O	S	0	0
			1134	717	207	204	6		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	122	Total	C	N	O	S	0	0
			921	571	173	173	4		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	146	Total	C	N	O	S	0	0
			1082	671	207	202	2		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	120	Total	C	N	O	S	0	0
			962	588	187	182	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	112	Total	C	N	O	0	0
			916	584	178	154		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	102	Total	C	N	O	S	0	0
			795	506	140	148	1		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	112	Total	C	N	O	S	0	0
			868	541	168	155	4		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	95	Total	C	N	O	S	0	0
			767	480	139	144	4		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	103	Total	C	N	O	S	0	0
			780	488	145	143	4		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	61	Total	C	N	O	S	0	0
			504	312	97	93	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

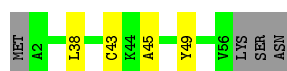
Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	56	Total	C	N	O	S	0	0
			441	273	86	81	1		

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: 50S ribosomal protein L32

Chain 0: 



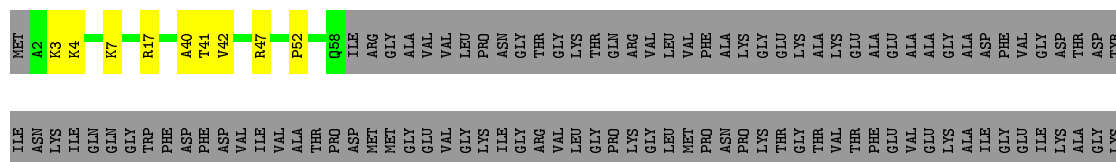
- Molecule 2: 50S ribosomal protein L34

Chain 2: 



- Molecule 3: 50S ribosomal protein L1

Chain 5: 



- Molecule 4: 50S ribosomal protein L11

Chain 6: 



- Molecule 5: ribosome RNA 23S

Chain A: 



A1021	C961	U901	A841	A781	G721	A861	U601	G541	U481	A421	G361	U301	C241	G181	G121	A61
G1022	C962	G902	C842	A782	A722	U662	G602	G542	C462	C422	C362	U302	U242	G182	G122	C62
G1023	G963	G903	C843	A783	A723	G663	G603	A543	C463	G423	C363	U303	G243	A183	A123	G63
G1024	A964	G904	C784	A784	A724	C664	C604	A544	C464	A244	G364	U304	A244	G184	G124	A64
A1025	A965	G905	C785	A785	C725	G665	G605	U545	U485	C425	U365	A305	G245	A185	A125	A65
A1026	U966	G906	C786	A786	C726	G666	U606	G546	A486	G426	G366	A306	U246	A186	A126	C66
A1027	G967	U907	A847	C787	A727	A667	G607	A547	C467	G427	G367	A307	A247	C187	C127	A67
C1028	C968	A908	C788	A788	G728	G668	C608	A548	U488	A248	C368	U308	C248	G188	C128	C68
A1029	C969	G909	C789	A789	G729	G669	C609	A549	U489	A249	A369	U309	C249	G189	C129	C69
G1030	A970	A910	U850	A790	U730	C670	U610	G550	A490	C430	G370	U310	G250	G190	A130	A71
C1031	A971	G911	A851	C791	U731	G671	U611	A551	C491	A431	G371	U311	G251	G191	C131	A72
G1032	G972	C912	G852	G792	A732	C672	U612	G552	C492	C432	U372	G312	G252	G192	C132	U72
C1033	G973	G913	C853	U793	U733	G673	U613	A553	G493	G433	A373	G313	G253	A193	A133	A73
A1034	A974	C914	U854	U794	C734	G674	G614	U554	A494	U434	A374	A314	A254	A194	C134	U74
G1035	C975	U915	G855	G795	U735	C675	U615	C555	U495	G435	A375	G315	G255	A195	U135	G75
A1036	U976	G916	G856	A796	U736	G676	A616	C556	U496	A436	A376	G316	C256	U196	C136	C76
C1037	U977	U917	U857	A797	C737	A677	G617	U557	G497	A437	G377	G317	G257	G197	G137	U77
G1038	A978	U918	U858	A798	C738	A678	A618	G558	U498	A438	C378	A318	A258	A198	U138	U78
C1039	U979	U919	C859	A799	C739	A679	A619	A559	U499	U439	C379	G319	A259	A199	A139	C79
G1040	C980	G920	U860	G800	A740	G680	U620	A560	A500	U440	C380	U320	A260	A200	A140	G80
C1041	C981	G921	C861	U801	U741	G681	U621	A561	A501	C441	U381	U321	C261	A201	U141	G81
A1042	U982	A922	U862	G802	G742	G682	A622	C562	C502	C442	G382	A322	G262	A202	G142	G82
G1043	U983	C923	C863	C803	U743	A683	G623	C563	C503	G443	G383	C323	G263	U203	G143	G83
C1044	G984	U924	G864	G804	C744	G684	C624	G564	A504	U444	A384	A324	G264	C204	A144	A84
U1045	G985	A925	G865	G805	G745	U685	C625	U565	G505	C445	G385	A325	A265	U205	G145	G85
A1046	G986	G926	A866	G806	A746	C866	G626	G566	U506	G446	U386	A326	U266	A206	U146	C86
A1047	A987	G927	A867	G807	G747	U687	G627	U567	A507	G447	C387	G327	U267	A207	G147	U87
G1048	U988	G928	A868	A808	G748	G688	C628	G568	C508	A448	A388	G328	A268	G208	G148	G88
U1049	U989	G929	U869	A809	G749	A689	G629	C569	C509	A449	A389	A329	G269	U209	U149	U89
U1050	C990	G930	A870	G810	U750	A690	A630	C570	G510	U450	A390	A330	C270	A210	A150	A90
C1051	A991	C931	G871	A811	G751	U691	U631	U571	U511	C451	A391	C331	C271	C211	U151	A91
C1052	G992	C932	C872	G812	A752	A692	U632	A572	G512	C452	C392	G332	C272	C212	C152	G92
C1053	A993	C933	U873	G813	A753	G693	U633	C573	A513	G453	U393	G333	A273	G213	G153	C93
A1054	C994	U934	U874	U814	G754	G694	A634	A574	G514	G454	U394	G334	A274	G214	A154	A94
A1055	U995	A935	U875	G815	U755	G695	C635	A575	G515	A455	C395	G335	A275	G215	U155	A95
A1056	G996	C936	A876	U816	U756	C696	G636	G576	G516	A456	G396	U336	C276	A216	A156	G96
G1057	C997	C937	G877	G817	C757	G697	A637	U577	A517	G457	U397	A337	C277	G217	U157	C97
U1058	G998	G938	C878	G818	A758	C698	U638	A578	A518	G458	U398	G338	A278	G218	C158	U98
A1059	A999	G939	G879	G819	G759	A699	C639	G579	A519	A459	C399	A339	A279	A219	U159	U99
G1060	U1000	G940	C880	U820	G760	U700	C640	U580	G520	C460	U400	U340	G280	A220	G160	U100
A1061	U1001	U941	U881	A821	U761	G701	C641	C581	U521	C461	C401	G341	A281	G221	A161	G101
C1062	U1002	U942	A882	G822	A762	A702	G642	A582	U522	A462	U402	A342	G282	A222	A162	A102
G1063	A1003	A943	G883	G823	A763	G703	U643	G583	G523	U463	C403	A343	G283	G223	U163	U103
U1064	G1064	C944	C884	G824	C764	U704	G644	A584	A524	C464	C404	G344	C284	A224	U164	C104
U1065	A1005	C945	C885	G825	A765	A705	C645	G585	A525	U465	U405	A345	U285	A225	C165	C105
A1066	C1066	G946	U886	U826	C766	C706	A646	C586	A526	C466	G406	G346	U286	A226	A166	G106
A1067	G1067	A947	C887	G827	U767	G707	A647	C587	A527	C467	A407	G347	G287	G227	U167	G107
G1068	A1008	A948	A888	A828	G768	U708	G648	C588	G528	C468	G408	U348	C288	C228	A168	A108
U1069	U1009	U949	A889	A829	A769	G709	G649	G589	C529	A469	U409	U349	G289	A229	G169	G109
G1070	C1010	U950	C890	A830	A770	G710	U650	U590	A530	A470	G410	U350	U290	A230	G170	A110
G1071	G1011	C951	G891	U831	U771	U711	U651	U591	C531	G471	G411	G351	C291	A231	A171	U111
A1072	G1012	A952	U892	G832	G772	C712	A652	A592	C532	G472	G412	G352	U292	U232	U172	U112
A1073	U1013	G953	C893	G833	G773	G713	A653	A593	C533	C473	U413	A353	U293	G233	A173	U113
A1074	A1014	U954	A894	C834	A774	U714	G654	C594	C534	U474	C414	A354	G294	C234	U174	G114
A1075	G1015	C955	G895	A835	G775	A715	G655	G595	G535	A475	C415	A355	G295	G235	G175	C115
G1076	U1016	A956	A896	A836	G776	G716	A656	G596	G536	A476	U416	G356	G296	G236	A176	G116
G1077	C1017	A957	G897	U837	G777	A717	G657	G597	A537	A477	G417	G357	G297	U237	G177	A117
A1078	G1018	C958	U898	C838	C778	C718	A658	U598	A538	U478	A418	C358	U298	U238	A178	A118
U1079	U1019	C959	C899	G839	C779	C719	A659	G599	G539	U479	G419	C359	U299	G239	A179	U119
G1080	A1020	U960	U900	A840	G780	C720	G660	A600	G540	C460	U420	C360	G300	C240	G180	G120

A1981	C1921	C1861	G1801	G1741	U1681	G1621	U1501	U1441	A1381	U1321	C1261	A1201	A1141	U1081
A1982	C1922	C1862	A1802	G1742	C1682	C1622	G1502	A1442	G1382	G1322	C1262	A1202	A1142	G1082
G1983	C1923	U1863	C1803	A1743	G1683	C1623	G1503	C1443	U1383	A1323	G1263	A1203	A1143	G1083
U1984	C1924	G1864	U1804	G1744	U1684	U1624	A1504	C1444	C1384	G1324	G1264	C1204	A1144	A1084
U1985	A1925	C1865	G1805	A1745	A1685	C1625	U1505	A1445	G1385	A1325	A1265	U1205	G1145	G1085
G1986	G1926	C1866	U1806	A1746	A1686	G1626	A1506	C1446	G1386	A1326	A1266	G1206	G1146	U1086
G1987	U1927	C1867	U1807	G1747	G1687	A1627	U1507	C1447	G1387	U1327	G1267	C1207	U1147	U1087
G1988	A1928	G1868	U1808	G1748	G1688	C1628	C1508	U1448	A1388	C1328	G1268	G1208	U1148	G1088
G1989	A1929	G1869	A1809	G1749	U1689	C1629	A1509	C1449	C1389	C1329	A1269	G1209	A1149	C1089
G1990	A1930	U1870	G1810	G1750	G1690	A1630	G1510	C1450	C1390	C1330	C1270	A1210	C1150	U1090
C1991	C1931	A1871	C1811	U1751	A1691	A1631	U1511	U1451	U1391	C1331	U1271	C1211	U1151	U1091
G1992	G1932	C1872	A1812	G1752	U1692	G1632	G1512	C1452	A1392	U1332	G1272	U1212	G1152	A1092
G1993	G1933	U1873	A1813	C1753	C1693	G1633	U1513	A1453	A1393	G1273	G1213	G1213	G1153	A1093
C1994	C1934	G1874	A1814	U1754	G1694	U1634	C1514	C1454	G1394	C1334	U1274	U1214	U1154	A1094
A1995	G1935	G1875	A1815	C1755	A1695	G1635	C1515	C1455	C1395	A1335	G1275	C1215	C1155	C1095
G1996	G1936	A1876	A1816	U1756	G1696	A1636	A1516	A1456	C1396	C1336	G1276	C1216	G1156	A1096
G1997	C1937	A1877	C1817	G1757	A1697	A1637	A1517	U1457	G1397	C1337	U1277	U1217	A1157	A1097
A1998	C1938	G	A1818	U1758	G1698	A1638	G1518	U1458	A1398	G1338	G1278	U1218	G1158	C1098
G1999	G1939	G	A1819	U1759	A1699	G1639	C1519	U1459	G1399	A1339	C1279	C1219	U1159	C1099
A2000	U1940	U	A1820	A1760	A1700	G1640	A1520	G1460	G1400	A1340	G1280	G1220	G1160	A1100
G2001	G1941	U	C1821	G1761	C1701	A1641	A1521	A1461	C1401	A1341	G1281	A1221	A1161	G1101
G2002	A1942	A	G1822	G1762	U1702	G1642	U1522	G1462	C1402	G1342	A1282	A1222	C1162	G1102
G2003	C1943	A	U1823	G1763	C1703	C1643	U1523	G1463	C1403	C1343	U1283	C1223	U1163	A1103
G2004	U1944	G	C1824	U1764	U1704	C1644	A1524	A1464	A1404	C1344	A1284	A1224	C1164	U1104
A2005	A1945	A	U1825	G1765	C1705	C1645	A1525	A1465	A1405	U1345	G1285	G1225	U1165	G1105
A2006	U1946	G	C1826	C1766	G1706	G1646	G1526	U1466	A1406	A1346	A1286	U1226	G1166	U1106
A2007	A1947	G	U1827	A1767	U1707	U1647	C1527	G1467	G1407	A1347	A1287	G1227	C1167	U1107
G2008	A1948	A	G1828	A1768	A1708	A1648	U1528	G1468	G1408	G1348	G1288	G1228	G1168	G1108
G2009	G1949	G	C1829	G1769	A1709	C1649	G1529	G1469	C1409	G1349	U1289	C1229	C1169	G1109
A2010	G1950	C	A1830	C1770	A1710	G1650	G1530	G1470	G1410	A1290	A1230	C1170	G1110	G110
U2011	G1951	C	A1831	C1771	G1711	G1651	G1531	G1471	U1411	U1351	A1291	G1231	G1171	U1111
C2012	U1952	C	A1832	C1772	G1712	C1652	A1532	G1472	A1412	U1352	G1292	G1232	A1172	U1112
G2013	C1953	C	G1833	G1773	A1713	A1653	A1533	A1473	G1413	C1353	A1293	A1233	A1173	A1113
G2014	G1954	U	C1834	A1774	A1714	A1654	A1534	C1474	G1414	C1354	A1294	G1234	A1174	G1114
G2015	U1955	A	G1835	G1775	C1715	A1655	U1535	G1475	C1415	U1355	U1295	A1235	A1175	A1115
G2016	A1956	G	G1836	A1776	U1716	C1656	A1536	C1476	G1416	G1356	G1296	G1236	U1176	A1116
C2017	A1957	C	U1837	G1777	C1717	C1657	G1537	A1477	A1417	A1357	C1297	C1237	G1177	G1117
A2018	G1958	G	A1838	A1778	G1718	G1658	G1538	G1478	U1418	G1358	C1298	G1238	U1178	C1118
G2019	G1959	U	A1839	G1779	G1719	A1659	C1539	G1479	G1419	G1359	G1299	U1239	A1179	A1119
U2020	U1960	A	G1840	C1780	C1720	C1660	A1540	A1480	G1420	A1360	G1300	U1240	C1180	G1120
G2021	A1961	A	G1841	C1781	A1721	A1661	A1541	G1481	A1421	A1361	U1301	C1241	C1181	C1121
U2022	G1962	G	C1842	G1782	A1722	C1662	A1542	G1482	C1422	G1362	A1302	U1242	G1182	C1122
C1963	C1963	C	G1843	G1783	A1723	A1663	U1543	A1483	A1423	G1363	U1303	A1243	G1183	A1123
U2024	G1964	G	A1844	A1784	A1724	G1664	C1544	U1484	A1424	C1364	G1304	A1244	G1184	C1124
C2025	A1965	A	A1845	G1785	U1725	G1665	C1545	A1485	C1425	U1365	A1305	G1245	G1185	C1125
A2026	A1966	A	G1846	U1786	G1726	U1666	G1546	G1486	A1426	C1366	G1306	G1246	C1186	A1126
A2027	A1967	G	U1847	G1787	A1727	A1667	U1547	G1487	G1427	G1367	U1307	G1247	U1187	U1127
C2028	U1968	G	A1848	A1788	C1728	G1668	A1548	G1488	G1428	C1368	A1308	C1248	A1188	U1128
G2029	U1969	U	U1849	A1789	C1729	G1669	U1549	U1489	U1429	C1369	G1309	U1249	A1189	G1129
A2030	C1970	G	A1850	U1790	C1730	C1670	C1550	A1490	U1430	C1370	C1310	G1250	A1190	A1130
G2031	C1971	C	G1851	A1791	C1731	G1671	C1551	A1491	G1431	G1371	C1311	U1251	C1191	A1131
A2032	U1972	G	G1852	G1792	G1732	A1672	C1552	G1492	A1432	C1372	A1312	G1252	G1192	A1132
G2033	G1973	A	C1853	G1793	U1733	C1673	A1553	G1493	A1433	C1373	A1313	A1253	U1193	G1133
A2034	C1974	A	G1854	C1794	A1734	A1674	U1554	G1494	A1434	C1374	A1314	A1254	A1194	A1134
C2035	U1975	U	C1855	A1795	A1735	G1675	A1555	C1495	U1435	U1375	G1315	G1255	U1195	G1135
U2036	C1976	U	U1856	C1796	C1736	A1676	A1556	G1496	U1436	G1376	A1316	C1256	C1196	U1136
C2037	G1977	G	G1857	A1797	U1737	A1677	G1557	G1497	C1437	G1377	G1317	C1257	A1197	G1137
G2038	G1978	A	A1858	U1798	U1738	A1678	G1558	U1498	C1438	G1378	G1318	A1258	C1198	G1138
G2039	G1979	A	C1859	G1799	C1739	A1679	A1559	A1499	A1439	U1379	G1319	G1259	C1199	G1139
U2040	U1980	G	G1860	C1800	G1740	A1680	U1560	U1500	G1440	U1380	G1320	A1260	G1200	U1140

G2881	G2882	G2883	G2884	G2885	G2886	G2887	G2888	G2889	G2890	G2891	G2892	G2893	G2894	G2895	G2896	G2897	A2898	G2899	A2900	G2901	A2902	G2903	A2904	G2905	G2906	A2907	A2908	G2909	G2910	G2911	A2912	G2913	G2914	G2915	G2916	G2917	G2918	A2919	G2920	G2921	G2922	A2923	A2924	G2925	A2926	A2927														
G2101	G2102	G2103	U2104	U2105	U2106	G2107	U2108	G2109	G2110	U2111	G2112	G2113	G2114	U2115	U2116	G2117	U2117	U2118	A2119	U2120	U2121	G2122	A2123	A2124	U2125	G2126	G2127	U2128	G2129	G2130	U2131	A2132	G2133	A2134	G2135	G2136	G2137	U2138	U2139	G2140	A2141	G2142	A2143	U2144	G2145	A2146	U2147	U2148	A2149	G2150	U2151	G2152	G2153	A2154	G2155	U2156	G2157	G2158	G2159	U2160
G2161	G2162	G2163	A2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	U2175	A2176	G2177	G2178	U2179	U2180	U2181	G2182	G2183	U2184	U2185	G2186	A2187	G2188	U2189	G2190	G2191	U2192	G2193	A2194	G2195	U2196	G2197	G2198	G2199	A2200	U2201	A2202	G2203	U2204	A2205	G2206	G2207	G2208	U2209	G2210	G2211	G2212	G2213	U2214	G2215	A2216	U2217	A2218	G2219	U2220	
G2221	G2222	G2223	U2224	G2225	U2226	A2227	A2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	U2239	U2240	U2241	U2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	A2254	G2255	A2256	G2257	U2258	G2259	U2260	G2261	A2262	G2263	G2264	U2265	G2266	G2267	G2268	G2269	A2270	G2271	G2272	U2273	U2274	A2275	A2276	G2277	U2278	G2279	G2280	
G2281	G2282	G2283	U2284	G2285	U2286	G2287	G2288	G2289	G2290	U2291	G2292	G2293	U2294	A2295	A2296	A2297	A2298	G2299	G2300	U2301	A2302	G2303	G2304	G2305	G2306	A2307	G2308	G2309	G2310	G2311	G2312	U2313	G2314	A2315	A2316	G2317	G2318	G2319	U2320	U2321	G2322	G2323	G2324	U2325	G2326	U2327	A2328	A2329	A2330	U2331	G2332	G2333	U2334	U2335	A2336	G2337	A2338	A2339	U2340	
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U2521	U2522	G2523	U2524	G2525	A2526	G2527	G2528	U2529	G2530	G2531	A2532	G2533	G2534	U2535	G2536	G2537	G2538	G2539	U2540	G2541	A2542	G2543	G2544	G2545	G2546	U2547	U2548	G2549	G2550	U2551	G2552	G2553	A2554	G2555	G2556	U2557	G2558	U2559	A2560	G2561	U2562	G2563	A2564	G2565	U2566	G2567	G2568	G2569	A2570	A2571	G2572	G2573	G2574	U2575	U2576	G2577	G2578	G2579	G2580	
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U2701	G2702	G2703	A2704	G2705	G2706	G2707	A2708	G2709	G2710	G2711	G2712	U2713	G2714	G2715	U2716	G2717	U2718	A2719	U2720	G2721	A2722	G2723	U2724	G2725	G2726	U2727	U2728	G2729	U2730	G2731	G2732	G2733	A2734	U2735	G2736	G2737	G2738	G2739	U2740	U2741	G2742	G2743	G2744	U2745	U2746	U2747	U2748	U2749	A2750	G2751	G2752	U2753	U2754	U2755	G2756	U2757	G2758	G2759	G2760	
G2761	A2762	G2763	G2764	G2765	G2766	A2767	U2768	A2769	A2770	G2771	U2772	G2773	G2774	U2775	G2776	A2777	A2778	A2779	G2780	G2781	A2782	U2783	G2784	U2785	A2786	U2787	G2788	G2789	A2790	U2791	G2792	A2793	G2794	G2795	G2796	G2797	G2798	G2799	G2800	U2801	U2802	G2803	A2804	A2805	G2806	A2807	U2808	G2809	A2810	G2811	A2812	U2813	U2814	U2815	U2816	C2817	A2818	A2819	U2820	
U2821	G2822	G2823	G2824	G2825	A2826	A2827	G2828	G2829	A2830	U2831	G2832	U2833	A2834	U2835	U2836	A2837	U2838	G2839	G2840	G2841	U2842	G2843	A2844	A2845	A2846	U2847	A2848	U2849	G2850	A2851	U2852	G2853	A2854	G2855	G2856	U2857	U2858	G2859	A2860	U2861	A2862	G2863	U2864	U2865	U2866	U2867	A2868	A2869	G2870	G2871	U2872	G2873	U2874	U2875	A2876	U2877	U2878	G2879	U2880	

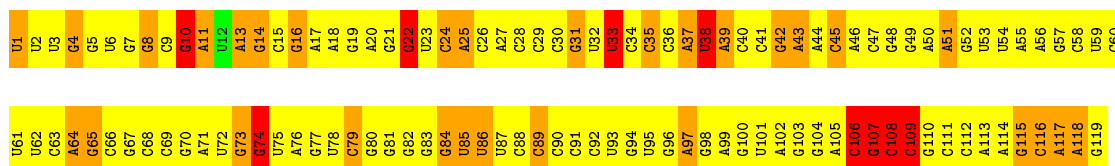
• Molecule 6: ribosome RNA 5S

Chain B: .

66%

25%

8%



- Molecule 7: 50S ribosomal protein L2

Chain C: 90% 9% •



- Molecule 8: 50S ribosomal protein L3

Chain D: 89% 9% ••



- Molecule 9: 50S ribosomal protein L4

Chain E: 86% 12% •



- Molecule 10: 50S ribosomal protein L5

Chain F: 86% 13% •



- Molecule 11: 50S ribosomal protein L6

Chain G: 87% 9% •



- Molecule 12: 50S ribosomal protein L13

Chain J: 86% 11% ••



- Molecule 13: 50S ribosomal protein L14

Chain K: 93% 7%



- Molecule 14: 50S ribosomal protein L15

Chain L: 85% 12% .



- Molecule 15: 50S ribosomal protein L17

Chain N: 94% 6%



- Molecule 16: 50S ribosomal protein L18

Chain O: 83% 15% .



- Molecule 17: 50S ribosomal protein L19

Chain P: 73% 20% . .



- Molecule 18: 50S ribosomal protein L20

Chain Q: 94% . . .



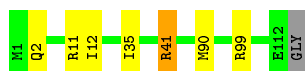
- Molecule 19: 50S ribosomal protein L21

Chain R: 88% 11% .




- Molecule 20: 50S ribosomal protein L22

Chain S: 93% 5% . .




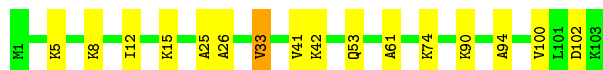
- Molecule 21: 50S ribosomal protein L23

Chain T:  86% 12%




- Molecule 22: 50S ribosomal protein L24

Chain U:  84% 15%



- Molecule 23: 50S ribosomal protein L29

Chain X:  85% 8% 8%



- Molecule 24: 50S ribosomal protein L30

Chain Y:  92% 5%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	21020	Depositor
Resolution determination method	SSNR-MAP(an optimized approach of Spectral Single-to Noise Ratio) at 1.0 cutoff	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI Eagle 4K*4K CCD	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0	1.04	0/440	1.06	1/584 (0.2%)
10	F	0.96	0/1432	1.09	2/1920 (0.1%)
11	G	0.98	0/1264	1.05	0/1709
12	J	0.94	0/1157	1.04	0/1557
13	K	1.03	0/928	1.05	0/1245
14	L	0.98	0/1094	1.09	2/1457 (0.1%)
15	N	1.08	0/969	1.06	0/1294
16	O	1.01	0/922	1.05	1/1236 (0.1%)
17	P	1.10	0/929	1.21	5/1243 (0.4%)
18	Q	1.06	0/952	1.08	4/1266 (0.3%)
19	R	0.91	0/806	1.09	0/1080
2	2	1.26	0/371	1.06	0/483
20	S	1.01	0/877	1.13	1/1179 (0.1%)
21	T	1.00	0/774	1.11	1/1030 (0.1%)
22	U	0.87	0/790	1.15	0/1054
23	X	1.05	0/505	1.02	0/671
24	Y	0.97	0/443	1.01	0/594
3	5	0.87	0/921	1.10	1/1239 (0.1%)
4	6	0.91	0/1058	1.02	0/1427
5	A	1.69	134/69349 (0.2%)	2.70	8798/108189 (8.1%)
6	B	1.64	4/2843 (0.1%)	2.64	336/4432 (7.6%)
7	C	1.01	0/2166	1.09	2/2902 (0.1%)
8	D	0.96	0/1590	1.07	0/2130
9	E	0.97	0/1586	1.08	2/2139 (0.1%)
All	All	1.55	138/94166 (0.1%)	2.45	9156/142060 (6.4%)

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
14	L	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
15	N	0	1
17	P	0	3
21	T	0	3
5	A	0	447
6	B	0	15
8	D	0	2
9	E	0	1
All	All	0	474

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1253	A	N7-C5	-7.44	1.34	1.39
5	A	353	A	N7-C5	-7.42	1.34	1.39
5	A	629	G	C2'-C1'	-7.08	1.45	1.53
5	A	1449	C	P-O5'	-7.08	1.52	1.59
5	A	2297	A	N7-C5	-6.86	1.35	1.39

The worst 5 of 9156 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	10	G	P-O3'-C3'	26.30	151.26	119.70
5	A	1339	A	P-O3'-C3'	26.04	150.94	119.70
5	A	178	A	P-O3'-C3'	22.26	146.41	119.70
5	A	2062	A	P-O3'-C3'	21.01	144.91	119.70
5	A	74	U	P-O3'-C3'	20.60	144.42	119.70

There are no chirality outliers.

5 of 474 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	14	A	Sidechain
5	A	15	G	Sidechain
5	A	27	G	Sidechain
5	A	28	A	Sidechain
5	A	3	U	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	433	0	454	0	0
2	2	368	0	410	0	0
3	5	910	0	944	2	0
4	6	1044	0	1098	1	0
5	A	61914	0	31166	148	0
6	B	2542	0	1288	6	0
7	C	2129	0	2225	0	0
8	D	1568	0	1635	2	0
9	E	1567	0	1652	3	0
10	F	1413	0	1479	2	0
11	G	1246	0	1273	0	0
12	J	1134	0	1178	3	0
13	K	921	0	977	0	0
14	L	1082	0	1132	3	0
15	N	962	0	995	0	0
16	O	913	0	947	4	0
17	P	916	0	987	2	0
18	Q	940	0	1005	1	0
19	R	795	0	838	0	0
20	S	868	0	930	0	0
21	T	767	0	813	0	0
22	U	780	0	838	1	0
23	X	504	0	541	0	0
24	Y	441	0	478	0	0
All	All	86157	0	55283	174	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 1.

The worst 5 of 174 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:A:1799:G:H1	5:A:2011:U:H3	1.32	0.76
5:A:2557:U:H3	5:A:2564:A:H61	1.39	0.68
5:A:1672:A:H61	5:A:1684:U:H3	1.43	0.65
5:A:1339:A:C2	5:A:1679:A:C2	2.87	0.62
5:A:1976:C:H2'	5:A:1977:G:H5''	1.80	0.62

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
1	0	53/59 (90%)	40 (76%)	10 (19%)	3 (6%)	2	28
2	2	42/44 (96%)	38 (90%)	2 (5%)	2 (5%)	3	32
3	5	116/232 (50%)	96 (83%)	11 (10%)	9 (8%)	1	20
4	6	139/141 (99%)	117 (84%)	15 (11%)	7 (5%)	3	31
7	C	275/277 (99%)	224 (82%)	33 (12%)	18 (6%)	1	25
8	D	204/209 (98%)	158 (78%)	38 (19%)	8 (4%)	4	36
9	E	204/207 (99%)	166 (81%)	19 (9%)	19 (9%)	1	16
10	F	177/179 (99%)	136 (77%)	27 (15%)	14 (8%)	1	19
11	G	161/179 (90%)	150 (93%)	9 (6%)	2 (1%)	16	61
12	J	141/145 (97%)	117 (83%)	14 (10%)	10 (7%)	1	22
13	K	120/122 (98%)	103 (86%)	11 (9%)	6 (5%)	3	31
14	L	144/146 (99%)	105 (73%)	24 (17%)	15 (10%)	1	12
15	N	118/120 (98%)	96 (81%)	19 (16%)	3 (2%)	7	46
16	O	118/120 (98%)	87 (74%)	18 (15%)	13 (11%)	0	11
17	P	110/115 (96%)	71 (64%)	23 (21%)	16 (14%)	0	6
18	Q	115/119 (97%)	104 (90%)	10 (9%)	1 (1%)	21	67
19	R	100/102 (98%)	79 (79%)	13 (13%)	8 (8%)	1	19
20	S	110/113 (97%)	97 (88%)	8 (7%)	5 (4%)	3	33
21	T	93/95 (98%)	70 (75%)	14 (15%)	9 (10%)	1	14
22	U	101/103 (98%)	71 (70%)	18 (18%)	12 (12%)	0	9
23	X	59/66 (89%)	53 (90%)	4 (7%)	2 (3%)	5	40
24	Y	54/59 (92%)	47 (87%)	5 (9%)	2 (4%)	4	38
All	All	2754/2952 (93%)	2225 (81%)	345 (12%)	184 (7%)	3	24

5 of 184 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	5	41	THR
3	5	209	VAL
3	5	212	VAL
4	6	93	ASN
7	C	34	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 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	
1	0	49/53 (92%)	49 (100%)	0	100	100
2	2	39/39 (100%)	38 (97%)	1 (3%)	54	80
3	5	98/185 (53%)	93 (95%)	5 (5%)	29	66
4	6	110/110 (100%)	110 (100%)	0	100	100
7	C	225/225 (100%)	213 (95%)	12 (5%)	28	64
8	D	167/170 (98%)	157 (94%)	10 (6%)	24	60
9	E	169/170 (99%)	163 (96%)	6 (4%)	42	74
10	F	154/154 (100%)	147 (96%)	7 (4%)	34	69
11	G	138/151 (91%)	133 (96%)	5 (4%)	42	74
12	J	122/123 (99%)	113 (93%)	9 (7%)	17	54
13	K	101/101 (100%)	98 (97%)	3 (3%)	48	77
14	L	110/110 (100%)	107 (97%)	3 (3%)	52	79
15	N	100/100 (100%)	97 (97%)	3 (3%)	48	77
16	O	93/93 (100%)	90 (97%)	3 (3%)	46	76
17	P	97/100 (97%)	90 (93%)	7 (7%)	18	55
18	Q	96/98 (98%)	95 (99%)	1 (1%)	82	92
19	R	84/84 (100%)	79 (94%)	5 (6%)	24	60
20	S	93/93 (100%)	91 (98%)	2 (2%)	60	83
21	T	85/85 (100%)	83 (98%)	2 (2%)	57	82
22	U	87/87 (100%)	84 (97%)	3 (3%)	44	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	54/57 (95%)	51 (94%)	3 (6%)	26	62
24	Y	51/53 (96%)	51 (100%)	0	100	100
All	All	2322/2441 (95%)	2232 (96%)	90 (4%)	43	72

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	F	169	LEU
12	J	69	LYS
21	T	91	GLU
11	G	28	LYS
11	G	164	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
10	F	37	ASN
10	F	172	GLN
15	N	61	GLN
10	F	2	ASN
16	O	103	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A	2882/2927 (98%)	895 (31%)	205 (7%)
6	B	118/119 (99%)	24 (20%)	3 (2%)
All	All	3000/3046 (98%)	919 (30%)	208 (6%)

5 of 919 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	2	G
5	A	3	U
5	A	4	U
5	A	8	U
5	A	10	A

5 of 208 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1417	A
5	A	1625	C
5	A	2821	U
5	A	1423	A
5	A	1497	G

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.