



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 08:25 AM EDT

PDB ID : 5GAG
EMDB ID: : EMD-8003
Title : RNC in complex with SRP-SR in the closed state
Authors : Jomaa, A.; Boehringer, D.; Leibundgut, M.; Ban, N.
Deposited on : unknown
Resolution : 3.80 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

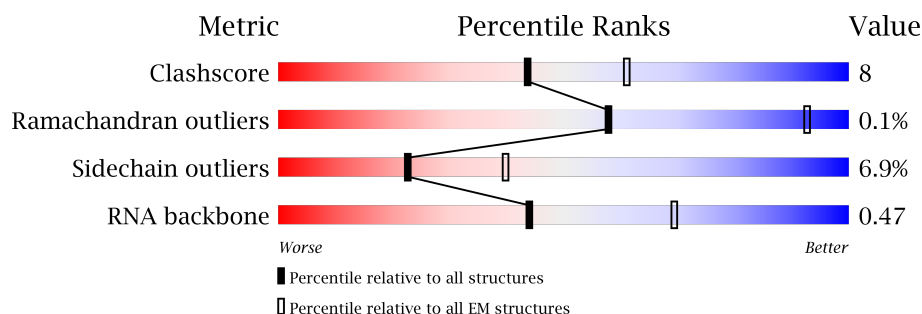
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.





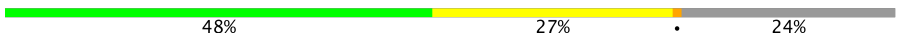


















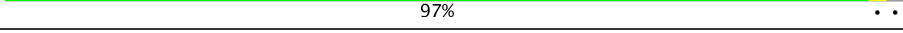



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	1	113	18% 15% 5% 62%
2	2	3	67% 33%
3	A	2903	58% 34% 6% ..
4	B	120	68% 30% .
5	C	273	71% 25% .
6	D	209	73% 24% .
7	E	201	78% 21%
8	F	179	64% 32% ..

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Mol	Chain	Length	Quality of chain
9	G	177	
10	H	149	
11	I	165	
12	J	142	
13	K	142	
14	L	123	
15	M	144	
16	N	136	
17	O	127	
18	P	117	
19	Q	115	
20	R	118	
21	S	103	
22	T	110	
23	U	100	
24	V	104	
25	W	94	
26	X	85	
27	Y	78	
28	Z	63	
29	a	59	
30	b	57	
31	c	55	
32	d	46	
33	e	65	

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Mol	Chain	Length	Quality of chain
34	f	38	<div><div></div><div>100%</div></div>
35	i	450	<div><div></div><div>26%</div><div></div><div>72%</div></div>
36	k	18	<div><div></div><div>100%</div></div>

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 94030 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 SRP 4.5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	43	Total	C	N	O	P	0	0
			926	413	174	296	43		

- Molecule 2 is a RNA chain called tRNA CCAend.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	2883	Total	C	N	O	P	0	0
			61902	27613	11397	20009	2883		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	178	Total	C	N	O	S	0	1
			1411	899	250	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	125	Total	C	N	O	S	0	0
			946	599	169	175	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	VAL	SER	conflict	UNP P0A7J3
I	86	THR	MET	conflict	UNP P0A7J3

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	95	Total	C	N	O	S	0	0
			756	479	141	135	1		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	103	Total	C	N	O	0	1
			780	492	147	141		

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	c	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 35 is a protein called Signal recognition particle protein Ffh.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	126	Total	C	N	O	S	0	0
			916	575	169	161	11		

- Molecule 36 is a protein called 1A9L SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	18	Total	C	N	O	S	0	0
			137	94	20	22	1		

- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	D	1	Total	Mg	0
			1	1	
37	B	12	Total	Mg	0
			12	12	
37	b	1	Total	Mg	0
			1	1	
37	C	2	Total	Mg	0
			2	2	
37	A	411	Total	Mg	0
			411	411	
37	O	1	Total	Mg	0
			1	1	
37	2	1	Total	Mg	0
			1	1	
37	Y	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	

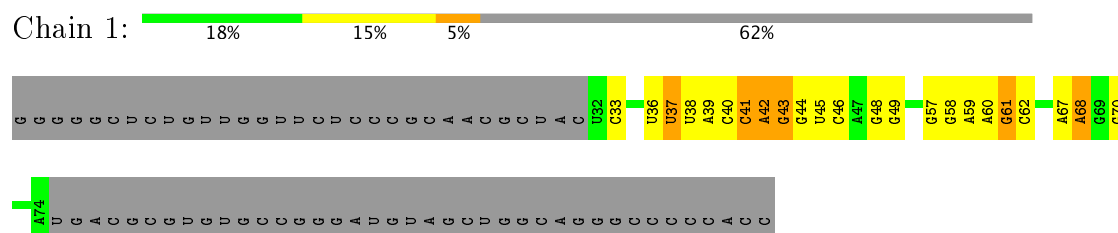
- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	

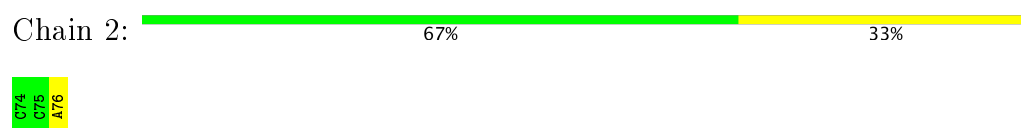
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

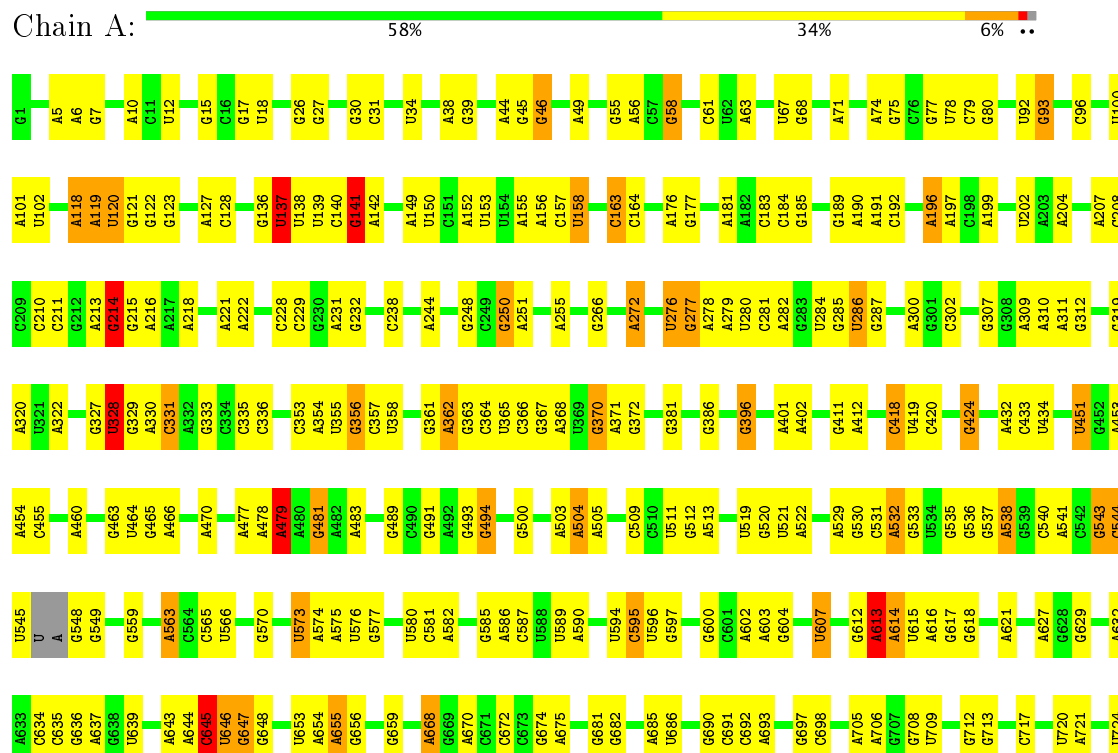
- Molecule 1: SRP 4.5S RNA



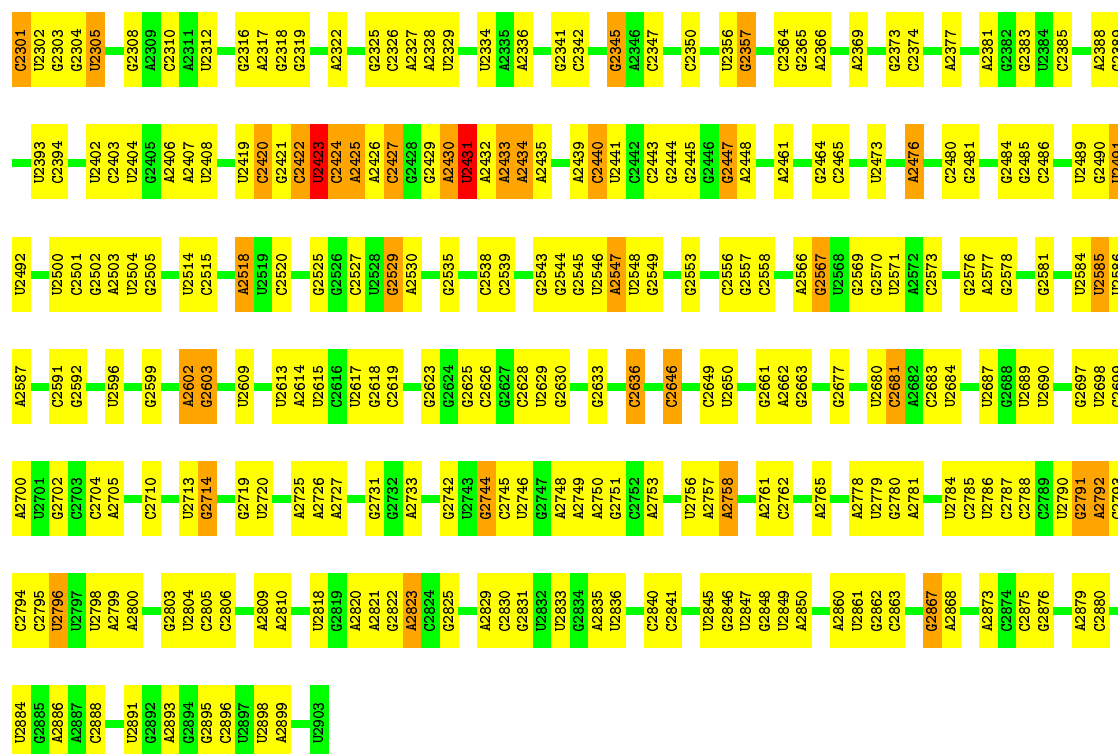
- Molecule 2: tRNA CCAend



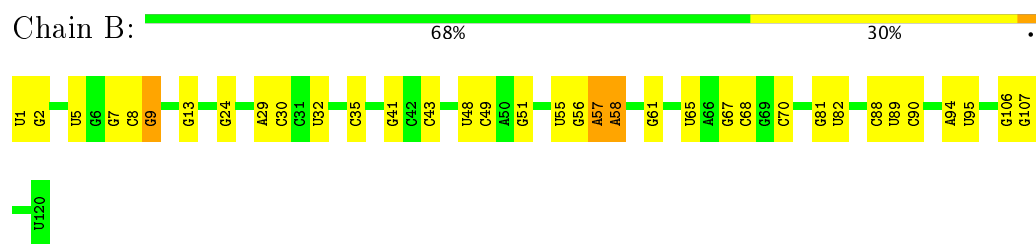
- Molecule 3: 23S rRNA



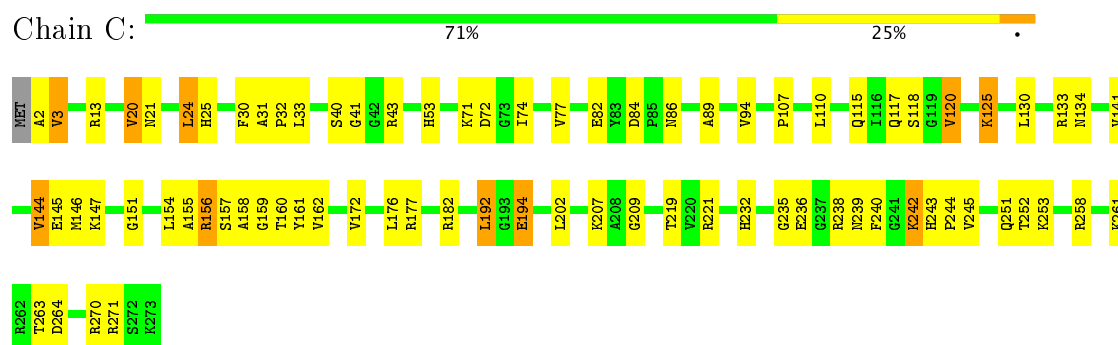
G2216	G2217	G2140	G1858	G1757	G1523	G1434	G1341	A1205	G1102	G1020	G914	U827	G726
G2221	G2222	G2145	U1859	A1757	G1524	A1434	A1342	G1206	A1103	A1021	G915	U828	G727
G2223	G2224	G2146	G1860	A1758	G1525	U1439	G1343	G1207	A1104	G1022	C916	G831	G728
G2225	G2226	G2147	G1866	C1764	C1526	U1440	U1344	C1208	U1105	A1023	C922	U832	G729
G2227	G2228	G2148	A1866	A1764	A1527	G1441	G1345	U1209	G1106	G1024	A827	A833	A730
G2229	G2230	G2149	G1869	A1773	G1529	U1443	G1346	G1212	G1107	G1025	G927	G834	G738
G2231	G2232	G2150	G1870	G1776	A1532	G1444	U1352	G1218	G1110	G1026	U932	U839	G739
G2233	G2234	G2151	A1871	G1777	C1533	G1445	A1353	G1219	A1111	A1027	U933	C840	U741
G2235	G2236	G2152	G1872	U1779	U1534	G1446	A1354	G1220	U934	A1028	U934	A742	A743
G2237	G2238	G2153	G1873	A1783	A1535	G1447	G1355	U1224	U1119	U1033	A843	A844	A744
G2239	G2240	G2154	G1874	A1784	G1537	G1448	G1356	G1227	U1120	G1038	A845	A846	U747
G2241	G2242	G2155	G1875	U1785	G1538	G1449	G1357	G1228	U1121	A1039	U847	U848	G748
G2243	G2244	G2156	U1880	A1786	G1539	G1450	G1358	G1229	U1122	G1040	A849	A850	A753
G2245	G2246	G2157	C1881	U1787	U1540	G1451	G1359	G1230	A1133	A1041	A851	A852	U754
G2247	G2248	G2158	U1882	C1790	U1541	G1452	C1362	G1231	A1134	G1042	A853	A854	A755
G2249	G2250	G2159	A1889	A1791	G1543	G1456	A1365	G1232	U1130	G1043	A855	A856	U756
G2251	G2252	G2160	A1890	U1796	A1544	U1457	A1366	G1233	U1131	A1044	A857	A858	G757
G2253	G2254	G2161	A1891	G1797	A1545	U1458	G1367	G1234	A1132	G1045	A859	A860	A764
G2255	G2256	G2162	A1900	U1798	A1546	G1459	G1368	G1235	G1133	A1046	A861	A862	G765
G2257	G2258	G2163	G1903	G1799	C1547	U1460	C1370	A1253	A1134	G1047	A863	A864	U766
G2259	G2260	G2164	G1904	A1801	A1548	C1461	G1371	G1254	U1135	A1048	A865	A866	U767
G2261	G2262	G2165	C1905	A1802	A1549	C1462	G1372	G1255	G1136	G1049	A867	A868	G774
G2263	G2264	G2166	G1906	U1803	A1550	G1463	A1373	G1256	U1137	A1050	A869	A870	G775
G2265	G2266	G2167	G1907	A1804	A1551	G1464	G1374	G1257	A1138	G1051	A871	A872	G776
G2267	G2268	G2168	G1908	U1805	A1552	G1465	A1375	G1258	G1139	G1052	A873	A874	G777
G2269	G2270	G2169	C1909	G1811	A1553	U1466	A1376	G1259	U1140	G1053	A875	A876	G778
G2271	G2272	G2170	U1911	G1812	A1554	U1467	G1377	G1260	A1141	G1054	A877	A878	G779
G2273	G2274	G2171	A1912	A1813	A1555	U1468	A1378	G1261	U1142	G1055	A879	A880	G780
G2275	G2276	G2172	C1913	G1814	A1556	U1469	G1379	G1262	A1143	G1056	A881	A882	A781
G2277	G2278	G2173	C1914	A1815	A1557	U1470	U1379	G1263	A1144	G1057	A883	A884	A782
G2279	G2280	G2174	U1915	G1816	A1558	U1471	U1380	G1264	G1145	G1058	A885	A886	A783
G2281	G2282	G2175	C1916	G1817	A1559	U1472	A1381	G1265	U1146	G1059	A887	A888	G784
G2283	G2284	G2176	U1917	A1818	A1560	U1473	G1382	G1266	G1147	G1060	A889	A890	G785
G2285	G2286	G2177	G1918	G1819	A1561	U1474	A1383	G1267	U1148	G1061	A891	A892	A789
G2287	G2288	G2178	U1919	A1820	A1562	U1475	G1384	G1268	U1149	G1062	A893	A894	U790
G2289	G2290	G2179	C1920	U1821	A1563	U1476	A1385	G1269	G1150	G1063	A895	A896	C791
G2291	G2292	G2180	U1921	G1822	A1564	U1477	G1386	G1270	U1151	G1064	A897	A898	A794
G2293	G2294	G2181	C1922	A1823	A1565	U1478	A1387	G1271	G1152	G1065	A899	A900	G797
G2295	G2296	G2182	U1923	U1824	A1566	U1479	U1388	G1272	U1153	G1066	A901	A902	A798
G2297	G2298	G2183	C1924	G1825	A1567	U1480	A1389	G1273	U1154	G1067	A903	A904	A800
G2299	G2300	G2184	U1925	U1826	A1568	U1481	G1390	G1274	G1155	G1068	A905	A906	G805
G2301	G2302	G2185	A1926	G1827	A1569	U1482	A1391	G1275	U1156	G1069	A907	A908	G806
G2303	G2304	G2186	C1927	U1828	A1570	U1483	G1392	G1276	U1157	G1070	A909	A910	U807
G2305	G2306	G2187	U1928	A1829	A1571	U1484	A1393	G1277	U1158	G1071	A911	A912	A812
G2307	G2308	G2188	G1929	U1830	A1572	U1485	G1394	G1278	U1159	G1072	A913	A914	U813
G2309	G2310	G2189	U1930	G1831	A1573	U1486	A1395	G1279	U1160	G1073	A915	A916	C814
G2311	G2312	G2190	C1931	U1832	A1574	U1487	A1396	G1280	U1161	G1074	A917	A918	C815
G2313	G2314	G2191	U1932	G1833	A1575	U1488	G1397	G1281	U1162	G1075	A919	A920	C816
G2315	G2316	G2192	A1933	U1834	A1576	U1489	A1398	G1282	U1163	G1076	A921	A922	A819
G2317	G2318	G2193	G1934	G1835	A1577	U1490	A1399	G1283	U1164	G1077	A923	A924	A820
G2319	G2320	G2194	U1935	U1836	A1578	U1491	G1400	G1284	U1165	G1078	A925	A926	A821
G2321	G2322	G2195	C1936	A1837	A1579	U1492	G1401	G1285	U1166	G1079	A927	A928	A822
G2323	G2324	G2196	U1937	G1838	A1580	U1493	A1402	G1286	U1167	G1080	A929	A930	A823
G2325	G2326	G2197	A1938	U1839	A1581	U1494	A1403	G1287	U1168	G1081	A931	A932	A824
G2327	G2328	G2198	U1939	G1840	A1582	U1495	G1404	G1288	U1169	G1082	A933	A934	A825
G2329	G2330	G2199	C1940	A1841	A1583	U1496	A1405	G1289	U1170	G1083	A935	A936	A826
G2331	G2332	G2200	U1941	U1842	A1584	U1497	G1406	G1290	U1171	G1084	A937	A938	A827
G2333	G2334	G2201	G1942	G1843	A1585	U1498	A1407	G1291	U1172	G1085	A939	A940	A828
G2335	G2336	G2202	C1943	U1844	A1586	U1499	G1408	G1292	U1173	G1086	A941	A942	A829
G2337	G2338	G2203	U1944	A1845	A1587	U1500	G1409	G1293	U1174	G1087	A943	A944	A830
G2339	G2340	G2204	A1945	G1846	A1588	U1501	A1410	G1294	U1175	G1088	A945	A946	A831
G2341	G2342	G2205	U1946	U1847	A1589	U1502	G1411	G1295	U1176	G1089	A947	A948	A832
G2343	G2344	G2206	C1947	A1848	A1590	U1503	A1412	G1296	U1177	G1090	A949	A950	A833
G2345	G2346	G2207	U1948	G1849	A1591	U1504	G1413	G1297	U1178	G1091	A951	A952	A834
G2347	G2348	G2208	G1949	U1850	A1592	U1505	A1414	G1298	U1179	G1092	A953	A954	A835
G2349	G2350	G2209	U1950	A1851	A1593	U1506	G1415	G1299	U1180	G1093	A955	A956	A836
G2351	G2352	G2210	C1951	G1852	A1594	U1507	A1416	G1300	U1181	G1094	A957	A958	A837
G2353	G2354	G2211	U1952	U1853	A1595	U1508	G1417	G1301	U1182	G1095	A959	A960	A838
G2355	G2356	G2212	G1953	A1854	A1596	U1509	A1418	G1302	U1183	G1096	A961	A962	A839
G2357	G2358	G2213	C1954	U1855	A1597	U1510	G1419	G1303	U1184	G1097	A963	A964	A840
G2359	G2360	G2214	U1955	A1856	A1598	U1511	A1420	G1304	U1185	G1098	A965	A966	A841
G2361	G2362	G2215	C1956	G1857	A1599	U1512	G1421	G1305	U1186	G1099	A967	A968	A842
G2363	G2364	G2216	U1957	U1858	A1600	U1513	G1422	G1306	U1187	G1100	A969	A970	A843
G2365	G2366	G2217	A1958	A1859	A1601	U1514	G1423	G1307	U1188	G1101	A971	A972	A844
G2367	G2368	G2218	C1959	G1860	A1602	U1515	G1424	G1308	U1189	G1102	A973	A974	A845
G2369	G2370	G2219	U1960	U1861	A1603	U1516	G1425	G1309	U1190	G1103	A975	A976	A846
G2371	G2372	G2220	G1961	A1862	A1604	U1517	G1426	G1310	U1191	G1104	A977	A978	A847
G2373	G2374	G2221	C1962	U1863	A1605	U1518	G1427	G1311	U1192	G1105	A979	A980	A848
G2375	G2376	G2222	U1962	A1864	A1606	U1519	G1428	G1312	U1193	G1106	A981	A982	A849
G2377	G2378	G2223	G1963	G1865	A1607	U1520	G1429	G1313	U1194	G1107	A983	A984	A850
G2379	G2380	G2224	U1964	U1866	A1608	U1521	G1430	G1314	U1195	G1108	A985	A986	A851
G2381	G2382	G2225	C1965	A1867	A1609	U1522	G1431	G1315	U1196	G1109	A987	A988	A852
G2383	G2384	G2226	U1966	U1868	A1610	U1523	G1432	G1316	U1197	G1110	A989	A990	A853
G2385	G2386	G2227	G1967	A1869	A1611	U1524	G1433	G1317	U1198	G1111	A991	A992	A854
G2387	G2388	G2228	U1968	G1869	A1612	U1525	G1434	G1318	U1199	G1112	A993	A994	A855
G2389	G2390	G2229	C1968	U1870	A1613	U1526	G1435	G1319	U1200	G1113	A995	A996	A856
G2391	G2392	G2230	U1969	A1871	A1614	U1527	G1436	G1320	U1201	G1114	A997	A998	A857
G2393	G2394	G2231	G1970	U1872	A1615	U1528	G1437	G1321	U1202	G1115	A999	A1000	A858
G2395	G2396	G2232	U1971	A1873	A1616	U1529	G1438	G1322	U1203	G1116	A1001	A1002	A859
G2397	G2398	G2233	C1972	G1874	A1617	U1530	G1439	G1323	U1204	G1117	A1003	A1004	A860
G2399	G2400	G2234	U1973	A1875	A1618	U1531	G1440	G1324	U1205	G1118	A1005	A1006	A861
G2401	G2402	G2235	G1974	U1876	A1619	U1532	G1441	G1325	U1206	G1119	A1007	A1008	A862
G2403	G2404	G2236	U1975	A1877	A1620	U1533	G1442	G1326	U1207	G1120	A1009	A1010	A863
G2405	G2406	G2237	C1976	G1878	A1621	U1534	G1443	G1327	U1208	G1121	A1011	A1012	A864
G2407	G2408	G2238	U1977	A1879	A1622	U153							



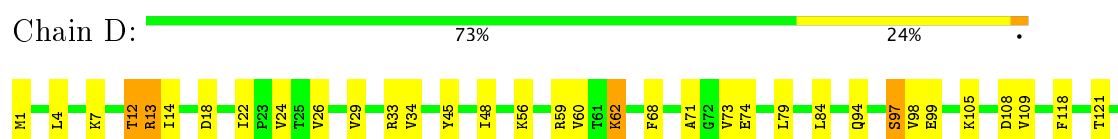
• Molecule 4: 5S rRNA

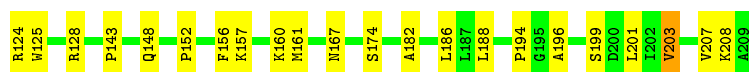


• Molecule 5: 50S ribosomal protein L2



• Molecule 6: 50S ribosomal protein L3





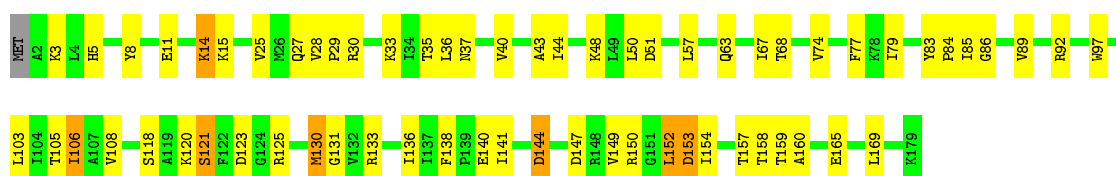
• Molecule 7: 50S ribosomal protein L4

Chain E: 78% 21%



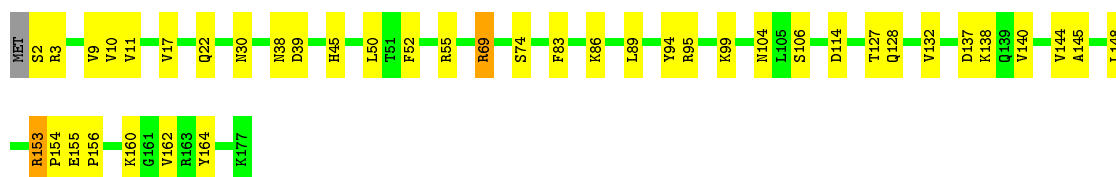
• Molecule 8: 50S ribosomal protein L5

Chain F: 64% 32%



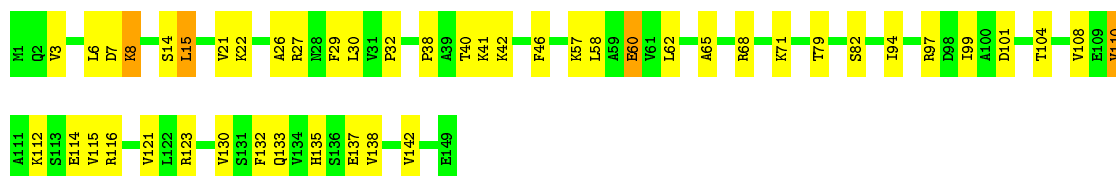
• Molecule 9: 50S ribosomal protein L6

Chain G: 76% 22%



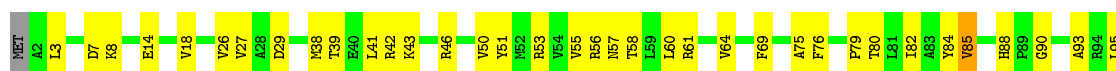
• Molecule 10: 50S ribosomal protein L9

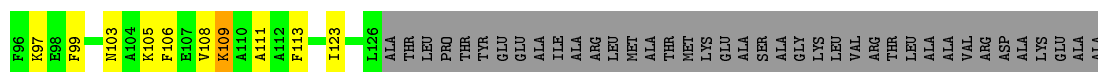
Chain H: 68% 29%



• Molecule 11: 50S ribosomal protein L10

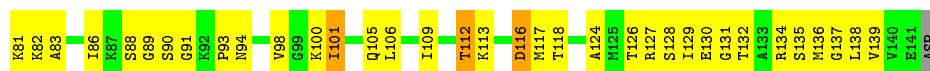
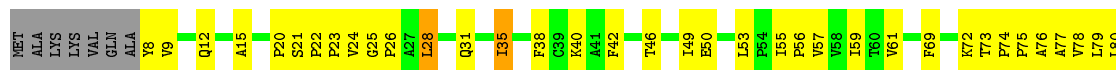
Chain I: 48% 27% 24%





- Molecule 12: 50S ribosomal protein L11

Chain J: 44% 46% 6%



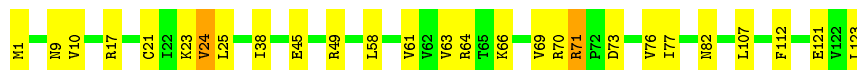
- Molecule 13: 50S ribosomal protein L13

Chain K: 73% 25% 2%



- Molecule 14: 50S ribosomal protein L14

Chain L: 78% 20% 2%



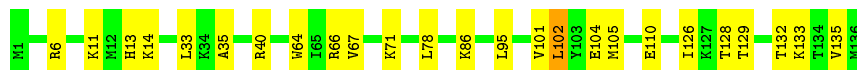
- Molecule 15: 50S ribosomal protein L15

Chain M: 77% 22% 1%



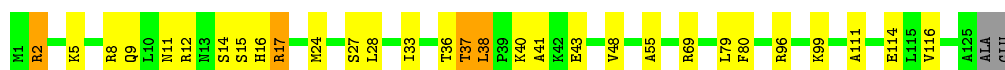
- Molecule 16: 50S ribosomal protein L16

Chain N: 82% 18% 0%

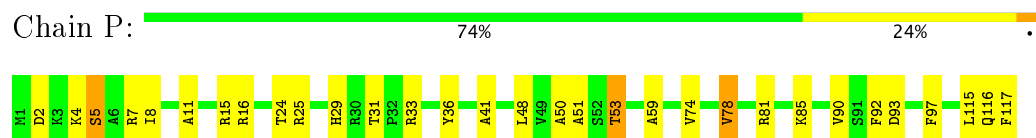


- Molecule 17: 50S ribosomal protein L17

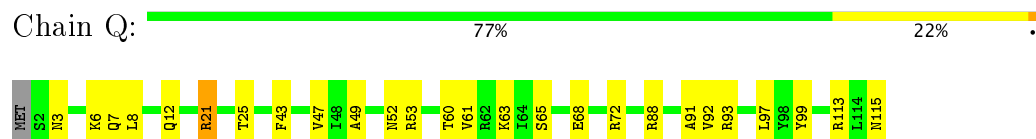
Chain O: 75% 20% 5%



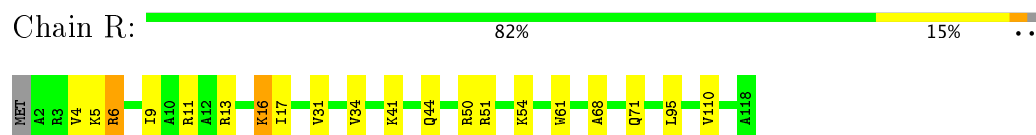
- Molecule 18: 50S ribosomal protein L18



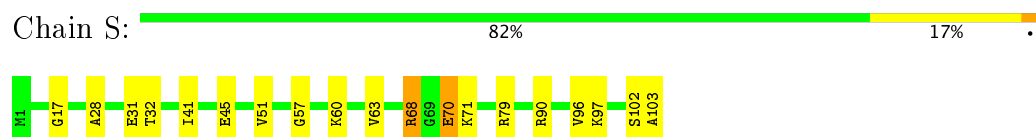
- Molecule 19: 50S ribosomal protein L19



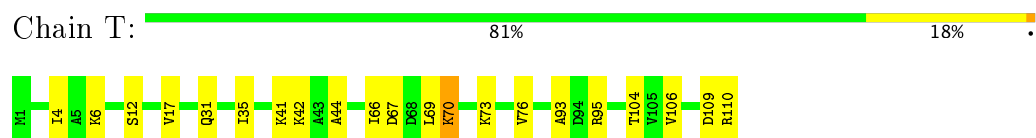
- Molecule 20: 50S ribosomal protein L20



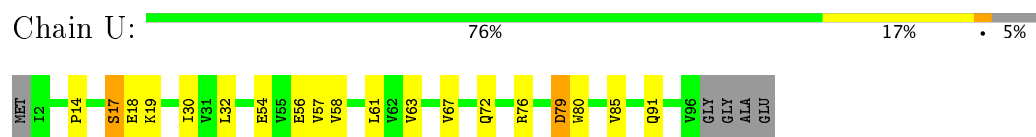
- Molecule 21: 50S ribosomal protein L21



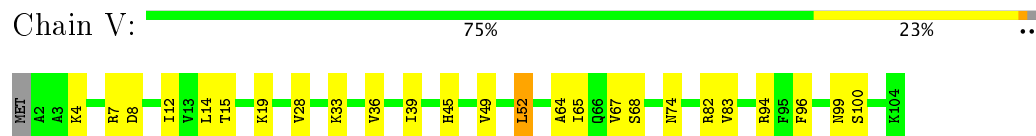
- Molecule 22: 50S ribosomal protein L22




- Molecule 23: 50S ribosomal protein L23



- Molecule 24: 50S ribosomal protein L24



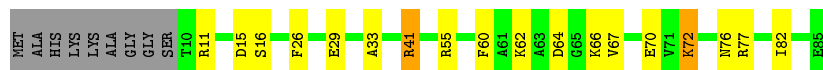
- Molecule 25: 50S ribosomal protein L25

Chain W:  82% 15% .



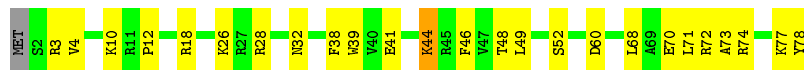
- Molecule 26: 50S ribosomal protein L27

Chain X:  68% 19% . 11%



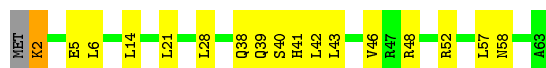
- Molecule 27: 50S ribosomal protein L28

Chain Y:  67% 31% ..



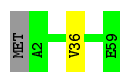
- Molecule 28: 50S ribosomal protein L29

Chain Z:  71% 25% ..




- Molecule 29: 50S ribosomal protein L30

Chain a:  97% ..




- Molecule 30: 50S ribosomal protein L32

Chain b:  86% 12% .




- Molecule 31: 50S ribosomal protein L33

Chain c:  87% 5% 7%



- Molecule 32: 50S ribosomal protein L34

Chain d:  87% 13%



- Molecule 33: 50S ribosomal protein L35

Chain e:  92% 6%



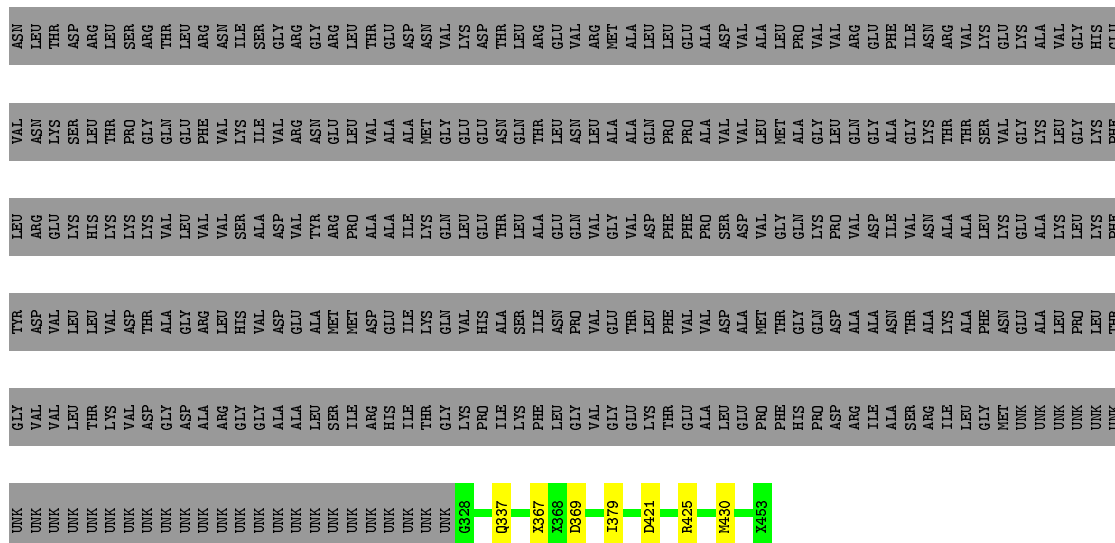
- Molecule 34: 50S ribosomal protein L36

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: Signal recognition particle protein Ffh

Chain i:  26% 2% 72%



- Molecule 36: 1A9L SS

Chain k: 100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	75942	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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	1	0.87	0/1037	1.34	8/1616 (0.5%)
10	H	0.47	0/1121	0.57	0/1515
11	I	0.58	0/958	0.62	0/1292
12	J	0.65	0/993	0.69	1/1341 (0.1%)
13	K	0.42	0/1152	0.55	0/1551
14	L	0.43	0/955	0.60	0/1279
15	M	0.40	0/1062	0.59	0/1413
16	N	0.43	0/1093	0.56	0/1460
17	O	0.45	0/1006	0.61	0/1345
18	P	0.40	0/910	0.56	0/1219
19	Q	0.42	0/929	0.56	0/1242
2	2	0.43	0/68	1.05	0/103
20	R	0.51	1/960 (0.1%)	0.56	0/1278
21	S	0.42	0/829	0.61	0/1107
22	T	0.46	0/864	0.67	0/1156
23	U	0.47	0/763	0.60	0/1021
24	V	0.45	0/788	0.58	0/1053
25	W	0.38	0/766	0.53	0/1025
26	X	0.45	0/587	0.58	0/776
27	Y	0.43	0/635	0.56	0/848
28	Z	0.43	0/502	0.60	0/667
29	a	0.37	0/453	0.55	0/605
3	A	0.63	8/69329 (0.0%)	1.10	112/108152 (0.1%)
30	b	0.45	0/450	0.64	0/599
31	c	0.40	0/421	0.58	0/561
32	d	0.42	0/380	0.60	0/498
33	e	0.41	0/513	0.58	0/676
34	f	0.45	0/303	0.56	0/397
35	i	0.46	0/672	0.57	0/883
36	k	0.74	0/137	0.85	0/186
4	B	0.48	0/2872	0.97	0/4478
5	C	0.43	0/2122	0.60	0/2854

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
6	D	0.43	0/1586	0.60	0/2134
7	E	0.41	0/1571	0.59	0/2113
8	F	0.41	0/1435	0.53	0/1928
9	G	0.39	0/1343	0.58	0/1816
All	All	0.58	9/101565 (0.0%)	1.00	121/152187 (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
35	i	0	1
5	C	0	1
All	All	0	2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1490	A	N9-C4	6.41	1.41	1.37
3	A	2117	A	N9-C4	6.03	1.41	1.37
3	A	1070	A	N9-C4	5.99	1.41	1.37
3	A	2158	A	N9-C4	5.74	1.41	1.37
3	A	2114	A	N9-C4	5.67	1.41	1.37

The worst 5 of 121 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1490	A	C8-N9-C4	-10.42	101.63	105.80
3	A	2422	C	O4'-C1'-N1	8.66	115.13	108.20
3	A	2427	C	C6-N1-C2	-8.57	116.87	120.30
3	A	2160	C	C6-N1-C2	-8.50	116.90	120.30
3	A	2423	U	C6-N1-C2	-8.23	116.06	121.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	C	232	HIS	Peptide
35	i	367	UNK	Peptide

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	1	926	0	467	11	0
2	2	62	0	34	0	0
3	A	61902	0	31133	666	0
4	B	2569	0	1301	22	0
5	C	2083	0	2154	49	0
6	D	1565	0	1616	37	0
7	E	1552	0	1619	31	0
8	F	1411	0	1444	41	0
9	G	1323	0	1371	25	0
10	H	1110	0	1148	30	0
11	I	946	0	978	31	0
12	J	979	0	1028	56	0
13	K	1129	0	1162	26	0
14	L	946	0	1023	18	0
15	M	1053	0	1129	22	0
16	N	1074	0	1157	12	0
17	O	993	0	1034	21	0
18	P	900	0	935	24	0
19	Q	917	0	962	17	0
20	R	947	0	1019	13	0
21	S	816	0	839	11	0
22	T	857	0	922	10	0
23	U	756	0	817	9	0
24	V	780	0	831	12	0
25	W	753	0	780	8	0
26	X	580	0	594	13	0
27	Y	625	0	652	16	0
28	Z	501	0	531	14	0
29	a	449	0	488	0	0
30	b	444	0	458	0	0
31	c	414	0	442	0	0
32	d	377	0	418	0	0
33	e	504	0	572	0	0
34	f	302	0	340	0	0
35	i	916	0	943	0	0
36	k	137	0	168	0	0
37	2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	A	411	0	0	0	0
37	B	12	0	0	0	0
37	C	2	0	0	0	0
37	D	1	0	0	0	0
37	O	1	0	0	0	0
37	R	1	0	0	0	0
37	Y	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
All	All	94030	0	62509	1122	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 8.

The worst 5 of 1122 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)
12:J:86:ILE:HD13	12:J:138:LEU:HD21	1.51	0.93
3:A:276:U:O2	3:A:278:A:N6	2.03	0.91
3:A:2584:U:H3'	3:A:2585:U:H5''	1.52	0.89
3:A:2304:G:H22	3:A:2312:U:H3	1.18	0.88
3:A:2128:G:H1	3:A:2160:C:H42	1.19	0.88

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	
5	C	270/273 (99%)	263 (97%)	7 (3%)	0	100	100
6	D	207/209 (99%)	202 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	E	199/201 (99%)	191 (96%)	7 (4%)	1 (0%)	32	73
8	F	176/179 (98%)	172 (98%)	4 (2%)	0	100	100
9	G	174/177 (98%)	172 (99%)	2 (1%)	0	100	100
10	H	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
11	I	123/165 (74%)	113 (92%)	9 (7%)	1 (1%)	22	65
12	J	132/142 (93%)	125 (95%)	7 (5%)	0	100	100
13	K	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	L	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
15	M	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
16	N	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
17	O	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
18	P	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
19	Q	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
20	R	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
21	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
22	T	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
23	U	93/100 (93%)	89 (96%)	4 (4%)	0	100	100
24	V	101/104 (97%)	99 (98%)	2 (2%)	0	100	100
25	W	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
26	X	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	Y	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Z	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
29	a	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
30	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
31	c	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
32	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	e	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
34	f	36/38 (95%)	36 (100%)	0	0	100	100
35	i	84/450 (19%)	84 (100%)	0	0	100	100
36	k	16/18 (89%)	12 (75%)	4 (25%)	0	100	100
All	All	3535/4042 (88%)	3426 (97%)	107 (3%)	2 (0%)	58	88

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	E	6	LYS
11	I	108	VAL

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	
5	C	216/218 (99%)	198 (92%)	18 (8%)	13	49
6	D	164/164 (100%)	155 (94%)	9 (6%)	25	63
7	E	165/165 (100%)	157 (95%)	8 (5%)	30	66
8	F	148/150 (99%)	135 (91%)	13 (9%)	12	46
9	G	137/138 (99%)	128 (93%)	9 (7%)	19	57
10	H	114/114 (100%)	104 (91%)	10 (9%)	12	46
11	I	95/123 (77%)	90 (95%)	5 (5%)	26	64
12	J	104/110 (94%)	95 (91%)	9 (9%)	12	46
13	K	116/116 (100%)	106 (91%)	10 (9%)	12	47
14	L	104/104 (100%)	95 (91%)	9 (9%)	12	46
15	M	103/103 (100%)	99 (96%)	4 (4%)	37	70
16	N	109/109 (100%)	101 (93%)	8 (7%)	16	54
17	O	102/103 (99%)	95 (93%)	7 (7%)	18	56
18	P	87/87 (100%)	83 (95%)	4 (5%)	31	67
19	Q	99/100 (99%)	95 (96%)	4 (4%)	36	69
20	R	89/90 (99%)	83 (93%)	6 (7%)	19	57
21	S	84/84 (100%)	80 (95%)	4 (5%)	30	66
22	T	93/93 (100%)	88 (95%)	5 (5%)	26	63
23	U	82/84 (98%)	77 (94%)	5 (6%)	22	60
24	V	83/85 (98%)	77 (93%)	6 (7%)	17	54
25	W	78/78 (100%)	72 (92%)	6 (8%)	15	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	57/63 (90%)	52 (91%)	5 (9%)	12	46
27	Y	67/68 (98%)	63 (94%)	4 (6%)	22	60
28	Z	54/55 (98%)	49 (91%)	5 (9%)	10	43
29	a	48/49 (98%)	47 (98%)	1 (2%)	59	82
30	b	47/48 (98%)	40 (85%)	7 (15%)	3	23
31	c	45/49 (92%)	42 (93%)	3 (7%)	19	57
32	d	38/38 (100%)	32 (84%)	6 (16%)	3	21
33	e	51/52 (98%)	47 (92%)	4 (8%)	15	51
34	f	34/34 (100%)	34 (100%)	0	100	100
35	i	71/313 (23%)	65 (92%)	6 (8%)	12	48
36	k	17/17 (100%)	17 (100%)	0	100	100
All	All	2901/3204 (90%)	2701 (93%)	200 (7%)	23	56

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	K	131	ASN
16	N	135	VAL
32	d	1	MET
14	L	24	VAL
15	M	59	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
12	J	31	GLN
17	O	11	ASN
30	b	19	HIS
12	J	111	GLN
16	N	3	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	42/113 (37%)	12 (28%)	0
2	2	2/3 (66%)	1 (50%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	A	2878/2903 (99%)	488 (16%)	17 (0%)
4	B	119/120 (99%)	16 (13%)	0
All	All	3041/3139 (96%)	517 (17%)	17 (0%)

5 of 517 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	33	C
1	1	36	U
1	1	37	U
1	1	38	U
1	1	39	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	1110	G
3	A	1344	U
3	A	2422	C
3	A	805	G
3	A	2430	A

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](#)

Of 432 ligands modelled in this entry, 432 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.