



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 10:43 AM UTC

PDB ID : 3JA1 / pdb_00003ja1
EMDB ID : EMD-6316
Title : Activation of GTP Hydrolysis in mRNA-tRNA Translocation by Elongation Factor G
Authors : Li, W.; Liu, Z.; Koripella, R.K.; Langlois, R.; Sanyal, S.; Frank, J.
Deposited on : 2015-03-30
Resolution : 3.60 Å(reported)
Based on initial model : 3J0U

This is a wwPDB EM 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/EMValidationReportHelp>

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:

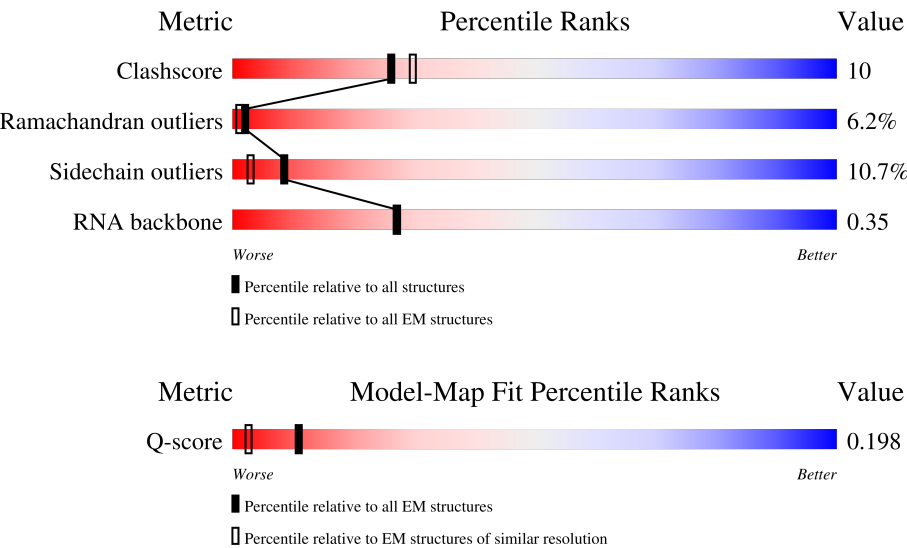
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.60 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.



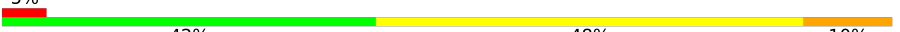
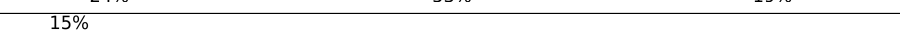
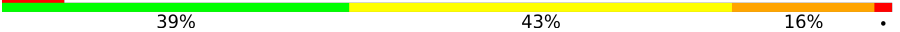
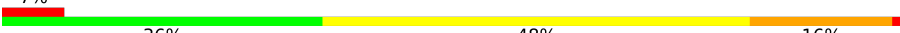
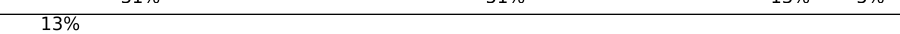
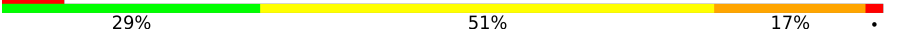
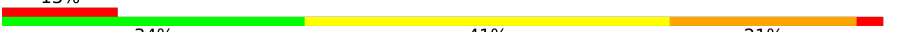
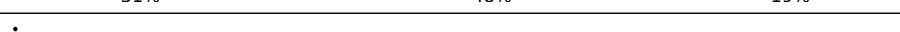
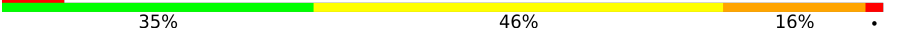
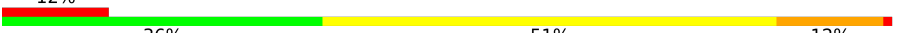
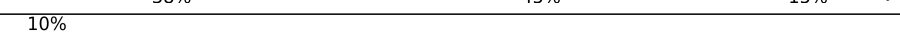
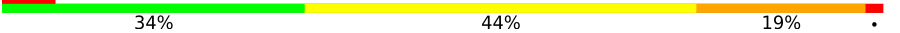
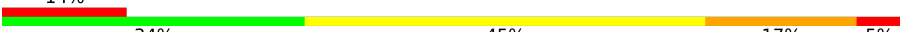
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	SS	91	
2	SA	1542	
3	S1	47	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	S2	77	
5	ST	86	
6	SU	70	
7	SG	178	
8	SH	129	
9	SI	129	
10	SJ	103	
11	SK	128	
12	SL	123	
13	SM	117	
14	SN	100	
15	SO	88	
16	SP	82	
17	SQ	83	
18	SB	240	
19	SC	232	
20	SD	205	
21	SE	166	
22	SF	135	
23	SR	74	
24	S3	702	
25	LB	120	
26	LA	2904	
27	LD	272	
28	LU	110	

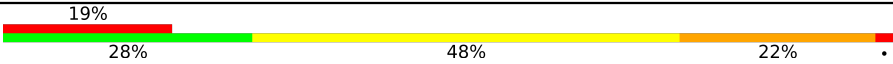
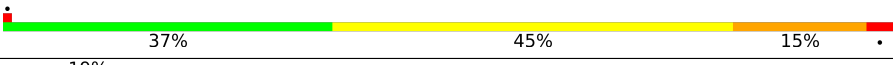
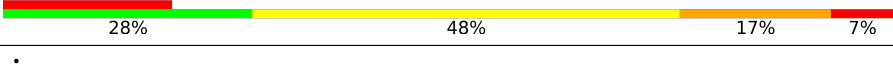
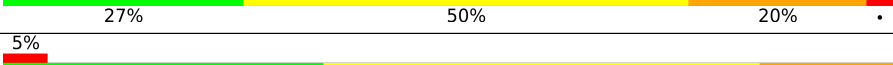
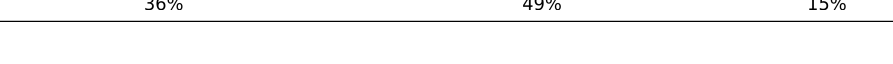
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LV	100	
30	LW	103	
31	LX	94	
32	LY	84	
33	LZ	77	
34	L0	63	
35	L1	58	
36	L2	70	
37	LC	234	
38	LE	209	
39	L3	56	
40	L4	54	
41	L5	46	
42	L6	64	
43	L7	38	
44	LF	201	
45	LG	178	
46	LH	176	
47	LJ	164	
48	LN	144	
49	LK	141	
50	LL	142	
51	LI	149	
52	LO	136	
53	LP	127	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	LM	123	
55	LQ	117	
56	LR	114	
57	LS	117	
58	LT	103	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 156127 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 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SS	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	1542	Total	C	N	O	P	0	0
			33076	14754	6064	10717	1541		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S1	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 4 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S2	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

- Molecule 5 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	ST	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 6 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SG	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SI	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SK	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SM	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SQ	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 18 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SB	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 19 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SC	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 20 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 21 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SE	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 22 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SF	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SR	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 24 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S3	702	Total	C	N	O	S	0	0
			5431	3420	938	1048	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S3	91	ALA	HIS	engineered mutation	UNP P0A6M8

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LA	2904	Total	C	N	O	P	0	0
			62330	27807	11462	20158	2903		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	1618	C	A	conflict	GB 33357927

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
LA	1915	C	U	conflict	GB 33357927
LA	2030	U	A	conflict	GB 33357927
LA	2251	U	G	conflict	GB 33357927

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 28 is a protein called 50S ribosomal protein L22.

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

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 30 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	LW	103	Total	C	N	O	0	0
			789	498	148	143		

- Molecule 31 is a protein called 50S ribosomal protein L25.

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

- Molecule 32 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 33 is a protein called 50S ribosomal protein L28.

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

- Molecule 34 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 35 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 36 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 37 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 38 is a protein called 50S ribosomal protein L3.

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

- Molecule 39 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 40 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	L4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 41 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	L5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 42 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 43 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 44 is a protein called 50S ribosomal protein L4.

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

- Molecule 45 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 46 is a protein called 50S ribosomal protein L6.

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

- Molecule 47 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 48 is a protein called 50S ribosomal protein L15.

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

- Molecule 49 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LK	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

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

- Molecule 51 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LI	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 52 is a protein called 50S ribosomal protein L16.

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

- Molecule 53 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LP	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 54 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LM	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 55 is a protein called 50S ribosomal protein L18.

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

- Molecule 56 is a protein called 50S ribosomal protein L19.

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

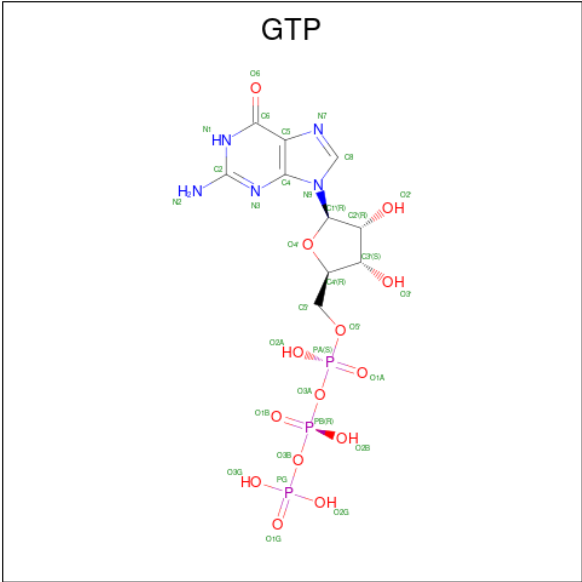
- Molecule 57 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LS	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 58 is a protein called 50S ribosomal protein L21.

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

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

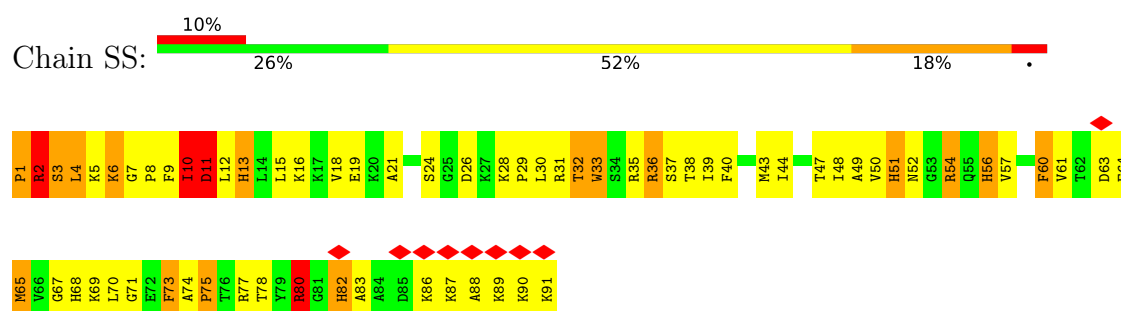


Mol	Chain	Residues	Atoms					AltConf
59	S3	1	Total	C	N	O	P	0
			32	10	5	14	3	

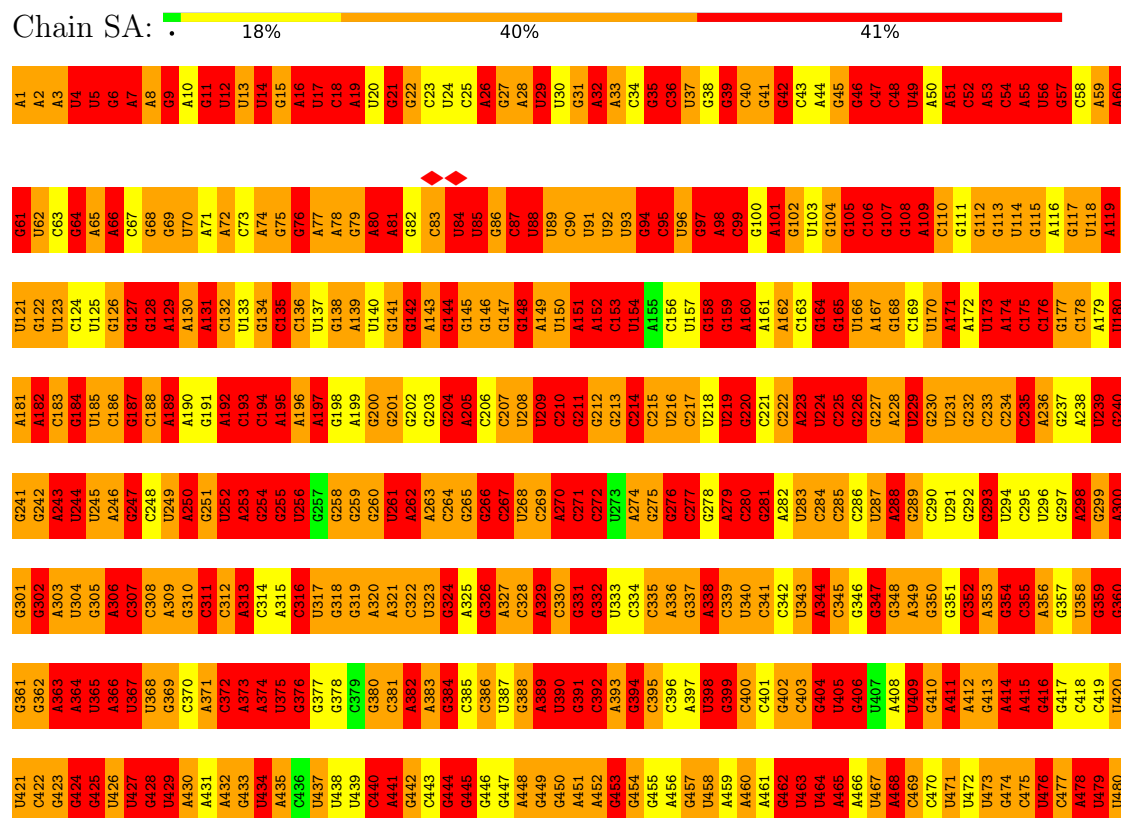
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 30S ribosomal protein S19



• Molecule 2: 16S ribosomal RNA



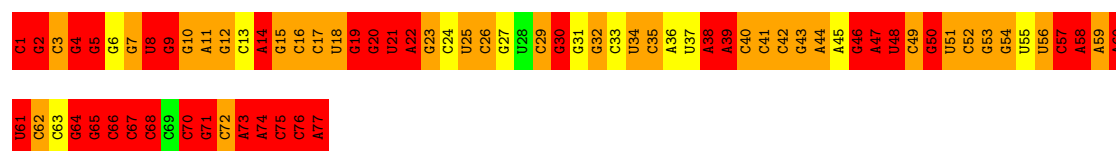




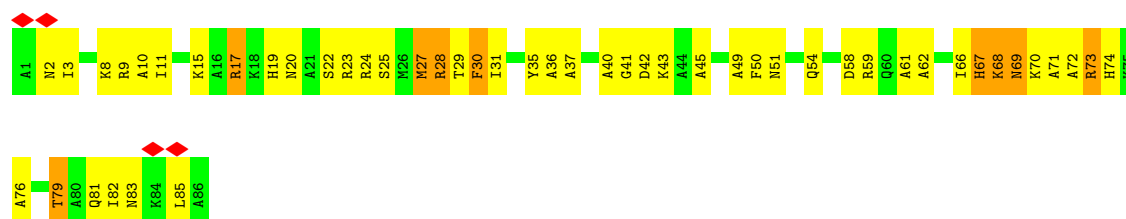
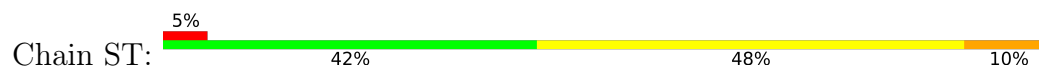
- Molecule 3: mRNA



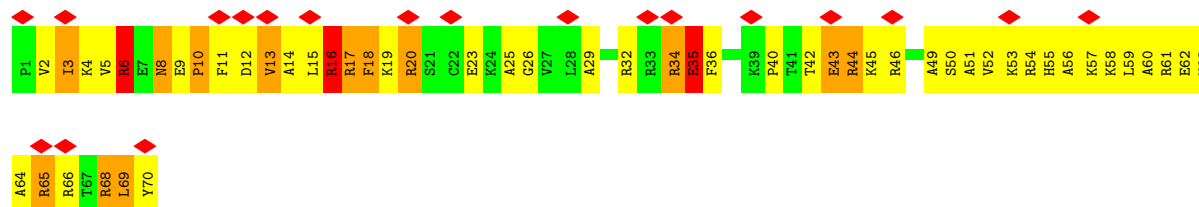
- Molecule 4: P/E-tRNA



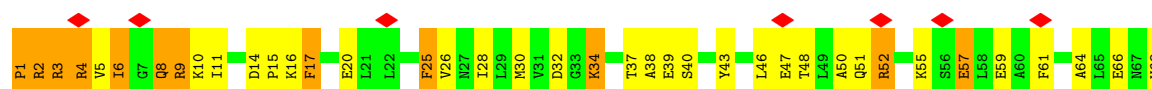
- Molecule 5: 30S ribosomal protein S20

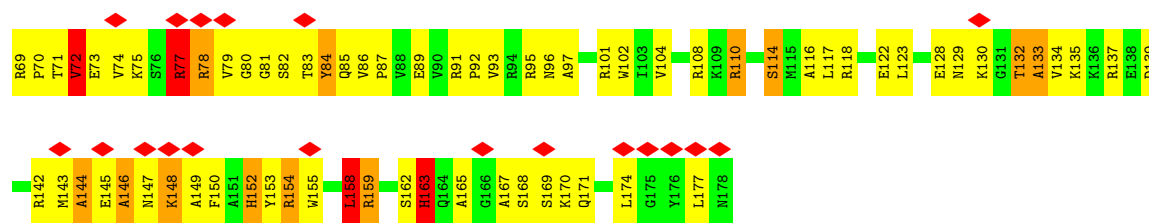


- Molecule 6: 30S ribosomal protein S21

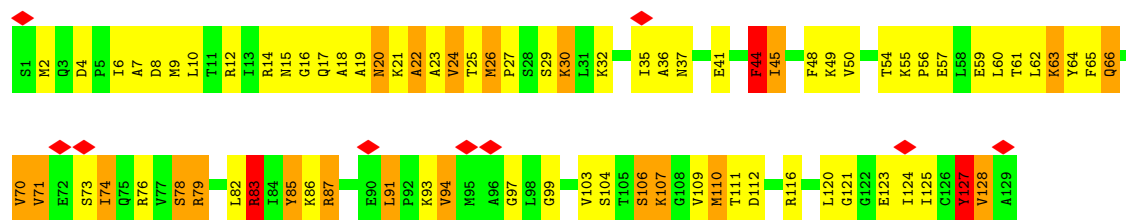


- Molecule 7: 30S ribosomal protein S7

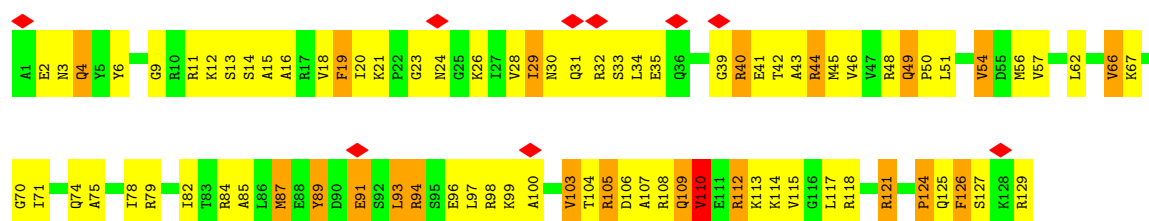




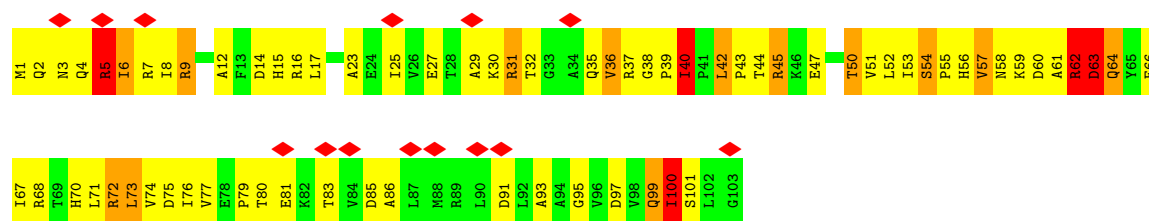
• Molecule 8: 30S ribosomal protein S8



• Molecule 9: 30S ribosomal protein S9

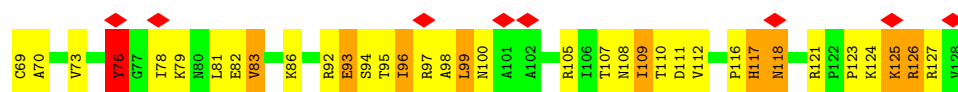


• Molecule 10: 30S ribosomal protein S10



• Molecule 11: 30S ribosomal protein S11

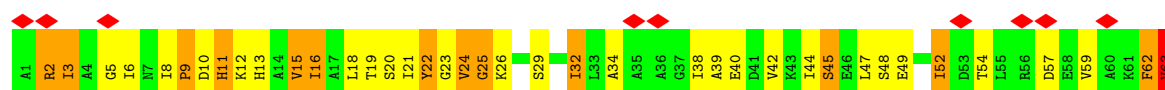




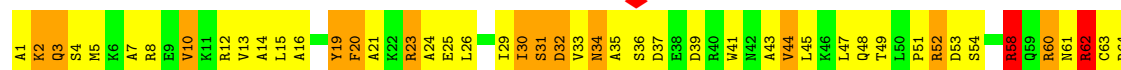
- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13



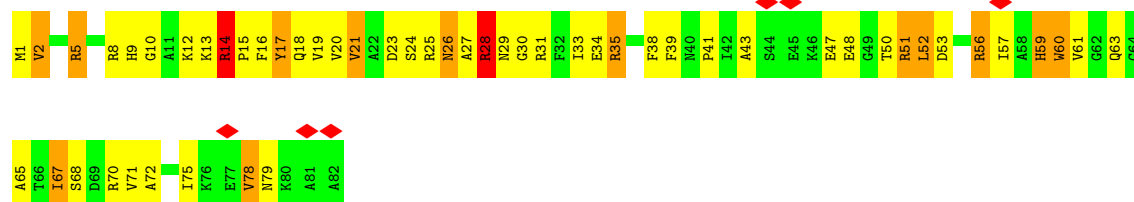
- Molecule 14: 30S ribosomal protein S14



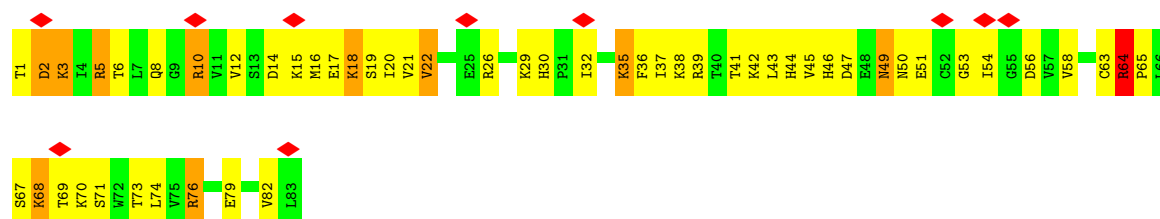
- Molecule 15: 30S ribosomal protein S15



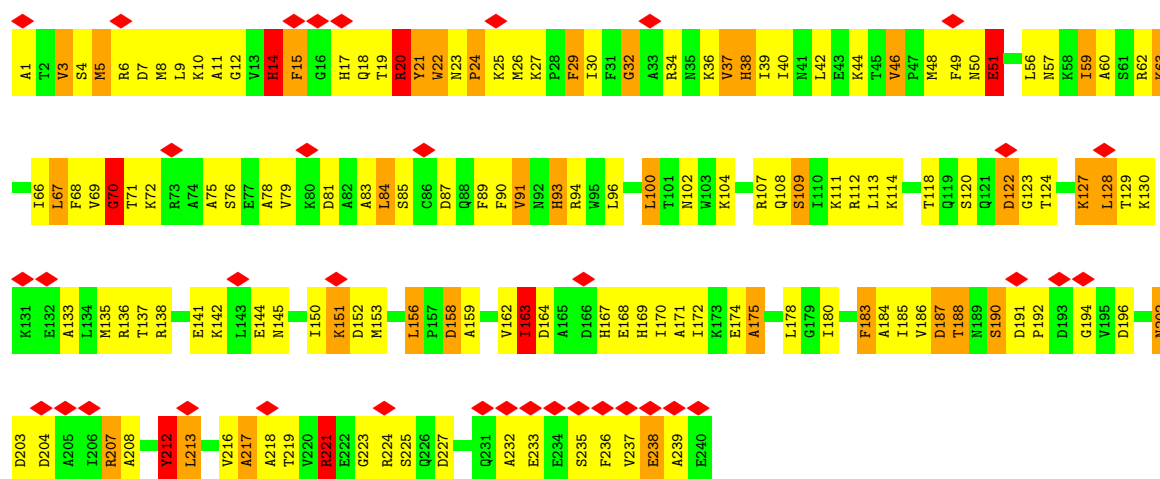
- Molecule 16: 30S ribosomal protein S16



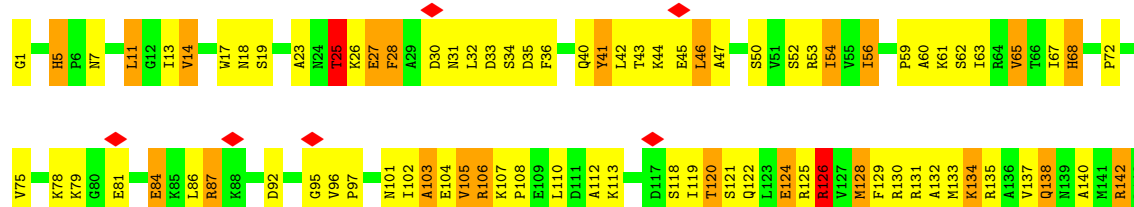
• Molecule 17: 30S ribosomal protein S17

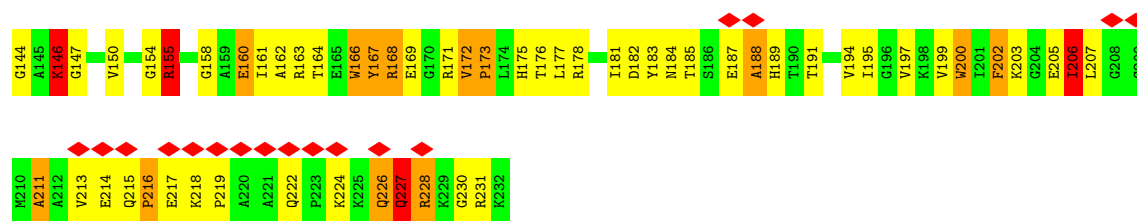


• Molecule 18: 30S ribosomal protein S2

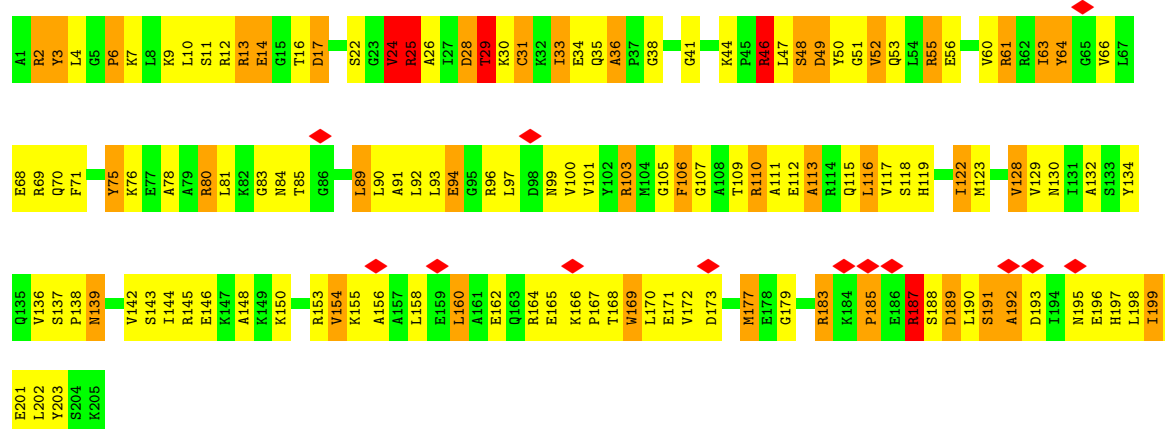


• Molecule 19: 30S ribosomal protein S3

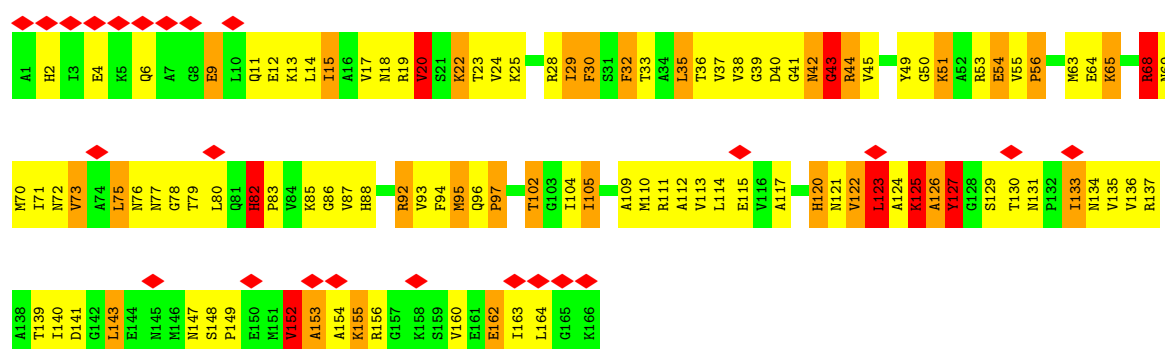




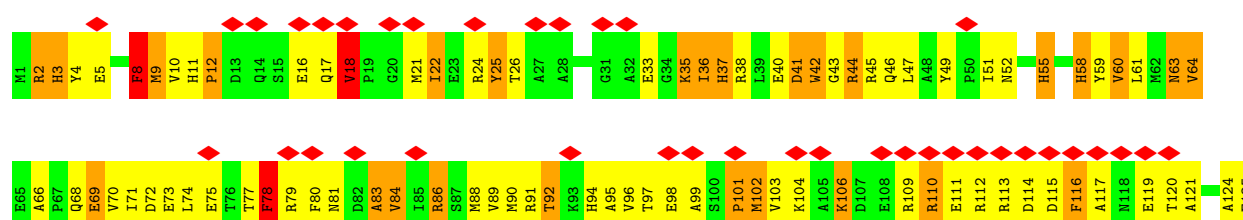
• Molecule 20: 30S ribosomal protein S4



• Molecule 21: 30S ribosomal protein S5

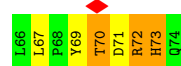


• Molecule 22: 30S ribosomal protein S6

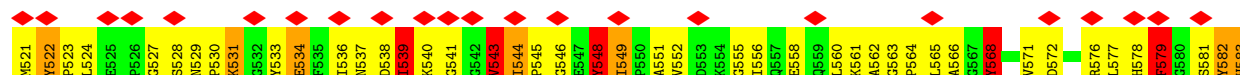
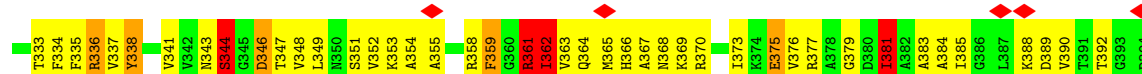
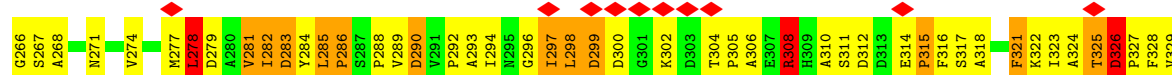
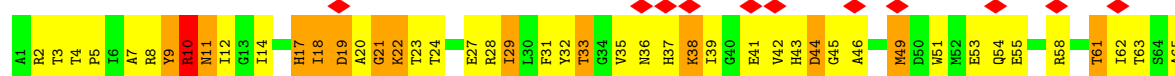


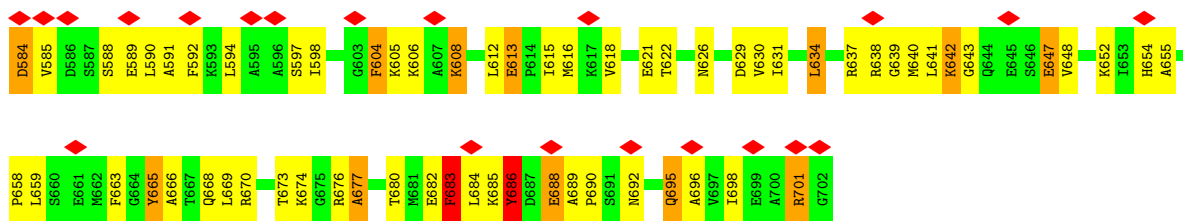


• Molecule 23: 30S ribosomal protein S18



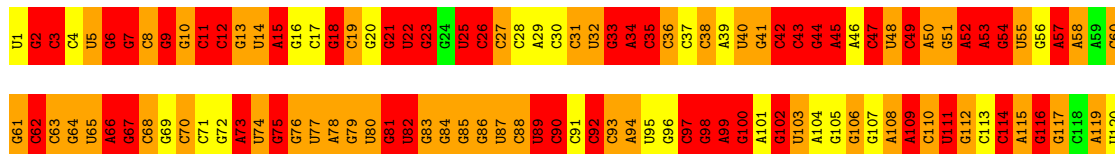
• Molecule 24: Elongation factor G





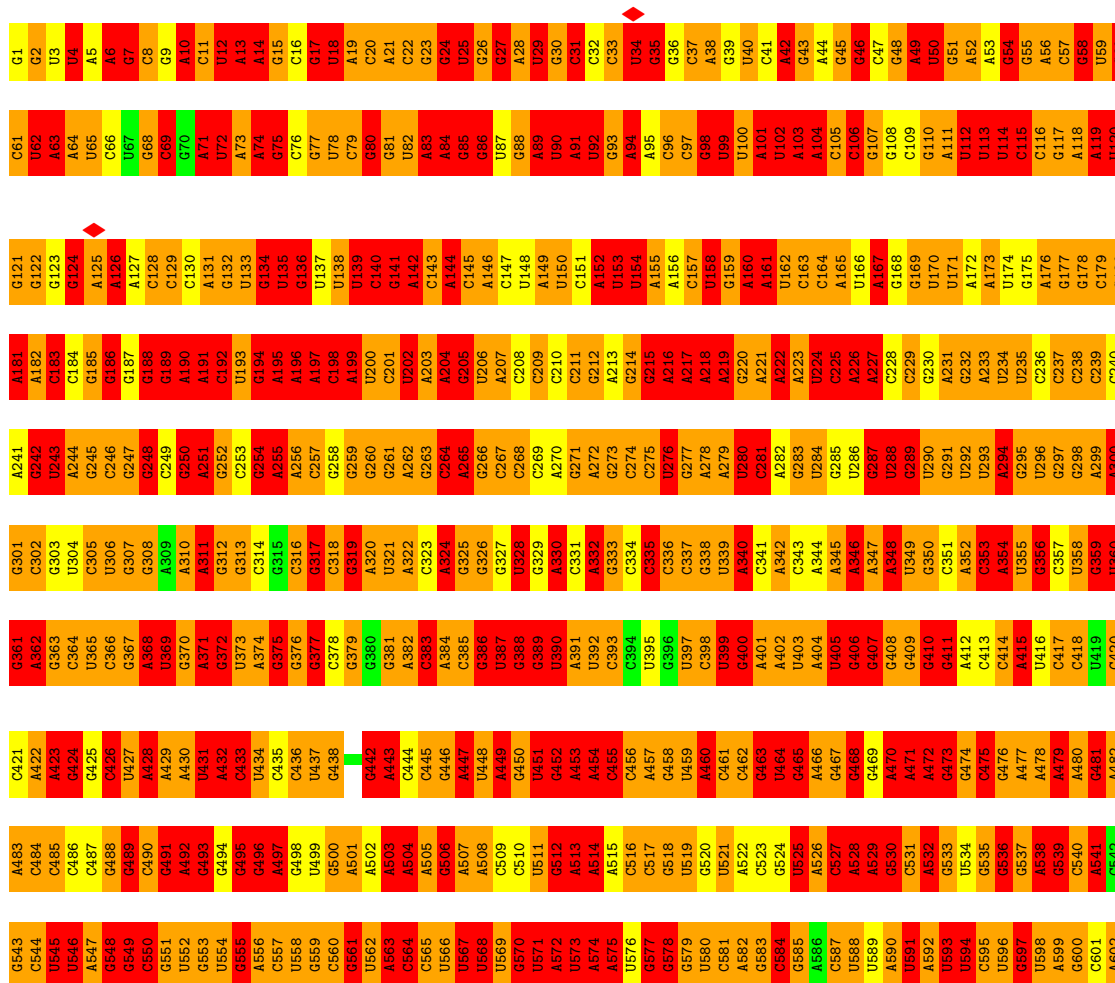
• Molecule 25: 5S ribosomal RNA

Chain LB: . 20% 39% 38%



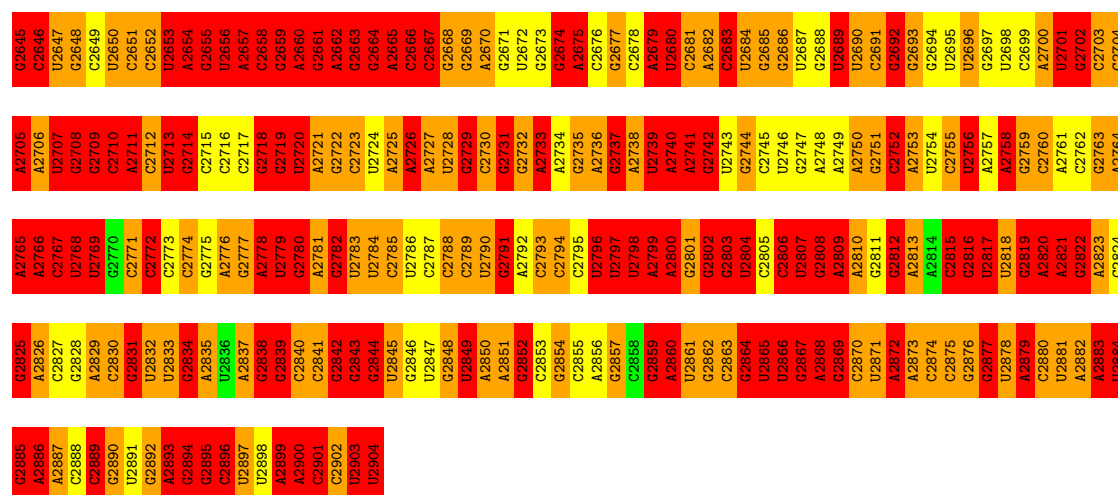
• Molecule 26: 23S ribosomal RNA

Chain LA: . 15% 41% 43%

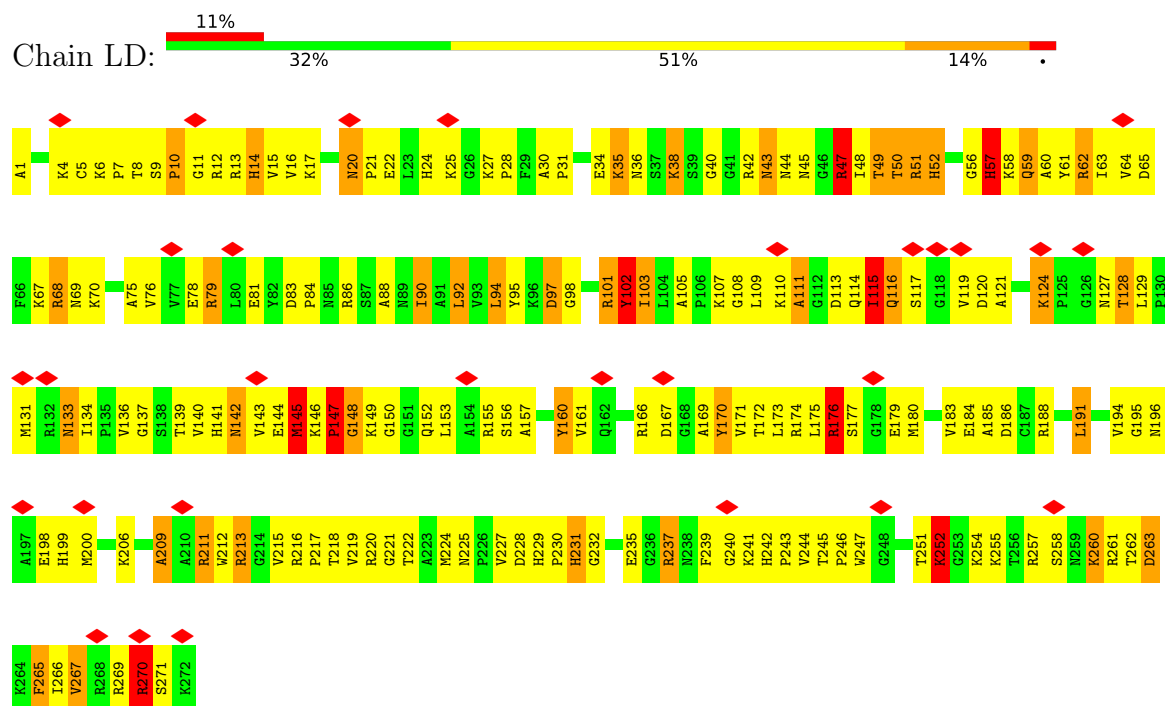


U1563	C1564	C1565	U1566	C1567	U1568	A1569	U1570	A1571	A1572	C1573	C1574	C1575	U1576	C1577	U1578	U1579	A1580	U1581	C1582	A1583	C1584	U1585	C1586	C1587	U1588	U1589	C1590	A1591	C1592	C1593	U1594	A1595	C1596	U1597	C1598	U1598	U1599	C1600	C1601	C1602	C1603	A1604	C1605	C1606	C1607	A1608	A1609	U1610	C1611	C1612	C1613	U1614	C1615	C1616	U1617	C1618	U1619	U1620	C1621	C1622	U1623						
U1443	C1444	G1445	C1446	C1447	C1448	U1449	U1450	C1451	C1452	C1453	C1454	C1455	U1456	U1457	U1458	U1459	U1460	C1461	C1462	C1463	C1464	C1465	U1466	U1467	U1468	U1469	U1470	C1471	C1472	C1473	U1474	C1475	U1476	C1477	C1478	C1479	U1480	C1481	U1482	C1483	U1484	U1485	U1486	U1487	C1488	A1489	U1490	C1491	C1492	C1493	C1494	A1495	U1496	U1497	C1498	U1499	U1500	C1501	A1502								
A1383	A1384	U1385	C1386	C1387	C1388	U1389	U1390	C1391	C1392	C1393	C1394	U1395	A1396	C1397	C1398	C1399	U1400	C1401	U1402	C1403	C1404	U1405	U1406	C1407	C1408	U1409	C1410	U1411	U1412	C1413	C1414	U1415	U1416	C1417	C1418	U1419	U1420	C1421	C1422	C1423	C1424	U1425	C1426	U1427	C1428	C1429	U1430	A1431	C1432	C1433	C1434	A1435	U1436	C1437	C1438	U1439	U1440	C1441	U1442								
C1323	C1324	U1325	U1326	C1327	C1328	U1329	C1330	C1331	C1332	C1333	C1334	C1335	A1336	C1337	C1338	C1339	U1340	C1341	A1342	C1343	C1344	C1345	C1346	A1347	C1348	C1349	C1350	C1351	U1352	C1353	A1354	C1355	C1356	C1357	C1358	A1359	C1360	C1361	C1362	C1363	C1364	A1365	A1366	C1367	C1368	C1369	C1370	C1371	U1372	U1373	C1374	C1375	C1376	C1377	C1378	U1379	C1380	C1381	C1382								
U1263	A1264	A1265	C1266	C1267	C1268	U1269	C1270	C1271	C1272	C1273	A1274	C1275	A1276	C1277	C1278	C1279	C1280	C1281	U1282	C1283	A1284	C1285	A1286	G1287	C1288	C1289	C1290	C1291	C1292	C1293	U1294	C1295	C1296	C1297	C1298	C1299	C1300	A1301	C1302	C1303	C1304	A1305	C1306	A1307	C1308	C1309	C1310	C1311	U1312	U1313	C1314	C1315	C1316	C1317	U1318	C1319	C1320	A1321	A1322								
U1203	A1204	C1205	C1206	C1207	C1208	U1209	C1210	C1211	C1212	C1213	A1214	C1215	G1216	C1217	C1218	U1219	C1220	C1221	U1222	C1223	U1224	C1225	A1226	G1227	C1228	C1229	C1230	C1231	C1232	C1233	U1234	C1235	C1236	U1237	C1238	C1239	U1240	C1241	C1242	C1243	C1244	U1245	G1246	A1247	C1248	U1249	C1250	C1251	U1252	C1253	A1254	U1255	C1256	C1257	U1258	C1259	A1260	U1261	A1262								
A1143	A1144	C1145	C1146	C1147	U1148	U1149	C1150	A1151	C1152	C1153	C1154	A1155	A1156	C1157	C1158	U1159	C1160	C1161	C1162	C1163	C1164	A1165	C1166	C1167	C1168	A1169	C1170	C1171	C1172	C1173	U1174	A1175	C1176	G1177	C1178	U1179	U1180	C1181	C1182	U1183	U1184	G1185	C1186	C1187	U1188	A1189	G1190	C1191	U1192	C1193	A1194	C1195	C1196	C1197	U1198	U1199	C1200	C1201	G1202								
U1083	C1084	A1085	C1086	C1087	U1088	A1089	C1090	C1091	C1092	C1093	U1094	A1095	A1096	U1097	C1098	U1099	C1100	C1101	C1102	A1103	C1104	C1105	C1106	C1107	U1108	C1109	C1110	A1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	U1119	C1120	C1121	C1122	C1123	C1124	C1125	A1126	C1127	C1128	A1129	U1130	C1131	U1132	U1133	A1134	C1135	C1136	C1137	U1138	C1139	C1140	U1141	A1142								
U1023	C1024	C1025	C1026	C1027	C1028	U1029	C1030	C1031	C1032	C1033	C1034	U1035	C1036	C1037	C1038	A1039	A1040	C1041	C1042	C1043	C1044	C1045	A1046	C1047	A1048	C1049	C1050	C1051	C1052	C1053	U1054	C1055	C1056	A1057	U1058	C1059	U1060	U1061	C1062	C1063	C1064	U1065	U1066	C1067	C1068	A1069	C1070	C1071	U1072	U1073	C1074	C1075	C1076	A1077	U1078	C1079	U1080	U1081	U1082								
U963	C964	C965	C966	C967	C968	C969	U970	C971	C972	A973	C974	A975	C976	C977	C978	A979	A980	C981	C982	C983	A984	C985	C986	C987	A988	C989	C990	C991	C992	C993	C994	C995	A996	C997	C998	U999	A1000	A1001	C1002	C1003	U1004	C1005	C1006	C1007	U1008	A1009	C949	C950	C951	G952	C953	C954	A1010	C1011	U1012	C1013	A1014	C1015	C1016	C956	C957	U1017	U1018	U1019	A1020	C961	G962
G843	A844	A845	U846	U847	C848	A849	U850	C851	C852	C853	C854	C855	C856	C857	C858	C859	U860	A861	C862	A863	A864	C865	A866	C867	U868	C869	U870	U871	C872	C873	C874	C875	C876	C877	C878	A879	C880	C881	C882	C883	U884	C885	A886	U887	C888	C889	C890	C891	A892	C893	C894	C895	U896	C897	C898	A899	A900	C901	C902								
A783	C784	C785	C786	C787	U788	A789	U790	C791	C792	C793	A794	C795	C796	C797	C798	C799	U800	A801	C802	U803	A804	C805	C806	U807	C808	C809	U810	U811	C812	C813	C814	C815	C816	C817	C818	A819	C820	A821	C822	C823	U824	A825	U826	U827	U828	A829	C830	C831	U832	C833	A834	C835	U836	C837	C838	U839	C840	A841	U842								
C723	U724	G725	C726	C727	U728	A729	U730	C731	C732	C733	A734	C735	C736	C737	C738	C739	U740	U741	C742	C743	U744	C745	U746	U747	C748	A749	U750	U751	C752	C753	U754	C755	U756	C757	C758	C759	U760	A761	U762	C763	C764	U765	U766	C767	U768	U769	C770	C771	U772	C773	U774	C775	U776	C777	C778	U779	C780	A781	U782								
G663	G664	U665	U666	C667	U668	A669	U670	C671	C672	C673	C674	C675	A676	C677	C678	C679	U680	U681	C682	U683	A684	C685	U686	C687	U688	A689	U690	C691	C692	C693	U694	C695	U696	C697	C698	A699	U700	C701	U702	C703	U704	A705	U706	C707	U708	U709	C710	C711	U712	C713	U714	A715	U716	C717	U718	C719	U720	A721	U722								
A603	G604	G605	U606	U607	A608	A609	C610	C611	C612	A613	A614	U615	A616	C617	C618	C619	U620	A621	C622	C623	C624	C625	A626	C627	U628	C629	U630	A631	C632	C633	C634	C635	C636	A637	C638	U639	C640	U641	U642	A643	A644	U645	U646	C647	U648	U649	C650	C651	U652	U653	A654	A655	C656	U657	U658	C659	C660	A661	C662								

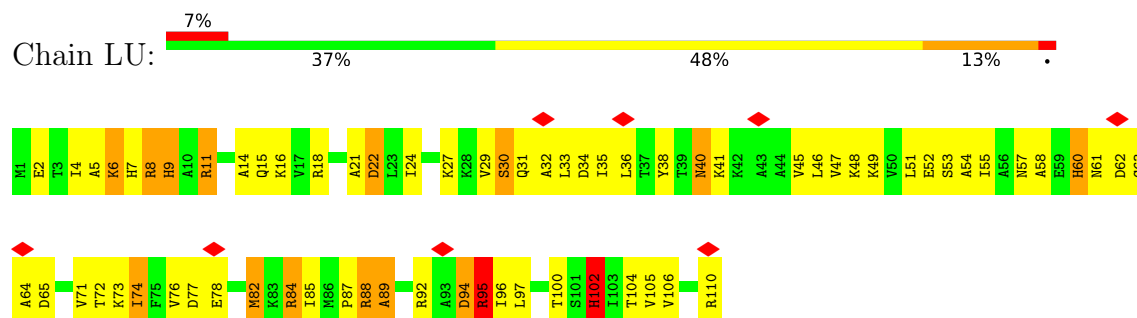




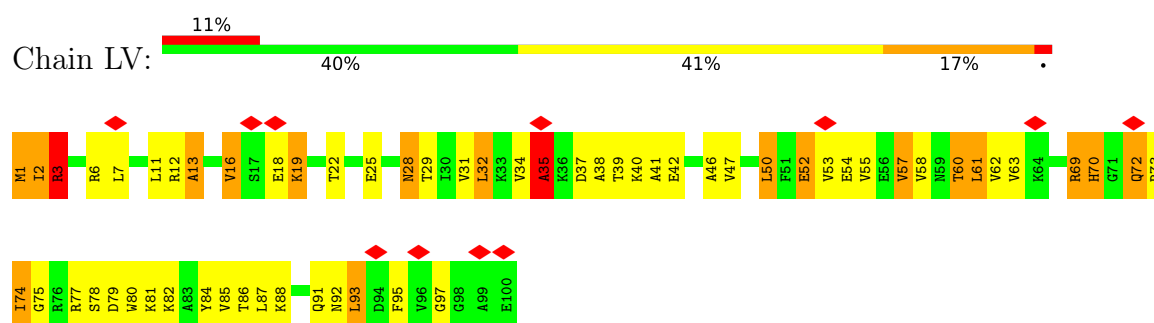
• Molecule 27: 50S ribosomal protein L2



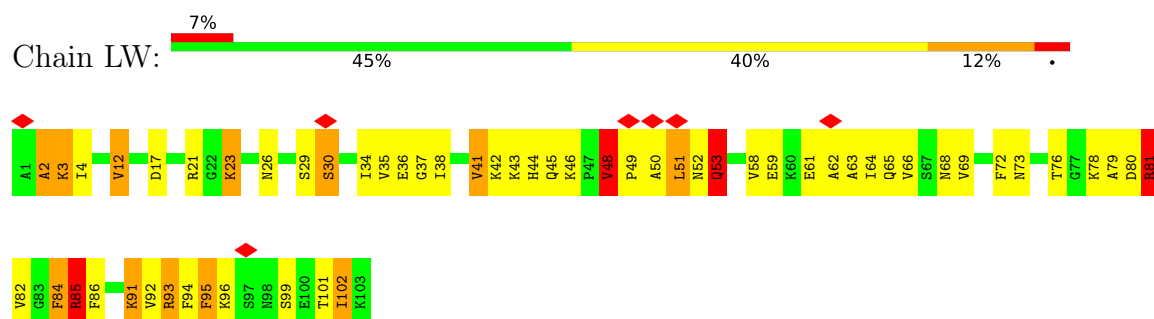
• Molecule 28: 50S ribosomal protein L22



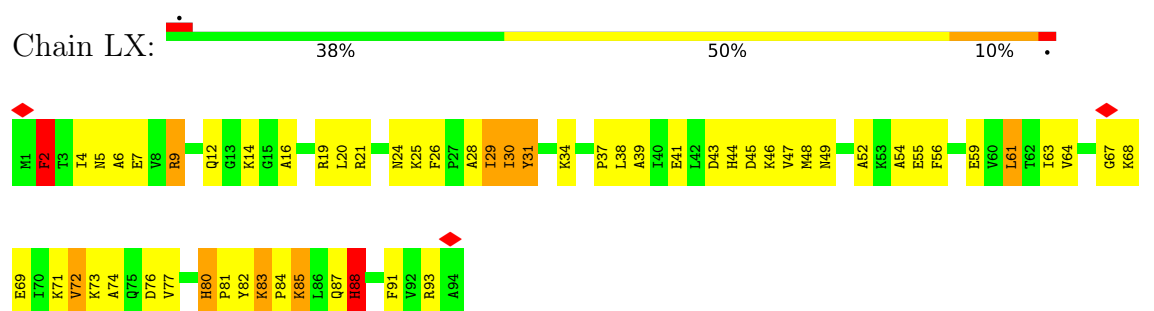
• Molecule 29: 50S ribosomal protein L23



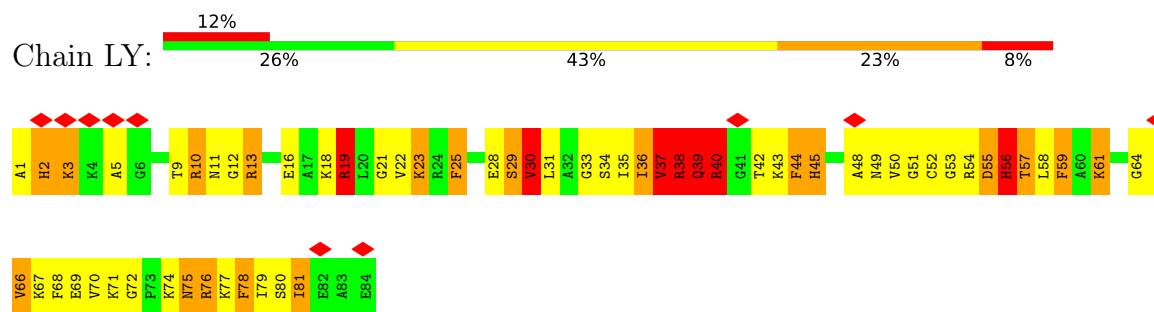
• Molecule 30: 50S ribosomal protein L24



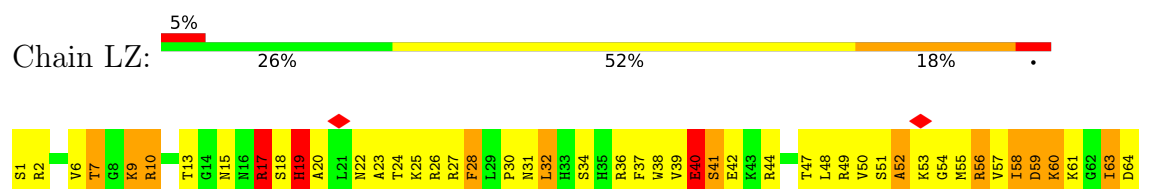
• Molecule 31: 50S ribosomal protein L25

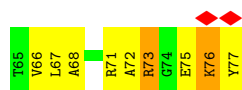


• Molecule 32: 50S ribosomal protein L27

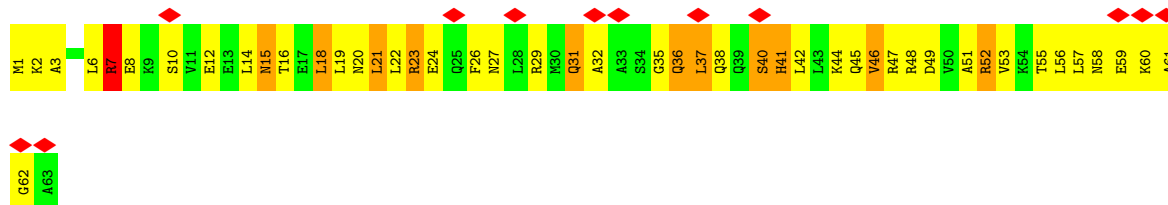


• Molecule 33: 50S ribosomal protein L28

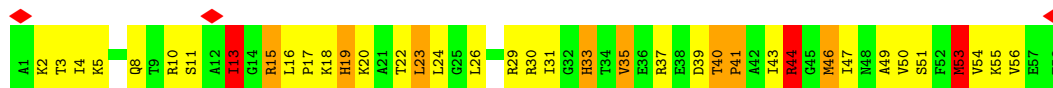




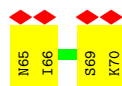
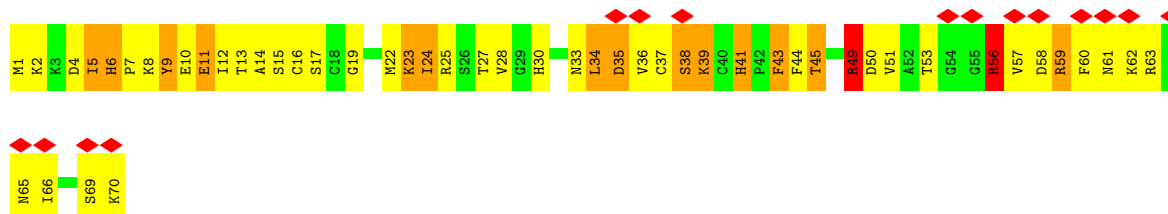
- Molecule 34: 50S ribosomal protein L29



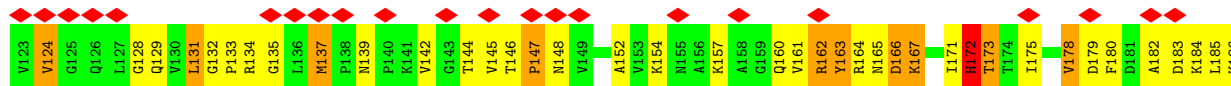
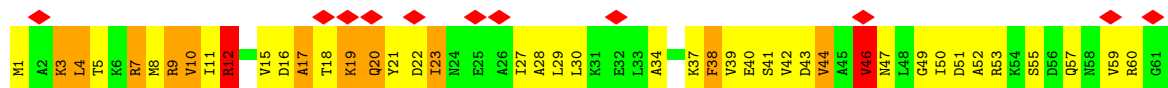
- Molecule 35: 50S ribosomal protein L30

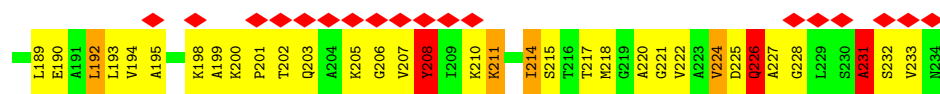


- Molecule 36: 50S ribosomal protein L31

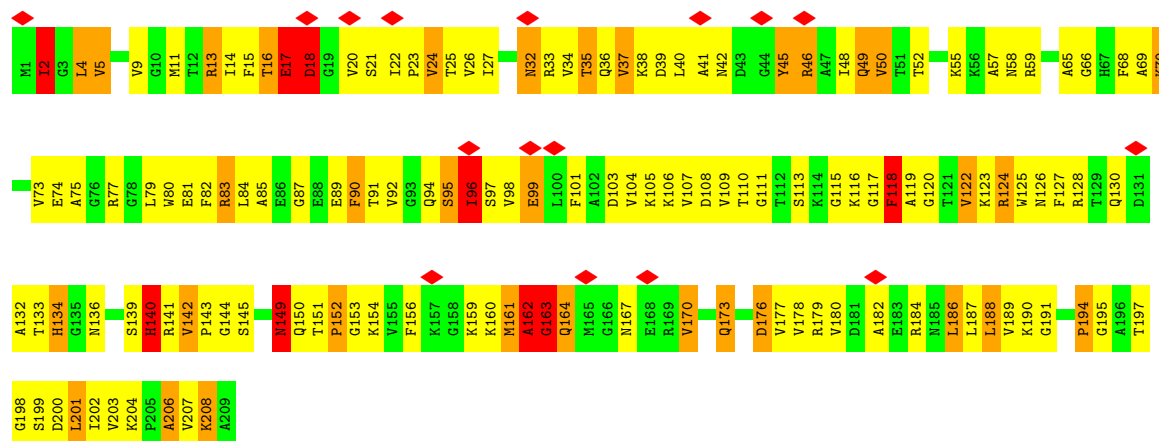


- Molecule 37: 50S ribosomal protein L1

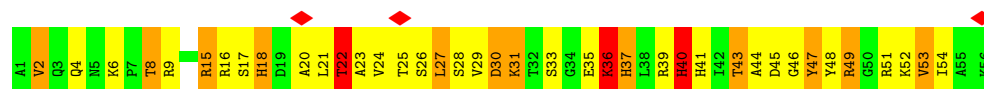




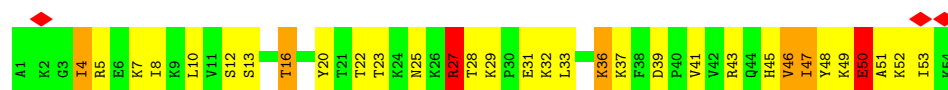
• Molecule 38: 50S ribosomal protein L3



• Molecule 39: 50S ribosomal protein L32



• Molecule 40: 50S ribosomal protein L33



• Molecule 41: 50S ribosomal protein L34

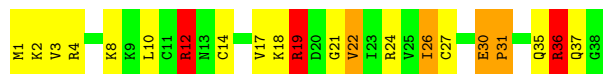


• Molecule 42: 50S ribosomal protein L35



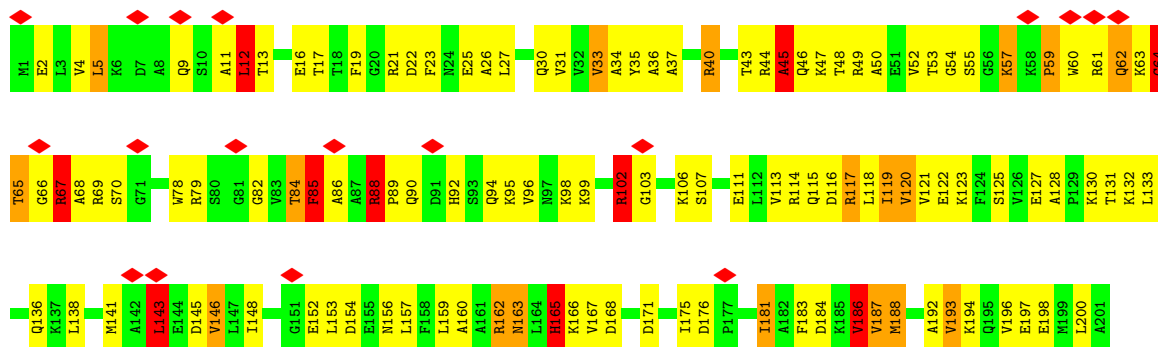
- Molecule 43: 50S ribosomal protein L36

Chain L7: 



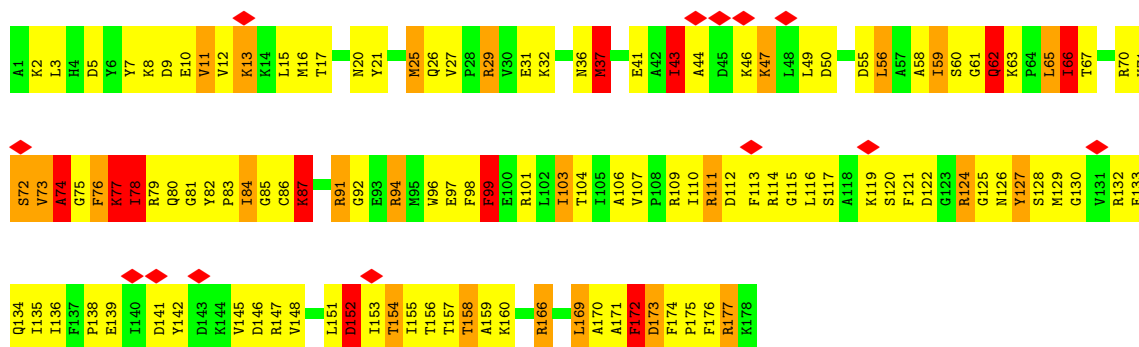
- Molecule 44: 50S ribosomal protein L4

Chain LF: 



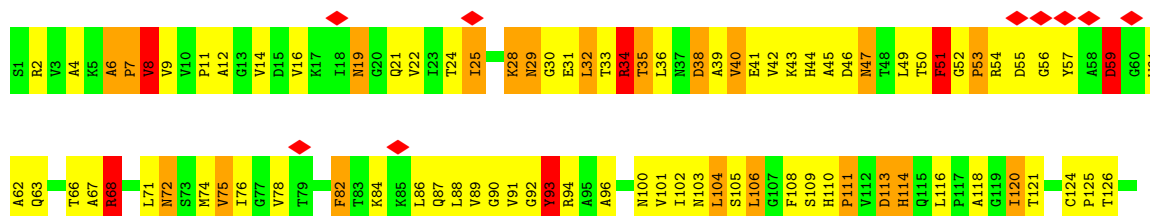
- Molecule 45: 50S ribosomal protein L5

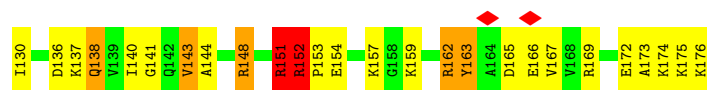
Chain LG: 



- Molecule 46: 50S ribosomal protein L6

Chain LH: 

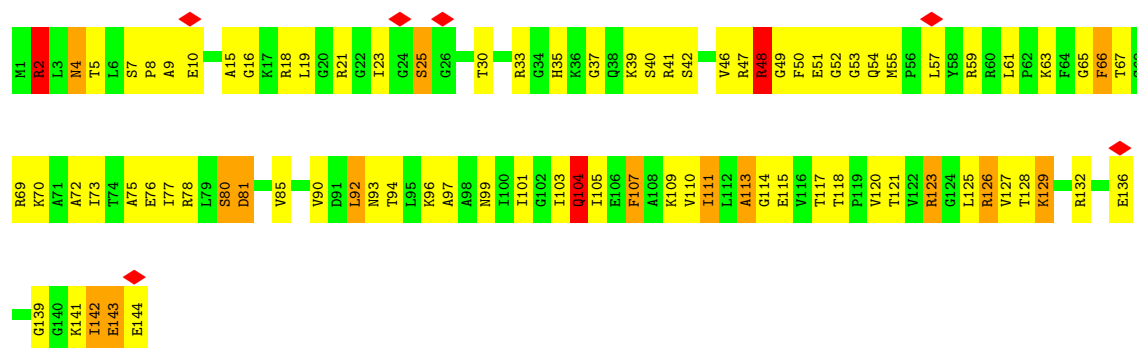




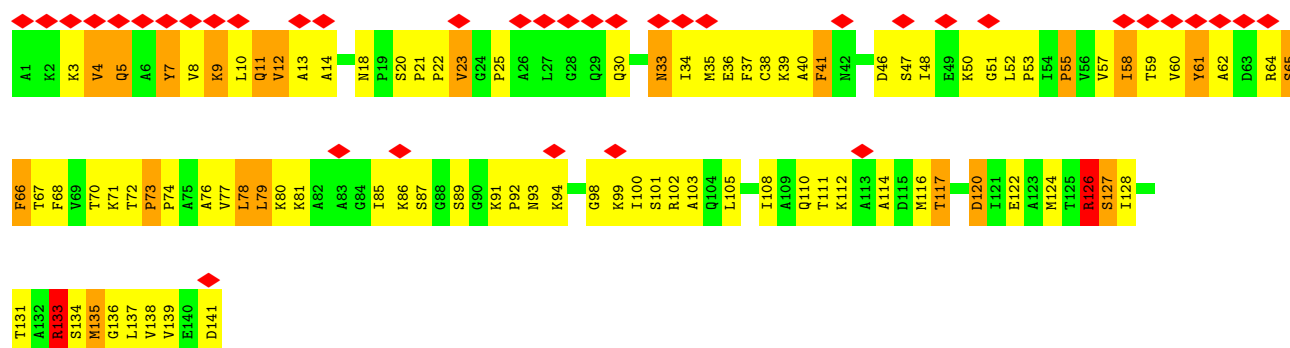
• Molecule 47: 50S ribosomal protein L10



• Molecule 48: 50S ribosomal protein L15

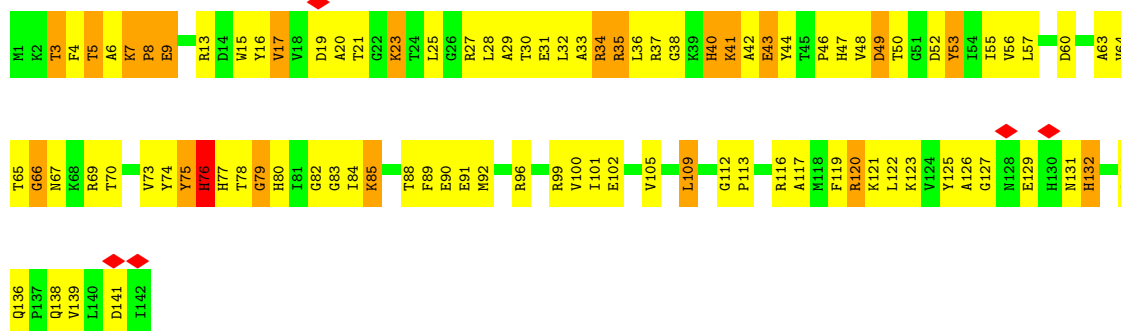


• Molecule 49: 50S ribosomal protein L11



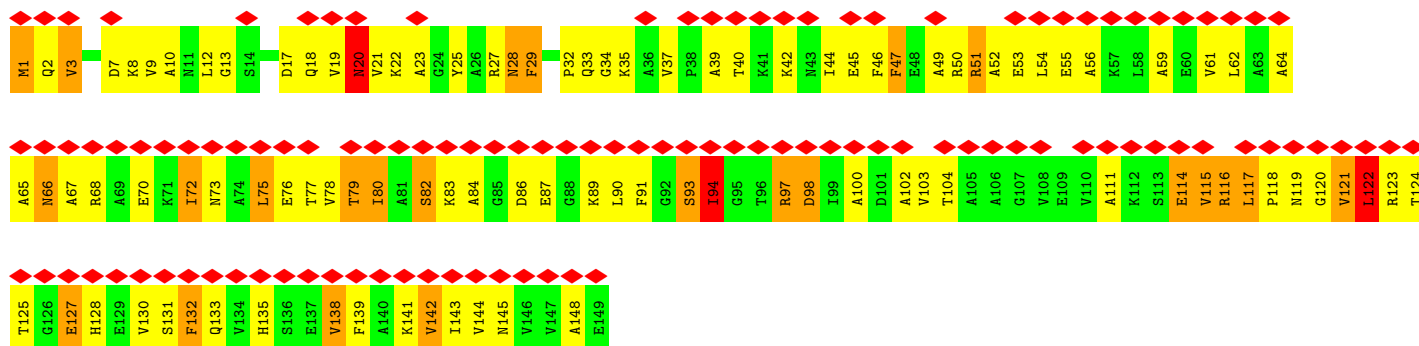
• Molecule 50: 50S ribosomal protein L13

Chain LL: 



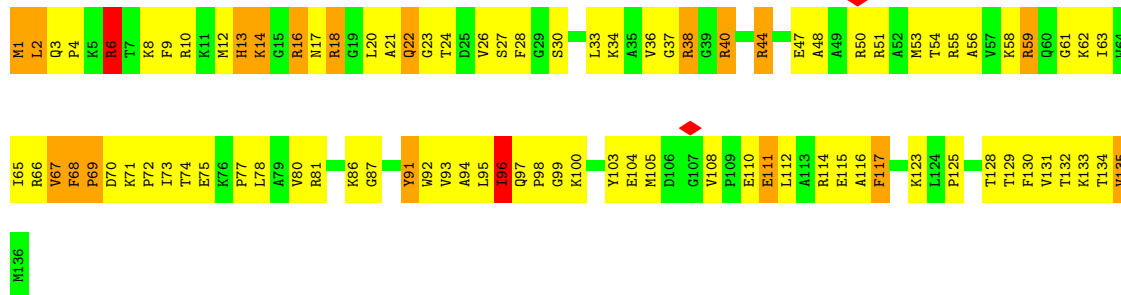
• Molecule 51: 50S ribosomal protein L9

Chain LI: 



• Molecule 52: 50S ribosomal protein L16

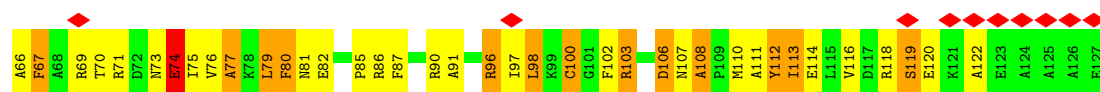
Chain LO: 



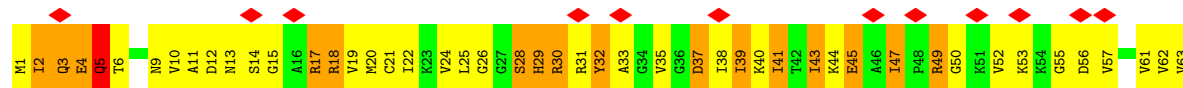
• Molecule 53: 50S ribosomal protein L17

Chain LP: 

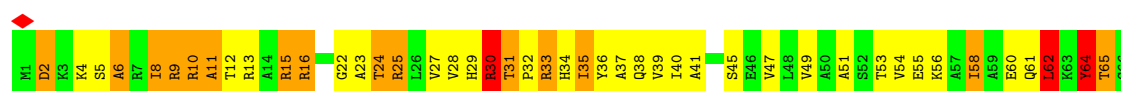




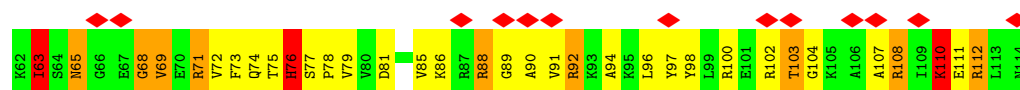
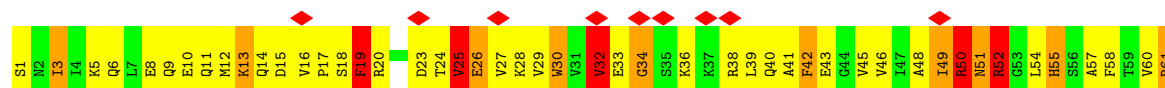
• Molecule 54: 50S ribosomal protein L14



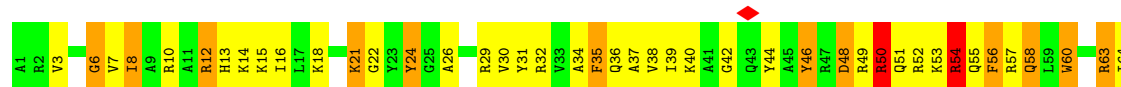
• Molecule 55: 50S ribosomal protein L18



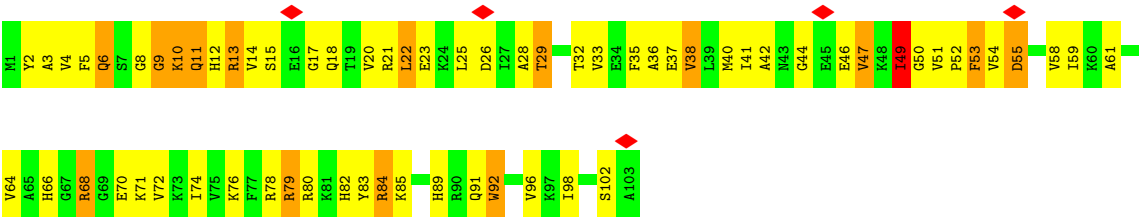
• Molecule 56: 50S ribosomal protein L19



• Molecule 57: 50S ribosomal protein L20



• Molecule 58: 50S ribosomal protein L21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	50000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3 and CTFIT	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	58000	Depositor
Image detector	DIRECT ELECTRON DE-12 (4k x 3k)	Depositor
Maximum map value	0.207	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	377.99997, 377.99997, 377.99997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	SS	2.19	21/744 (2.8%)	2.73	73/995 (7.3%)
2	SA	2.12	1123/37035 (3.0%)	2.13	2301/57774 (4.0%)
3	S1	2.24	49/1108 (4.4%)	2.28	78/1724 (4.5%)
4	S2	2.11	50/1831 (2.7%)	2.24	142/2853 (5.0%)
5	ST	2.34	26/676 (3.8%)	2.60	48/895 (5.4%)
6	SU	2.18	18/598 (3.0%)	2.72	45/792 (5.7%)
7	SG	2.23	54/1422 (3.8%)	2.53	106/1908 (5.6%)
8	SH	2.16	34/989 (3.4%)	2.55	70/1326 (5.3%)
9	SI	2.18	26/1048 (2.5%)	2.50	74/1394 (5.3%)
10	SJ	2.32	38/835 (4.6%)	2.63	79/1127 (7.0%)
11	SK	2.27	31/982 (3.2%)	2.67	80/1323 (6.0%)
12	SL	2.32	37/969 (3.8%)	2.58	77/1300 (5.9%)
13	SM	2.21	31/919 (3.4%)	2.69	84/1226 (6.9%)
14	SN	2.10	21/817 (2.6%)	2.59	72/1088 (6.6%)
15	SO	2.16	21/724 (2.9%)	2.58	54/966 (5.6%)
16	SP	2.10	19/659 (2.9%)	2.52	51/884 (5.8%)
17	SQ	2.20	16/681 (2.3%)	2.52	53/913 (5.8%)
18	SB	2.20	54/1904 (2.8%)	2.66	172/2565 (6.7%)
19	SC	2.13	54/1852 (2.9%)	2.48	132/2490 (5.3%)
20	SD	2.21	56/1665 (3.4%)	2.48	120/2227 (5.4%)
21	SE	2.13	35/1239 (2.8%)	2.64	99/1664 (5.9%)
22	SF	2.17	33/1121 (2.9%)	2.60	85/1509 (5.6%)
23	SR	2.22	16/637 (2.5%)	2.51	49/851 (5.8%)
24	S3	2.22	184/5532 (3.3%)	2.60	475/7485 (6.3%)
25	LB	2.13	79/2869 (2.8%)	2.09	161/4474 (3.6%)
26	LA	2.15	2159/69808 (3.1%)	2.12	4286/108905 (3.9%)
27	LD	2.27	76/2131 (3.6%)	2.56	159/2863 (5.6%)
28	LU	2.15	27/864 (3.1%)	2.50	63/1156 (5.4%)
29	LV	2.17	24/794 (3.0%)	2.54	46/1060 (4.3%)
30	LW	2.17	22/797 (2.8%)	2.49	57/1062 (5.4%)
31	LX	2.18	28/766 (3.7%)	2.58	53/1025 (5.2%)
32	LY	2.40	33/642 (5.1%)	2.71	54/848 (6.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	2.38	33/635 (5.2%)	2.65	57/848 (6.7%)
34	L0	2.15	17/510 (3.3%)	2.86	59/677 (8.7%)
35	L1	2.16	12/453 (2.6%)	2.62	31/605 (5.1%)
36	L2	2.14	18/559 (3.2%)	2.55	36/745 (4.8%)
37	LC	2.24	58/1748 (3.3%)	2.74	169/2355 (7.2%)
38	LE	2.26	51/1586 (3.2%)	2.60	119/2134 (5.6%)
39	L3	2.28	19/450 (4.2%)	2.46	33/599 (5.5%)
40	L4	2.30	18/448 (4.0%)	2.40	25/594 (4.2%)
41	L5	2.28	21/380 (5.5%)	2.79	40/498 (8.0%)
42	L6	2.19	18/513 (3.5%)	2.49	34/676 (5.0%)
43	L7	2.17	6/303 (2.0%)	2.34	14/397 (3.5%)
44	LF	2.24	60/1571 (3.8%)	2.47	103/2113 (4.9%)
45	LG	2.10	35/1444 (2.4%)	2.67	129/1937 (6.7%)
46	LH	2.17	45/1343 (3.4%)	2.69	116/1816 (6.4%)
47	LJ	2.17	46/1247 (3.7%)	2.59	102/1679 (6.1%)
48	LN	2.13	32/1062 (3.0%)	2.59	81/1413 (5.7%)
49	LK	2.21	37/1046 (3.5%)	2.78	102/1410 (7.2%)
50	LL	2.28	42/1152 (3.6%)	2.58	101/1551 (6.5%)
51	LI	2.23	43/1122 (3.8%)	2.70	94/1515 (6.2%)
52	LO	2.24	46/1093 (4.2%)	2.52	68/1460 (4.7%)
53	LP	2.30	42/1021 (4.1%)	2.52	78/1364 (5.7%)
54	LM	2.24	29/956 (3.0%)	2.59	82/1279 (6.4%)
55	LQ	2.27	36/910 (4.0%)	2.53	72/1219 (5.9%)
56	LR	2.29	40/929 (4.3%)	2.70	79/1242 (6.4%)
57	LS	2.19	31/960 (3.2%)	2.66	83/1278 (6.5%)
58	LT	2.17	29/829 (3.5%)	2.62	68/1107 (6.1%)
All	All	2.16	5359/168928 (3.2%)	2.28	11473/251183 (4.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	SS	0	11
2	SA	0	979
3	S1	0	36
4	S2	0	48
5	ST	0	5
6	SU	0	11
7	SG	0	19
8	SH	0	10

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
9	SI	0	7
10	SJ	0	9
11	SK	0	7
12	SL	0	10
13	SM	0	8
14	SN	0	11
15	SO	0	7
16	SP	0	9
17	SQ	0	6
18	SB	0	13
19	SC	0	11
20	SD	0	18
21	SE	0	11
22	SF	0	12
23	SR	0	9
24	S3	0	38
25	LB	0	68
26	LA	5	1948
27	LD	0	24
28	LU	0	8
29	LV	0	5
30	LW	0	8
31	LX	0	5
32	LY	0	8
33	LZ	0	7
34	L0	0	2
35	L1	0	3
36	L2	0	9
37	LC	0	17
38	LE	0	15
39	L3	0	5
40	L4	0	4
41	L5	0	7
42	L6	0	2
43	L7	0	4
44	LF	0	10
45	LG	0	15
46	LH	0	13
47	LJ	0	10
48	LN	0	12
49	LK	0	10
50	LL	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
51	LI	0	7
52	LO	0	8
53	LP	0	10
54	LM	0	9
55	LQ	0	14
56	LR	0	11
57	LS	0	12
58	LT	0	8
All	All	5	3608

The worst 5 of 5359 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	LG	107	VAL	CA-CB	-12.88	1.45	1.53
27	LD	28	PRO	CA-C	-11.50	1.39	1.52
33	LZ	10	ARG	CA-C	-11.50	1.39	1.52
18	SB	100	LEU	CA-C	11.23	1.60	1.52
52	LO	68	PHE	CA-C	-11.17	1.41	1.52

The worst 5 of 11473 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	LA	1568	G	P-O5'-C5'	25.30	158.84	120.90
26	LA	826	U	P-O3'-C3'	22.14	153.42	120.20
26	LA	2516	A	P-O5'-C5'	19.57	150.25	120.90
26	LA	1409	U	P-O5'-C5'	19.31	149.86	120.90
2	SA	1344	C	O3'-P-O5'	18.31	131.47	104.00

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
26	LA	2451	A	C1'
26	LA	2503	A	C2'
26	LA	2504	U	C3',C2'
26	LA	2575	C	C4'

5 of 3608 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	SS	1	PRO	Peptide
1	SS	10	ILE	Peptide
1	SS	2	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	SS	3	SER	Peptide
1	SS	8	PRO	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	SS	727	0	769	10	0
2	SA	33076	0	16190	635	0
3	S1	993	0	496	16	0
4	S2	1639	0	816	32	0
5	ST	670	0	722	2	0
6	SU	590	0	631	6	0
7	SG	1400	0	1449	13	0
8	SH	979	0	1034	5	0
9	SI	1036	0	1084	9	0
10	SJ	825	0	865	10	0
11	SK	965	0	997	14	0
12	SL	955	0	1019	12	0
13	SM	910	0	981	10	0
14	SN	805	0	847	5	0
15	SO	716	0	742	5	0
16	SP	649	0	666	3	0
17	SQ	672	0	716	4	0
18	SB	1872	0	1885	15	0
19	SC	1822	0	1913	14	0
20	SD	1643	0	1710	23	0
21	SE	1225	0	1273	22	0
22	SF	1101	0	1050	11	0
23	SR	626	0	651	6	0
24	S3	5431	0	5403	50	0
25	LB	2566	0	1269	48	0
26	LA	62330	0	30424	1512	0
27	LD	2092	0	2170	22	0
28	LU	857	0	922	6	0
29	LV	787	0	846	6	0
30	LW	789	0	847	8	0
31	LX	753	0	780	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	LY	634	0	656	18	0
33	LZ	625	0	655	4	0
34	L0	509	0	543	5	0
35	L1	449	0	491	4	0
36	L2	549	0	552	5	0
37	LC	1733	0	1824	19	0
38	LE	1565	0	1616	22	0
39	L3	444	0	461	9	0
40	L4	441	0	485	3	0
41	L5	377	0	418	8	0
42	L6	504	0	574	4	0
43	L7	302	0	343	4	0
44	LF	1552	0	1619	18	0
45	LG	1420	0	1460	17	0
46	LH	1323	0	1374	6	0
47	LJ	1233	0	1283	6	0
48	LN	1053	0	1129	8	0
49	LK	1032	0	1088	4	0
50	LL	1129	0	1162	9	0
51	LI	1111	0	1148	8	0
52	LO	1074	0	1157	18	0
53	LP	1008	0	1045	11	0
54	LM	947	0	1023	11	0
55	LQ	900	0	935	9	0
56	LR	917	0	965	6	0
57	LS	947	0	1022	17	0
58	LT	816	0	839	7	0
59	S3	32	0	12	0	0
All	All	156127	0	107046	2656	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 10.

The worst 5 of 2656 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)
21:SE:123:LEU:HD13	21:SE:124:ALA:H	1.44	0.83
2:SA:1381:U:H1'	7:SG:152:HIS:CE1	2.16	0.80
26:LA:1853:A:H61	26:LA:2087:G:H1'	1.47	0.80
26:LA:1965:C:C2	26:LA:1966:A:H2'	2.18	0.78
2:SA:803:G:C5	2:SA:804:U:C4	2.72	0.78

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	SS	89/91 (98%)	71 (80%)	13 (15%)	5 (6%)	1	14
5	ST	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
6	SU	68/70 (97%)	46 (68%)	14 (21%)	8 (12%)	0	4
7	SG	176/178 (99%)	154 (88%)	14 (8%)	8 (4%)	2	17
8	SH	127/129 (98%)	103 (81%)	16 (13%)	8 (6%)	1	12
9	SI	127/129 (98%)	99 (78%)	22 (17%)	6 (5%)	2	17
10	SJ	101/103 (98%)	83 (82%)	11 (11%)	7 (7%)	1	11
11	SK	126/128 (98%)	102 (81%)	18 (14%)	6 (5%)	2	16
12	SL	121/123 (98%)	95 (78%)	14 (12%)	12 (10%)	0	6
13	SM	115/117 (98%)	97 (84%)	11 (10%)	7 (6%)	1	13
14	SN	98/100 (98%)	81 (83%)	12 (12%)	5 (5%)	1	15
15	SO	86/88 (98%)	76 (88%)	7 (8%)	3 (4%)	3	23
16	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	1	16
17	SQ	81/83 (98%)	67 (83%)	9 (11%)	5 (6%)	1	12
18	SB	238/240 (99%)	212 (89%)	14 (6%)	12 (5%)	1	16
19	SC	230/232 (99%)	196 (85%)	18 (8%)	16 (7%)	1	10
20	SD	203/205 (99%)	166 (82%)	26 (13%)	11 (5%)	1	14
21	SE	164/166 (99%)	127 (77%)	24 (15%)	13 (8%)	1	8
22	SF	133/135 (98%)	114 (86%)	11 (8%)	8 (6%)	1	13
23	SR	72/74 (97%)	57 (79%)	10 (14%)	5 (7%)	1	11
24	S3	700/702 (100%)	611 (87%)	61 (9%)	28 (4%)	2	20
27	LD	270/272 (99%)	215 (80%)	42 (16%)	13 (5%)	2	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LU	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	6	33
29	LV	98/100 (98%)	75 (76%)	13 (13%)	10 (10%)	0	5
30	LW	101/103 (98%)	84 (83%)	12 (12%)	5 (5%)	1	16
31	LX	92/94 (98%)	83 (90%)	5 (5%)	4 (4%)	2	18
32	LY	82/84 (98%)	57 (70%)	15 (18%)	10 (12%)	0	4
33	LZ	75/77 (97%)	63 (84%)	10 (13%)	2 (3%)	4	27
34	L0	61/63 (97%)	51 (84%)	8 (13%)	2 (3%)	3	24
35	L1	56/58 (97%)	45 (80%)	7 (12%)	4 (7%)	1	10
36	L2	68/70 (97%)	44 (65%)	15 (22%)	9 (13%)	0	3
37	LC	232/234 (99%)	192 (83%)	29 (12%)	11 (5%)	2	17
38	LE	207/209 (99%)	151 (73%)	34 (16%)	22 (11%)	0	5
39	L3	54/56 (96%)	40 (74%)	7 (13%)	7 (13%)	0	3
40	L4	52/54 (96%)	45 (86%)	5 (10%)	2 (4%)	2	21
41	L5	44/46 (96%)	34 (77%)	7 (16%)	3 (7%)	1	11
42	L6	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	7	36
43	L7	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	3
44	LF	199/201 (99%)	163 (82%)	21 (11%)	15 (8%)	1	9
45	LG	176/178 (99%)	133 (76%)	26 (15%)	17 (10%)	0	6
46	LH	174/176 (99%)	127 (73%)	29 (17%)	18 (10%)	0	5
47	LJ	162/164 (99%)	143 (88%)	11 (7%)	8 (5%)	1	16
48	LN	142/144 (99%)	116 (82%)	22 (16%)	4 (3%)	4	26
49	LK	139/141 (99%)	114 (82%)	17 (12%)	8 (6%)	1	13
50	LL	140/142 (99%)	116 (83%)	14 (10%)	10 (7%)	1	10
51	LI	147/149 (99%)	121 (82%)	16 (11%)	10 (7%)	1	11
52	LO	134/136 (98%)	111 (83%)	14 (10%)	9 (7%)	1	11
53	LP	125/127 (98%)	109 (87%)	10 (8%)	6 (5%)	2	16
54	LM	121/123 (98%)	91 (75%)	18 (15%)	12 (10%)	0	6
55	LQ	115/117 (98%)	108 (94%)	5 (4%)	2 (2%)	7	35
56	LR	112/114 (98%)	79 (70%)	17 (15%)	16 (14%)	0	3
57	LS	115/117 (98%)	104 (90%)	5 (4%)	6 (5%)	1	15
58	LT	101/103 (98%)	87 (86%)	11 (11%)	3 (3%)	3	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7019/7125 (98%)	5781 (82%)	805 (12%)	433 (6%)	2	12

5 of 433 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	SS	11	ASP
1	SS	37	SER
1	SS	75	PRO
6	SU	10	PRO
6	SU	18	PHE

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	SS	78/78 (100%)	67 (86%)	11 (14%)	3	19
5	ST	65/65 (100%)	59 (91%)	6 (9%)	8	33
6	SU	60/60 (100%)	53 (88%)	7 (12%)	5	25
7	SG	146/146 (100%)	137 (94%)	9 (6%)	16	44
8	SH	104/104 (100%)	90 (86%)	14 (14%)	4	21
9	SI	106/106 (100%)	89 (84%)	17 (16%)	2	15
10	SJ	90/90 (100%)	80 (89%)	10 (11%)	6	27
11	SK	98/98 (100%)	90 (92%)	8 (8%)	10	36
12	SL	103/103 (100%)	95 (92%)	8 (8%)	11	38
13	SM	95/95 (100%)	81 (85%)	14 (15%)	3	17
14	SN	83/83 (100%)	76 (92%)	7 (8%)	10	35
15	SO	76/76 (100%)	70 (92%)	6 (8%)	11	37
16	SP	65/65 (100%)	57 (88%)	8 (12%)	4	23
17	SQ	77/77 (100%)	73 (95%)	4 (5%)	21	48
18	SB	198/198 (100%)	184 (93%)	14 (7%)	13	40
19	SC	189/189 (100%)	168 (89%)	21 (11%)	6	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	SD	172/172 (100%)	149 (87%)	23 (13%)	4	21
21	SE	125/125 (100%)	109 (87%)	16 (13%)	4	22
22	SF	116/116 (100%)	99 (85%)	17 (15%)	3	17
23	SR	64/64 (100%)	59 (92%)	5 (8%)	11	38
24	S3	575/575 (100%)	518 (90%)	57 (10%)	7	31
27	LD	217/217 (100%)	190 (88%)	27 (12%)	4	23
28	LU	93/93 (100%)	81 (87%)	12 (13%)	4	22
29	LV	84/84 (100%)	73 (87%)	11 (13%)	4	21
30	LW	84/84 (100%)	78 (93%)	6 (7%)	13	40
31	LX	78/78 (100%)	72 (92%)	6 (8%)	12	38
32	LY	62/62 (100%)	54 (87%)	8 (13%)	4	22
33	LZ	67/67 (100%)	57 (85%)	10 (15%)	3	17
34	L0	55/55 (100%)	49 (89%)	6 (11%)	6	27
35	L1	48/48 (100%)	39 (81%)	9 (19%)	1	10
36	L2	62/62 (100%)	53 (86%)	9 (14%)	3	18
37	LC	181/181 (100%)	159 (88%)	22 (12%)	5	23
38	LE	164/164 (100%)	143 (87%)	21 (13%)	4	22
39	L3	47/47 (100%)	43 (92%)	4 (8%)	10	35
40	L4	48/48 (100%)	44 (92%)	4 (8%)	10	35
41	L5	38/38 (100%)	34 (90%)	4 (10%)	6	29
42	L6	51/51 (100%)	49 (96%)	2 (4%)	28	54
43	L7	34/34 (100%)	31 (91%)	3 (9%)	9	33
44	LF	165/165 (100%)	156 (94%)	9 (6%)	19	47
45	LG	149/149 (100%)	133 (89%)	16 (11%)	6	28
46	LH	137/137 (100%)	120 (88%)	17 (12%)	4	23
47	LJ	122/122 (100%)	110 (90%)	12 (10%)	7	31
48	LN	103/103 (100%)	91 (88%)	12 (12%)	5	25
49	LK	109/109 (100%)	93 (85%)	16 (15%)	3	17
50	LL	116/116 (100%)	108 (93%)	8 (7%)	14	41
51	LI	114/114 (100%)	95 (83%)	19 (17%)	2	14
52	LO	109/109 (100%)	97 (89%)	12 (11%)	6	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	LP	103/103 (100%)	95 (92%)	8 (8%)	11	38
54	LM	104/104 (100%)	95 (91%)	9 (9%)	9	34
55	LQ	87/87 (100%)	80 (92%)	7 (8%)	11	37
56	LR	99/99 (100%)	87 (88%)	12 (12%)	5	23
57	LS	89/89 (100%)	78 (88%)	11 (12%)	4	23
58	LT	84/84 (100%)	77 (92%)	7 (8%)	10	35
All	All	5788/5788 (100%)	5167 (89%)	621 (11%)	8	28

5 of 621 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	LG	65	LEU
53	LP	113	ILE
46	LH	51	PHE
45	LG	59	ILE
49	LK	57	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
50	LL	86	GLN
53	LP	3	HIS
58	LT	6	GLN
24	S3	258	ASN
24	S3	219	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	SA	1541/1542 (99%)	372 (24%)	122 (7%)
25	LB	119/120 (99%)	22 (18%)	9 (7%)
26	LA	2903/2904 (99%)	663 (22%)	221 (7%)
3	S1	46/47 (97%)	36 (78%)	12 (26%)
4	S2	77/77 (100%)	21 (27%)	10 (12%)
All	All	4686/4690 (99%)	1114 (23%)	374 (7%)

5 of 1114 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	SA	3	A
2	SA	4	U
2	SA	5	U
2	SA	8	A
2	SA	9	G

5 of 374 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	LA	1061	U
26	LA	1818	U
26	LA	1133	A
26	LA	1392	A
26	LA	2042	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
59	GTP	S3	801	-	33,34,34	3.55	9 (27%)	50,54,54	1.43	6 (12%)

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
59	GTP	S3	801	-	-	0/22/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	S3	801	GTP	PA-O3A	-11.93	1.46	1.59
59	S3	801	GTP	PB-O3A	-11.50	1.47	1.59
59	S3	801	GTP	PB-O3B	-8.91	1.49	1.59
59	S3	801	GTP	C1'-N9	-2.58	1.40	1.47
59	S3	801	GTP	C5-N7	-2.50	1.34	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S3	801	GTP	O3A-PA-O1A	4.95	125.61	110.70
59	S3	801	GTP	O5'-PA-O1A	-3.17	96.38	108.94
59	S3	801	GTP	O4'-C4'-C3'	-2.79	99.61	105.15
59	S3	801	GTP	C6-C5-C4	-2.70	114.77	118.83
59	S3	801	GTP	C2'-C3'-C4'	2.33	107.12	102.61

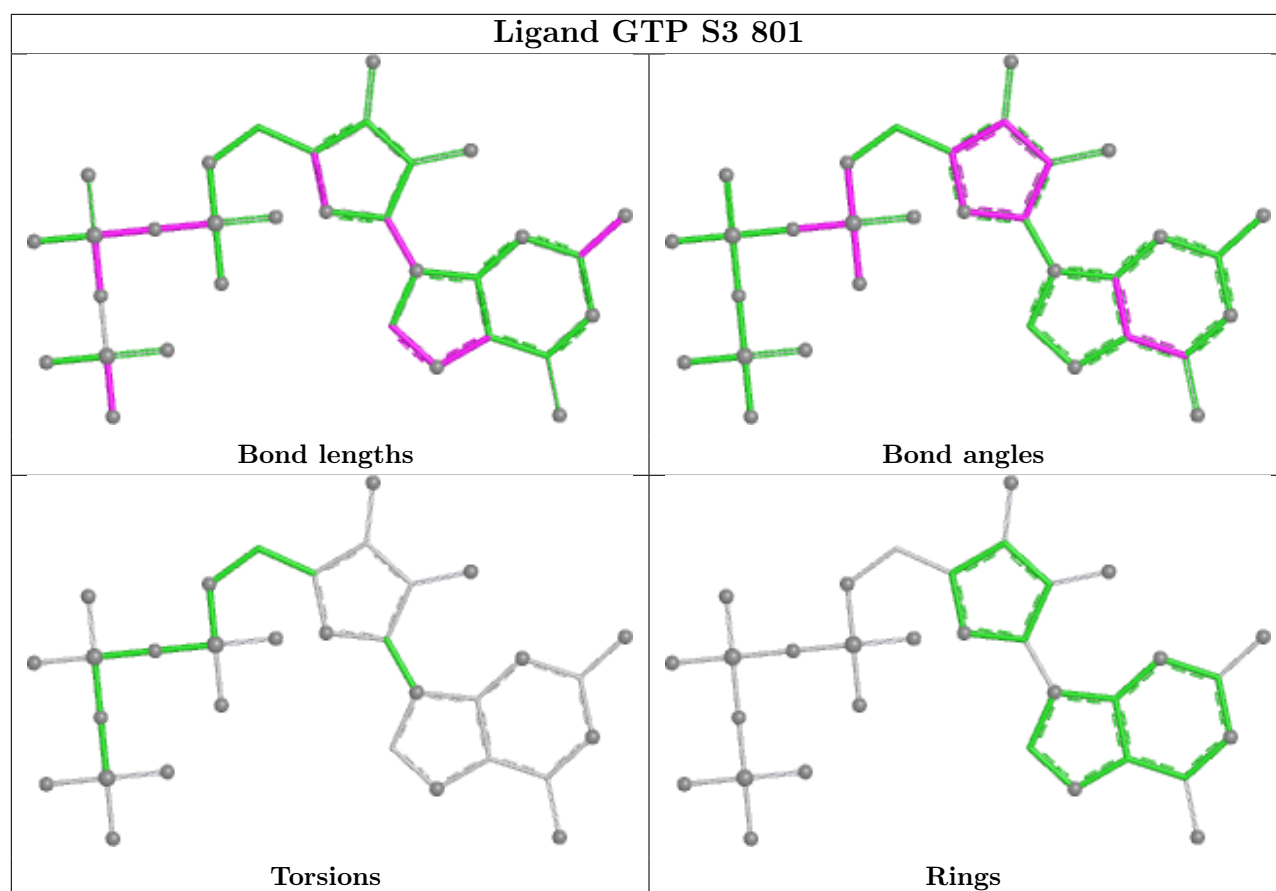
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

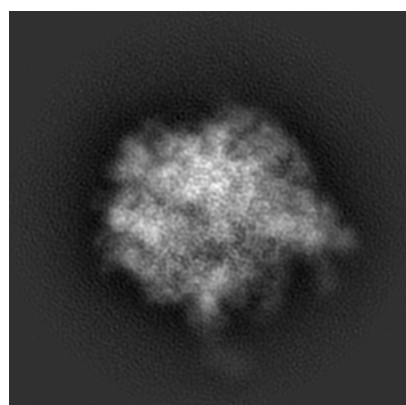
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6316. These allow visual inspection of the internal detail of the map and identification of artifacts.

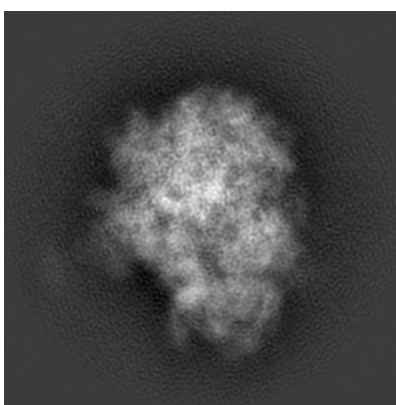
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

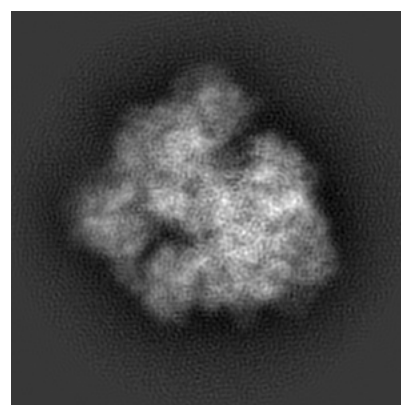
6.1.1 Primary map



X



Y

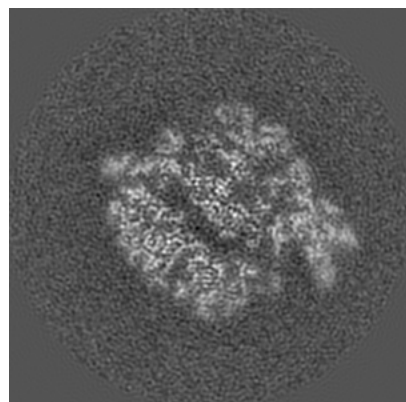


Z

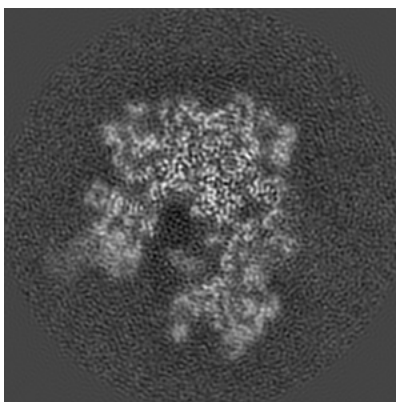
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

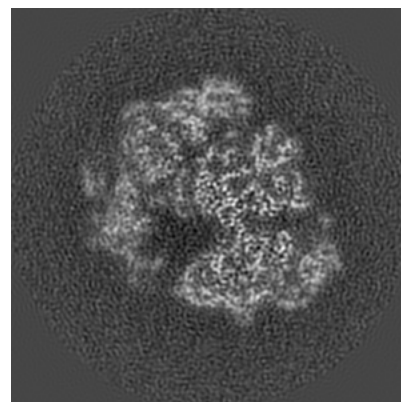
6.2.1 Primary map



X Index: 180



Y Index: 180

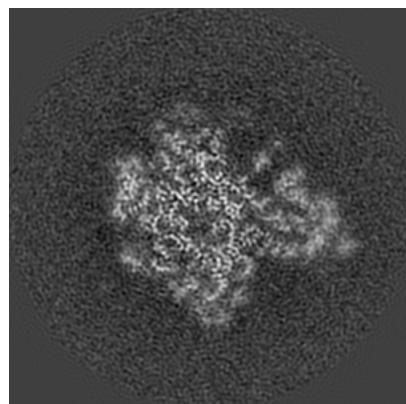


Z Index: 180

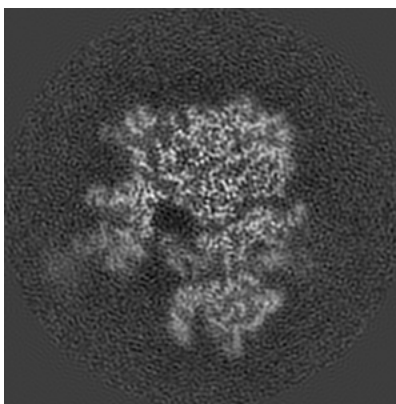
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

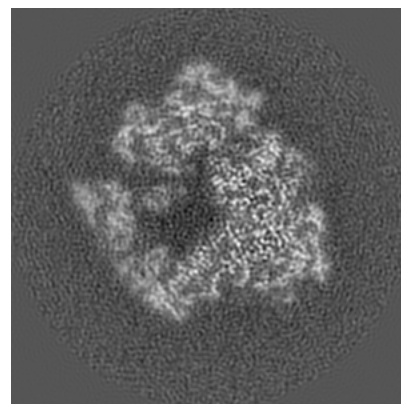
6.3.1 Primary map



X Index: 191



Y Index: 188

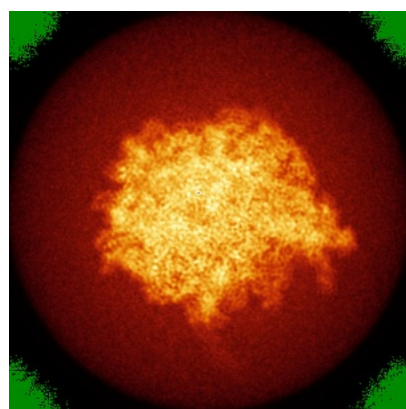


Z Index: 161

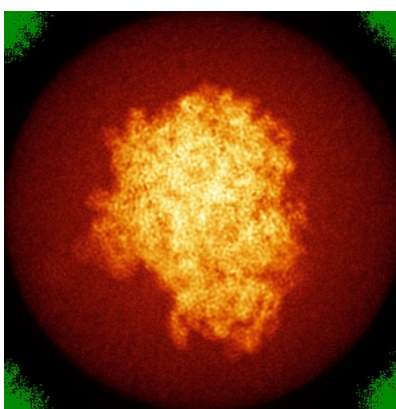
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

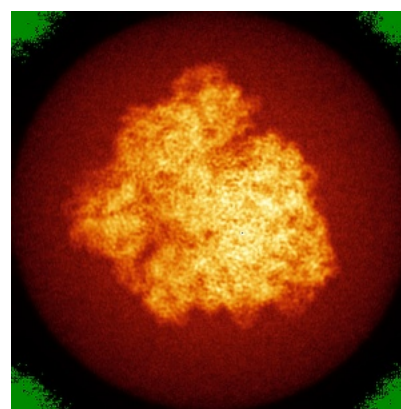
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

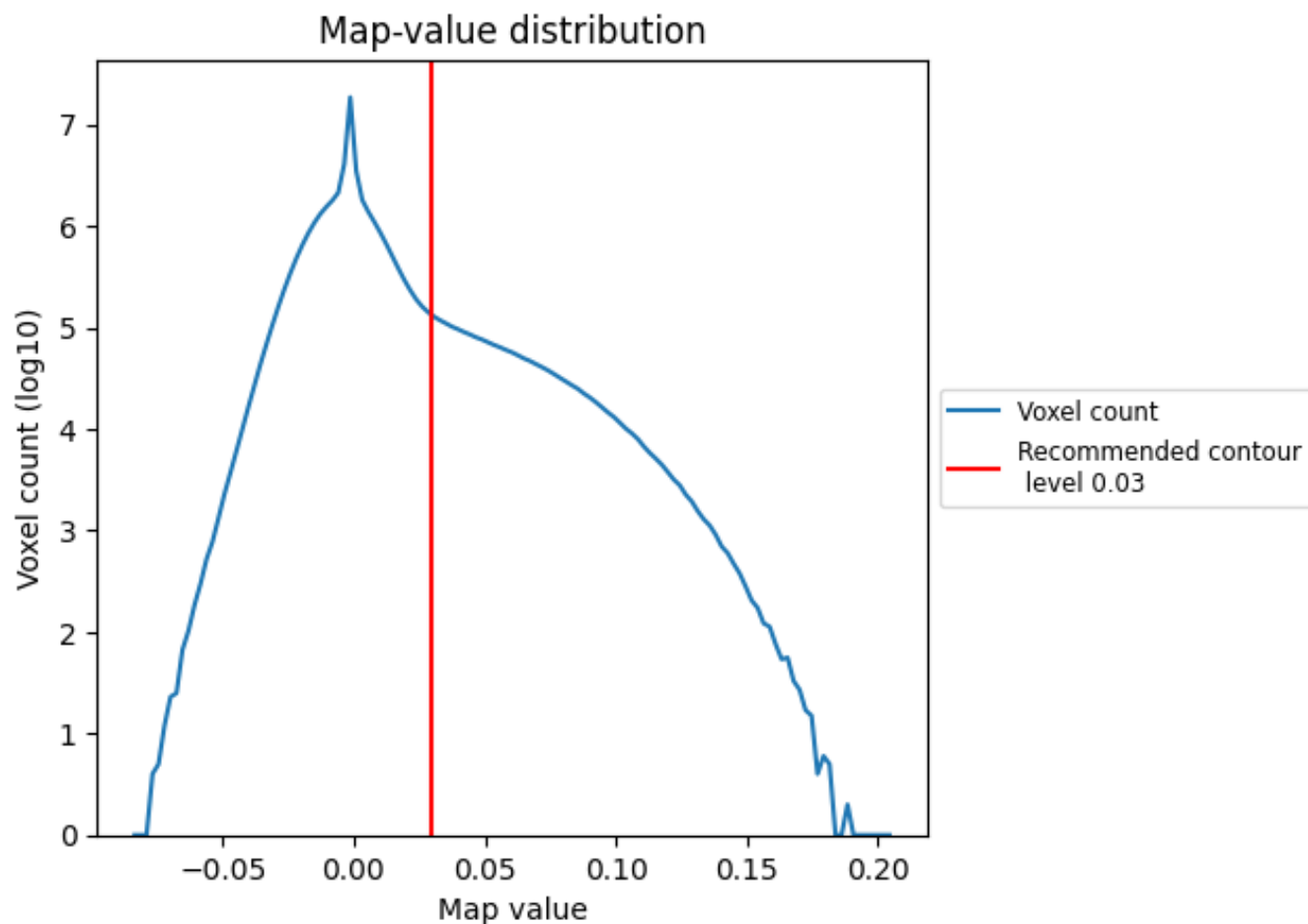
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

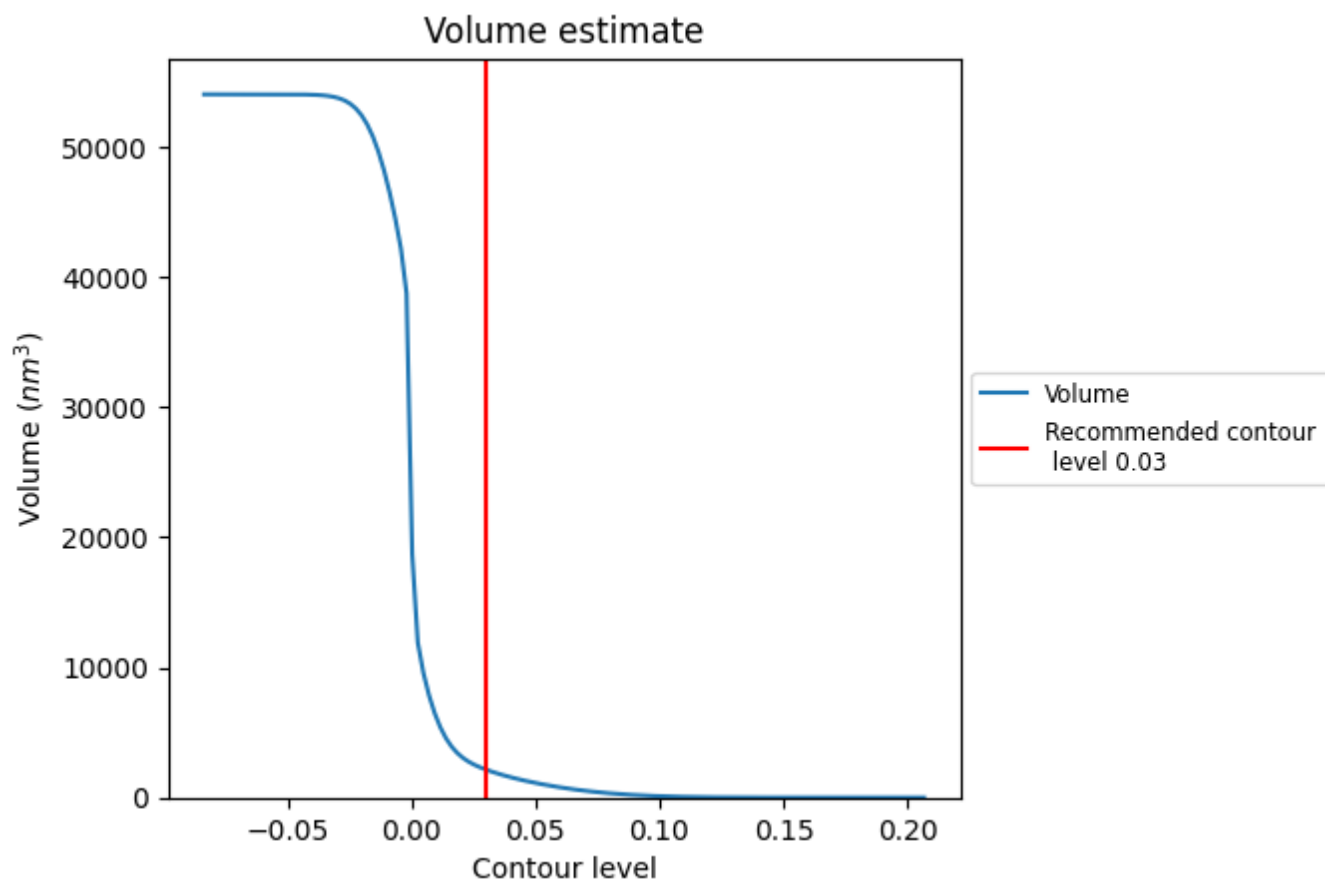
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

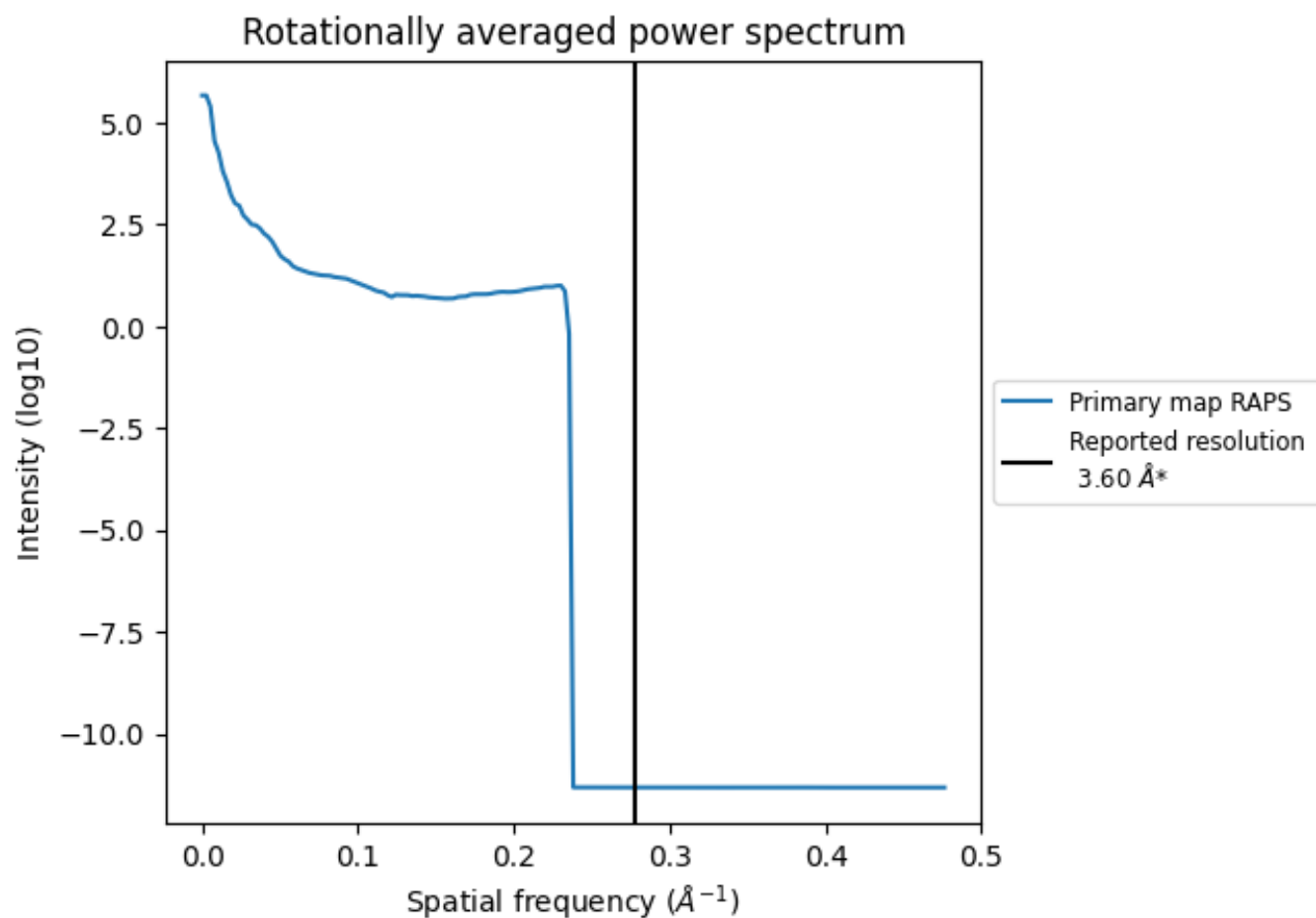
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2151 nm³; this corresponds to an approximate mass of 1943 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

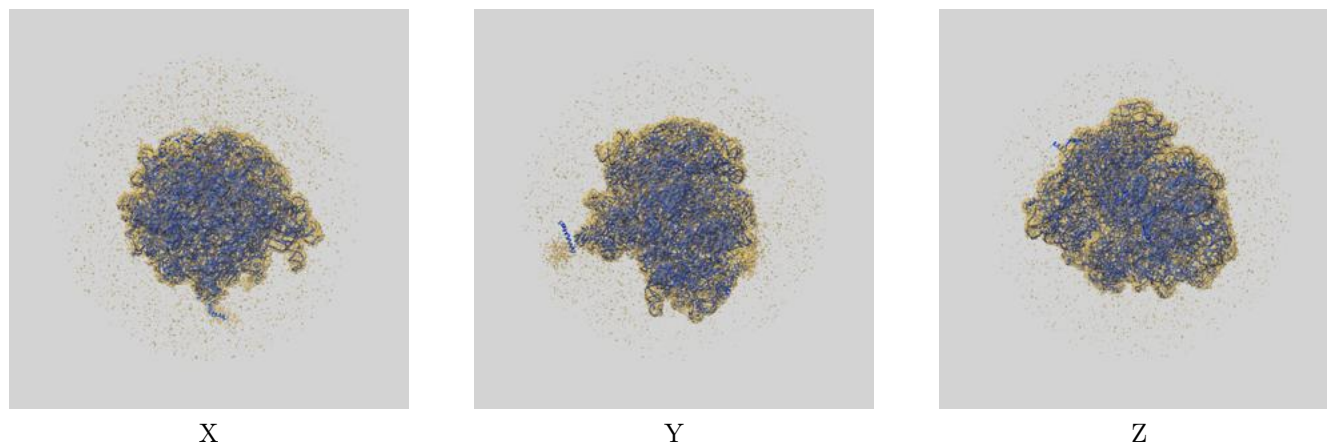
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

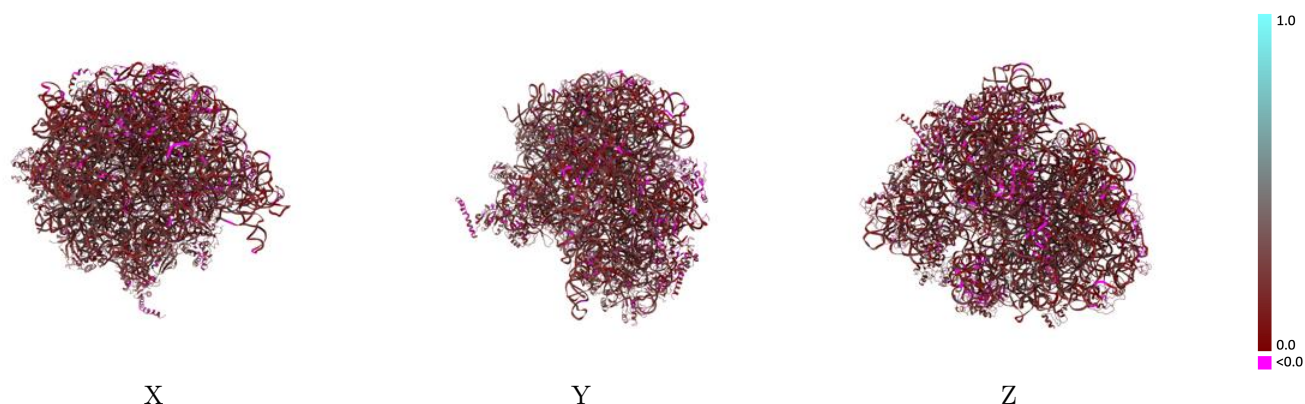
This section contains information regarding the fit between EMDB map EMD-6316 and PDB model 3JA1. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



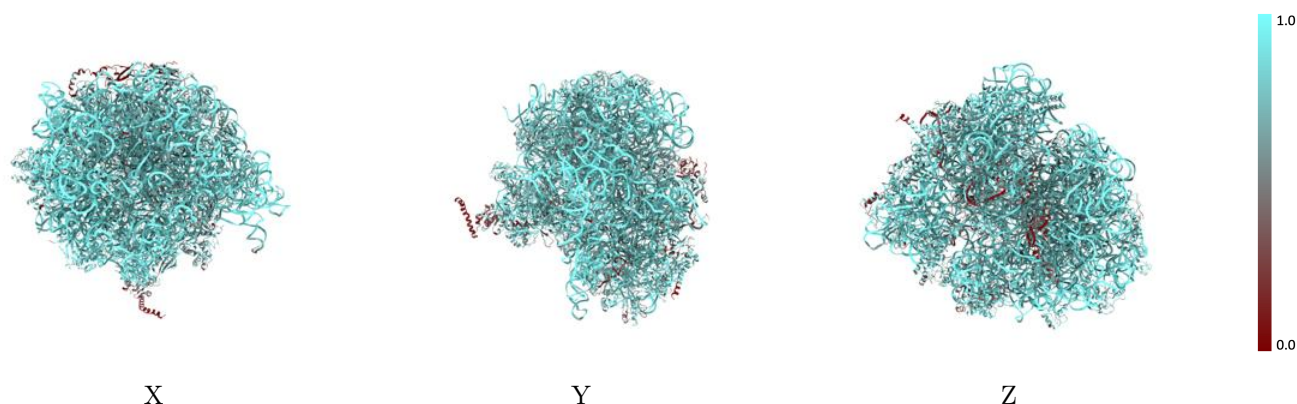
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



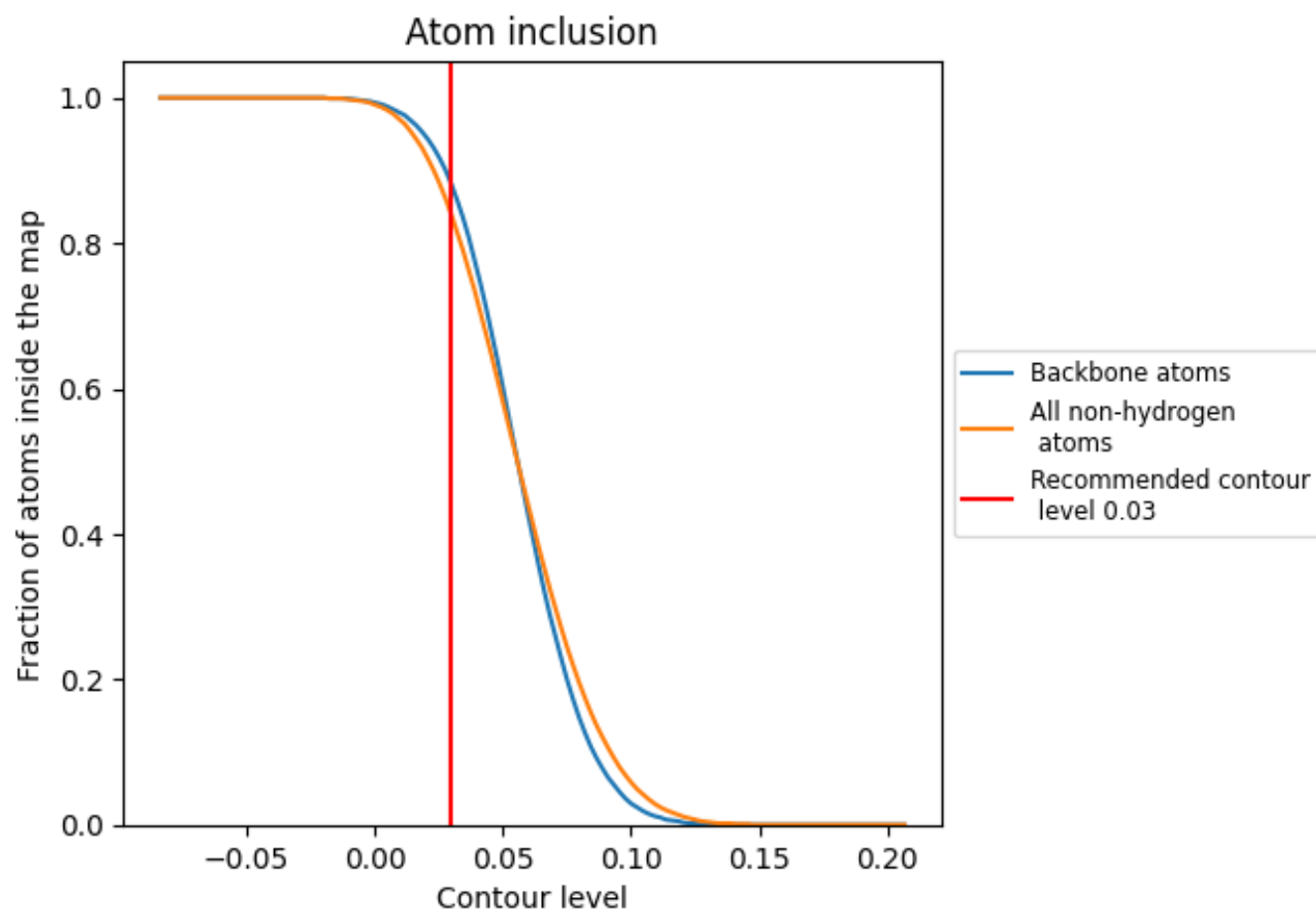
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.1980
L0	 0.6980	 0.0780
L1	 0.7940	 0.2550
L2	 0.7100	 0.2320
L3	 0.8130	 0.2120
L4	 0.8010	 0.2200
L5	 0.7130	 0.1580
L6	 0.8310	 0.2520
L7	 0.8390	 0.2520
LA	 0.9060	 0.2080
LB	 0.9630	 0.2520
LC	 0.5670	 0.1420
LD	 0.7030	 0.1620
LE	 0.7480	 0.2040
LF	 0.7470	 0.1930
LG	 0.7990	 0.2160
LH	 0.7970	 0.2420
LI	 0.2460	 0.0930
LJ	 0.3820	 0.1930
LK	 0.6220	 0.1940
LL	 0.8150	 0.2350
LM	 0.6190	 0.1840
LN	 0.8070	 0.2280
LO	 0.8130	 0.2710
LP	 0.7750	 0.1480
LQ	 0.8970	 0.2430
LR	 0.6620	 0.1500
LS	 0.8280	 0.2360
LT	 0.8120	 0.2220
LU	 0.7360	 0.1850
LV	 0.6940	 0.1090
LW	 0.8190	 0.1440
LX	 0.8420	 0.2880
LY	 0.7770	 0.2540
LZ	 0.7590	 0.1900



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
S1	 0.4400	 0.1220
S2	 0.8660	 0.1970
S3	 0.6700	 0.2040
SA	 0.9160	 0.1960
SB	 0.6690	 0.1540
SC	 0.7290	 0.2070
SD	 0.7940	 0.1780
SE	 0.7070	 0.1600
SF	 0.5420	 0.0470
SG	 0.6780	 0.1610
SH	 0.7280	 0.1580
SI	 0.8110	 0.1870
SJ	 0.7180	 0.1920
SK	 0.6980	 0.1770
SL	 0.7100	 0.2180
SM	 0.7300	 0.2250
SN	 0.8280	 0.2130
SO	 0.7480	 0.1270
SP	 0.8020	 0.1580
SQ	 0.7300	 0.1010
SR	 0.7280	 0.1310
SS	 0.7450	 0.2230
ST	 0.7890	 0.1410
SU	 0.6040	 0.1850