



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Feb 21, 2017 – 09:00 PM EST

PDB ID : 5MMI  
EMDB ID: : EMD-3531  
Title : Structure of the large subunit of the chloroplast ribosome  
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.  
Deposited on : 2016-12-10  
Resolution : 3.25 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](mailto: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.

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

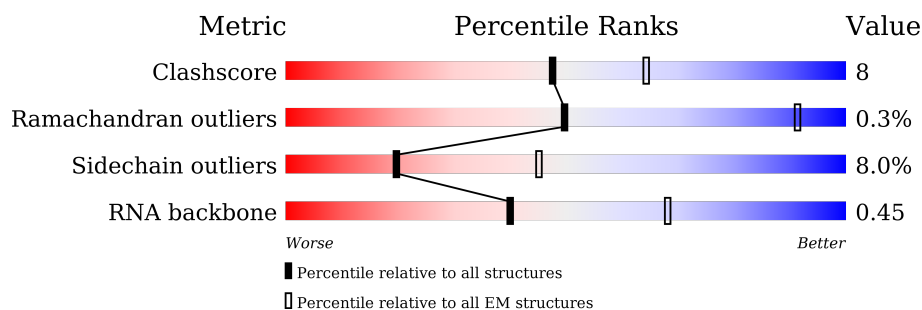
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




















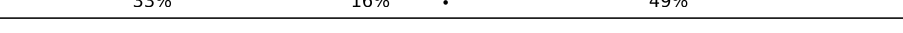






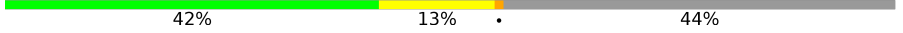
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	0	130	13% 18% . 66%
2	1	57	54% 30% 16%
3	2	66	67% 23% . 9%
4	3	152	24% 15% . 61%
5	4	159	32% 12% . 55%
6	5	37	62% 35% .
7	6	142	24% 8% .. 65%
8	7	116	32% . . 60%

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Mol	Chain	Length	Quality of chain
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	
29	U	198	
30	V	192	
31	W	106	
32	X	194	
33	Y	148	

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Mol	Chain	Length	Quality of chain
34	Z	168	<div><div></div><div>43%</div><div>16%</div><div>•</div><div>40%</div></div>
35	z	2	<div><div></div><div>100%</div></div>

## 2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 95397 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	44	Total	C	N	O	S	0	0
			359	226	61	70	2		

- Molecule 2 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	48	Total	C	N	O	0	0
			396	261	75	60		

- Molecule 3 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 4 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	60	Total	C	N	O	S	0	0
			467	282	107	75	3		

- Molecule 5 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	72	Total	C	N	O	S	0	0
			588	370	124	93	1		

- Molecule 6 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 7 is a protein called plastid ribosomal protein cL37, PSRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 8 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2798	Total	C	N	O	P	0	0
			60083	26804	11116	19365	2798		

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	121	Total	C	N	O	P	0	0
			2584	1154	466	843	121		

- Molecule 11 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	253	Total	C	N	O	S	0	0
			1952	1209	401	336	6		

- Molecule 12 is a protein called plastid ribosomal protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	221	Total	C	N	O	S	0	0
			1686	1066	308	301	11		

- Molecule 13 is a protein called plastid ribosomal protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	212	Total	C	N	O	S	0	0
			1676	1061	312	300	3		

- Molecule 14 is a protein called plastid ribosomal protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	193	Total	C	N	O	S	0	0
			1454	923	255	268	8		

- Molecule 15 is a protein called plastid ribosomal protein uL6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	178	Total	C	N	O	S	0	0
			1391	878	256	253	4		

- Molecule 16 is a protein called plastid ribosomal protein bL9c.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	H	48	Total	C	N	O	0	0
			382	251	69	62		

- Molecule 17 is a protein called plastid ribosomal protein uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	137	Total	C	N	O	S	0	0
			1106	711	186	203	6		

- Molecule 18 is a protein called 50S ribosomal protein L11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	133	Total	C	N	O	S	0	0
			977	624	161	186	6		

- Molecule 19 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	203	Total	C	N	O	S	0	0
			1648	1047	307	289	5		

- Molecule 20 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 21 is a protein called plastid ribosomal protein uL15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	185	Total	C	N	O	S	0	0
			1410	879	280	245	6		

- Molecule 22 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	135	Total	C	N	O	S	0	0
			1075	677	218	174	6		

- Molecule 23 is a protein called plastid ribosomal protein bL17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 24 is a protein called plastid ribosomal protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	122	Total	C	N	O	S	0	0
			962	598	186	173	5		

- Molecule 25 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	118	Total	C	N	O	S	0	0
			953	611	186	155	1		

- Molecule 26 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	119	Total	C	N	O	S	0	0
			1029	652	213	162	2		

- Molecule 27 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	S	170	Total	C	N	O	0	0
			1310	844	227	239		

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



Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	172	Total	C	N	O	S	0	0
			1395	892	257	237	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	96	Total	C	N	O	S	0	0
			776	503	135	136	2		

- Molecule 30 is a protein called plastid ribosomal protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	134	Total	C	N	O	S	0	0
			1078	677	203	195	3		

- Molecule 31 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 32 is a protein called plastid ribosomal protein bL27c.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	109	Total	C	N	O	0	0
			888	560	175	153		

- Molecule 33 is a protein called plastid ribosomal protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	S	0	0
			634	402	128	103	1		

- Molecule 34 is a protein called plastid ribosomal protein uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	101	Total	C	N	O	S	0	0
			846	529	167	147	3		

- Molecule 35 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 36 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	2	1	Total	Zn	0
			1	1	
36	5	1	Total	Zn	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
37	P	1	Total	Mg	0
			1	1	
37	D	2	Total	Mg	0
			2	2	
37	E	1	Total	Mg	0
			1	1	
37	H	1	Total	Mg	0
			1	1	
37	B	15	Total	Mg	0
			15	15	
37	C	1	Total	Mg	0
			1	1	
37	6	1	Total	Mg	0
			1	1	
37	7	1	Total	Mg	0
			1	1	
37	A	453	Total	Mg	0
			453	453	
37	4	1	Total	Mg	0
			1	1	
37	V	2	Total	Mg	0
			2	2	
37	N	1	Total	Mg	0
			1	1	
37	U	1	Total	Mg	0
			1	1	
37	X	1	Total	Mg	0
			1	1	
37	T	1	Total	Mg	0
			1	1	

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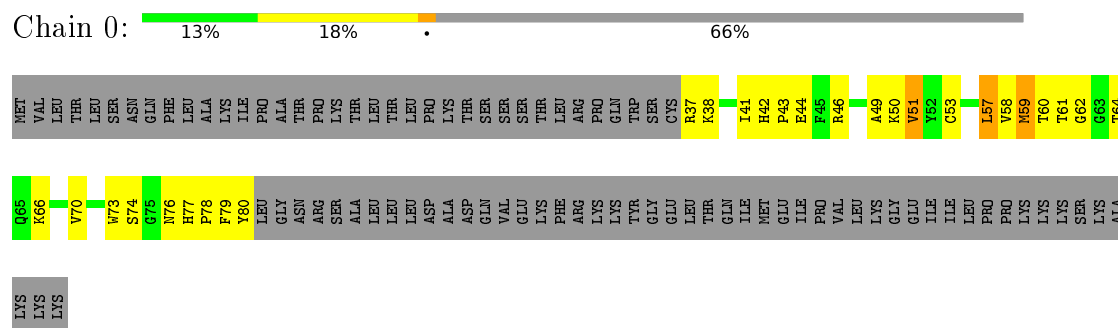
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Mol	Chain	Residues	Atoms		AltConf
37	R	1	Total 1	Mg 1	0
37	Y	1	Total 1	Mg 1	0
37	W	14	Total 14	Mg 14	0
37	M	2	Total 2	Mg 2	0

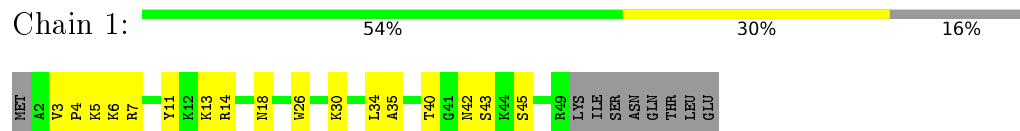
### 3 Residue-property plots

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

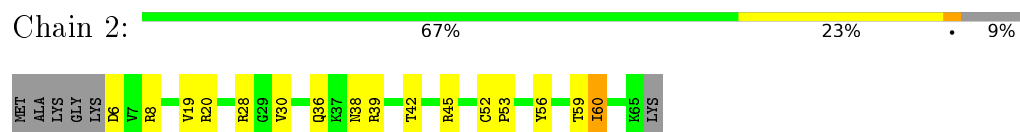
- Molecule 1: 50S ribosomal protein L31



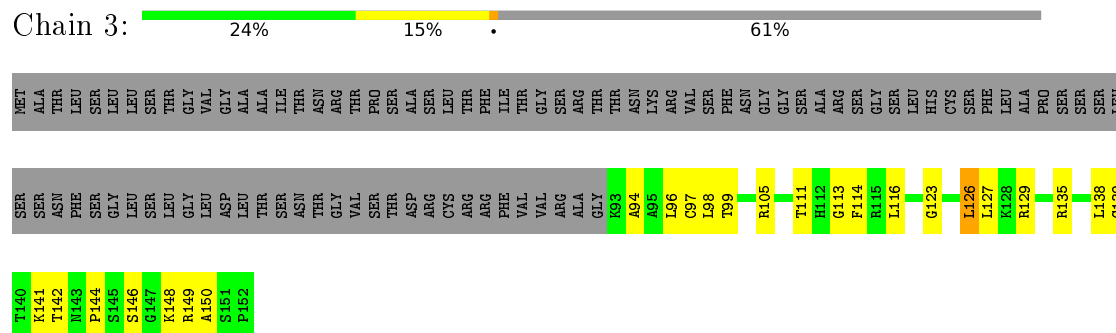
- Molecule 2: 50S ribosomal protein L32, chloroplastic




- Molecule 3: 50S ribosomal protein L33, chloroplastic

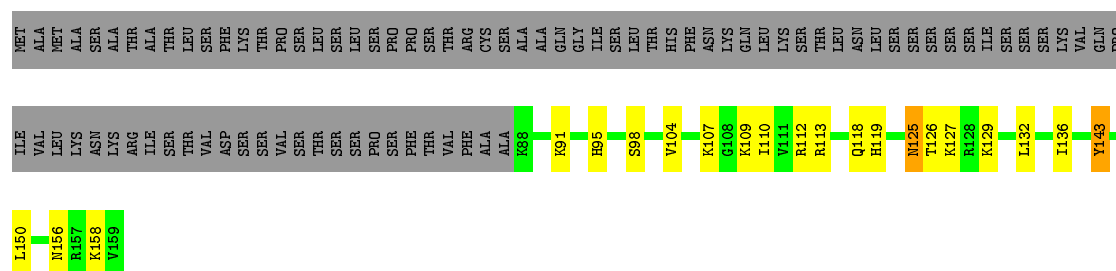


- Molecule 4: 50S ribosomal protein L34, chloroplastic



- Molecule 5: 50S ribosomal protein L35, chloroplastic

Chain 4: 



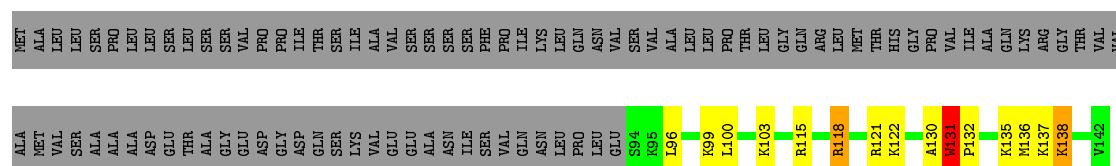
- Molecule 6: 50S ribosomal protein L36, chloroplastic

Chain 5: 



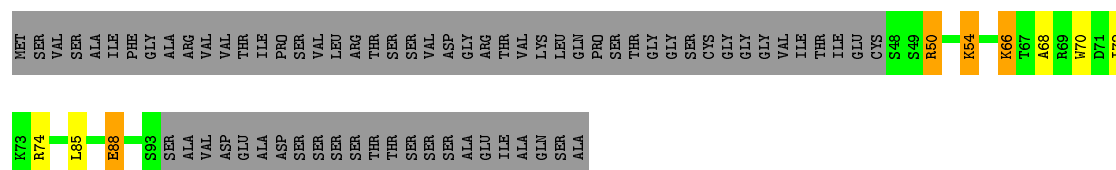
- Molecule 7: plastid ribosomal protein cL37, PSRP5

Chain 6: 



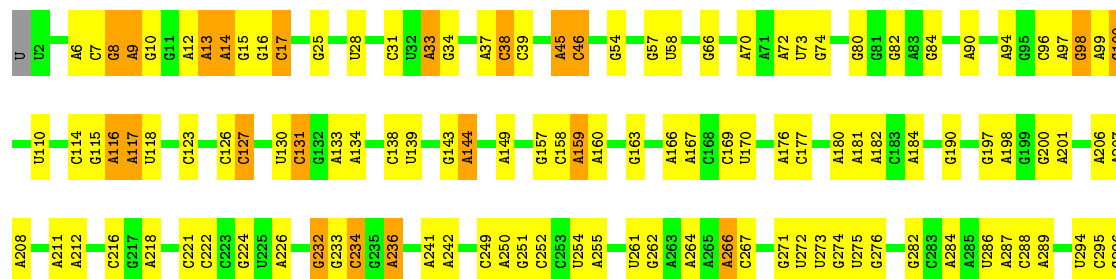
- Molecule 8: 50S ribosomal protein 6, chloroplastic

Chain 7: 

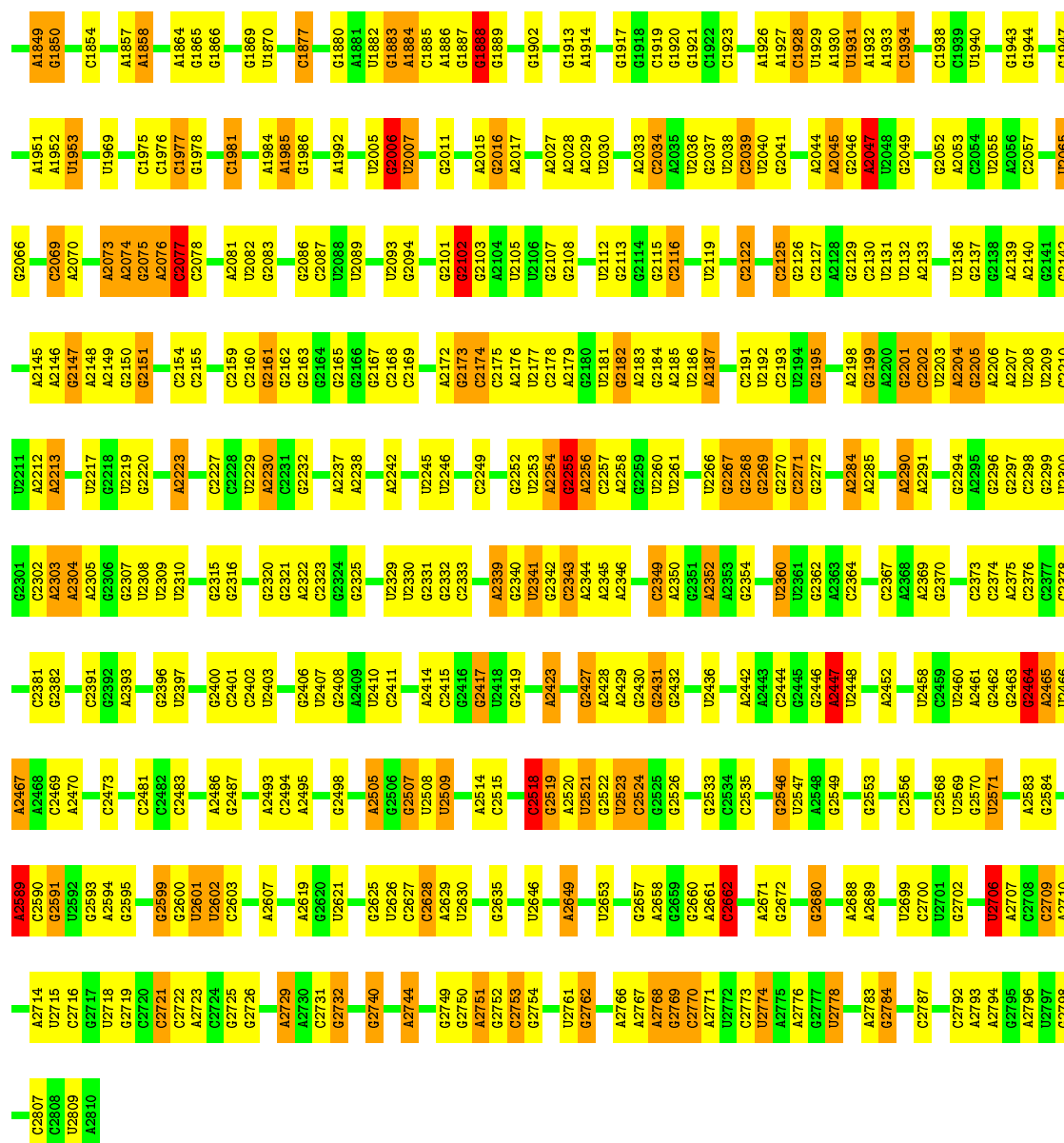


- Molecule 9: 23S ribosomal RNA

Chain A: 

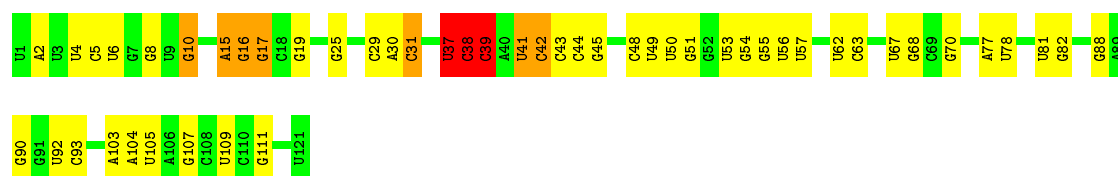


A	G1634	A1535	A1448	G1360	C1264	A1160	G1071	G866	A772	A681	C590	U411	U297
G1756	C1635	A1536	G1449	U1361	C1264	A1161	A1072	G869	A773	G685	C591	U415	G298
G1760	U1638	G1543	G1450	A1363	G1269	G1163	A1074	A876	G774	A696	G593	C416	C299
G1761	G1642	A1544	G1454	U1364	A1272	U1168	G1075	A879	G775	U697	A596	G417	A304
G1762	G1643	G1545	G1455	U1365	G1273	A1169	A1076	G893	G776	U697	C597	G418	A305
G1766	A1644	C1546	G1456	C1366	A1274	A1170	G1082	G894	G776	C698	C598	G419	G306
C1547	G1457	G1458	G1459	G1370	G1277	G1173	G1083	G895	G776	U701	C599	G423	U311
A1549	C1371	C1372	C1373	C1374	G1281	U1177	A1085	U881	G782	G702	C600	A424	C312
U1550	A1465	U1373	U1374	U1375	G1282	U1178	G1086	U882	G783	G703	C601	C425	A313
C1564	A1472	G1473	G1474	U1378	U1284	G1184	G1087	U883	G784	U705	C602	A427	G316
G1567	G1475	U1476	U1477	U1379	G1285	G1189	U1090	G888	G785	G709	C603	G436	G317
U1568	G1476	A1380	G1381	U1382	U1286	G1190	G1091	G889	G786	U710	C604	G437	A318
C1569	G1477	U1383	U1384	U1385	G1287	G1191	C1092	G890	G787	G712	C605	C448	U320
U1570	G1478	U1386	U1387	U1388	U1288	G1192	G1093	G891	G788	A713	C606	G451	A325
G1571	A1480	G1389	U1400	U1390	C1291	U1193	A1094	C892	G789	A716	C607	G452	A326
G1572	G1481	U1401	U1402	U1391	G1292	G1194	G1095	C893	G790	A717	C608	U453	A331
C1573	G1482	U1403	U1404	U1392	U1293	U1195	C1106	C894	G791	U720	C609	G454	G332
G1574	G1483	U1405	U1406	U1393	C1294	U1196	G1111	G	U801	G721	C610	C457	A333
U1583	G1484	U1407	U1408	U1394	U1295	A1197	G1112	A	G802	G722	C611	G458	G338
U1584	U1485	U1409	U1410	U1395	A1296	A1198	A1113	G	G803	G723	C612	G459	A339
C1487	U1486	U1411	U1412	U1396	U1297	A1199	A1114	A	G804	G724	C613	G460	A340
A1488	U1487	U1413	U1414	U1397	U1298	A1200	G1115	G	C807	A727	C614	C474	G344
G1491	U1488	U1415	U1416	U1398	C1310	A1201	G1116	G902	C808	A728	C615	G466	C345
A1492	U1489	U1417	U1418	U1399	U1311	A1202	G1117	G903	G809	A729	C616	G467	U346
G1493	U1490	U1419	U1420	U1400	G1312	U1203	G1118	U904	G810	G730	C617	U468	A349
G1494	U1491	U1421	U1422	U1401	U1313	U1204	U1119	U905	G811	G731	C618	U469	G350
A1497	U1492	U1423	U1424	U1402	U1314	U1205	U1120	C907	G812	A732	C619	G470	A362
G1498	U1493	U1425	U1426	U1403	U1315	U1206	U1121	U908	G813	A733	C620	U471	C363
U1499	U1494	U1427	U1428	U1404	U1316	U1207	U1122	U909	G814	A734	C621	C474	U364
U1500	U1495	U1429	U1430	U1405	U1317	U1208	U1123	A910	G815	G735	C622	G475	A368
G1501	U1496	U1431	U1432	U1406	U1318	U1209	U1124	A911	G816	G736	C623	G476	C369
A1502	U1497	U1433	U1434	U1407	U1319	U1210	U1125	A912	G817	A737	C624	C477	U365
U1511	U1498	U1435	U1436	U1408	U1320	U1211	U1126	A913	G818	A738	C625	G478	U366
U1512	U1499	U1437	U1438	U1409	U1321	U1212	U1127	A914	G819	A739	C626	G479	U367
C1513	U1500	U1439	U1440	U1410	U1322	U1213	U1128	A915	G820	A740	C627	G480	A370
U1514	U1501	U1441	U1442	U1411	U1323	U1214	U1129	A916	G821	G741	C628	G481	U371
U1515	U1502	U1443	U1444	U1412	U1324	U1215	U1130	A917	G822	G742	C629	G482	C372
U1516	U1503	U1445	U1446	U1413	U1325	U1216	U1131	A918	G823	G743	C630	G483	G373
U1517	U1504	U1447	U1448	U1414	U1326	U1217	U1132	A919	G824	G744	C631	G484	C374
A1603	U1505	U1449	U1450	U1415	U1327	U1218	U1133	A920	G825	A745	C632	G485	U375
A1604	U1506	U1451	U1452	U1416	U1328	U1219	U1134	A921	G826	A746	C633	G486	U376
A1605	U1507	U1453	U1454	U1417	U1329	U1220	U1135	A922	G827	A747	C634	G487	G377
U1610	U1508	U1455	U1456	U1418	U1330	U1221	U1136	A923	G828	A748	C635	G488	A378
G1611	U1509	U1457	U1458	U1419	U1331	U1222	U1137	A924	G829	A749	C636	G489	C379
A1612	U1510	U1459	U1460	U1420	U1332	U1223	U1138	A925	G830	A750	C637	G490	U380
G1615	U1511	U1461	U1462	U1421	U1333	U1224	U1139	A926	G831	A751	C638	G491	U381
A1616	U1512	U1463	U1464	U1422	U1334	U1225	U1140	A927	G832	A752	C639	G492	G390
U1620	U1513	U1465	U1466	U1423	U1335	U1226	U1141	A928	G833	A753	C640	G493	A383
C1621	U1514	U1467	U1468	U1424	U1336	U1227	U1142	A929	G834	A754	C641	G494	G384
U1622	U1515	U1469	U1470	U1425	U1337	U1228	U1143	A930	G835	A755	C642	G495	U399
G1629	U1516	U1471	U1472	U1426	U1338	U1229	U1144	A931	G836	A756	C643	G496	U400
G1630	U1517	U1473	U1474	U1427	U1339	U1230	U1145	A932	G837	A757	C644	G497	G401
G1631	U1518	U1475	U1476	U1428	U1340	U1231	U1146	A933	G838	A758	C645	G498	C402
U1632	U1519	U1477	U1478	U1429	U1341	U1232	U1147	A934	G839	A759	C646	G499	G403
A1633	U1520	U1479	U1480	U1430	U1342	U1233	U1148	A935	G840	A760	C647	G500	C404
G1634	U1521	U1481	U1482	U1431	U1343	U1234	U1149	A936	G841	A761	C648	G501	C405
G1635	U1522	U1483	U1484	U1432	U1344	U1235	U1150	A937	G842	A762	C649	G502	C406
G1636	U1523	U1485	U1486	U1433	U1345	U1236	U1151	A938	G843	A763	C650	G503	C407
G1637	U1524	U1487	U1488	U1434	U1346	U1237	U1152	A939	G844	A764	C651	G504	C408
G1638	U1525	U1489	U1490	U1435	U1347	U1238	U1153	A940	G845	A765	C652	G505	C409
G1639	U1526	U1491	U1492	U1436	U1348	U1239	U1154	A941	G846	A766	C653	G506	C410
G1640	U1527	U1493	U1494	U1437	U1349	U1240	U1155	A942	G847	A767	C654	G507	C411
G1641	U1528	U1495	U1496	U1438	U1350	U1241	U1156	A943	G848	A768	C655	G508	C412
G1642	U1529	U1497	U1498	U1439	U1351	U1242	U1157	A944	G849	A769	C656	G509	C413
G1643	U1530	U1499	U1499	U1440	U1352	U1243	U1158	A945	G850	A770	C657	G510	C414
G1644	U1531	U1501	U1501	U1441	U1353	U1244	U1159	A946	G851	A771	C658	G511	C415
G1645	U1532	U1503	U1503	U1442	U1354	U1245	U1160	A947	G852	A772	C659	G512	C416
G1646	U1533	U1505	U1505	U1443	U1355	U1246	U1161	A948	G853	A773	C660	G513	C417
G1647	U1534	U1507	U1507	U1444	U1356	U1247	U1162	A949	G854	A774	C661	G514	C418
G1648	U1535	U1509	U1509	U1445	U1357	U1248	U1163	A950	G855	A775	C662	G515	C419
G1649	U1536	U1511	U1511	U1446	U1358	U1249	U1164	A951	G856	A776	C663	G516	C420
G1650	U1537	U1513	U1513	U1447	U1359	U1250	U1165	A952	G857	A777	C664	G517	C421
G1651	U1538	U1515	U1515	U1448	U1360	U1251	U1166	A953	G858	A778	C665	G518	C422
G1652	U1539	U1517	U1517	U1449	U1361	U1252	U1167	A954	G859	A779	C666	G519	C423
G1653	U1540	U1519	U1519	U1450	U1362	U1253	U1168	A955	G860	A780	C667	G520	C424
G1654	U1541	U1521	U1521	U1451	U1363	U1254	U1169	A956	G861	A781	C668	G521	C425
G1655	U1542	U1523	U1523	U1452	U1364	U1255	U1170	A957	G862	A782	C669	G522	C426
G1656	U1543	U1525	U1525	U1453	U1365	U1256	U1171	A958	G863	A783	C670	G523	C427
G1657	U1544	U1527	U1527	U1454	U1366	U1257	U1172	A959	G864	A784	C671	G524	C428
G1658	U1545	U1529	U1529	U1455	U1367	U1258	U1173	A960	G865	A785	C672	G525	C429
G1659	U1546	U1531	U1531	U1456	U1368	U1259	U1174	A961	G866	A786	C673	G526	C430
G1660	U1547	U1533	U1533	U1457	U1369	U1260	U1175	A962	G867	A787	C674	G527	C431
G1661	U1548	U1535	U1535	U1458	U1370	U1261	U1176	A963	G868	A788	C675	G528	C432
G1662	U1549	U1537	U1537	U1459	U1371	U1262	U1177	A964	G869	A789	C676	G529	C433
G1663	U1550	U1539	U1539	U1460	U1372	U1263	U1178	A965	G870	A790	C677	G530	C434
G1664	U1551	U1541	U1541	U1461	U1373	U1264	U1179	A966	G871	A791	C678	G531	C435
G1665	U1552	U1543	U1543	U1462	U1374	U1265	U1180	A967	G872	A792	C679	G532	C436
G1666	U1553	U1545	U1545	U1463	U1375	U1266	U1181	A968	G873	A793	C680	G533	C437
G1667	U1554	U1547	U1547	U1464	U1376	U1267	U1182	A969	G874	A794	C681	G534	C438
G1668	U1555	U1549	U1549	U1465	U1377	U1268	U1183	A970	G875	A795	C682	G535	C439
G1669	U1556	U1551	U1551	U1466	U1378	U1269	U1184	A971	G876	A796	C683	G536	C440
G1670	U1557	U1553	U1553	U1467	U1379	U1270	U1185	A972	G877	A797	C684	G537	C441
G1671	U1558	U1555	U1555	U1468	U1380	U1271	U1186	A973	G878	A798	C685	G538	C442
G1672	U1559	U1557	U1557										



• Molecule 10: 5S ribosomal RNA

Chain B: 59% 33% 6% .



• Molecule 11: 50S ribosomal protein L2, chloroplastic

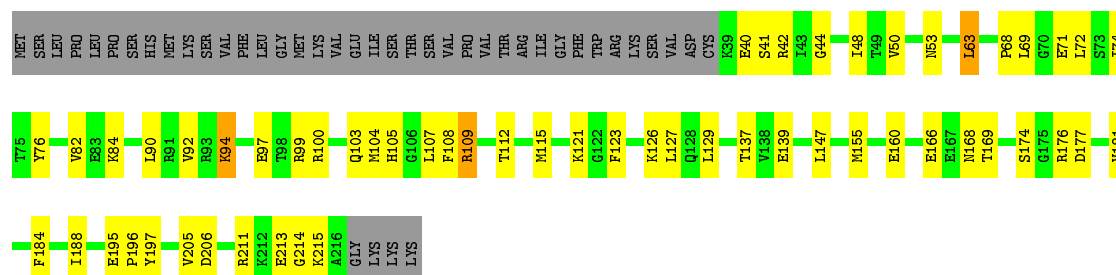
Chain C: 61% 29% . 7%





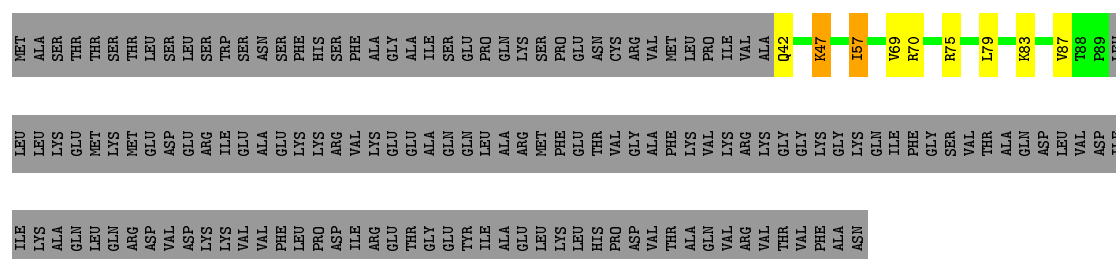


Chain G:



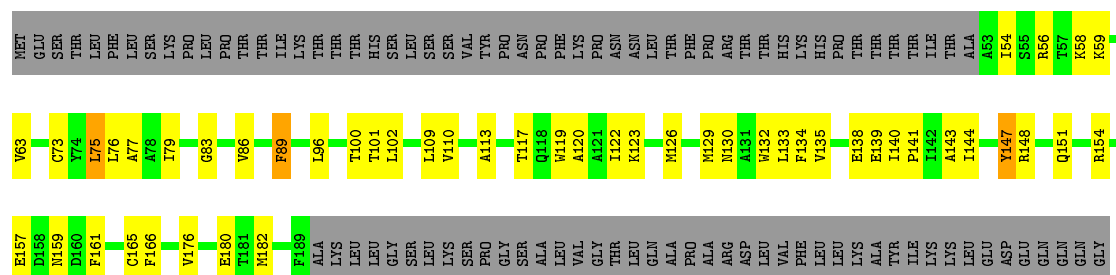
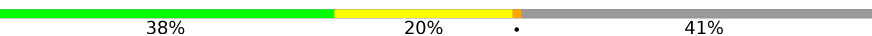
- Molecule 16: plastid ribosomal protein bL9c

Chain H:



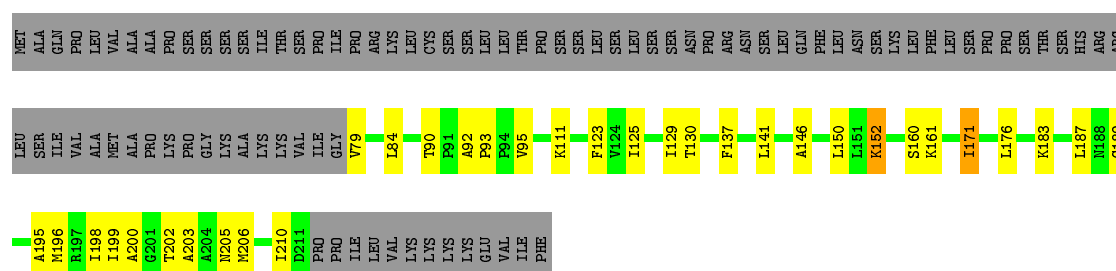
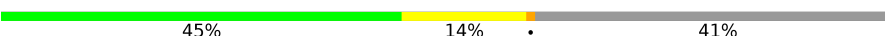
- Molecule 17: plastid ribosomal protein uL10c

Chain I:



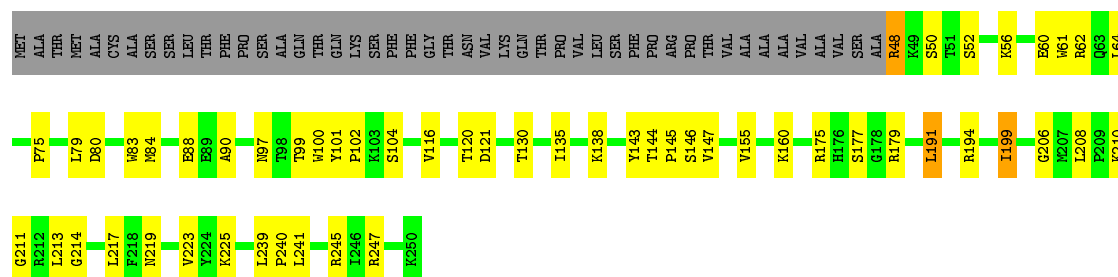
- Molecule 18: 50S ribosomal protein L11, chloroplastic

Chain J:



- Molecule 19: 50S ribosomal protein L13, chloroplastic

Chain K:  59% 21% • 19%



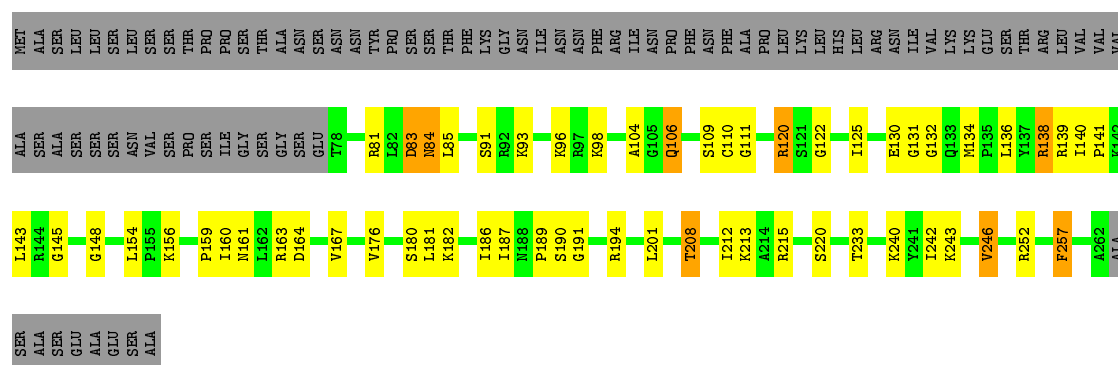
- Molecule 20: 50S ribosomal protein L14, chloroplastic

Chain L:  67% 31% .



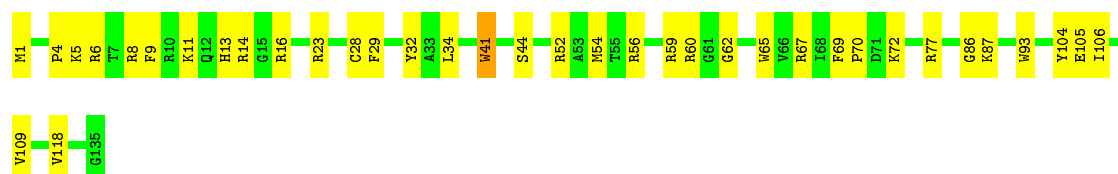
- Molecule 21: plastid ribosomal protein uL15c

Chain M:  46% 19% • 32%



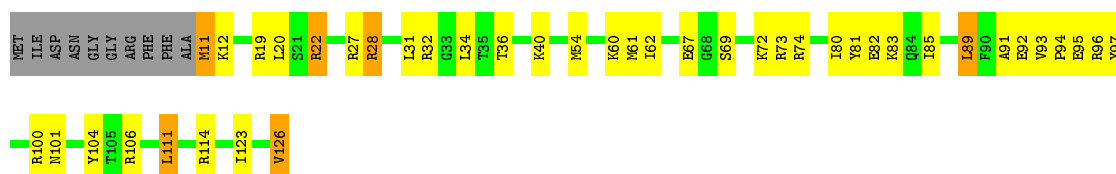
- Molecule 22: 50S ribosomal protein L16, chloroplastic

Chain N:  73% 27%

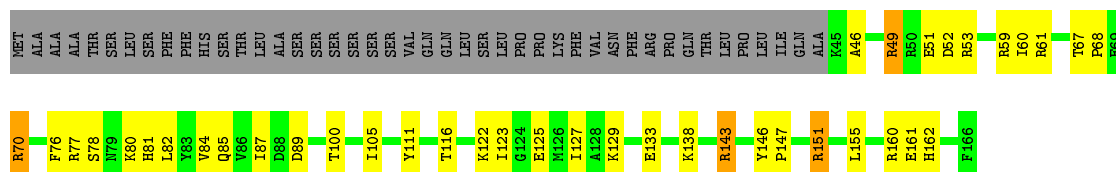


- Molecule 23: plastid ribosomal protein bL17c

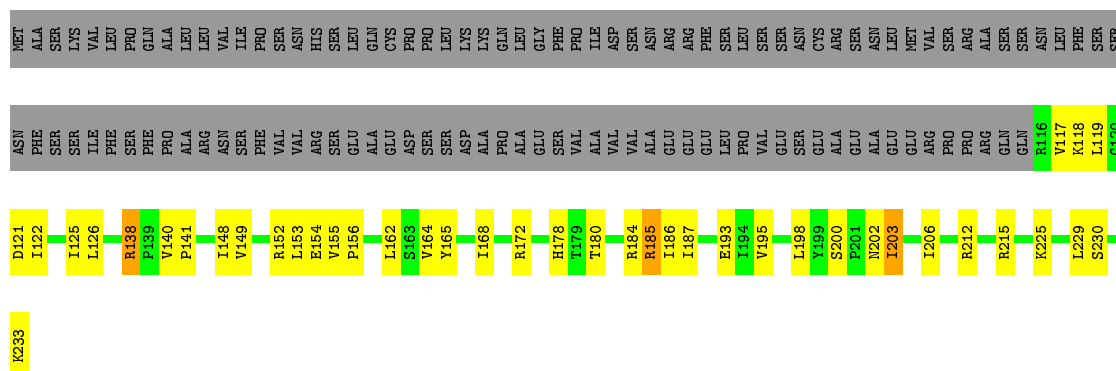
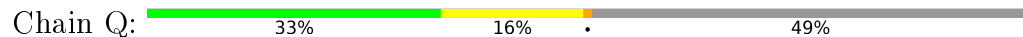
Chain O:  59% 29% 5% 8%



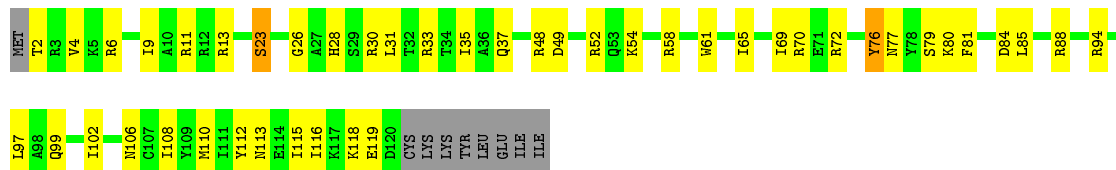
- Molecule 24: plastid ribosomal protein uL18c



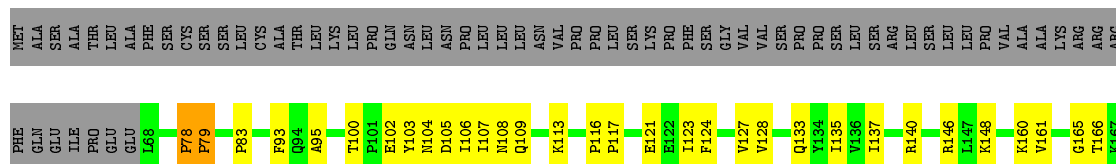
- Molecule 25: 50S ribosomal protein L19, chloroplastic

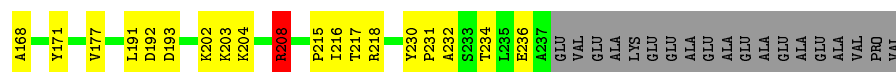


- Molecule 26: 50S ribosomal protein L20, chloroplastic



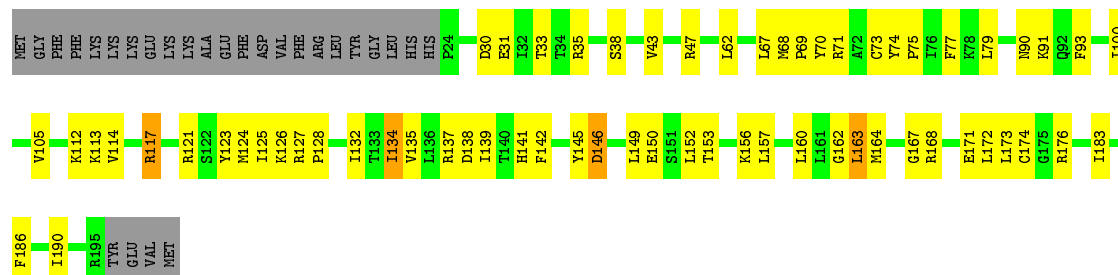
- Molecule 27: 50S ribosomal protein L21, chloroplastic





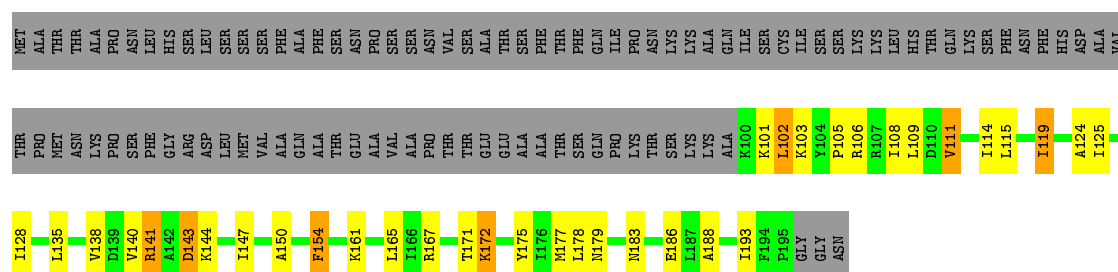
- Molecule 28: 50S ribosomal protein L22, chloroplastic

Chain T: 54% 30% 14%



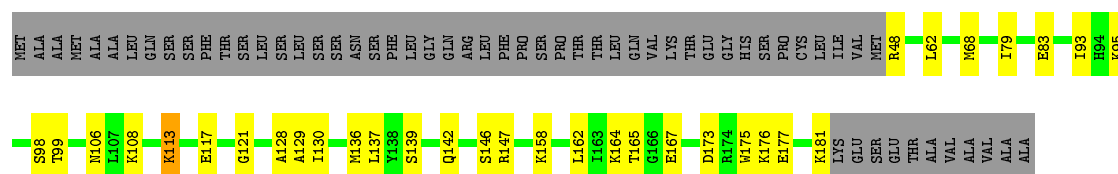
- Molecule 29: 50S ribosomal protein L23, chloroplastic

Chain U: 30% 15% 52%



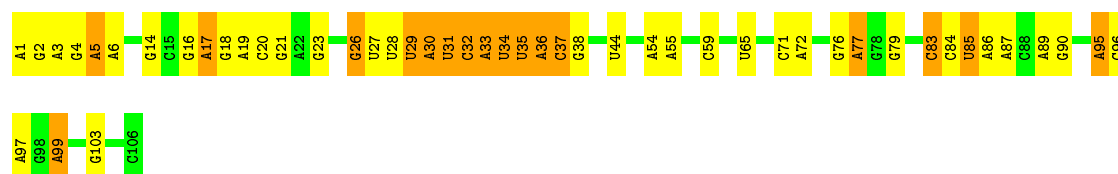
- Molecule 30: plastid ribosomal protein uL24c

Chain V: 53% 17% 30%



- Molecule 31: 4.5S ribosomal RNA

Chain W: 54% 30% 16%



- Molecule 32: plastid ribosomal protein bL27c

Chain X: 42% 13% 44%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	154332	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	Not provided	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	0	0.46	0/369	0.67	0/499
10	B	0.45	1/2890 (0.0%)	1.00	5/4503 (0.1%)
11	C	0.52	0/1986	0.73	1/2666 (0.0%)
12	D	0.56	0/1713	0.72	0/2291
13	E	0.56	0/1707	0.80	1/2298 (0.0%)
14	F	0.42	0/1475	0.61	1/1990 (0.1%)
15	G	0.39	0/1412	0.60	0/1898
16	H	0.41	0/386	0.62	0/514
17	I	0.49	0/1129	0.53	0/1521
18	J	0.50	0/992	0.55	0/1343
19	K	0.51	0/1688	0.64	0/2279
2	1	0.62	0/405	0.69	0/537
20	L	0.48	0/951	0.66	0/1282
21	M	0.52	0/1430	0.71	0/1896
22	N	0.48	0/1097	0.64	1/1471 (0.1%)
23	O	0.57	0/959	0.77	0/1280
24	P	0.38	0/978	0.56	0/1311
25	Q	0.52	0/967	0.67	0/1299
26	R	0.61	0/1046	0.74	0/1395
27	S	0.51	0/1339	0.72	3/1826 (0.2%)
28	T	0.50	0/1420	0.64	0/1900
29	U	0.50	0/787	0.68	0/1056
3	2	0.49	0/497	0.66	0/664
30	V	0.43	0/1093	0.63	0/1457
31	W	0.74	0/2551	1.15	3/3977 (0.1%)
32	X	0.47	0/905	0.61	0/1204
33	Y	0.51	0/644	0.64	0/856
34	Z	0.41	0/854	0.58	0/1131
35	z	0.89	0/46	1.88	2/69 (2.9%)
4	3	0.62	0/470	0.80	0/619
5	4	0.61	0/594	0.75	0/784
6	5	0.39	0/307	0.53	0/403

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
7	6	0.53	0/425	0.84	1/551 (0.2%)
8	7	0.53	0/382	0.58	0/520
9	A	0.85	39/67297 (0.1%)	1.19	236/104984 (0.2%)
All	All	0.75	40/103191 (0.0%)	1.07	254/154274 (0.2%)

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
21	M	0	1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	591	C	N1-C6	-7.28	1.32	1.37
9	A	1272	A	N9-C4	-7.03	1.33	1.37
9	A	1272	A	N3-C4	-6.93	1.30	1.34
9	A	1272	A	N7-C5	-6.68	1.35	1.39
9	A	810	G	C6-N1	-6.13	1.35	1.39

The worst 5 of 254 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1272	A	C2-N3-C4	-11.16	105.02	110.60
9	A	1272	A	N1-C2-N3	9.97	134.28	129.30
9	A	1272	A	C6-C5-N7	-9.58	125.60	132.30
9	A	2464	G	C8-N9-C4	9.23	110.09	106.40
9	A	2464	G	N9-C4-C5	-9.22	101.71	105.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	M	104	ALA	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	0	359	0	330	26	0
2	1	396	0	437	15	0
3	2	489	0	507	10	0
4	3	467	0	526	13	0
5	4	588	0	658	12	0
6	5	305	0	344	9	0
7	6	422	0	508	16	0
8	7	368	0	386	5	0
9	A	60083	0	30260	543	0
10	B	2584	0	1305	37	0
11	C	1952	0	2038	56	0
12	D	1686	0	1772	49	0
13	E	1676	0	1737	38	0
14	F	1454	0	1488	50	0
15	G	1391	0	1458	34	0
16	H	382	0	437	5	0
17	I	1106	0	1122	40	0
18	J	977	0	1027	28	0
19	K	1648	0	1684	41	0
20	L	942	0	996	25	0
21	M	1410	0	1495	45	0
22	N	1075	0	1134	27	0
23	O	944	0	1004	31	0
24	P	962	0	984	28	0
25	Q	953	0	1050	26	0
26	R	1029	0	1092	34	0
27	S	1310	0	1315	37	0
28	T	1395	0	1482	41	0
29	U	776	0	837	23	0
30	V	1078	0	1144	23	0
31	W	2277	0	1146	27	0
32	X	888	0	923	13	0
33	Y	634	0	684	12	0
34	Z	846	0	918	17	0
35	z	42	0	23	0	0
36	2	1	0	0	0	0
36	5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	4	1	0	0	0	0
37	6	1	0	0	0	0
37	7	1	0	0	0	0
37	A	453	0	0	0	0
37	B	15	0	0	0	0
37	C	1	0	0	0	0
37	D	2	0	0	0	0
37	E	1	0	0	0	0
37	H	1	0	0	0	0
37	M	2	0	0	0	0
37	N	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	T	1	0	0	0	0
37	U	1	0	0	0	0
37	V	2	0	0	0	0
37	W	14	0	0	0	0
37	X	1	0	0	0	0
37	Y	1	0	0	0	0
All	All	95397	0	64251	1211	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 1211 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)
9:A:652:C:N4	9:A:657:U:O4	1.86	1.08
9:A:2077:C:H42	9:A:2464:G:H1	1.10	0.98
20:L:15:GLY:HA3	20:L:50:THR:HG21	1.51	0.90
9:A:817:C:OP2	21:M:120:ARG:NH1	2.06	0.89
9:A:540:A:H62	9:A:2055:U:H3	1.18	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	
1	0	42/130 (32%)	39 (93%)	3 (7%)	0	100	100
2	1	46/57 (81%)	44 (96%)	2 (4%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	35 (100%)	0	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	9	45
8	7	44/116 (38%)	40 (91%)	3 (7%)	1 (2%)	8	42
11	C	251/272 (92%)	238 (95%)	12 (5%)	1 (0%)	39	78
12	D	219/305 (72%)	205 (94%)	13 (6%)	1 (0%)	34	75
13	E	210/293 (72%)	193 (92%)	17 (8%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	167 (95%)	9 (5%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100
19	K	201/250 (80%)	194 (96%)	7 (4%)	0	100	100
20	L	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
21	M	183/271 (68%)	169 (92%)	12 (7%)	2 (1%)	17	60
22	N	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
23	O	114/126 (90%)	110 (96%)	4 (4%)	0	100	100
24	P	120/166 (72%)	114 (95%)	6 (5%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	157 (94%)	9 (5%)	2 (1%)	16	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	T	170/199 (85%)	161 (95%)	8 (5%)	1 (1%)	30	72
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	121 (92%)	10 (8%)	1 (1%)	24	66
32	X	107/194 (55%)	95 (89%)	12 (11%)	0	100	100
33	Y	75/148 (51%)	74 (99%)	1 (1%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	19	62
All	All	3707/5644 (66%)	3499 (94%)	197 (5%)	11 (0%)	50	83

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	C	232	GLU
21	M	131	GLY
27	S	78	PRO
34	Z	151	SER
7	6	131	TRP

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	39/117 (33%)	36 (92%)	3 (8%)	16	52
2	1	41/50 (82%)	39 (95%)	2 (5%)	31	70
3	2	56/60 (93%)	51 (91%)	5 (9%)	12	43
4	3	50/125 (40%)	45 (90%)	5 (10%)	9	36
5	4	62/140 (44%)	55 (89%)	7 (11%)	7	31
6	5	34/34 (100%)	30 (88%)	4 (12%)	6	29
7	6	46/124 (37%)	44 (96%)	2 (4%)	35	73
8	7	40/96 (42%)	35 (88%)	5 (12%)	6	26
11	C	201/217 (93%)	181 (90%)	20 (10%)	9	36
12	D	182/259 (70%)	167 (92%)	15 (8%)	14	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	E	179/255 (70%)	160 (89%)	19 (11%)	8	34
14	F	152/214 (71%)	141 (93%)	11 (7%)	18	55
15	G	151/190 (80%)	141 (93%)	10 (7%)	21	60
16	H	42/170 (25%)	37 (88%)	5 (12%)	6	28
17	I	119/204 (58%)	113 (95%)	6 (5%)	30	70
18	J	106/189 (56%)	103 (97%)	3 (3%)	51	82
19	K	176/213 (83%)	168 (96%)	8 (4%)	34	73
20	L	101/101 (100%)	94 (93%)	7 (7%)	19	58
21	M	141/215 (66%)	126 (89%)	15 (11%)	8	34
22	N	108/108 (100%)	101 (94%)	7 (6%)	21	60
23	O	96/103 (93%)	84 (88%)	12 (12%)	6	26
24	P	100/139 (72%)	90 (90%)	10 (10%)	9	36
25	Q	104/207 (50%)	94 (90%)	10 (10%)	10	38
26	R	106/115 (92%)	98 (92%)	8 (8%)	17	53
27	S	137/223 (61%)	134 (98%)	3 (2%)	60	86
28	T	152/176 (86%)	138 (91%)	14 (9%)	11	40
29	U	85/171 (50%)	74 (87%)	11 (13%)	5	24
30	V	121/169 (72%)	116 (96%)	5 (4%)	37	75
32	X	92/163 (56%)	83 (90%)	9 (10%)	10	38
33	Y	67/130 (52%)	60 (90%)	7 (10%)	9	34
34	Z	93/153 (61%)	87 (94%)	6 (6%)	21	60
All	All	3179/4830 (66%)	2925 (92%)	254 (8%)	20	50

5 of 254 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	I	89	PHE
21	M	138	ARG
32	X	85	GLN
17	I	147	TYR
19	K	191	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
20	L	73	ASN
23	O	18	HIS
28	T	90	ASN
20	L	92	ASN
21	M	133	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	19 (15%)	0
31	W	105/106 (99%)	38 (36%)	0
35	z	1/2 (50%)	1 (100%)	0
9	A	2794/2810 (99%)	642 (22%)	8 (0%)
All	All	3020/3039 (99%)	700 (23%)	8 (0%)

5 of 700 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A
9	A	14	A

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	795	U
9	A	2753	C
9	A	2447	A
9	A	680	G
9	A	1520	A

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 503 ligands modelled in this entry, 503 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.