



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:40 AM EST

PDB ID : 4V61
EMDB ID : EMD-1417
Title : Homology model for the Spinach chloroplast 30S subunit fitted to 9.4Å cryo-EM map of the 70S chlororibosome.
Authors : Sharma, M.R.; Wilson, D.N.; Datta, P.P.; Barat, C.; Schlutzenzen, F.; Fucini, P.; Agrawal, R.K.
Deposited on : 2007-11-09
Resolution : 9.40 Å(reported)
Based on initial models : 2ZXY, 2XYZ

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

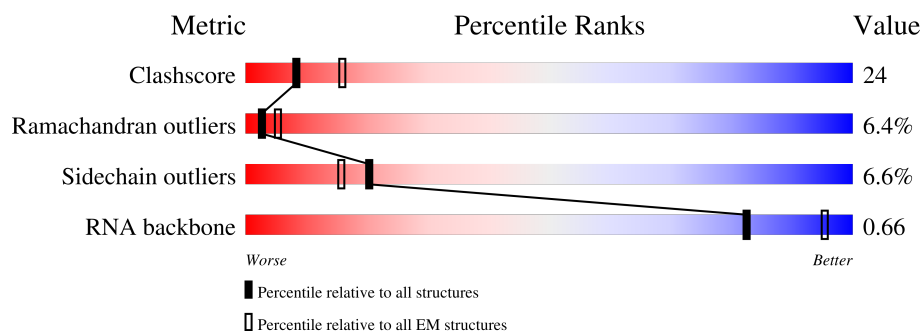
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.40 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.















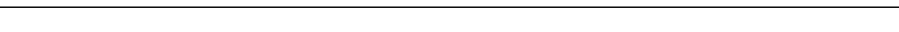

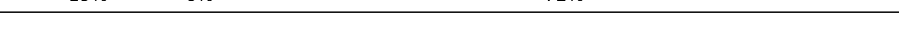

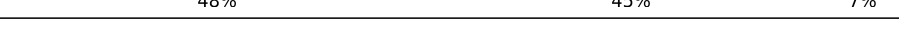

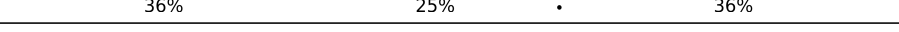


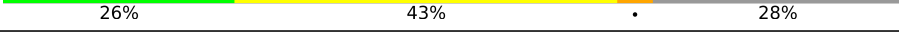


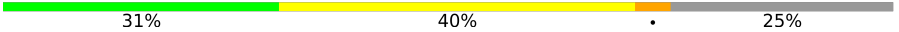
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	AA	1491	39% 46% 14% .
2	AB	231	84% 13% .
3	AC	218	85% 13% .
4	AD	201	84% 15% .
5	AE	308	43% 7% . 49%
6	AF	168	48% 15% . 36%
7	AG	155	87% 10% ..


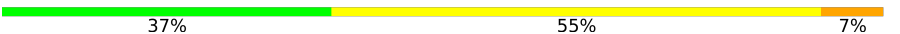


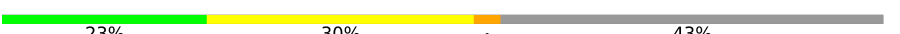
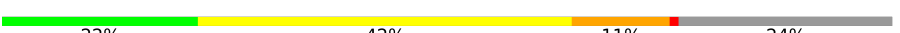








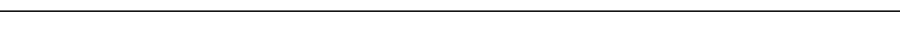
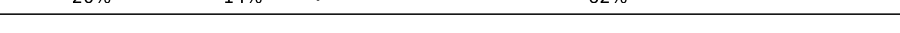
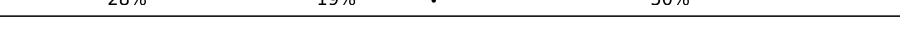
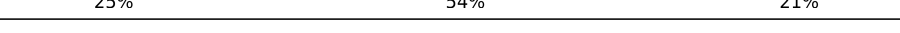



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Mol	Chain	Length	Quality of chain
8	AH	134	
9	AI	197	
10	AJ	197	
11	AK	140	
12	AL	123	
13	AM	145	
14	AN	100	
15	AO	90	
16	AP	88	
17	AQ	142	
18	AR	103	
19	AS	92	
20	AT	202	
21	AU	190	
22	BA	2810	
23	BB	117	
24	BC	103	
25	BD	352	
26	BE	269	
27	BF	259	
28	BG	293	
29	BH	220	
30	BI	223	
31	BJ	197	
32	BK	224	

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Mol	Chain	Length	Quality of chain
33	BL	250	
34	BM	121	
35	BN	257	
36	BO	135	
37	BP	205	
38	BQ	161	
39	BR	233	
40	BS	119	
41	BT	257	
42	BU	199	
43	BV	198	
44	BW	191	
45	BX	198	
46	BY	151	
47	BZ	173	
48	B1	144	
49	B2	57	
50	B3	66	
51	B4	152	
52	B5	159	
53	B6	104	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142250 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1478	Total	C	N	O	P	0	0
			31745	14154	5865	10249	1477		

- Molecule 2 is a protein called Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0
			1827	1152	334	328	13		

- Molecule 3 is a protein called Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	217	Total	C	N	O	S	0	0
			1744	1113	314	310	7		

- Molecule 4 is a protein called Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	199	Total	C	N	O	S	0	0
			1632	1032	318	277	5		

- Molecule 5 is a protein called Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	158	Total	C	N	O	S	0	0
			1190	742	230	212	6		

- Molecule 6 is a protein called Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	107	Total	C	N	O	S	0	0
			872	558	145	166	3		

- Molecule 7 is a protein called Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	154	Total	C	N	O	S	0	0
			1211	753	244	211	3		

- Molecule 8 is a protein called Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	134	Total	C	N	O	S	0	0
			1088	684	211	187	6		

- Molecule 9 is a protein called Ribosomal Protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			988	627	188	172	1		

- Molecule 10 is a protein called Ribosomal Protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	99	Total	C	N	O	S	0	0
			803	515	144	139	5		

- Molecule 11 is a protein called Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	118	Total	C	N	O	S	0	0
			888	549	182	152	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	21	SER	-	insertion	UNP P06506
AK	22	ALA	-	insertion	UNP P06506

- Molecule 12 is a protein called Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0
			968	604	198	163	3		

- Molecule 13 is a protein called Ribosomal Protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	99	Total	C	N	O	S	0	0
			824	513	168	141	2		

- Molecule 14 is a protein called Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	99	Total	C	N	O	S	0	0
			820	507	174	136	3		

- Molecule 15 is a protein called Ribosomal Protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	85	Total	C	N	O	S	0	0
			713	454	134	124	1		

- Molecule 16 is a protein called Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 17 is a protein called Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	83	Total	C	N	O	S	0	0
			662	416	130	112	4		

- Molecule 18 is a protein called Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	58	Total	C	N	O	S	0	0
			478	300	94	83	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	81	GLU	-	insertion	UNP Q9M3K7
AR	82	LYS	-	insertion	UNP Q9M3K7

- Molecule 19 is a protein called Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	92	Total	C	N	O	S	0	0
			747	472	146	126	3		

- Molecule 20 is a protein called Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	102	Total	C	N	O	S	0	0
			799	493	163	142	1		

- Molecule 21 is a protein called Ribosomal Protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	53	Total	C	N	O	S	0	0
			455	276	96	81	2		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BA	2732	Total	C	N	O	P	0	0
			58665	26173	10857	18904	2731		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BB	117	Total	C	N	O	P	0	0
			2497	1116	452	813	116		

- Molecule 24 is a RNA chain called 4.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BC	103	Total	C	N	O	P	0	0
			2207	987	408	710	102		

- Molecule 25 is a protein called Ribosomal Protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BD	227	Total	C	N	O	S	0	0
			1760	1117	307	329	7		

- Molecule 26 is a protein called Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BE	266	Total	C	N	O	S	0	0
			2049	1268	418	357	6		

- Molecule 27 is a protein called Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BF	154	Total	C	N	O	S	0	0
			1196	756	230	205	5		

- Molecule 28 is a protein called Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BG	211	Total	C	N	O	S	0	0
			1664	1057	309	295	3		

- Molecule 29 is a protein called Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BH	175	Total	C	N	O	S	0	0
			1351	862	233	248	8		

- Molecule 30 is a protein called Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BI	182	Total	C	N	O	S	0	0
			1429	907	257	262	3		

- Molecule 31 is a protein called Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BJ	148	Total	C	N	O	S	0	0
			1177	753	206	215	3		

- Molecule 32 is a protein called Ribosomal Protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BK	145	Total	C	N	O	S	0	0
			1060	679	177	198	6		

- Molecule 33 is a protein called Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BL	125	Total	C	N	O	S	0	0
			998	634	192	169	3		

- Molecule 34 is a protein called Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BM	121	Total	C	N	O	S	0	0
			943	588	179	171	5		

- Molecule 35 is a protein called Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BN	176	Total	C	N	O	S	0	0
			1333	835	257	235	6		

- Molecule 36 is a protein called Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BO	135	Total	C	N	O	S	0	0
			1076	677	218	175	6		

- Molecule 37 is a protein called Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BP	116	Total	C	N	O	S	0	0
			948	594	195	155	4		

- Molecule 38 is a protein called Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BQ	122	Total	C	N	O	S	0	0
			962	597	183	178	4		

- Molecule 39 is a protein called Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BR	113	Total	C	N	O	S	0	0
			915	586	177	151	1		

- Molecule 40 is a protein called Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BS	119	Total	C	N	O	S	0	0
			1030	653	213	161	3		

- Molecule 41 is a protein called Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BT	104	Total	C	N	O	S	0	0
			826	537	150	139			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	122	ILE	-	insertion	UNP P24613

- Molecule 42 is a protein called Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BU	122	Total	C	N	O	S	0	0
			986	627	178	175	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	126	LEU	LYS	conflict	UNP P09594

- Molecule 43 is a protein called Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BV	85	Total	C	N	O	S	0	0
			677	436	115	124	2		

- Molecule 44 is a protein called Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BW	110	Total	C	N	O	S	0	0
			869	548	160	160	1		

- Molecule 45 is a protein called Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BX	86	Total	C	N	O	S	0	0
			660	419	127	114			

- Molecule 46 is a protein called Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BY	76	Total	C	N	O	S	0	0
			619	395	120	103	1		

- Molecule 47 is a protein called Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BZ	65	Total	C	N	O	S	0	0
			551	341	106	101	3		

- Molecule 48 is a protein called Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B1	72	Total	C	N	O	S	0	0
			581	369	99	109	4		

- Molecule 49 is a protein called Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B2	57	Total	C	N	O	S	0	0
			469	305	87	76	1		

- Molecule 50 is a protein called Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B3	65	Total	C	N	O	S	0	0
			524	326	105	88	5		

- Molecule 51 is a protein called Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B4	37	Total	C	N	O	S	0	0
			297	180	70	45	2		

- Molecule 52 is a protein called Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B5	62	Total	C	N	O	S	0	0
			504	315	107	81	1		

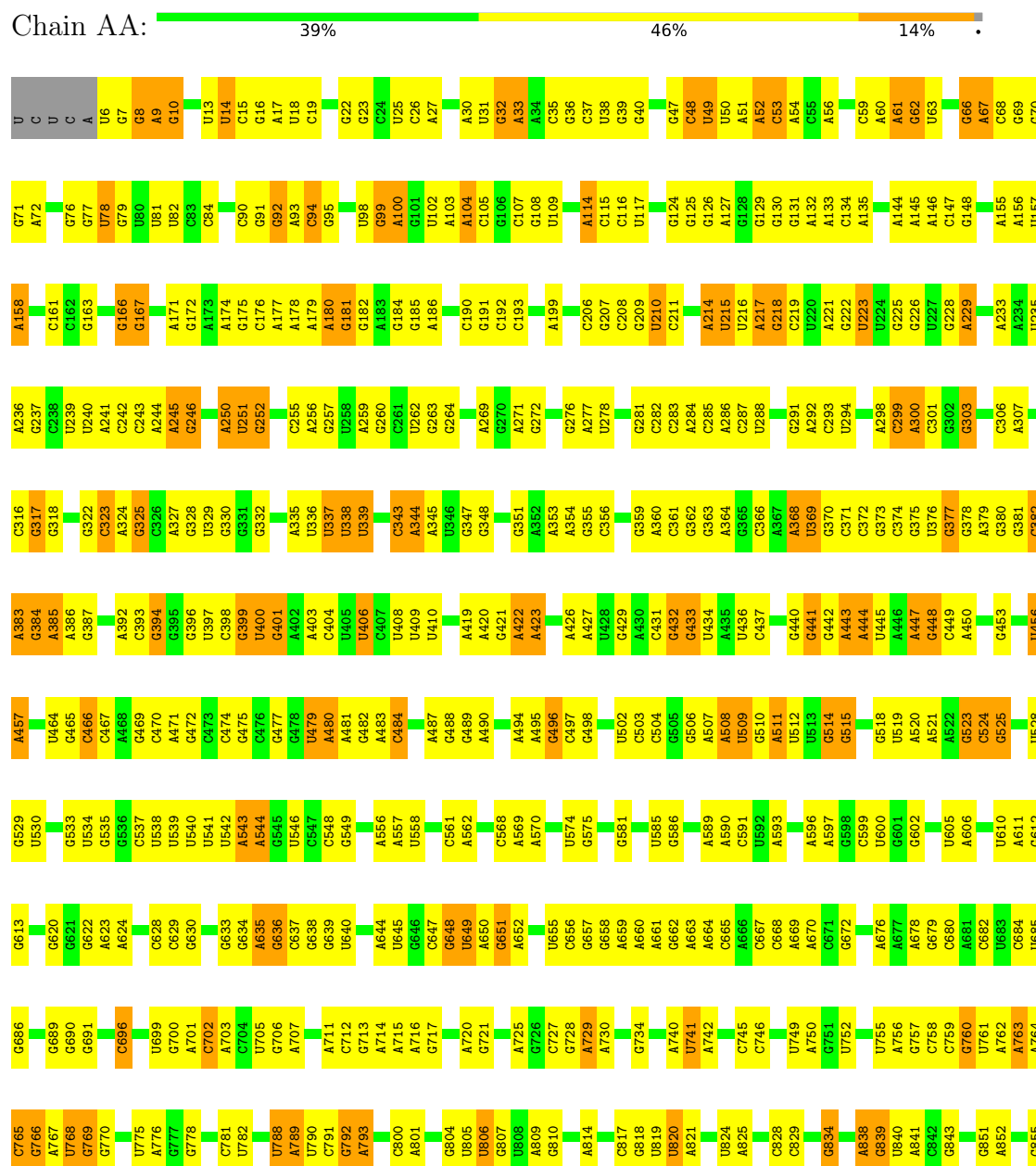
- Molecule 53 is a protein called Ribosomal Protein L36.

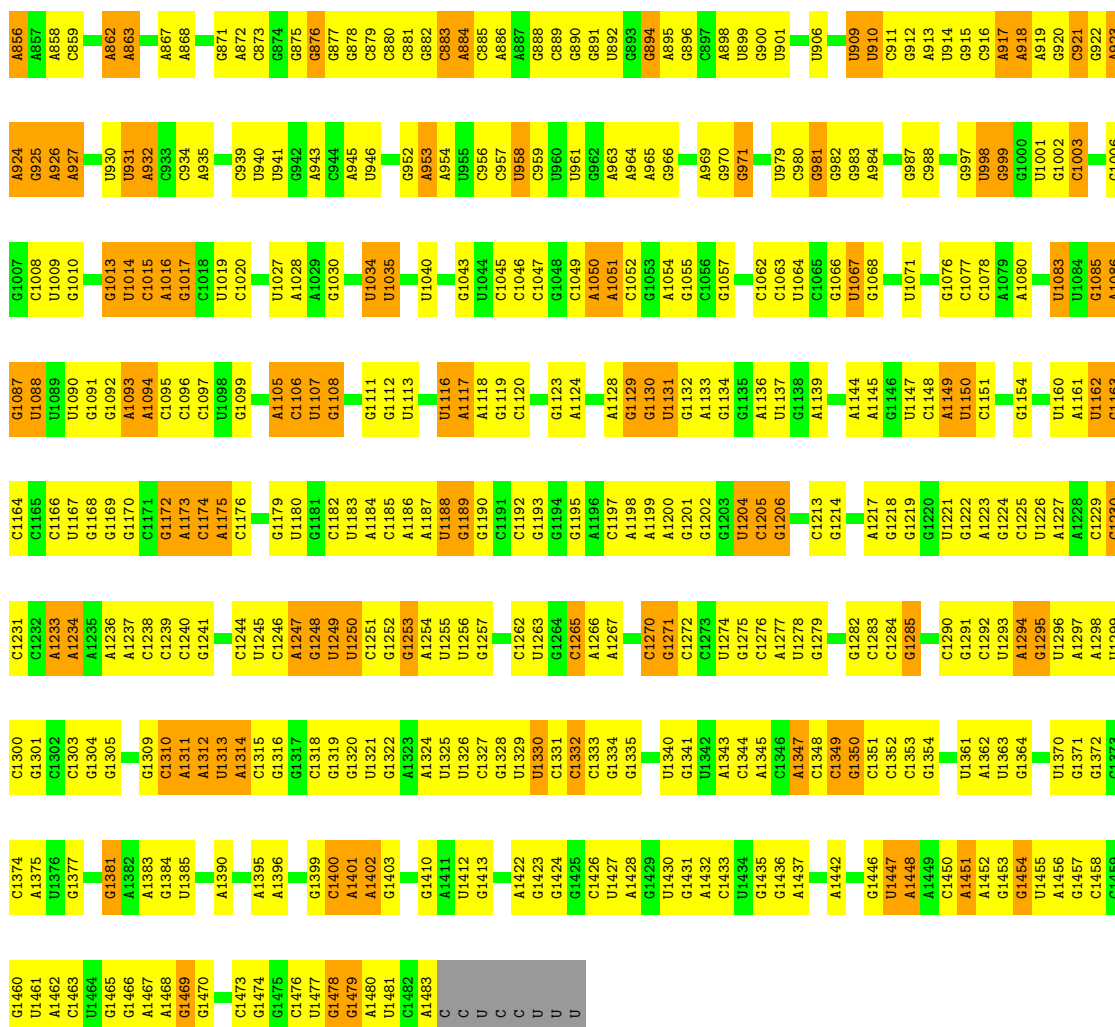
Mol	Chain	Residues	Atoms					AltConf	Trace
53	B6	38	Total	C	N	O	S	0	0
			309	190	65	49	5		

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. 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.

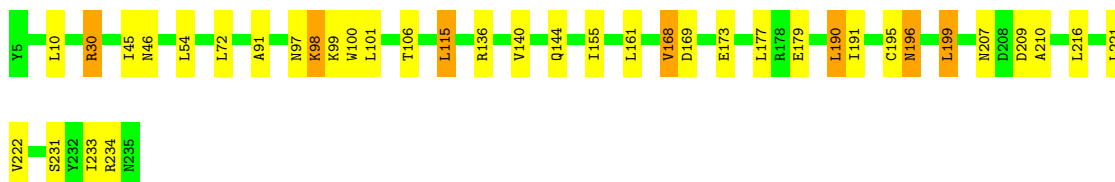
• Molecule 1: 16S rRNA





• Molecule 2: Ribosomal Protein S2

Chain AB: 84% 13%



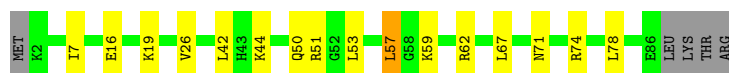
• Molecule 3: Ribosomal Protein S3

Chain AC: 85% 13%



• Molecule 4: Ribosomal Protein S4

Chain AD: 84% 15%



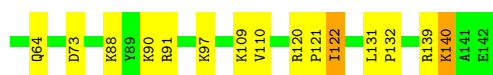
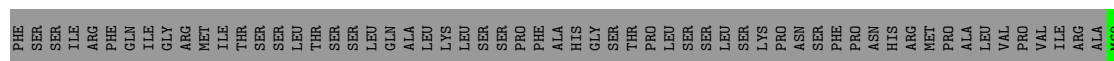
• Molecule 16: Ribosomal Protein S16

Chain AP: 61% 20% 8% 9%



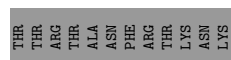
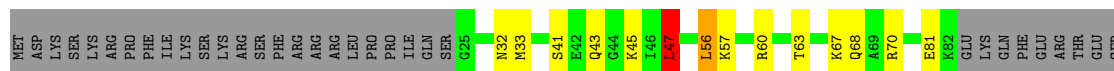
• Molecule 17: Ribosomal Protein S17

Chain AQ: 48% 9% 42%



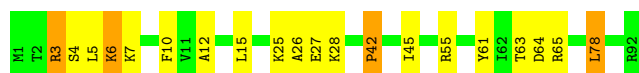
• Molecule 18: Ribosomal Protein S18

Chain AR: 43% 12% 44%



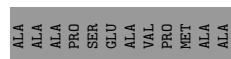
• Molecule 19: Ribosomal Protein S19

Chain AS: 78% 17%



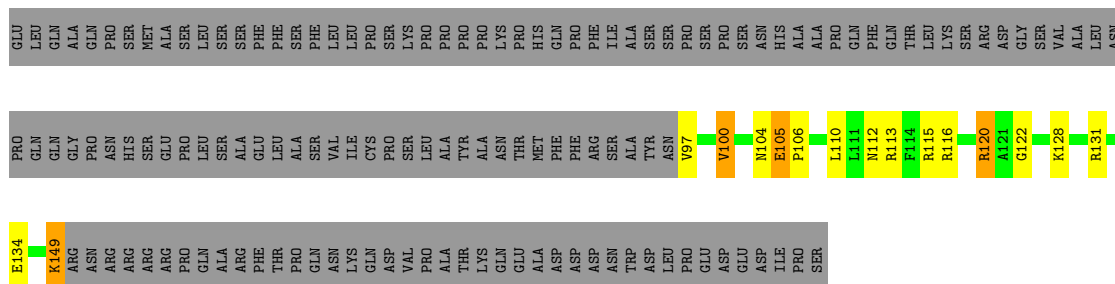
• Molecule 20: Ribosomal Protein S20

Chain AT: 43% 7% 50%



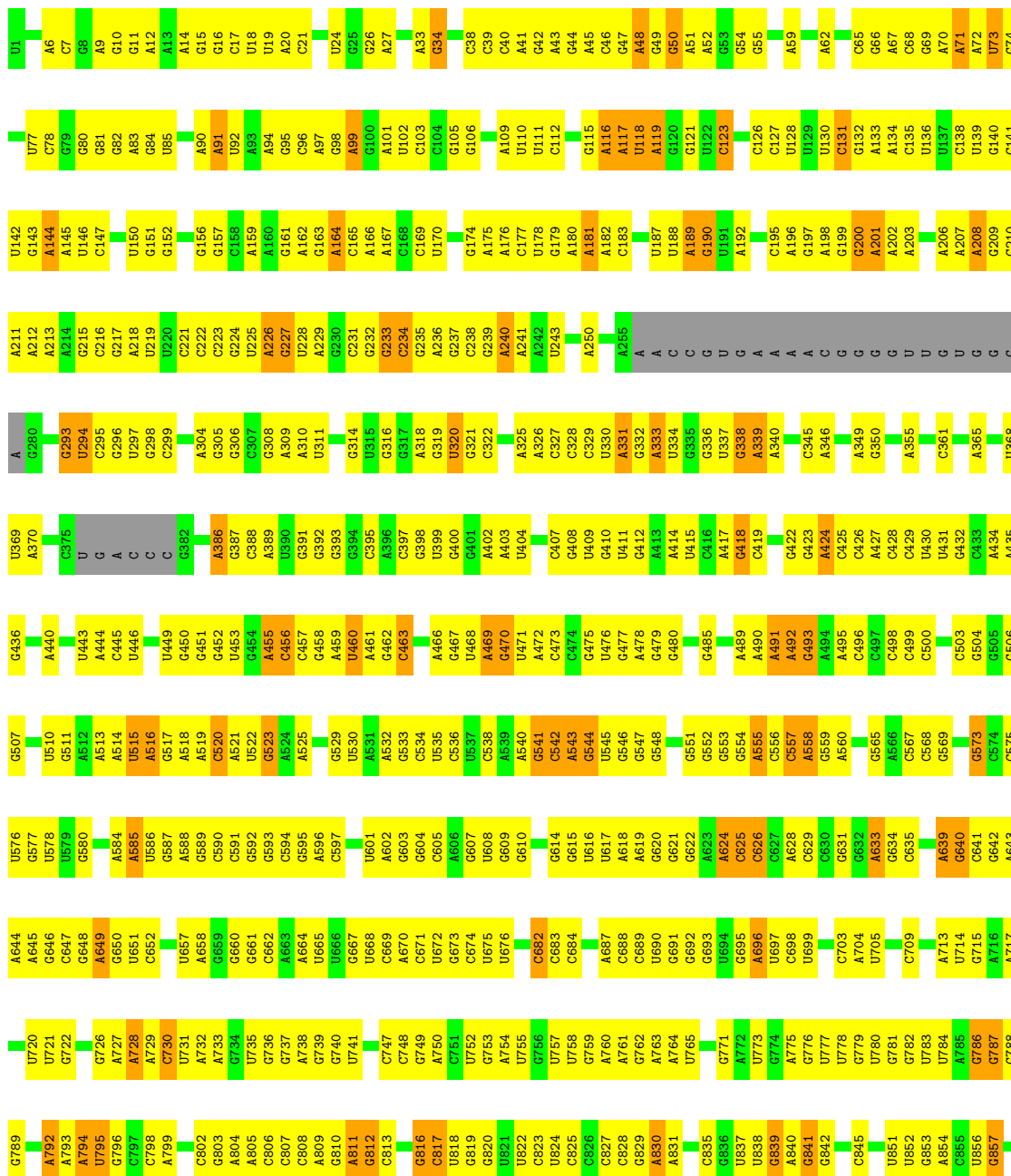
• Molecule 21: Ribosomal Protein S21

Chain AU: 19% 6% 72%

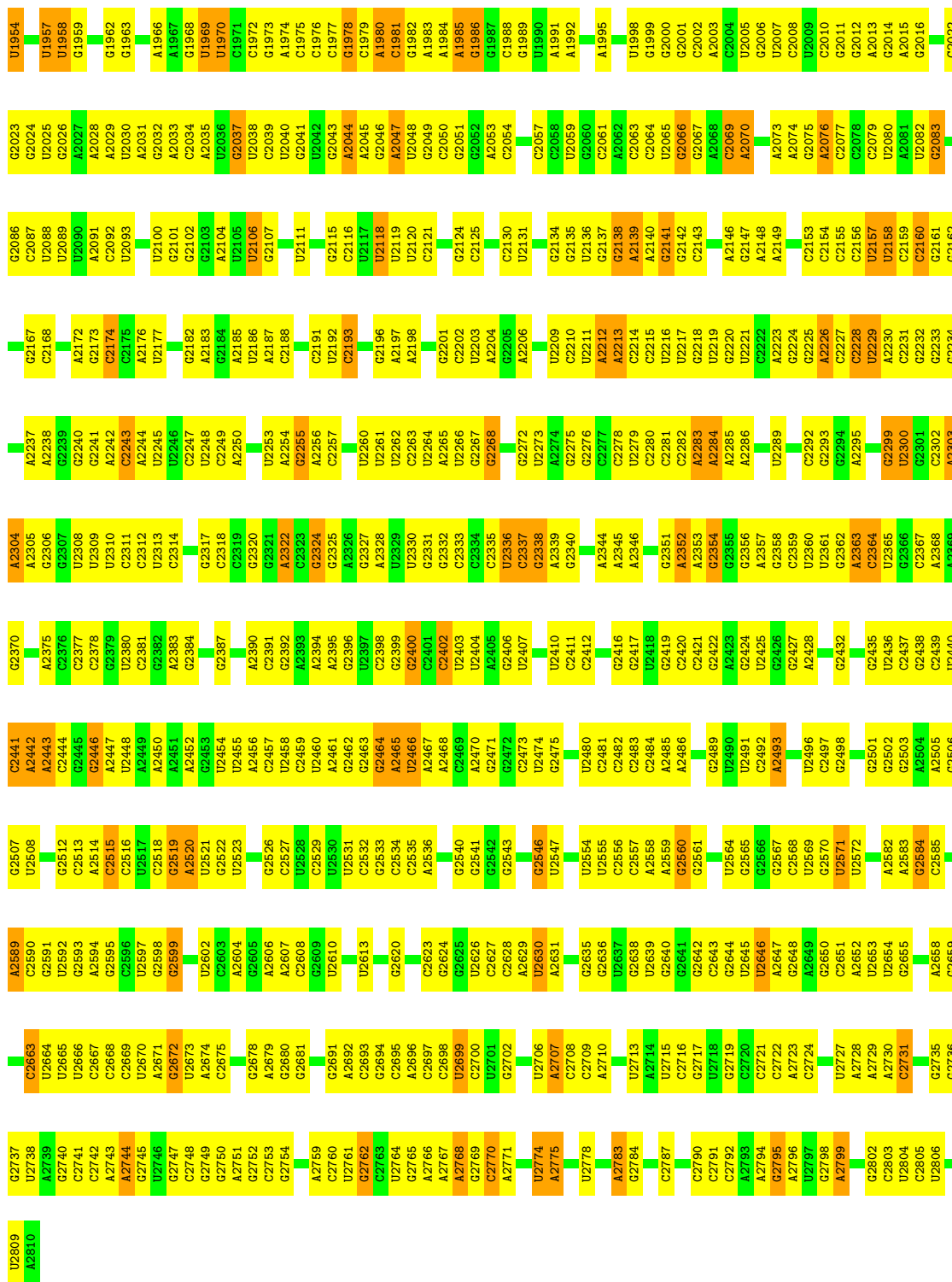


• Molecule 22: 23S rRNA

Chain BA:

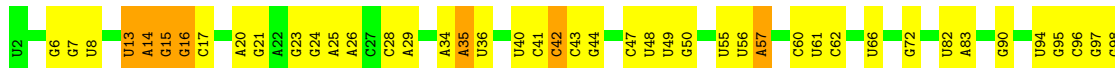


U1874	U1804	C1730	A1652	C1570	C1495	A1427	A1363	U1299	A1228	C1162	A1078	A1003	U862
G1875	C1805	G1731	C1653	G1571	A1496	C1428	G1364	U1300	G1229	C1163	A1079	G1004	C863
A1876	C1806	G1732	A1654	G1572	A1497	C1429	U1365	G1301	G1230	G1164	G1079	G1005	U864
C1877	C1807	G1733	U1661	U1576	G1499	U1433	A1367	U1302	A1232	G1165	C1081	G1006	A865
U1878	C1808	A1734	G1662	U1583	U1500	G1434	G1368	G1303	G1233	G1166	A1082	C1010	G866
G1880	C1810	G1735	G1663	C1584	G	U1435	A1369	A1305	A1234	C1167	G1083	C1011	G867
A1881	A1811	A1736	G1664	C1585	C	U1436	C1372	G1306	A1235	U1168	U	G1012	G868
U1882	A1812	A1737	A1670	C	C	G1437	A1374	A1307	A1236	A1169	C	G1013	U870
G1883	A1813	G1738	A1671	C	C	U1438	A1375	A1308	C1239	U1170	A	A	A871
C1885	A1814	G1739	A1672	U1593	U	U1439	A1376	U1309	G1240	U1175	A	G1016	A872
A1886	A1815	U1741	C1673	A1594	C	C1440	A1377	C1310	U1241	C1176	U1089	G1017	A873
		U1742	C1674	U1595	U	C1441	A1377		G1242	U1177	U1090	A1018	G874
		G1743	C1675	U1596	U	C1442			C1243	C1178	C1092	U1019	C875
		G1744	U1676	U1597	U	C1443				C1179			
		C1745	A1677	U1598	U	G1444	A1380		G1246	C1180	A1097	C1023	U882
		G1746	G1678	U1599	U	U1445	G1381	C1317	U1247	G1181	A1098	A1024	G884
		C1747	G1679	C	C	G1446	G1382	G1318	A1247	C1182	G1099	G1025	G885
		G1748	G1680	U1599	A	G1447	C1383	C1319	U1284	A1183	C1100	C1026	U886
		U1749	G1681	A1600	G	A1448	C1384	C1320	U1285		A1101		G887
		C1750	C1682	G1601	G	C1449	G1385	G1321	G1286	U1187	C1104	A1029	C888
		A1751	G1683	G1602	G	G1450	A1386	A1322	G1287	U1188		G1031	G889
		C1752	G1684	A1603	U	G1451	A1387	A1323	U1258	G1189		C1032	G890
		A1753	G1685	A1604	A	A1452	A1388	A1324	C1259			C1033	C893
		A1754	A1686	A1605	A	G1453	G1389	C1325	G1260	U1190			C894
		A1755	G1687	A1606	G	G1454		C1326	A1261				C
			A1688	G1607	A	U1455	U1393	U1327	A1262	U1195		C1035	G
		C1762	G1689	U1609	G	G1456	A1394	A1328	G1263	A1196		U1036	A
		G1763	C1690	C1610	U	G1457	G1395	A1329	G1264	A1197		A1037	A
			A1691	C1611	U	C1458	U1396	G1330	G1265	A1198		A1038	G
		G1766	C1692	G1611	U	U1459	C1397	C1331		A1199		A1039	A
		U1767	A1528	U1619	U	A1460	G1398	G1332	G1269	A1200		U1040	G
		G1768	A1529	C1621	A	A1461	A1399	U1333	G1270	A1201		G1041	C901
			G1530	G1615	G	G1462	U1400	U1334	G1271	A1202		A1042	G902
		G1773	G1531	C1617	U	U1463	G1401	C1335	A1272	C1203		C1043	G903
		G1774	G1532	C1618	U	U1464	G1402	G1336	G1273	A1204		G1044	
			A1533	U1618	U			U1337	A1274	U1205		G1045	C906
			A1534	U1619	U		A1403	C1338	A1275	G1206		C1046	C907
			U1620	C1621	U	C1468	C1404	C1339	U1276	G1207		U1047	A908
			A1535		U	G1469	A1405	G1340	G1277	G1208		C1048	
			A1536		U	A1470	A1406	G1341	U1278	G1209		A1049	C912
			C1542	G1628	U	A1471	C1407	A1342	C1279	A1210		G1050	G913
			G1543	G1629	U		G1408	A1343	G1280	G1211		U1051	A914
			A1544		U	A1474	G1409	U1344	G1281	G1212		G1052	G915
			G1545		U	U1475	G1410	G1345		G1213		A1053	G916
				C1634	U		U1411	U1346	U1284	G1214		U1054	C917
			U1553		U	U1479	A1412	U1347	G1285	A1215		A1055	A918
			C1554	G1637	U	U1480	A1413	C1348	U1286	A1216		A1056	A919
			G1555	U1638	U	U1481	A1414	G1349	A1287	G1217		G1061	A920
			A1556	A1639	U	C1482	U1415	U1350	U1288	U1218			C921
			G1557	C1640	U	G1483	U1416	C1351		G1219		G1066	G925
			U1558	C1641	U	G1484	U1417	C1352	U1289	U1220		G1067	A926
			A1559	U1485	U	U1485	U1418	A1353	G1292	C1221		C996	A927
			C1560	G1642	U	A1488	C1419	C1354	C1293	G1222		U1068	U928
			G1643	U1645	U	G1490	G1420		A1294	G1223		U1069	A929
			A1561	A1644	U	U1421	U1421	G1359	A1295	U1224			
			A1562	A1645	U	G1422		U1360	A1296	G1225		G1073	A934
			G1563	A1646	U	A1492		G1361	C1297	U1226		A1074	U935
			U1564	C1647	U	G1494		G1362	A1298	U1227		G1075	
			G1569	C1651	U				A1298				



• Molecule 23: 5S rRNA

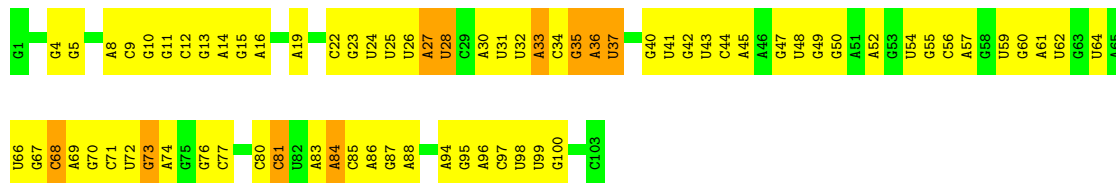
Chain BB: 48% 45% 7%





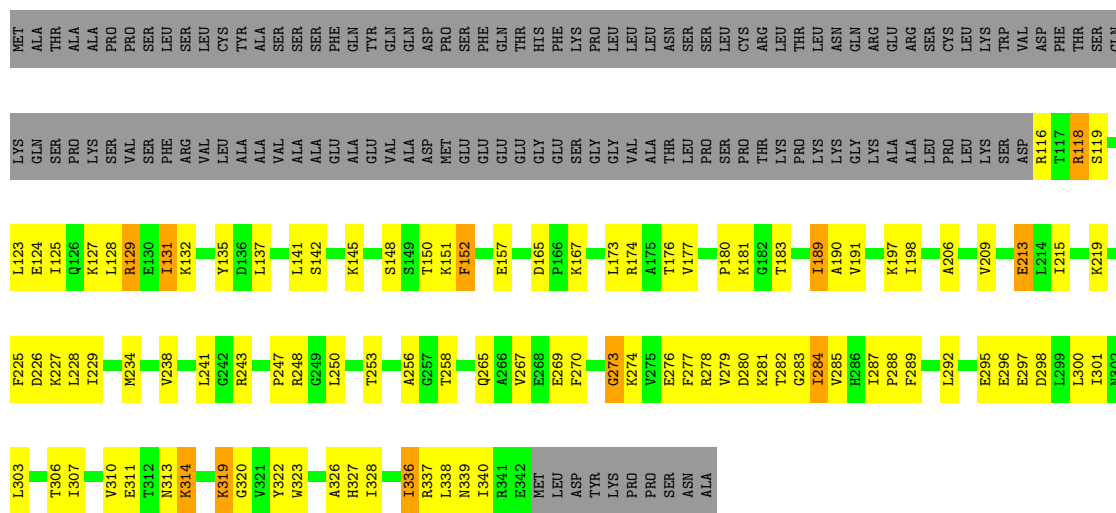
• Molecule 24: 4.8S rRNA

Chain BC: 29% 61% 10%



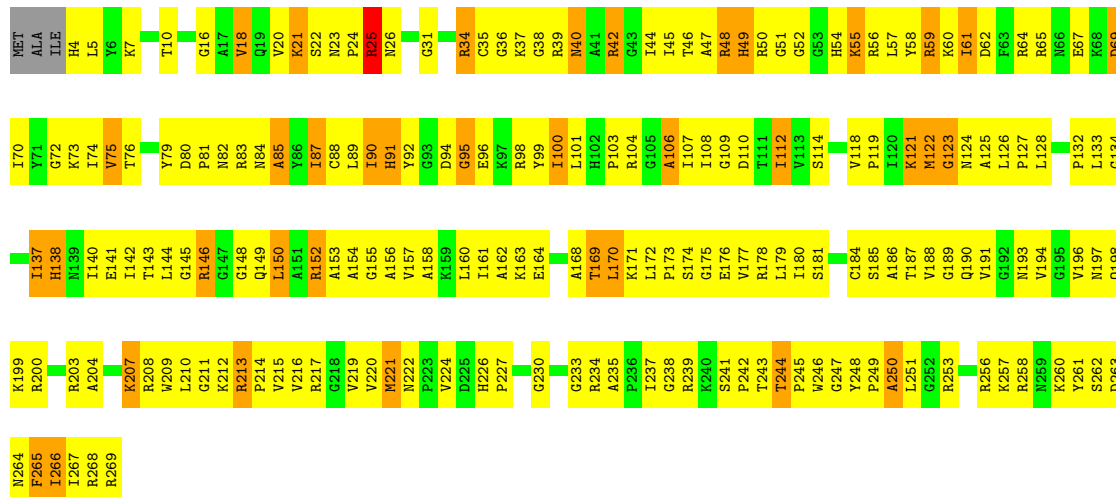
• Molecule 25: Ribosomal Protein L1

Chain BD: 36% 25% 36%

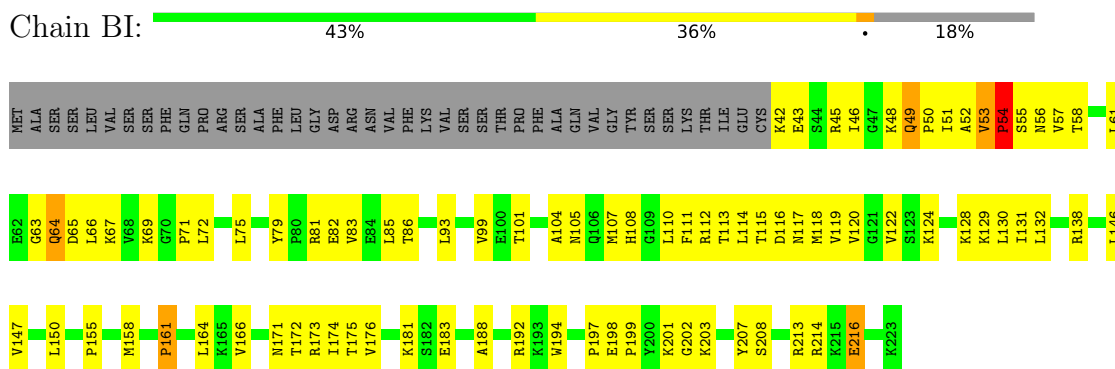


• Molecule 26: Ribosomal Protein L2

Chain BE: 26% 59% 14%

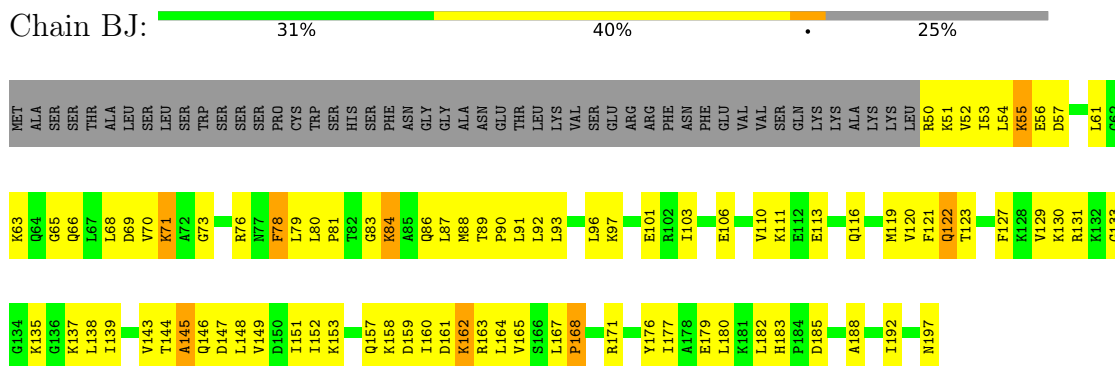


Chain BI:



- Molecule 31: Ribosomal Protein L9

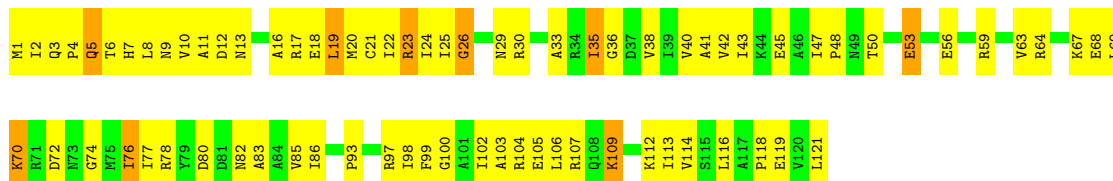
Chain BJ:





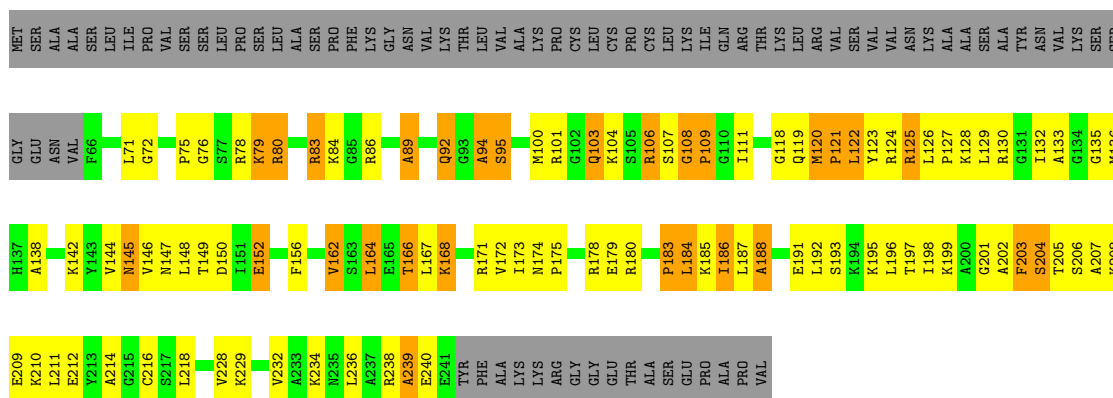
• Molecule 34: Ribosomal Protein L14

Chain BM: 37% 55% 7%



• Molecule 35: Ribosomal Protein L15

Chain BN: 29% 28% 11% 32%



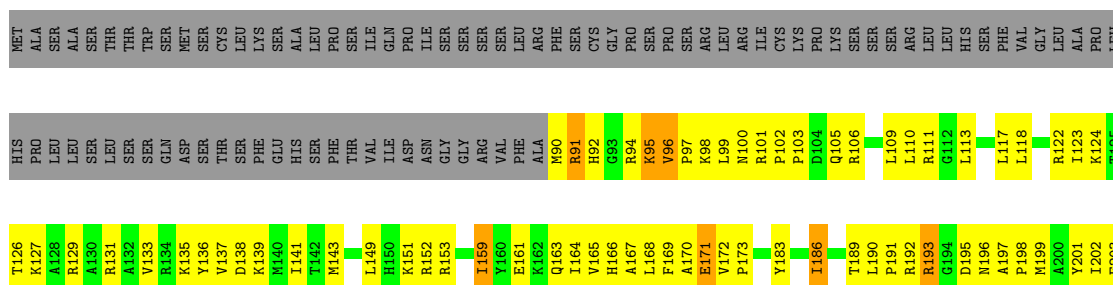
• Molecule 36: Ribosomal Protein L16

Chain BO: 34% 56% 10%

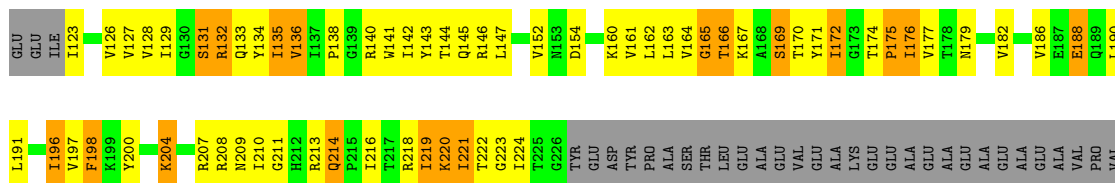


• Molecule 37: Ribosomal Protein L17

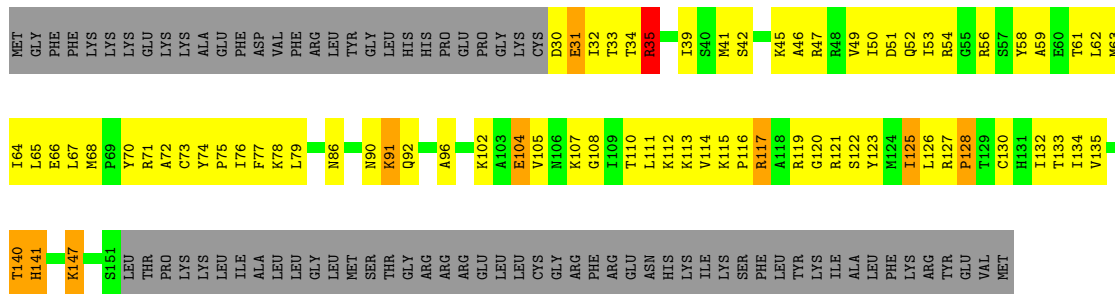
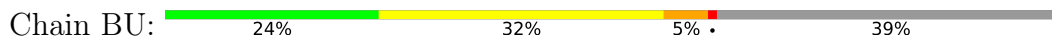
Chain BP: 23% 30% 43%



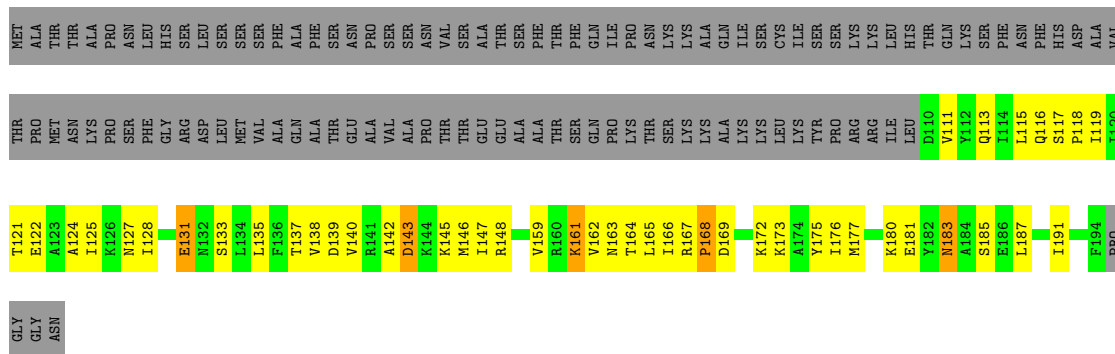
PHE	GLN	GLU	ILE	PRO	GLU	LEU	LYS	ALA	PHE	PHE	GLN	ARG	PRO	ASN	GLN	LYS	GLN	LEU	SER	ASP	VAL	PRO	ASP	PHE	GLN	ALA	PRO	GLU	GLY	THR	PRO	GLU	Tyr	ASN	ASP	ILE	ILE	ASN	GLN	PHE	LEU	PRO	PRO	PRO	PRO	PRO
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



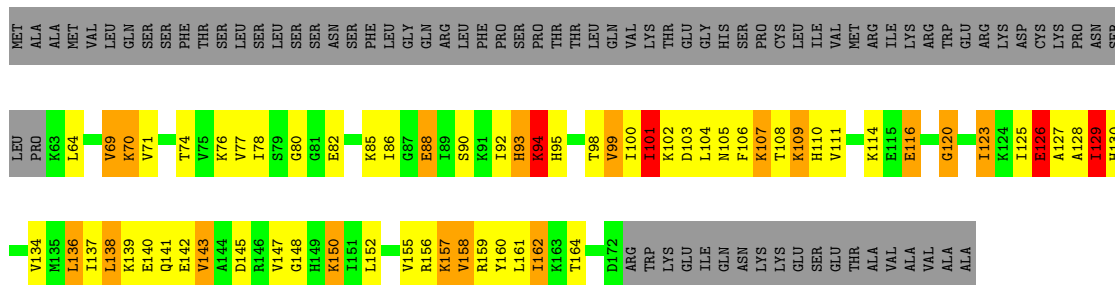
• Molecule 42: Ribosomal Protein L22



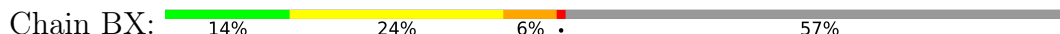
• Molecule 43: Ribosomal Protein L23

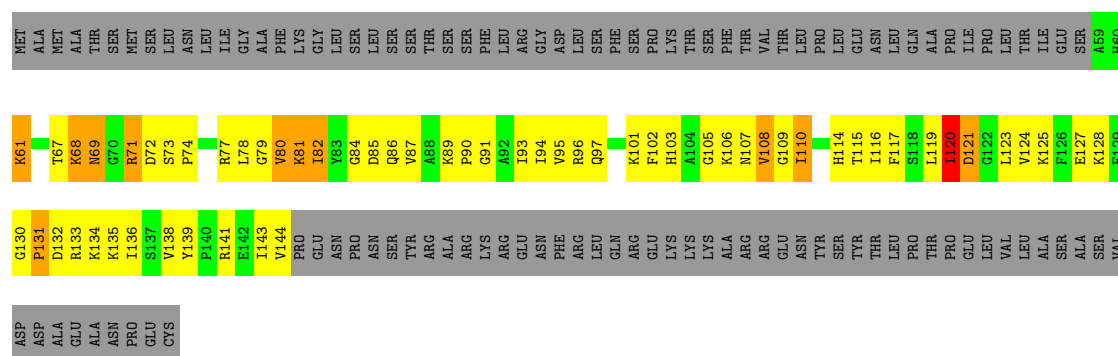


• Molecule 44: Ribosomal Protein L24



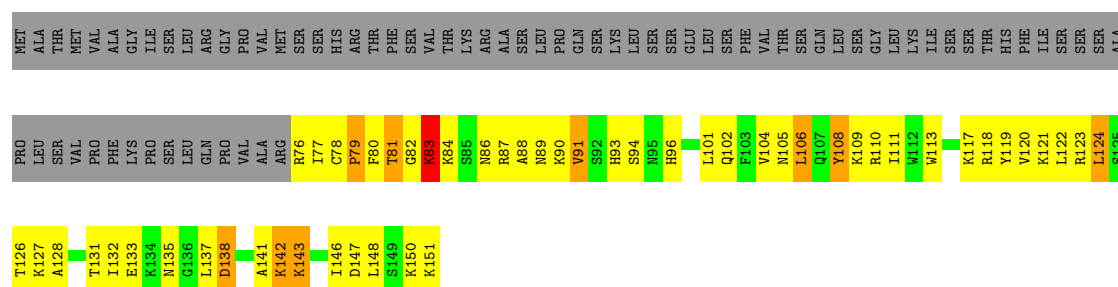
• Molecule 45: Ribosomal Protein L27





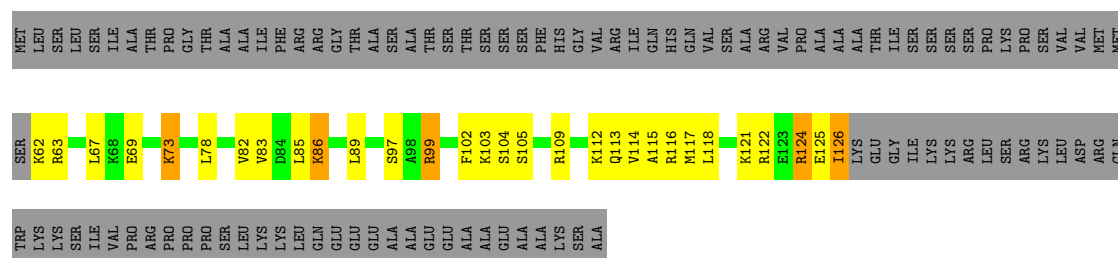
• Molecule 46: Ribosomal Protein L28

Chain BY: 15% 28% 6% 50%



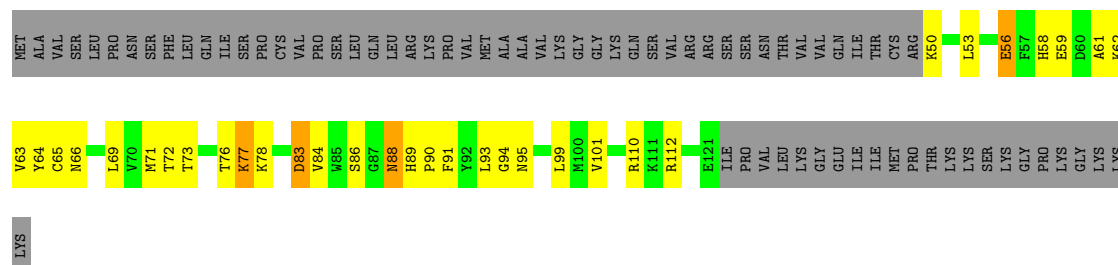
• Molecule 47: Ribosomal Protein L29

Chain BZ: 20% 14% 62%



• Molecule 48: Ribosomal Protein L31

Chain B1: 28% 19% 50%



• Molecule 49: Ribosomal Protein L32

Chain B2: 25% 54% 21%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86370	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction for each Micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	50760	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	AA	0.22	0/35552	0.66	1/55472 (0.0%)
2	AB	0.62	0/1860	0.69	3/2512 (0.1%)
3	AC	0.63	0/1771	0.75	3/2380 (0.1%)
4	AD	0.61	0/1660	0.74	1/2228 (0.0%)
5	AE	0.56	0/1204	0.64	0/1620
6	AF	0.71	0/887	0.76	2/1195 (0.2%)
7	AG	0.56	0/1227	0.70	2/1641 (0.1%)
8	AH	0.59	0/1103	0.70	0/1477
9	AI	0.63	0/1004	0.75	1/1347 (0.1%)
10	AJ	0.59	0/820	0.69	0/1108
11	AK	0.57	0/902	0.68	0/1214
12	AL	0.56	0/984	0.71	1/1323 (0.1%)
13	AM	0.60	0/833	0.78	1/1108 (0.1%)
14	AN	0.53	0/836	0.77	0/1116
15	AO	0.63	0/721	0.69	0/956
16	AP	0.72	0/674	0.86	2/902 (0.2%)
17	AQ	0.57	0/672	0.69	1/898 (0.1%)
18	AR	0.57	0/481	0.79	1/641 (0.2%)
19	AS	0.59	0/762	0.67	0/1021
20	AT	0.47	0/803	0.64	0/1063
21	AU	0.59	0/458	0.76	0/608
22	BA	0.13	0/65708	0.63	0/102501
23	BB	0.13	0/2793	0.63	0/4353
24	BC	0.13	0/2472	0.63	0/3854
25	BD	0.24	0/1786	0.40	0/2397
26	BE	0.21	0/2085	0.42	0/2800
27	BF	0.24	0/1214	0.42	0/1613
28	BG	0.25	0/1696	0.43	0/2283
29	BH	0.24	0/1372	0.41	0/1848
30	BI	0.23	0/1451	0.42	0/1944
31	BJ	0.24	0/1189	0.40	0/1589
32	BK	0.23	0/1077	0.43	0/1456
33	BL	0.23	0/1019	0.40	0/1369
34	BM	0.22	0/952	0.42	0/1282

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BN	0.23	0/1354	0.40	0/1806
36	BO	0.24	0/1098	0.41	0/1471
37	BP	0.23	0/964	0.41	0/1288
38	BQ	0.23	0/976	0.41	0/1305
39	BR	0.22	0/929	0.46	0/1248
40	BS	0.24	0/1047	0.40	0/1394
41	BT	0.23	0/839	0.43	0/1135
42	BU	0.23	0/1003	0.40	0/1348
43	BV	0.24	0/685	0.40	0/920
44	BW	0.21	0/878	0.42	0/1171
45	BX	0.25	0/672	0.41	0/896
46	BY	0.25	0/629	0.44	0/835
47	BZ	0.25	0/553	0.40	0/728
48	B1	0.26	0/594	0.37	0/797
49	B2	0.28	0/478	0.39	0/633
50	B3	0.23	0/532	0.40	0/708
51	B4	0.25	0/298	0.39	0/390
52	B5	0.23	0/509	0.38	0/672
53	B6	0.25	0/312	0.37	0/409
All	All	0.27	0/154378	0.62	19/230273 (0.0%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	AF	132	LEU	CA-CB-CG	7.67	132.94	115.30
13	AM	82	LEU	CA-CB-CG	7.39	132.30	115.30
16	AP	6	LEU	CA-CB-CG	7.02	131.45	115.30
7	AG	31	LEU	CA-CB-CG	6.96	131.32	115.30
16	AP	33	LEU	CA-CB-CG	6.96	131.30	115.30

There are no chirality outliers.

There are no planarity outliers.

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	AA	31745	0	15984	1134	0
2	AB	1827	0	1867	17	0
3	AC	1744	0	1831	18	0
4	AD	1632	0	1734	17	0
5	AE	1190	0	1245	18	0
6	AF	872	0	884	41	0
7	AG	1211	0	1284	11	0
8	AH	1088	0	1149	14	0
9	AI	988	0	1047	12	0
10	AJ	803	0	845	14	0
11	AK	888	0	933	10	0
12	AL	968	0	1046	12	0
13	AM	824	0	872	26	0
14	AN	820	0	858	13	0
15	AO	713	0	765	48	0
16	AP	664	0	703	13	0
17	AQ	662	0	715	11	0
18	AR	478	0	519	14	0
19	AS	747	0	787	22	0
20	AT	799	0	879	11	0
21	AU	455	0	466	10	0
22	BA	58665	0	29550	2028	0
23	BB	2497	0	1264	51	0
24	BC	2207	0	1114	89	0
25	BD	1760	0	1834	107	0
26	BE	2049	0	2128	412	0
27	BF	1196	0	1282	135	0
28	BG	1664	0	1731	187	0
29	BH	1351	0	1405	129	0
30	BI	1429	0	1510	94	0
31	BJ	1177	0	1259	86	0
32	BK	1060	0	1129	59	0
33	BL	998	0	1038	94	0
34	BM	943	0	996	101	0
35	BN	1333	0	1406	155	0
36	BO	1076	0	1134	127	0
37	BP	948	0	1009	96	0
38	BQ	962	0	992	120	0
39	BR	915	0	1001	153	0
40	BS	1030	0	1100	150	0
41	BT	826	0	900	83	0
42	BU	986	0	1025	106	0
43	BV	677	0	716	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BW	869	0	929	107	0
45	BX	660	0	693	92	0
46	BY	619	0	672	97	0
47	BZ	551	0	587	38	0
48	B1	581	0	562	46	0
49	B2	469	0	516	77	0
50	B3	524	0	557	64	0
51	B4	297	0	336	40	0
52	B5	504	0	559	77	0
53	B6	309	0	340	25	0
All	All	142250	0	97687	5825	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 24.

The worst 5 of 5825 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)
1:AA:755:U:H3	26:BE:5:LEU:CD1	1.02	1.62
1:AA:1423:G:C4'	22:BA:1737:A:C2	1.80	1.61
15:AO:44:LYS:HE3	26:BE:7:LYS:CE	1.25	1.61
1:AA:660:A:C5'	26:BE:161:ILE:HA	1.32	1.54
1:AA:1423:G:H4'	22:BA:1737:A:C2	1.37	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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
2	AB	229/231 (99%)	201 (88%)	25 (11%)	3 (1%)	12 48
3	AC	215/218 (99%)	179 (83%)	29 (14%)	7 (3%)	4 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AD	197/201 (98%)	179 (91%)	17 (9%)	1 (0%)	29	69
5	AE	156/308 (51%)	138 (88%)	16 (10%)	2 (1%)	12	48
6	AF	105/168 (62%)	92 (88%)	10 (10%)	3 (3%)	4	29
7	AG	152/155 (98%)	136 (90%)	14 (9%)	2 (1%)	12	48
8	AH	132/134 (98%)	118 (89%)	13 (10%)	1 (1%)	19	60
9	AI	125/197 (64%)	110 (88%)	13 (10%)	2 (2%)	9	44
10	AJ	97/197 (49%)	85 (88%)	10 (10%)	2 (2%)	7	36
11	AK	116/140 (83%)	95 (82%)	16 (14%)	5 (4%)	2	22
12	AL	121/123 (98%)	99 (82%)	17 (14%)	5 (4%)	3	23
13	AM	97/145 (67%)	75 (77%)	15 (16%)	7 (7%)	1	14
14	AN	97/100 (97%)	83 (86%)	13 (13%)	1 (1%)	15	55
15	AO	83/90 (92%)	77 (93%)	6 (7%)	0	100	100
16	AP	78/88 (89%)	59 (76%)	12 (15%)	7 (9%)	1	11
17	AQ	81/142 (57%)	69 (85%)	11 (14%)	1 (1%)	13	50
18	AR	56/103 (54%)	51 (91%)	4 (7%)	1 (2%)	8	40
19	AS	90/92 (98%)	75 (83%)	12 (13%)	3 (3%)	4	26
20	AT	100/202 (50%)	93 (93%)	7 (7%)	0	100	100
21	AU	51/190 (27%)	37 (72%)	10 (20%)	4 (8%)	1	13
25	BD	225/352 (64%)	189 (84%)	33 (15%)	3 (1%)	12	48
26	BE	264/269 (98%)	126 (48%)	94 (36%)	44 (17%)	0	3
27	BF	152/259 (59%)	91 (60%)	32 (21%)	29 (19%)	0	2
28	BG	209/293 (71%)	159 (76%)	39 (19%)	11 (5%)	2	19
29	BH	173/220 (79%)	130 (75%)	32 (18%)	11 (6%)	1	16
30	BI	180/223 (81%)	143 (79%)	30 (17%)	7 (4%)	3	23
31	BJ	146/197 (74%)	105 (72%)	33 (23%)	8 (6%)	2	19
32	BK	143/224 (64%)	115 (80%)	22 (15%)	6 (4%)	3	22
33	BL	123/250 (49%)	92 (75%)	24 (20%)	7 (6%)	1	18
34	BM	119/121 (98%)	96 (81%)	20 (17%)	3 (2%)	5	32
35	BN	174/257 (68%)	98 (56%)	48 (28%)	28 (16%)	0	3
36	BO	133/135 (98%)	93 (70%)	30 (23%)	10 (8%)	1	13
37	BP	114/205 (56%)	94 (82%)	16 (14%)	4 (4%)	3	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	BQ	120/161 (74%)	81 (68%)	23 (19%)	16 (13%)	0	5
39	BR	111/233 (48%)	66 (60%)	25 (22%)	20 (18%)	0	3
40	BS	117/119 (98%)	96 (82%)	12 (10%)	9 (8%)	1	13
41	BT	102/257 (40%)	62 (61%)	23 (22%)	17 (17%)	0	3
42	BU	120/199 (60%)	92 (77%)	20 (17%)	8 (7%)	1	15
43	BV	83/198 (42%)	63 (76%)	15 (18%)	5 (6%)	1	17
44	BW	108/191 (56%)	59 (55%)	34 (32%)	15 (14%)	0	4
45	BX	84/198 (42%)	52 (62%)	21 (25%)	11 (13%)	0	5
46	BY	74/151 (49%)	43 (58%)	20 (27%)	11 (15%)	0	3
47	BZ	63/173 (36%)	58 (92%)	5 (8%)	0	100	100
48	B1	70/144 (49%)	52 (74%)	14 (20%)	4 (6%)	1	18
49	B2	55/57 (96%)	32 (58%)	11 (20%)	12 (22%)	0	2
50	B3	63/66 (96%)	33 (52%)	23 (36%)	7 (11%)	0	7
51	B4	35/152 (23%)	28 (80%)	7 (20%)	0	100	100
52	B5	60/159 (38%)	39 (65%)	15 (25%)	6 (10%)	0	9
53	B6	36/104 (35%)	26 (72%)	6 (17%)	4 (11%)	0	7
All	All	5834/8791 (66%)	4464 (76%)	997 (17%)	373 (6%)	3	16

5 of 373 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	88	ARG
3	AC	89	PRO
3	AC	202	THR
5	AE	218	THR
6	AF	155	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	196/196 (100%)	177 (90%)	19 (10%)	8	27
3	AC	187/188 (100%)	177 (95%)	10 (5%)	22	47
4	AD	178/180 (99%)	167 (94%)	11 (6%)	18	43
5	AE	121/255 (48%)	118 (98%)	3 (2%)	47	68
6	AF	95/144 (66%)	84 (88%)	11 (12%)	5	21
7	AG	125/126 (99%)	113 (90%)	12 (10%)	8	27
8	AH	117/117 (100%)	105 (90%)	12 (10%)	7	25
9	AI	101/159 (64%)	93 (92%)	8 (8%)	12	35
10	AJ	91/178 (51%)	79 (87%)	12 (13%)	4	18
11	AK	92/110 (84%)	86 (94%)	6 (6%)	17	42
12	AL	106/106 (100%)	98 (92%)	8 (8%)	13	38
13	AM	90/126 (71%)	80 (89%)	10 (11%)	6	22
14	AN	89/90 (99%)	77 (86%)	12 (14%)	4	17
15	AO	80/85 (94%)	75 (94%)	5 (6%)	18	43
16	AP	71/79 (90%)	58 (82%)	13 (18%)	1	10
17	AQ	72/125 (58%)	67 (93%)	5 (7%)	15	40
18	AR	54/98 (55%)	49 (91%)	5 (9%)	9	28
19	AS	81/81 (100%)	74 (91%)	7 (9%)	10	32
20	AT	80/163 (49%)	72 (90%)	8 (10%)	7	26
21	AU	49/170 (29%)	46 (94%)	3 (6%)	18	44
25	BD	190/297 (64%)	181 (95%)	9 (5%)	26	51
26	BE	212/214 (99%)	205 (97%)	7 (3%)	38	61
27	BF	127/217 (58%)	123 (97%)	4 (3%)	40	62
28	BG	177/254 (70%)	172 (97%)	5 (3%)	43	65
29	BH	148/183 (81%)	139 (94%)	9 (6%)	18	44
30	BI	156/192 (81%)	152 (97%)	4 (3%)	46	66
31	BJ	128/171 (75%)	125 (98%)	3 (2%)	50	70
32	BK	114/189 (60%)	109 (96%)	5 (4%)	28	53
33	BL	104/213 (49%)	101 (97%)	3 (3%)	42	64
34	BM	101/101 (100%)	94 (93%)	7 (7%)	15	40
35	BN	136/203 (67%)	126 (93%)	10 (7%)	13	38
36	BO	108/108 (100%)	100 (93%)	8 (7%)	13	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BP	97/177 (55%)	92 (95%)	5 (5%)	23	48
38	BQ	103/135 (76%)	94 (91%)	9 (9%)	10	31
39	BR	100/207 (48%)	89 (89%)	11 (11%)	6	22
40	BS	106/106 (100%)	101 (95%)	5 (5%)	26	51
41	BT	90/224 (40%)	86 (96%)	4 (4%)	28	53
42	BU	108/176 (61%)	104 (96%)	4 (4%)	34	58
43	BV	74/171 (43%)	72 (97%)	2 (3%)	44	65
44	BW	98/171 (57%)	88 (90%)	10 (10%)	7	25
45	BX	68/167 (41%)	62 (91%)	6 (9%)	10	31
46	BY	66/133 (50%)	63 (96%)	3 (4%)	27	52
47	BZ	61/149 (41%)	55 (90%)	6 (10%)	8	26
48	B1	62/126 (49%)	61 (98%)	1 (2%)	62	79
49	B2	50/50 (100%)	46 (92%)	4 (8%)	12	35
50	B3	59/60 (98%)	55 (93%)	4 (7%)	16	41
51	B4	31/125 (25%)	29 (94%)	2 (6%)	17	42
52	B5	53/140 (38%)	50 (94%)	3 (6%)	20	45
53	B6	36/87 (41%)	36 (100%)	0	100	100
All	All	5038/7522 (67%)	4705 (93%)	333 (7%)	20	41

5 of 333 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	BM	35	ILE
41	BT	198	PHE
35	BN	83	ARG
38	BQ	46	GLU
44	BW	129	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
30	BI	117	ASN
51	B4	112	HIS
34	BM	29	ASN
50	B3	40	HIS

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Mol	Chain	Res	Type
45	BX	107	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1477/1491 (99%)	245 (16%)	51 (3%)
22	BA	2726/2810 (97%)	387 (14%)	12 (0%)
23	BB	116/117 (99%)	12 (10%)	0
24	BC	102/103 (99%)	14 (13%)	0
All	All	4421/4521 (97%)	658 (14%)	63 (1%)

5 of 658 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	A
1	AA	10	G
1	AA	14	U
1	AA	15	C
1	AA	32	G

5 of 63 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	862	A
22	BA	639	A
1	AA	1014	U
22	BA	625	C
22	BA	1927	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-1417. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.