



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 5, 2017 – 06:13 AM EDT

PDB ID : 5X8P
EMDB ID: : EMD-6709
Title : Structure of the 70S chloroplast ribosome from spinach
Authors : Ahmed, T.; Shi, J.; Bhushan, S.
Deposited on : unknown
Resolution : 3.40 Å(reported)

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

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

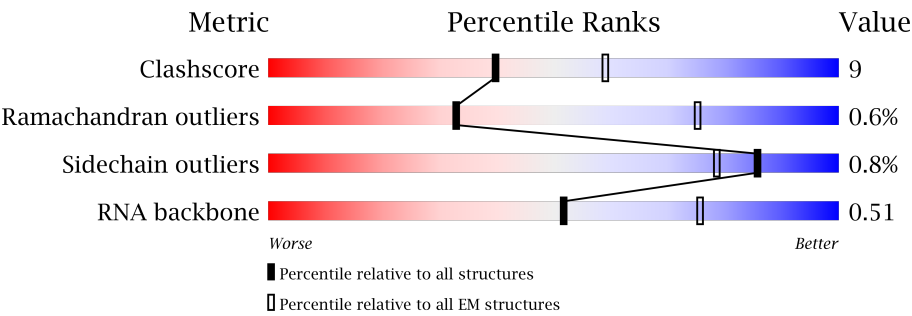
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	1	56	<div><div>70%13%18%</div></div>
2	2	65	<div><div>58%18%•22%</div></div>
3	3	61	<div><div>72%21%7%</div></div>
4	4	73	<div><div>77%16%•5%</div></div>
5	5	37	<div><div>78%22%</div></div>
6	6	142	<div><div>30%5%65%</div></div>
7	7	116	<div><div>29%10%60%</div></div>
8	B	121	<div><div>66%23%7%•</div></div>

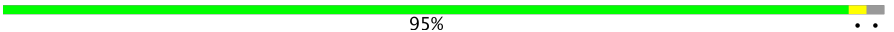


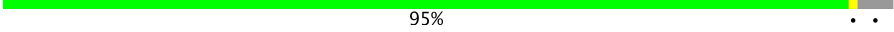
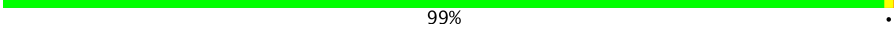



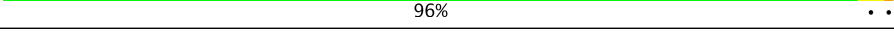

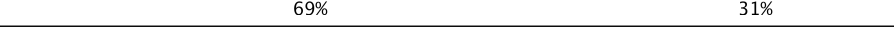
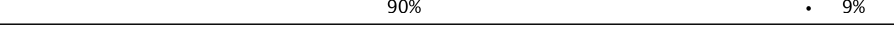
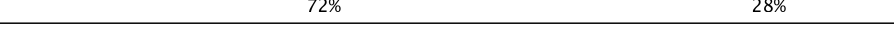


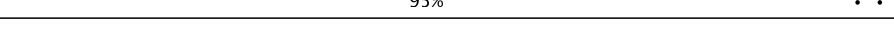









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Mol	Chain	Length	Quality of chain
9	C	271	
10	D	221	
11	E	243	
12	F	220	
13	G	182	
14	H	155	
15	K	197	
16	L	121	
17	M	192	
18	N	135	
19	O	116	
20	P	123	
21	Q	156	
22	R	127	
23	S	201	
24	T	199	
25	U	122	
26	V	145	
27	W	106	
28	X	137	
29	Y	77	
30	Z	109	
31	A	2810	
32	0	94	
33	b	236	

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Mol	Chain	Length	Quality of chain
34	c	218	
35	e	253	
36	f	146	
37	g	155	
38	h	134	
39	i	157	
40	j	122	
41	k	138	
42	l	123	
43	m	126	
44	o	90	
45	p	88	
46	q	108	
47	r	101	
48	s	92	
49	t	108	
50	u	137	
51	y	236	
52	a	1491	
53	w	121	
54	d	201	
55	v	198	
56	n	100	
57	x	47	
58	8	370	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 147126 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	46	Total	C	N	O	0	0
			378	250	70	58		

- Molecule 2 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	51	Total	C	N	O	S	0	0
			415	258	83	70	4		

- Molecule 3 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	57	Total	C	N	O	S	0	0
			445	268	103	71	3		

- Molecule 4 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	69	Total	C	N	O	S	0	0
			563	353	119	90	1		

- Molecule 5 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	37	Total	C	N	O	S	0	0
			304	186	70	44	4		

- Molecule 6 is a protein called protein cL37.

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

- Molecule 7 is a protein called protein cL38.

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

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	117	Total	C	N	O	P	0	0
			2500	1116	452	815	117		

- Molecule 9 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	247	Total	C	N	O	S	0	0
			1904	1181	390	327	6		

- Molecule 10 is a protein called protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	212	Total	C	N	O	S	0	0
			1620	1025	295	289	11		

- Molecule 11 is a protein called 50S ribosomal protein L4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	210	Total	C	N	O	S	0	0
			1655	1052	308	292	3		

- Molecule 12 is a protein called 50S ribosomal protein L5, chloroplastic.

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

- Molecule 13 is a protein called protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	173	Total	C	N	O	S	0	0
			1353	855	249	245	4		

- Molecule 14 is a protein called protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	53	Total	C	N	O	S	0	0
			423	280	74	68	1		

- Molecule 15 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	193	Total	C	N	O	S	0	0
			1568	1000	289	274	5		

- Molecule 16 is a protein called 50S ribosomal protein L14, chloroplastic.

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

- Molecule 17 is a protein called protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	177	Total	C	N	O	S	0	0
			1342	836	264	236	6		

- Molecule 18 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	134	Total	C	N	O	S	0	0
			1067	672	217	173	5		

- Molecule 19 is a protein called protein L17.

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

- Molecule 20 is a protein called protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	120	Total	C	N	O	S	0	0
			947	589	183	170	5		

- Molecule 21 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	118	Total	C	N	O	S	0	0
			953	610	186	156	1		

- Molecule 22 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	115	Total	C	N	O	S	0	0
			996	633	208	153	2		

- Molecule 23 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	147	Total	C	N	O		0	0
			1171	759	202	210			

- Molecule 24 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	144	Total	C	N	O	S	0	0
			1149	731	210	200	8		

- Molecule 25 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	92	Total	C	N	O	S	0	0
			740	477	129	132	2		

- Molecule 26 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	124	Total	C	N	O	S	0	0
			993	624	187	180	2		

- Molecule 27 is a RNA chain called 4.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	102	Total	C	N	O	P	0	0
			2187	977	403	705	102		

- Molecule 28 is a protein called protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	X	100	Total	C	N	O	0	0
			810	511	159	140		

- Molecule 29 is a protein called protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	74	Total	C	N	O	S	0	0
			605	385	121	98	1		

- Molecule 30 is a protein called protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	90	Total	C	N	O	S	0	0
			754	470	150	131	3		

- Molecule 31 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	2809	Total	C	N	O	P	0	0
			60324	26912	11166	19437	2809		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	0	64	Total	C	N	O	S	0	0
			521	330	89	100	2		

- Molecule 33 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	227	Total	C	N	O	S	0	0
			1787	1127	326	321	13		

- Molecule 34 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	213	Total	C	N	O	S	0	0
			1719	1099	310	304	6		

- Molecule 35 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	171	Total	C	N	O	S	0	0
			1292	806	250	230	6		

- Molecule 36 is a protein called 30S ribosomal protein S6 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	111	Total	C	N	O	S	0	0
			886	566	145	171	4		

- Molecule 37 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	149	Total	C	N	O	S	0	0
			1161	723	231	204	3		

- Molecule 38 is a protein called 30S ribosomal protein S8, chloroplastic.

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

- Molecule 39 is a protein called 30S ribosomal protein S9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	133	Total	C	N	O	S	0	0
			1020	650	191	178	1		

- Molecule 40 is a protein called protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	98	Total	C	N	O	S	0	0
			796	512	142	137	5		

- Molecule 41 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	118	Total	C	N	O	S	0	0
			887	549	182	151	5		

- Molecule 42 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	123	Total	C	N	O	S	0	0
			967	604	198	162	3		

- Molecule 43 is a protein called 30S ribosomal protein S13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	110	Total	C	N	O	S	0	0
			898	559	183	153	3		

- Molecule 44 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	62	Total	C	N	O	S	0	0
			525	339	100	85	1		

- Molecule 45 is a protein called 30S ribosomal protein S16, chloroplastic.

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

- Molecule 46 is a protein called protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	78	Total	C	N	O	S	0	0
			635	399	124	108	4		

- Molecule 47 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	64	Total	C	N	O	S	0	0
			518	326	101	90	1		

- Molecule 48 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	78	Total	C	N	O	S	0	0
			627	403	118	104	2		

- Molecule 49 is a protein called protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	105	Total	C	N	O	S	0	0
			832	514	169	148	1		

- Molecule 50 is a protein called protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	44	Total	C	N	O	S	0	0
			393	238	87	66	2		

- Molecule 51 is a protein called protein plastid pY.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	108	Total	C	N	O	S	0	0
			845	521	164	159	1		

- Molecule 52 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	1480	Total	C	N	O	P	0	0
			31777	14168	5863	10266	1480		

- Molecule 53 is a protein called protein cS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	84	Total	C	N	O	S	0	0
			689	454	115	118	2		

- Molecule 54 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 55 is a protein called protein cS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	190	Total	C	N	O	S	0	0
			1464	908	255	298	3		

- Molecule 56 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	n	99	Total	C	N	O	S	0	0
			819	507	174	135	3		

- Molecule 57 is a protein called protein bTHXc.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	x	37	Total	C	N	O	0	0
			289	179	65	45		

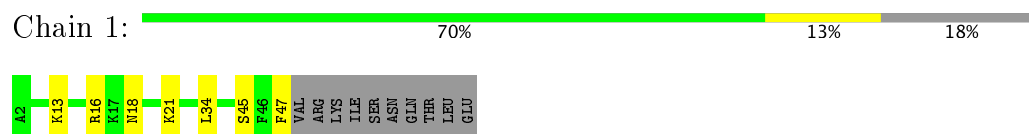
- Molecule 58 is a protein called 30S ribosomal protein S1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	154	Total	C	N	O	S	0	0
			1201	744	222	227	8		

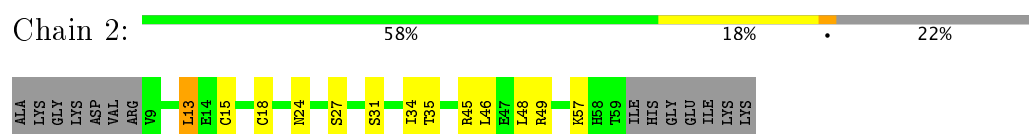
3 Residue-property plots [i](#)

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

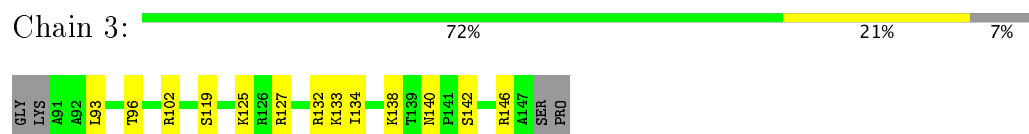
- Molecule 1: 50S ribosomal protein L32, chloroplastic



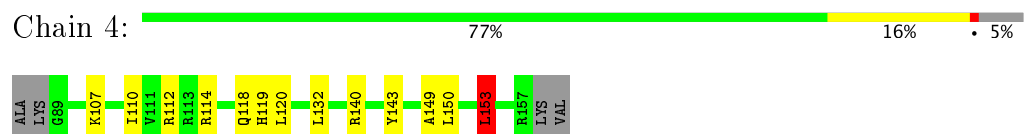
- Molecule 2: 50S ribosomal protein L33, chloroplastic



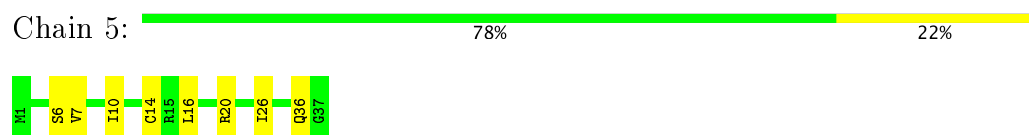
- Molecule 3: 50S ribosomal protein L34, chloroplastic



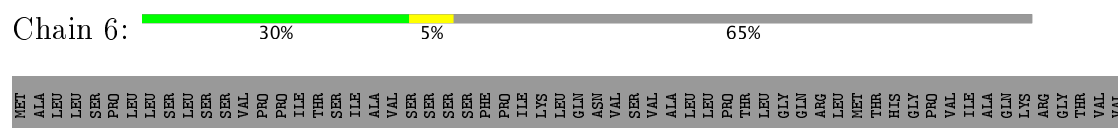
- Molecule 4: 50S ribosomal protein L35, chloroplastic

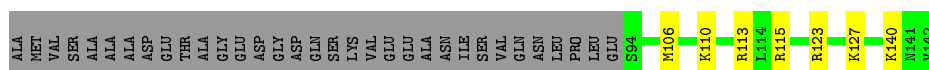


- Molecule 5: 50S ribosomal protein L36, chloroplastic

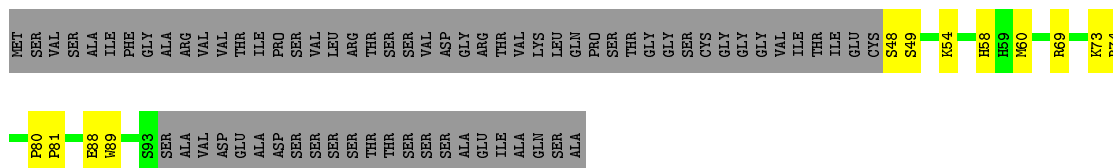


- Molecule 6: protein cL37

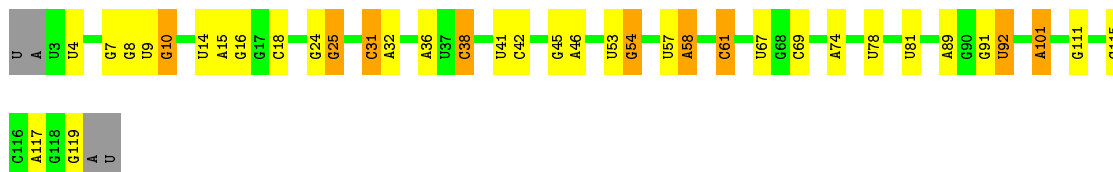




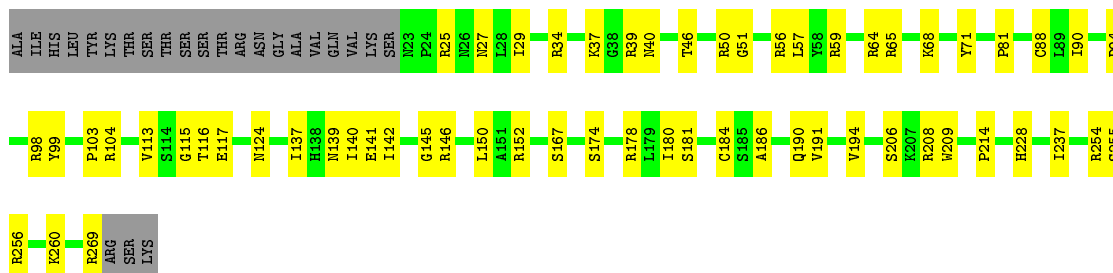
- Molecule 7: protein cL38



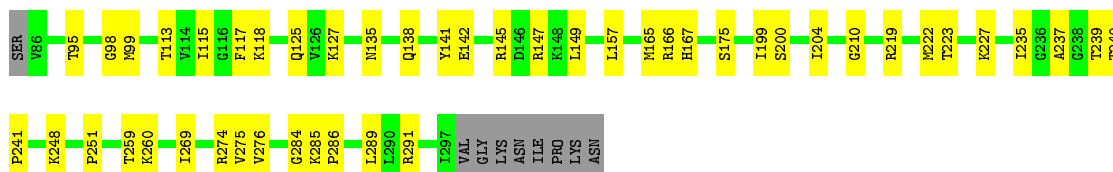
- Molecule 8: 5S rRNA



- Molecule 9: 50S ribosomal protein L2, chloroplastic

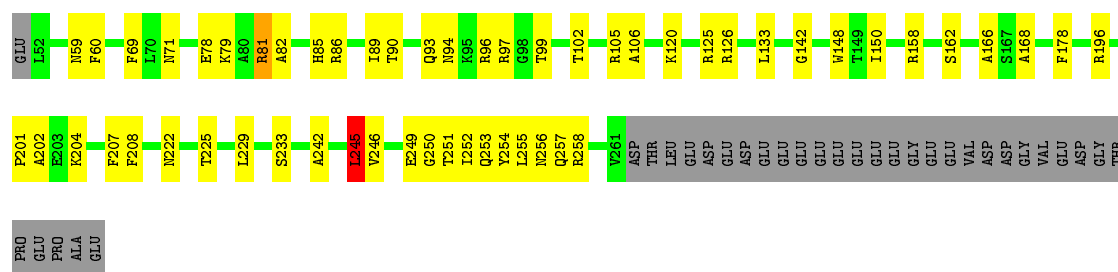


- Molecule 10: protein L3

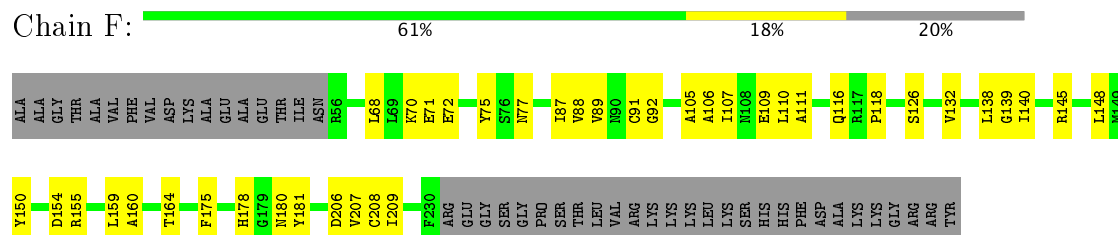


- Molecule 11: 50S ribosomal protein L4, chloroplastic

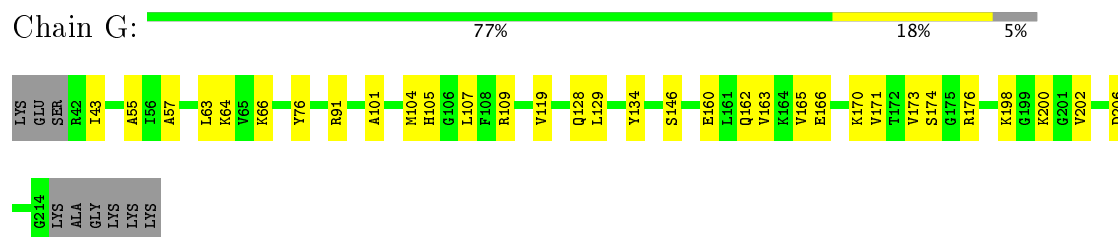




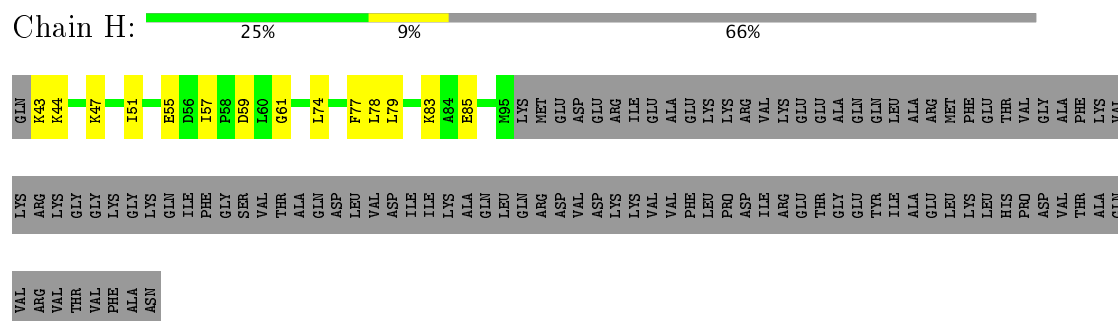
- Molecule 12: 50S ribosomal protein L5, chloroplastic



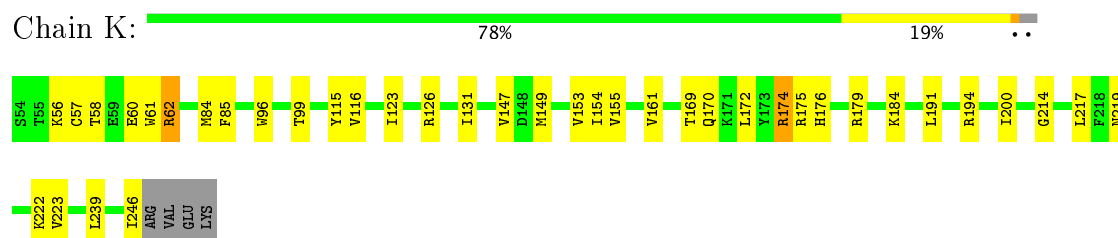
- Molecule 13: protein L6



- Molecule 14: protein L9

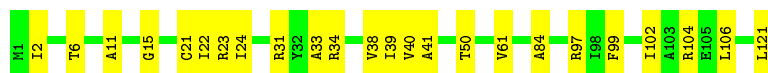


- Molecule 15: 50S ribosomal protein L13, chloroplastic



- Molecule 16: 50S ribosomal protein L14, chloroplastic

Chain L:  80% 20%



- Molecule 17: protein L15

Chain M:  80% 11% 8%




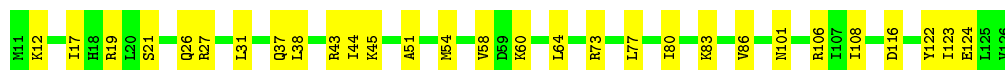
- Molecule 18: 50S ribosomal protein L16, chloroplastic

Chain N:  73% 26%



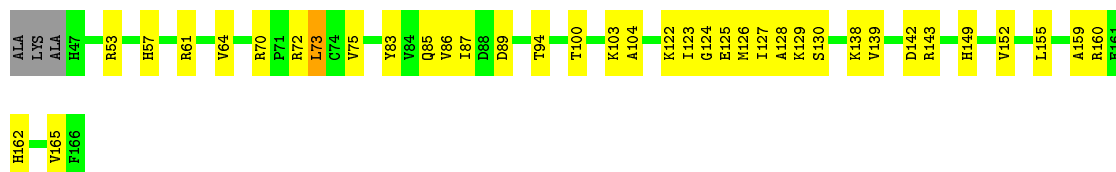
- Molecule 19: protein L17

Chain O:  75% 25%



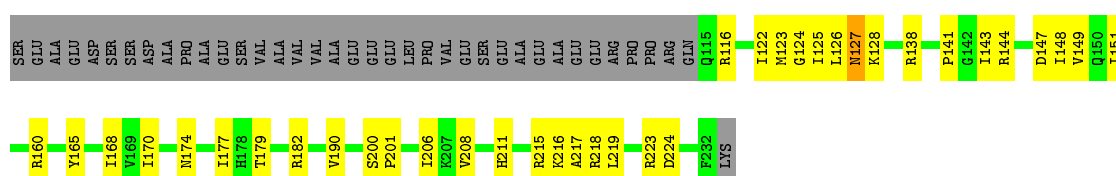
- Molecule 20: protein L18

Chain P:  67% 29%

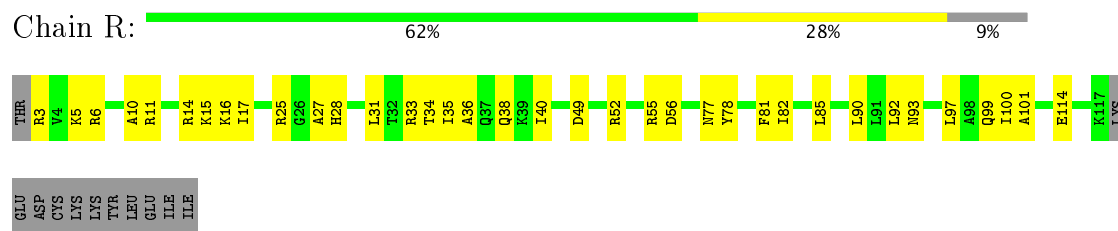


- Molecule 21: 50S ribosomal protein L19, chloroplastic

Chain Q:  52% 23% 24%



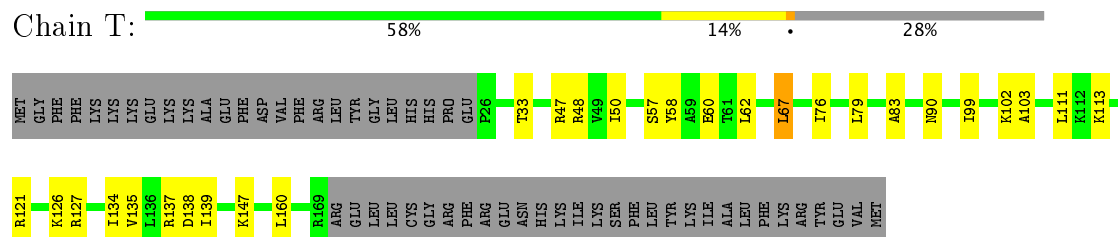
- Molecule 22: 50S ribosomal protein L20, chloroplastic



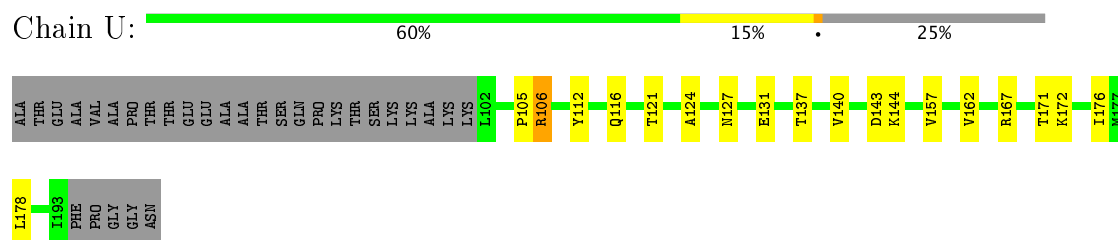
- Molecule 23: 50S ribosomal protein L21, chloroplastic



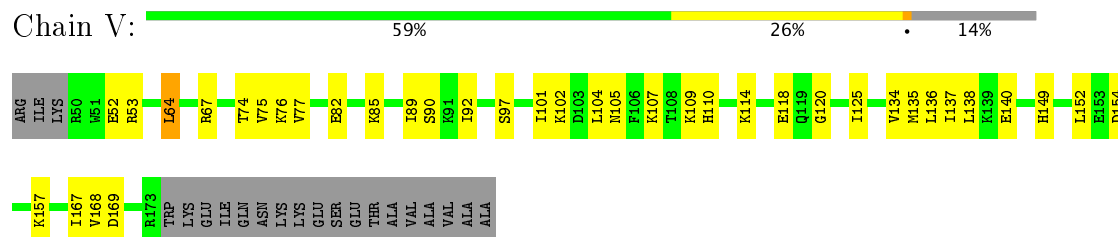
- Molecule 24: 50S ribosomal protein L22, chloroplastic



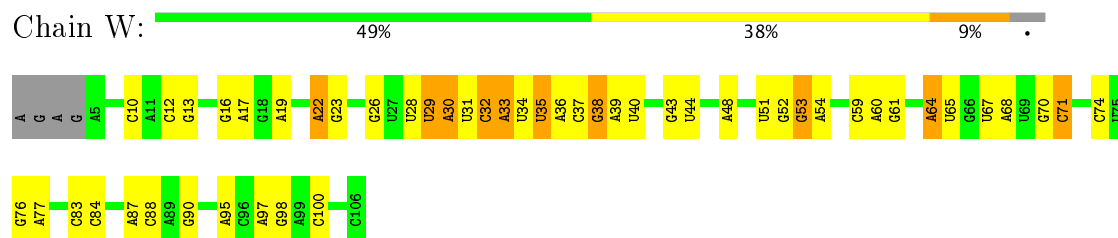
- Molecule 25: 50S ribosomal protein L23, chloroplastic



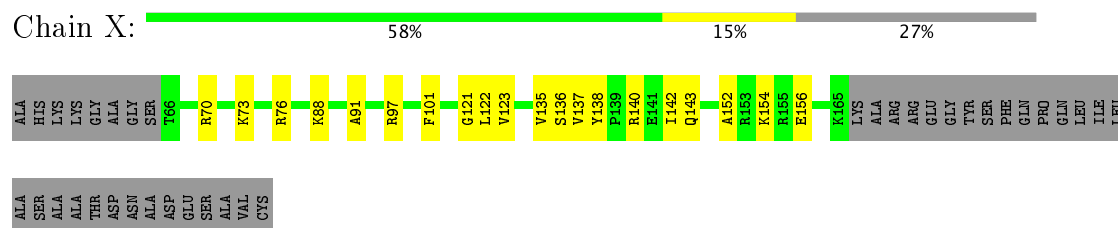
- Molecule 26: 50S ribosomal protein L24, chloroplastic



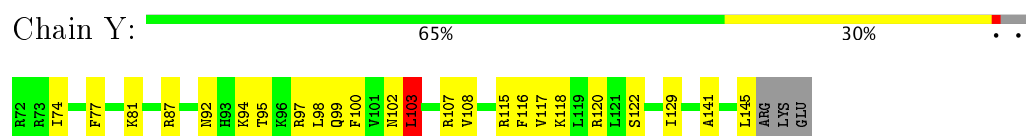
- Molecule 27: 4.8S rRNA



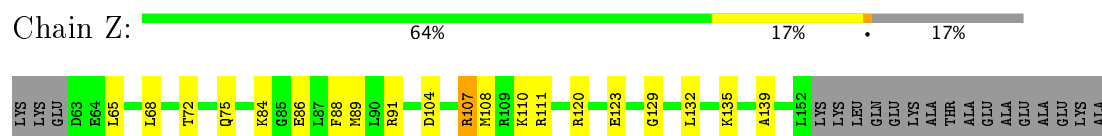
• Molecule 28: protein L27



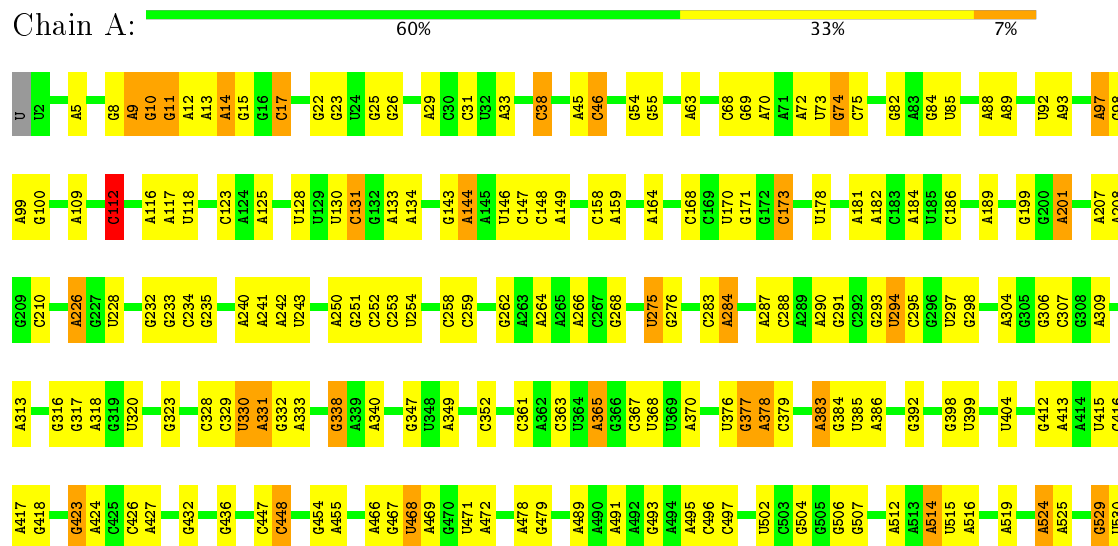
• Molecule 29: protein L28



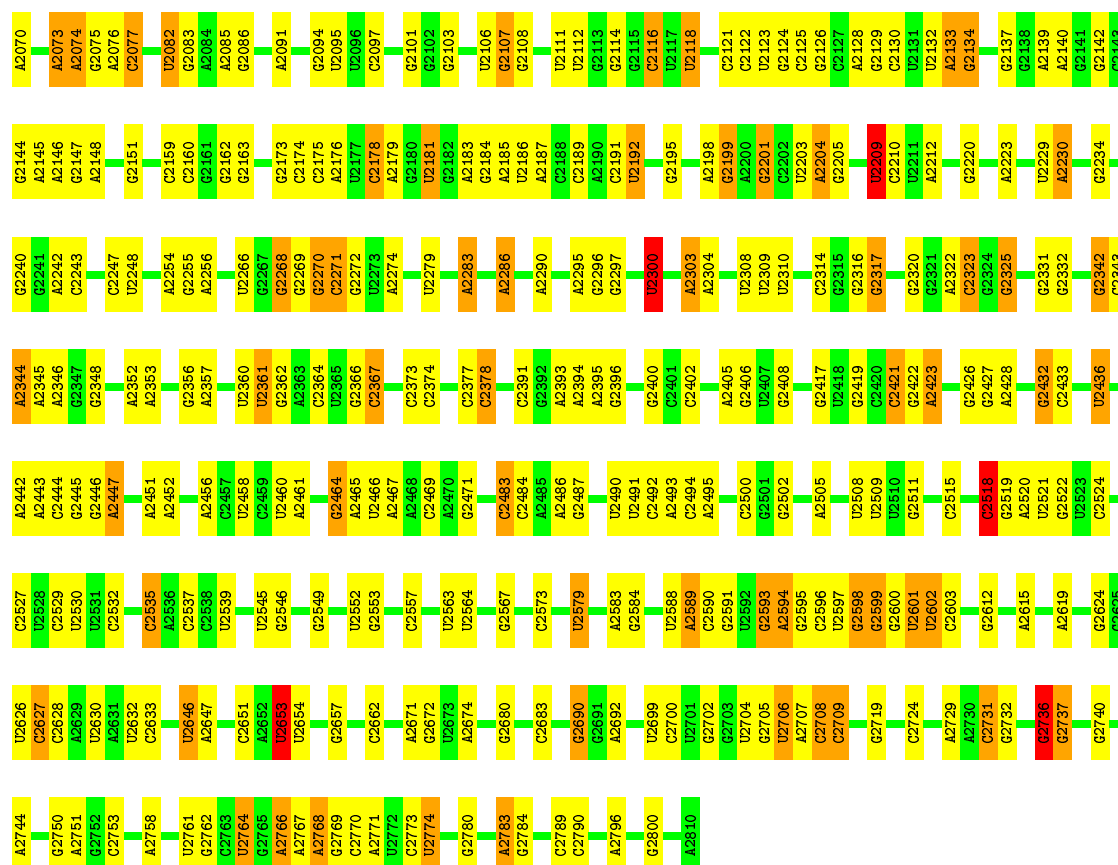
• Molecule 30: protein L29



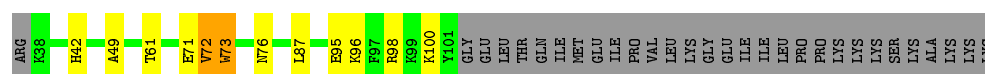
• Molecule 31: 23S rRNA



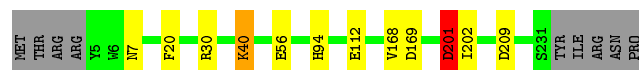
U1957	A1839	U1749	A1616	A1519	G1437	G1344	G1253	C1149	G1075	G981	G887	A804	C702	G614	A531
G1962	C1843	C1750	U1620	A1520	G1438	G1345	U1254	G1150	A1076	G982	C888	A805	C703	G615	A540
U1968	U1844	C1752	C1621	G1522	U1439	U1346	U1255	A1154	C1077	G983	G889	A811	U705	G621	A541
U1969	G1845	A1753	A1622	A1523	G1443	C1348	G1257	A1155	A1078	G984	G891	G812	G706	A621	C542
U1970	C1884	A1755	A1628	G1524	G1444	C1354	C1259	A1157	C1081	A985	C892	C813		A623	A543
C1971		G1756	G1445	G1525	G1446	G1355	G1260	U1158	G1084	U986	C893		C709	A624	C544
	G1889	G1757	A1448		A1448		A1261	G1159	G1087	A987	C894	G816			C630
	G1860	G1758	C1449	U1528	C1449	C1366	G1269	A1160		G989	C895	C817	G715		C631
			G1450	A1529	G1450	C1367	G1270	A1161	G1092	U992	A897	U818	U721	G632	A554
	G1871	G1762	G1451	A1530	G1451	C1371	C1271	G1162		C993	A898	G820	G722	A633	A555
	G1873	G1763	A1452	A1531	A1452	C1372	A1272	G1163	G1096		A899		G723		C556
C1981	U1874	G1766	G1453	A1533	G1453	U1373	G1273	A1169	A1097	A1001	G900	C823	G724	U638	C557
			G1454		G1454	U1374	A1274	A1170	A1098	G1002	C901	C826		A639	A558
	A1894	G1770	G1456	A1544	G1456	C1379	U1276	U1175	G1100	A1008	G904	G827	C730	G641	A560
A1985	A1876	C1770	A1646	G1545	C1458		G1277	C1176	A1101		U905	C828	U731	A643	C563
G1986		G1774	A1650	C1546	U1459	G1384	U1278	U1177	G1102	A1011	C906		A732	A644	U564
G1987	G1882	G1778	A1662	G1547	A1460	G1385		A1183	G1103	G1012	C907	U833	A733	A645	C568
	G1883		A1666	A1548	G1461	A1386	G1281	G1189	C1104	C1013	A908	G834	G734	G646	C569
	A1894	A1783		A1549	G1462	A1387	U1283	G1189	A1105	C1014				C647	C570
	G1994	C1784	U1665	U1550	G1462	A1388	U1284		C1106	G1015	U911	U838	G737	A649	C571
A1995	G1887		A1666		G1466		U1285	A1196	C1107	G1016				G650	A571
U1996	G1888	U1769	C1662	G1555	C1467	G1391	G1286	A1197	G1108	G1017	G915	G841	G740	G651	U572
	G1889	A1790	G1683	A1557	C1468	U1392	A1286	A1198		A1018	G916	G842	U741	C652	G573
U2005	C1901	C1792	C1684	A1559	A1472		C1291		A1112	U1019	A919	G844	G744	A656	C577
G2006	G1906	A1793	G1685		U1475	C1397	G1292	A1201	A1113	A1028	A920	C845	A745	U657	U578
U2007	C1907	A1794	C1689	U1568	G1476	A1399	C1293	G1206	A1114	A1024	U924	A846			U579
C2010	C1907	A1795		A1569	U1476	U1400	A1294	U1209	G1115		G925		G756	A663	U580
G2011	A1914	A1796	C1692	C1570	U1481	G1401	A1296	U1210	U1117	A1028	A926	U856	G757	A664	A581
A2012	A1915			G1571	U1481	G1402	C1297	G1211	U1118	A1037	U928		U758	A665	A582
C2013	G1920	A1801	C1696	G1573	U1481	A1403	A1298	G1211	G1119		U928		G759	U666	A583
				C1574	G1484	C1404		U1219	G1120	U1040	A932		A763	G667	A584
C2020	C1808	C1808	A1704	G1574	U1485	A1405	A1305	U1219	G1121	U1041	U937	U854	G770	U668	A585
U2021	G1809	C1810	A1705	A1578	U1486	A1406	A1308	U1220	U1122	G1050	A946	A865	U773	G680	C591
G2022	A1926	A1811	C1706		U1487	C1407	U1309	G1225	A1123	G1051	A947	G866	A775	A681	C592
G2023	C1927	A1812	U1707	C1584	A1488	A1408	C1310	U1226	U1124	G1052	U938	G867	G776	C682	C593
	C1928	A1813	C1708		A1489	A1408	C1311	U1227	A1125	U1053	A947	G868		C683	C594
C2034	U1929	G1814	G1709	A1592	G1490	A1413	C1311	A1228	G1126	U1054	A960	G869	G776	C684	A596
A2035	U1930	U1815		U1593	G1493	A1416	G1315	A1234	C1130	U1055	G961	U870	U783	G685	C599
U2036	U1931	C1710	C1711	A1594	G1494	U1417	C1316	A1235	A1131	A1056	G962	A871	G783	A686	A600
G2037		U1818	A1712		U1495	U1418	G1317	U1239	G1134	A1057		A872		A687	
A2045	C1934	A1819	A1725	A1600	G1497	U1419	A1321	G1238	G1137		G966		G786	C688	C605
G2046	G1935	A1820	A1726		G1501	U1423	A1322	C1239	G1138	A1060		C877	G787	G693	A606
A2047	G1936	G1821	G1732	A1603	A1502	A1424	G1330	U1240	A1139	G1061	G970	U878	G788	A696	G607
U2048	A1941	A1825	G1733	A1604	G1505	A1427	G1331	U1245	G1140	G1062	U971	U880		A697	U608
G2049	G1942	U1826	A1734	A1605	C1506		G1332	U1245	G1141	U1063	G972	A793	A793	A697	G609
C2051	G1943	U1827	G1739	G1607	G1507	C1431	U1333	G1248	G1142	A1064	G973	U795		C698	G610
G2052	G1944	A1829	G1740	C1608	U1511	U1432	U1334	G1249	G1143	G1065	G974			U701	C611
	U1945	U1830		G1611	U1512	U1433	C1335	C1250	U1147		A975	G883		A699	U612
U2055	G1949	U1836	C1746	A1612	C1513	U1434	A1342	G1251		A1072	G976	G884	C802	U700	G611
C2063	A1950	U1837	C1747	U1615	U1514	U1435	A1342	G1251				G885		A700	U612
	A1951	G1838	C1748		G1515	U1436	A1343	C1252	G1148		G977	U886			U613



- Molecule 32: 50S ribosomal protein L31



- Molecule 33: 30S ribosomal protein S2, chloroplastic



- Molecule 34: 30S ribosomal protein S3, chloroplastic



- Molecule 35: 30S ribosomal protein S5, chloroplastic



CYS ILE LYS LYS ASP ASP ILE ASP THR THR PHE PHE GLU GLN ASP ASP ASN PRO PRO ASP ASP GLU GLU ILE ILE THR PHE ASP PRO PRO LYS LYS PRO GLU GLY TYR ILE PRO PRO ARG ALA VAL ASP GLU PRO PRO PHE GLU SER SER GLU GLU GLU ILE ALA LEU ALA TYR GLU GLU LEU TYR GLY ALA ALA

TYR SER GLY GLU SER LEU LEU GLY ASN VAL TYR MET ASP SER LYS ILE LYS LYS ALA THR G138 K144 K147 I148 L266 P302 K303 E304 E305 K308

- Molecule 36: 30S ribosomal protein S6 alpha, chloroplastic

Chain f:  75% 24%

ASP PHE SER GLY SER PHE PHE GLU GLY GLY PHE PHE GLY GLY LEU ASP ASP ASP PRO PRO SER THR PRO PRO ALA GLY LEU VAL VAL GLU GLU LYS P97 P102 K207 LYS ARG LYS TYR

- Molecule 37: 30S ribosomal protein S7, chloroplastic

Chain g:  95% ..


MET SER ARG R4 E8 E9 A152 HIS PHE ARG

- Molecule 38: 30S ribosomal protein S8, chloroplastic

Chain h:  99% ..


M1 R67 L79 W134

- Molecule 39: 30S ribosomal protein S9, chloroplastic

Chain i:  82% 15%


THR SER ALA THR ALA VAL VAL VAL VAL THR THR ASP LEU GLU LYS PHE VAL LYS SER ARG L63 R78 T96 A159 R176 S195 LYS ARG

- Molecule 40: protein S10

Chain j:  80% 20%

SER PHE GLU ASP THR GLY SER GLU THR SER LYS ILE ILE SER ARG ASN GLY ARG ASP ASP ASP MET ALA LYS LYS K38 L135 L195

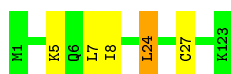
- Molecule 41: 30S ribosomal protein S11, chloroplastic

Chain k:  86% 14%

MET ALA LYS PRO PRO ILE PRO LYS ILE GLY SER ARG ARG ASN GLY ARG ILE ILE SER SER ARG LYS S21 V138

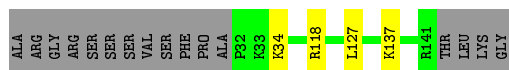
- Molecule 42: 30S ribosomal protein S12, chloroplastic

Chain l:  96% ..



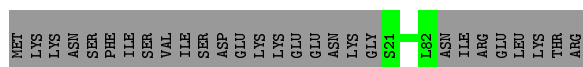
- Molecule 43: 30S ribosomal protein S13, chloroplastic

Chain m: 84% 13%



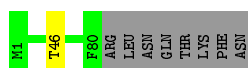
- Molecule 44: 30S ribosomal protein S15, chloroplastic

Chain o: 69% 31%



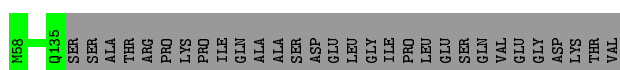
- Molecule 45: 30S ribosomal protein S16, chloroplastic

Chain p: 90% 9%



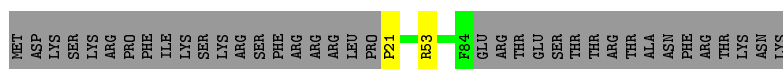
- Molecule 46: protein S17

Chain q: 72% 28%



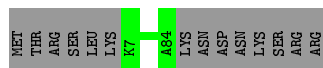
- Molecule 47: 30S ribosomal protein S18, chloroplastic

Chain r: 61% 37%



- Molecule 48: 30S ribosomal protein S19 alpha, chloroplastic

Chain s: 85% 15%



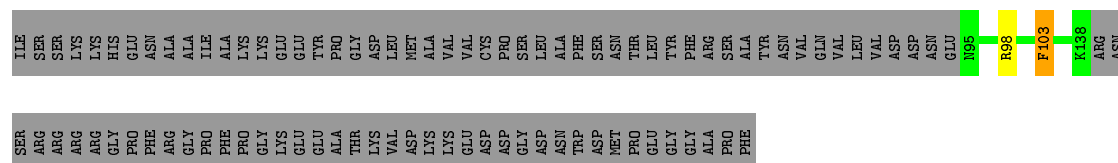
- Molecule 49: protein S20

Chain t: 95% 2%



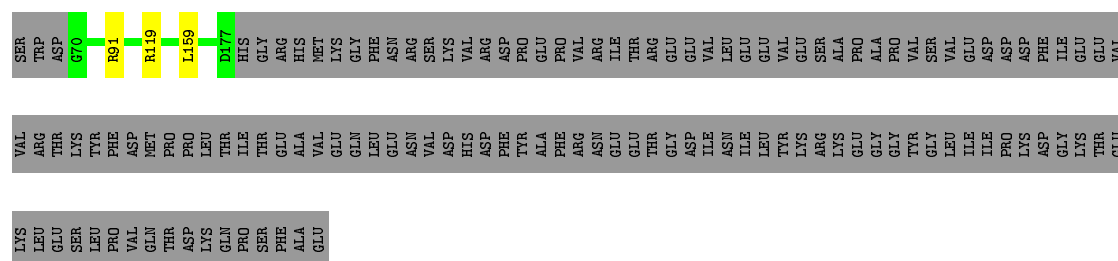
- Molecule 50: protein S21

Chain u:  31% .. 68%



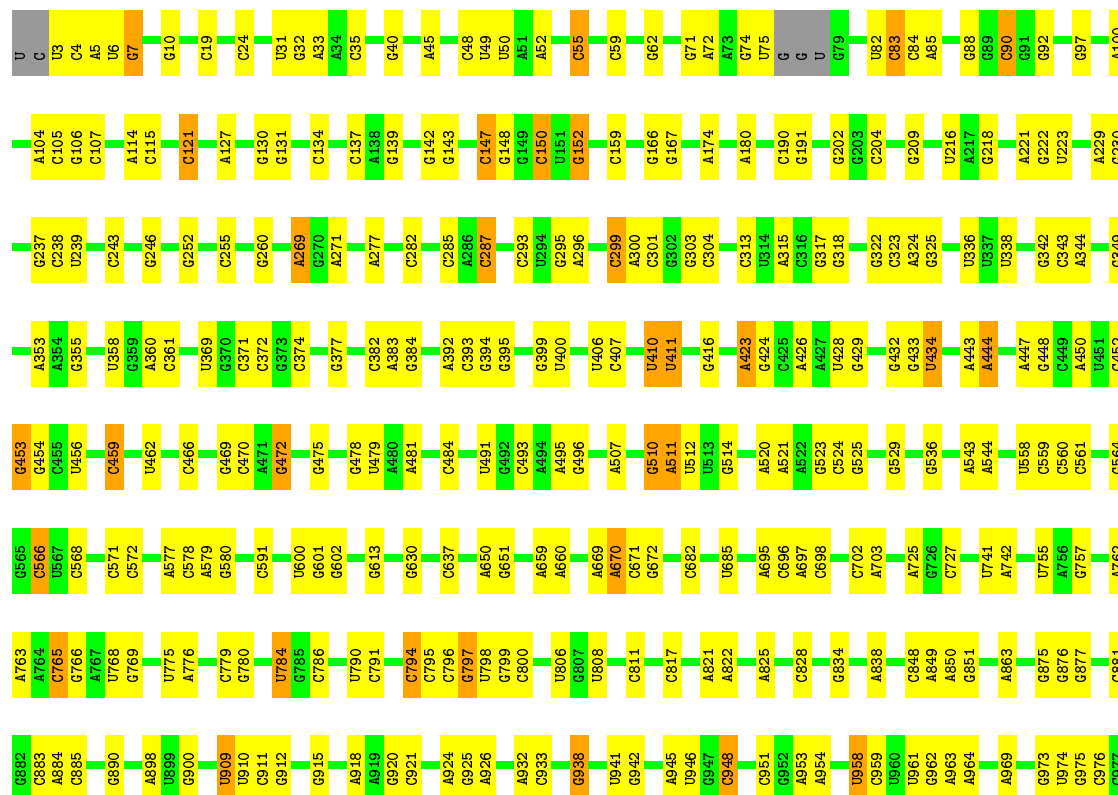
- Molecule 51: protein plastid pY

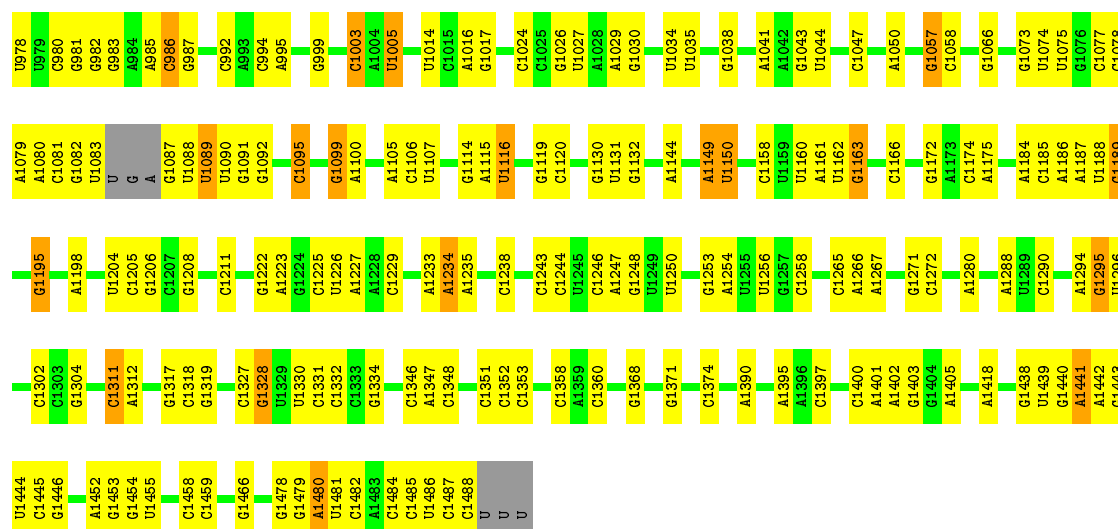
Chain y:  44% 54%



- Molecule 52: 16S rRNA

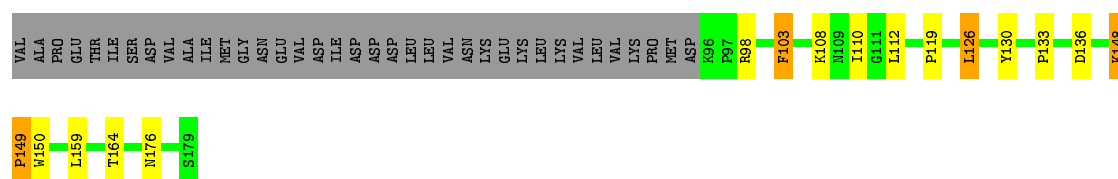
Chain a: 67% 29% .





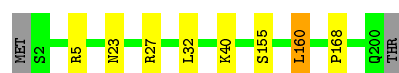
• Molecule 53: protein cS23

Chain w: 56% 10% 31%



• Molecule 54: 30S ribosomal protein S4, chloroplastic

Chain d: 95%



• Molecule 55: protein cS22

Chain v: 81% 12%



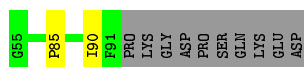
• Molecule 56: 30S ribosomal protein S14, chloroplastic

Chain n: 99%



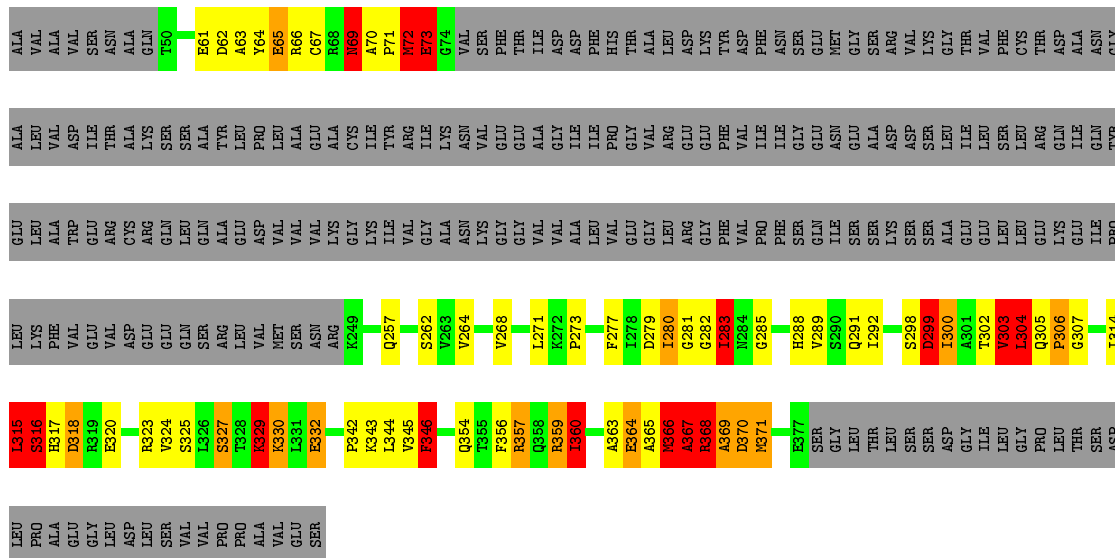
• Molecule 57: protein bTHXc

Chain x: 74% 21%



- Molecule 58: 30S ribosomal protein S1, chloroplastic

Chain 8:  23% 11% • • 58%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	81305	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3700	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	1	0.27	0/387	0.51	0/513
10	D	0.31	0/1646	0.65	0/2201
11	E	0.30	0/1687	0.65	1/2271 (0.0%)
12	F	0.28	0/1372	0.61	0/1848
13	G	0.26	0/1374	0.55	1/1849 (0.1%)
14	H	0.26	0/427	0.59	0/568
15	K	0.28	0/1608	0.57	2/2174 (0.1%)
16	L	0.31	0/951	0.59	0/1282
17	M	0.28	0/1361	0.53	0/1806
18	N	0.31	0/1089	0.61	0/1461
19	O	0.28	0/959	0.61	0/1280
2	2	0.32	0/422	0.75	1/564 (0.2%)
20	P	0.26	0/963	0.55	1/1293 (0.1%)
21	Q	0.31	0/967	0.71	2/1300 (0.2%)
22	R	0.33	0/1013	0.61	0/1351
23	S	0.31	0/1199	0.61	0/1633
24	T	0.29	0/1168	0.60	1/1566 (0.1%)
25	U	0.27	0/749	0.58	0/1006
26	V	0.27	0/1006	0.64	1/1343 (0.1%)
27	W	0.35	0/2449	1.07	10/3817 (0.3%)
28	X	0.30	0/825	0.57	0/1099
29	Y	0.28	0/615	0.65	2/819 (0.2%)
3	3	0.27	0/447	0.66	1/588 (0.2%)
30	Z	0.27	0/762	0.57	0/1012
31	A	0.35	1/67572 (0.0%)	1.05	315/105421 (0.3%)
32	0	0.29	0/533	0.66	1/718 (0.1%)
33	b	0.75	8/1819 (0.4%)	0.96	8/2458 (0.3%)
34	c	0.48	0/1746	0.72	1/2348 (0.0%)
35	e	0.61	0/1307	0.77	2/1754 (0.1%)
36	f	0.44	0/904	0.69	0/1225
37	g	0.36	0/1175	0.62	0/1574
38	h	0.88	5/1103 (0.5%)	1.69	6/1477 (0.4%)
39	i	0.43	0/1038	0.70	0/1397
4	4	0.31	0/569	0.66	1/752 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	j	0.51	0/813	0.70	1/1099 (0.1%)
41	k	0.40	0/901	0.63	0/1214
42	l	0.62	0/983	0.80	4/1323 (0.3%)
43	m	0.45	0/909	0.75	2/1209 (0.2%)
44	o	0.42	0/532	0.65	0/707
45	p	0.52	0/674	0.71	0/902
46	q	0.50	0/647	0.64	0/867
47	r	0.49	0/522	0.76	2/697 (0.3%)
48	s	0.44	0/642	0.70	0/866
49	t	0.46	0/842	0.68	0/1127
5	5	0.30	0/306	0.67	0/403
50	u	1.10	3/396 (0.8%)	0.94	3/518 (0.6%)
51	y	0.45	0/852	0.70	0/1139
52	a	1.13	32/35582 (0.1%)	1.39	473/55510 (0.9%)
53	w	0.80	2/709 (0.3%)	1.23	11/965 (1.1%)
54	d	0.40	0/1661	0.72	2/2230 (0.1%)
55	v	1.49	16/1481 (1.1%)	1.24	13/1991 (0.7%)
56	n	0.37	0/835	0.62	0/1116
57	x	0.55	0/296	0.74	1/390 (0.3%)
58	8	0.87	5/1216 (0.4%)	1.61	28/1631 (1.7%)
6	6	0.25	0/425	0.46	0/551
7	7	0.28	0/382	0.54	0/520
8	B	0.31	0/2796	1.05	12/4357 (0.3%)
9	C	0.29	0/1938	0.64	0/2603
All	All	0.65	72/159552 (0.0%)	1.08	909/237703 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	M	0	1
21	Q	0	1
23	S	0	1
32	0	0	1
33	b	0	2
34	c	0	3
35	e	0	1
36	f	0	1
37	g	0	1
39	i	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	j	0	1
42	l	0	3
43	m	0	2
50	u	0	1
53	w	0	7
54	d	0	2
55	v	0	15
58	8	0	17
All	All	0	62

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	142	PHE	CE1-CZ	-18.97	1.01	1.37
55	v	142	PHE	CE2-CZ	-17.85	1.03	1.37
55	v	142	PHE	CG-CD2	-15.89	1.15	1.38
38	h	67	ARG	CZ-NH2	-15.34	1.13	1.33
55	v	165	PHE	CE2-CZ	-14.94	1.08	1.37

The worst 5 of 909 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	h	67	ARG	NE-CZ-NH1	50.54	145.57	120.30
33	b	201	ASP	CB-CG-OD2	20.66	136.90	118.30
52	a	1440	G	N3-C2-N2	-20.49	105.56	119.90
52	a	7	G	C2-N3-C4	20.20	122.00	111.90
52	a	1441	A	N1-C2-N3	20.05	139.32	129.30

There are no chirality outliers.

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	0	73	TRP	Peptide
17	M	143	LEU	Peptide
21	Q	190	VAL	Peptide
23	S	174	THR	Peptide
33	b	168	VAL	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	378	0	415	7	0
2	2	415	0	434	7	0
3	3	445	0	501	12	0
4	4	563	0	623	9	0
5	5	304	0	345	7	0
6	6	422	0	508	8	0
7	7	368	0	386	7	0
8	B	2500	0	1263	15	0
9	C	1904	0	1985	42	0
10	D	1620	0	1699	34	0
11	E	1655	0	1725	41	0
12	F	1351	0	1407	29	0
13	G	1353	0	1416	18	0
14	H	423	0	490	8	0
15	K	1568	0	1595	24	0
16	L	942	0	995	17	0
17	M	1342	0	1417	24	0
18	N	1067	0	1122	31	0
19	O	944	0	1004	28	0
20	P	947	0	966	29	0
21	Q	953	0	1042	37	0
22	R	996	0	1062	35	0
23	S	1171	0	1216	23	0
24	T	1149	0	1220	22	0
25	U	740	0	795	14	0
26	V	993	0	1055	25	0
27	W	2187	0	1102	18	0
28	X	810	0	847	13	0
29	Y	605	0	652	17	0
30	Z	754	0	808	13	0
31	A	60324	0	30373	516	0
32	0	521	0	498	14	0
33	b	1787	0	1828	0	0
34	c	1719	0	1807	0	0
35	e	1292	0	1355	0	0
36	f	886	0	888	0	0
37	g	1161	0	1237	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	h	1088	0	1149	0	0
39	i	1020	0	1072	0	0
40	j	796	0	841	0	0
41	k	887	0	933	0	0
42	l	967	0	1046	0	0
43	m	898	0	949	0	0
44	o	525	0	572	0	0
45	p	664	0	703	0	0
46	q	635	0	667	0	0
47	r	518	0	544	0	0
48	s	627	0	653	0	0
49	t	832	0	883	0	0
50	u	393	0	406	0	0
51	y	845	0	892	0	0
52	a	31777	0	16003	0	0
53	w	689	0	706	0	0
54	d	1633	0	1727	0	0
55	v	1464	0	1456	0	0
56	n	819	0	858	0	0
57	x	289	0	301	0	0
58	8	1201	0	1220	46	0
All	All	147126	0	101662	970	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 9.

The worst 5 of 970 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)
31:A:1466:G:C8	31:A:1934:C:OP1	108.10	1.24
21:Q:160:ARG:HH12	31:A:317:G:H1'	136.27	1.14
21:Q:160:ARG:HH22	31:A:317:G:C1'	136.78	1.10
21:Q:160:ARG:NH1	31:A:317:G:H1'	136.21	1.10
17:M:122:GLY:O	31:A:897:A:O2'	108.58	1.07

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	1	44/56 (79%)	40 (91%)	4 (9%)	0	100	100
2	2	49/65 (75%)	39 (80%)	10 (20%)	0	100	100
3	3	55/61 (90%)	49 (89%)	6 (11%)	0	100	100
4	4	67/73 (92%)	59 (88%)	8 (12%)	0	100	100
5	5	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
6	6	47/142 (33%)	46 (98%)	1 (2%)	0	100	100
7	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
9	C	245/271 (90%)	213 (87%)	32 (13%)	0	100	100
10	D	210/221 (95%)	188 (90%)	22 (10%)	0	100	100
11	E	208/243 (86%)	180 (86%)	28 (14%)	0	100	100
12	F	173/220 (79%)	161 (93%)	12 (7%)	0	100	100
13	G	171/182 (94%)	161 (94%)	10 (6%)	0	100	100
14	H	51/155 (33%)	47 (92%)	4 (8%)	0	100	100
15	K	191/197 (97%)	178 (93%)	13 (7%)	0	100	100
16	L	119/121 (98%)	104 (87%)	15 (13%)	0	100	100
17	M	175/192 (91%)	163 (93%)	11 (6%)	1 (1%)	28	68
18	N	132/135 (98%)	111 (84%)	21 (16%)	0	100	100
19	O	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
20	P	118/123 (96%)	116 (98%)	2 (2%)	0	100	100
21	Q	116/156 (74%)	100 (86%)	16 (14%)	0	100	100
22	R	113/127 (89%)	105 (93%)	8 (7%)	0	100	100
23	S	145/201 (72%)	118 (81%)	27 (19%)	0	100	100
24	T	142/199 (71%)	125 (88%)	17 (12%)	0	100	100
25	U	90/122 (74%)	86 (96%)	4 (4%)	0	100	100
26	V	122/145 (84%)	109 (89%)	13 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	X	98/137 (72%)	87 (89%)	11 (11%)	0	100	100
29	Y	72/77 (94%)	66 (92%)	6 (8%)	0	100	100
30	Z	88/109 (81%)	87 (99%)	1 (1%)	0	100	100
32	0	62/94 (66%)	54 (87%)	6 (10%)	2 (3%)	5	34
33	b	225/236 (95%)	195 (87%)	29 (13%)	1 (0%)	38	75
34	c	211/218 (97%)	181 (86%)	28 (13%)	2 (1%)	20	61
35	e	169/253 (67%)	150 (89%)	17 (10%)	2 (1%)	15	54
36	f	109/146 (75%)	85 (78%)	24 (22%)	0	100	100
37	g	147/155 (95%)	130 (88%)	16 (11%)	1 (1%)	25	65
38	h	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
39	i	131/157 (83%)	107 (82%)	23 (18%)	1 (1%)	22	62
40	j	96/122 (79%)	83 (86%)	13 (14%)	0	100	100
41	k	116/138 (84%)	104 (90%)	12 (10%)	0	100	100
42	l	121/123 (98%)	100 (83%)	21 (17%)	0	100	100
43	m	108/126 (86%)	90 (83%)	18 (17%)	0	100	100
44	o	60/90 (67%)	59 (98%)	1 (2%)	0	100	100
45	p	78/88 (89%)	61 (78%)	17 (22%)	0	100	100
46	q	76/108 (70%)	64 (84%)	12 (16%)	0	100	100
47	r	62/101 (61%)	58 (94%)	4 (6%)	0	100	100
48	s	76/92 (83%)	61 (80%)	15 (20%)	0	100	100
49	t	103/108 (95%)	93 (90%)	10 (10%)	0	100	100
50	u	42/137 (31%)	39 (93%)	3 (7%)	0	100	100
51	y	106/236 (45%)	96 (91%)	10 (9%)	0	100	100
53	w	82/121 (68%)	79 (96%)	0	3 (4%)	4	30
54	d	197/201 (98%)	173 (88%)	22 (11%)	2 (1%)	18	59
55	v	188/198 (95%)	171 (91%)	14 (7%)	3 (2%)	11	48
56	n	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
57	x	35/47 (74%)	30 (86%)	4 (11%)	1 (3%)	5	36
58	8	150/370 (40%)	116 (77%)	18 (12%)	16 (11%)	0	6
All	All	6213/7898 (79%)	5499 (88%)	679 (11%)	35 (1%)	33	68

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	0	72	VAL
35	e	148	ILE
53	w	149	PRO
55	v	105	MET
58	8	72	MET

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	1	39/49 (80%)	39 (100%)	0	100	100
2	2	48/59 (81%)	46 (96%)	2 (4%)	34	70
3	3	47/50 (94%)	47 (100%)	0	100	100
4	4	59/62 (95%)	58 (98%)	1 (2%)	66	86
5	5	34/34 (100%)	34 (100%)	0	100	100
6	6	46/124 (37%)	46 (100%)	0	100	100
7	7	40/96 (42%)	40 (100%)	0	100	100
9	C	195/216 (90%)	194 (100%)	1 (0%)	91	96
10	D	174/182 (96%)	174 (100%)	0	100	100
11	E	176/205 (86%)	173 (98%)	3 (2%)	66	86
12	F	148/183 (81%)	148 (100%)	0	100	100
13	G	147/154 (96%)	147 (100%)	0	100	100
14	H	47/134 (35%)	47 (100%)	0	100	100
15	K	167/171 (98%)	165 (99%)	2 (1%)	75	89
16	L	101/101 (100%)	101 (100%)	0	100	100
17	M	135/144 (94%)	133 (98%)	2 (2%)	70	87
18	N	107/108 (99%)	107 (100%)	0	100	100
19	O	96/96 (100%)	96 (100%)	0	100	100
20	P	99/100 (99%)	99 (100%)	0	100	100
21	Q	104/135 (77%)	103 (99%)	1 (1%)	80	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	R	102/114 (90%)	102 (100%)	0	100	100
23	S	129/174 (74%)	129 (100%)	0	100	100
24	T	126/176 (72%)	126 (100%)	0	100	100
25	U	81/103 (79%)	80 (99%)	1 (1%)	75	89
26	V	112/129 (87%)	111 (99%)	1 (1%)	82	92
28	X	85/111 (77%)	84 (99%)	1 (1%)	75	89
29	Y	64/67 (96%)	63 (98%)	1 (2%)	68	86
30	Z	83/97 (86%)	82 (99%)	1 (1%)	75	89
32	0	56/83 (68%)	55 (98%)	1 (2%)	64	85
33	b	192/201 (96%)	188 (98%)	4 (2%)	59	83
34	c	185/188 (98%)	185 (100%)	0	100	100
35	e	132/203 (65%)	128 (97%)	4 (3%)	46	78
36	f	98/125 (78%)	98 (100%)	0	100	100
37	g	120/126 (95%)	120 (100%)	0	100	100
38	h	117/117 (100%)	115 (98%)	2 (2%)	66	86
39	i	103/123 (84%)	102 (99%)	1 (1%)	80	91
40	j	90/110 (82%)	90 (100%)	0	100	100
41	k	92/109 (84%)	92 (100%)	0	100	100
42	l	106/106 (100%)	106 (100%)	0	100	100
43	m	97/109 (89%)	97 (100%)	0	100	100
44	o	58/85 (68%)	58 (100%)	0	100	100
45	p	71/79 (90%)	70 (99%)	1 (1%)	71	88
46	q	70/95 (74%)	70 (100%)	0	100	100
47	r	56/96 (58%)	56 (100%)	0	100	100
48	s	67/81 (83%)	67 (100%)	0	100	100
49	t	86/89 (97%)	84 (98%)	2 (2%)	56	82
50	u	40/118 (34%)	40 (100%)	0	100	100
51	y	97/213 (46%)	94 (97%)	3 (3%)	45	77
53	w	75/109 (69%)	74 (99%)	1 (1%)	73	89
54	d	178/180 (99%)	175 (98%)	3 (2%)	66	86
55	v	160/168 (95%)	158 (99%)	2 (1%)	73	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	n	89/90 (99%)	89 (100%)	0	100	100
57	x	28/37 (76%)	28 (100%)	0	100	100
58	8	129/310 (42%)	125 (97%)	4 (3%)	45	77
All	All	5383/6724 (80%)	5338 (99%)	45 (1%)	86	93

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	b	94	HIS
35	e	305	GLU
58	8	283	ILE
35	e	144	LYS
38	h	67	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
24	T	106	ASN
38	h	19	ASN
55	v	96	ASN
26	V	130	HIS
34	c	187	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	W	101/106 (95%)	30 (29%)	4 (3%)
31	A	2808/2810 (99%)	596 (21%)	4 (0%)
52	a	1477/1491 (99%)	310 (20%)	0
8	B	116/121 (95%)	21 (18%)	1 (0%)
All	All	4502/4528 (99%)	957 (21%)	9 (0%)

5 of 957 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	B	4	U
8	B	10	G
8	B	14	U
8	B	15	A

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Mol	Chain	Res	Type
8	B	16	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	W	97	A
31	A	556	C
31	A	97	A
27	W	32	C
31	A	5	A

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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.