



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Feb 21, 2017 – 11:29 AM EST

PDB ID : 5MMM
EMDB ID: : EMD-3533
Title : Structure of the 70S chloroplast ribosome
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.
Deposited on : 2016-12-11
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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

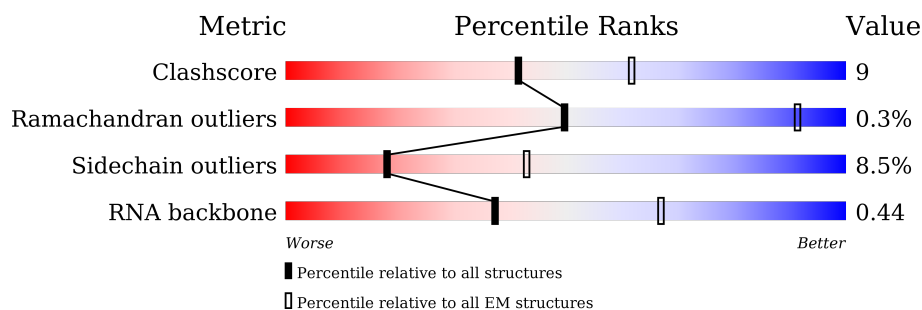
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.








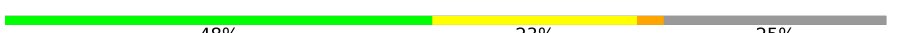



















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	0	130	25% 23% . 49%
2	1	57	58% 23% . 16%
3	2	66	68% 20% . 9%
4	3	152	26% 13% . 61%
5	4	159	30% 13% . 55%
6	5	37	59% 35% 5%
7	6	142	27% 6% . 65%
8	7	116	26% 12% . 60%

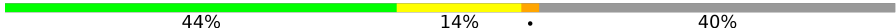

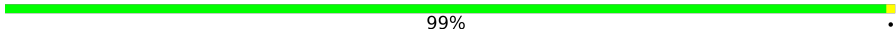


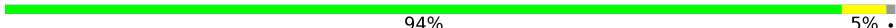



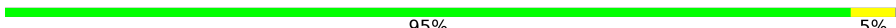


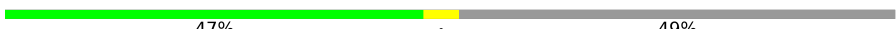












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Mol	Chain	Length	Quality of chain
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	
29	U	198	
30	V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

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Mol	Chain	Length	Quality of chain
34	Z	168	
35	z	76	
36	8	174	
37	a	1491	
38	b	236	
39	c	218	
40	d	201	
41	e	308	
42	f	211	
43	g	155	
44	h	134	
45	i	208	
46	j	195	
47	k	138	
48	l	123	
49	m	172	
50	n	100	
51	o	90	
52	p	88	
53	q	165	
54	r	101	
55	s	92	
56	t	183	
57	u	180	
58	v	260	

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Mol	Chain	Length	Quality of chain
59	w	179	<div><div></div><div>46%</div><div>54%</div></div>
60	x	101	<div><div></div><div>40%</div><div>60%</div></div>
61	y	302	<div><div></div><div>37%</div><div>62%</div></div>

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 152465 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	66	Total	C	N	O	S	0	0
			536	338	94	102	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 23 is a protein called plastid ribosomal protein uL14c.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 35 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 36 is a protein called plastid ribosomal protein bS1c.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	8	174	Total	C	N	O		0	0
			870	522	174	174			

- Molecule 37 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	1484	Total	C	N	O	P	0	0
			31868	14208	5881	10295	1484		

- Molecule 38 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	233	Total	C	N	O	S	0	0
			1844	1163	339	329	13		

- Molecule 39 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	216	Total	C	N	O	S	0	0
			1736	1108	313	309	6		

- Molecule 40 is a protein called 30S ribosomal protein S4, chloroplastic.

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

- Molecule 41 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	187	Total	C	N	O	S	0	0
			1331	826	259	240	6		

- Molecule 42 is a protein called plastid ribosomal protein bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	113	Total	C	N	O	S	0	0
			911	583	152	172	4		

- Molecule 43 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	154	Total	C	N	O	S	0	0
			1210	753	244	210	3		

- Molecule 44 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	133	Total	C	N	O	S	0	0
			1079	679	210	185	5		

- Molecule 45 is a protein called plastid ribosomal protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	144	Total	C	N	O	S	0	0
			1119	712	211	195	1		

- Molecule 46 is a protein called plastid ribosomal protein uS10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	99	Total	C	N	O	S	0	0
			805	517	144	139	5		

- Molecule 47 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	117	Total	C	N	O	S	0	0
			882	546	181	150	5		

- Molecule 48 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	l	122	Total	C	N	O	S	0	0
			959	599	197	161	2		

- Molecule 49 is a protein called plastid ribosomal protein uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	m	110	Total	C	N	O	S	0	0
			904	556	182	161	5		

- Molecule 50 is a protein called 30S ribosomal protein S14, chloroplastic.

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

- Molecule 51 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	o	75	Total	C	N	O	S	0	0
			635	404	123	107	1		

- Molecule 52 is a protein called 30S ribosomal protein S16, chloroplastic.

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

- Molecule 53 is a protein called plastid ribosomal protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	q	86	Total	C	N	O	S	0	0
			693	434	136	119	4		

- Molecule 54 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	60	Total	C	N	O	S	0	0
			490	308	96	85	1		

- Molecule 55 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	s	78	Total	C	N	O	S	0	0
			631	406	119	104	2		

- Molecule 56 is a protein called plastid ribosomal protein bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	t	107	Total	C	N	O	S	0	0
			853	528	173	151	1		

- Molecule 57 is a protein called plastid ribosomal protein bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	65	Total	C	N	O	S	0	0
			568	339	127	100	2		

- Molecule 58 is a protein called 30S ribosomal protein 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	v	80	Total	C	N	O	S	0	0
			613	388	104	121			

- Molecule 59 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	w	82	Total	C	N	O	S	0	0
			686	454	113	116	3		

- Molecule 60 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	x	40	Total	C	N	O	S	0	0
			309	192	69	48			

- Molecule 61 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	y	116	Total	C	N	O	S	0	0
			919	567	181	169	2		

- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	2	1	Total	Zn	0
			1	1	
62	5	1	Total	Zn	0
			1	1	

- Molecule 63 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
63	P	1	Total Mg 1 1	0
63	B	15	Total Mg 15 15	0
63	6	1	Total Mg 1 1	0
63	W	14	Total Mg 14 14	0
63	S	1	Total Mg 1 1	0
63	k	1	Total Mg 1 1	0
63	E	1	Total Mg 1 1	0
63	V	1	Total Mg 1 1	0
63	A	511	Total Mg 511 511	0
63	n	1	Total Mg 1 1	0
63	x	1	Total Mg 1 1	0
63	R	1	Total Mg 1 1	0
63	M	2	Total Mg 2 2	0
63	D	1	Total Mg 1 1	0
63	a	219	Total Mg 219 219	0
63	4	1	Total Mg 1 1	0
63	U	1	Total Mg 1 1	0
63	H	1	Total Mg 1 1	0
63	C	1	Total Mg 1 1	0
63	7	1	Total Mg 1 1	0
63	T	1	Total Mg 1 1	0
63	l	1	Total Mg 1 1	0

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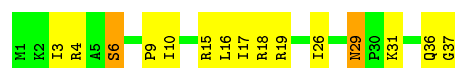
Mol	Chain	Residues	Atoms		AltConf
63	F	1	Total	Mg	0
			1	1	

- Molecule 1: 50S ribosomal protein L31



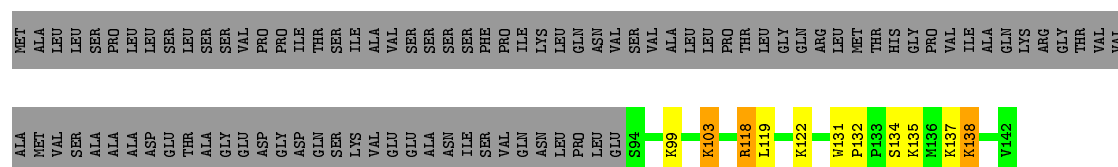
- Molecule 6: 50S ribosomal protein L36, chloroplastic

Chain 5:  59% 35% 5%



- Molecule 7: plastid ribosomal protein cL37, PSRP5

Chain 6: 27% 6% 65%



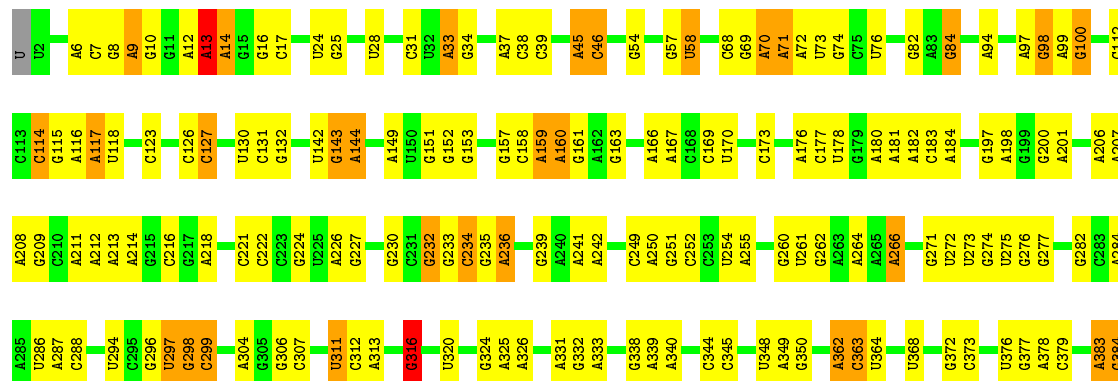
- Molecule 8: 50S ribosomal protein 6, chloroplastic

Chain 7:  26% 12% 60%

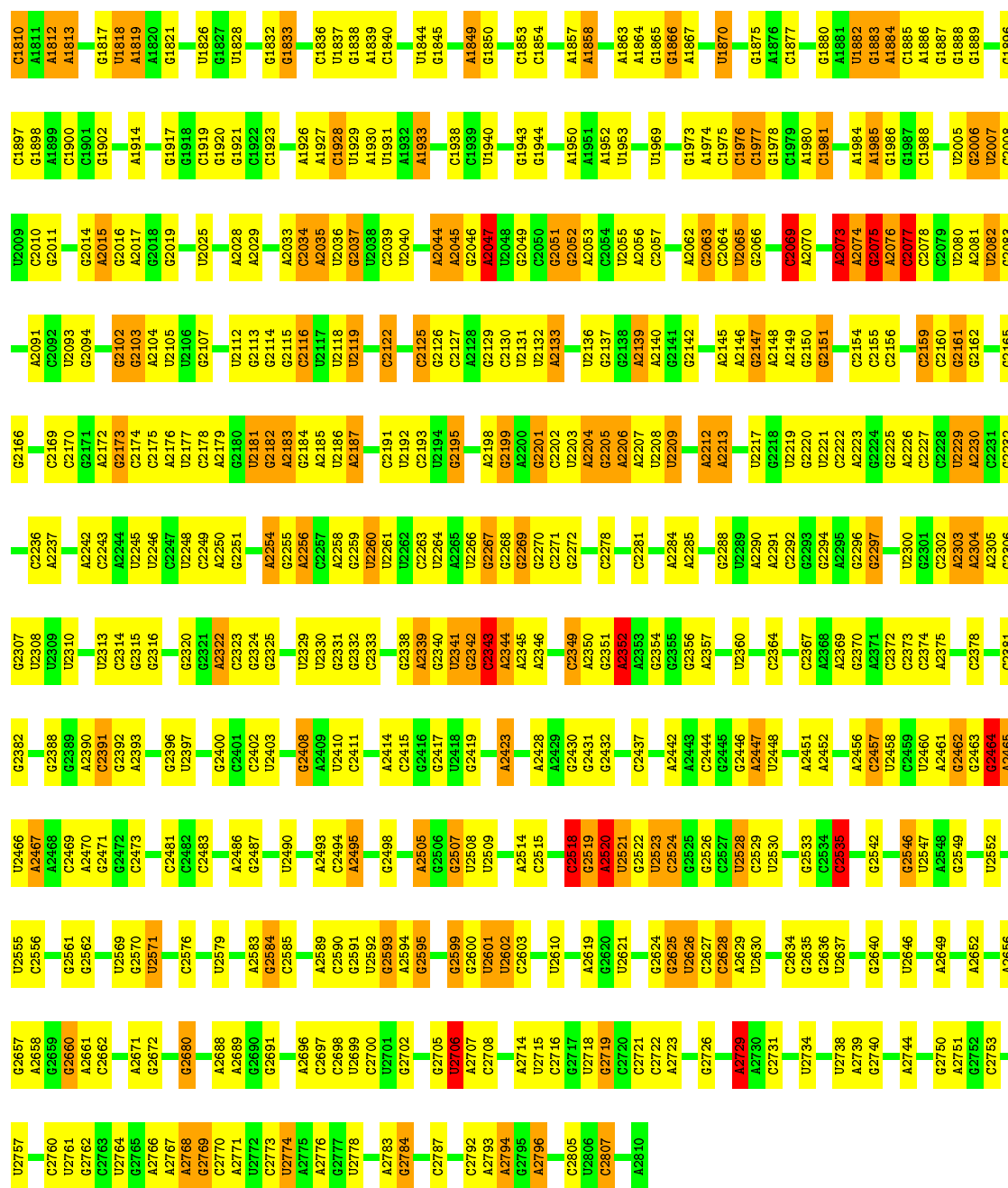


- Molecule 9: 23S ribosomal RNA

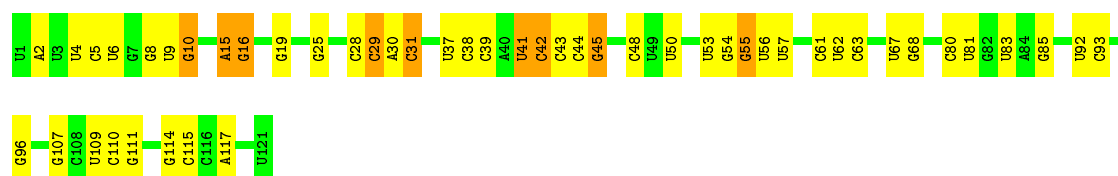
Chain A:  52% 37% 10%




A1688	C1689	A1582	G1491	A1416	U1219	U1133	A1060	G966	G885	U801	U720	A639	A555	G484	G394
C1690	A1492	A1417	A1492	U1417	U1220	G1134	G1061	C967	U886	C802	U721	G640	C556	G485	G395
A1691	C1493	U1418	G1493	U1418	C1221	A1135	U1062	G970	G887	G803	G722	G641	C557	G486	G396
C1692	A1494	C1420	A1322	G1322	U1226	U1136	U1063	U971	C888	A804	G723	G642	A558	U487	G398
U1693	A1497	U1423	U1327	U1327	G1231	G1138	G1065	G974	G889	A805	G724	A643	G559	G488	U404
C1694	G1498	A1424	U1432	U1432	G1239	A1139	G1070	G975	G890	A809	A727	A644	A560	A490	U405
U1695	G1498	C1425	U1436	U1436	G1241	G1140	G1071	C976	G894	G810	A728	A645	A561	A491	C406
A1700	A1501	A1426	U1332	A1332	A1234	C1141	C1072	G978	G894	A811	A729	G646	U564	A492	C407
C1701	A1502	U1431	U1333	U1333	A1235	G1142	A1072	G980	C895	G812	C730	G648	G565	G408	U409
G1702	G1507	U1432	C1335	C1335	G1239	U1143	G1073	G981	G	G813	U731	G650	A494	G409	G410
G1703	U1511	U1433	C1336	C1336	G1240	U1144	G1074	G982	G	U814	A732	G651	U571	G410	G411
A1704	U1512	U1434	U1337	U1337	U1241	U1147	G1075	G983	A	G815	A733	U651	U572	U411	
A1705	C1512	G1435	C1338	C1338	U1245	U1153	A1078	G984	G	G816	G734	C852	G573	U802	
C1710	C1513	U1436	A1342	A1342	U1246	G1154	A1082	G989	C901	U818	G737	A656	U576	C503	U415
A1711	U1518	U1437	C1348	C1348	G1248	A1155	G1083	G993	G902	G819	A739	U657	G577	G504	U416
A1712	A1519	U1438	U1353	U1353	G1253	U1158	G1084	C996	A905	G820	U741	A658	U578	G505	A417
A1713	A1520	U1439	U1357	U1357	U1254	G1159	A1085	C996	C906	C823	A745	A663	A581	G511	A421
A1715	G1522	A1444	A1357	A1357	U1255	U1160	G1086	G1000	A908	U824	A745	U665	A582	A512	G422
U1620	A1523	G1445	G1358	G1358	G1256	A1161	U1087	G1001	A909	C825	G749	U666	A583	A513	G423
C1621	G1524	G1446	C1359	C1359	G1257	G1162	U1088	A1001	A910	C826	G749	G667	A585	A514	A424
G1731	G1525	G1447	G1359	G1359	G1258	G1163	U1090	G1002	U911	C827	A750	U668	U	C425	
A1734	G1526	A1448	U1363	U1363	C1259	G1166	G1091	A1003		A830	C751	C669	A588	C426	
C1746	G1527	G1449	G1364	G1364	G1260	C1167	C1092	A1007	G915	A670	U752	A670	G589	C427	
G1750	U1528	U1450	U1365	U1365	A1261	C1167	C1093	A1008	G916	C671	U752	C671	C590	A428	
A	A1529	G1451	C1366	C1366	G1264	G1169	G1096	A1009	C917	U837	A754	C674	C591	C429	
C	U1530	A1452	U1367	U1367	U1269	A1170	A1097	C1010	A918	G839	U757	U675	G592	G523	A434
A	A1531	G1453	C1371	C1371	C1270	G1173	A1098	A1011	A919	A840	U758	U676	A596	A524	A435
C1634	G1532	U1454	A1374	A1374	A1272	G1178	C1100	G1017	C921	C843	U759	A677	C597	A526	G436
C1635	A1533	G1456	A1375	A1375	A1273	G1178	C1101	G1018	U922	C844	A761	U678	G597	C527	
U1636	U1534	G1457	C1375	C1375	G1274	G1178	G1102	U1019	U924	C845	A761	G680	C605	C528	G448
A1535	A1535	C1458	U1378	U1378	A1274	G1184	A1105	C1020	U925	A846	A767	A681	A606	G529	G452
G1642	G1536	U1458	C1379	C1379	A1275	G1189	A1106	C1023	A926		G768	C684	C609	U530	U453
A1644	U1544	A1465	A1380	A1380	U1276	G1190	C1105	A1024	A927	G850	G771	C688	G610	A531	G454
G1761	G1545	C1466	U1381	U1381	G1277	G1191	U1109	A1028	U931	U851	G771	U612	G611	C457	
G1763	U1546	C1467	G1385	G1385	A1289	G1192	U1110	A1029	U937	U852	A772	G695	U613	G536	C458
A1764	C1546	G1468	A1386	A1386	C1231	G1193	G1111	A1038	G938	G853	G773	A696	G614	C537	
G1685	U1550	U1469	A1394	A1394	G1282	U1195	A1113	A1039	A939	U856	A775	U697	G615	C538	G462
U1661	G1557	G1472	C1397	C1397	C1283	U1196	A1114	A1038	C940	G857	G776	C702	G621	A540	A466
U1661	A1559	U1474	A1398	A1398	A1294	A1197	G1115	A1039	U948	G858	G776	U701	G622	G541	A467
A1666	C1560	G1476	A1399	A1399	A1295	A1198	A1116	U1040	C941	C702	G782	U705	A623	C542	U468
G1670	U1563	G1477	U1400	U1400	A1296	A1199	G1117	G1041	C944	G866	A785	U705	G623	A543	U469
U1788	G1563	A1480	G1401	G1401	U1299	A1202	U1118	G1045	A945	G869	G786	U705	G623	G544	G470
U1789	G1566	G1483	U1402	U1402	U1300	C1206	G1119	G1045	A946	G869	G787	G711	G629	U545	G471
C1791	C1567	U1484	G1301	G1301	G1301	U1207	C1120	G1050	U948	C874	G788	G712	G630	G546	U471
A1801	U1568	A1405	A1405	A1405	A1307	G1207	U1121	U1051	C949	C875	G791	A713	G631	G547	A472
G1683	A1569	U1485	A1406	A1406	A1308	G1208	U1122	G1052	A949	G875	A792	U714	G632	A549	C473
C1684	C1570	U1486	A1407	A1407	U1309	G1209	A1123	A1053	G951	G879	A793	G715	A633	G550	C474
G1571	G1571	C1487	A1408	A1408	U1210	A1210	U1124	U1054	A952	U880	A794	A716	G634	G551	G480
C1685	G1572	A1488	G1409	G1409	C1310	G1211	U1125	A1055	G953	U881	U795	A717	G635	G552	G481
A1686	C1573	A1489	U1415	U1415	C1311	G1218	A1131	A1056	G954	U882	G796	G718	G636	G553	A482
G1687	G1574	G1490					C1132					C719		G554	A483



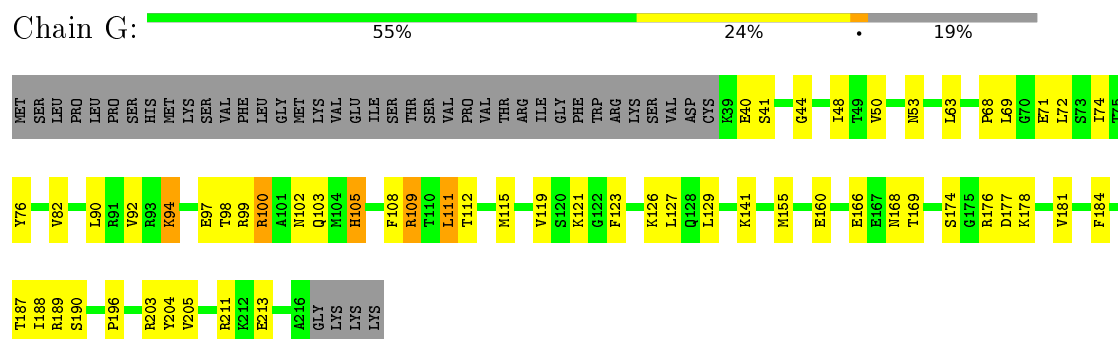
- Molecule 10: 5S ribosomal RNA



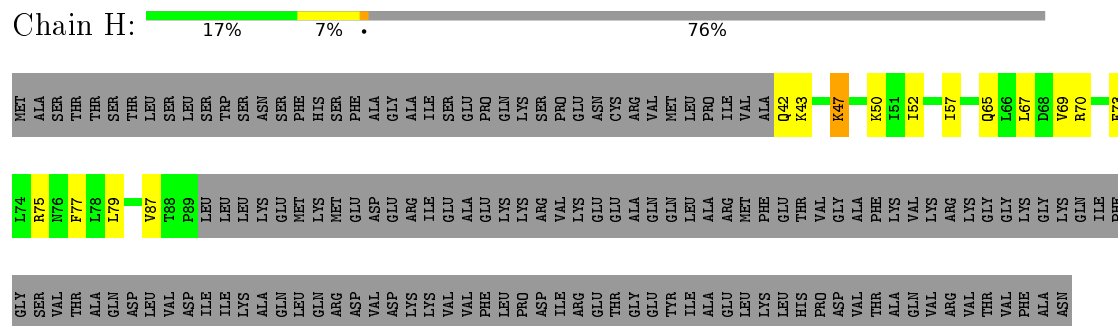
- Molecule 11: 50S ribosomal protein L2, chloroplastic

Chain F: 

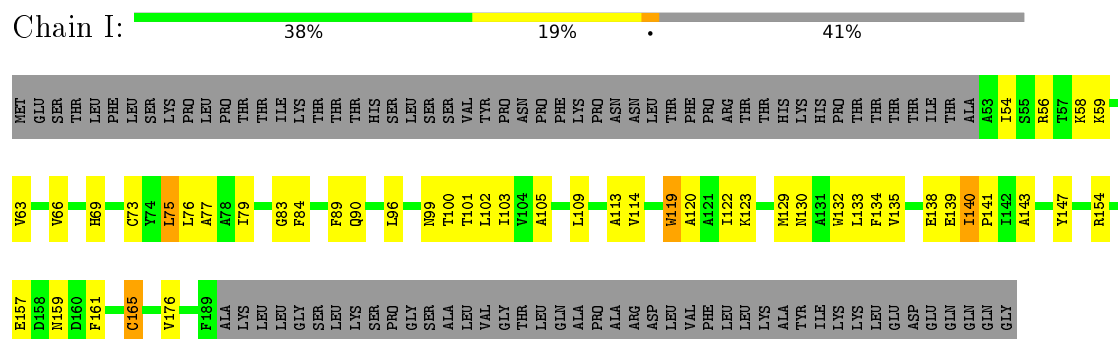
- Molecule 15: plastid ribosomal protein uL6c



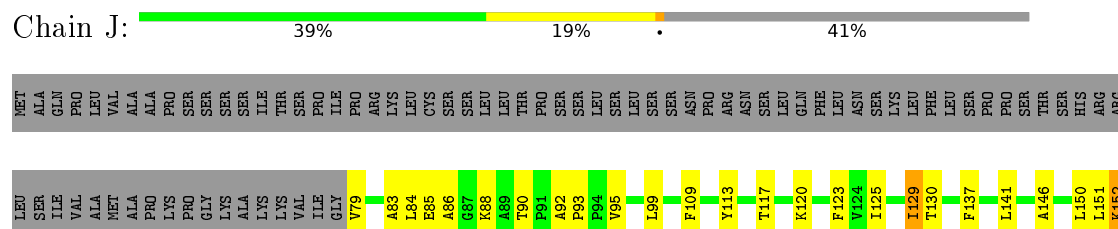
- Molecule 16: plastid ribosomal protein bL9c



- Molecule 17: plastid ribosomal protein uL10c



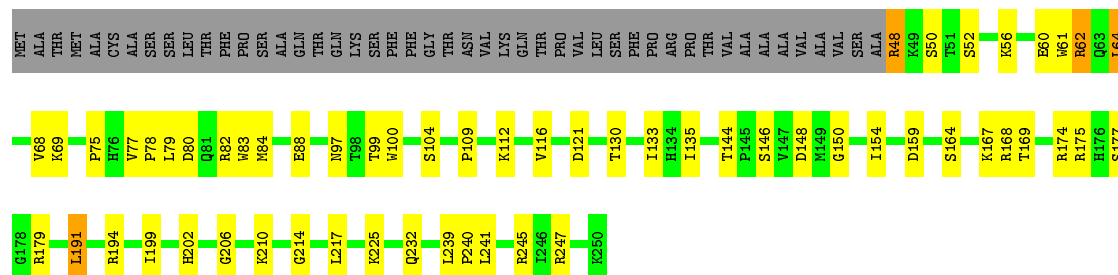
- Molecule 18: 50S ribosomal protein L11, chloroplastic





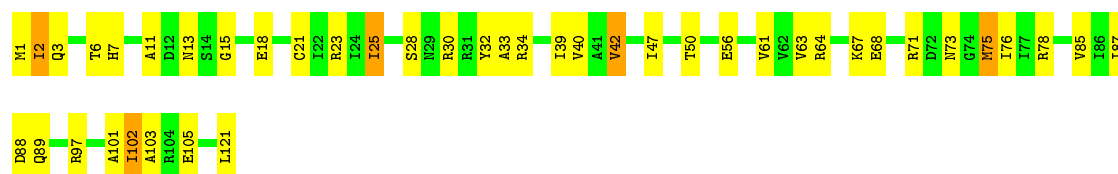
- Molecule 19: 50S ribosomal protein L13, chloroplastic

Chain K: 58% 22% 19%



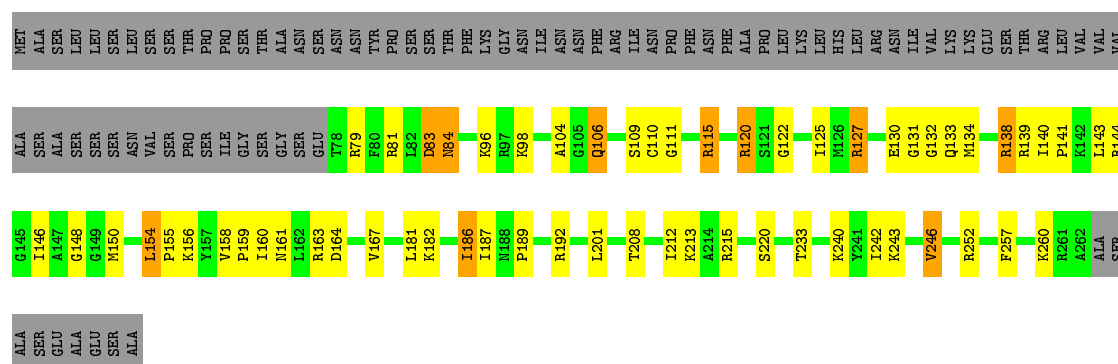
- Molecule 20: 50S ribosomal protein L14, chloroplastic

Chain L: 64% 31% 5%



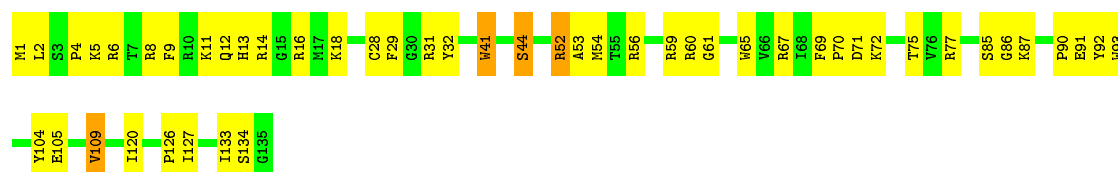
- Molecule 21: plastid ribosomal protein uL15c


Chain M: 46% 18% 32%

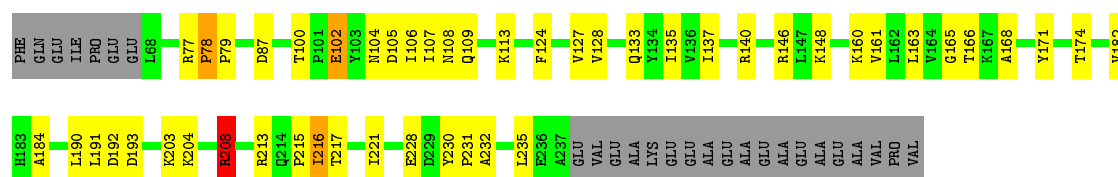


- Molecule 22: 50S ribosomal protein L16, chloroplastic

Chain N: 64% 33% 3%

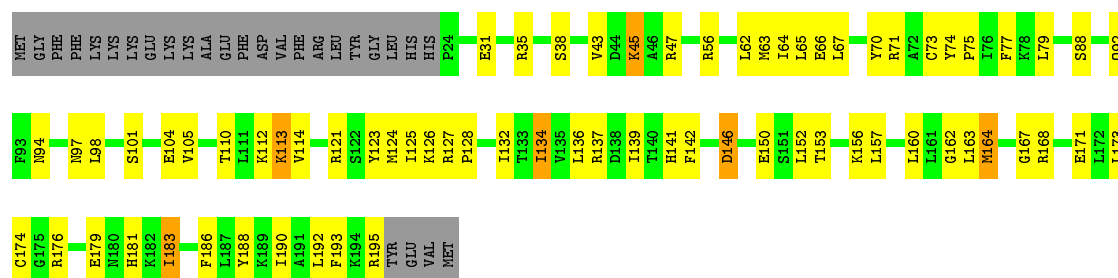


- Chain S: 



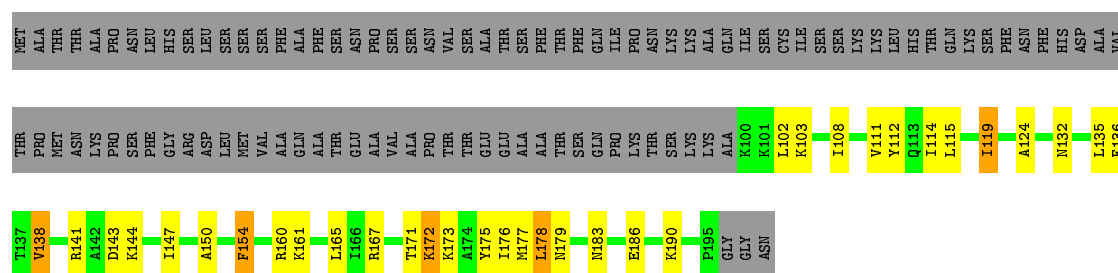
- Molecule 28: 50S ribosomal protein L22, chloroplastic

Chain T:



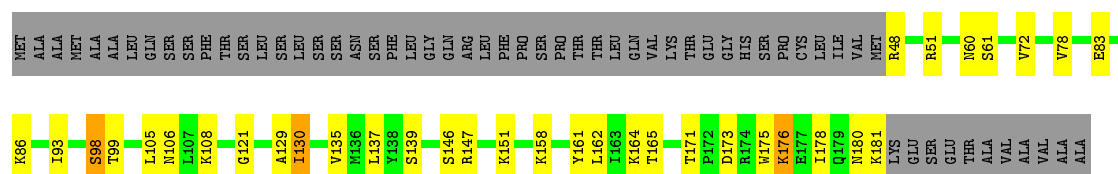
- Molecule 29: 50S ribosomal protein L23, chloroplastic

Chain U:



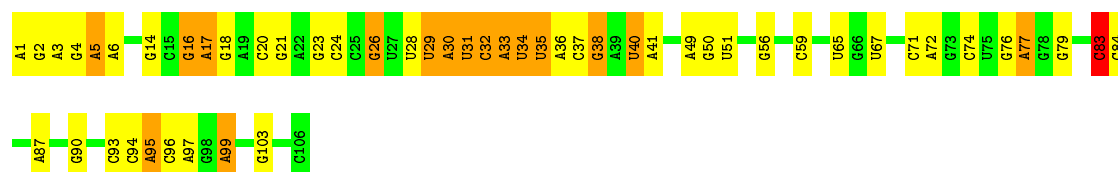
- Molecule 30: plastid ribosomal protein uL24c

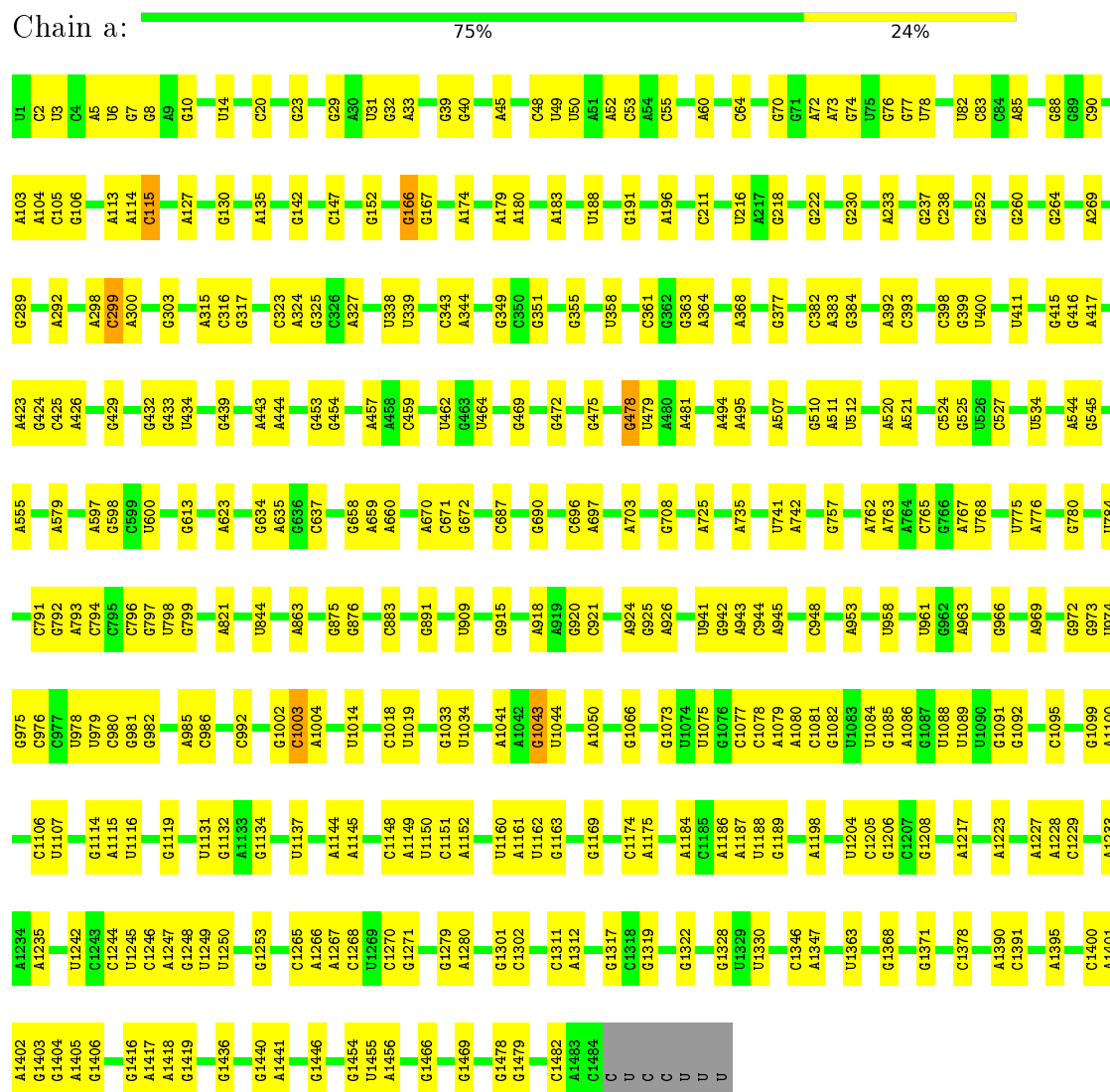
Chain V:



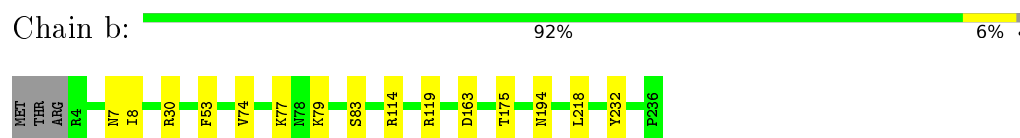
- Molecule 31: 4.5S ribosomal RNA

Chain W:

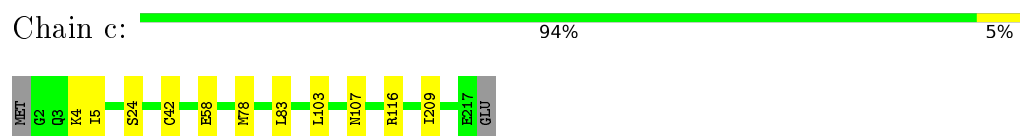




- Molecule 38: 30S ribosomal protein S2, chloroplastic



- Molecule 39: 30S ribosomal protein S3, chloroplastic



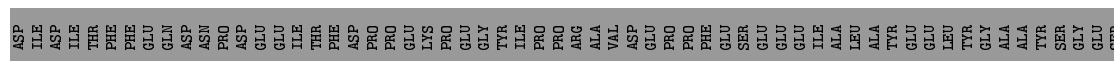
- Molecule 40: 30S ribosomal protein S4, chloroplastic





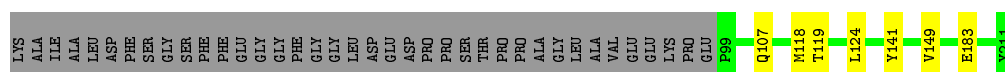
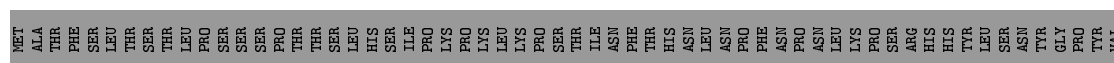
- Molecule 41: 30S ribosomal protein S5, chloroplastic

Chain e: 58% 39%



- Molecule 42: plastid ribosomal protein bS6c

Chain f: 50% 46%



- Molecule 43: 30S ribosomal protein S7, chloroplastic

Chain g: 95% 5%



- Molecule 44: 30S ribosomal protein S8, chloroplastic

Chain h: 92% 7%



- Molecule 45: plastid ribosomal protein uS9c

Chain i: 62% 7% 31%



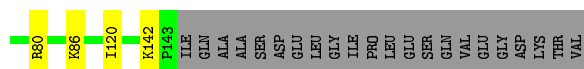
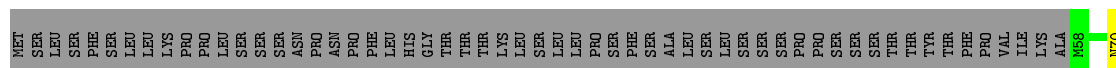
- Molecule 46: plastid ribosomal protein uS10c

Chain p: 82% 9% 9%



- Molecule 53: plastid ribosomal protein uS17c

Chain q: 49% 48%



- Molecule 54: 30S ribosomal protein S18, chloroplastic

Chain r: 54% 5% 41%



- Molecule 55: 30S ribosomal protein S19 alpha, chloroplastic

Chain s: 80% 15%



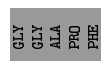
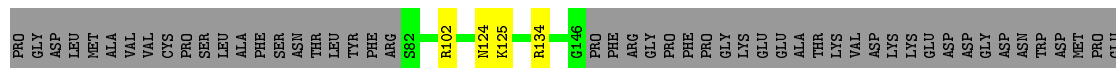
- Molecule 56: plastid ribosomal protein bS20c

Chain t: 54% 42%

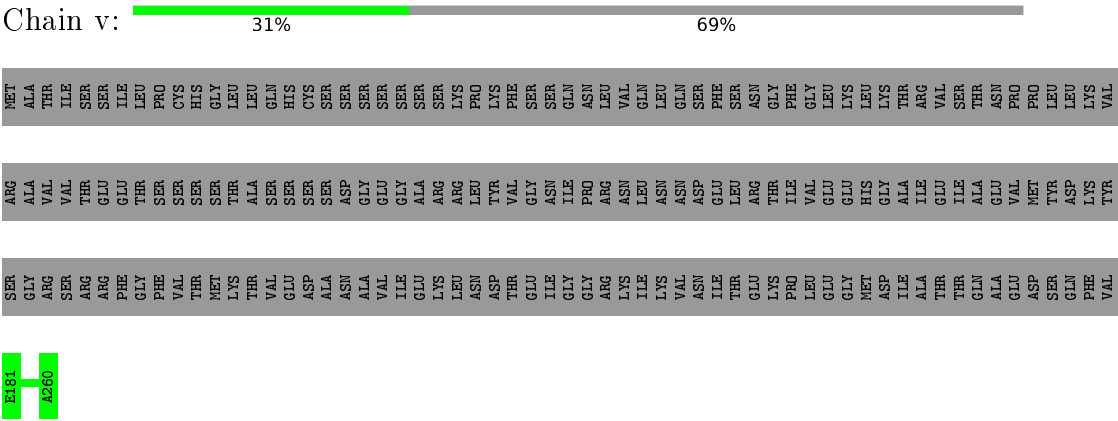


- Molecule 57: plastid ribosomal protein bS21c

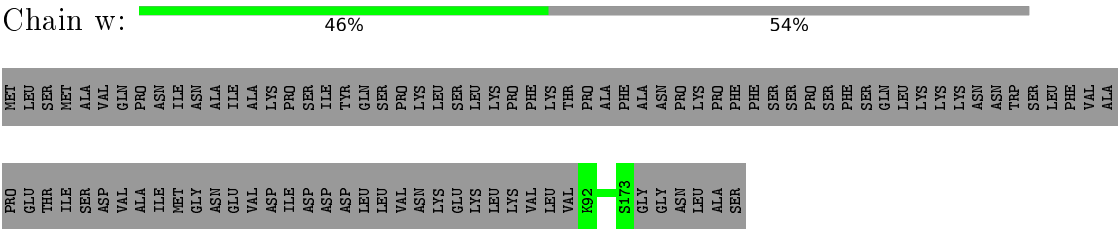
Chain u: 34% 64%



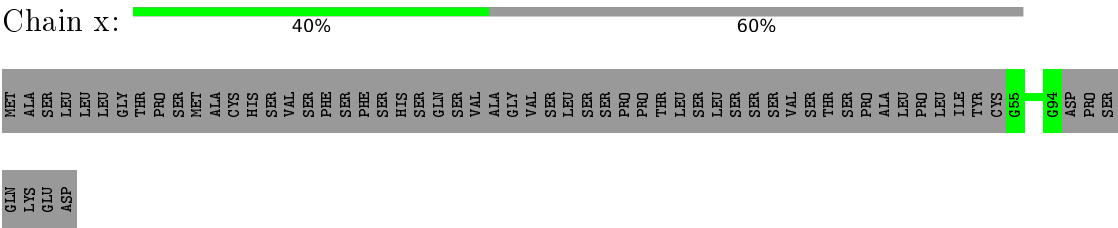
- Molecule 58: 30S ribosomal protein 2, chloroplastic



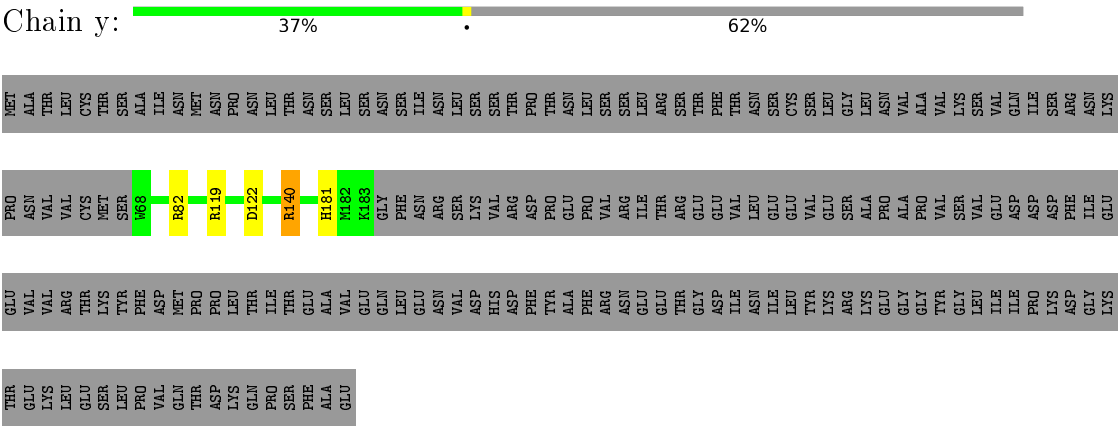
- Molecule 59: 30S ribosomal protein 3, chloroplastic



- Molecule 60: 30S ribosomal protein S31, chloroplastic



- Molecule 61: Ribosome-binding factor PSRP1, chloroplastic



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	140583	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 2$	RMSZ	# $ Z > 2$
1	0	0.65	0/548	0.88	1/737 (0.1%)
10	B	0.49	0/2890	1.01	3/4503 (0.1%)
11	C	0.49	0/1986	0.69	2/2666 (0.1%)
12	D	0.54	0/1713	0.70	0/2291
13	E	0.54	0/1707	0.77	1/2298 (0.0%)
14	F	0.39	0/1475	0.60	1/1990 (0.1%)
15	G	0.39	0/1412	0.57	0/1898
16	H	0.41	0/386	0.59	0/514
17	I	0.54	0/1129	0.56	0/1521
18	J	0.56	0/992	0.58	0/1343
19	K	0.50	0/1688	0.63	0/2279
2	1	0.61	0/405	0.71	0/537
20	L	0.48	0/951	0.63	0/1282
21	M	0.50	0/1430	0.69	0/1896
22	N	0.45	0/1097	0.61	0/1471
23	O	0.55	0/959	0.72	0/1280
24	P	0.40	0/978	0.57	0/1311
25	Q	0.57	0/967	0.69	0/1299
26	R	0.60	0/1046	0.72	0/1395
27	S	0.48	0/1339	0.69	3/1826 (0.2%)
28	T	0.50	0/1420	0.63	0/1900
29	U	0.50	0/787	0.69	0/1056
3	2	0.47	0/497	0.74	1/664 (0.2%)
30	V	0.42	0/1093	0.61	0/1457
31	W	0.74	0/2551	1.18	4/3977 (0.1%)
32	X	0.45	0/905	0.60	0/1204
33	Y	0.46	0/644	0.62	0/856
34	Z	0.41	0/854	0.56	0/1131
35	z	1.35	7/1813 (0.4%)	1.93	81/2823 (2.9%)
37	a	0.57	0/35687	1.00	35/55680 (0.1%)
38	b	0.40	0/1878	0.55	0/2538
39	c	0.39	0/1763	0.58	0/2370

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
4	3	0.55	0/470	0.71	0/619
40	d	0.37	0/1661	0.57	0/2230
41	e	0.44	0/1345	0.61	0/1817
42	f	0.34	0/929	0.54	0/1255
43	g	0.37	0/1226	0.53	0/1641
44	h	0.37	0/1094	0.57	0/1467
45	i	0.37	0/1138	0.60	0/1526
46	j	0.42	0/822	0.58	0/1111
47	k	0.35	0/896	0.59	0/1206
48	l	0.45	0/975	0.60	0/1312
49	m	0.37	0/912	0.61	0/1219
5	4	0.57	0/594	0.67	0/784
50	n	0.39	0/836	0.55	0/1116
51	o	0.38	0/642	0.49	0/852
52	p	0.39	0/674	0.62	0/902
53	q	0.37	0/707	0.55	0/949
54	r	0.37	0/494	0.56	0/660
55	s	0.40	0/646	0.61	0/870
56	t	0.41	0/862	0.63	1/1151 (0.1%)
57	u	0.34	0/572	0.47	0/754
58	v	0.58	0/621	0.49	0/833
59	w	0.58	0/707	0.55	0/962
6	5	0.38	0/307	0.54	0/403
60	x	0.46	0/317	0.62	0/418
61	y	0.40	0/930	0.71	2/1243 (0.2%)
7	6	0.46	0/425	0.77	0/551
8	7	0.43	0/382	0.57	0/520
9	A	0.82	39/67297 (0.1%)	1.21	253/104984 (0.2%)
All	All	0.67	46/163471 (0.0%)	1.03	388/243348 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	E	0	1
21	M	0	1
38	b	0	1
41	e	0	1
56	t	0	2
All	All	0	6

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	z	1	G	OP3-P	-10.61	1.48	1.61
9	A	1272	A	N3-C4	-8.41	1.29	1.34
9	A	1272	A	N9-C4	-7.74	1.33	1.37
9	A	727	A	N3-C4	7.72	1.39	1.34
9	A	830	A	N3-C4	-7.35	1.30	1.34

The worst 5 of 388 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	727	A	N1-C2-N3	-17.96	120.32	129.30
35	z	34	G	N1-C2-N2	-13.39	104.15	116.20
9	A	1272	A	C2-N3-C4	-12.32	104.44	110.60
61	y	140	ARG	NE-CZ-NH2	-11.37	114.62	120.30
9	A	727	A	C6-N1-C2	10.68	125.01	118.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	E	134	ARG	Peptide
21	M	104	ALA	Peptide
38	b	74	VAL	Peptide
41	e	144	LYS	Peptide
56	t	75	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	536	0	515	27	0
2	1	396	0	437	11	0
3	2	489	0	507	8	0
4	3	467	0	526	11	0
5	4	588	0	658	15	0
6	5	305	0	344	14	0
7	6	422	0	508	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	7	368	0	386	7	0
9	A	60083	0	30259	664	0
10	B	2584	0	1305	36	0
11	C	1952	0	2038	58	0
12	D	1686	0	1772	55	0
13	E	1676	0	1737	46	0
14	F	1454	0	1488	46	0
15	G	1391	0	1458	36	0
16	H	382	0	437	10	0
17	I	1106	0	1122	38	0
18	J	977	0	1027	33	0
19	K	1648	0	1684	44	0
20	L	942	0	996	27	0
21	M	1410	0	1495	46	0
22	N	1075	0	1134	38	0
23	O	944	0	1004	29	0
24	P	962	0	984	31	0
25	Q	953	0	1050	33	0
26	R	1029	0	1092	40	0
27	S	1310	0	1315	32	0
28	T	1395	0	1482	45	0
29	U	776	0	837	22	0
30	V	1078	0	1144	21	0
31	W	2277	0	1146	27	0
32	X	888	0	923	20	0
33	Y	634	0	684	13	0
34	Z	846	0	918	17	0
35	z	1623	0	821	0	0
36	8	870	0	184	1	0
37	a	31868	0	16050	0	0
38	b	1844	0	1887	0	0
39	c	1736	0	1819	0	0
40	d	1633	0	1730	0	0
41	e	1331	0	1312	0	0
42	f	911	0	923	0	0
43	g	1210	0	1284	0	0
44	h	1079	0	1137	0	0
45	i	1119	0	1181	0	0
46	j	805	0	849	0	0
47	k	882	0	928	0	0
48	l	959	0	1035	0	0
49	m	904	0	943	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	n	820	0	858	0	0
51	o	635	0	686	0	0
52	p	664	0	703	0	0
53	q	693	0	729	0	0
54	r	490	0	532	0	0
55	s	631	0	661	0	0
56	t	853	0	915	0	0
57	u	568	0	576	0	0
58	v	613	0	621	0	0
59	w	686	0	706	0	0
60	x	309	0	323	0	0
61	y	919	0	958	0	0
62	2	1	0	0	0	0
62	5	1	0	0	0	0
63	4	1	0	0	0	0
63	6	1	0	0	0	0
63	7	1	0	0	0	0
63	A	511	0	0	0	0
63	B	15	0	0	0	0
63	C	1	0	0	0	0
63	D	1	0	0	0	0
63	E	1	0	0	0	0
63	F	1	0	0	0	0
63	H	1	0	0	0	0
63	M	2	0	0	0	0
63	P	1	0	0	0	0
63	R	1	0	0	0	0
63	S	1	0	0	0	0
63	T	1	0	0	0	0
63	U	1	0	0	0	0
63	V	1	0	0	0	0
63	W	14	0	0	0	0
63	a	219	0	0	0	0
63	k	1	0	0	0	0
63	l	1	0	0	0	0
63	n	1	0	0	0	0
63	x	1	0	0	0	0
All	All	152465	0	104763	1383	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 1383 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1857:A:HO2'	9:A:1858:A:H8	1.05	0.97
17:I:122:ILE:HD12	17:I:165:CYS:HB2	1.50	0.94
9:A:652:C:N4	9:A:657:U:O4	2.01	0.94
10:B:54:G:HO2'	10:B:55:G:H8	1.00	0.93
9:A:817:C:OP2	21:M:120:ARG:NH1	2.03	0.92

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	
1	0	64/130 (49%)	56 (88%)	5 (8%)	3 (5%)	3	26
2	1	46/57 (81%)	45 (98%)	1 (2%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	9	47
8	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
11	C	251/272 (92%)	235 (94%)	15 (6%)	1 (0%)	39	79
12	D	219/305 (72%)	206 (94%)	12 (6%)	1 (0%)	34	75
13	E	210/293 (72%)	196 (93%)	14 (7%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	165 (94%)	11 (6%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	K	201/250 (80%)	193 (96%)	8 (4%)	0	100	100
20	L	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
21	M	183/271 (68%)	168 (92%)	13 (7%)	2 (1%)	17	61
22	N	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
23	O	114/126 (90%)	108 (95%)	6 (5%)	0	100	100
24	P	120/166 (72%)	113 (94%)	7 (6%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	158 (94%)	8 (5%)	2 (1%)	16	59
28	T	170/199 (85%)	162 (95%)	7 (4%)	1 (1%)	30	72
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	123 (93%)	9 (7%)	0	100	100
32	X	107/194 (55%)	96 (90%)	11 (10%)	0	100	100
33	Y	75/148 (51%)	73 (97%)	2 (3%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	19	63
38	b	231/236 (98%)	221 (96%)	10 (4%)	0	100	100
39	c	214/218 (98%)	201 (94%)	13 (6%)	0	100	100
40	d	197/201 (98%)	186 (94%)	11 (6%)	0	100	100
41	e	185/308 (60%)	182 (98%)	3 (2%)	0	100	100
42	f	111/211 (53%)	106 (96%)	4 (4%)	1 (1%)	21	65
43	g	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
44	h	131/134 (98%)	127 (97%)	2 (2%)	2 (2%)	13	54
45	i	142/208 (68%)	136 (96%)	6 (4%)	0	100	100
46	j	97/195 (50%)	93 (96%)	3 (3%)	1 (1%)	19	63
47	k	115/138 (83%)	108 (94%)	7 (6%)	0	100	100
48	l	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
49	m	108/172 (63%)	101 (94%)	6 (6%)	1 (1%)	21	65
50	n	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
51	o	73/90 (81%)	72 (99%)	1 (1%)	0	100	100
52	p	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
53	q	84/165 (51%)	78 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	r	58/101 (57%)	55 (95%)	3 (5%)	0	100	100
55	s	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
56	t	105/183 (57%)	100 (95%)	3 (3%)	2 (2%)	10	49
57	u	63/180 (35%)	62 (98%)	1 (2%)	0	100	100
58	v	78/260 (30%)	76 (97%)	2 (3%)	0	100	100
59	w	80/179 (45%)	78 (98%)	2 (2%)	0	100	100
60	x	38/101 (38%)	37 (97%)	1 (3%)	0	100	100
61	y	114/302 (38%)	106 (93%)	8 (7%)	0	100	100
All	All	6476/9784 (66%)	6138 (95%)	319 (5%)	19 (0%)	50	82

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	92	ASP
27	S	78	PRO
49	m	53	VAL
56	t	174	TYR
11	C	232	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	57/117 (49%)	54 (95%)	3 (5%)	28	67
2	1	41/50 (82%)	37 (90%)	4 (10%)	10	40
3	2	56/60 (93%)	50 (89%)	6 (11%)	8	35
4	3	50/125 (40%)	42 (84%)	8 (16%)	3	16
5	4	62/140 (44%)	52 (84%)	10 (16%)	3	16
6	5	34/34 (100%)	30 (88%)	4 (12%)	6	29
7	6	46/124 (37%)	42 (91%)	4 (9%)	13	47
8	7	40/96 (42%)	33 (82%)	7 (18%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	C	201/217 (93%)	185 (92%)	16 (8%)	15	51
12	D	182/259 (70%)	164 (90%)	18 (10%)	10	39
13	E	179/255 (70%)	158 (88%)	21 (12%)	7	30
14	F	152/214 (71%)	140 (92%)	12 (8%)	15	52
15	G	151/190 (80%)	137 (91%)	14 (9%)	11	42
16	H	42/170 (25%)	37 (88%)	5 (12%)	6	29
17	I	119/204 (58%)	109 (92%)	10 (8%)	14	49
18	J	106/189 (56%)	101 (95%)	5 (5%)	32	72
19	K	176/213 (83%)	166 (94%)	10 (6%)	25	65
20	L	101/101 (100%)	91 (90%)	10 (10%)	10	39
21	M	141/215 (66%)	123 (87%)	18 (13%)	5	26
22	N	108/108 (100%)	100 (93%)	8 (7%)	17	55
23	O	96/103 (93%)	81 (84%)	15 (16%)	3	18
24	P	100/139 (72%)	90 (90%)	10 (10%)	9	38
25	Q	104/207 (50%)	94 (90%)	10 (10%)	10	40
26	R	106/115 (92%)	93 (88%)	13 (12%)	6	28
27	S	137/223 (61%)	131 (96%)	6 (4%)	35	73
28	T	152/176 (86%)	134 (88%)	18 (12%)	6	29
29	U	85/171 (50%)	74 (87%)	11 (13%)	5	26
30	V	121/169 (72%)	111 (92%)	10 (8%)	14	49
32	X	92/163 (56%)	76 (83%)	16 (17%)	2	13
33	Y	67/130 (52%)	59 (88%)	8 (12%)	6	29
34	Z	93/153 (61%)	84 (90%)	9 (10%)	10	40
38	b	198/201 (98%)	184 (93%)	14 (7%)	18	58
39	c	186/188 (99%)	175 (94%)	11 (6%)	24	64
40	d	178/180 (99%)	164 (92%)	14 (8%)	15	52
41	e	121/255 (48%)	113 (93%)	8 (7%)	21	61
42	f	100/186 (54%)	94 (94%)	6 (6%)	24	64
43	g	125/126 (99%)	118 (94%)	7 (6%)	26	66
44	h	116/117 (99%)	108 (93%)	8 (7%)	19	59
45	i	114/169 (68%)	99 (87%)	15 (13%)	5	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	j	91/173 (53%)	85 (93%)	6 (7%)	21	61
47	k	91/109 (84%)	83 (91%)	8 (9%)	12	46
48	l	105/106 (99%)	98 (93%)	7 (7%)	20	60
49	m	99/151 (66%)	92 (93%)	7 (7%)	18	58
50	n	89/90 (99%)	81 (91%)	8 (9%)	12	45
51	o	70/85 (82%)	68 (97%)	2 (3%)	50	82
52	p	71/79 (90%)	63 (89%)	8 (11%)	7	32
53	q	77/149 (52%)	72 (94%)	5 (6%)	21	61
54	r	56/96 (58%)	51 (91%)	5 (9%)	12	45
55	s	68/81 (84%)	64 (94%)	4 (6%)	24	64
56	t	89/156 (57%)	84 (94%)	5 (6%)	26	66
57	u	59/160 (37%)	55 (93%)	4 (7%)	20	60
58	v	67/225 (30%)	67 (100%)	0	100	100
59	w	76/162 (47%)	76 (100%)	0	100	100
60	x	30/85 (35%)	30 (100%)	0	100	100
61	y	104/275 (38%)	99 (95%)	5 (5%)	31	71
All	All	5577/8434 (66%)	5101 (92%)	476 (8%)	18	48

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	P	143	ARG
29	U	103	LYS
51	o	40	LEU
25	Q	198	LEU
27	S	87	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
30	V	180	ASN
41	e	225	HIS
55	s	69	HIS
33	Y	99	GLN
39	c	125	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	20 (16%)	0
31	W	105/106 (99%)	34 (32%)	1 (0%)
35	z	75/76 (98%)	22 (29%)	0
37	a	1483/1491 (99%)	349 (23%)	0
9	A	2794/2810 (99%)	658 (23%)	8 (0%)
All	All	4577/4604 (99%)	1083 (23%)	9 (0%)

5 of 1083 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	8	G
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1520	A
31	W	77	A
9	A	2447	A
9	A	556	C
9	A	2035	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 781 ligands modelled in this entry, 781 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	1068:UNK	C	1101:UNK	N	66.30
1	8	1143:UNK	C	1201:UNK	N	11.98