



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:06 PM UTC

PDB ID : 7K50 / pdb_00007k50
EMDB ID : EMD-22669
Title : Pre-translocation non-frameshifting(CCA-A) complex (Structure I)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2020-09-16
Resolution : 3.40 Å(reported)
Based on initial models : 6ENJ, 5UYM

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

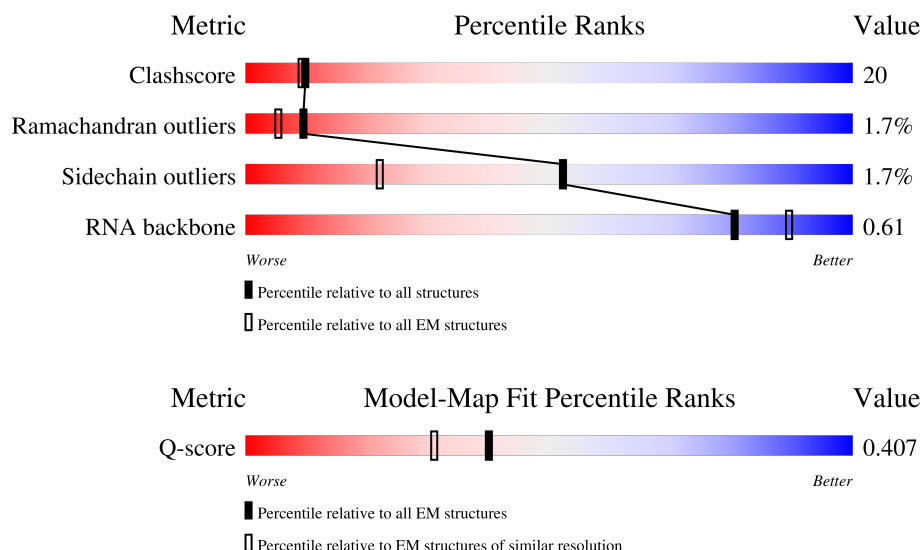
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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.



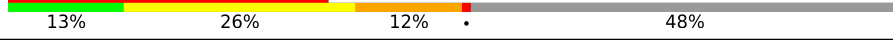
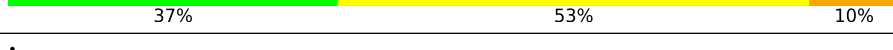
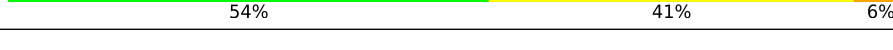
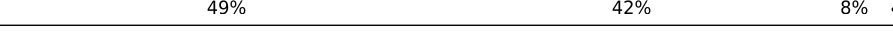
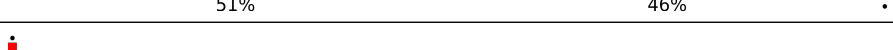
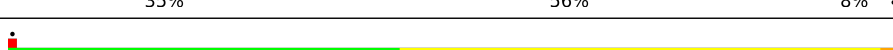
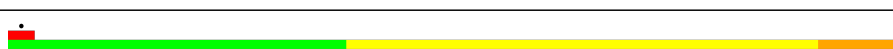
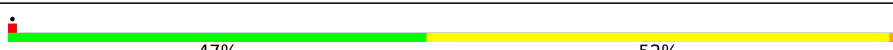
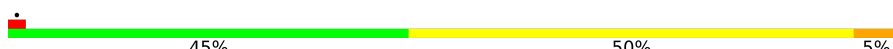
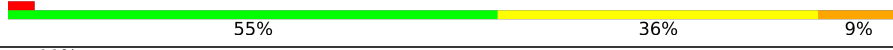
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	271	
2	c	209	
3	d	201	

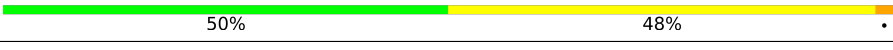
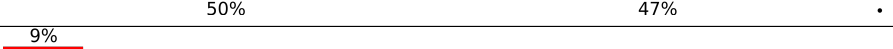
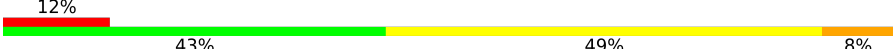
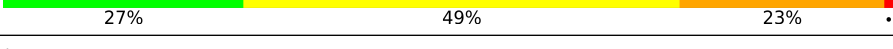
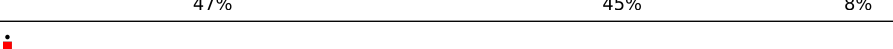
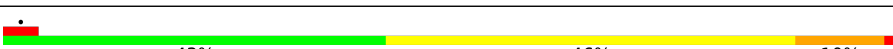
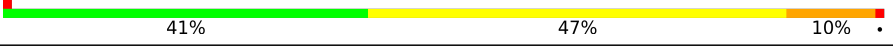
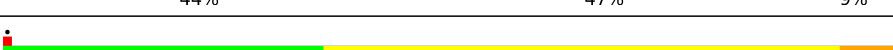
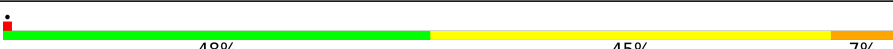
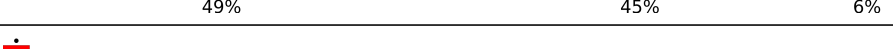
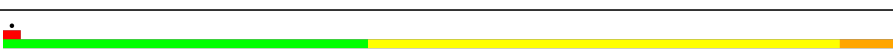
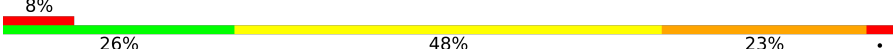
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	A	66	
27	B	56	
28	C	50	

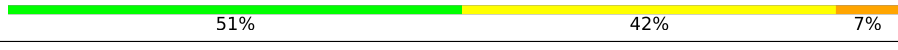
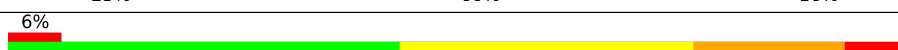
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Mol	Chain	Length	Quality of chain
29	D	46	
30	E	64	
31	F	38	
32	G	225	
33	H	206	
34	I	205	
35	J	157	
36	K	100	
37	L	151	
38	M	129	
39	N	127	
40	O	98	
41	P	116	
42	Q	123	
43	R	114	
44	S	100	
45	T	88	
46	U	82	
47	V	80	
48	W	65	
49	X	79	
50	Y	85	
51	Z	65	
52	a	223	
53	3	1539	

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Mol	Chain	Length	Quality of chain
54	1	2903	
55	2	120	
56	5	77	
56	6	77	
57	4	18	
58	7	77	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 149700 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	125	Total	C	N	O	S	0	0
			936	590	166	179	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	84	Total	C	N	O	S	0	0
			633	397	114	118	4		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	74	Total	C	N	O	S	0	0
			551	358	91	99	3		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O		0
			947	604	192	151		0

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

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

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

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

- Molecule 30 is a protein called 50S ribosomal protein L35.

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

- Molecule 31 is a protein called 50S ribosomal protein L36.

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

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	G	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	4	18	Total	C	N	O	P	0	0
			390	176	80	117	17		

- Molecule 58 is a RNA chain called tRNAPro.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	7	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S) (labeled as "Ligand of Interest" by depositor).

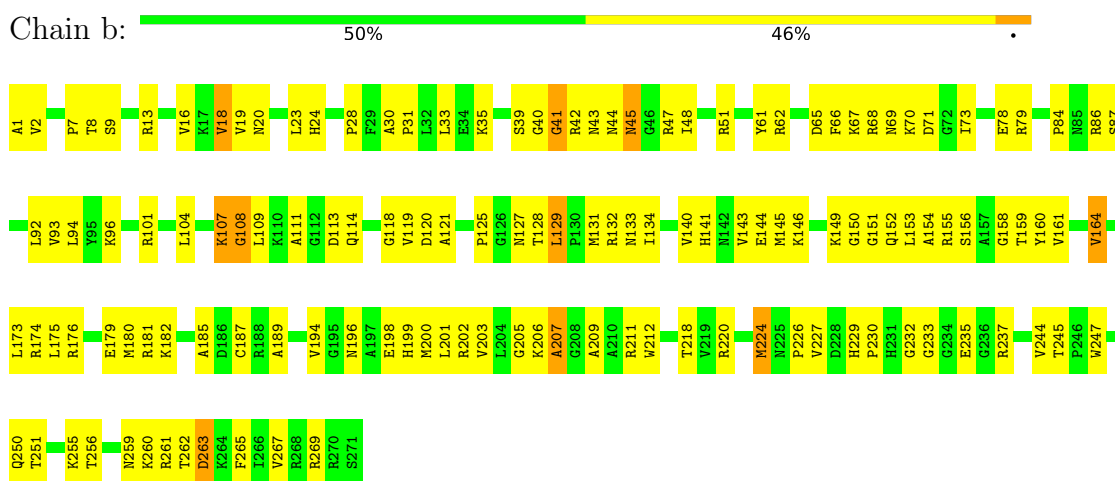


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	5	1	10	6	1	2	1	0

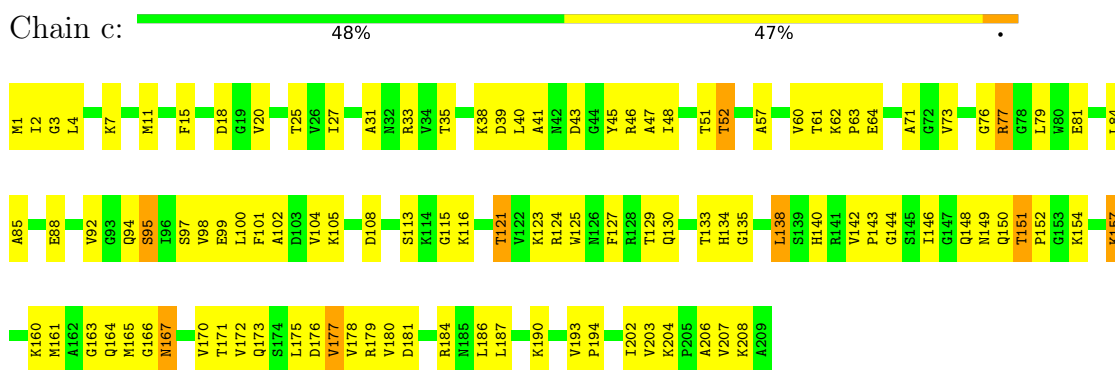
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

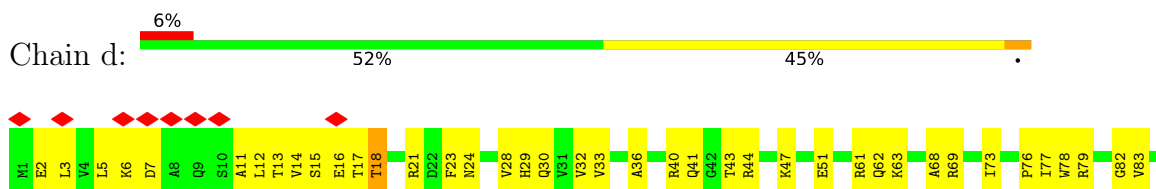
• Molecule 1: 50S ribosomal protein L2

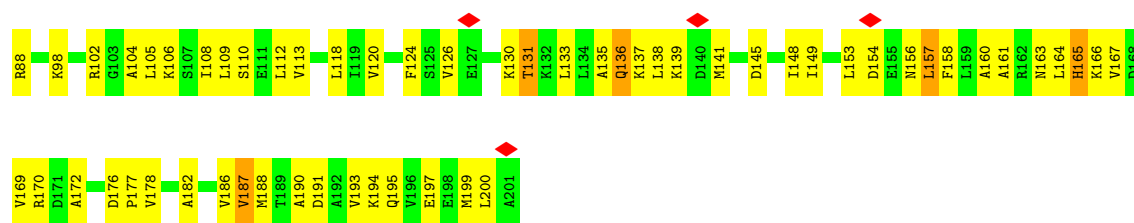


• Molecule 2: 50S ribosomal protein L3

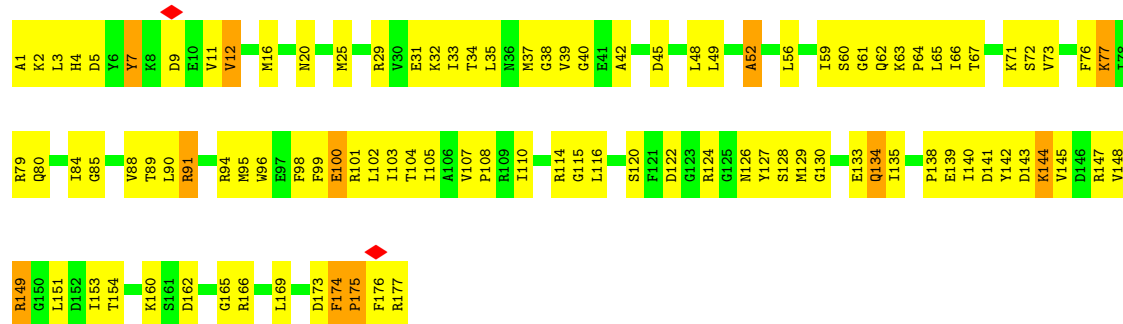


• Molecule 3: 50S ribosomal protein L4

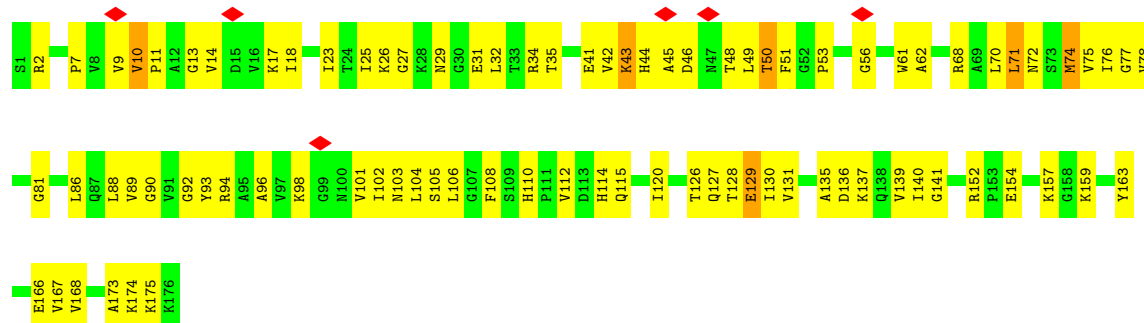




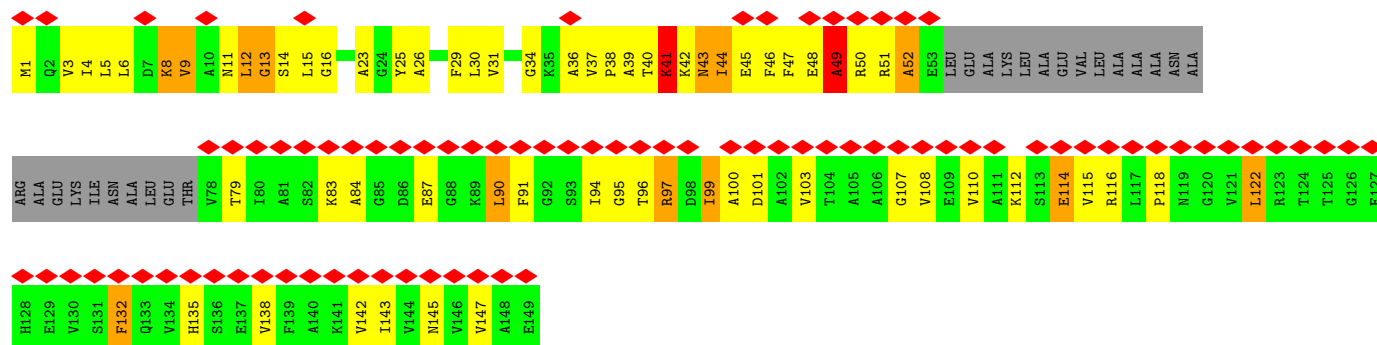
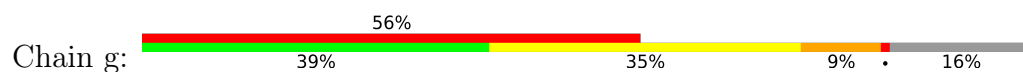
• Molecule 4: 50S ribosomal protein L5



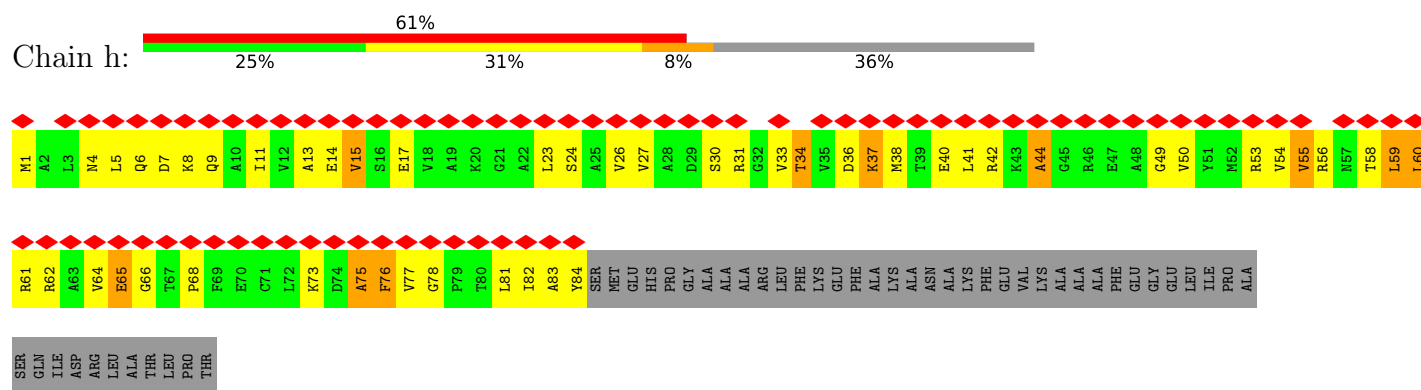
• Molecule 5: 50S ribosomal protein L6



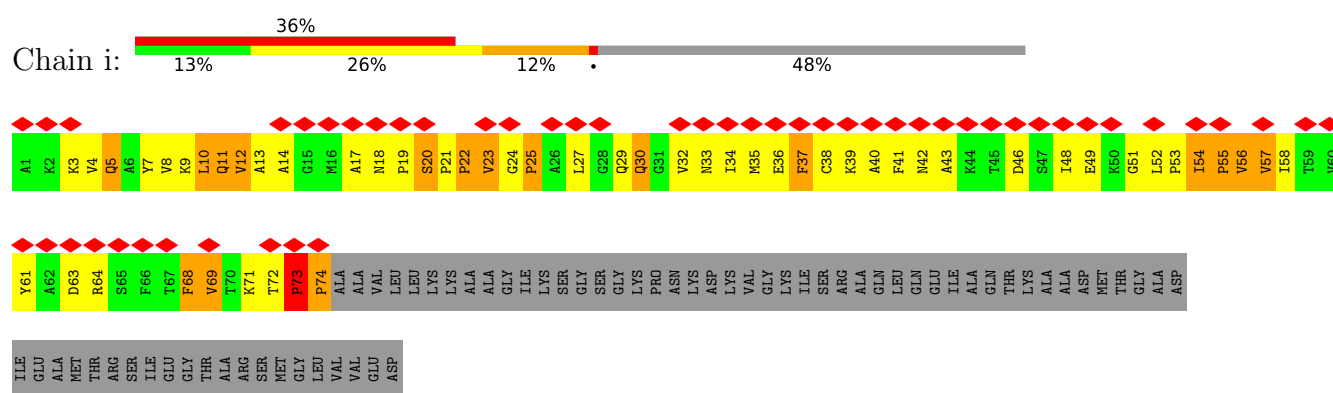
• Molecule 6: 50S ribosomal protein L9



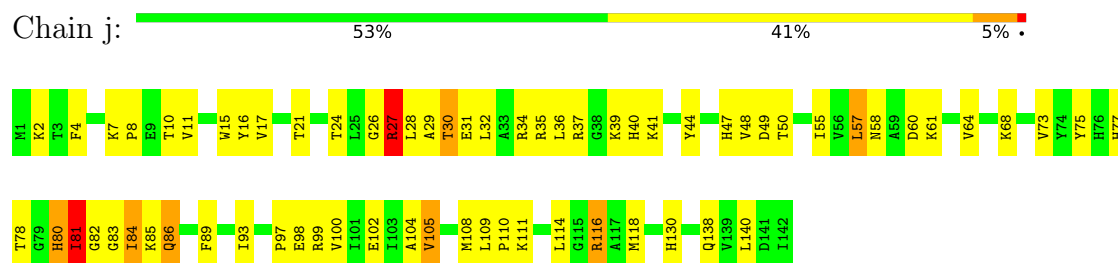
- Molecule 7: 50S ribosomal protein L10



- Molecule 8: 50S ribosomal protein L11



- Molecule 9: 50S ribosomal protein L13

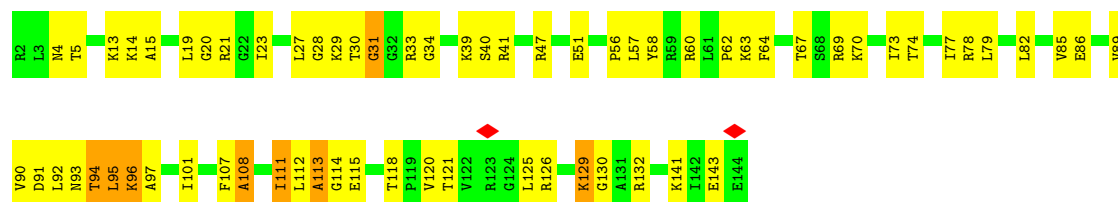


- Molecule 10: 50S ribosomal protein L14



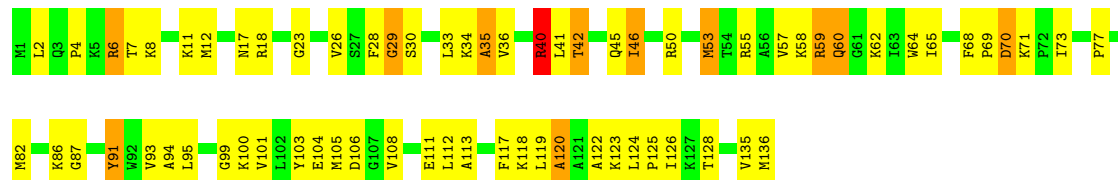
- Molecule 11: 50S ribosomal protein L15





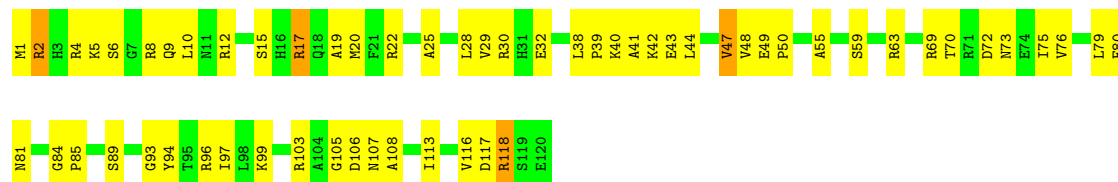
• Molecule 12: 50S ribosomal protein L16

Chain m: 49% 42% 8% .



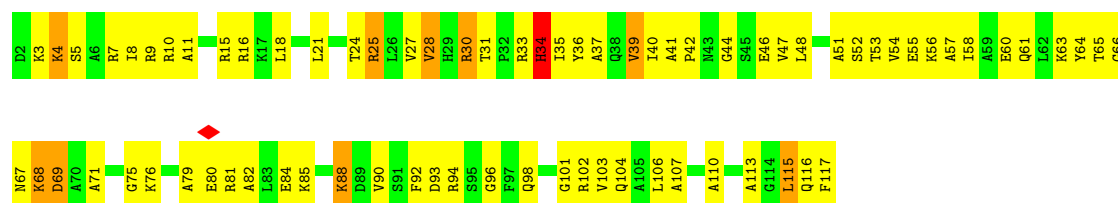
• Molecule 13: 50S ribosomal protein L17

Chain n: 51% 46% .



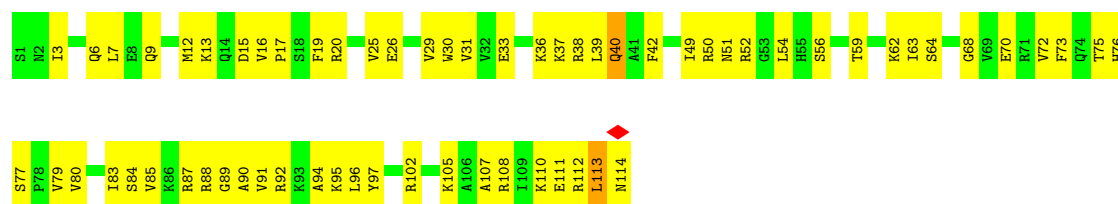
• Molecule 14: 50S ribosomal protein L18

Chain o: 35% 56% 8% .

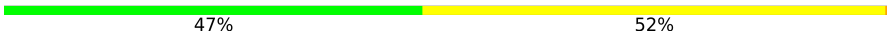


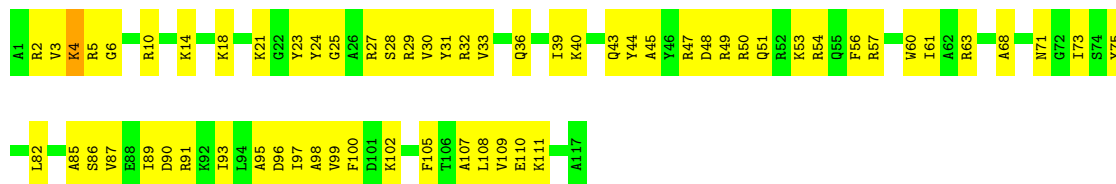
• Molecule 15: 50S ribosomal protein L19

Chain p: 44% 54% .



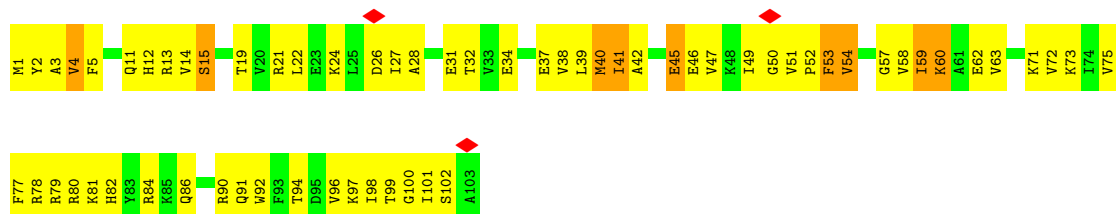
• Molecule 16: 50S ribosomal protein L20

Chain q: 



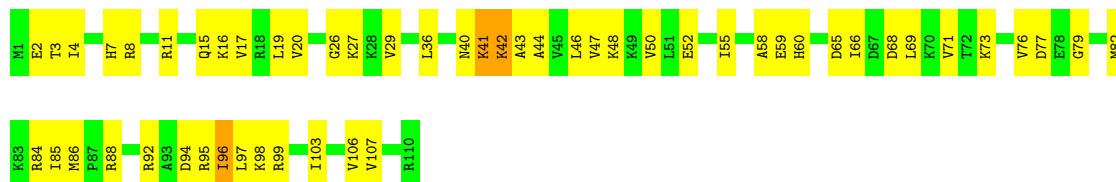
• Molecule 17: 50S ribosomal protein L21

Chain r: 



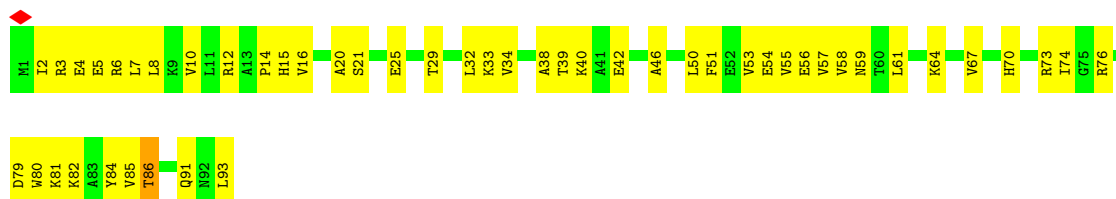
• Molecule 18: 50S ribosomal protein L22

Chain s: 



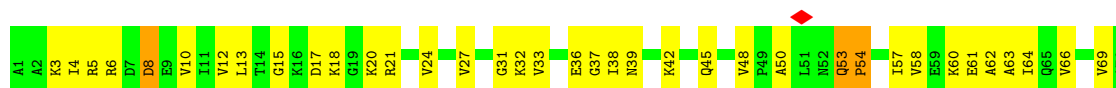
• Molecule 19: 50S ribosomal protein L23

Chain t: 



• Molecule 20: 50S ribosomal protein L24

Chain u: 

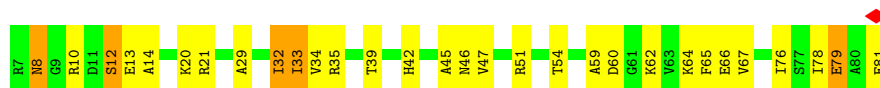




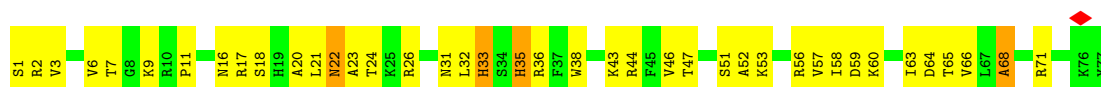
- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



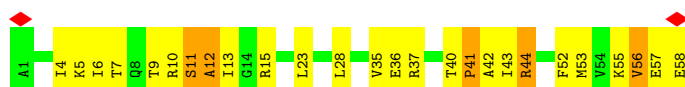
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

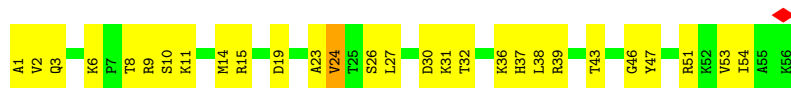


- Molecule 26: 50S ribosomal protein L31

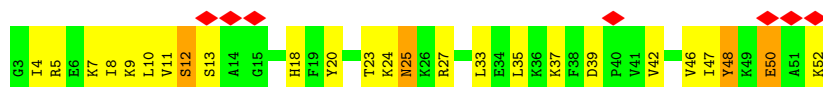




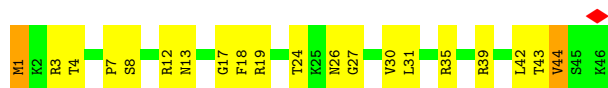
- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



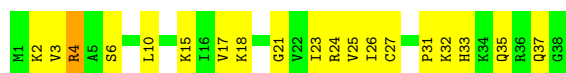
- Molecule 29: 50S ribosomal protein L34



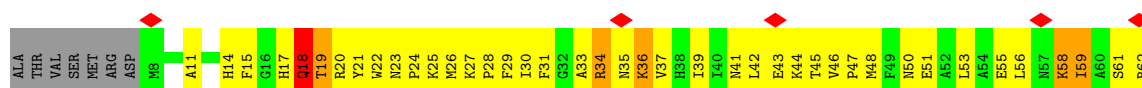
- Molecule 30: 50S ribosomal protein L35

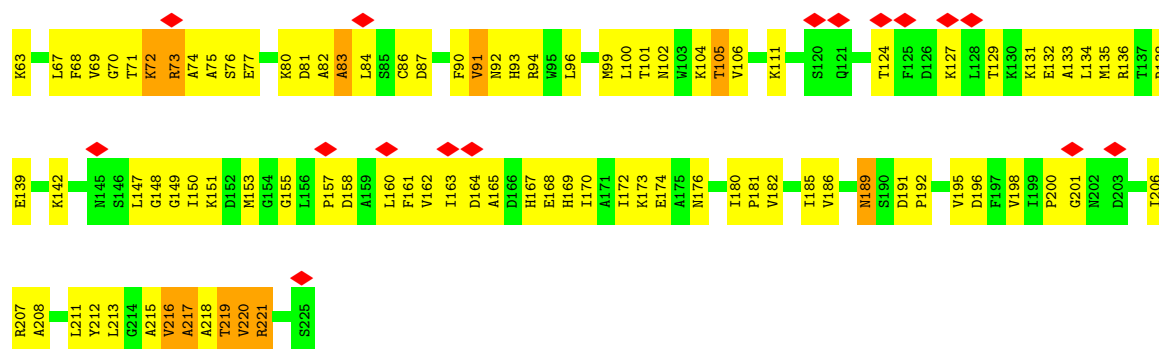


- Molecule 31: 50S ribosomal protein L36



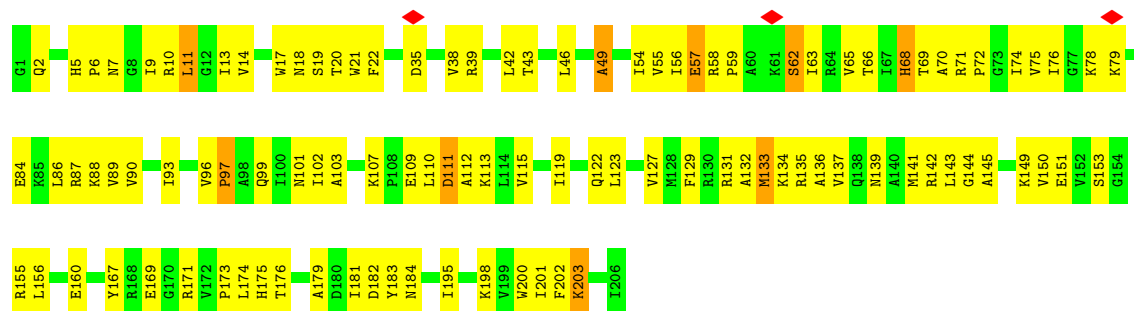
- Molecule 32: 30S ribosomal protein S2





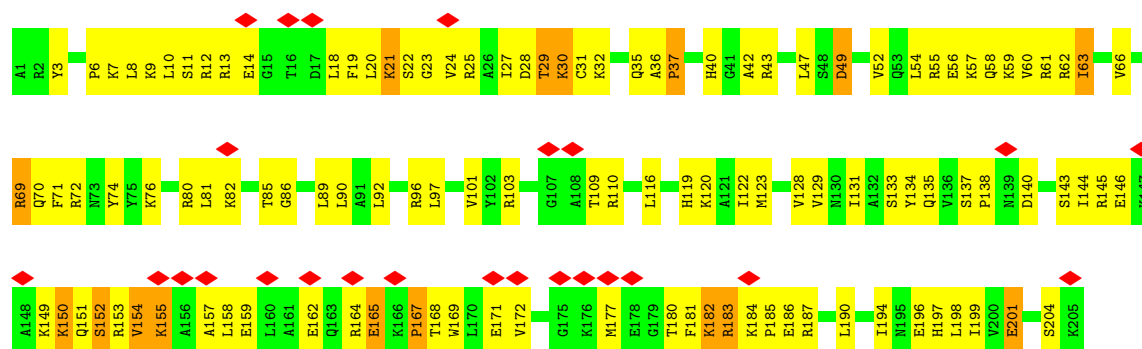
• Molecule 33: 30S ribosomal protein S3

Chain H: 49% 47%



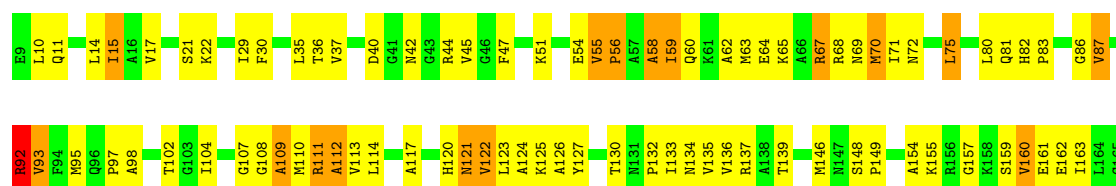
• Molecule 34: 30S ribosomal protein S4

Chain I: 12% 43% 49% 8%

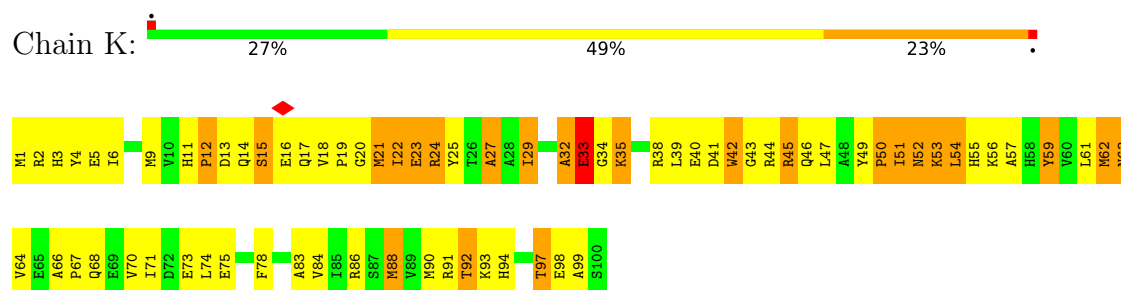


• Molecule 35: 30S ribosomal protein S5

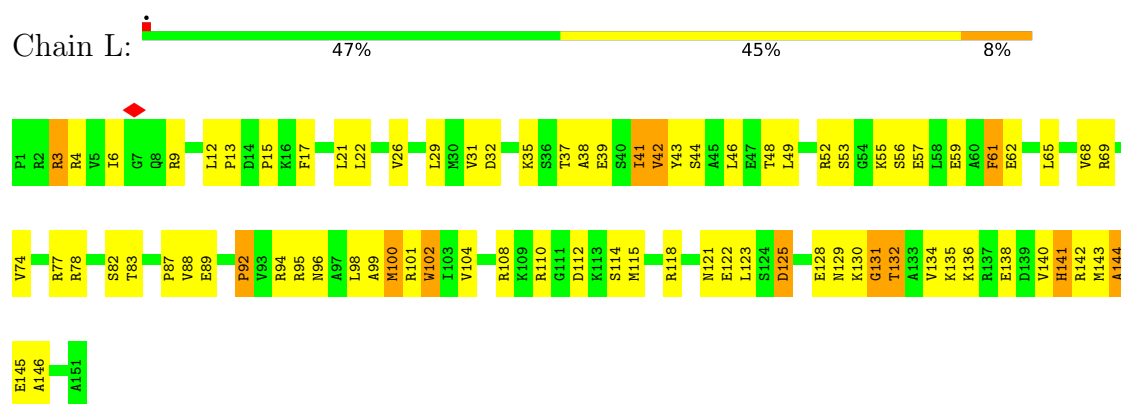
Chain J: 46% 43% 10%



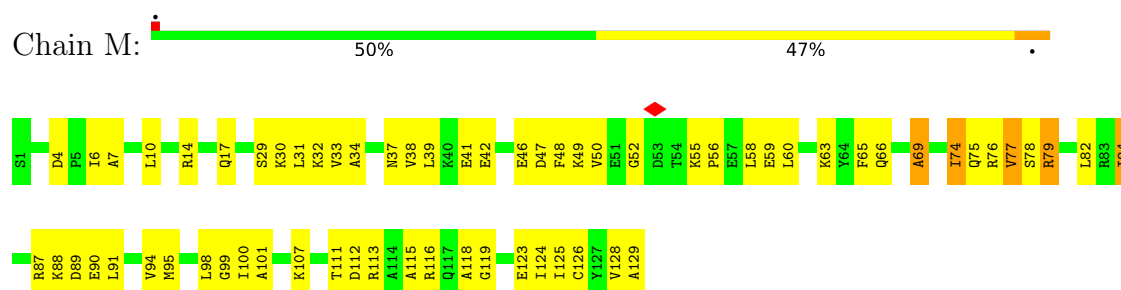
- Molecule 36: 30S ribosomal protein S6



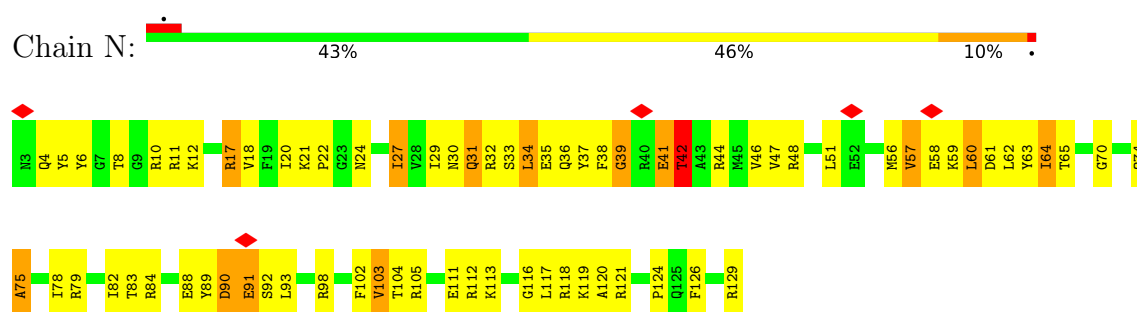
- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8

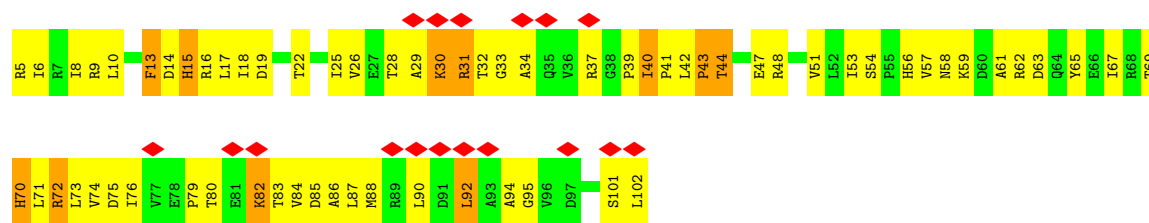


- Molecule 39: 30S ribosomal protein S9

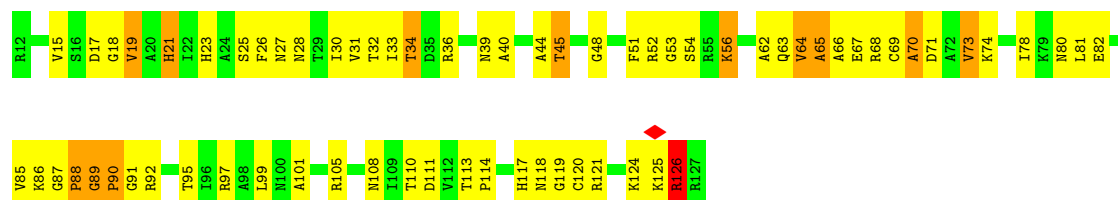


- Molecule 40: 30S ribosomal protein S10

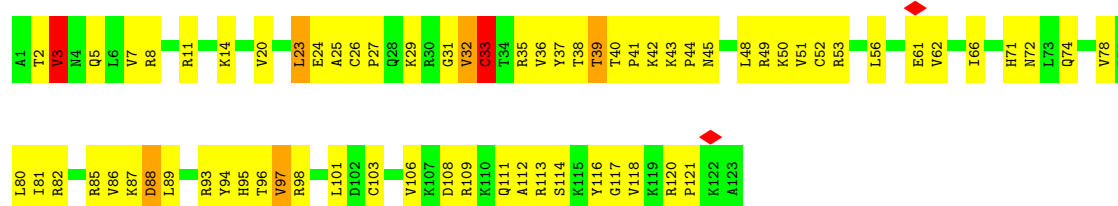




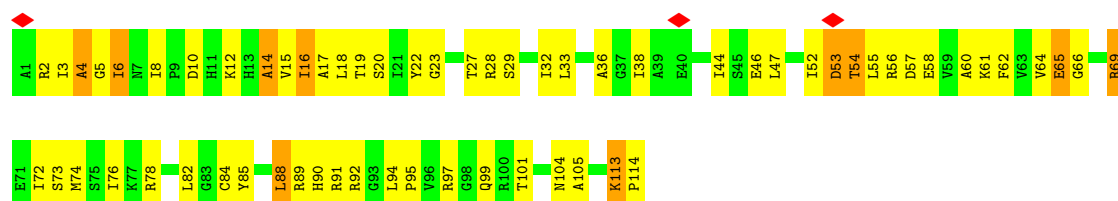
• Molecule 41: 30S ribosomal protein S11



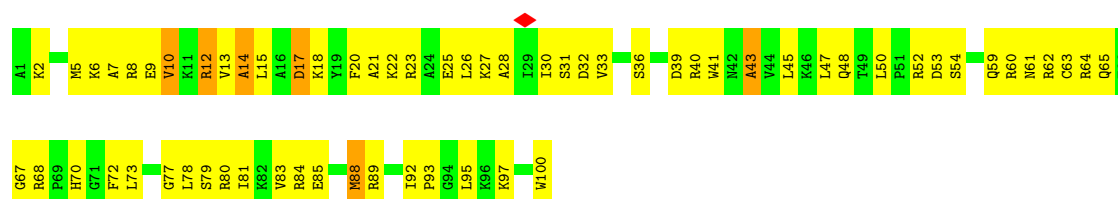
• Molecule 42: 30S ribosomal protein S12



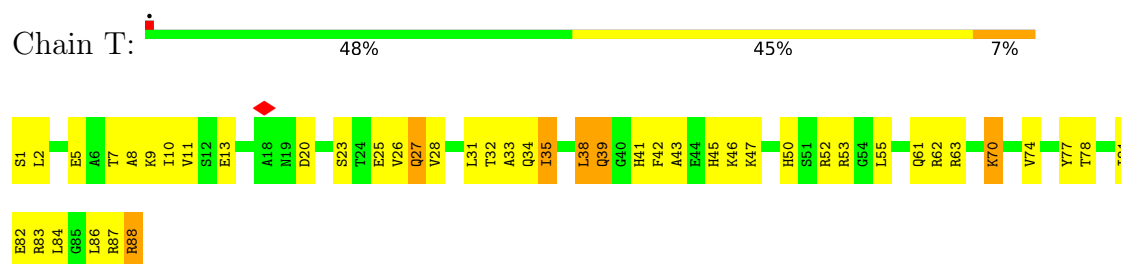
• Molecule 43: 30S ribosomal protein S13



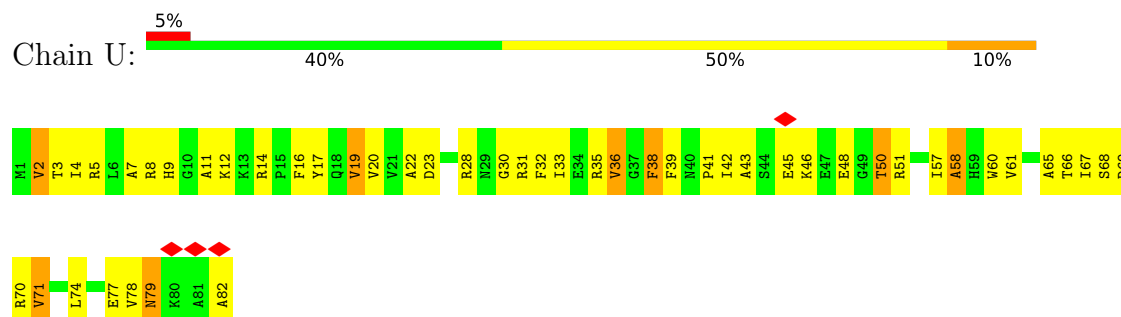
• Molecule 44: 30S ribosomal protein S14



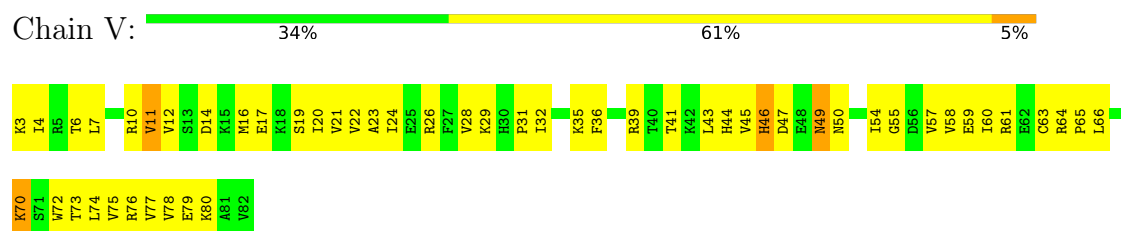
- Molecule 45: 30S ribosomal protein S15



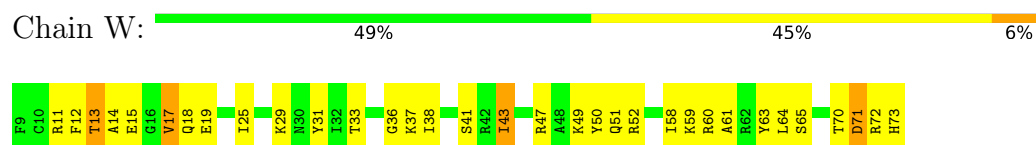
- Molecule 46: 30S ribosomal protein S16



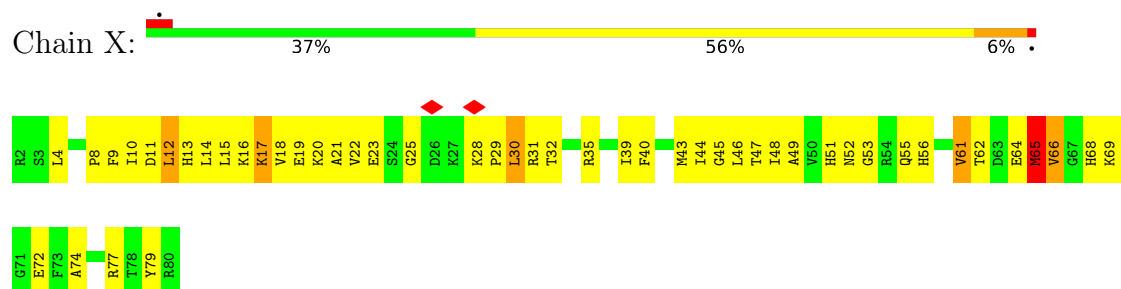
- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18

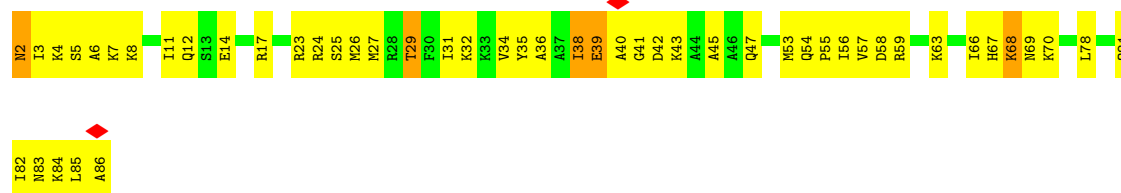


- Molecule 49: 30S ribosomal protein S19

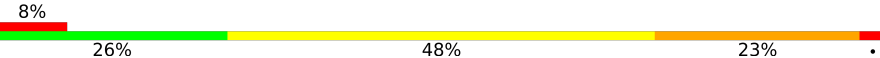


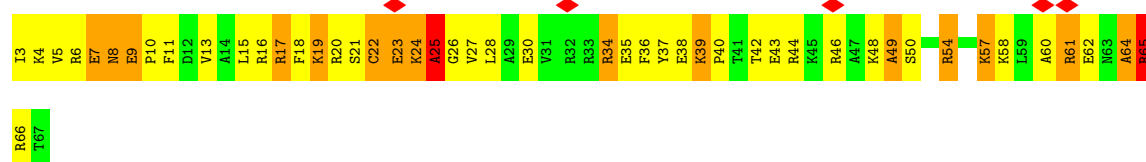
- Molecule 50: 30S ribosomal protein S20

Chain Y: 

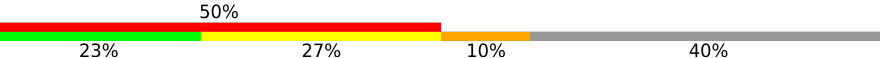


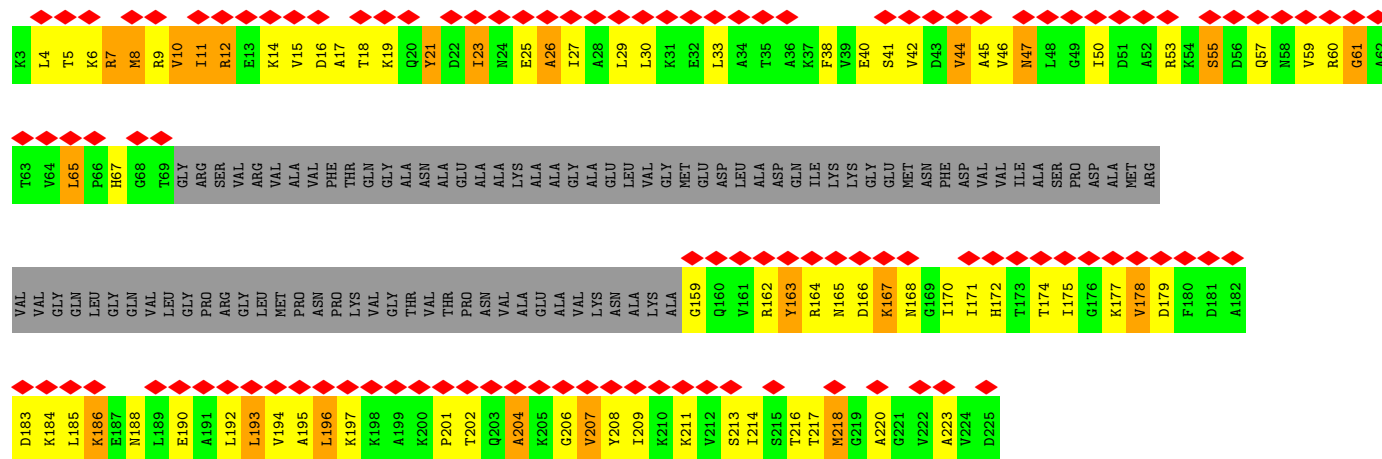
- Molecule 51: 30S ribosomal protein S21

Chain Z: 



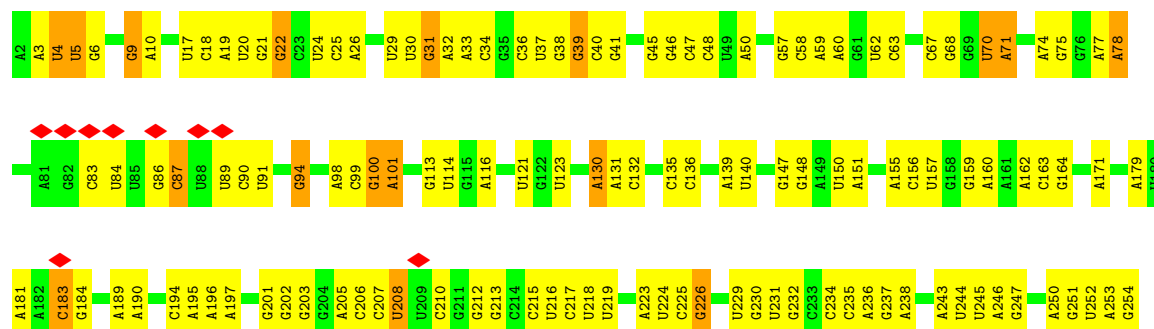
- Molecule 52: 50S ribosomal protein L1

Chain a: 



- Molecule 53: 16S ribosomal RNA

Chain 3: 

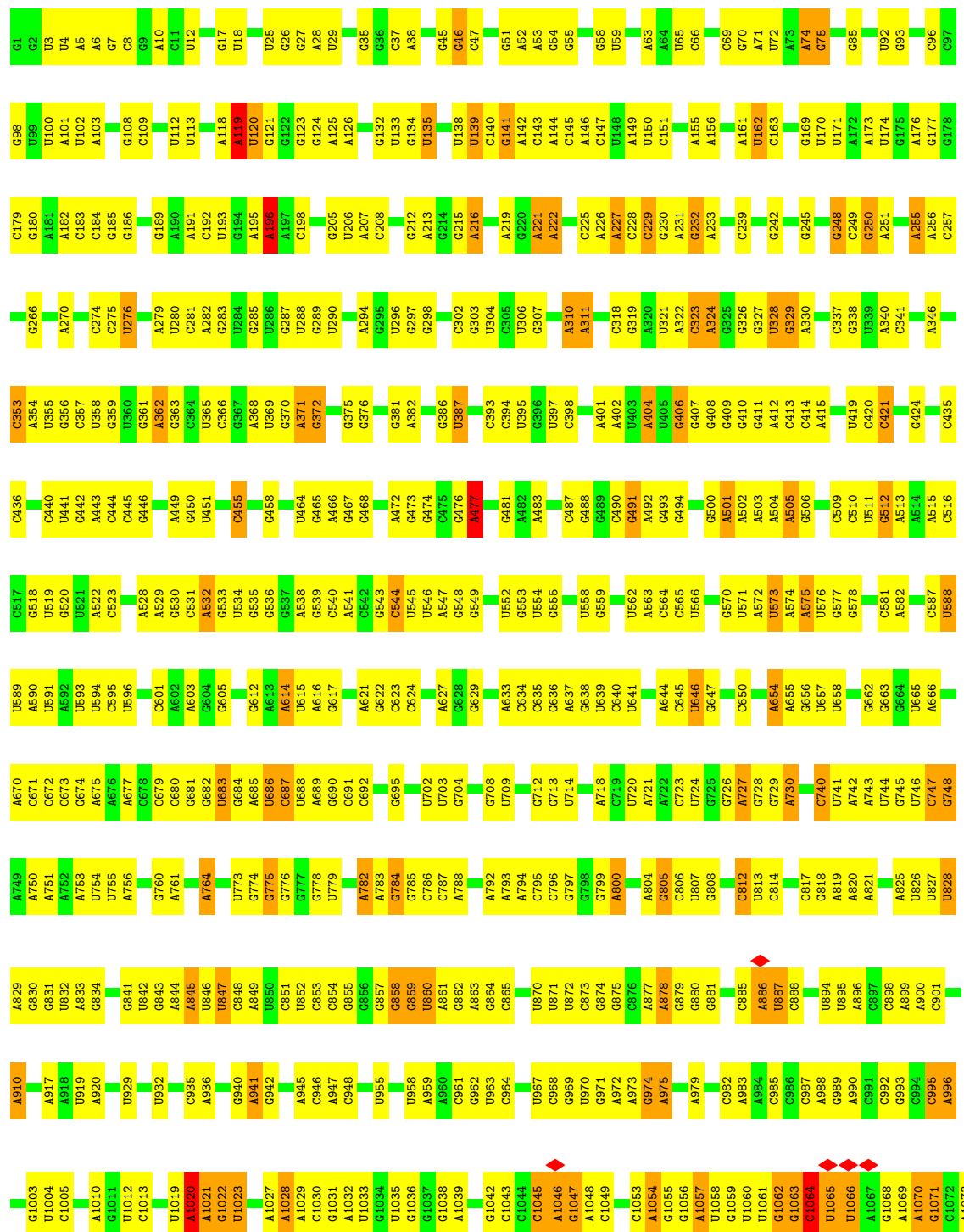


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C1195	A1196	A1197	U1198	U1199	C1200	A1201	U1202	C1203	A1204	U1205	U1211	U1212	A1213	C1218	A1219	G1220	G1221	G1222	A1225	C1226	A1227	C1228	A1229	C1230	G1233	C1234	U1235	A1236	C1237	A1238	U1239	G1240	G1241	C1242	G1243	G1244	C1245	A1248	C1249	A1250	A1251	A1252	G1253	A1254	G1258	C1259	A1260	C1273	A1274	A1275	G1276		
C1277	G1278	G1279	A1280	C1281	C1282	A1285	U1286	U1287	A1288	A1289	U1295	G1296	G1300	U1301	C1302	C1303	G1304	G1305	A1306	U1307	U1308	G1309	G1310	C1314	U1315	G1316	C1317	A1318	A1319	C1320	G1323	A1324	C1325	U1326	C1327	C1328	A1329	U1330	G1331	A1332	A1333	G1334	G1337	C1342	G1343	A1346	G1347	U1348	A1349	A1350	U1351		
C1352	G1353	U1354	U1364	G1365	G1366	C1367	A1368	U1369	G1370	U1371	U1372	G1373	A1374	G1379	U1380	U1381	C1382	U1390	U1391	G1392	U1393	A1394	C1395	A1396	C1397	G1403	C1404	A1408	G1409	A1410	C1411	A1412	A1413	G1414	G1415	G1416	G1417	G1422	A1513	G1514	G1515	G1516	G1517	A1518	A1519	U1522	G1523	C1524	G1525	U1526	G1527	C1528	G1529

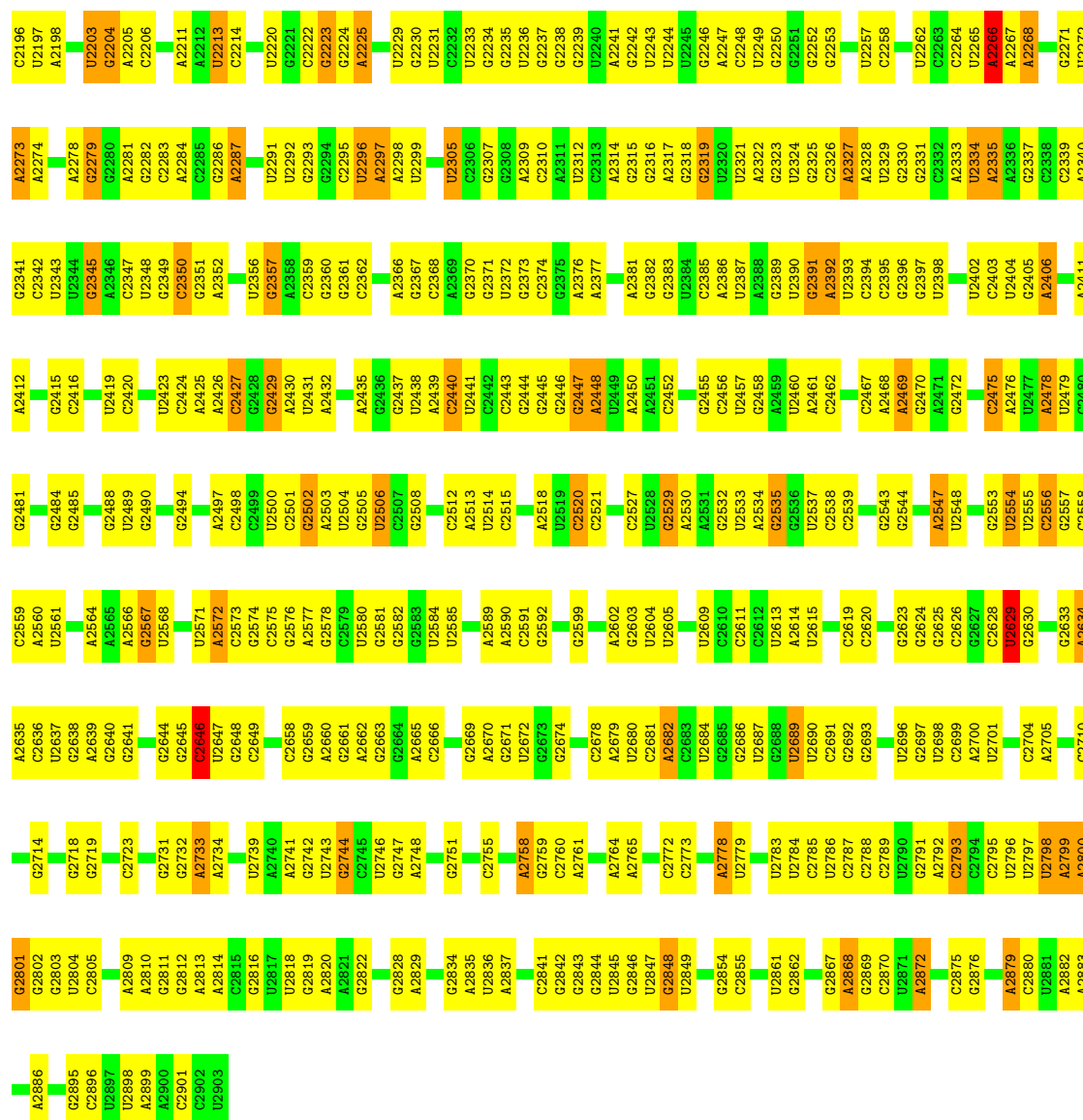


● Molecule 54: 23S ribosomal RNA

Chain 1: 43% 49% 8%

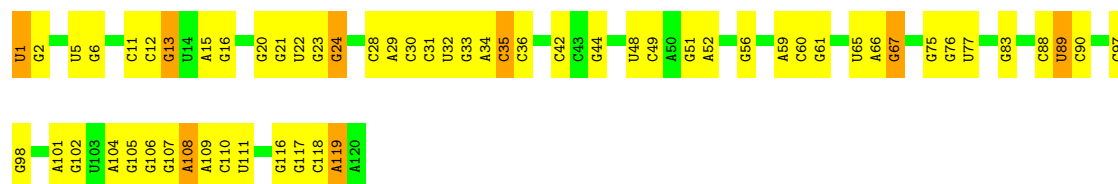


U2132	C2066	G1811	G1743	G1686	A1569	G1483	G1401	C1315	G1225	C1153	G1074
G2133	G2067	U1812	U1742	A1666	A1570	U1484	U1402	U1316	G1225	C1153	C1075
A2134	U2068	C1816	G1743	A1669	A1571	U1485	A1403	G1317	C1229	G1154	C1076
A2135	G2069	C1817	A1744	C1670	A1572	U1486	C1404	U1318	C1229	A1155	U1077
G2136	A2070	U1818	A1745	U1671	A1583	U1487	U1405	C1319	U1231	A1156	U1078
U2137	C2072	A1819	U1747	G1672	U1584	U1488	U1406	A1321	G1232	C1181	C1079
G2138	G2073	U1820	C1748	G1673	C1585	C1489	G1410	A1322	G1233	G1182	A1080
U2139	U2074	G1906	A1749	G1674	A1586	G1491	U1411	U1326	U1234	G1183	U1081
G2140	A2075	G1907	G1750	A1676	A1590	G1492	A1412	U1327	U1234	C1184	U1082
G2141	A2009	A1912	U1751	A1677	A1591	C1493	A1413	A1328	A1241	A1165	U1083
A2142	G2010	A1913	G1752	A1678	A1592	C1498	G1416	U1329	G1248	G1166	A1084
C2143	U2011	U1915	A1754	U1680	C1593	C1499	G1416	A1329	G1249	C1167	A1085
G2144	G2012	U1916	G1756	G1681	A1597	A1503	A1419	U1330	U1250	G1168	A1086
C2145	A2013	A1917	U1757	U1683	A1598	A1504	A1420	G1341	C1251	A1169	G1087
G2146	A2014	G1832	U1758	G1684	U1599	U1506	G1426	C1345	G1252	C1170	U1088
A2147	A2015	U1834	U1759	C1685	C1600	C1507	A1427	C1345	A1253	G1171	A1089
U2151	G2018	U1837	C1760	C1686	G1601	U1508	G1430	A1353	U1254	C1172	A1090
G2152	A2019	C1838	C1761	U1688	U1602	A1509	A1431	A1354	U1255	U1174	G1091
C2153	A2020	U1838	A1762	U1688	A1603	U1510	G1432	G1355	U1257	U1176	C1092
A2154	C2021	G1842	G1763	A1689	A1608	G1511	A1434	G1357	G1259	C1177	A1096
U2155	G2022	U1844	C1764	A1690	C1611	A1516	G1435	G1358	G1262	G1179	G1099
G2156	A2023	G1845	A1773	G1695	C1611	G1516	G1438	G1361	A1262	U1180	C1102
U2157	G2024	U1846	C1774	G1696	A1616	G1516	U1438	C1362	A1265	U1181	A1103
G2158	C2025	A1847	U1775	A1698	A1616	A1522	A1439	C1363	A1265	G1182	C1104
C2159	U2026	G1848	G1776	U1698	U1621	G1526	U1440	G1364	A1269	U1183	U1105
G2160	G2027	U1849	U1777	C1698	G1622	G1527	G1441	A1365	C1270	U1184	G1106
C2161	U2028	G1849	U1778	G1703	G1622	G1528	U1442	A1366	G1271	G1185	G1107
A2162	A2029	U1857	U1779	C1704	U1624	G1529	U1443	A1367	A1272	G1186	U1108
G2163	G2030	A1859	A1780	G1704	U1624	G1529	U1444	G1368	A1275	C1109	G1110
C2164	A2031	U1859	U1781	U1709	A1630	A1535	G1445	G1369	A1275	G1111	A1111
U2167	G2032	U1859	A1784	G1710	G1631	C1536	G1449	C1370	A1276	G1112	A1112
G2168	A2033	U1865	C1788	U1712	G1631	G1537	G1450	C1371	G1277	U1113	U1113
A2169	G2034	A1866	A1789	U1713	A1635	G1537	G1451	U1372	C1278	G1192	G1119
U2170	C2035	G1867	C1790	A1714	U1636	G1538	G1452	A1373	G1279	G1193	U1120
A2171	U2041	C1868	A1791	G1715	A1637	U1539	G1453	G1378	G1280	A1194	C1121
G2172	A2042	G1869	G1792	U1716	C1638	G1540	C1454	U1379	G1281	G1197	G1122
C2173	C2043	C1870	C1793	A1717	A1641	U1541	C1454	A1383	A1287	U1198	U1130
U2111	C2044	A1871	C1794	G1718	G1642	U1542	C1461	A1384	C1288	C1200	G1131
G2112	C2045	A1872	C1795	G1719	G1645	A1548	G1464	A1385	C1289	U1203	U1132
U2113	G2046	C1873	U1796	U1720	G1645	A1549	G1465	C1386	G1292	A1204	A1133
G2115	C2047	A1874	G1797	G1721	U1646	G1555	G1466	A1387	C1293	A1205	A1134
C2116	U2048	G1875	U1798	A1723	U1647	G1555	U1467	G1388	G1296	G1206	C1135
U2117	G2048	G1875	G1799	G1723	U1648	C1558	U1468	G1389	G1297	C1211	G1139
G2118	A2051	G1878	C1800	G1724	U1649	U1559	A1469	U1390	C1297	G1212	C1140
A2119	A2052	C1879	A1801	U1729	G1653	U1560	A1470	U1391	G1300	A1213	U1141
G2120	G2053	U1881	A1802	C1730	A1654	C1561	U1474	A1392	A1301	A1214	A1142
C2121	A2054	U1882	C1803	G1731	A1655	U1562	G1475	A1393	A1302	G1215	A1143
U2122	C2055	A1883	A1805	C1732	C1556	C1563	G1479	U1394	G1309	U1216	C1146
G2123	G2056	G1884	C1806	G1733	U1657	C1564	U1480	A1395	U1313	U1217	A1147
C2124	A2060	A1885	G1807	G1738	C1658	C1565	U1481	U1396	C1314	G1218	U1148
U2127	G2061	U1889	A1808	A1739	A1664	U1566	U1482	U1397	U1314	U1219	G1149
G2128	U2130	U1889	A1809	G1740	A1665	G1567	G1482	U1400			
C2129	U2131	U1890	A1810								
U2130											
U2131											



• Molecule 55: 5S ribosomal RNA

Chain 2: 51% 42% 7%

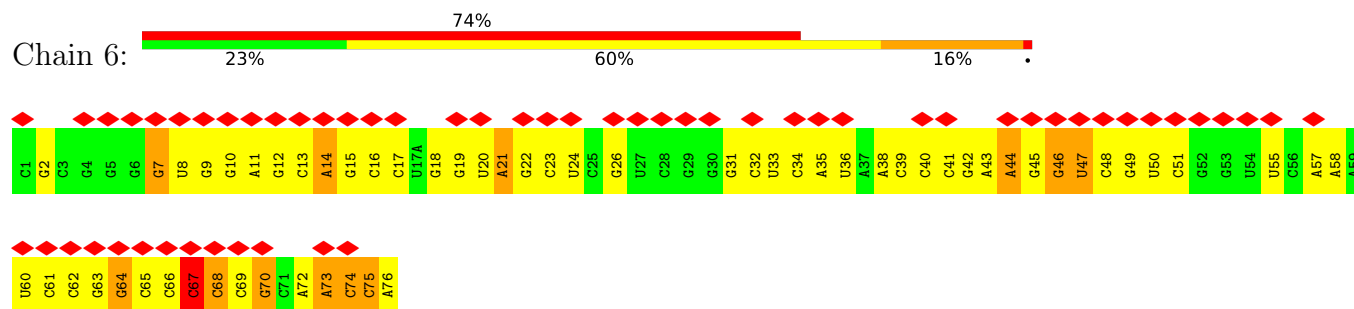


• Molecule 56: tRNA^{fMet}

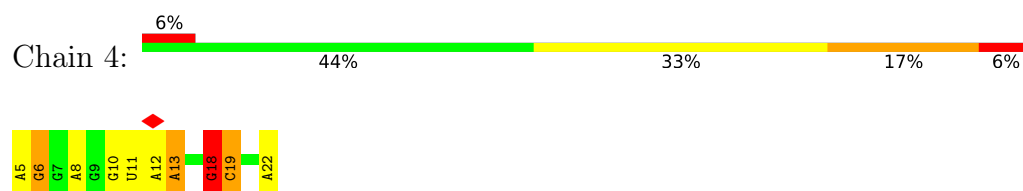
Chain 5: 55% 38% 8%



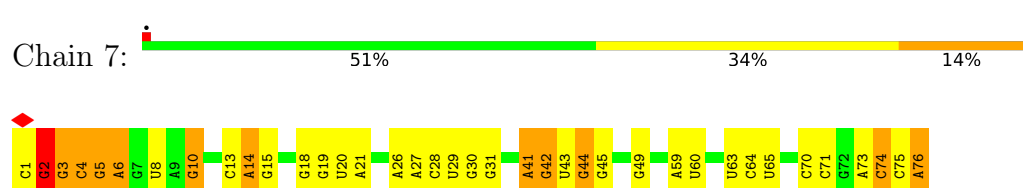
- Molecule 56: tRNA^{fMet}



- Molecule 57: mRNA



- Molecule 58: tRNA^{Pro}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4263	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	22.510	Depositor
Minimum map value	-7.018	Depositor
Average map value	0.018	Depositor
Map value standard deviation	1.404	Depositor
Recommended contour level	3.7	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.85	8/2122 (0.4%)	1.12	9/2852 (0.3%)
2	c	0.95	8/1586 (0.5%)	1.13	9/2134 (0.4%)
3	d	1.07	15/1571 (1.0%)	1.18	13/2113 (0.6%)
4	e	0.91	8/1435 (0.6%)	1.09	9/1926 (0.5%)
5	f	0.94	8/1343 (0.6%)	1.13	8/1816 (0.4%)
6	g	1.35	17/946 (1.8%)	1.51	22/1275 (1.7%)
7	h	1.34	10/638 (1.6%)	1.36	10/860 (1.2%)
8	i	2.18	24/564 (4.3%)	1.93	30/768 (3.9%)
9	j	1.10	11/1152 (1.0%)	1.12	13/1551 (0.8%)
10	k	1.01	8/948 (0.8%)	1.30	11/1268 (0.9%)
11	l	0.76	4/1054 (0.4%)	1.02	6/1403 (0.4%)
12	m	1.18	13/1093 (1.2%)	1.22	15/1460 (1.0%)
13	n	0.81	3/974 (0.3%)	1.03	6/1301 (0.5%)
14	o	1.26	14/902 (1.6%)	1.20	7/1209 (0.6%)
15	p	0.67	1/929 (0.1%)	0.95	4/1242 (0.3%)
16	q	0.79	3/960 (0.3%)	1.04	3/1278 (0.2%)
17	r	1.00	6/829 (0.7%)	1.29	11/1107 (1.0%)
18	s	0.92	5/864 (0.6%)	1.07	5/1156 (0.4%)
19	t	0.89	3/745 (0.4%)	0.99	5/994 (0.5%)
20	u	0.69	1/788 (0.1%)	0.98	2/1051 (0.2%)
21	v	0.77	2/766 (0.3%)	0.96	4/1025 (0.4%)
22	w	0.84	2/582 (0.3%)	1.01	0/769
23	x	0.76	2/635 (0.3%)	0.98	1/848 (0.1%)
24	y	1.16	6/510 (1.2%)	1.25	6/677 (0.9%)
25	z	0.86	2/453 (0.4%)	0.98	2/605 (0.3%)
26	A	0.82	3/532 (0.6%)	0.98	2/709 (0.3%)
27	B	0.60	1/450 (0.2%)	0.87	0/599
28	C	0.92	4/417 (1.0%)	1.01	3/554 (0.5%)
29	D	0.65	0/380	0.90	0/498
30	E	0.84	3/513 (0.6%)	0.90	0/676
31	F	0.83	1/303 (0.3%)	0.93	0/397
32	G	1.16	15/1736 (0.9%)	1.20	16/2338 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	1.03	12/1652 (0.7%)	1.10	13/2225 (0.6%)
34	I	0.99	14/1665 (0.8%)	1.22	16/2227 (0.7%)
35	J	0.95	8/1170 (0.7%)	1.18	9/1573 (0.6%)
36	K	1.76	22/836 (2.6%)	1.57	21/1128 (1.9%)
37	L	1.03	10/1196 (0.8%)	1.17	7/1602 (0.4%)
38	M	1.17	9/989 (0.9%)	1.20	9/1326 (0.7%)
39	N	0.85	6/1034 (0.6%)	1.14	6/1375 (0.4%)
40	O	0.97	5/797 (0.6%)	1.22	10/1077 (0.9%)
41	P	0.97	7/886 (0.8%)	1.20	9/1195 (0.8%)
42	Q	0.88	3/969 (0.3%)	1.15	8/1300 (0.6%)
43	R	1.08	9/893 (1.0%)	1.24	7/1193 (0.6%)
44	S	1.03	8/817 (1.0%)	1.05	4/1088 (0.4%)
45	T	0.93	7/722 (1.0%)	1.15	4/964 (0.4%)
46	U	0.95	4/659 (0.6%)	0.97	0/884
47	V	0.66	1/658 (0.2%)	1.04	4/881 (0.5%)
48	W	0.91	1/545 (0.2%)	1.09	3/731 (0.4%)
49	X	1.00	6/653 (0.9%)	1.13	4/877 (0.5%)
50	Y	1.17	4/671 (0.6%)	1.16	7/888 (0.8%)
51	Z	1.48	11/551 (2.0%)	1.50	12/728 (1.6%)
52	a	1.59	26/1034 (2.5%)	1.43	26/1387 (1.9%)
53	3	0.48	0/36963	0.55	3/57662 (0.0%)
54	1	0.48	0/69796	0.57	18/108888 (0.0%)
55	2	0.46	0/2872	0.58	1/4479 (0.0%)
56	5	0.45	0/1832	0.54	0/2855
56	6	0.52	0/1832	0.63	2/2855 (0.1%)
57	4	0.51	0/439	0.64	1/684 (0.1%)
58	7	0.48	0/1840	0.62	3/2868 (0.1%)
All	All	0.69	384/162691 (0.2%)	0.77	439/243399 (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
6	g	0	2
35	J	0	1
53	3	0	11
54	1	0	45
55	2	0	3
All	All	0	62

The worst 5 of 384 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	K	13	ASP	C-O	18.60	1.47	1.24
36	K	17	GLN	N-CA	16.38	1.65	1.46
12	m	119	LEU	C-O	16.32	1.43	1.24
9	j	27	ARG	C-O	16.23	1.43	1.24
32	G	59	ILE	C-O	16.21	1.43	1.24

The worst 5 of 439 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	K	50	PRO	CA-C-N	-12.70	110.89	122.96
36	K	50	PRO	C-N-CA	-12.70	110.89	122.96
2	c	144	GLY	O-C-N	-12.23	114.47	123.52
34	I	154	VAL	CA-C-N	-12.12	104.65	120.65
34	I	154	VAL	C-N-CA	-12.12	104.65	120.65

There are no chirality outliers.

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	3	159	G	Sidechain
53	3	94	G	Sidechain
35	J	92	ARG	Mainchain
6	g	41	LYS	Mainchain
6	g	49	ALA	Mainchain

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	b	2083	0	2157	134	0
2	c	1565	0	1616	96	0
3	d	1552	0	1619	78	0
4	e	1411	0	1447	93	0
5	f	1323	0	1374	70	0
6	g	936	0	961	73	0
7	h	633	0	666	57	0
8	i	551	0	577	62	0
9	j	1129	0	1162	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	k	939	0	1012	89	0
11	l	1045	0	1117	69	0
12	m	1074	0	1157	53	0
13	n	961	0	1000	54	0
14	o	892	0	923	62	0
15	p	917	0	965	58	0
16	q	947	0	1022	66	0
17	r	816	0	839	65	0
18	s	857	0	922	47	0
19	t	739	0	807	42	0
20	u	780	0	834	49	0
21	v	753	0	780	55	0
22	w	575	0	592	38	0
23	x	625	0	655	32	0
24	y	509	0	543	33	0
25	z	449	0	491	23	0
26	A	523	0	524	31	0
27	B	444	0	461	32	0
28	C	410	0	440	21	0
29	D	377	0	418	21	0
30	E	504	0	574	36	0
31	F	302	0	343	21	0
32	G	1705	0	1732	121	0
33	H	1625	0	1699	84	0
34	I	1643	0	1710	113	0
35	J	1157	0	1199	83	0
36	K	818	0	808	81	0
37	L	1182	0	1240	70	0
38	M	979	0	1034	51	0
39	N	1022	0	1070	79	0
40	O	787	0	828	73	0
41	P	870	0	878	66	0
42	Q	955	0	1019	76	0
43	R	884	0	944	57	0
44	S	805	0	847	71	0
45	T	714	0	737	45	0
46	U	649	0	666	52	0
47	V	649	0	691	59	0
48	W	536	0	552	37	0
49	X	638	0	665	48	0
50	Y	665	0	714	44	0
51	Z	545	0	579	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	a	1027	0	1092	77	0
53	3	33012	0	16618	723	0
54	1	62317	0	31346	1400	0
55	2	2568	0	1303	44	0
56	5	1640	0	836	24	0
56	6	1640	0	837	49	0
57	4	390	0	198	8	0
58	7	1647	0	832	32	0
59	5	10	0	10	1	0
All	All	149700	0	100682	4908	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 20.

The worst 5 of 4908 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)
54:1:1063:G:H1	54:1:1075:C:N4	1.40	1.17
54:1:1300:G:H4'	54:1:1301:A:H5''	1.28	1.15
6:g:9:VAL:HG12	6:g:11:ASN:H	0.97	1.11
42:Q:23:LEU:HD22	42:Q:29:LYS:HD3	1.33	1.06
36:K:3:HIS:H	36:K:92:THR:HG22	1.24	1.02

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	b	269/271 (99%)	235 (87%)	30 (11%)	4 (2%)	8	30
2	c	207/209 (99%)	182 (88%)	22 (11%)	3 (1%)	9	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	d	199/201 (99%)	176 (88%)	22 (11%)	1 (0%)	24	54
4	e	175/177 (99%)	152 (87%)	18 (10%)	5 (3%)	3	19
5	f	174/176 (99%)	148 (85%)	25 (14%)	1 (1%)	21	50
6	g	121/149 (81%)	99 (82%)	19 (16%)	3 (2%)	4	21
7	h	82/131 (63%)	62 (76%)	19 (23%)	1 (1%)	10	35
8	i	72/141 (51%)	56 (78%)	15 (21%)	1 (1%)	9	31
9	j	140/142 (99%)	124 (89%)	15 (11%)	1 (1%)	18	47
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	17
11	l	141/143 (99%)	121 (86%)	18 (13%)	2 (1%)	9	31
12	m	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	5	24
13	n	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	44
14	o	114/116 (98%)	99 (87%)	14 (12%)	1 (1%)	14	42
15	p	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	42
16	q	115/117 (98%)	106 (92%)	7 (6%)	2 (2%)	7	28
17	r	101/103 (98%)	85 (84%)	15 (15%)	1 (1%)	12	40
18	s	108/110 (98%)	95 (88%)	13 (12%)	0	100	100
19	t	91/93 (98%)	80 (88%)	11 (12%)	0	100	100
20	u	100/102 (98%)	81 (81%)	18 (18%)	1 (1%)	12	40
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	65 (89%)	7 (10%)	1 (1%)	9	31
23	x	75/77 (97%)	67 (89%)	7 (9%)	1 (1%)	9	33
24	y	61/63 (97%)	53 (87%)	7 (12%)	1 (2%)	7	29
25	z	56/58 (97%)	50 (89%)	4 (7%)	2 (4%)	2	16
26	A	64/66 (97%)	59 (92%)	5 (8%)	0	100	100
27	B	54/56 (96%)	44 (82%)	8 (15%)	2 (4%)	2	16
28	C	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
29	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
30	E	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	7	29
31	F	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
32	G	216/225 (96%)	178 (82%)	34 (16%)	4 (2%)	6	26
33	H	204/206 (99%)	189 (93%)	15 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	I	203/205 (99%)	165 (81%)	36 (18%)	2 (1%)	12	40
35	J	155/157 (99%)	132 (85%)	18 (12%)	5 (3%)	3	17
36	K	98/100 (98%)	78 (80%)	18 (18%)	2 (2%)	6	25
37	L	149/151 (99%)	123 (83%)	25 (17%)	1 (1%)	18	47
38	M	127/129 (98%)	111 (87%)	16 (13%)	0	100	100
39	N	125/127 (98%)	106 (85%)	15 (12%)	4 (3%)	3	17
40	O	96/98 (98%)	77 (80%)	17 (18%)	2 (2%)	5	24
41	P	114/116 (98%)	90 (79%)	21 (18%)	3 (3%)	4	21
42	Q	121/123 (98%)	92 (76%)	23 (19%)	6 (5%)	1	10
43	R	112/114 (98%)	92 (82%)	16 (14%)	4 (4%)	2	16
44	S	98/100 (98%)	82 (84%)	16 (16%)	0	100	100
45	T	86/88 (98%)	75 (87%)	10 (12%)	1 (1%)	10	35
46	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	21
47	V	78/80 (98%)	63 (81%)	12 (15%)	3 (4%)	2	15
48	W	63/65 (97%)	49 (78%)	11 (18%)	3 (5%)	2	11
49	X	77/79 (98%)	63 (82%)	14 (18%)	0	100	100
50	Y	83/85 (98%)	78 (94%)	3 (4%)	2 (2%)	4	22
51	Z	63/65 (97%)	40 (64%)	14 (22%)	9 (14%)	0	0
52	a	130/223 (58%)	105 (81%)	24 (18%)	1 (1%)	16	44
All	All	5836/6178 (94%)	4960 (85%)	778 (13%)	98 (2%)	9	28

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	108	GLY
2	c	77	ARG
3	d	83	VAL
4	e	175	PRO
6	g	9	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	213 (99%)	3 (1%)	59	70
2	c	164/164 (100%)	160 (98%)	4 (2%)	43	62
3	d	165/165 (100%)	162 (98%)	3 (2%)	51	67
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	70
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	98/114 (86%)	98 (100%)	0	100	100
7	h	66/100 (66%)	66 (100%)	0	100	100
8	i	60/109 (55%)	57 (95%)	3 (5%)	22	49
9	j	116/116 (100%)	113 (97%)	3 (3%)	40	61
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	66
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	75
12	m	109/109 (100%)	107 (98%)	2 (2%)	51	67
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	63
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	72
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	82 (99%)	1 (1%)	63	72
21	v	78/78 (100%)	76 (97%)	2 (3%)	40	61
22	w	57/57 (100%)	54 (95%)	3 (5%)	20	47
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	67
25	z	48/48 (100%)	47 (98%)	1 (2%)	47	64
26	A	59/59 (100%)	58 (98%)	1 (2%)	53	67
27	B	47/47 (100%)	47 (100%)	0	100	100
28	C	45/45 (100%)	44 (98%)	1 (2%)	45	63
29	D	38/38 (100%)	35 (92%)	3 (8%)	11	36
30	E	51/51 (100%)	51 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	F	34/34 (100%)	33 (97%)	1 (3%)	37	60
32	G	180/186 (97%)	178 (99%)	2 (1%)	65	74
33	H	170/170 (100%)	169 (99%)	1 (1%)	78	80
34	I	172/172 (100%)	170 (99%)	2 (1%)	63	72
35	J	119/119 (100%)	114 (96%)	5 (4%)	26	52
36	K	87/87 (100%)	83 (95%)	4 (5%)	24	50
37	L	124/124 (100%)	124 (100%)	0	100	100
38	M	104/104 (100%)	102 (98%)	2 (2%)	50	66
39	N	105/105 (100%)	103 (98%)	2 (2%)	50	66
40	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
41	P	89/89 (100%)	87 (98%)	2 (2%)	45	63
42	Q	103/103 (100%)	100 (97%)	3 (3%)	37	60
43	R	92/92 (100%)	90 (98%)	2 (2%)	45	63
44	S	83/83 (100%)	83 (100%)	0	100	100
45	T	76/76 (100%)	74 (97%)	2 (3%)	40	61
46	U	65/65 (100%)	60 (92%)	5 (8%)	12	37
47	V	74/74 (100%)	74 (100%)	0	100	100
48	W	56/56 (100%)	54 (96%)	2 (4%)	31	56
49	X	70/70 (100%)	68 (97%)	2 (3%)	37	60
50	Y	65/65 (100%)	64 (98%)	1 (2%)	57	69
51	Z	55/55 (100%)	54 (98%)	1 (2%)	51	67
52	a	110/174 (63%)	107 (97%)	3 (3%)	39	60
All	All	4862/5031 (97%)	4777 (98%)	85 (2%)	52	67

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	M	74	ILE
46	U	2	VAL
39	N	42	THR
42	Q	33	CYS
46	U	66	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
48	W	73	HIS
50	Y	20	ASN
52	a	172	HIS
13	n	9	GLN
12	m	45	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	168 (10%)	2 (0%)
54	1	2902/2903 (99%)	367 (12%)	11 (0%)
55	2	119/120 (99%)	10 (8%)	0
56	5	76/77 (98%)	11 (14%)	0
56	6	76/77 (98%)	25 (32%)	0
57	4	17/18 (94%)	5 (29%)	1 (5%)
58	7	76/77 (98%)	15 (19%)	3 (3%)
All	All	4804/4811 (99%)	601 (12%)	17 (0%)

5 of 601 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	4	U
53	3	5	U
53	3	6	G
53	3	9	G
53	3	22	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	7	2	G
58	7	41	A
54	1	1130	U
54	1	1930	G
54	1	2061	G

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	5	101	56	8,9,10	0.73	0	8,9,11	1.08	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	5	101	56	-	1/7/9/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	5	101	FME	O-C-CA	-2.59	118.11	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

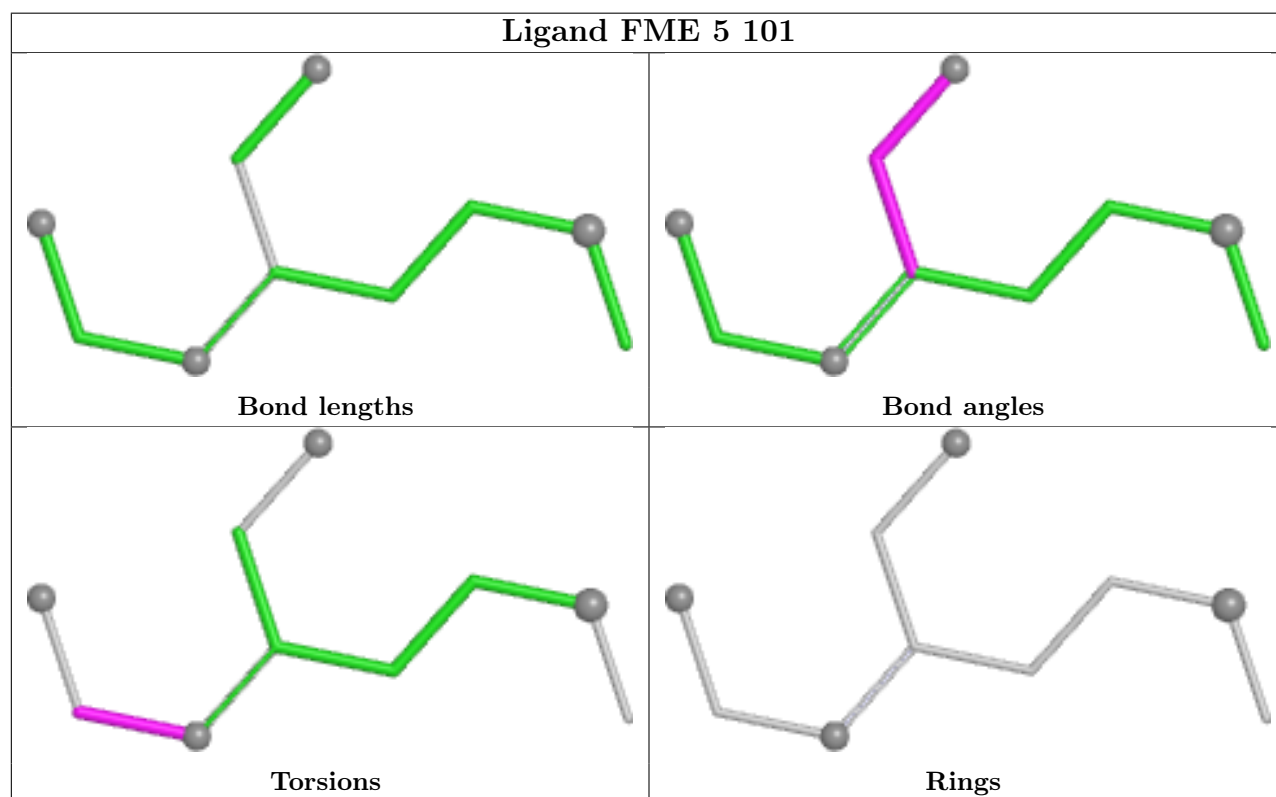
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	5	101	FME	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

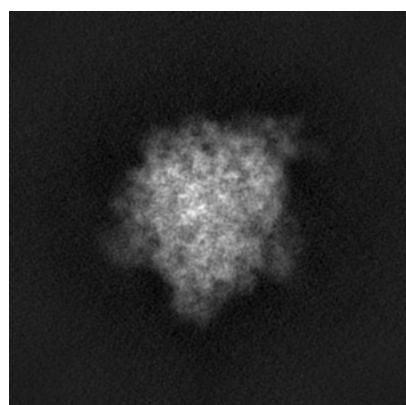
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22669. These allow visual inspection of the internal detail of the map and identification of artifacts.

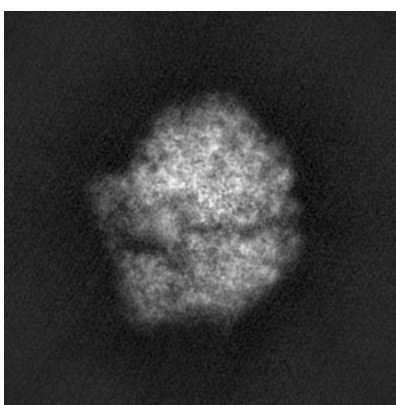
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

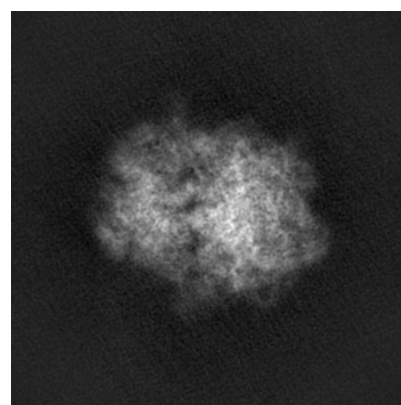
6.1.1 Primary map



X



Y

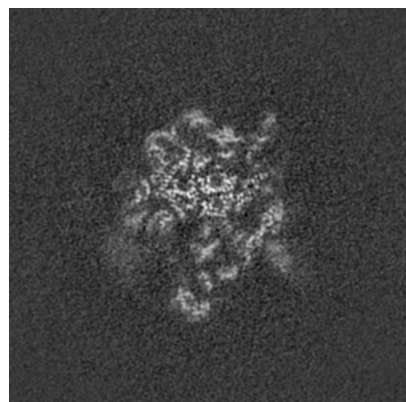


Z

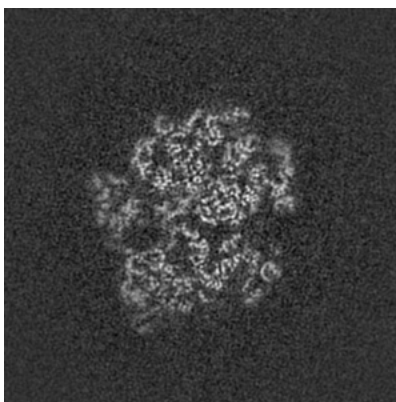
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

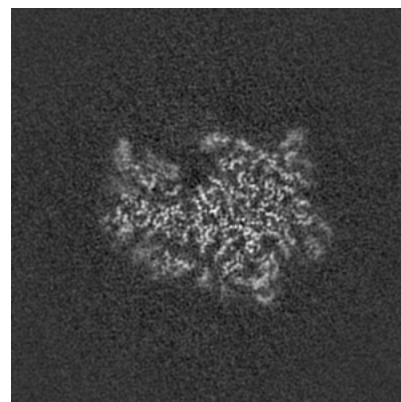
6.2.1 Primary map



X Index: 200



Y Index: 200

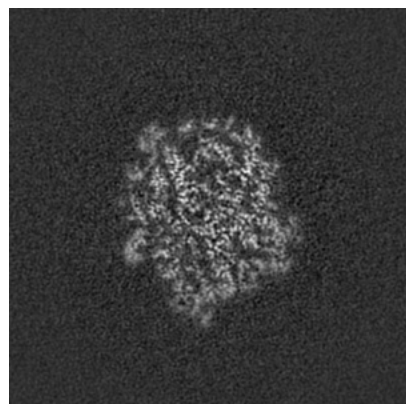


Z Index: 200

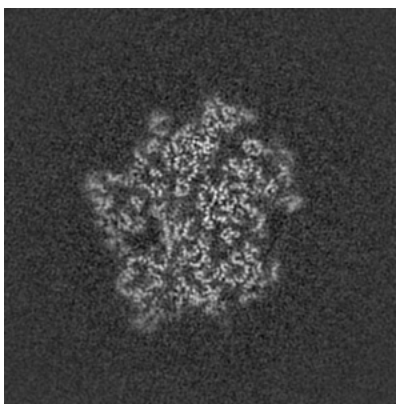
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

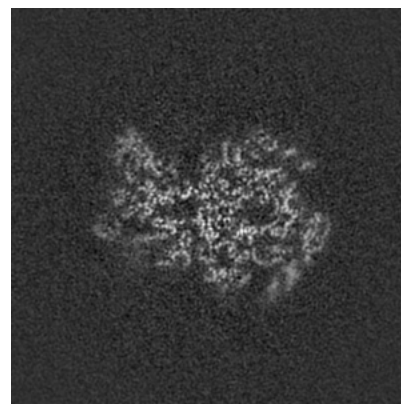
6.3.1 Primary map



X Index: 226



Y Index: 193

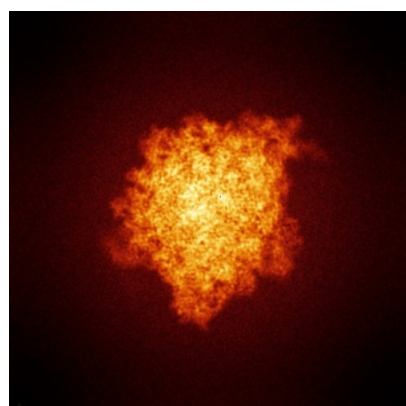


Z Index: 214

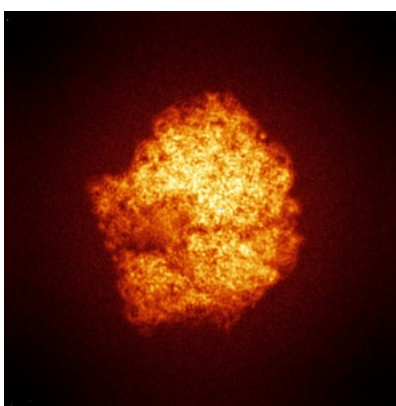
The images above show the largest variance slices of the map in three orthogonal directions.

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

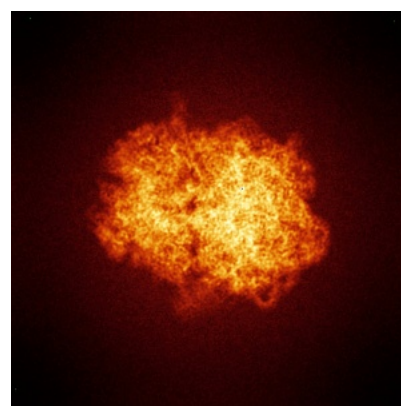
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

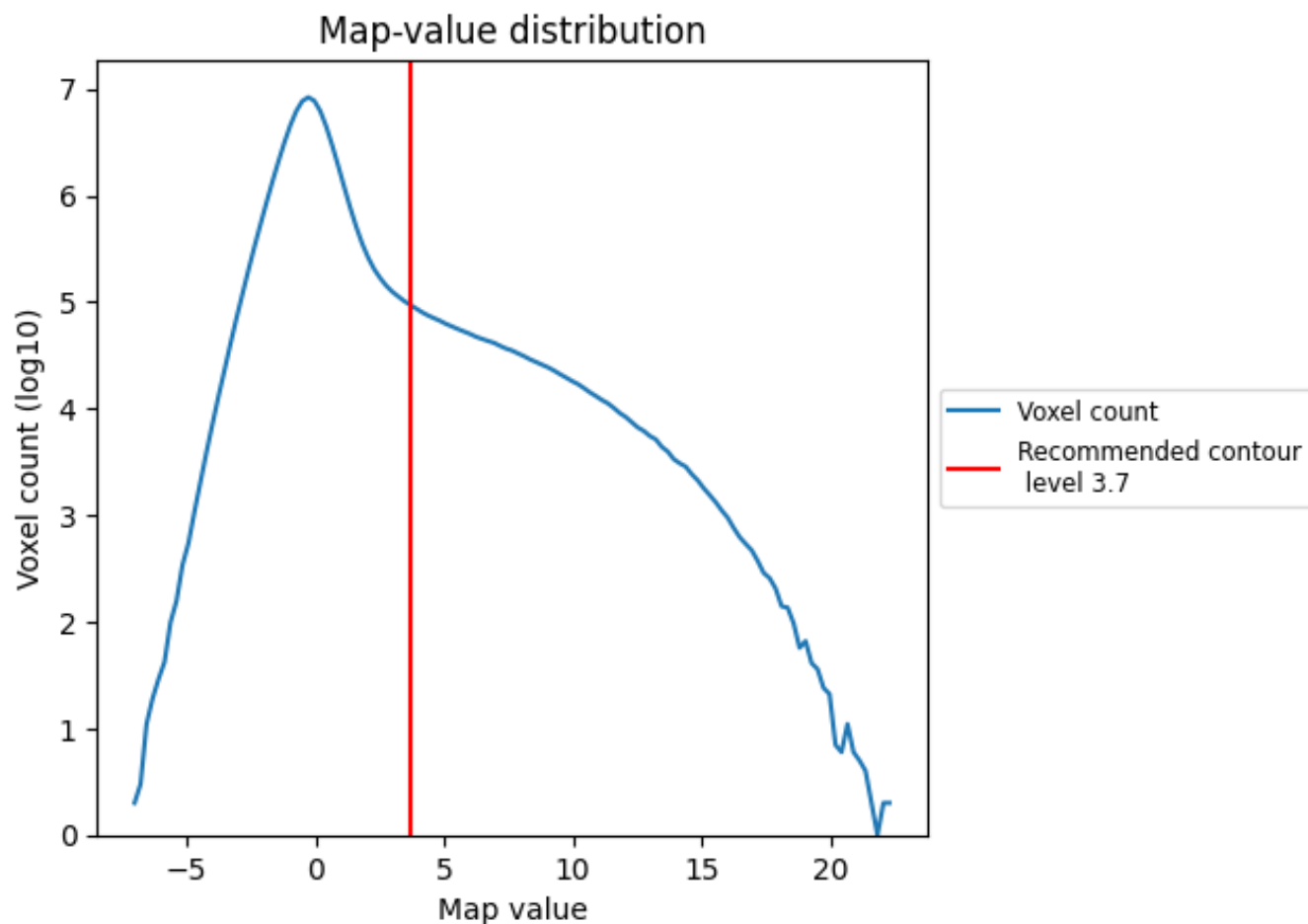
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

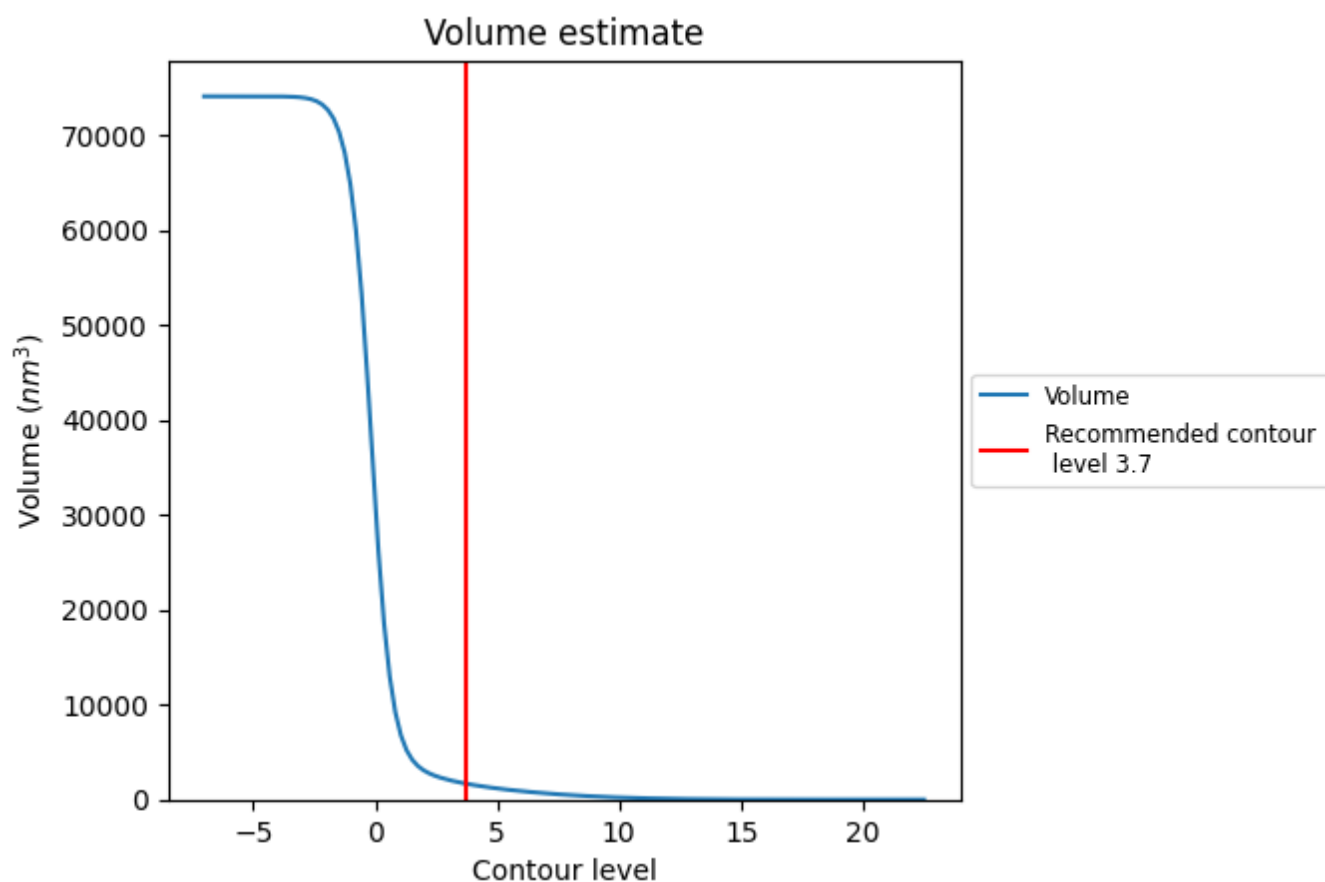
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

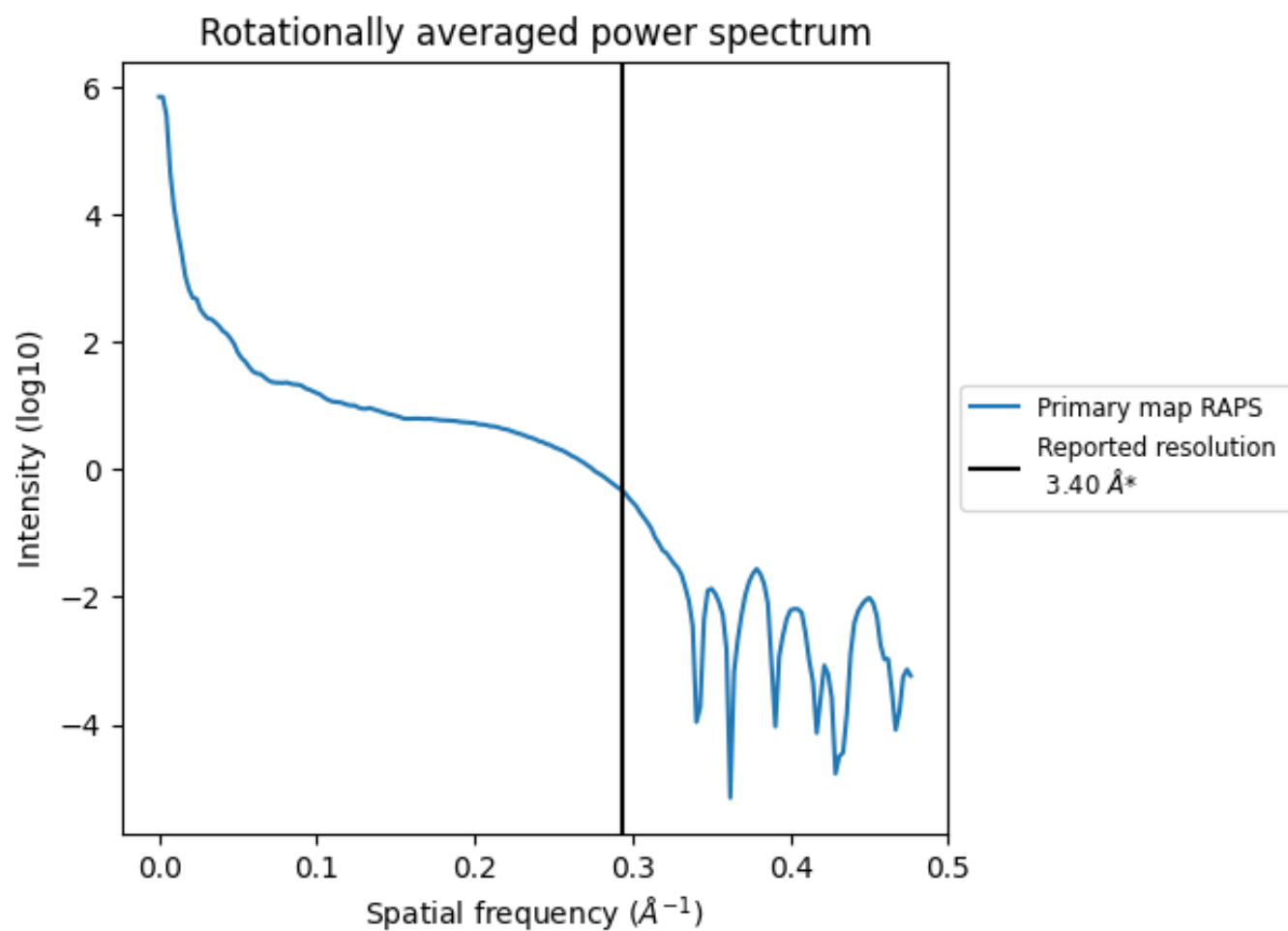
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1687 nm^3 ; this corresponds to an approximate mass of 1524 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

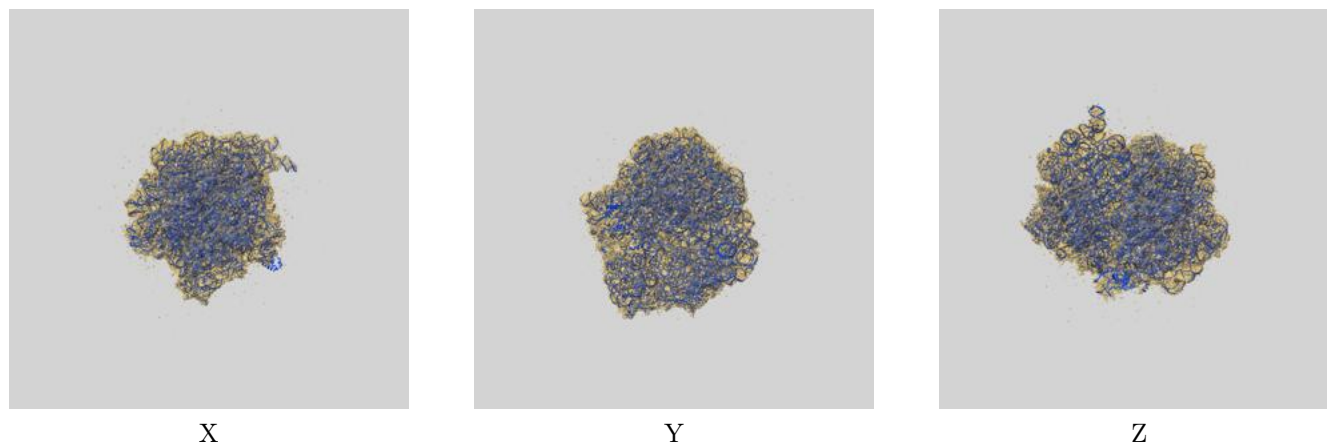
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

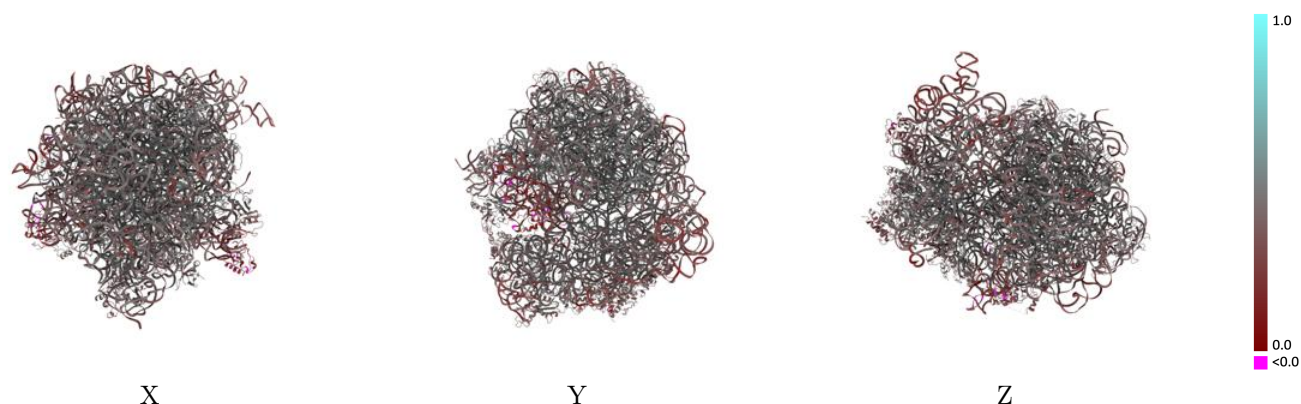
This section contains information regarding the fit between EMDB map EMD-22669 and PDB model 7K50. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



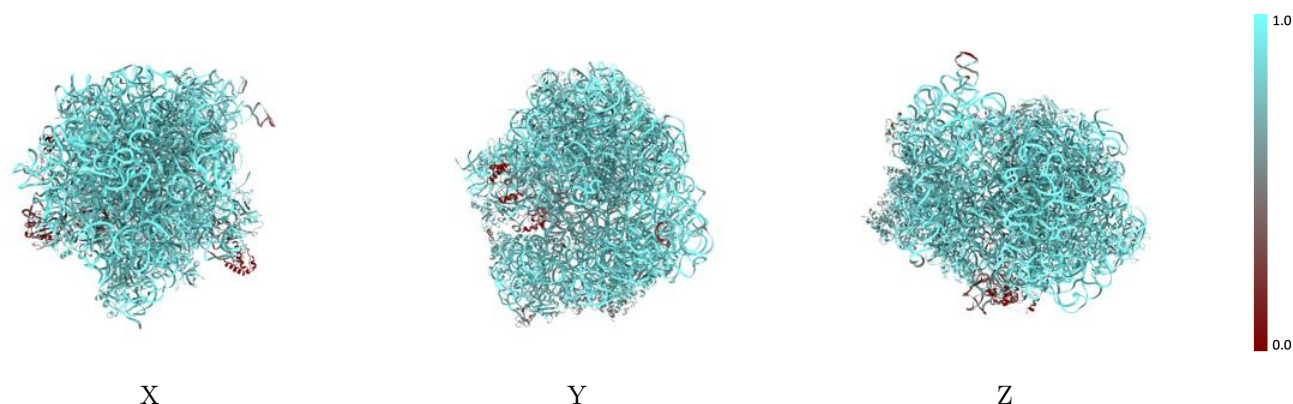
The images above show the 3D surface view of the map at the recommended contour level 3.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



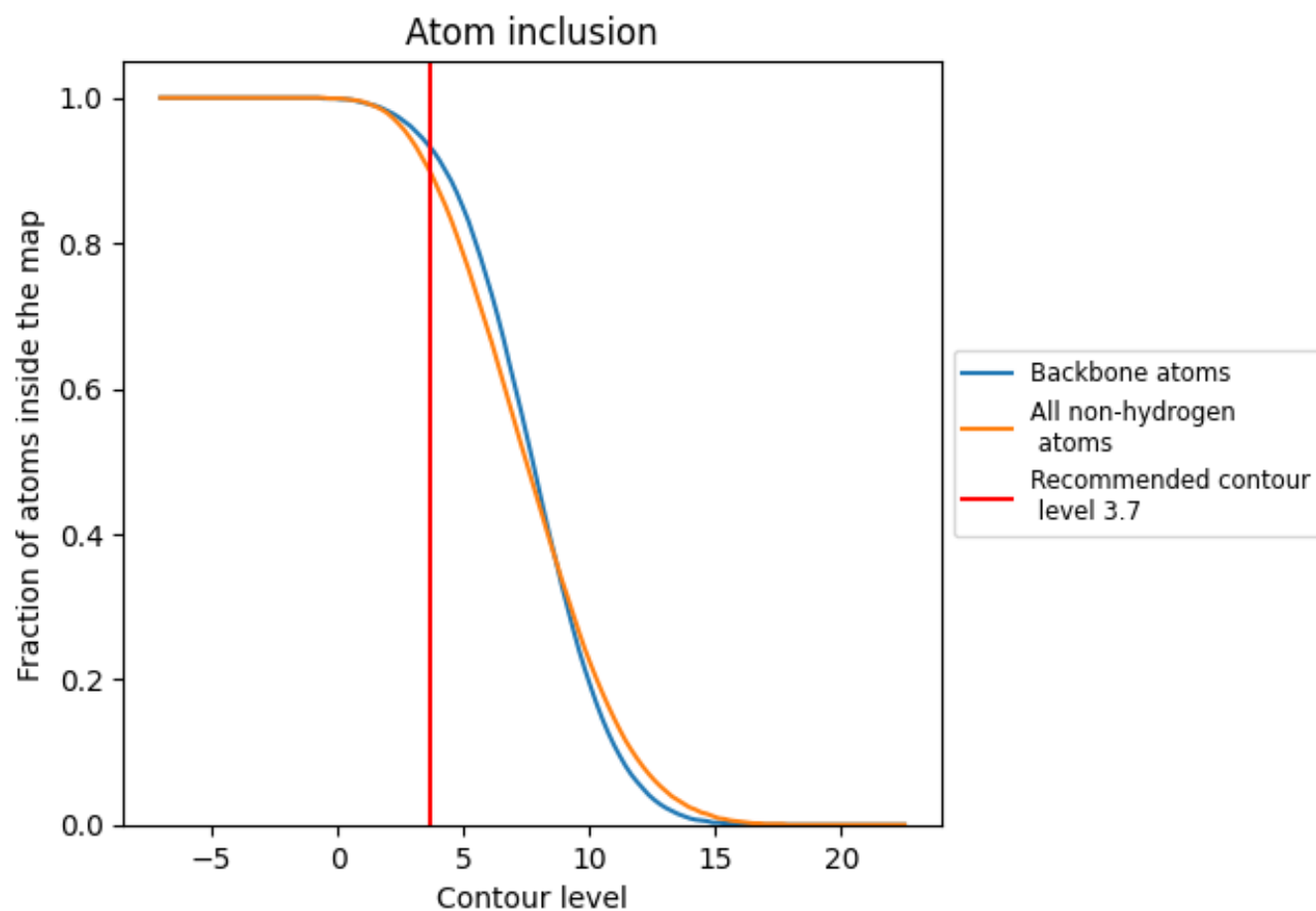
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.7).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.4070
1	 0.9590	 0.4180
2	 0.9640	 0.4020
3	 0.9520	 0.4030
4	 0.8280	 0.3170
5	 0.9420	 0.3770
6	 0.3010	 0.2080
7	 0.8300	 0.2860
A	 0.7320	 0.3540
B	 0.8810	 0.4490
C	 0.6720	 0.4250
D	 0.9300	 0.4570
E	 0.9160	 0.4720
F	 0.8560	 0.4570
G	 0.6520	 0.3740
H	 0.8000	 0.4180
I	 0.7470	 0.3540
J	 0.8750	 0.4390
K	 0.8560	 0.4070
L	 0.8150	 0.3830
M	 0.8480	 0.4320
N	 0.7760	 0.3930
O	 0.6420	 0.3920
P	 0.8690	 0.4210
Q	 0.8640	 0.3970
R	 0.8070	 0.3910
S	 0.8170	 0.4060
T	 0.8840	 0.4210
U	 0.8310	 0.3960
V	 0.8470	 0.4070
W	 0.8470	 0.4020
X	 0.7940	 0.3880
Y	 0.8140	 0.3810
Z	 0.7200	 0.3420
a	 0.1940	 0.2500



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Chain	Atom inclusion	Q-score
b	 0.9230	 0.4750
c	 0.8990	 0.4600
d	 0.7970	 0.4240
e	 0.8130	 0.3980
f	 0.8060	 0.3840
g	 0.2960	 0.3170
h	 0.0990	 0.1940
i	 0.2810	 0.2320
j	 0.8940	 0.4480
k	 0.8650	 0.4570
l	 0.8800	 0.4470
m	 0.8800	 0.4610
n	 0.9020	 0.4470
o	 0.8370	 0.3910
p	 0.8770	 0.4530
q	 0.8910	 0.4430
r	 0.8370	 0.4260
s	 0.8550	 0.4430
t	 0.8480	 0.4330
u	 0.8480	 0.4130
v	 0.8350	 0.4140
w	 0.8750	 0.4680
x	 0.8880	 0.4510
y	 0.7990	 0.3680
z	 0.8400	 0.4300