Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 10:16 AM EST

PDB ID	:	7MT3
EMDB ID	:	EMD-23975
Title	:	Mtb 70S with P/E tRNA
Authors	:	Cui, Z.; Zhang, J.
Deposited on	:	2021-05-12
Resolution	:	2.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

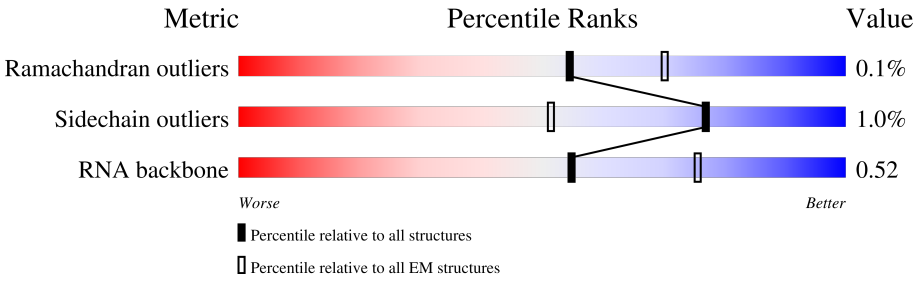
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	0	57	11% 95% 5%
2	1	55	87% 13%
3	2	47	91% 6%
4	3	64	97%
5	4	37	97%
6	6	80	18% 70% 29%
7	7	24	58% 63% 38%
8	8	235	93% 96%

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Mol	Chain	Length	Quality of chain
9	A	3138	10% 81% 17%
10	B	115	88% 12%
11	C	280	96%
12	D	217	98%
13	E	223	92% 7%
14	F	187	6% 94% 5%
15	G	179	10% 97%
16	H	152	23% 30% 69%
17	J	195	75% 25%
18	K	122	99%
19	L	146	98%
20	M	138	5% 96%
21	N	180	64% 36%
22	O	122	98%
23	P	113	99%
24	Q	129	95%
25	R	104	94%
26	S	197	57% 43%
27	T	100	94% 5%
28	U	105	83% 14%
29	V	215	11% 80% 18%
30	W	86	83% 16%
31	X	64	94%
32	Y	77	88% 12%
33	Z	65	88% 9%

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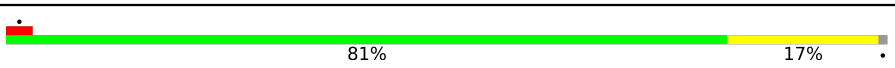
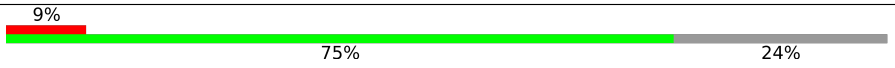
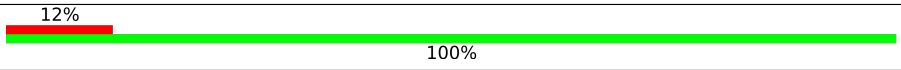
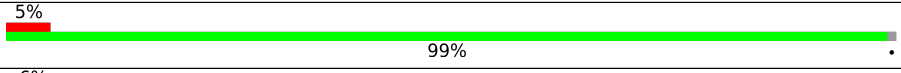
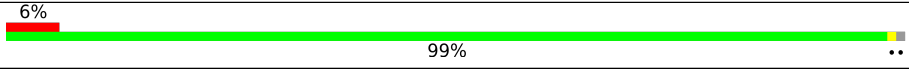
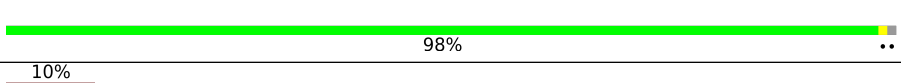
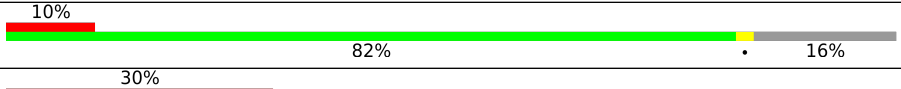
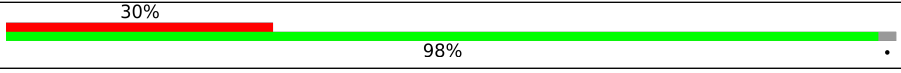
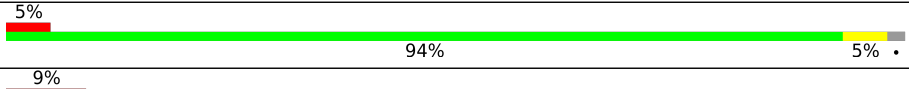
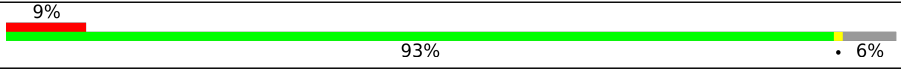
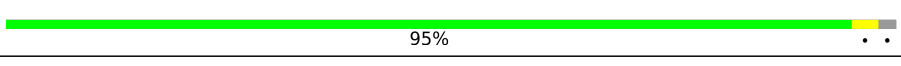
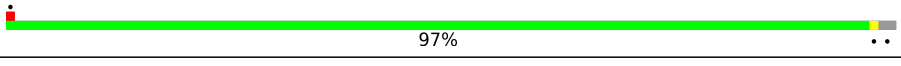
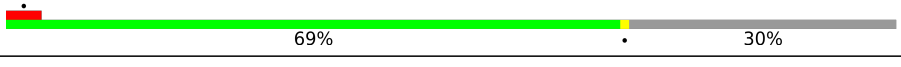
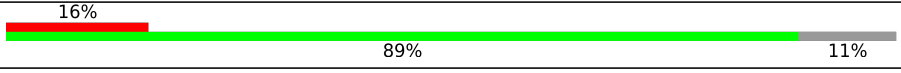
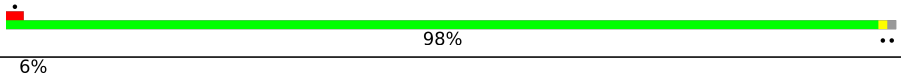
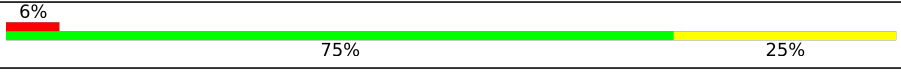
Mol	Chain	Length	Quality of chain
34	a	1537	
35	c	274	
36	d	201	
37	e	220	
38	f	96	
39	g	156	
40	h	132	
41	i	151	
42	j	101	
43	k	139	
44	l	124	
45	m	124	
46	n	61	
47	o	89	
48	p	162	
49	q	135	
50	r	84	
51	s	93	
52	t	86	
53	y	77	
54	z	26	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147942 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	0	54	429	266	94	69	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	48	400	245	84	67	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	44	374	222	97	54	1	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	3	62	494	298	112	84	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	299	182	66	47	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	1	VAL	MET	conflict	UNP P9WH89

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	57	Total	C	N	O	S	0	0
			446	277	82	82	5		

- Molecule 7 is a protein called 50S ribosomal protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	7	15	Total	C	N	O	0	0
			120	71	32	17		

- Molecule 8 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	230	Total	C	N	O	S	0	0
			1704	1068	310	323	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	3118	Total	C	N	O	P	0	0
			66958	29847	12340	21653	3118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	115	Total	C	N	O	P	0	0
			2458	1097	456	790	115		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	272	Total	C	N	O	S	0	0
			2088	1277	437	369	5		

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	213	Total	C	N	O	S	0	0
			1590	985	307	292	6		

- Molecule 13 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	207	Total	C	N	O	S	0	0
			1552	958	303	289	2		

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	178	Total	C	N	O	S	0	0
			1408	885	267	251	5		

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	174	Total	C	N	O	S	0	0
			1330	836	249	244	1		

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	47	Total	C	N	O	S	0	0
			350	220	64	65	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	146	Total	C	N	O	S	0	0
			1143	724	217	199	3		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			941	590	180	169	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	VAL	MET	conflict	UNP A0A045HTP7

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	144	Total	C	N	O	S	0	0
			1075	666	217	190	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	134	Total	C	N	O	S	0	0
			1072	679	215	177	1		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	116	Total	C	N	O	S	0	0
			908	574	175	158	1		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	O	119	Total	C	N	O	0	0
			905	552	191	162		

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	112	Total	C	N	O	S	0	0
			907	573	174	159	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Q	124	Total	C	N	O	0	0
			993	616	207	170		

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	R	100	Total	C	N	O	0	0
			757	482	138	137		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	MET	-	insertion	UNP P9WHC3

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	S	113	Total	C	N	O	0	0
			860	533	178	149		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	T	95	Total	C	N	O	0	0
			741	469	138	134		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	90	Total	C	N	O	S	0	0
			699	430	138	129	2		

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	V	177	Total	C	N	O	0	0
			1319	822	243	254		

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	W	72	Total	C	N	O	0	0
			537	331	112	94		

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	62	Total	C	N	O	S	0	0
			468	284	100	80	4		

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	68	Total	C	N	O	S	0	0
			560	343	109	107	1		

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z	59	Total	C	N	O	0	0
			476	293	101	82		

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1519	Total	C	N	O	P	0	0
			32620	14535	5961	10605	1519		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	207	Total	C	N	O	S	0	0
			1654	1030	322	298	4		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	200	Total	C	N	O	S	0	0
			1650	1036	316	296	2		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	169	Total	C	N	O	S	0	0
			1222	770	231	218	3		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	95	Total	C	N	O	S	0	0
			757	480	133	141	3		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	155	Total	C	N	O	S	0	0
			1230	768	241	219	2		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	131	Total	C	N	O	S	0	0
			1006	631	188	186	1		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	i	127	Total	C	N	O	0	0
			992	628	195	169		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	99	Total	C	N	O	S	0	0
			789	496	146	144	3		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	k	117	Total	C	N	O	0	0
			873	540	175	158		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	122	Total	C	N	O	S	0	0
			959	594	197	166	2		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	116	Total	C	N	O	S	0	0
			945	578	196	168	3		

- Molecule 46 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	60	Total	C	N	O	S	0	0
			468	294	96	73	5		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	o	87	Total	C	N	O	0	0
			718	449	144	125		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	p	113	Total	C	N	O	0	0
			884	564	166	154		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	95	Total	C	N	O	S	0	0
			770	482	152	133	3		

- Molecule 50 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	64	Total	C	N	O	S	0	0
			506	315	98	90	3		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	83	Total	C	N	O	S	0	0
			672	432	125	114	1		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	t	85	Total	C	N	O	0	0
			652	394	141	117		

- Molecule 53 is a RNA chain called tRNA (Met).

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	6	Total	C	N	O	P	0	0
			129	58	25	40	6		

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	1	1	Total	Zn	0
			1	1	
55	4	1	Total	Zn	0
			1	1	
55	6	1	Total	Zn	0
			1	1	
55	X	1	Total	Zn	0
			1	1	
55	n	1	Total	Zn	0
			1	1	
55	r	1	Total	Zn	0
			1	1	

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	298	Total	Mg	0
			298	298	
56	B	5	Total	Mg	0
			5	5	
56	C	2	Total	Mg	0
			2	2	
56	D	1	Total	Mg	0
			1	1	
56	L	1	Total	Mg	0
			1	1	
56	a	125	Total	Mg	0
			125	125	
56	r	1	Total	Mg	0
			1	1	

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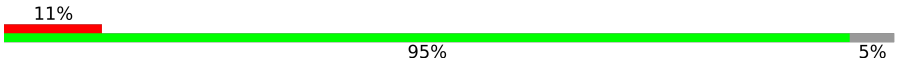
Mol	Chain	Residues	Atoms	AltConf
56	t	1	Total Mg 1 1	0
56	z	1	Total Mg 1 1	0

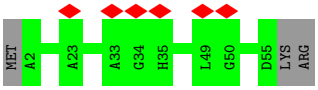
3 Residue-property plots (i)

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 L32

Chain 0:



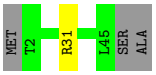


• Molecule 2: 50S ribosomal protein L33 2

Chain 1:

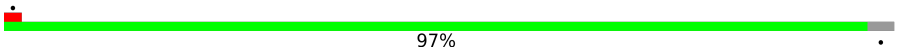
• Molecule 3: 50S ribosomal protein L34

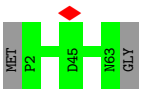
Chain 2:



• Molecule 4: 50S ribosomal protein L35

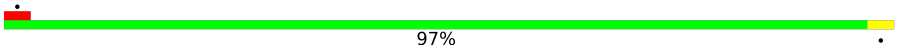
Chain 3:

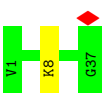




• Molecule 5: 50S ribosomal protein L36

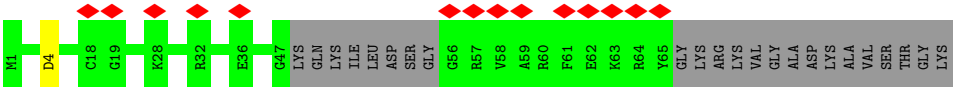
Chain 4:





• Molecule 6: 50S ribosomal protein L31

Chain 6:

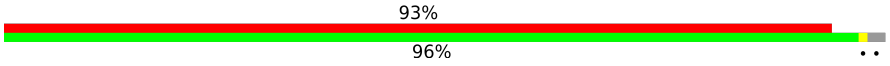


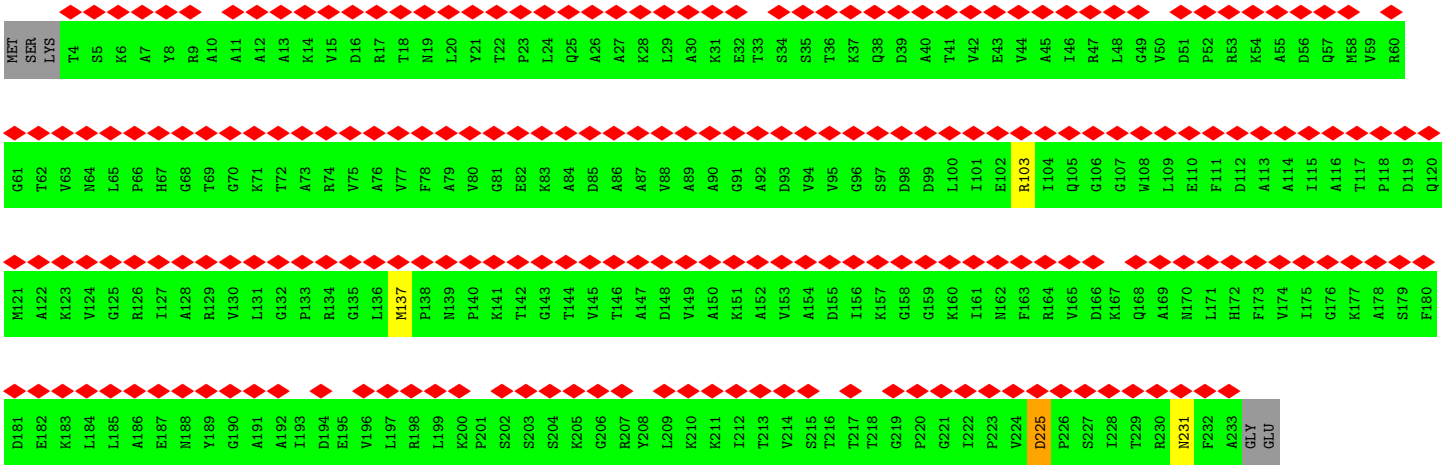
• Molecule 7: 50S ribosomal protein L37

Chain 7:

• Molecule 8: 50S ribosomal protein L1

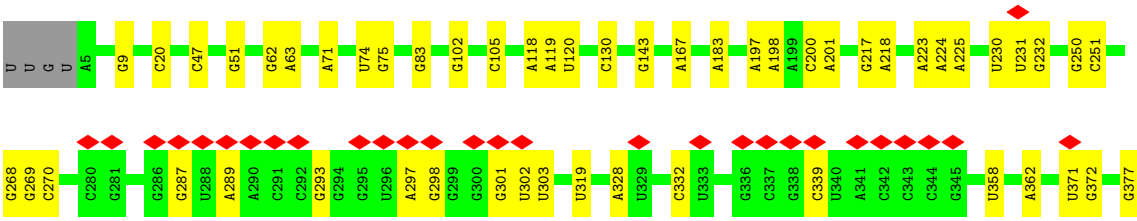
Chain 8:

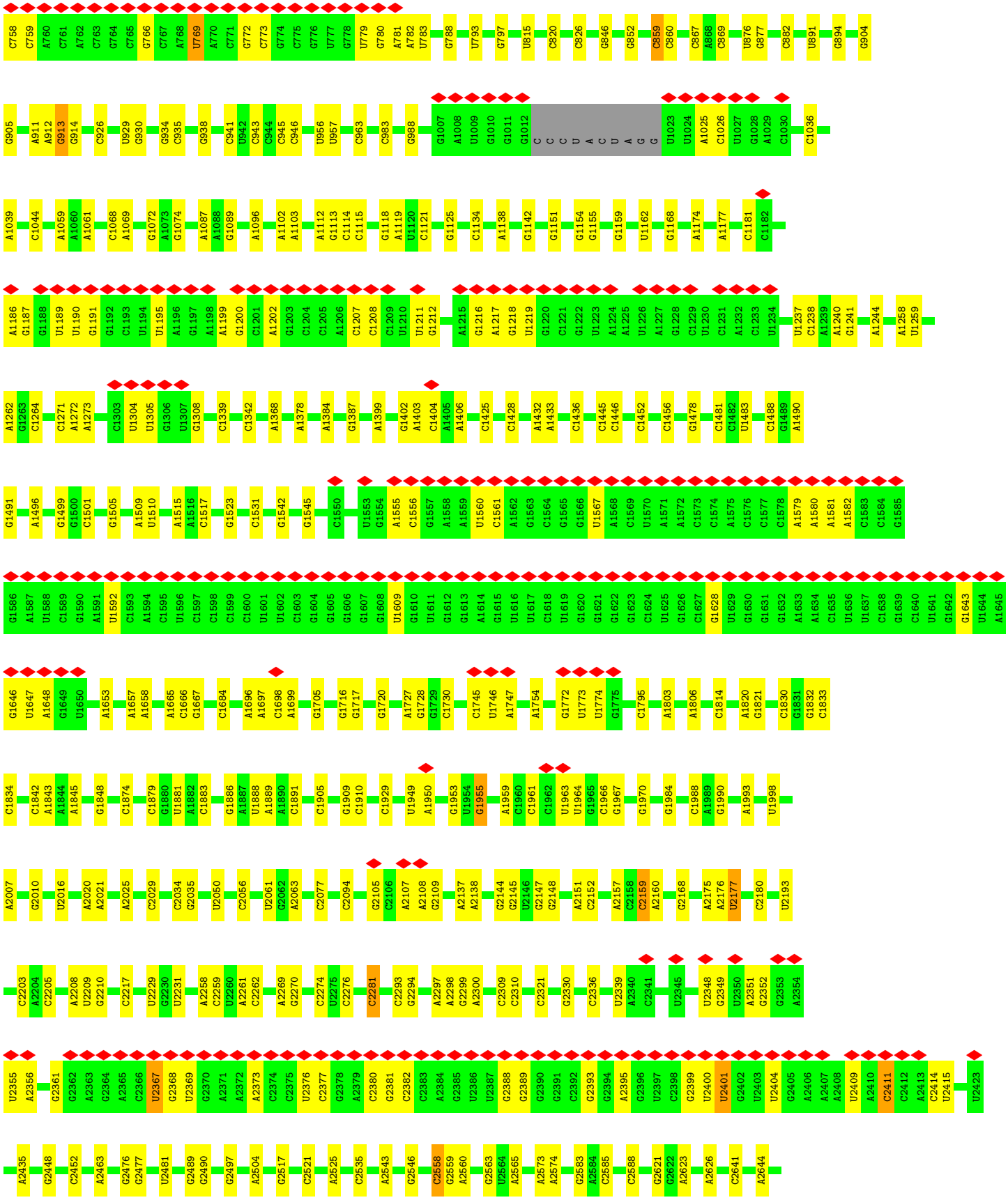




• Molecule 9: 23S rRNA

Chain A:

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G905 A911 A912 G913 G914 C926 U929 G930 G934 C935 G938 C941 U942 C943 C944 C945 C946 U956 U957 C963 C983 G988 G1007 A1008 U1009 G1010 G1011 G1012 C C C C U A C U A G G U1023 U1024 A1025 C1026 U1027 G1028 A1029 C1030 C1036
A1039 C1044 A1059 A1060 A1061 C1068 A1069 G1072 A1073 G1074 A1087 A1088 G1089 A1096 A1102 A1103 A1112 G1113 C1114 C1115 G1118 A1119 U1120 C1121 G1125 C1134 A1138 G1142 G1151 G1154 G1155 G1159 U1162 G1168 A1174 A1177 C1181 C1182
A1186 G1187 G1188 U1189 U1190 G1191 G1192 C1193 U1194 U1195 A1196 G1197 A1198 A1199 G1200 C1201 A1202 G1203 C1204 C1205 A1206 C1207 C1208 C1209 U1210 U1211 G1212 A1215 G1216 A1217 G1218 U1219 G1220 C1221 G1222 U1223 A1224 A1225 U1226 A1227 G1228 C1229 U1230 C1231 A1232 C1233 U1234 U1237 C1238 A1239 A1240 G1241 A1244 A1258 U1259
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G1491 A1496 G1499 G1500 C1501 G1505 A1509 U1510 A1515 A1516 C1517 G1523 C1531 G1542 G1545 C1550 U1553 G1554 A1555 C1556 G1557 A1558 A1559 U1560 C1561 A1562 G1563 C1564 G1565 G1566 U1567 A1568 C1569 U1570 A1571 A1572 C1573 C1574 A1575 C1576 C1577 C1578 A1579 A1580 A1581 A1582 C1583 C1584 G1585
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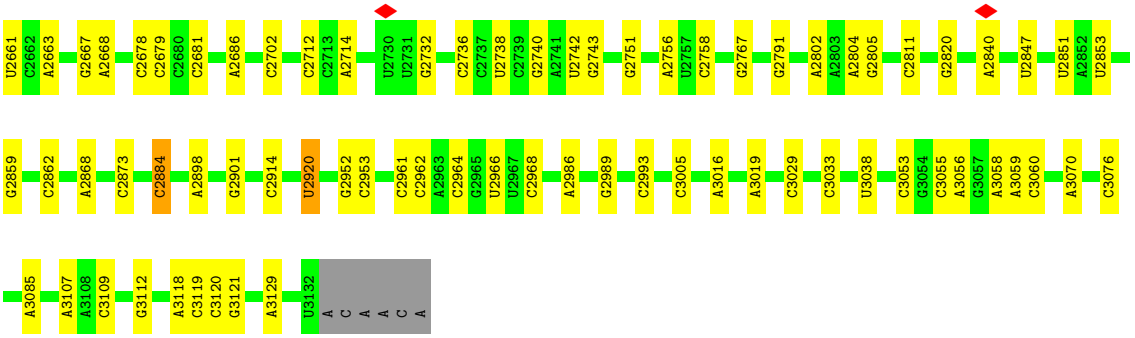
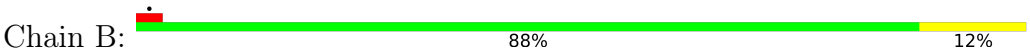
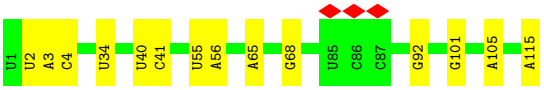
C1834 C1842 A1843 A1844 A1845 G1848 C1874 C1879 G1880 U1881 A1882 C1883 G1886 A1887 U1888 A1889 A1890 C1891 C1905 G1909 C1910 C1929 U1949 A1950 G1953 U1954 G1955 A1959 C1960 C1961 C1962 U1963 U1964 G1965 C1966 G1967 G1970 G1984 C1988 A1989 G1990 A1993 U1998
A2007 G2010 U2016 A2020 A2021 A2025 C2029 C2034 G2035 U2050 C2056 U2061 G2062 A2063 C2077 C2094 G2105 C2106 A2107 A2108 G2109 A2137 A2138 G2144 G2145 U2146 G2147 G2148 A2151 C2152 A2157 C2158 C2159 A2160 G2168 A2175 A2176 U2177 C2180 U2193
C2203 A2204 C2205 A2208 U2209 G2210 C2217 U2229 G2230 U2231 A2258 C2259 U2260 A2261 C2262 A2269 G2270 C2274 U2275 C2276 C2281 C2293 G2294 A2297 A2298 G2299 A2300 C2309 C2310 C2321 G2330 C2336 U2339 A2340 C2341 U2345 U2348 G2349 U2350 A2351 G2352 G2353 A2354
U2355 A2356 G2361 G2362 A2363 G2364 A2365 C2366 U2367 G2368 U2369 G2370 A2371 A2372 A2373 C2374 C2375 U2376 C2377 G2378 A2379 C2380 G2381 C2382 C2383 A2384 G2385 U2386 U2387 G2388 G2389 G2390 G2391 C2392 G2393 G2394 A2395 G2396 U2397 C2398 G2399 U2400 U2401 G2402 U2403 U2404 G2405 A2406 A2407 A2408 U2409 A2410 C2411 C2412 A2413 C2414 U2415 U2423
A2435 G2448 C2452 A2463 G2476 G2477 U2481 G2489 G2490 G2497 A2504 G2517 C2521 A2525 C2535 A2543 G2546 C2558 G2559 A2560 G2563 U2564 A2565 A2573 A2574 G2583 A2584 C2585 C2588 G2621 G2622 A2623 A2626 C2641 A2644

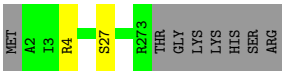


• Molecule 10: 5S rRNA

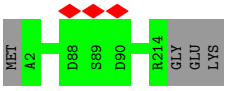




• Molecule 11: 50S ribosomal protein L2

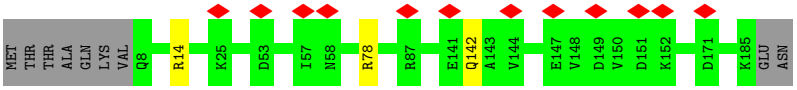


• Molecule 12: 50S ribosomal protein L3

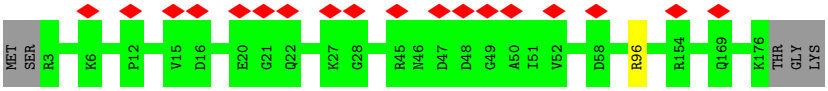


• Molecule 13: 50S ribosomal protein L4

• Molecule 14: 50S ribosomal protein L5

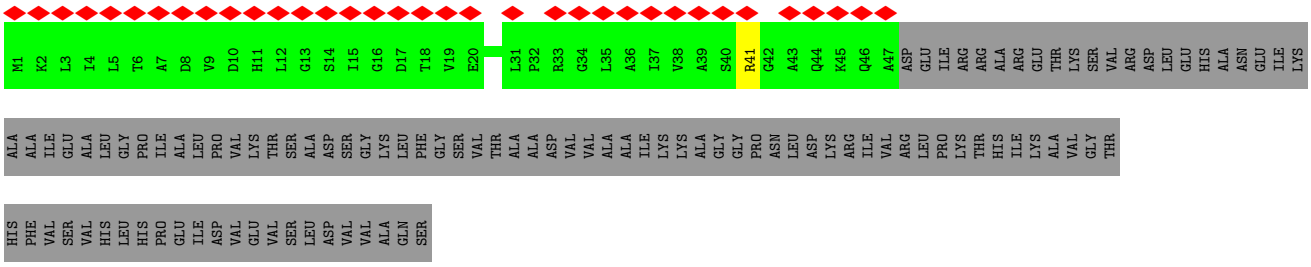


• Molecule 15: 50S ribosomal protein L6



• Molecule 16: 50S ribosomal protein L9

Chain H:

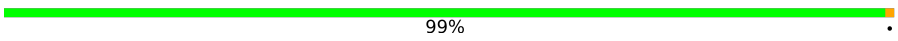


• Molecule 17: 50S ribosomal protein L13

Chain J:

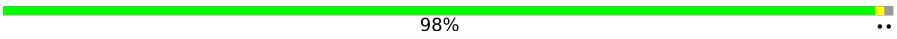
• Molecule 18: 50S ribosomal protein L14

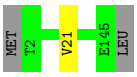
Chain K:



• Molecule 19: 50S ribosomal protein L15

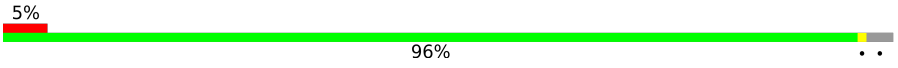
Chain L:

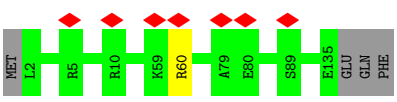




• Molecule 20: 50S ribosomal protein L16

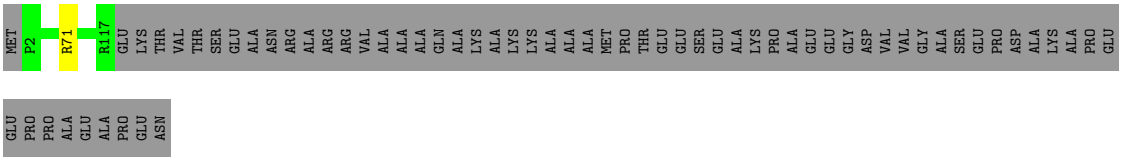
Chain M:





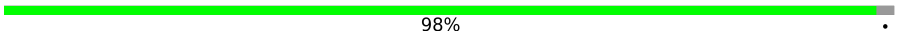
• Molecule 21: 50S ribosomal protein L17

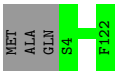
Chain N:



• Molecule 22: 50S ribosomal protein L18

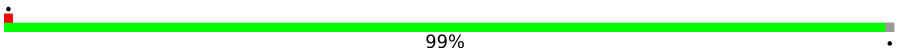
Chain O:

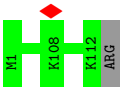




• Molecule 23: 50S ribosomal protein L19

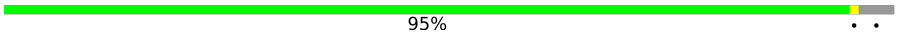
Chain P:

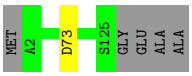




• Molecule 24: 50S ribosomal protein L20

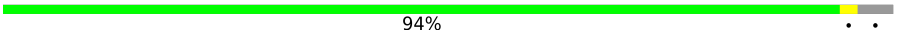
Chain Q:

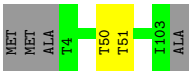




• Molecule 25: 50S ribosomal protein L21

Chain R:



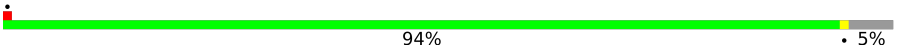


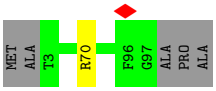
• Molecule 26: 50S ribosomal protein L22

Chain S:

• Molecule 27: 50S ribosomal protein L23

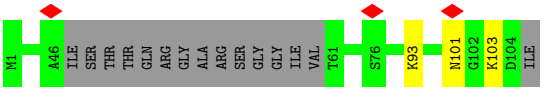
Chain T:





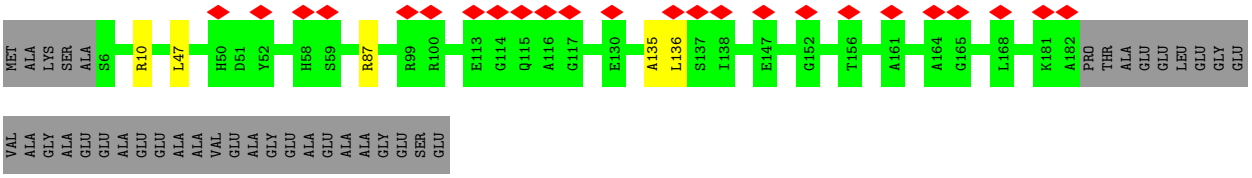
• Molecule 28: 50S ribosomal protein L24

Chain U:



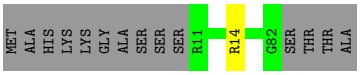
• Molecule 29: 50S ribosomal protein L25

Chain V:



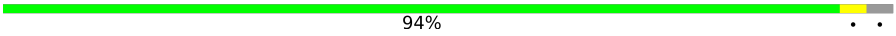
• Molecule 30: 50S ribosomal protein L27

Chain W:



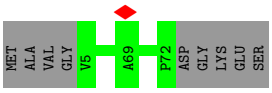
• Molecule 31: 50S ribosomal protein L28

Chain X:



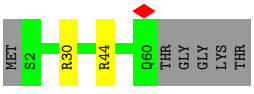
• Molecule 32: 50S ribosomal protein L29

Chain Y:



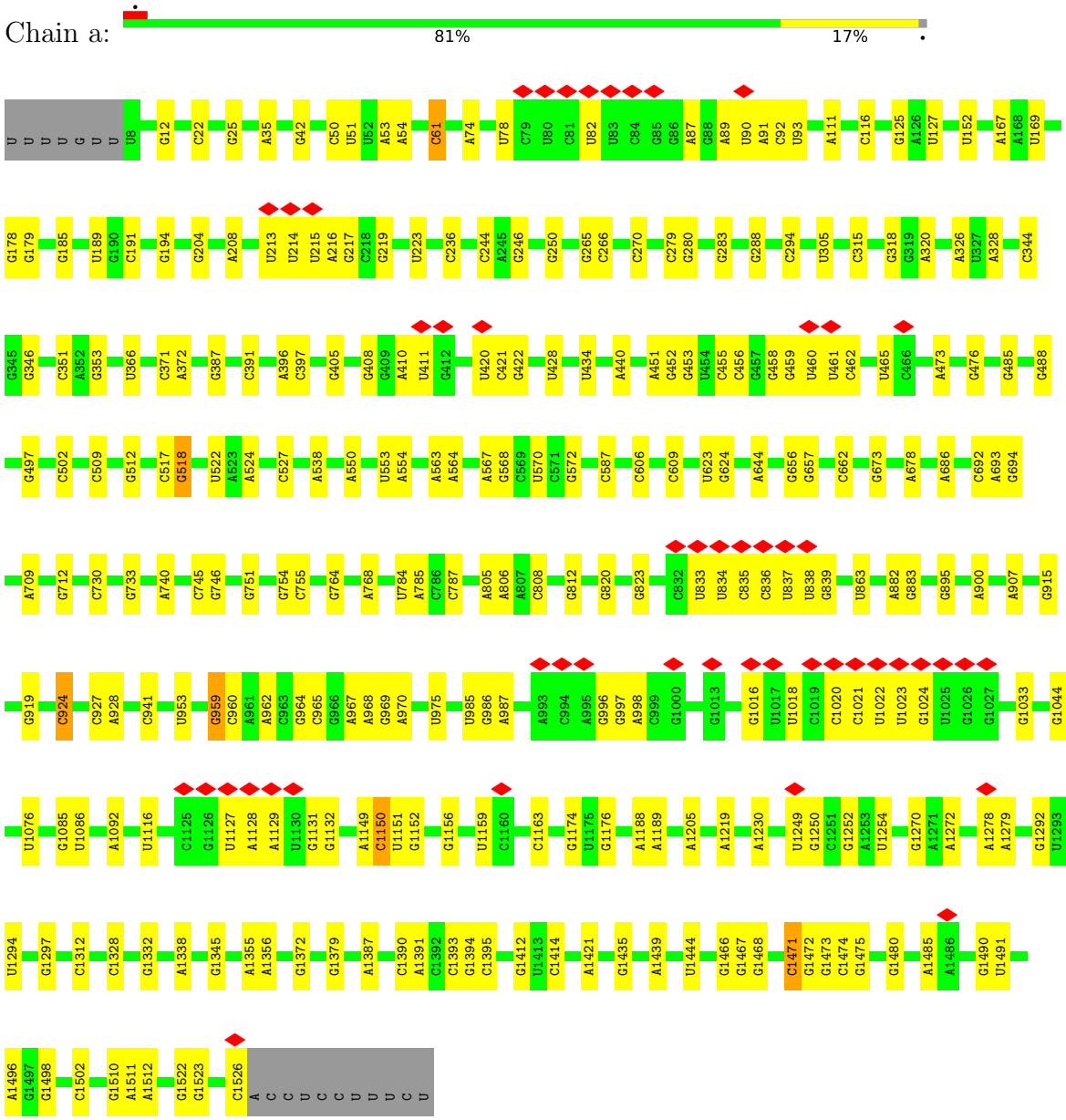
• Molecule 33: 50S ribosomal protein L30

Chain Z:



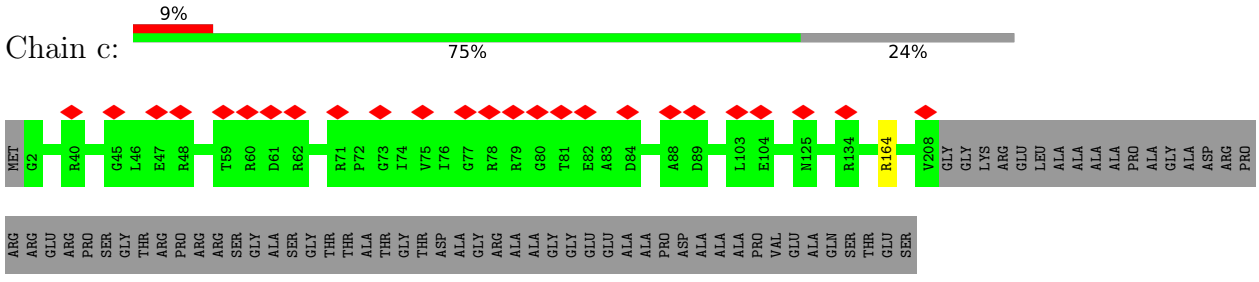
• Molecule 34: 16S rRNA

Chain a:



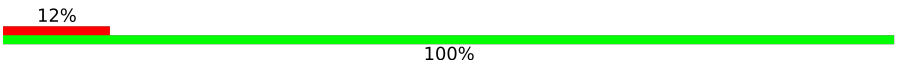
• Molecule 35: 30S ribosomal protein S3

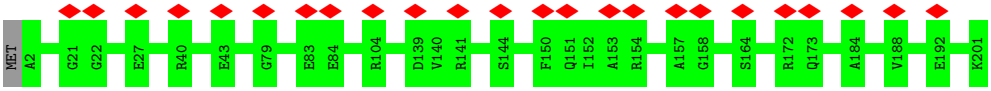
Chain c:



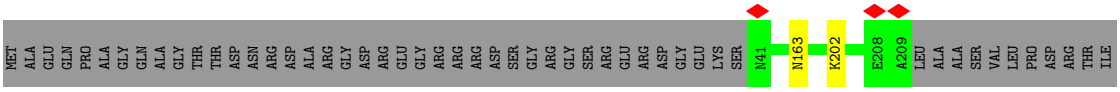
• Molecule 36: 30S ribosomal protein S4

Chain d:

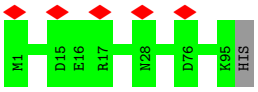




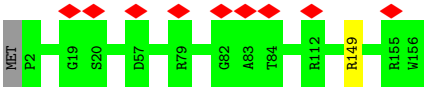
• Molecule 37: 30S ribosomal protein S5



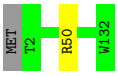
• Molecule 38: 30S ribosomal protein S6



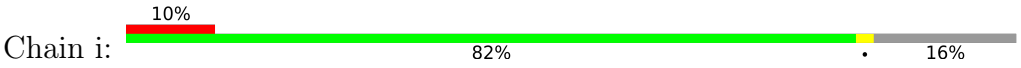
• Molecule 39: 30S ribosomal protein S7

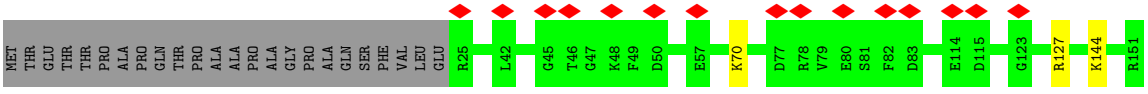


• Molecule 40: 30S ribosomal protein S8

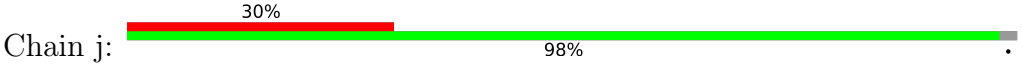


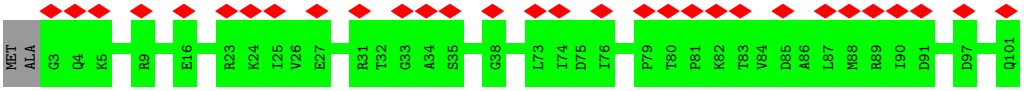
• Molecule 41: 30S ribosomal protein S9





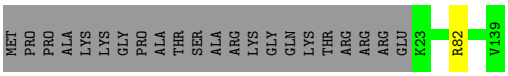
• Molecule 42: 30S ribosomal protein S10





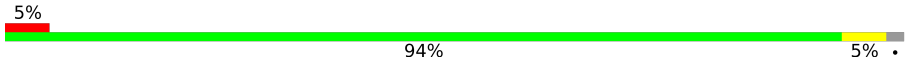
• Molecule 43: 30S ribosomal protein S11

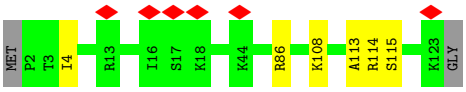
Chain k:



• Molecule 44: 30S ribosomal protein S12

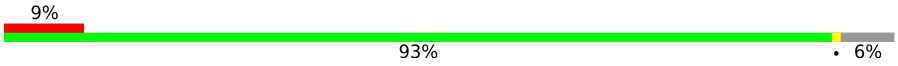
Chain l:

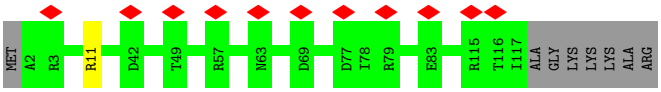




• Molecule 45: 30S ribosomal protein S13

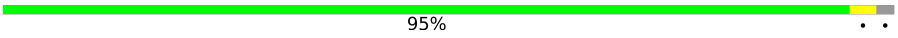
Chain m:





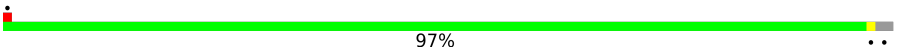
• Molecule 46: 30S ribosomal protein S14 type Z

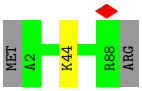
Chain n:



• Molecule 47: 30S ribosomal protein S15

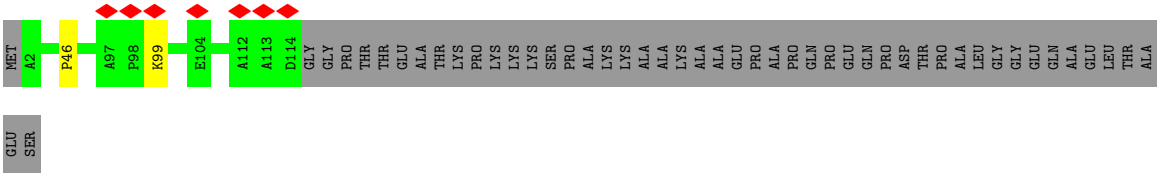
Chain o:





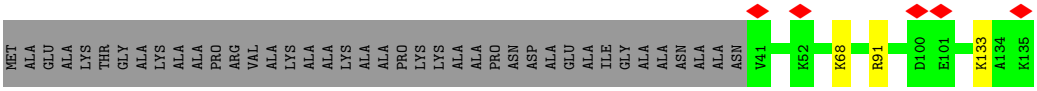
• Molecule 48: 30S ribosomal protein S16

Chain p:

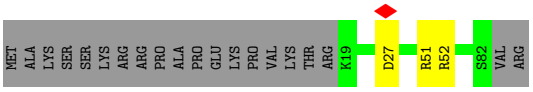


• Molecule 49: 30S ribosomal protein S17

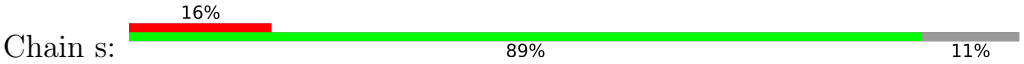
Chain q:

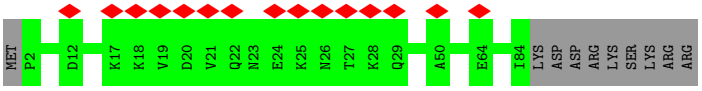


• Molecule 50: 30S ribosomal protein S18 1

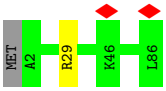


• Molecule 51: 30S ribosomal protein S19



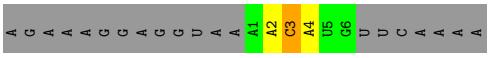


• Molecule 52: 30S ribosomal protein S20



• Molecule 53: tRNA (Met)

• Molecule 54: mRNA



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	134676	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.453	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, 5MU, 2MG, 4OC, G7M, 5MC, MG, ZN, OMG, UR3

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	0	0.41	0/435	0.53	0/581
2	1	0.40	0/407	0.53	0/543
3	2	0.46	0/377	0.59	0/494
4	3	0.38	0/499	0.54	0/664
5	4	0.38	0/303	0.59	0/402
6	6	0.29	0/455	0.62	1/611 (0.2%)
7	7	0.23	0/120	0.45	0/153
8	8	0.29	1/1728 (0.1%)	0.49	0/2339
9	A	0.90	1/74925 (0.0%)	1.01	169/116904 (0.1%)
10	B	0.66	0/2748	0.94	0/4280
11	C	0.49	0/2129	0.61	0/2861
12	D	0.47	0/1613	0.60	0/2174
13	E	0.44	0/1575	0.58	0/2129
14	F	0.33	0/1429	0.53	0/1921
15	G	0.29	0/1351	0.55	0/1824
16	H	0.29	0/353	0.60	0/474
17	J	0.49	0/1170	0.57	0/1584
18	K	0.49	0/951	0.63	1/1278 (0.1%)
19	L	0.42	0/1088	0.59	0/1453
20	M	0.32	0/1098	0.51	0/1481
21	N	0.46	0/925	0.57	0/1242
22	O	0.36	0/914	0.57	0/1228
23	P	0.47	0/922	0.58	0/1236
24	Q	0.53	0/1006	0.60	1/1349 (0.1%)
25	R	0.49	0/766	0.57	0/1030
26	S	0.46	0/874	0.55	0/1186
27	T	0.43	0/751	0.60	0/1012
28	U	0.39	0/705	0.67	0/941
29	V	0.29	0/1336	0.64	1/1820 (0.1%)
30	W	0.47	0/542	0.58	0/721
31	X	0.52	0/476	0.66	1/638 (0.2%)
32	Y	0.37	0/564	0.56	0/756

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Z	0.39	0/480	0.60	0/645
34	a	0.71	0/36331	0.93	40/56686 (0.1%)
35	c	0.30	0/1678	0.52	0/2254
36	d	0.29	0/1683	0.51	0/2269
37	e	0.37	0/1238	0.55	0/1673
38	f	0.33	0/767	0.52	0/1036
39	g	0.28	0/1250	0.51	0/1686
40	h	0.41	0/1021	0.59	0/1379
41	i	0.32	0/1010	0.57	1/1356 (0.1%)
42	j	0.34	0/803	0.61	0/1086
43	k	0.36	0/891	0.53	0/1204
44	l	0.40	0/970	0.64	0/1295
45	m	0.29	0/953	0.56	0/1274
46	n	0.36	0/477	0.58	1/634 (0.2%)
47	o	0.33	0/727	0.54	0/973
48	p	0.36	0/901	0.59	0/1217
49	q	0.35	0/782	0.63	0/1045
50	r	0.38	0/511	0.61	1/685 (0.1%)
51	s	0.29	0/690	0.55	0/928
52	t	0.30	0/654	0.46	0/867
53	y	0.53	1/1836 (0.1%)	0.97	4/2859 (0.1%)
54	z	0.70	0/144	1.35	1/222 (0.5%)
All	All	0.74	3/160332 (0.0%)	0.90	222/240582 (0.1%)

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
8	8	0	1
14	F	0	1
25	R	0	1
28	U	0	1
29	V	0	1
44	l	0	2
47	o	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	y	1	C	OP3-P	-10.70	1.48	1.61
9	A	616	A	N9-C4	-6.45	1.33	1.37
8	8	225	ASP	C-N	5.18	1.44	1.34

All (222) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	946	C	N3-C2-O2	-10.41	114.61	121.90
9	A	946	C	C2-N1-C1'	9.86	129.65	118.80
9	A	946	C	N1-C2-O2	9.81	124.78	118.90
9	A	882	C	C2-N1-C1'	9.69	129.46	118.80
9	A	2558	C	N1-C2-O2	9.50	124.60	118.90
34	a	1471	C	N1-C2-O2	9.21	124.43	118.90
9	A	946	C	C6-N1-C2	-8.86	116.76	120.30
34	a	1471	C	C2-N1-C1'	8.85	128.54	118.80
9	A	2309	C	N3-C2-O2	-8.80	115.74	121.90
9	A	2411	C	N1-C2-O2	8.78	124.17	118.90
9	A	3060	C	C2-N1-C1'	8.77	128.45	118.80
9	A	739	C	C2-N1-C1'	8.68	128.35	118.80
9	A	1134	C	C6-N1-C2	-8.65	116.84	120.30
9	A	1961	C	N1-C2-O2	8.63	124.08	118.90
9	A	1134	C	C5-C6-N1	8.49	125.25	121.00
9	A	3060	C	N3-C2-O2	-8.28	116.10	121.90
29	V	47	LEU	CA-CB-CG	8.14	134.03	115.30
34	a	1498	G	C4-N9-C1'	8.08	137.00	126.50
9	A	739	C	N3-C2-O2	-8.01	116.30	121.90
34	a	1471	C	N3-C2-O2	-7.99	116.31	121.90
9	A	2309	C	N1-C2-O2	7.96	123.68	118.90
9	A	2217	C	N3-C2-O2	-7.93	116.35	121.90
9	A	1517	C	N1-C2-O2	7.89	123.64	118.90
9	A	1517	C	C2-N1-C1'	7.77	127.35	118.80
9	A	739	C	N1-C2-O2	7.76	123.56	118.90
9	A	2558	C	N3-C2-O2	-7.75	116.48	121.90
34	a	22	C	C6-N1-C2	-7.44	117.33	120.30
9	A	2217	C	C2-N1-C1'	7.44	126.98	118.80
9	A	200	C	C6-N1-C2	-7.36	117.36	120.30
9	A	2411	C	N3-C2-O2	-7.35	116.75	121.90
9	A	2953	C	C6-N1-C2	-7.34	117.36	120.30
9	A	3060	C	N1-C2-O2	7.34	123.31	118.90
9	A	2411	C	C2-N1-C1'	7.31	126.84	118.80
9	A	3060	C	C6-N1-C2	-7.29	117.38	120.30
9	A	2559	G	C4-N9-C1'	7.27	135.95	126.50
9	A	882	C	N1-C2-O2	7.23	123.24	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	882	C	N3-C2-O2	-7.12	116.92	121.90
9	A	882	C	C6-N1-C1'	-7.09	112.30	120.80
9	A	2558	C	C2-N1-C1'	7.07	126.58	118.80
9	A	2411	C	C6-N1-C2	-7.07	117.47	120.30
9	A	1961	C	N3-C2-O2	-7.05	116.97	121.90
9	A	2217	C	N1-C2-O2	7.03	123.11	118.90
34	a	1498	G	N3-C4-N9	7.02	130.21	126.00
34	a	1471	C	C6-N1-C2	-6.95	117.52	120.30
9	A	1955	G	N3-C4-N9	-6.91	121.86	126.00
34	a	1498	G	C8-N9-C1'	-6.76	118.21	127.00
34	a	1498	G	N3-C4-C5	-6.73	125.24	128.60
9	A	1425	C	C6-N1-C2	-6.67	117.63	120.30
9	A	1833	C	C6-N1-C2	-6.67	117.63	120.30
34	a	22	C	C5-C6-N1	6.62	124.31	121.00
9	A	2884	C	C6-N1-C2	-6.60	117.66	120.30
9	A	1517	C	N3-C2-O2	-6.55	117.32	121.90
9	A	2310	C	C6-N1-C2	-6.50	117.70	120.30
34	a	1150	C	C2-N1-C1'	6.47	125.91	118.80
34	a	223	U	C2-N1-C1'	6.44	125.43	117.70
9	A	1115	C	C6-N1-C2	-6.43	117.73	120.30
9	A	754	C	C6-N1-C2	-6.42	117.73	120.30
9	A	1874	C	N1-C2-O2	6.32	122.69	118.90
9	A	2862	C	C6-N1-C2	-6.32	117.77	120.30
34	a	1498	G	C6-C5-N7	-6.31	126.61	130.40
9	A	2448	G	C4-N9-C1'	6.30	134.69	126.50
9	A	739	C	C6-N1-C1'	-6.29	113.26	120.80
9	A	2309	C	C2-N1-C1'	6.28	125.71	118.80
9	A	2559	G	C8-N9-C1'	-6.27	118.85	127.00
9	A	2884	C	C5-C6-N1	6.27	124.13	121.00
9	A	935	C	C6-N1-C2	-6.24	117.80	120.30
9	A	1961	C	C6-N1-C2	-6.13	117.85	120.30
9	A	576	C	C6-N1-C2	-6.12	117.85	120.30
9	A	1874	C	N3-C2-O2	-6.10	117.63	121.90
34	a	169	U	C2-N1-C1'	6.07	124.98	117.70
9	A	913	G	P-O3'-C3'	6.05	126.97	119.70
9	A	473	C	N1-C2-O2	6.05	122.53	118.90
9	A	2953	C	C5-C6-N1	6.03	124.01	121.00
9	A	2641	C	C6-N1-C2	-6.02	117.89	120.30
9	A	946	C	C6-N1-C1'	-6.00	113.59	120.80
9	A	1072	G	C4-N9-C1'	6.00	134.30	126.50
9	A	1955	G	N3-C2-N2	-5.97	115.72	119.90
9	A	912	A	C2-N3-C4	5.93	113.56	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	2321	C	C6-N1-C2	-5.93	117.93	120.30
9	A	1445	C	C6-N1-C2	-5.92	117.93	120.30
34	a	730	C	C6-N1-C2	-5.91	117.94	120.30
9	A	473	C	N3-C2-O2	-5.89	117.77	121.90
9	A	963	C	C6-N1-C2	-5.88	117.95	120.30
9	A	1339	C	C6-N1-C2	-5.88	117.95	120.30
9	A	604	C	C6-N1-C2	-5.88	117.95	120.30
9	A	1425	C	C5-C6-N1	5.83	123.92	121.00
9	A	945	C	C6-N1-C2	-5.81	117.97	120.30
34	a	527	C	C6-N1-C2	-5.81	117.98	120.30
9	A	130	C	C6-N1-C2	-5.80	117.98	120.30
9	A	2966	U	C5-C6-N1	5.80	125.60	122.70
9	A	695	G	C4-N9-C1'	5.79	134.03	126.50
9	A	2056	C	C6-N1-C2	-5.79	117.98	120.30
53	y	35	C	C2-N1-C1'	5.77	125.14	118.80
9	A	2559	G	N3-C4-N9	5.74	129.45	126.00
34	a	1254	U	C2-N1-C1'	5.73	124.57	117.70
34	a	1471	C	C6-N1-C1'	-5.72	113.94	120.80
9	A	200	C	C5-C6-N1	5.70	123.85	121.00
9	A	697	C	C6-N1-C2	-5.70	118.02	120.30
34	a	223	U	N3-C2-O2	-5.70	118.21	122.20
9	A	820	C	C5-C6-N1	5.67	123.83	121.00
9	A	1953	G	N3-C2-N2	-5.67	115.94	119.90
9	A	1684	C	C6-N1-C2	-5.65	118.04	120.30
9	A	2558	C	C6-N1-C2	-5.64	118.04	120.30
34	a	1414	C	C6-N1-C2	-5.63	118.05	120.30
9	A	2159	C	C6-N1-C2	-5.63	118.05	120.30
34	a	315	C	N1-C2-O2	5.62	122.28	118.90
34	a	169	U	N1-C2-O2	5.62	126.73	122.80
9	A	1833	C	C5-C6-N1	5.60	123.80	121.00
9	A	550	C	C6-N1-C2	-5.60	118.06	120.30
9	A	869	C	N1-C2-O2	5.60	122.26	118.90
9	A	1905	C	N1-C2-O2	5.59	122.25	118.90
9	A	2968	C	C6-N1-C2	-5.58	118.07	120.30
9	A	200	C	C2-N1-C1'	5.57	124.93	118.80
9	A	2961	C	C6-N1-C2	-5.57	118.07	120.30
53	y	35	C	N1-C2-O2	5.56	122.24	118.90
54	z	3	C	O4'-C1'-N1	5.55	112.64	108.20
41	i	144	LYS	C-N-CA	5.54	135.56	121.70
9	A	912	A	C4-N9-C1'	5.54	136.27	126.30
9	A	3060	C	C6-N1-C1'	-5.53	114.16	120.80
9	A	2452	C	C6-N1-C2	-5.53	118.09	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	2559	G	N3-C4-C5	-5.53	125.84	128.60
9	A	769	U	C2-N1-C1'	5.52	124.33	117.70
9	A	2993	C	C6-N1-C2	-5.51	118.10	120.30
34	a	554	A	N7-C8-N9	5.51	116.56	113.80
31	X	14	PHE	CB-CG-CD1	5.51	124.65	120.80
34	a	1472	G	O4'-C1'-N9	5.50	112.60	108.20
9	A	485	C	C6-N1-C2	-5.50	118.10	120.30
9	A	2535	C	N1-C2-O2	5.50	122.20	118.90
9	A	2993	C	C2-N1-C1'	5.49	124.83	118.80
9	A	1428	C	C6-N1-C2	-5.48	118.11	120.30
34	a	294	C	C6-N1-C2	-5.46	118.11	120.30
9	A	1874	C	C6-N1-C2	-5.46	118.12	120.30
9	A	2702	C	C6-N1-C2	-5.44	118.12	120.30
9	A	912	A	C8-N9-C4	-5.43	103.63	105.80
46	n	53	LEU	CA-CB-CG	5.43	127.80	115.30
9	A	1113	G	C4-N9-C1'	5.43	133.56	126.50
9	A	1961	C	C2-N1-C1'	5.43	124.78	118.80
9	A	2873	C	C6-N1-C2	-5.43	118.13	120.30
9	A	912	A	N7-C8-N9	5.43	116.51	113.80
9	A	2993	C	N1-C2-O2	5.42	122.15	118.90
9	A	1436	C	C6-N1-C2	-5.41	118.14	120.30
9	A	1121	C	C6-N1-C2	-5.41	118.14	120.30
34	a	1150	C	N1-C2-O2	5.40	122.14	118.90
9	A	1684	C	C5-C6-N1	5.40	123.70	121.00
9	A	2217	C	C6-N1-C2	-5.39	118.14	120.30
34	a	236	C	C6-N1-C2	-5.39	118.14	120.30
9	A	1891	C	C6-N1-C2	-5.38	118.15	120.30
9	A	2920	U	N3-C2-O2	-5.37	118.44	122.20
9	A	2411	C	C5-C6-N1	5.37	123.69	121.00
9	A	1988	C	C6-N1-C2	-5.37	118.15	120.30
9	A	2262	C	C6-N1-C2	-5.37	118.15	120.30
9	A	1834	C	C6-N1-C2	-5.36	118.16	120.30
34	a	61	C	N1-C2-O2	5.36	122.12	118.90
9	A	20	C	C6-N1-C2	-5.36	118.16	120.30
9	A	2535	C	N3-C2-O2	-5.34	118.16	121.90
9	A	1879	C	C6-N1-C2	-5.34	118.16	120.30
34	a	745	C	C2-N1-C1'	5.34	124.67	118.80
9	A	1517	C	C6-N1-C1'	-5.33	114.41	120.80
9	A	1272	A	O4'-C1'-N9	5.32	112.46	108.20
9	A	2993	C	C5-C6-N1	5.31	123.66	121.00
9	A	867	C	N1-C2-O2	5.31	122.09	118.90
50	r	27	ASP	CB-CG-OD1	5.31	123.08	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	3029	C	N1-C2-O2	5.30	122.08	118.90
9	A	2355	U	C2-N1-C1'	5.30	124.06	117.70
9	A	1955	G	N3-C4-C5	5.30	131.25	128.60
53	y	1	C	N1-C2-O2	5.30	122.08	118.90
9	A	2029	C	C6-N1-C2	-5.29	118.18	120.30
9	A	2281	C	C5-C6-N1	5.29	123.64	121.00
9	A	2321	C	C5-C6-N1	5.29	123.64	121.00
9	A	877	G	O4'-C1'-N9	5.28	112.42	108.20
9	A	2989	G	C4-N9-C1'	5.27	133.35	126.50
9	A	860	C	C6-N1-C2	-5.26	118.19	120.30
9	A	859	C	C6-N1-C2	-5.26	118.20	120.30
34	a	61	C	C6-N1-C2	-5.25	118.20	120.30
9	A	2681	C	C6-N1-C2	-5.25	118.20	120.30
34	a	745	C	N1-C2-O2	5.25	122.05	118.90
9	A	2077	C	C6-N1-C2	-5.25	118.20	120.30
9	A	826	C	C6-N1-C2	-5.24	118.20	120.30
9	A	926	C	C5-C6-N1	5.23	123.62	121.00
9	A	506	C	C6-N1-C2	-5.22	118.21	120.30
9	A	2276	C	C5-C6-N1	5.22	123.61	121.00
9	A	2448	G	C8-N9-C1'	-5.22	120.21	127.00
34	a	22	C	N1-C2-O2	5.21	122.03	118.90
34	a	787	C	C6-N1-C2	-5.21	118.22	120.30
9	A	1488	C	C6-N1-C2	-5.20	118.22	120.30
34	a	315	C	C5-C6-N1	5.19	123.60	121.00
9	A	3076	C	C6-N1-C2	-5.18	118.23	120.30
34	a	1502	C	C6-N1-C2	-5.18	118.23	120.30
34	a	924	C	C6-N1-C2	-5.18	118.23	120.30
9	A	600	G	O4'-C1'-N9	5.18	112.34	108.20
9	A	1834	C	C5-C6-N1	5.18	123.59	121.00
9	A	1517	C	C6-N1-C2	-5.17	118.23	120.30
18	K	110	ARG	CA-CB-CG	5.17	124.78	113.40
9	A	1446	C	C6-N1-C2	-5.17	118.23	120.30
34	a	755	C	C6-N1-C2	-5.16	118.24	120.30
9	A	882	C	C6-N1-C2	-5.16	118.24	120.30
9	A	1953	G	N3-C4-N9	-5.15	122.91	126.00
9	A	270	C	C6-N1-C2	-5.15	118.24	120.30
9	A	820	C	C6-N1-C2	-5.14	118.24	120.30
9	A	507	C	C6-N1-C2	-5.13	118.25	120.30
9	A	473	C	C6-N1-C2	-5.13	118.25	120.30
34	a	1498	G	N7-C8-N9	5.13	115.66	113.10
9	A	408	C	C6-N1-C2	-5.11	118.26	120.30
34	a	1471	C	C5-C6-N1	5.10	123.55	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	2401	U	C2-N1-C1'	5.10	123.82	117.70
9	A	739	C	O4'-C1'-N1	5.09	112.27	108.20
9	A	2914	C	C6-N1-C2	-5.09	118.27	120.30
53	y	41	C	C6-N1-C2	-5.08	118.27	120.30
9	A	1531	C	C6-N1-C2	-5.08	118.27	120.30
9	A	943	C	C6-N1-C2	-5.07	118.27	120.30
9	A	47	C	C6-N1-C2	-5.07	118.27	120.30
9	A	913	G	OP1-P-O3'	5.07	116.34	105.20
24	Q	73	ASP	CB-CG-OD1	5.06	122.85	118.30
9	A	983	C	C6-N1-C2	-5.04	118.28	120.30
9	A	1068	C	C5-C6-N1	5.04	123.52	121.00
9	A	105	C	C6-N1-C2	-5.04	118.28	120.30
34	a	965	C	C6-N1-C2	-5.04	118.29	120.30
9	A	769	U	N1-C2-O2	5.01	126.31	122.80
9	A	3005	C	N1-C2-O2	5.01	121.91	118.90
9	A	505	C	C6-N1-C2	-5.01	118.30	120.30
6	6	4	ASP	CB-CG-OD1	5.00	122.80	118.30
9	A	2367	U	C2-N1-C1'	5.00	123.70	117.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	8	225	ASP	Mainchain
14	F	142	GLN	Peptide
25	R	50	THR	Peptide
28	U	101	ASN	Peptide
29	V	136	LEU	Peptide
44	l	113	ALA	Peptide
44	l	115	SER	Peptide
47	o	44	LYS	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	52/57 (91%)	52 (100%)	0	0	100	100
2	1	46/55 (84%)	46 (100%)	0	0	100	100
3	2	42/47 (89%)	42 (100%)	0	0	100	100
4	3	60/64 (94%)	60 (100%)	0	0	100	100
5	4	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
6	6	53/80 (66%)	46 (87%)	7 (13%)	0	100	100
7	7	11/24 (46%)	11 (100%)	0	0	100	100
8	8	228/235 (97%)	214 (94%)	14 (6%)	0	100	100
11	C	270/280 (96%)	259 (96%)	10 (4%)	1 (0%)	34	66
12	D	211/217 (97%)	194 (92%)	17 (8%)	0	100	100
13	E	205/223 (92%)	198 (97%)	7 (3%)	0	100	100
14	F	176/187 (94%)	160 (91%)	16 (9%)	0	100	100
15	G	172/179 (96%)	157 (91%)	15 (9%)	0	100	100
16	H	45/152 (30%)	39 (87%)	6 (13%)	0	100	100
17	J	144/195 (74%)	142 (99%)	2 (1%)	0	100	100
18	K	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
19	L	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
20	M	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
21	N	114/180 (63%)	112 (98%)	2 (2%)	0	100	100
22	O	117/122 (96%)	110 (94%)	7 (6%)	0	100	100
23	P	110/113 (97%)	102 (93%)	8 (7%)	0	100	100
24	Q	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
25	R	98/104 (94%)	90 (92%)	7 (7%)	1 (1%)	15	44
26	S	111/197 (56%)	111 (100%)	0	0	100	100
27	T	93/100 (93%)	88 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	U	86/105 (82%)	76 (88%)	10 (12%)	0	100 100
29	V	175/215 (81%)	142 (81%)	32 (18%)	1 (1%)	25 56
30	W	70/86 (81%)	65 (93%)	5 (7%)	0	100 100
31	X	60/64 (94%)	59 (98%)	1 (2%)	0	100 100
32	Y	66/77 (86%)	63 (96%)	3 (4%)	0	100 100
33	Z	57/65 (88%)	55 (96%)	2 (4%)	0	100 100
35	c	205/274 (75%)	189 (92%)	16 (8%)	0	100 100
36	d	198/201 (98%)	180 (91%)	18 (9%)	0	100 100
37	e	167/220 (76%)	152 (91%)	15 (9%)	0	100 100
38	f	93/96 (97%)	91 (98%)	2 (2%)	0	100 100
39	g	153/156 (98%)	149 (97%)	4 (3%)	0	100 100
40	h	129/132 (98%)	123 (95%)	6 (5%)	0	100 100
41	i	125/151 (83%)	110 (88%)	15 (12%)	0	100 100
42	j	97/101 (96%)	85 (88%)	12 (12%)	0	100 100
43	k	115/139 (83%)	104 (90%)	11 (10%)	0	100 100
44	l	120/124 (97%)	89 (74%)	29 (24%)	2 (2%)	9 29
45	m	114/124 (92%)	103 (90%)	11 (10%)	0	100 100
46	n	58/61 (95%)	56 (97%)	1 (2%)	1 (2%)	9 29
47	o	85/89 (96%)	79 (93%)	6 (7%)	0	100 100
48	p	111/162 (68%)	98 (88%)	12 (11%)	1 (1%)	17 46
49	q	93/135 (69%)	82 (88%)	11 (12%)	0	100 100
50	r	62/84 (74%)	58 (94%)	4 (6%)	0	100 100
51	s	81/93 (87%)	69 (85%)	12 (15%)	0	100 100
52	t	83/86 (96%)	81 (98%)	2 (2%)	0	100 100
All	All	5512/6423 (86%)	5118 (93%)	387 (7%)	7 (0%)	54 81

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	R	51	THR
44	l	114	ARG
46	n	17	ALA
29	V	135	ALA
48	p	46	PRO

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Mol	Chain	Res	Type
11	C	27	SER
44	l	4	ILE

5.3.2 Protein sidechains (i)

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	44/47 (94%)	44 (100%)	0	100	100
2	1	45/51 (88%)	45 (100%)	0	100	100
3	2	38/40 (95%)	37 (97%)	1 (3%)	46	79
4	3	53/54 (98%)	53 (100%)	0	100	100
5	4	35/35 (100%)	34 (97%)	1 (3%)	42	76
6	6	49/66 (74%)	49 (100%)	0	100	100
7	7	11/20 (55%)	11 (100%)	0	100	100
8	8	175/179 (98%)	172 (98%)	3 (2%)	60	87
11	C	212/219 (97%)	211 (100%)	1 (0%)	88	96
12	D	163/166 (98%)	163 (100%)	0	100	100
13	E	159/172 (92%)	157 (99%)	2 (1%)	69	91
14	F	147/155 (95%)	145 (99%)	2 (1%)	67	90
15	G	143/147 (97%)	142 (99%)	1 (1%)	84	95
16	H	36/121 (30%)	35 (97%)	1 (3%)	43	77
17	J	120/161 (74%)	120 (100%)	0	100	100
18	K	101/101 (100%)	100 (99%)	1 (1%)	76	93
19	L	108/110 (98%)	107 (99%)	1 (1%)	78	94
20	M	110/114 (96%)	109 (99%)	1 (1%)	78	94
21	N	94/139 (68%)	93 (99%)	1 (1%)	73	92
22	O	91/93 (98%)	91 (100%)	0	100	100
23	P	98/99 (99%)	98 (100%)	0	100	100
24	Q	97/99 (98%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	R	81/83 (98%)	81 (100%)	0	100	100
26	S	87/140 (62%)	86 (99%)	1 (1%)	73	92
27	T	81/83 (98%)	80 (99%)	1 (1%)	71	92
28	U	77/88 (88%)	75 (97%)	2 (3%)	46	79
29	V	142/164 (87%)	140 (99%)	2 (1%)	67	90
30	W	52/62 (84%)	51 (98%)	1 (2%)	57	85
31	X	51/52 (98%)	50 (98%)	1 (2%)	55	84
32	Y	60/66 (91%)	60 (100%)	0	100	100
33	Z	51/55 (93%)	49 (96%)	2 (4%)	32	66
35	c	170/210 (81%)	169 (99%)	1 (1%)	86	96
36	d	176/177 (99%)	176 (100%)	0	100	100
37	e	121/159 (76%)	119 (98%)	2 (2%)	60	87
38	f	84/85 (99%)	84 (100%)	0	100	100
39	g	130/131 (99%)	129 (99%)	1 (1%)	81	94
40	h	107/108 (99%)	106 (99%)	1 (1%)	78	94
41	i	102/120 (85%)	100 (98%)	2 (2%)	55	84
42	j	89/90 (99%)	89 (100%)	0	100	100
43	k	90/107 (84%)	89 (99%)	1 (1%)	73	92
44	l	104/105 (99%)	102 (98%)	2 (2%)	57	85
45	m	99/104 (95%)	98 (99%)	1 (1%)	76	93
46	n	46/47 (98%)	46 (100%)	0	100	100
47	o	77/79 (98%)	77 (100%)	0	100	100
48	p	90/125 (72%)	89 (99%)	1 (1%)	73	92
49	q	85/105 (81%)	82 (96%)	3 (4%)	36	70
50	r	54/72 (75%)	52 (96%)	2 (4%)	34	68
51	s	75/85 (88%)	75 (100%)	0	100	100
52	t	64/65 (98%)	63 (98%)	1 (2%)	62	88
All	All	4574/5155 (89%)	4530 (99%)	44 (1%)	77	93

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	2	31	ARG

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Mol	Chain	Res	Type
5	4	8	LYS
8	8	103	ARG
8	8	137	MET
8	8	231	ASN
11	C	4	ARG
13	E	19	LYS
13	E	81	ARG
14	F	14	ARG
14	F	78	ARG
15	G	96	ARG
16	H	41	ARG
18	K	110	ARG
19	L	21	VAL
20	M	60	ARG
21	N	71	ARG
26	S	102	ARG
27	T	70	ARG
28	U	93	LYS
28	U	103	LYS
29	V	10	ARG
29	V	87	ARG
30	W	14	ARG
31	X	27	ARG
33	Z	30	ARG
33	Z	44	ARG
35	c	164	ARG
37	e	163	ASN
37	e	202	LYS
39	g	149	ARG
40	h	50	ARG
41	i	70	LYS
41	i	127	ARG
43	k	82	ARG
44	l	86	ARG
44	l	108	LYS
45	m	11	ARG
48	p	99	LYS
49	q	68	LYS
49	q	91	ARG
49	q	133	LYS
50	r	51	ARG
50	r	52	ARG

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Mol	Chain	Res	Type
52	t	29	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
7	7	17	ASN
8	8	170	ASN
8	8	231	ASN
12	D	34	ASN
12	D	183	HIS
13	E	47	GLN
14	F	142	GLN
17	J	147	GLN
23	P	79	ASN
24	Q	44	ASN
24	Q	122	ASN
29	V	43	GLN
29	V	91	GLN
29	V	127	ASN
35	c	176	HIS
36	d	111	GLN
36	d	115	HIS
37	e	163	ASN
40	h	38	GLN
41	i	65	HIS
41	i	66	GLN
47	o	51	HIS
51	s	23	ASN
51	s	29	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	113/115 (98%)	14 (12%)	0
34	a	1515/1537 (98%)	250 (16%)	0
53	y	76/77 (98%)	16 (21%)	0
54	z	5/26 (19%)	3 (60%)	0
9	A	3116/3138 (99%)	475 (15%)	2 (0%)
All	All	4825/4893 (98%)	758 (15%)	2 (0%)

All (758) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	9	G
9	A	51	G
9	A	62	G
9	A	63	A
9	A	71	A
9	A	74	U
9	A	75	G
9	A	83	G
9	A	102	G
9	A	118	A
9	A	119	A
9	A	120	U
9	A	143	G
9	A	167	A
9	A	183	A
9	A	197	A
9	A	198	A
9	A	201	A
9	A	217	G
9	A	218	A
9	A	223	A
9	A	224	A
9	A	225	A
9	A	230	U
9	A	231	U
9	A	232	G
9	A	250	G
9	A	251	C
9	A	268	G
9	A	269	G
9	A	287	G
9	A	289	A
9	A	293	G
9	A	297	A
9	A	298	G
9	A	301	G
9	A	302	U
9	A	303	U
9	A	319	U
9	A	328	A
9	A	332	C
9	A	339	C

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Mol	Chain	Res	Type
9	A	358	U
9	A	362	A
9	A	371	U
9	A	372	G
9	A	377	G
9	A	385	G
9	A	405	A
9	A	413	A
9	A	414	G
9	A	425	G
9	A	426	C
9	A	428	A
9	A	446	A
9	A	447	G
9	A	475	G
9	A	485	C
9	A	494	C
9	A	500	G
9	A	501	A
9	A	505	C
9	A	510	U
9	A	527	C
9	A	544	U
9	A	545	U
9	A	554	G
9	A	566	A
9	A	570	G
9	A	573	C
9	A	582	G
9	A	589	A
9	A	592	G
9	A	593	A
9	A	595	U
9	A	596	A
9	A	597	C
9	A	616	A
9	A	618	U
9	A	619	C
9	A	620	C
9	A	621	G
9	A	634	U
9	A	635	U

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Mol	Chain	Res	Type
9	A	636	U
9	A	637	C
9	A	639	U
9	A	641	U
9	A	643	C
9	A	644	G
9	A	645	G
9	A	646	A
9	A	664	U
9	A	665	G
9	A	666	C
9	A	671	U
9	A	672	G
9	A	674	A
9	A	675	G
9	A	677	A
9	A	688	A
9	A	689	G
9	A	694	G
9	A	695	G
9	A	706	A
9	A	718	G
9	A	719	U
9	A	735	A
9	A	738	G
9	A	741	A
9	A	749	U
9	A	758	C
9	A	759	C
9	A	766	G
9	A	769	U
9	A	772	G
9	A	773	C
9	A	779	U
9	A	780	G
9	A	781	A
9	A	782	A
9	A	783	U
9	A	788	G
9	A	793	U
9	A	797	G
9	A	815	U

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Mol	Chain	Res	Type
9	A	846	G
9	A	852	G
9	A	859	C
9	A	876	U
9	A	891	U
9	A	894	G
9	A	904	G
9	A	905	G
9	A	911	A
9	A	913	G
9	A	914	G
9	A	929	U
9	A	930	G
9	A	934	G
9	A	938	G
9	A	941	C
9	A	956	U
9	A	957	U
9	A	988	G
9	A	1025	A
9	A	1026	C
9	A	1036	C
9	A	1039	A
9	A	1044	C
9	A	1059	A
9	A	1061	A
9	A	1069	A
9	A	1074	G
9	A	1087	A
9	A	1089	G
9	A	1096	A
9	A	1102	A
9	A	1103	A
9	A	1112	A
9	A	1114	C
9	A	1118	G
9	A	1119	A
9	A	1125	G
9	A	1138	A
9	A	1142	G
9	A	1151	G
9	A	1154	G

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Mol	Chain	Res	Type
9	A	1155	G
9	A	1159	G
9	A	1162	U
9	A	1168	G
9	A	1174	A
9	A	1177	A
9	A	1181	C
9	A	1186	A
9	A	1187	G
9	A	1189	U
9	A	1190	U
9	A	1191	G
9	A	1195	U
9	A	1199	A
9	A	1200	G
9	A	1202	A
9	A	1207	C
9	A	1208	C
9	A	1211	U
9	A	1212	G
9	A	1216	G
9	A	1217	A
9	A	1218	G
9	A	1219	U
9	A	1237	U
9	A	1238	C
9	A	1240	A
9	A	1241	G
9	A	1244	A
9	A	1258	A
9	A	1259	U
9	A	1262	A
9	A	1264	C
9	A	1271	C
9	A	1273	A
9	A	1304	U
9	A	1305	U
9	A	1308	G
9	A	1342	C
9	A	1368	A
9	A	1378	A
9	A	1384	A

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Mol	Chain	Res	Type
9	A	1387	G
9	A	1399	A
9	A	1402	G
9	A	1403	A
9	A	1404	C
9	A	1406	A
9	A	1432	A
9	A	1433	A
9	A	1452	C
9	A	1456	C
9	A	1478	G
9	A	1481	C
9	A	1483	U
9	A	1490	A
9	A	1491	G
9	A	1496	A
9	A	1499	G
9	A	1501	C
9	A	1505	G
9	A	1509	A
9	A	1510	U
9	A	1515	A
9	A	1523	G
9	A	1542	G
9	A	1545	G
9	A	1555	A
9	A	1556	C
9	A	1560	U
9	A	1561	C
9	A	1567	U
9	A	1579	A
9	A	1580	A
9	A	1581	A
9	A	1582	A
9	A	1592	U
9	A	1609	U
9	A	1628	G
9	A	1643	G
9	A	1646	G
9	A	1647	U
9	A	1648	A
9	A	1653	A

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Mol	Chain	Res	Type
9	A	1657	A
9	A	1658	A
9	A	1665	A
9	A	1666	C
9	A	1667	G
9	A	1696	A
9	A	1697	A
9	A	1698	C
9	A	1699	A
9	A	1705	G
9	A	1716	G
9	A	1717	G
9	A	1720	G
9	A	1727	A
9	A	1728	G
9	A	1730	C
9	A	1745	C
9	A	1746	U
9	A	1747	A
9	A	1754	A
9	A	1772	G
9	A	1773	U
9	A	1774	U
9	A	1795	C
9	A	1803	A
9	A	1806	A
9	A	1814	C
9	A	1820	A
9	A	1821	G
9	A	1830	C
9	A	1832	G
9	A	1842	C
9	A	1843	A
9	A	1845	A
9	A	1848	G
9	A	1881	U
9	A	1883	C
9	A	1886	G
9	A	1888	U
9	A	1889	A
9	A	1909	G
9	A	1910	C

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Mol	Chain	Res	Type
9	A	1929	C
9	A	1949	U
9	A	1950	A
9	A	1955	G
9	A	1959	A
9	A	1963	U
9	A	1964	U
9	A	1966	C
9	A	1967	G
9	A	1970	G
9	A	1984	G
9	A	1990	G
9	A	1993	A
9	A	1998	U
9	A	2007	A
9	A	2010	G
9	A	2016	U
9	A	2020	A
9	A	2021	A
9	A	2025	A
9	A	2034	C
9	A	2035	G
9	A	2050	U
9	A	2061	U
9	A	2063	A
9	A	2094	C
9	A	2105	G
9	A	2107	A
9	A	2108	A
9	A	2109	G
9	A	2137	A
9	A	2138	A
9	A	2144	G
9	A	2145	G
9	A	2147	G
9	A	2148	G
9	A	2151	A
9	A	2152	C
9	A	2157	A
9	A	2159	C
9	A	2160	A
9	A	2168	G

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Mol	Chain	Res	Type
9	A	2175	A
9	A	2176	A
9	A	2177	5MU
9	A	2180	C
9	A	2193	U
9	A	2203	C
9	A	2205	C
9	A	2208	A
9	A	2209	U
9	A	2210	G
9	A	2229	U
9	A	2231	U
9	A	2258	A
9	A	2259	C
9	A	2261	A
9	A	2269	A
9	A	2270	G
9	A	2274	C
9	A	2281	C
9	A	2293	C
9	A	2294	G
9	A	2297	A
9	A	2298	A
9	A	2299	G
9	A	2300	A
9	A	2330	G
9	A	2336	C
9	A	2339	U
9	A	2348	U
9	A	2349	G
9	A	2351	A
9	A	2352	G
9	A	2356	A
9	A	2361	G
9	A	2367	U
9	A	2368	G
9	A	2369	U
9	A	2373	A
9	A	2376	U
9	A	2377	C
9	A	2380	C
9	A	2381	G

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Mol	Chain	Res	Type
9	A	2382	C
9	A	2388	G
9	A	2389	G
9	A	2393	G
9	A	2395	A
9	A	2399	G
9	A	2400	U
9	A	2401	U
9	A	2404	U
9	A	2409	U
9	A	2411	C
9	A	2414	C
9	A	2415	U
9	A	2435	A
9	A	2463	A
9	A	2476	G
9	A	2477	G
9	A	2481	U
9	A	2489	G
9	A	2490	G
9	A	2497	G
9	A	2504	A
9	A	2517	G
9	A	2521	C
9	A	2525	A
9	A	2543	A
9	A	2546	G
9	A	2558	C
9	A	2560	A
9	A	2563	G
9	A	2565	A
9	A	2573	A
9	A	2574	A
9	A	2583	G
9	A	2585	C
9	A	2588	C
9	A	2621	G
9	A	2623	A
9	A	2626	A
9	A	2644	A
9	A	2661	U
9	A	2663	A

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Mol	Chain	Res	Type
9	A	2667	G
9	A	2668	A
9	A	2678	C
9	A	2679	C
9	A	2686	A
9	A	2712	C
9	A	2714	A
9	A	2732	G
9	A	2736	C
9	A	2738	U
9	A	2740	G
9	A	2742	U
9	A	2743	G
9	A	2751	G
9	A	2756	A
9	A	2758	C
9	A	2767	G
9	A	2802	A
9	A	2804	A
9	A	2805	G
9	A	2811	C
9	A	2820	G
9	A	2840	A
9	A	2847	U
9	A	2851	U
9	A	2853	U
9	A	2859	G
9	A	2868	A
9	A	2884	C
9	A	2898	A
9	A	2901	G
9	A	2920	U
9	A	2952	G
9	A	2962	C
9	A	2964	C
9	A	2986	A
9	A	3016	A
9	A	3019	A
9	A	3033	C
9	A	3038	U
9	A	3053	C
9	A	3055	C

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Mol	Chain	Res	Type
9	A	3056	A
9	A	3058	A
9	A	3059	A
9	A	3070	A
9	A	3085	A
9	A	3107	A
9	A	3109	C
9	A	3112	G
9	A	3118	A
9	A	3119	C
9	A	3120	C
9	A	3121	G
9	A	3129	A
10	B	2	U
10	B	3	A
10	B	4	C
10	B	34	U
10	B	40	U
10	B	41	C
10	B	55	U
10	B	56	A
10	B	65	A
10	B	68	G
10	B	92	G
10	B	101	G
10	B	105	A
10	B	115	A
34	a	12	G
34	a	25	G
34	a	35	A
34	a	42	G
34	a	50	C
34	a	51	U
34	a	53	A
34	a	54	A
34	a	61	C
34	a	74	A
34	a	78	U
34	a	82	U
34	a	87	A
34	a	89	A
34	a	90	U

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Mol	Chain	Res	Type
34	a	91	A
34	a	92	C
34	a	93	U
34	a	111	A
34	a	116	C
34	a	125	G
34	a	127	U
34	a	152	U
34	a	167	A
34	a	178	G
34	a	179	G
34	a	185	G
34	a	189	U
34	a	191	C
34	a	194	G
34	a	204	G
34	a	208	A
34	a	213	U
34	a	214	U
34	a	215	U
34	a	216	A
34	a	217	G
34	a	219	G
34	a	244	C
34	a	246	G
34	a	250	G
34	a	265	G
34	a	266	C
34	a	270	C
34	a	279	C
34	a	280	G
34	a	283	G
34	a	288	G
34	a	305	U
34	a	318	G
34	a	320	A
34	a	326	A
34	a	328	A
34	a	344	C
34	a	346	G
34	a	351	C
34	a	353	G

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Mol	Chain	Res	Type
34	a	366	U
34	a	371	C
34	a	372	A
34	a	387	G
34	a	391	C
34	a	396	A
34	a	397	C
34	a	405	G
34	a	408	G
34	a	410	A
34	a	411	U
34	a	420	U
34	a	421	C
34	a	422	G
34	a	428	U
34	a	434	U
34	a	440	A
34	a	451	A
34	a	452	G
34	a	453	G
34	a	455	C
34	a	456	C
34	a	458	G
34	a	459	G
34	a	460	U
34	a	461	U
34	a	462	C
34	a	465	U
34	a	473	A
34	a	476	G
34	a	485	G
34	a	488	G
34	a	497	G
34	a	502	C
34	a	509	C
34	a	512	G
34	a	517	C
34	a	518	G7M
34	a	522	U
34	a	524	A
34	a	538	A
34	a	550	A

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Mol	Chain	Res	Type
34	a	553	U
34	a	563	A
34	a	564	A
34	a	567	A
34	a	568	G
34	a	570	U
34	a	572	G
34	a	587	C
34	a	606	C
34	a	609	C
34	a	623	U
34	a	624	G
34	a	644	A
34	a	656	G
34	a	657	G
34	a	662	C
34	a	673	G
34	a	678	A
34	a	686	A
34	a	692	C
34	a	693	A
34	a	694	G
34	a	709	A
34	a	712	G
34	a	733	G
34	a	740	A
34	a	746	G
34	a	751	G
34	a	754	G
34	a	764	G
34	a	768	A
34	a	784	U
34	a	785	A
34	a	805	A
34	a	806	A
34	a	808	C
34	a	812	G
34	a	820	G
34	a	823	G
34	a	833	U
34	a	834	U
34	a	835	C

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Mol	Chain	Res	Type
34	a	836	C
34	a	837	U
34	a	838	U
34	a	839	G
34	a	863	U
34	a	882	A
34	a	883	G
34	a	895	G
34	a	900	A
34	a	907	A
34	a	915	G
34	a	919	G
34	a	924	C
34	a	927	C
34	a	928	A
34	a	941	C
34	a	953	U
34	a	959	2MG
34	a	962	A
34	a	964	G
34	a	967	A
34	a	968	A
34	a	969	G
34	a	970	A
34	a	975	U
34	a	985	U
34	a	986	G
34	a	987	A
34	a	996	G
34	a	997	G
34	a	998	A
34	a	1016	G
34	a	1018	U
34	a	1020	C
34	a	1021	C
34	a	1022	U
34	a	1023	U
34	a	1024	G
34	a	1033	G
34	a	1044	G
34	a	1056	U
34	a	1076	U

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Mol	Chain	Res	Type
34	a	1085	G
34	a	1086	U
34	a	1092	A
34	a	1116	U
34	a	1127	U
34	a	1128	A
34	a	1129	A
34	a	1131	G
34	a	1132	G
34	a	1149	A
34	a	1150	C
34	a	1151	U
34	a	1152	G
34	a	1156	G
34	a	1159	U
34	a	1163	C
34	a	1174	G
34	a	1176	G
34	a	1188	A
34	a	1189	A
34	a	1205	A
34	a	1219	A
34	a	1230	A
34	a	1249	U
34	a	1250	G
34	a	1252	G
34	a	1270	G
34	a	1272	A
34	a	1278	A
34	a	1279	A
34	a	1292	G
34	a	1294	U
34	a	1297	G
34	a	1312	C
34	a	1328	C
34	a	1332	G
34	a	1338	A
34	a	1345	G
34	a	1355	A
34	a	1356	A
34	a	1372	G
34	a	1379	G

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Mol	Chain	Res	Type
34	a	1387	A
34	a	1390	C
34	a	1391	A
34	a	1393	C
34	a	1394	G
34	a	1412	G
34	a	1421	A
34	a	1435	G
34	a	1439	A
34	a	1444	U
34	a	1466	G
34	a	1467	G
34	a	1468	G
34	a	1471	C
34	a	1473	G
34	a	1474	C
34	a	1475	G
34	a	1480	G
34	a	1485	A
34	a	1490	G
34	a	1496	A
34	a	1510	G
34	a	1522	G
34	a	1523	G
34	a	1526	C
53	y	3	C
53	y	4	G
53	y	5	G
53	y	13	C
53	y	17	C
53	y	19	G
53	y	20	G
53	y	21	U
53	y	22	A
53	y	49	C
53	y	51	U
53	y	53	G
53	y	66	C
53	y	68	C
53	y	74	A
53	y	77	A
54	z	2	A

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Mol	Chain	Res	Type
54	z	3	C
54	z	4	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	913	G
9	A	2177	5MU

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

9 non-standard protein/DNA/RNA residues are 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	$\#\|Z\| > 2$
34	5MC	a	960	34	18,22,23	3.47	7 (38%)	26,32,35	1.00	1 (3%)
34	4OC	a	1395	34	20,23,24	2.93	8 (40%)	26,32,35	0.91	1 (3%)
34	MA6	a	1511	34	19,26,27	1.13	2 (10%)	18,38,41	3.28	2 (11%)
34	MA6	a	1512	34	19,26,27	1.12	2 (10%)	18,38,41	3.53	2 (11%)
34	G7M	a	518	34	20,26,27	3.95	10 (50%)	17,39,42	1.13	1 (5%)
9	OMG	A	2791	9	18,26,27	2.45	8 (44%)	19,38,41	1.48	4 (21%)
34	UR3	a	1491	34	19,22,23	2.65	5 (26%)	26,32,35	1.17	1 (3%)
9	5MU	A	2177	9	19,22,23	4.66	7 (36%)	28,32,35	3.72	9 (32%)
34	2MG	a	959	34	18,26,27	2.39	7 (38%)	16,38,41	1.44	4 (25%)

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
34	5MC	a	960	34	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	4OC	a	1395	34	-	2/9/29/30	0/2/2/2
34	MA6	a	1511	34	-	0/7/29/30	0/3/3/3
34	MA6	a	1512	34	-	3/7/29/30	0/3/3/3
34	G7M	a	518	34	-	0/3/25/26	0/3/3/3
9	OMG	A	2791	9	-	0/5/27/28	0/3/3/3
34	UR3	a	1491	34	-	0/7/25/26	0/2/2/2
9	5MU	A	2177	9	-	2/7/25/26	0/2/2/2
34	2MG	a	959	34	-	2/5/27/28	0/3/3/3

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2177	5MU	C6-N1	10.67	1.56	1.38
34	a	518	G7M	C8-N7	9.90	1.51	1.33
34	a	518	G7M	C8-N9	9.66	1.50	1.33
9	A	2177	5MU	C2-N1	9.64	1.53	1.38
34	a	960	5MC	C6-C5	8.97	1.49	1.34
9	A	2177	5MU	C4-C5	8.94	1.59	1.44
9	A	2177	5MU	C4-N3	-7.88	1.24	1.38
34	a	1491	UR3	C6-C5	6.54	1.50	1.35
9	A	2177	5MU	C6-C5	6.34	1.45	1.34
34	a	960	5MC	C4-N3	6.24	1.44	1.34
34	a	1395	4OC	C4-N3	6.22	1.43	1.32
34	a	1395	4OC	C6-C5	6.06	1.49	1.35
34	a	960	5MC	C2-N3	5.88	1.48	1.36
34	a	1491	UR3	C2-N1	5.86	1.46	1.38
34	a	1395	4OC	C2-N3	5.75	1.48	1.36
9	A	2791	OMG	C2-N3	5.48	1.46	1.33
34	a	518	G7M	C2-N3	5.47	1.46	1.33
34	a	959	2MG	C2-N2	5.16	1.44	1.33
34	a	1491	UR3	C2-N3	5.12	1.48	1.39
34	a	959	2MG	C4-N3	4.93	1.49	1.37
34	a	518	G7M	C2-N2	4.79	1.45	1.34
9	A	2791	OMG	C4-N3	4.77	1.48	1.37
34	a	518	G7M	C6-N1	4.48	1.44	1.37
34	a	1395	4OC	C4-N4	4.40	1.44	1.35
34	a	959	2MG	C2-N1	4.32	1.43	1.36
34	a	960	5MC	C4-N4	4.27	1.45	1.34
34	a	960	5MC	C6-N1	4.25	1.45	1.38
9	A	2791	OMG	C2-N2	3.92	1.43	1.34
34	a	960	5MC	C2-N1	3.89	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	518	G7M	C4-N3	3.85	1.46	1.37
34	a	1395	4OC	C2-N1	3.70	1.48	1.40
9	A	2791	OMG	C6-N1	3.50	1.43	1.37
34	a	518	G7M	C2-N1	3.49	1.46	1.37
9	A	2177	5MU	O4-C4	-3.43	1.17	1.23
34	a	1395	4OC	C5-C4	3.32	1.47	1.40
34	a	959	2MG	C6-N1	3.18	1.42	1.37
34	a	1395	4OC	C6-N1	3.04	1.45	1.38
34	a	1491	UR3	C6-N1	3.01	1.45	1.38
34	a	960	5MC	O2-C2	-2.94	1.18	1.23
9	A	2177	5MU	O2-C2	-2.92	1.17	1.23
34	a	1511	MA6	C5-C4	-2.85	1.33	1.40
34	a	1395	4OC	O2-C2	-2.85	1.18	1.23
34	a	1512	MA6	C5-C4	-2.82	1.33	1.40
34	a	959	2MG	C5-C4	-2.72	1.36	1.43
34	a	959	2MG	C5-C6	2.70	1.52	1.47
9	A	2791	OMG	C5-C4	-2.70	1.36	1.43
9	A	2791	OMG	C5-C6	2.68	1.52	1.47
34	a	518	G7M	C5-C6	2.65	1.52	1.45
9	A	2791	OMG	O6-C6	-2.49	1.18	1.23
34	a	518	G7M	O6-C6	-2.40	1.18	1.23
34	a	959	2MG	O6-C6	-2.37	1.18	1.23
34	a	1491	UR3	O2-C2	-2.35	1.18	1.22
9	A	2791	OMG	C2-N1	2.30	1.43	1.37
34	a	1512	MA6	C2-N3	2.12	1.35	1.32
34	a	518	G7M	C5-C4	2.01	1.43	1.39
34	a	1511	MA6	C2-N3	2.00	1.35	1.32

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	a	1512	MA6	N1-C6-N6	-13.57	102.78	117.06
9	A	2177	5MU	C5-C4-N3	12.57	126.04	115.31
34	a	1511	MA6	N1-C6-N6	-12.52	103.88	117.06
9	A	2177	5MU	C5-C6-N1	-10.57	112.46	123.34
34	a	1512	MA6	N3-C2-N1	-5.86	119.52	128.68
34	a	1511	MA6	N3-C2-N1	-5.45	120.16	128.68
9	A	2177	5MU	O4-C4-C5	-5.20	118.87	124.90
9	A	2177	5MU	C4-N3-C2	-5.07	120.79	127.35
9	A	2177	5MU	N3-C2-N1	4.63	121.03	114.89
34	a	1491	UR3	C4-N3-C2	-4.04	120.76	124.56
34	a	959	2MG	C5-C6-N1	3.73	120.54	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	2791	OMG	C5-C6-N1	3.49	120.11	113.95
9	A	2177	5MU	O2-C2-N1	-3.35	118.33	122.79
9	A	2791	OMG	C2-N1-C6	-3.07	119.44	125.10
34	a	960	5MC	C5-C6-N1	-3.01	120.24	123.34
9	A	2177	5MU	C5M-C5-C6	-2.88	119.00	122.85
34	a	518	G7M	C2-N1-C6	-2.71	120.10	125.10
9	A	2791	OMG	C8-N7-C5	2.65	108.03	102.99
9	A	2177	5MU	O4-C4-N3	-2.63	115.08	120.12
9	A	2177	5MU	C5M-C5-C4	2.61	121.64	118.77
34	a	959	2MG	C8-N7-C5	2.55	107.85	102.99
34	a	959	2MG	O6-C6-C5	-2.49	119.50	124.37
34	a	1395	4OC	CM4-N4-C4	-2.39	117.79	122.45
9	A	2791	OMG	O6-C6-C5	-2.37	119.75	124.37
34	a	959	2MG	CM2-N2-C2	-2.16	119.09	123.86

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	2177	5MU	O4'-C4'-C5'-O5'
34	a	959	2MG	O4'-C4'-C5'-O5'
34	a	959	2MG	C3'-C4'-C5'-O5'
34	a	1395	4OC	O4'-C4'-C5'-O5'
34	a	1512	MA6	O4'-C4'-C5'-O5'
34	a	1512	MA6	C3'-C4'-C5'-O5'
9	A	2177	5MU	C3'-C4'-C5'-O5'
34	a	1395	4OC	C3'-C4'-C5'-O5'
34	a	1512	MA6	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 441 ligands modelled in this entry, 441 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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	76:U	O3'	77:A	P	3.18

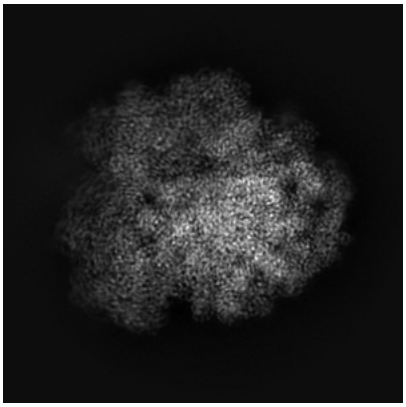
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-23975. These allow visual inspection of the internal detail of the map and identification of artifacts.

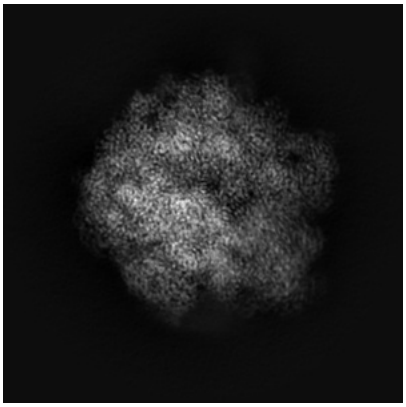
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

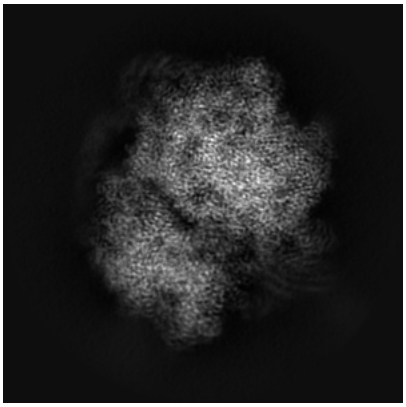
6.1.1 Primary map



X



Y

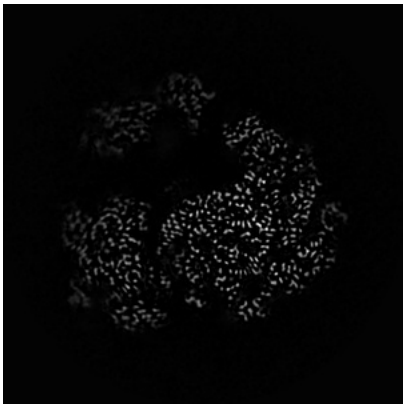


Z

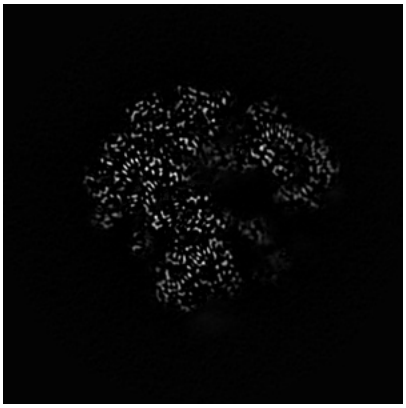
The images above show the map projected in three orthogonal directions.

6.2 Central slices

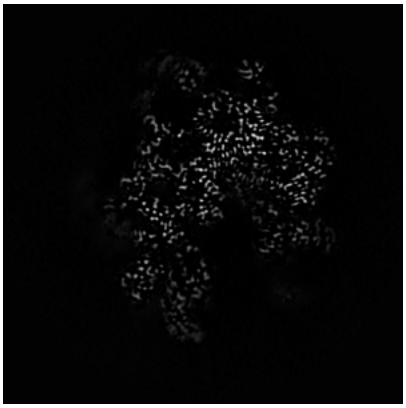
6.2.1 Primary map



X Index: 160



Y Index: 160

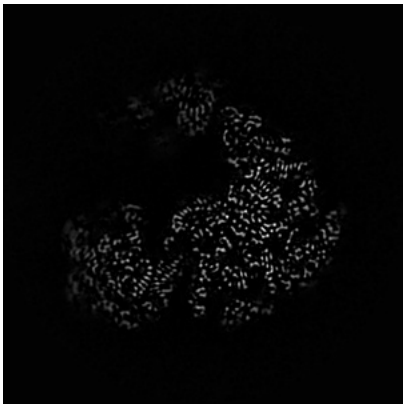


Z Index: 160

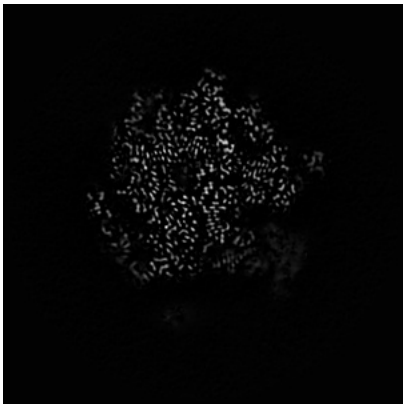
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

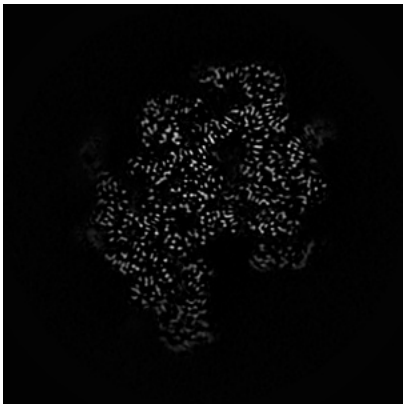
6.3.1 Primary map



X Index: 166



Y Index: 196



Z Index: 142

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

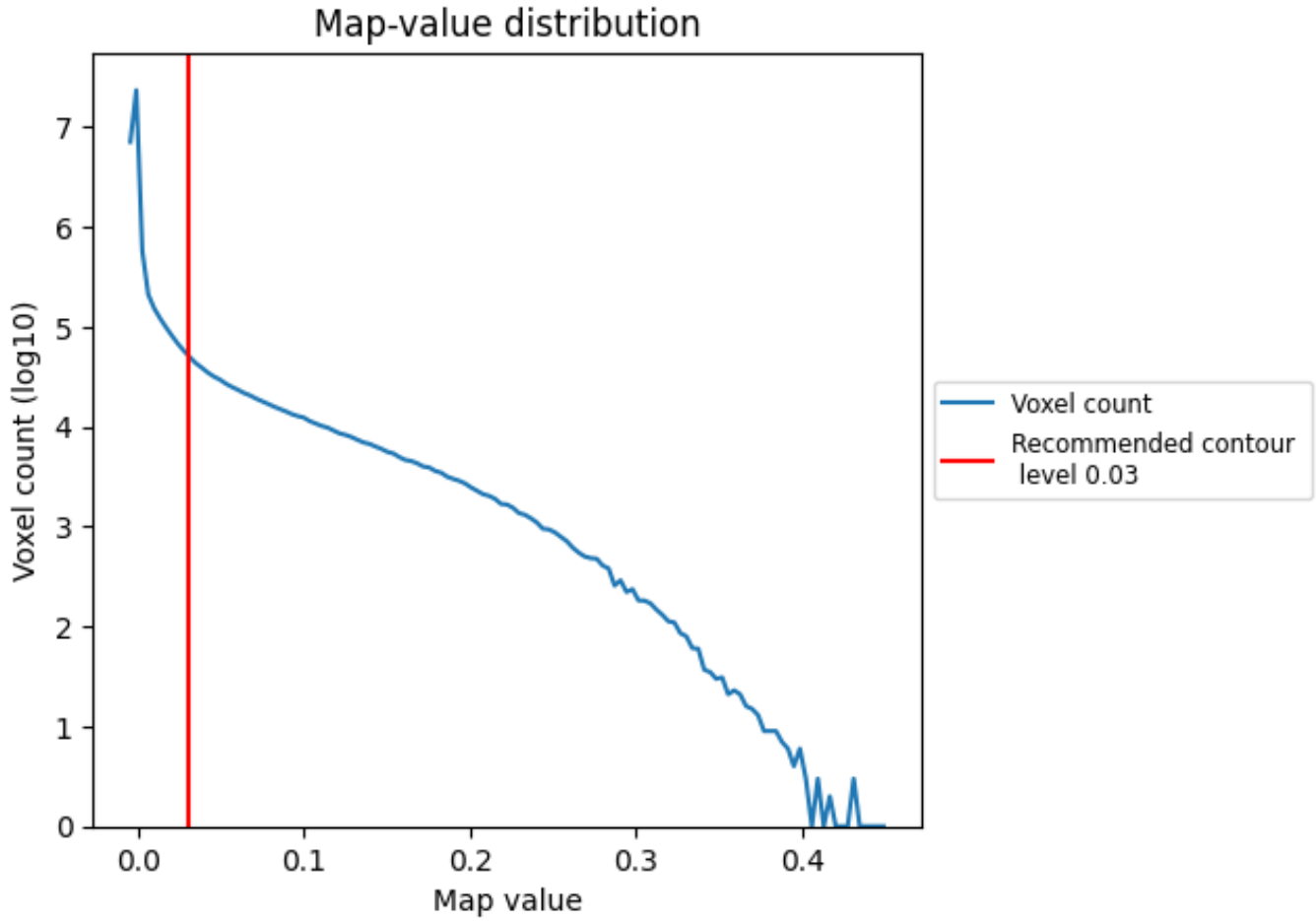
6.5 Mask visualisation (i)

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

7 Map analysis

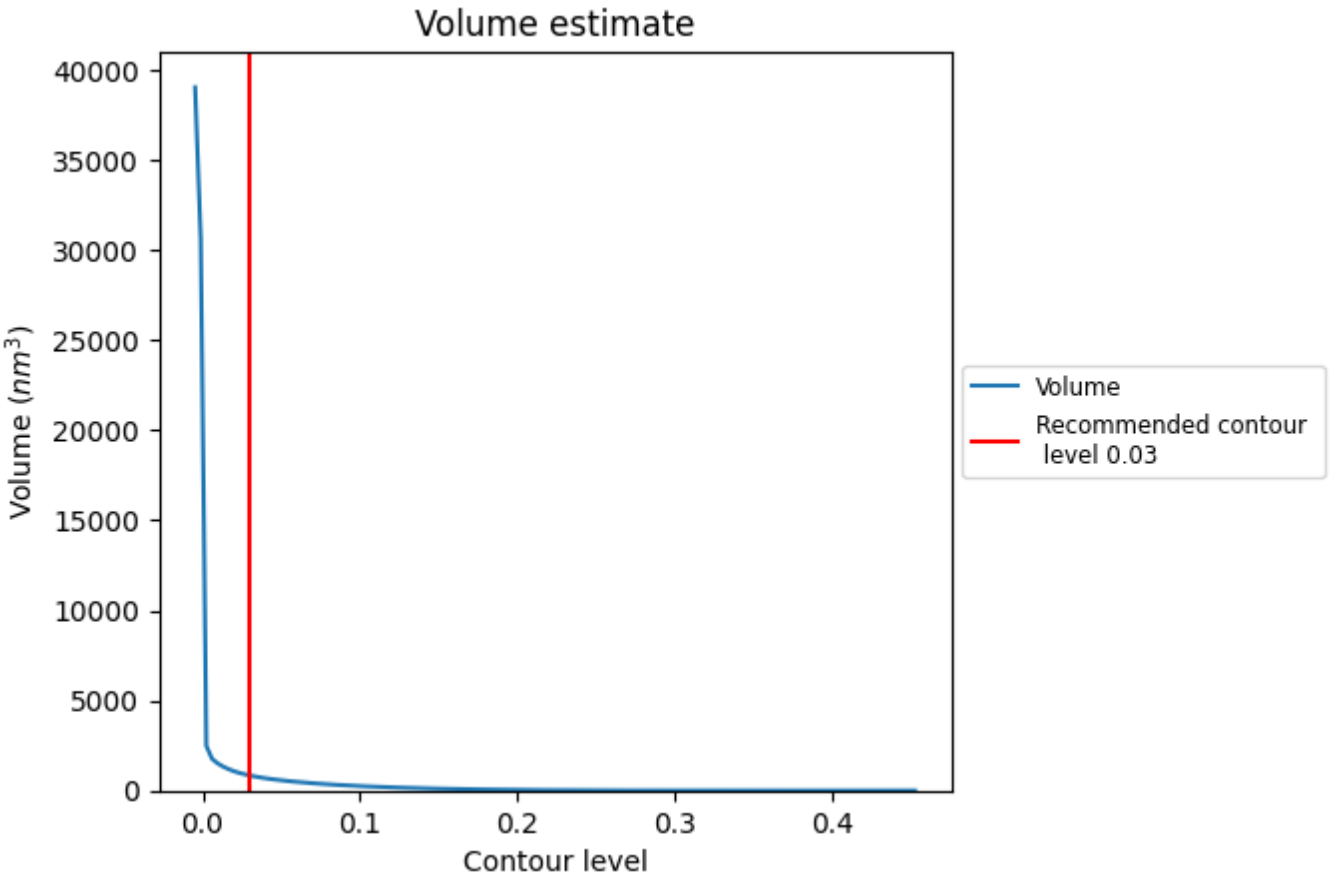
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

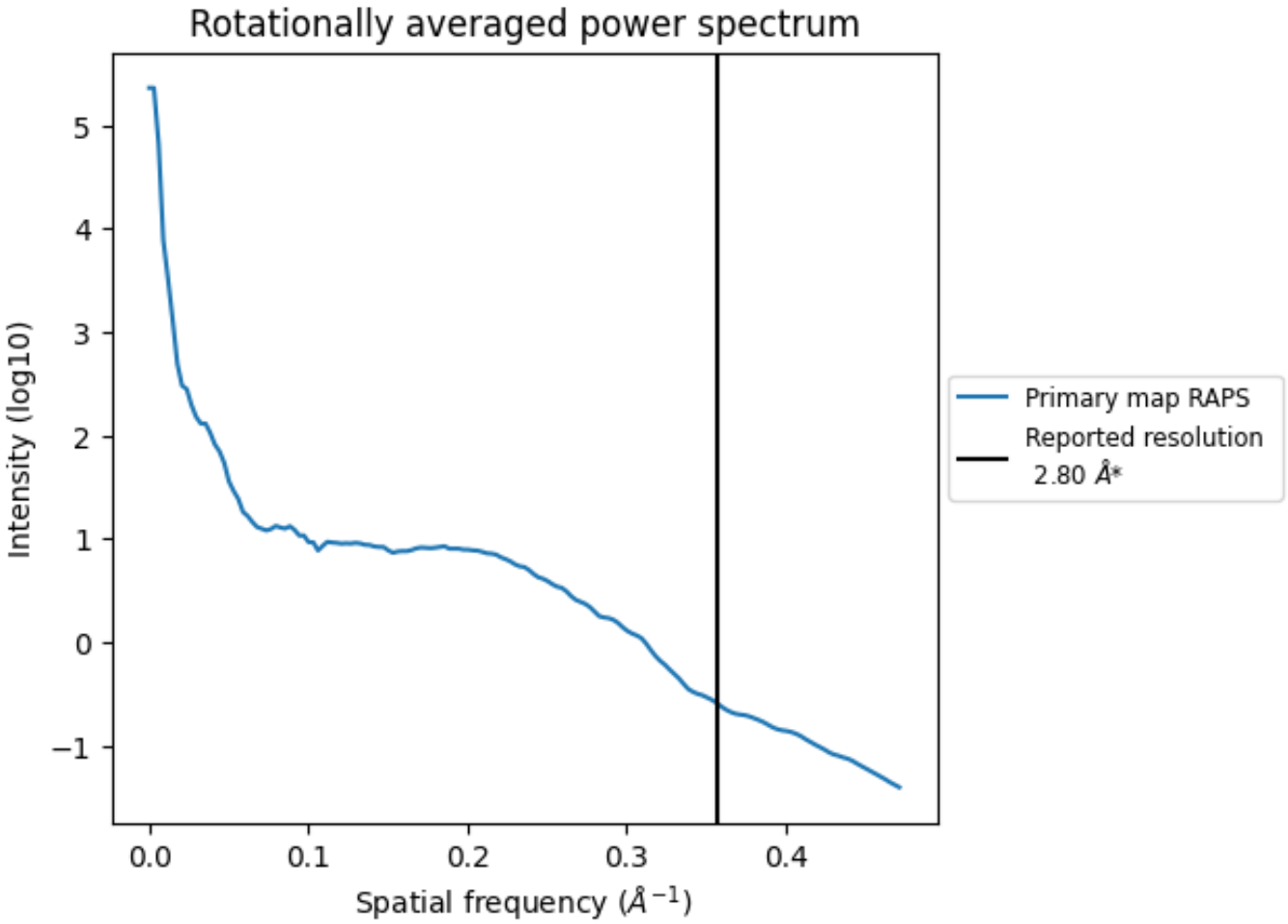
7.2 Volume estimate



The volume at the recommended contour level is 836 nm^3; this corresponds to an approximate mass of 755 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 (i)

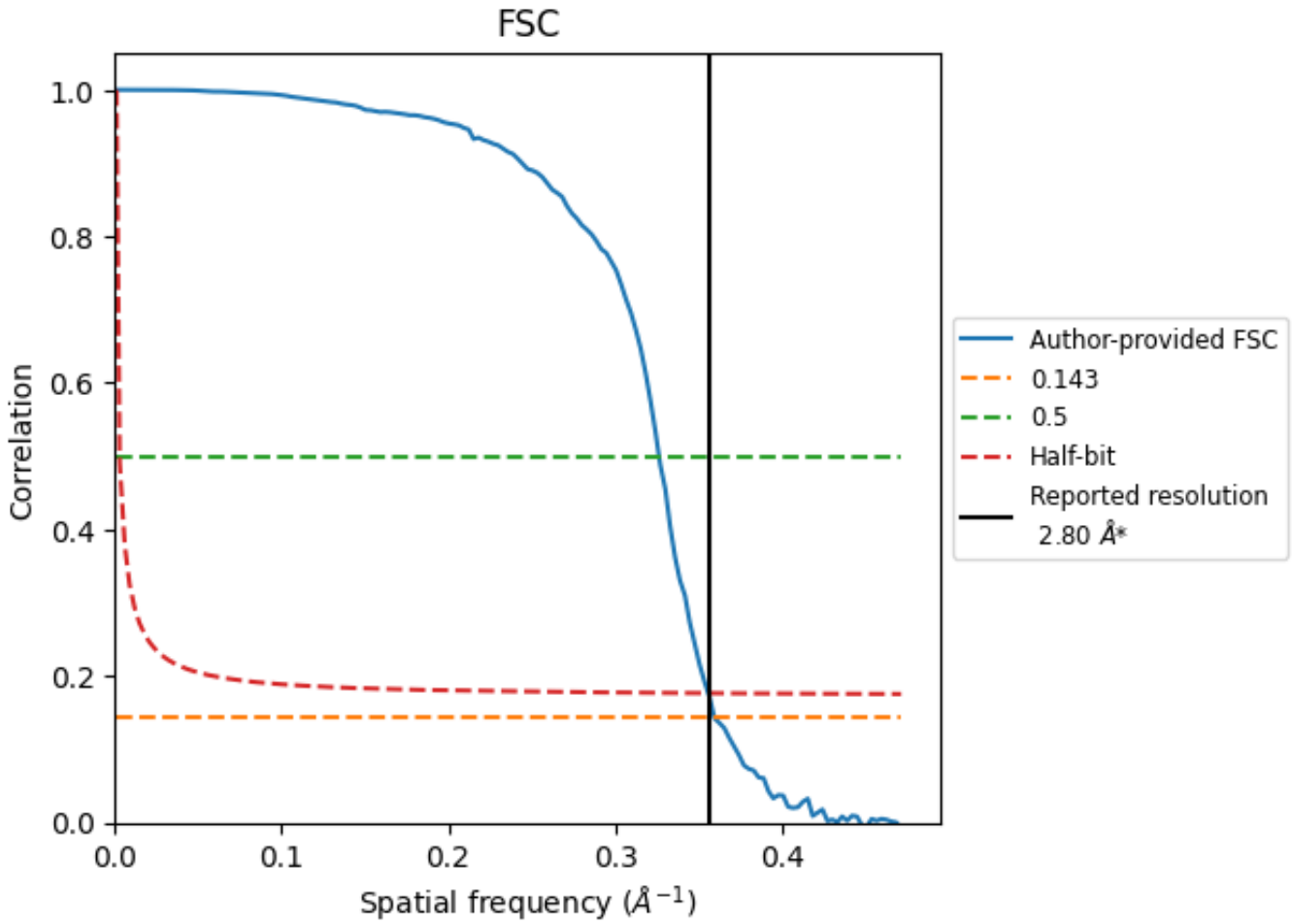


*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8.2 Resolution estimates (i)

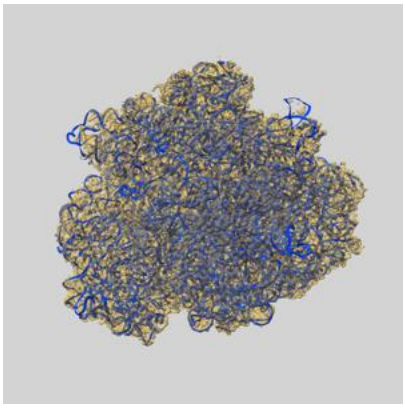
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.78	3.06	2.81
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

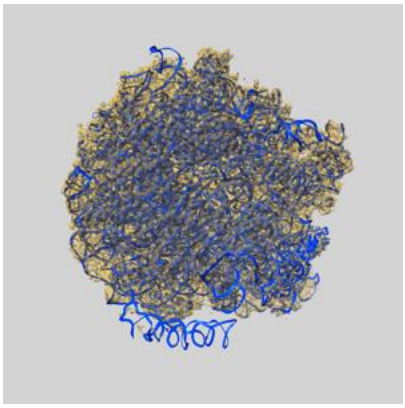
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-23975 and PDB model 7MT3. Per-residue inclusion information can be found in section 3 on page 15.

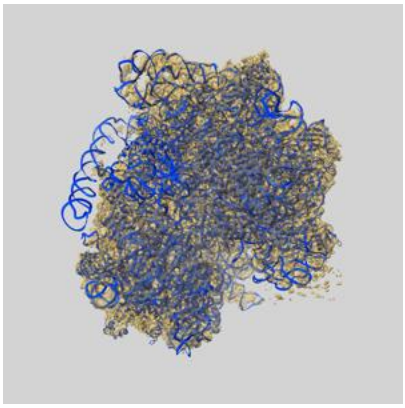
9.1 Map-model overlay



X



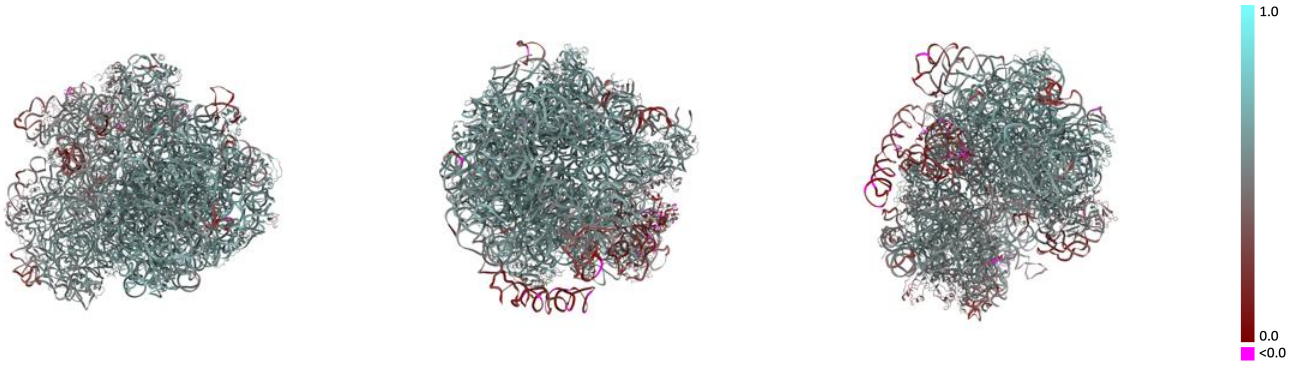
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03 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.

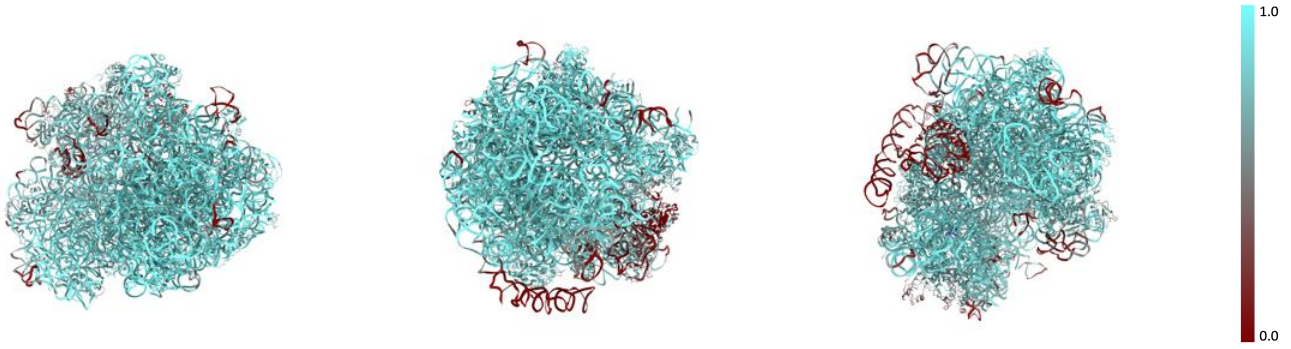
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

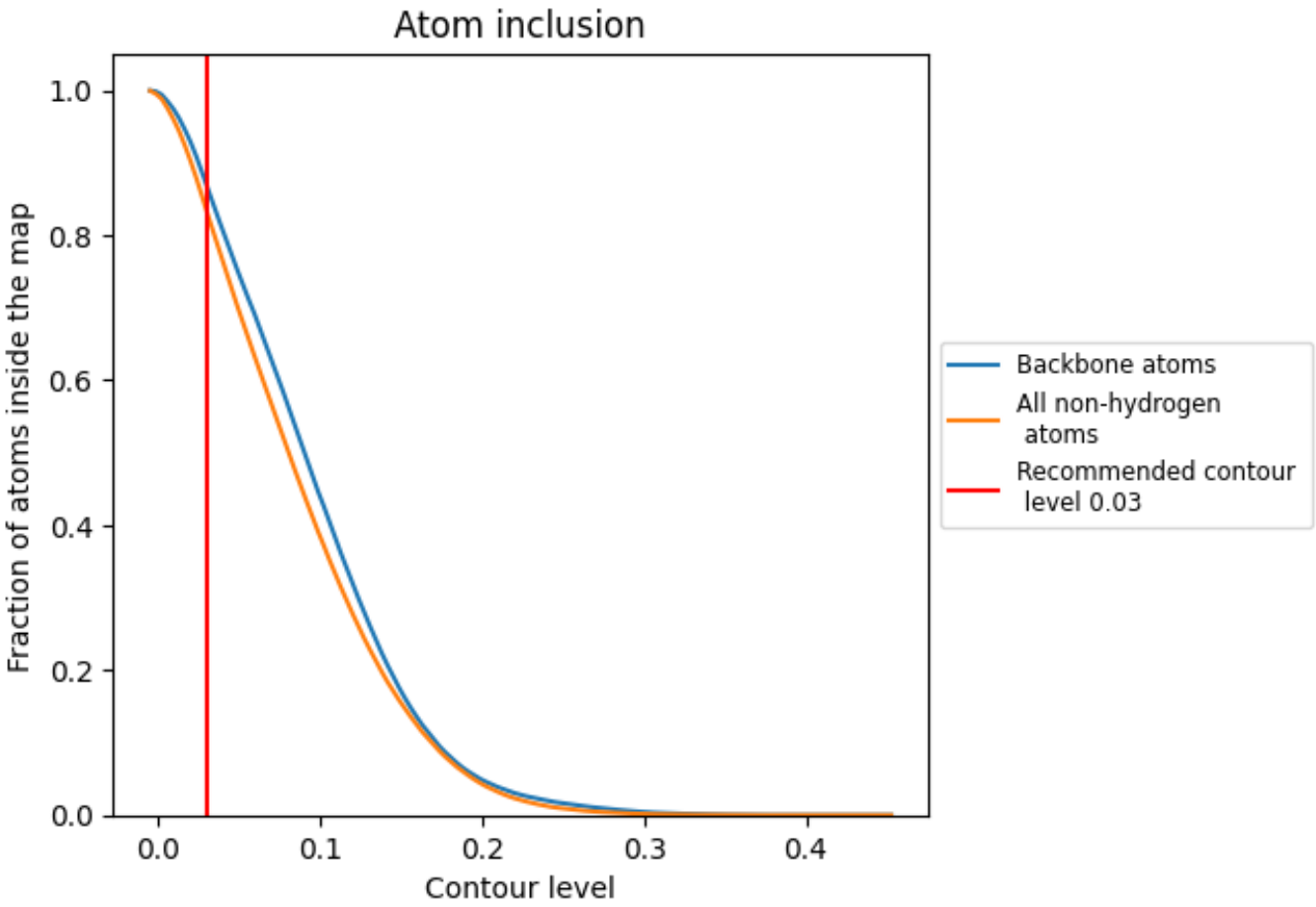
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.03).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 83% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8339	0.5360
0	0.7488	0.5620
1	0.8686	0.5700
2	0.9273	0.6080
3	0.8729	0.6010
4	0.8403	0.5650
6	0.5783	0.3590
7	0.1491	0.3620
8	0.0910	0.2090
A	0.8557	0.5480
B	0.9147	0.5550
C	0.9105	0.5980
D	0.8861	0.5840
E	0.8828	0.5730
F	0.7100	0.4700
G	0.6950	0.4600
H	0.2303	0.4160
J	0.8815	0.5790
K	0.8650	0.5750
L	0.8708	0.5790
M	0.7625	0.5280
N	0.9050	0.5910
O	0.8131	0.5410
P	0.8519	0.5620
Q	0.8988	0.5940
R	0.8890	0.5870
S	0.8991	0.5850
T	0.8764	0.5560
U	0.8341	0.5260
V	0.6448	0.4450
W	0.9208	0.5820
X	0.9317	0.5940
Y	0.8231	0.5480
Z	0.8659	0.5680
a	0.8844	0.5420

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Chain	Atom inclusion	Q-score
c	0.6853	0.4730
d	0.6700	0.4410
e	0.8040	0.5320
f	0.7259	0.4950
g	0.6768	0.4810
h	0.8484	0.5560
i	0.6799	0.4630
j	0.5716	0.4100
k	0.8150	0.5440
l	0.7892	0.5210
m	0.6767	0.4670
n	0.8133	0.5360
o	0.8104	0.5380
p	0.7369	0.4940
q	0.7847	0.5070
r	0.8049	0.5270
s	0.6263	0.4260
t	0.7984	0.5270
y	0.7415	0.4720
z	0.7769	0.4760