Full wwPDB EM Validation Report (i)

May 27, 2024 – 07:29 AM EDT

PDB ID	:	7SSW
EMDB ID	:	EMD-25415
Title	:	Late translocation intermediate with EF-G dissociated (Structure VI)
Authors	:	Carbone, C.E.; Korostelev, A.A.
Deposited on	:	2021-11-11
Resolution	:	3.80 Å(reported)
Based on initial model	:	5U9F

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 (i) 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 (i)) were used in the production of this report:

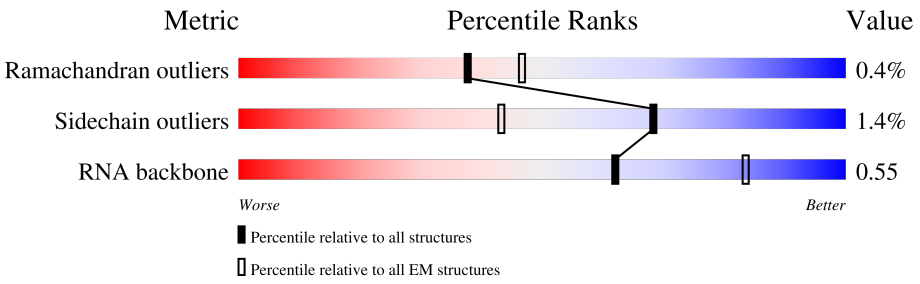
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	3	1539	81% 19%
2	1	2903	82% 18%
3	2	120	90% 10%
4	6	77	78% 21% •
5	b	271	98% •
6	c	209	96% •
7	d	201	99% •
8	e	177	• 99% •

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Mol	Chain	Length	Quality of chain
9	f	176	98%
10	g	149	22%, 99%
11	a	223	60%, 40%
12	i	142	25%, 97%
13	j	142	98%
14	k	122	96%
15	l	143	94%, 6%
16	m	136	98%
17	n	120	98%
18	o	116	98%
19	p	114	96%
20	q	117	99%
21	r	103	99%
22	s	110	98%
23	t	93	100%
24	u	102	98%
25	v	94	98%
26	w	75	99%
27	x	77	99%
28	y	63	97%
29	z	58	97%
30	B	56	98%
31	C	50	8%, 100%
32	D	46	100%
33	E	64	94%, 5%

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Mol	Chain	Length	Quality of chain
34	F	38	100%
35	4	39	5% 38% 13% 49%
36	5	77	81% 19%
37	G	225	8% 93%
38	H	206	15% 99%
39	I	205	100%
40	J	157	97%
41	K	100	99%
42	L	151	11% 99%
43	M	129	99%
44	N	127	98%
45	O	98	7% 97%
46	P	116	96%
47	Q	123	95%
48	R	114	99%
49	S	100	96%
50	T	88	98%
51	U	82	99%
52	V	80	95% 5%
53	W	65	97%
54	X	79	97%
55	Y	85	100%
56	Z	65	92% 6%

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 147596 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	3	1539	33012	14725	6052	10697	1538	0	0

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 4 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	6	77	1640	732	297	535	76	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	g	149	1111	699	197	214	1	0	0

- Molecule 11 is a protein called 50S ribosomal protein L1.

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

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	i	141	1032	651	179	196	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

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

- Molecule 15 is a protein called 50S ribosomal protein L15.

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

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

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

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

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

- Molecule 24 is a protein called 50S ribosomal protein L24.

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

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

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

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

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

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	4	20	436	195	87	134	20	0	0

- Molecule 36 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	5	77	1647	733	295	542	77	0	0

- Molecule 37 is a protein called 30S ribosomal protein S2.

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

- Molecule 38 is a protein called 30S ribosomal protein S3.

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

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called 30S ribosomal protein S5.

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

- Molecule 41 is a protein called 30S ribosomal protein S6.

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

- Molecule 42 is a protein called 30S ribosomal protein S7.

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

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

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

- Molecule 46 is a protein called 30S ribosomal protein S11.

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

- Molecule 47 is a protein called 30S ribosomal protein S12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

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

- Molecule 49 is a protein called 30S ribosomal protein S14.

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

- Molecule 50 is a protein called 30S ribosomal protein S15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

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

- Molecule 52 is a protein called 30S ribosomal protein S17.

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

- Molecule 53 is a protein called 30S ribosomal protein S18.

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

- Molecule 54 is a protein called 30S ribosomal protein S19.

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

- Molecule 55 is a protein called 30S ribosomal protein S20.

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

- Molecule 56 is a protein called 30S ribosomal protein S21.

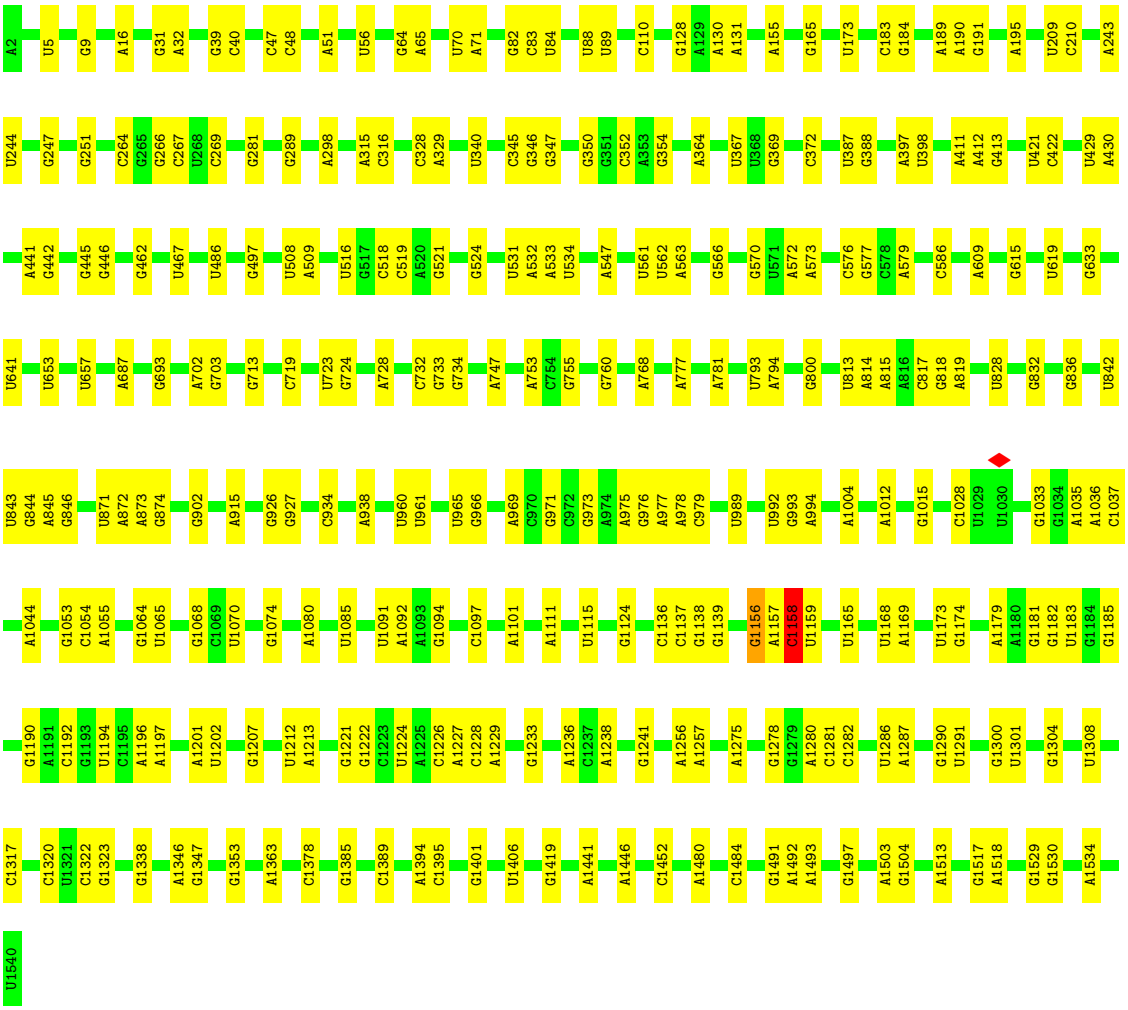
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Z	65	545	335	117	92	1	0	0

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.

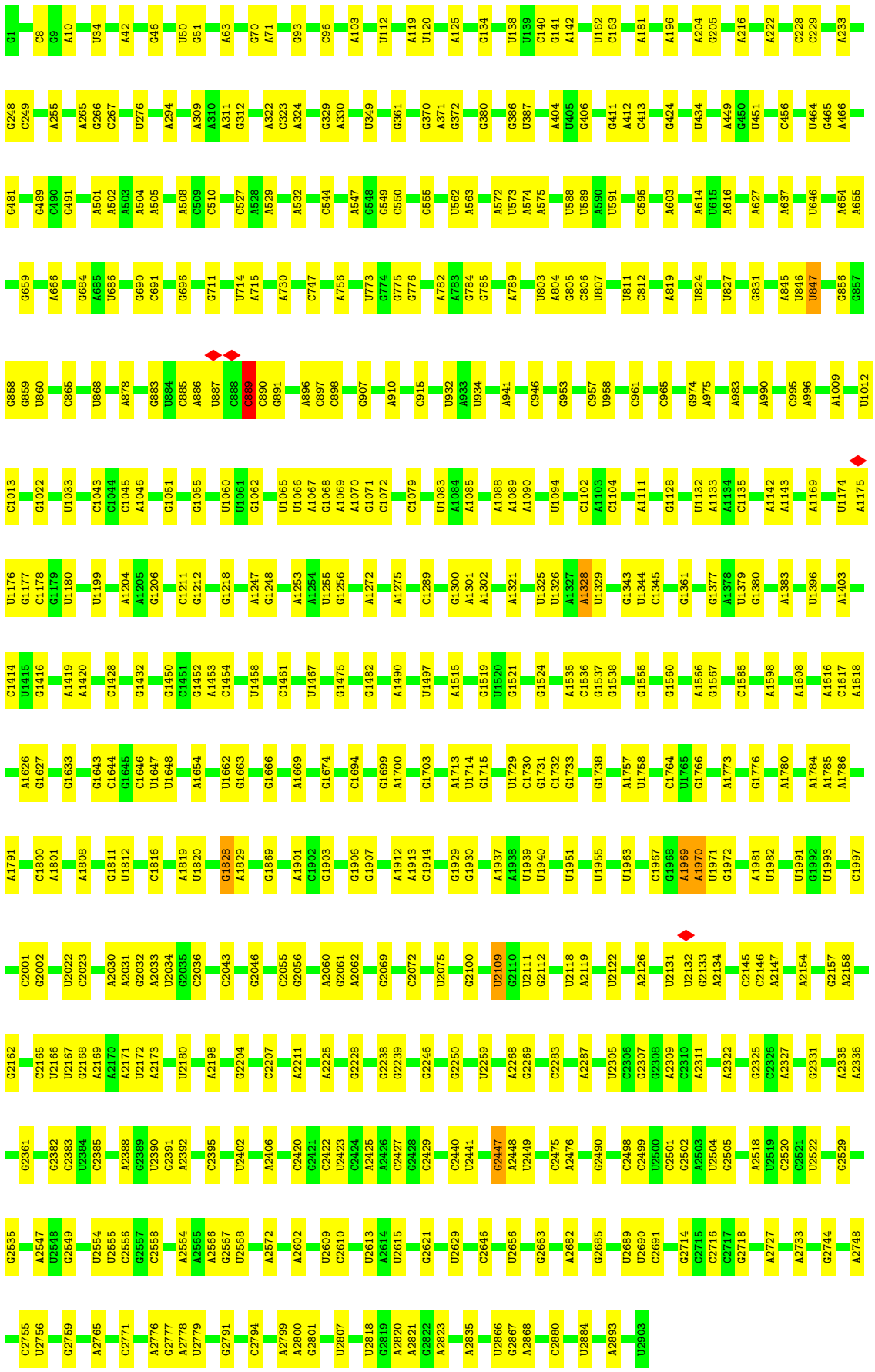
- Molecule 1: 16S rRNA

Chain 3: 81% 19%



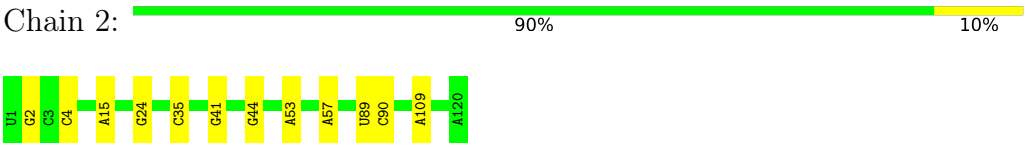
- Molecule 2: 23S rRNA

Chain 1: 82% 18%


G1 C8 G9 A10 U34 A42 G46 U50 G51 A63 G70 A71 G93 C96 A103 U112 A119 U120 A125 G134 U138 U139 C140 G141 A142 U162 C163 A181 A196 A204 G205 A216 A222 C228 C229 A233
G248 C249 A255 A265 G266 C267 U276 A294 A309 A310 A311 G312 A322 C323 A324 G329 A330 U349 G361 G370 A371 G372 G380 G386 U387 A404 U405 G406 G411 A412 C413 G424 U434 A449 G450 U451 C456 U464 G465 A466
G481 G489 C490 G491 A501 A502 A503 A504 A505 A508 C509 C510 C527 A528 A529 A532 C544 A547 G548 G549 C550 G555 U562 A563 A572 U573 A574 A575 U588 U589 A590 U591 C595 A603 A614 U615 A616 A627 A637 U646 A654 A655
G659 A666 G684 A685 U686 G690 C691 G696 G711 U714 A715 A730 C747 A756 U773 G774 G775 G776 A782 A783 G784 G785 A789 U803 A804 G805 C806 U807 U811 C812 A819 U824 U827 G831 A845 U846 U847 G856 G857
G858 G859 U860 C865 U868 A878 G883 U884 C885 A886 U887 C888 C889 C890 G891 A896 C897 C898 G907 A910 C915 U932 A933 U934 A941 C946 G953 C957 U958 C961 C965 G974 A975 A983 A990 C995 A996 A1009 U1012
C1013 G1022 U1033 C1043 C1044 C1045 A1046 G1051 G1055 U1060 U1061 G1062 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 C1079 U1083 A1084 A1085 A1088 A1089 A1090 U1094 C1102 A1103 C1104 A1111 G1128 U1132 A1133 A1134 C1135 A1142 A1143 A1169 U1174 A1175
U1176 G1177 C1178 G1179 U1180 U1199 A1204 A1205 G1206 C1211 G1212 G1218 A1247 G1248 A1253 A1254 U1255 G1256 A1272 A1275 C1289 G1300 A1301 A1302 A1321 U1325 U1326 A1327 A1328 U1329 G1343 U1344 C1345 G1361 G1377 A1378 U1379 G1380 A1383 U1396 A1403
C1414 U1415 G1416 A1419 A1420 C1428 G1432 G1450 C1451 G1452 A1453 C1454 U1458 C1461 U1467 G1475 G1482 A1490 U1497 A1515 G1519 U1520 G1521 G1524 A1535 C1536 G1537 G1538 G1555 G1560 A1566 G1567 C1585 A1598 A1608 A1616 C1617 A1618
A1626 G1627 G1633 G1643 C1644 G1645 C1646 U1647 U1648 A1654 U1662 G1663 G1666 A1669 G1674 C1694 G1699 A1700 G1703 A1713 U1714 G1715 U1729 C1730 G1731 C1732 G1733 G1738 A1757 U1758 C1764 U1765 G1766 A1773 G1776 A1780 A1784 A1785 A1786
A1791 C1800 A1801 A1808 G1811 U1812 C1816 A1819 U1820 G1828 A1829 G1869 A1901 C1902 G1903 G1906 G1907 A1912 A1913 C1914 G1929 G1930 A1937 A1938 U1939 U1940 U1951 U1955 U1963 C1967 G1968 A1969 A1970 U1971 G1972 A1981 U1982 U1991 G1992 U1993 C1997
C2001 G2002 U2022 C2023 A2030 A2031 G2032 A2033 U2034 G2035 C2036 C2043 G2046 C2055 G2056 A2060 G2061 A2062 G2069 C2072 U2075 G2100 U2109 C2110 U2111 G2112 U2118 A2119 U2122 A2126 U2131 U2132 G2133 A2134 C2145 C2146 A2147 A2154 G2157 A2158
G2162 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 U2180 A2198 G2204 C2207 A2211 A2225 G2228 G2238 G2239 G2246 G2250 U2259 A2268 G2269 C2283 A2287 U2305 C2306 G2307 G2308 A2309 C2310 A2311 A2322 G2325 C2326 A2327 G2331 A2335 A2336
G2361 G2382 G2383 U2384 C2385 A2388 G2389 U2390 G2391 A2392 C2395 U2402 A2406 C2420 G2421 C2422 U2423 C2424 A2425 A2426 C2427 G2428 G2429 C2440 U2441 G2447 A2448 U2449 C2475 A2476 G2490 C2498 C2499 U2500 C2501 G2502 A2503 U2504 G2505 A2518 U2519 C2520 C2521 U2522 G2529
G2535 A2547 U2548 G2549 U2554 U2555 C2556 G2557 C2558 A2564 A2565 A2566 G2567 U2568 A2572 A2602 U2609 C2610 U2613 A2614 U2615 G2621 U2629 C2646 U2656 G2663 A2682 G2685 U2689 U2690 C2691 G2714 C2715 C2716 C2717 G2718 A2727 A2733 G2744 A2748
C2755 U2756 G2759 A2765 C2771 A2776 G2777 A2778 U2779 G2791 C2794 A2799 A2800 G2801 U2807 U2818 G2819 A2820 A2821 G2822 A2823 A2835 U2866 G2867 A2868 C2880 U2884 A2893 U2903

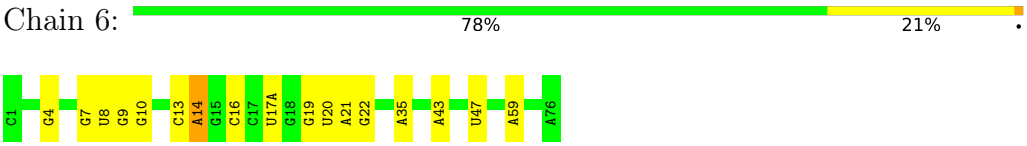
- Molecule 3: 5S rRNA

Chain 2:



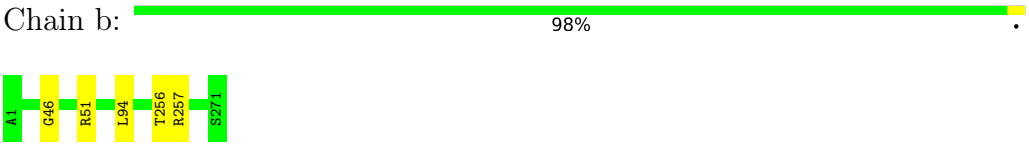
- Molecule 4: tRNA fMet

Chain 6:



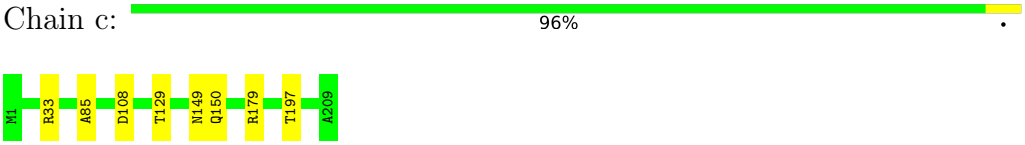
- Molecule 5: 50S ribosomal protein L2

Chain b:



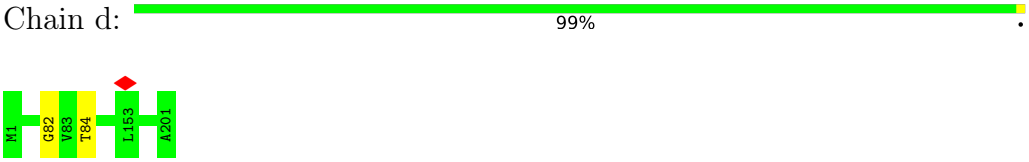
- Molecule 6: 50S ribosomal protein L3

Chain c:



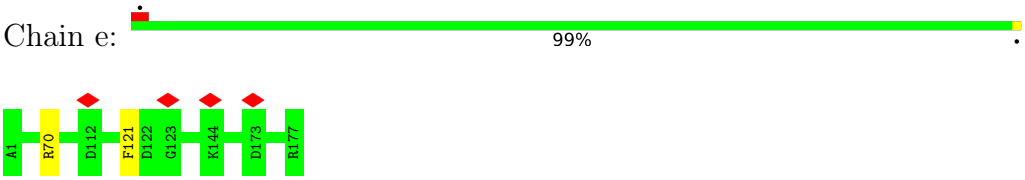
- Molecule 7: 50S ribosomal protein L4

Chain d:



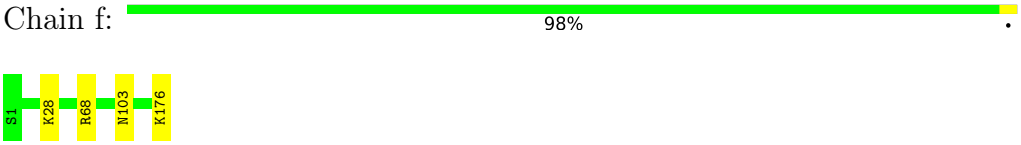
- Molecule 8: 50S ribosomal protein L5

Chain e:



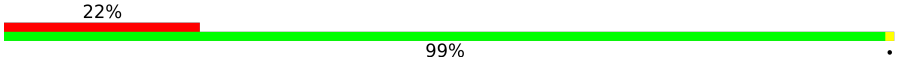
- Molecule 9: 50S ribosomal protein L6

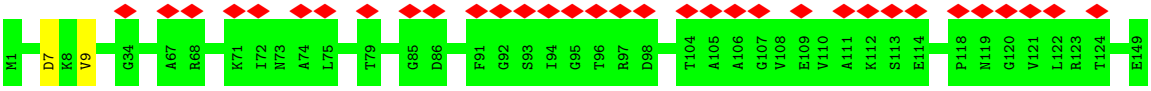
Chain f:



• Molecule 10: 50S ribosomal protein L9

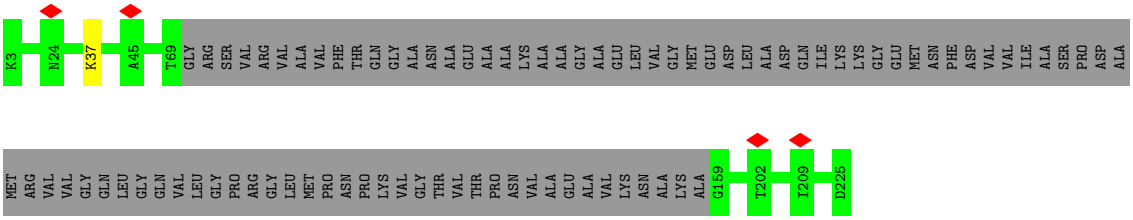
Chain g:





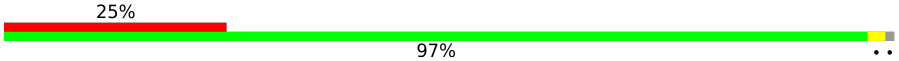
• Molecule 11: 50S ribosomal protein L1

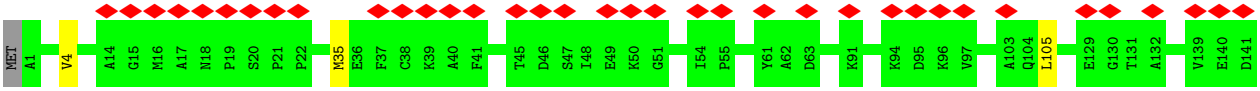
Chain a:



• Molecule 12: 50S ribosomal protein L11

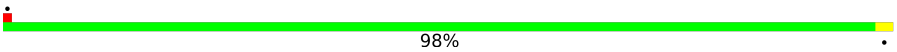
Chain i:

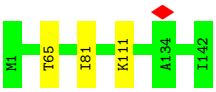




• Molecule 13: 50S ribosomal protein L13

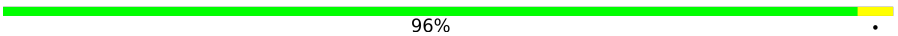
Chain j:

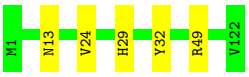




• Molecule 14: 50S ribosomal protein L14

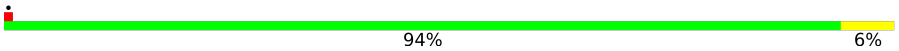
Chain k:

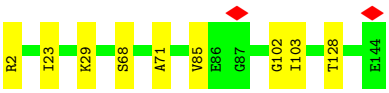




• Molecule 15: 50S ribosomal protein L15

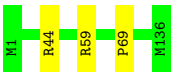
Chain l:





• Molecule 16: 50S ribosomal protein L16

Chain m: 98%



• Molecule 17: 50S ribosomal protein L17

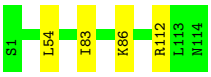
Chain n: 98%

• Molecule 18: 50S ribosomal protein L18

Chain o: 98%

• Molecule 19: 50S ribosomal protein L19

Chain p: 96%



• Molecule 20: 50S ribosomal protein L20

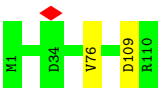
Chain q: 99%

• Molecule 21: 50S ribosomal protein L21

Chain r: 99%

• Molecule 22: 50S ribosomal protein L22

Chain s: 98%



• Molecule 23: 50S ribosomal protein L23

Chain t: 100%

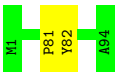
There are no outlier residues recorded for this chain.

• Molecule 24: 50S ribosomal protein L24

Chain u: 98%

• Molecule 25: 50S ribosomal protein L25

Chain v: 98%



• Molecule 26: 50S ribosomal protein L27

Chain w: 99%

• Molecule 27: 50S ribosomal protein L28

Chain x: 99%

• Molecule 28: 50S ribosomal protein L29

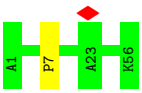
Chain y: 97%

• Molecule 29: 50S ribosomal protein L30

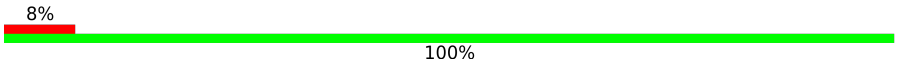
Chain z: 97%

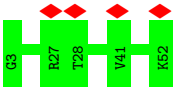
• Molecule 30: 50S ribosomal protein L32

Chain B: 98%

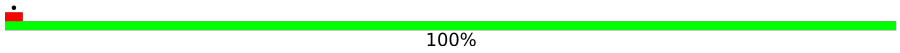


• Molecule 31: 50S ribosomal protein L33

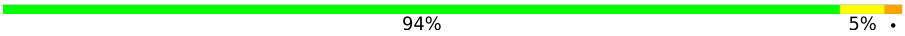
Chain C: 

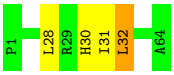


• Molecule 32: 50S ribosomal protein L34

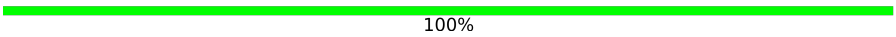
Chain D: 

• Molecule 33: 50S ribosomal protein L35

Chain E: 



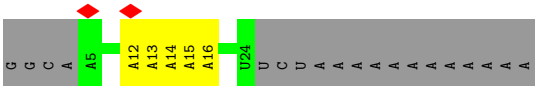
• Molecule 34: 50S ribosomal protein L36

Chain F: 

There are no outlier residues recorded for this chain.

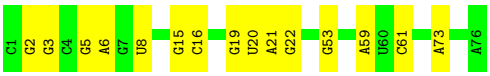
• Molecule 35: mRNA

Chain 4:

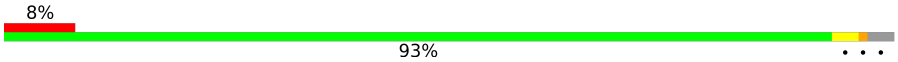


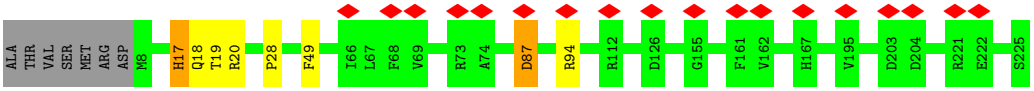
• Molecule 36: tRNA Pro

Chain 5:



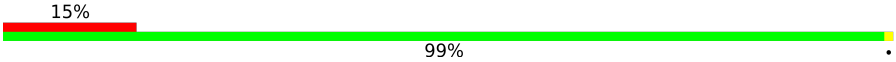
• Molecule 37: 30S ribosomal protein S2

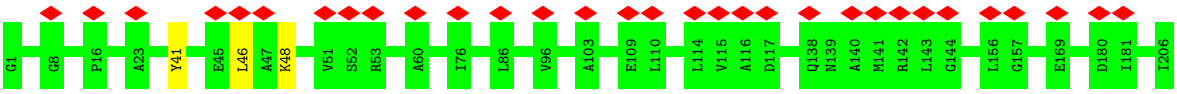
Chain G: 



• Molecule 38: 30S ribosomal protein S3

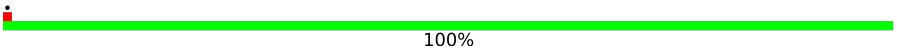
Chain H:

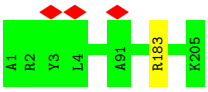




• Molecule 39: 30S ribosomal protein S4

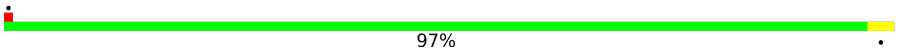
Chain I:

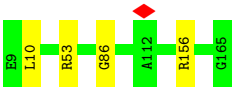




• Molecule 40: 30S ribosomal protein S5

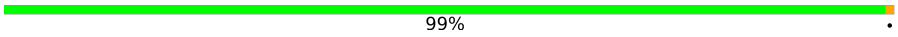
Chain J:





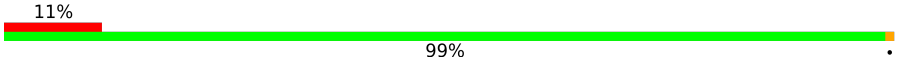
• Molecule 41: 30S ribosomal protein S6

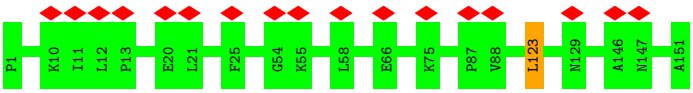
Chain K:



• Molecule 42: 30S ribosomal protein S7

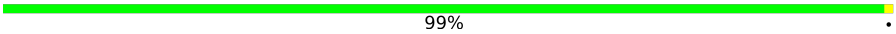
Chain L:





• Molecule 43: 30S ribosomal protein S8

Chain M:

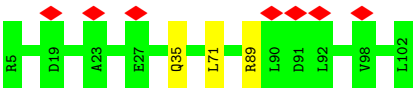


• Molecule 44: 30S ribosomal protein S9

Chain N: 98%

• Molecule 45: 30S ribosomal protein S10

Chain O: 7% 97%

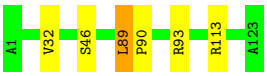


• Molecule 46: 30S ribosomal protein S11

Chain P: 96%

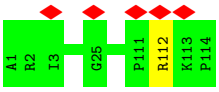
• Molecule 47: 30S ribosomal protein S12

Chain Q: 95%



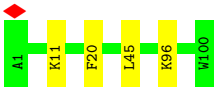
• Molecule 48: 30S ribosomal protein S13

Chain R: 99%



• Molecule 49: 30S ribosomal protein S14

Chain S: 96%



• Molecule 50: 30S ribosomal protein S15

Chain T: 98%

• Molecule 51: 30S ribosomal protein S16

Chain U: 99%

• Molecule 52: 30S ribosomal protein S17

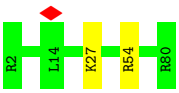
Chain V: 95% 5%

• Molecule 53: 30S ribosomal protein S18

Chain W: 97%

• Molecule 54: 30S ribosomal protein S19

Chain X: 97%



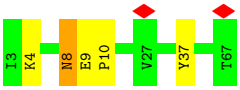
• Molecule 55: 30S ribosomal protein S20

Chain Y: 100%

There are no outlier residues recorded for this chain.

• Molecule 56: 30S ribosomal protein S21

Chain Z: 92% 6%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1163	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 ($e^-/Å^2$)	47.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.281	Depositor
Minimum map value	-12.230	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.851	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	370.5408, 370.5408, 370.5408	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8271, 0.8271, 0.8271	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	3	0.57	0/36963	0.68	4/57662 (0.0%)
2	1	0.56	0/69796	0.69	7/108888 (0.0%)
3	2	0.55	0/2872	0.68	0/4479
4	6	0.66	2/1832 (0.1%)	0.85	4/2855 (0.1%)
5	b	0.48	0/2122	0.72	1/2852 (0.0%)
6	c	0.43	0/1586	0.70	0/2134
7	d	0.37	0/1571	0.60	0/2113
8	e	0.37	0/1435	0.63	0/1926
9	f	0.34	0/1343	0.61	0/1816
10	g	0.34	0/1122	0.66	0/1515
11	a	0.28	0/1034	0.61	0/1387
12	i	0.33	0/1046	0.66	1/1410 (0.1%)
13	j	0.40	0/1152	0.64	0/1551
14	k	0.46	0/948	0.72	0/1268
15	l	0.40	0/1054	0.71	0/1403
16	m	0.44	0/1093	0.65	0/1460
17	n	0.43	0/974	0.68	0/1301
18	o	0.36	0/902	0.59	1/1209 (0.1%)
19	p	0.41	0/929	0.63	2/1242 (0.2%)
20	q	0.47	0/960	0.56	0/1278
21	r	0.43	0/829	0.68	1/1107 (0.1%)
22	s	0.38	0/864	0.59	0/1156
23	t	0.39	0/745	0.61	0/994
24	u	0.37	0/788	0.64	1/1051 (0.1%)
25	v	0.39	0/766	0.64	0/1025
26	w	0.42	0/582	0.64	0/769
27	x	0.43	0/635	0.64	0/848
28	y	0.29	0/510	0.66	0/677
29	z	0.35	0/453	0.62	1/605 (0.2%)
30	B	0.36	0/450	0.68	0/599
31	C	0.34	0/417	0.53	0/554
32	D	0.43	0/380	0.59	0/498
33	E	0.43	0/513	0.76	2/676 (0.3%)
34	F	0.38	0/303	0.68	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	4	0.68	0/490	0.75	0/763
36	5	0.64	0/1840	0.72	0/2868
37	G	0.35	0/1736	0.64	2/2338 (0.1%)
38	H	0.31	0/1652	0.58	0/2225
39	I	0.33	0/1665	0.58	0/2227
40	J	0.38	0/1170	0.69	1/1573 (0.1%)
41	K	0.39	0/836	0.64	1/1128 (0.1%)
42	L	0.30	0/1196	0.59	1/1602 (0.1%)
43	M	0.35	0/989	0.64	1/1326 (0.1%)
44	N	0.32	0/1034	0.64	0/1375
45	O	0.31	0/797	0.69	2/1077 (0.2%)
46	P	0.34	0/886	0.62	0/1195
47	Q	0.42	0/969	0.72	0/1300
48	R	0.31	0/893	0.65	0/1193
49	S	0.31	0/817	0.62	1/1088 (0.1%)
50	T	0.32	0/722	0.60	0/964
51	U	0.34	0/659	0.62	0/884
52	V	0.38	0/658	0.73	0/881
53	W	0.36	0/545	0.65	0/731
54	X	0.34	0/653	0.69	0/877
55	Y	0.30	0/671	0.53	0/888
56	Z	0.37	0/551	0.72	0/728
All	All	0.52	2/160398 (0.0%)	0.68	34/239936 (0.0%)

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
1	3	1	4
2	1	1	12
5	b	0	2
6	c	0	2
7	d	0	1
8	e	0	1
10	g	0	1
12	i	0	1
14	k	0	3
15	l	0	4
17	n	0	1
18	o	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	p	0	1
25	v	0	1
30	B	0	1
33	E	0	1
35	4	1	0
37	G	0	1
40	J	0	1
44	N	0	1
46	P	0	2
47	Q	0	2
51	U	0	1
52	V	0	2
56	Z	0	1
All	All	3	48

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	6	13	C	O3'-P	7.85	1.70	1.61
4	6	14	A	P-OP1	6.58	1.60	1.49

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	6	13	C	OP1-P-O3'	16.79	142.15	105.20
4	6	13	C	O3'-P-O5'	-15.05	75.40	104.00
4	6	13	C	P-O3'-C3'	9.45	131.04	119.70
4	6	14	A	O5'-P-OP1	-8.90	97.69	105.70
2	1	1828	G	N9-C1'-C2'	8.41	124.94	114.00
24	u	28	LEU	CA-CB-CG	7.26	132.00	115.30
18	o	26	LEU	CA-CB-CG	6.75	130.84	115.30
1	3	1156	G	N9-C1'-C2'	-6.43	104.93	112.00
33	E	32	LEU	CA-CB-CG	6.36	129.92	115.30
37	G	87	ASP	CB-CG-OD2	6.27	123.94	118.30
49	S	45	LEU	CA-CB-CG	6.12	129.38	115.30
1	3	1158	C	C3'-C2'-O2'	6.11	131.01	113.30
2	1	889	C	O4'-C1'-N1	5.88	112.90	108.20
33	E	28	LEU	CA-CB-CG	5.86	128.78	115.30
43	M	60	LEU	CA-CB-CG	5.74	128.50	115.30
19	p	54	LEU	CA-CB-CG	5.63	128.24	115.30
2	1	1669	A	N9-C1'-C2'	5.55	121.21	114.00
5	b	94	LEU	CA-CB-CG	5.53	128.01	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	J	10	LEU	CA-CB-CG	5.50	127.94	115.30
37	G	17	HIS	C-N-CA	5.47	135.38	121.70
2	1	847	U	N1-C1'-C2'	5.47	121.11	114.00
2	1	1328	A	N9-C1'-C2'	5.37	120.99	114.00
45	O	71	LEU	CA-CB-CG	5.37	127.65	115.30
29	z	47	ILE	CG1-CB-CG2	-5.35	99.63	111.40
12	i	105	LEU	CA-CB-CG	5.30	127.50	115.30
2	1	2109	U	N1-C1'-C2'	5.25	120.83	114.00
42	L	123	LEU	CA-CB-CG	5.25	127.37	115.30
19	p	83	ILE	CG1-CB-CG2	-5.19	99.98	111.40
41	K	61	LEU	CA-CB-CG	5.18	127.22	115.30
2	1	1970	A	C5'-C4'-O4'	5.18	115.31	109.10
45	O	35	GLN	CA-CB-CG	5.17	124.76	113.40
1	3	1158	C	C1'-C2'-O2'	5.09	125.89	110.60
1	3	563	A	N9-C1'-C2'	5.07	120.59	114.00
21	r	39	LEU	CA-CB-CG	5.07	126.96	115.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	3	1158	C	C2'
2	1	889	C	C2'
35	4	13	A	C4'

All (48) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	1328	A	Sidechain
2	1	1377	G	Sidechain
2	1	1432	G	Sidechain
2	1	1666	G	Sidechain
2	1	1828	G	Sidechain
2	1	1969	A	Sidechain
2	1	2109	U	Sidechain
2	1	2180	U	Sidechain
2	1	2447	G	Sidechain
2	1	370	G	Sidechain
2	1	775	G	Sidechain
2	1	889	C	Sidechain
1	3	1156	G	Sidechain
1	3	1158	C	Sidechain
1	3	1194	U	Sidechain

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Mol	Chain	Res	Type	Group
1	3	800	G	Sidechain
30	B	7	PRO	Peptide
33	E	30	HIS	Peptide
37	G	17	HIS	Peptide
40	J	86	GLY	Peptide
44	N	56	MET	Peptide
46	P	124	LYS	Peptide
46	P	125	LYS	Peptide
47	Q	46	SER	Peptide
47	Q	89	LEU	Peptide
51	U	44	SER	Peptide
52	V	42	LYS	Peptide
52	V	49	ASN	Peptide
56	Z	8	ASN	Peptide
5	b	46	GLY	Peptide
5	b	51	ARG	Peptide
6	c	149	ASN	Peptide
6	c	85	ALA	Peptide
7	d	82	GLY	Peptide
8	e	121	PHE	Peptide
10	g	7	ASP	Peptide
12	i	4	VAL	Peptide
14	k	13	ASN	Peptide
14	k	24	VAL	Peptide
14	k	29	HIS	Peptide
15	l	102	GLY	Peptide
15	l	23	ILE	Peptide
15	l	68	SER	Peptide
15	l	71	ALA	Peptide
17	n	43	GLU	Peptide
18	o	33	ARG	Peptide
19	p	112	ARG	Peptide
25	v	81	PRO	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	
5	b	269/271 (99%)	221 (82%)	48 (18%)	0	100	100
6	c	207/209 (99%)	172 (83%)	33 (16%)	2 (1%)	15	52
7	d	199/201 (99%)	167 (84%)	32 (16%)	0	100	100
8	e	175/177 (99%)	144 (82%)	31 (18%)	0	100	100
9	f	174/176 (99%)	154 (88%)	20 (12%)	0	100	100
10	g	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	22	60
11	a	130/223 (58%)	113 (87%)	17 (13%)	0	100	100
12	i	139/142 (98%)	117 (84%)	22 (16%)	0	100	100
13	j	140/142 (99%)	126 (90%)	13 (9%)	1 (1%)	22	60
14	k	120/122 (98%)	92 (77%)	28 (23%)	0	100	100
15	l	141/143 (99%)	106 (75%)	32 (23%)	3 (2%)	7	40
16	m	134/136 (98%)	109 (81%)	24 (18%)	1 (1%)	22	60
17	n	118/120 (98%)	96 (81%)	22 (19%)	0	100	100
18	o	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
19	p	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
20	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
21	r	101/103 (98%)	84 (83%)	17 (17%)	0	100	100
22	s	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
23	t	91/93 (98%)	75 (82%)	16 (18%)	0	100	100
24	u	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
25	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	14	51
26	w	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
27	x	75/77 (97%)	65 (87%)	10 (13%)	0	100	100
28	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	9	44
29	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	B	54/56 (96%)	42 (78%)	12 (22%)	0	100	100
31	C	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
32	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	E	62/64 (97%)	52 (84%)	8 (13%)	2 (3%)	4	32
34	F	36/38 (95%)	25 (69%)	11 (31%)	0	100	100
37	G	216/225 (96%)	187 (87%)	27 (12%)	2 (1%)	17	54
38	H	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
39	I	203/205 (99%)	178 (88%)	25 (12%)	0	100	100
40	J	155/157 (99%)	130 (84%)	25 (16%)	0	100	100
41	K	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
42	L	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
43	M	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
44	N	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
45	O	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
46	P	114/116 (98%)	98 (86%)	16 (14%)	0	100	100
47	Q	121/123 (98%)	93 (77%)	26 (22%)	2 (2%)	9	43
48	R	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
49	S	98/100 (98%)	87 (89%)	10 (10%)	1 (1%)	15	52
50	T	86/88 (98%)	77 (90%)	9 (10%)	0	100	100
51	U	80/82 (98%)	63 (79%)	17 (21%)	0	100	100
52	V	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
53	W	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
54	X	77/79 (98%)	62 (80%)	14 (18%)	1 (1%)	12	48
55	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	Z	63/65 (97%)	41 (65%)	18 (29%)	4 (6%)	1	20
All	All	5783/5982 (97%)	4926 (85%)	835 (14%)	22 (0%)	38	70

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	E	31	ILE
56	Z	37	TYR
10	g	9	VAL

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Mol	Chain	Res	Type
56	Z	10	PRO
15	l	103	ILE
15	l	128	THR
25	v	82	TYR
28	y	24	GLU
33	E	32	LEU
54	X	27	LYS
6	c	150	GLN
16	m	69	PRO
47	Q	90	PRO
56	Z	8	ASN
37	G	18	GLN
49	S	20	PHE
56	Z	9	GLU
6	c	129	THR
13	j	81	ILE
37	G	28	PRO
15	l	85	VAL
47	Q	32	VAL

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
5	b	216/216 (100%)	214 (99%)	2 (1%)	78 88
6	c	164/164 (100%)	160 (98%)	4 (2%)	49 71
7	d	165/165 (100%)	164 (99%)	1 (1%)	86 92
8	e	148/148 (100%)	147 (99%)	1 (1%)	84 91
9	f	137/137 (100%)	133 (97%)	4 (3%)	42 67
10	g	114/114 (100%)	114 (100%)	0	100 100
11	a	110/174 (63%)	109 (99%)	1 (1%)	78 88
12	i	109/110 (99%)	108 (99%)	1 (1%)	78 88
13	j	116/116 (100%)	114 (98%)	2 (2%)	60 78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	k	103/103 (100%)	101 (98%)	2 (2%)	57	76
15	l	102/102 (100%)	100 (98%)	2 (2%)	55	75
16	m	109/109 (100%)	107 (98%)	2 (2%)	59	77
17	n	100/100 (100%)	99 (99%)	1 (1%)	76	86
18	o	86/86 (100%)	86 (100%)	0	100	100
19	p	99/99 (100%)	98 (99%)	1 (1%)	76	86
20	q	89/89 (100%)	88 (99%)	1 (1%)	73	85
21	r	84/84 (100%)	84 (100%)	0	100	100
22	s	93/93 (100%)	91 (98%)	2 (2%)	52	72
23	t	80/80 (100%)	80 (100%)	0	100	100
24	u	83/83 (100%)	82 (99%)	1 (1%)	71	84
25	v	78/78 (100%)	78 (100%)	0	100	100
26	w	57/57 (100%)	56 (98%)	1 (2%)	59	77
27	x	67/67 (100%)	66 (98%)	1 (2%)	65	81
28	y	55/55 (100%)	54 (98%)	1 (2%)	59	77
29	z	48/48 (100%)	47 (98%)	1 (2%)	53	74
30	B	47/47 (100%)	47 (100%)	0	100	100
31	C	45/45 (100%)	45 (100%)	0	100	100
32	D	38/38 (100%)	38 (100%)	0	100	100
33	E	51/51 (100%)	51 (100%)	0	100	100
34	F	34/34 (100%)	34 (100%)	0	100	100
37	G	180/186 (97%)	175 (97%)	5 (3%)	43	68
38	H	170/170 (100%)	167 (98%)	3 (2%)	59	77
39	I	172/172 (100%)	171 (99%)	1 (1%)	86	92
40	J	119/119 (100%)	117 (98%)	2 (2%)	60	78
41	K	87/87 (100%)	86 (99%)	1 (1%)	73	85
42	L	124/124 (100%)	123 (99%)	1 (1%)	81	89
43	M	104/104 (100%)	104 (100%)	0	100	100
44	N	105/105 (100%)	103 (98%)	2 (2%)	57	76
45	O	86/86 (100%)	85 (99%)	1 (1%)	71	84
46	P	89/89 (100%)	86 (97%)	3 (3%)	37	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Q	103/103 (100%)	100 (97%)	3 (3%)	42	67
48	R	92/92 (100%)	91 (99%)	1 (1%)	73	85
49	S	83/83 (100%)	81 (98%)	2 (2%)	49	71
50	T	76/76 (100%)	74 (97%)	2 (3%)	46	69
51	U	65/65 (100%)	65 (100%)	0	100	100
52	V	74/74 (100%)	72 (97%)	2 (3%)	44	69
53	W	56/56 (100%)	54 (96%)	2 (4%)	35	63
54	X	70/70 (100%)	69 (99%)	1 (1%)	67	81
55	Y	65/65 (100%)	65 (100%)	0	100	100
56	Z	55/55 (100%)	54 (98%)	1 (2%)	59	77
All	All	4802/4873 (98%)	4737 (99%)	65 (1%)	68	81

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	b	256	THR
5	b	257	ARG
6	c	33	ARG
6	c	108	ASP
6	c	179	ARG
6	c	197	THR
7	d	84	THR
8	e	70	ARG
9	f	28	LYS
9	f	68	ARG
9	f	103	ASN
9	f	176	LYS
11	a	37	LYS
12	i	35	MET
13	j	65	THR
13	j	111	LYS
14	k	32	TYR
14	k	49	ARG
15	l	2	ARG
15	l	29	LYS
16	m	44	ARG
16	m	59	ARG
17	n	57	THR

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Mol	Chain	Res	Type
19	p	86	LYS
20	q	94	LEU
22	s	76	VAL
22	s	109	ASP
24	u	81	ARG
26	w	10	ARG
27	x	32	LEU
28	y	7	ARG
29	z	30	ARG
37	G	19	THR
37	G	20	ARG
37	G	49	PHE
37	G	87	ASP
37	G	94	ARG
38	H	41	TYR
38	H	46	LEU
38	H	48	LYS
39	I	183	ARG
40	J	53	ARG
40	J	156	ARG
41	K	61	LEU
42	L	123	LEU
44	N	26	LYS
44	N	128	LYS
45	O	89	ARG
46	P	12	ARG
46	P	105	ARG
46	P	121	ARG
47	Q	89	LEU
47	Q	93	ARG
47	Q	113	ARG
48	R	112	ARG
49	S	11	LYS
49	S	96	LYS
50	T	16	ARG
50	T	88	ARG
52	V	5	ARG
52	V	26	ARG
53	W	11	ARG
53	W	69	TYR
54	X	54	ARG
56	Z	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (76) such sidechains are listed below:

Mol	Chain	Res	Type
5	b	20	ASN
5	b	24	HIS
5	b	44	ASN
5	b	116	GLN
5	b	238	ASN
6	c	36	GLN
8	e	20	ASN
9	f	63	GLN
9	f	103	ASN
10	g	2	GLN
10	g	43	ASN
10	g	133	GLN
12	i	5	GLN
13	j	130	HIS
13	j	132	HIS
14	k	9	ASN
15	l	35	HIS
15	l	38	GLN
15	l	99	ASN
16	m	22	GLN
17	n	9	GLN
17	n	11	ASN
18	o	38	GLN
19	p	2	ASN
19	p	65	ASN
20	q	55	GLN
20	q	58	GLN
21	r	11	GLN
21	r	91	GLN
23	t	59	ASN
24	u	73	ASN
24	u	98	ASN
25	v	44	HIS
25	v	49	ASN
26	w	42	HIS
26	w	72	ASN
28	y	15	ASN
29	z	48	ASN
32	D	16	HIS
32	D	29	GLN
33	E	25	HIS

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Mol	Chain	Res	Type
34	F	33	HIS
37	G	121	GLN
37	G	176	ASN
37	G	177	ASN
38	H	7	ASN
38	H	31	ASN
38	H	139	ASN
39	I	58	GLN
39	I	88	ASN
40	J	72	ASN
40	J	82	HIS
40	J	96	GLN
40	J	131	ASN
41	K	11	HIS
41	K	17	GLN
42	L	67	ASN
42	L	141	HIS
43	M	3	GLN
43	M	17	GLN
43	M	75	GLN
44	N	31	GLN
45	O	20	GLN
46	P	63	GLN
47	Q	58	ASN
48	R	13	HIS
49	S	3	GLN
49	S	59	GLN
50	T	34	GLN
51	U	63	GLN
52	V	30	HIS
53	W	51	GLN
54	X	52	ASN
54	X	55	GLN
55	Y	12	GLN
55	Y	60	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	282 (18%)	4 (0%)
2	1	2902/2903 (99%)	511 (17%)	10 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	119/120 (99%)	12 (10%)	0
35	4	19/39 (48%)	5 (26%)	1 (5%)
36	5	76/77 (98%)	15 (19%)	0
4	6	76/77 (98%)	16 (21%)	0
All	All	4730/4755 (99%)	841 (17%)	15 (0%)

All (841) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	5	U
1	3	9	G
1	3	16	A
1	3	31	G
1	3	32	A
1	3	39	G
1	3	40	C
1	3	47	C
1	3	48	C
1	3	51	A
1	3	56	U
1	3	64	G
1	3	65	A
1	3	71	A
1	3	82	G
1	3	83	C
1	3	84	U
1	3	88	U
1	3	89	U
1	3	110	C
1	3	128	G
1	3	130	A
1	3	131	A
1	3	155	A
1	3	165	G
1	3	173	U
1	3	183	C
1	3	184	G
1	3	189	A
1	3	190	A
1	3	191	G
1	3	195	A
1	3	209	U

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Mol	Chain	Res	Type
1	3	210	C
1	3	243	A
1	3	244	U
1	3	247	G
1	3	251	G
1	3	264	C
1	3	266	G
1	3	267	C
1	3	269	C
1	3	281	G
1	3	289	G
1	3	298	A
1	3	315	A
1	3	316	C
1	3	328	C
1	3	329	A
1	3	340	U
1	3	345	C
1	3	346	G
1	3	347	G
1	3	350	G
1	3	352	C
1	3	354	G
1	3	364	A
1	3	367	U
1	3	369	G
1	3	372	C
1	3	387	U
1	3	388	G
1	3	397	A
1	3	398	U
1	3	411	A
1	3	412	A
1	3	413	G
1	3	421	U
1	3	422	C
1	3	429	U
1	3	430	A
1	3	441	A
1	3	442	G
1	3	445	G
1	3	446	G

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Mol	Chain	Res	Type
1	3	462	G
1	3	467	U
1	3	486	U
1	3	497	G
1	3	508	U
1	3	509	A
1	3	516	U
1	3	518	C
1	3	519	C
1	3	521	G
1	3	524	G
1	3	531	U
1	3	532	A
1	3	533	A
1	3	534	U
1	3	547	A
1	3	561	U
1	3	562	U
1	3	566	G
1	3	570	G
1	3	572	A
1	3	573	A
1	3	576	C
1	3	577	G
1	3	579	A
1	3	586	C
1	3	609	A
1	3	615	G
1	3	619	U
1	3	633	G
1	3	641	U
1	3	653	U
1	3	657	U
1	3	687	A
1	3	693	G
1	3	702	A
1	3	703	G
1	3	713	G
1	3	719	C
1	3	723	U
1	3	724	G
1	3	728	A

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Mol	Chain	Res	Type
1	3	732	C
1	3	733	G
1	3	734	G
1	3	747	A
1	3	753	A
1	3	755	G
1	3	760	G
1	3	768	A
1	3	777	A
1	3	781	A
1	3	793	U
1	3	794	A
1	3	813	U
1	3	814	A
1	3	815	A
1	3	817	C
1	3	818	G
1	3	819	A
1	3	828	U
1	3	832	G
1	3	836	G
1	3	842	U
1	3	843	U
1	3	844	G
1	3	845	A
1	3	846	G
1	3	871	U
1	3	872	A
1	3	873	A
1	3	874	G
1	3	902	G
1	3	915	A
1	3	926	G
1	3	927	G
1	3	934	C
1	3	938	A
1	3	960	U
1	3	961	U
1	3	965	U
1	3	966	G
1	3	969	A
1	3	971	G

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Mol	Chain	Res	Type
1	3	973	G
1	3	975	A
1	3	976	G
1	3	977	A
1	3	978	A
1	3	979	C
1	3	989	U
1	3	992	U
1	3	993	G
1	3	994	A
1	3	1004	A
1	3	1012	A
1	3	1015	G
1	3	1028	C
1	3	1033	G
1	3	1035	A
1	3	1036	A
1	3	1037	C
1	3	1044	A
1	3	1053	G
1	3	1054	C
1	3	1055	A
1	3	1064	G
1	3	1065	U
1	3	1068	G
1	3	1070	U
1	3	1074	G
1	3	1080	A
1	3	1085	U
1	3	1091	U
1	3	1092	A
1	3	1094	G
1	3	1097	C
1	3	1101	A
1	3	1111	A
1	3	1115	U
1	3	1124	G
1	3	1136	C
1	3	1137	C
1	3	1138	G
1	3	1139	G
1	3	1157	A

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Mol	Chain	Res	Type
1	3	1158	C
1	3	1159	U
1	3	1165	U
1	3	1168	U
1	3	1169	A
1	3	1173	U
1	3	1174	G
1	3	1179	A
1	3	1181	G
1	3	1182	G
1	3	1183	U
1	3	1185	G
1	3	1190	G
1	3	1192	C
1	3	1196	A
1	3	1197	A
1	3	1201	A
1	3	1202	U
1	3	1207	G
1	3	1212	U
1	3	1213	A
1	3	1221	G
1	3	1222	G
1	3	1224	U
1	3	1226	C
1	3	1227	A
1	3	1228	C
1	3	1229	A
1	3	1233	G
1	3	1236	A
1	3	1238	A
1	3	1241	G
1	3	1256	A
1	3	1257	A
1	3	1275	A
1	3	1278	G
1	3	1280	A
1	3	1281	C
1	3	1282	C
1	3	1286	U
1	3	1287	A
1	3	1290	G

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Mol	Chain	Res	Type
1	3	1291	U
1	3	1300	G
1	3	1301	U
1	3	1304	G
1	3	1308	U
1	3	1317	C
1	3	1320	C
1	3	1322	C
1	3	1323	G
1	3	1338	G
1	3	1346	A
1	3	1347	G
1	3	1353	G
1	3	1363	A
1	3	1378	C
1	3	1385	G
1	3	1389	C
1	3	1394	A
1	3	1395	C
1	3	1401	G
1	3	1406	U
1	3	1419	G
1	3	1441	A
1	3	1446	A
1	3	1452	C
1	3	1480	A
1	3	1484	C
1	3	1491	G
1	3	1492	A
1	3	1493	A
1	3	1497	G
1	3	1503	A
1	3	1504	G
1	3	1513	A
1	3	1517	G
1	3	1518	A
1	3	1529	G
1	3	1530	G
1	3	1534	A
2	1	8	C
2	1	10	A
2	1	34	U

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Mol	Chain	Res	Type
2	1	42	A
2	1	46	G
2	1	50	U
2	1	51	G
2	1	63	A
2	1	70	G
2	1	71	A
2	1	93	G
2	1	96	C
2	1	103	A
2	1	112	U
2	1	119	A
2	1	120	U
2	1	125	A
2	1	134	G
2	1	138	U
2	1	140	C
2	1	141	G
2	1	142	A
2	1	162	U
2	1	163	C
2	1	181	A
2	1	196	A
2	1	204	A
2	1	205	G
2	1	216	A
2	1	222	A
2	1	228	C
2	1	229	C
2	1	233	A
2	1	248	G
2	1	249	C
2	1	255	A
2	1	265	A
2	1	266	G
2	1	267	C
2	1	276	U
2	1	294	A
2	1	309	A
2	1	311	A
2	1	312	G
2	1	322	A

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Mol	Chain	Res	Type
2	1	323	C
2	1	324	A
2	1	329	G
2	1	330	A
2	1	349	U
2	1	361	G
2	1	371	A
2	1	372	G
2	1	380	G
2	1	386	G
2	1	387	U
2	1	404	A
2	1	406	G
2	1	411	G
2	1	412	A
2	1	413	C
2	1	424	G
2	1	434	U
2	1	449	A
2	1	451	U
2	1	456	C
2	1	464	U
2	1	465	G
2	1	466	A
2	1	481	G
2	1	489	G
2	1	491	G
2	1	501	A
2	1	502	A
2	1	504	A
2	1	505	A
2	1	508	A
2	1	510	C
2	1	527	C
2	1	529	A
2	1	532	A
2	1	544	C
2	1	547	A
2	1	549	G
2	1	550	C
2	1	555	G
2	1	562	U

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Mol	Chain	Res	Type
2	1	563	A
2	1	572	A
2	1	573	U
2	1	574	A
2	1	575	A
2	1	588	U
2	1	589	U
2	1	591	U
2	1	595	C
2	1	603	A
2	1	614	A
2	1	616	A
2	1	627	A
2	1	637	A
2	1	646	U
2	1	654	A
2	1	655	A
2	1	659	G
2	1	666	A
2	1	684	G
2	1	686	U
2	1	690	G
2	1	691	C
2	1	696	G
2	1	711	G
2	1	714	U
2	1	715	A
2	1	730	A
2	1	747	C
2	1	756	A
2	1	773	U
2	1	776	G
2	1	782	A
2	1	784	G
2	1	785	G
2	1	789	A
2	1	803	U
2	1	804	A
2	1	805	G
2	1	806	C
2	1	807	U
2	1	811	U

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Mol	Chain	Res	Type
2	1	812	C
2	1	819	A
2	1	824	U
2	1	827	U
2	1	831	G
2	1	845	A
2	1	846	U
2	1	847	U
2	1	856	G
2	1	858	G
2	1	859	G
2	1	860	U
2	1	865	C
2	1	868	U
2	1	878	A
2	1	883	G
2	1	885	C
2	1	886	A
2	1	887	U
2	1	890	C
2	1	891	G
2	1	897	C
2	1	898	C
2	1	907	G
2	1	910	A
2	1	915	C
2	1	932	U
2	1	934	U
2	1	941	A
2	1	946	C
2	1	953	G
2	1	957	C
2	1	958	U
2	1	961	C
2	1	965	C
2	1	974	G
2	1	975	A
2	1	983	A
2	1	990	A
2	1	995	C
2	1	996	A
2	1	1009	A

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Mol	Chain	Res	Type
2	1	1012	U
2	1	1013	C
2	1	1022	G
2	1	1033	U
2	1	1043	C
2	1	1045	C
2	1	1046	A
2	1	1051	G
2	1	1055	G
2	1	1060	U
2	1	1062	G
2	1	1065	U
2	1	1066	U
2	1	1067	A
2	1	1068	G
2	1	1069	A
2	1	1070	A
2	1	1071	G
2	1	1072	C
2	1	1079	C
2	1	1083	U
2	1	1085	A
2	1	1088	A
2	1	1089	A
2	1	1090	A
2	1	1094	U
2	1	1102	C
2	1	1104	C
2	1	1111	A
2	1	1128	G
2	1	1132	U
2	1	1133	A
2	1	1135	C
2	1	1142	A
2	1	1143	A
2	1	1169	A
2	1	1174	U
2	1	1175	A
2	1	1176	U
2	1	1177	G
2	1	1178	C
2	1	1180	U

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Mol	Chain	Res	Type
2	1	1199	U
2	1	1204	A
2	1	1206	G
2	1	1211	C
2	1	1212	G
2	1	1218	G
2	1	1247	A
2	1	1248	G
2	1	1253	A
2	1	1255	U
2	1	1256	G
2	1	1272	A
2	1	1275	A
2	1	1289	C
2	1	1300	G
2	1	1301	A
2	1	1302	A
2	1	1321	A
2	1	1325	U
2	1	1326	U
2	1	1329	U
2	1	1344	U
2	1	1345	C
2	1	1361	G
2	1	1379	U
2	1	1380	G
2	1	1383	A
2	1	1396	U
2	1	1403	A
2	1	1414	C
2	1	1416	G
2	1	1419	A
2	1	1420	A
2	1	1428	C
2	1	1450	G
2	1	1452	G
2	1	1453	A
2	1	1454	C
2	1	1458	U
2	1	1461	C
2	1	1467	U
2	1	1475	G

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Mol	Chain	Res	Type
2	1	1482	G
2	1	1490	A
2	1	1497	U
2	1	1515	A
2	1	1519	G
2	1	1521	G
2	1	1524	G
2	1	1535	A
2	1	1536	C
2	1	1537	G
2	1	1538	G
2	1	1555	G
2	1	1560	G
2	1	1566	A
2	1	1567	G
2	1	1585	C
2	1	1598	A
2	1	1608	A
2	1	1616	A
2	1	1617	C
2	1	1618	A
2	1	1627	G
2	1	1633	G
2	1	1643	G
2	1	1644	C
2	1	1646	C
2	1	1647	U
2	1	1648	U
2	1	1654	A
2	1	1662	U
2	1	1663	G
2	1	1674	G
2	1	1694	C
2	1	1699	G
2	1	1700	A
2	1	1703	G
2	1	1713	A
2	1	1714	U
2	1	1715	G
2	1	1729	U
2	1	1730	C
2	1	1731	G

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Mol	Chain	Res	Type
2	1	1732	C
2	1	1733	G
2	1	1738	G
2	1	1757	A
2	1	1758	U
2	1	1764	C
2	1	1766	G
2	1	1773	A
2	1	1776	G
2	1	1780	A
2	1	1784	A
2	1	1785	A
2	1	1786	A
2	1	1791	A
2	1	1800	C
2	1	1801	A
2	1	1808	A
2	1	1811	G
2	1	1812	U
2	1	1816	C
2	1	1819	A
2	1	1820	U
2	1	1829	A
2	1	1869	G
2	1	1901	A
2	1	1903	G
2	1	1906	G
2	1	1907	G
2	1	1912	A
2	1	1913	A
2	1	1914	C
2	1	1929	G
2	1	1930	G
2	1	1937	A
2	1	1939	U
2	1	1940	U
2	1	1951	U
2	1	1955	U
2	1	1963	U
2	1	1967	C
2	1	1969	A
2	1	1970	A

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Mol	Chain	Res	Type
2	1	1971	U
2	1	1972	G
2	1	1981	A
2	1	1982	U
2	1	1991	U
2	1	1993	U
2	1	1997	C
2	1	2001	C
2	1	2002	G
2	1	2022	U
2	1	2023	C
2	1	2030	A
2	1	2031	A
2	1	2032	G
2	1	2033	A
2	1	2034	U
2	1	2036	C
2	1	2043	C
2	1	2046	G
2	1	2055	C
2	1	2056	G
2	1	2060	A
2	1	2061	G
2	1	2062	A
2	1	2069	G
2	1	2072	C
2	1	2075	U
2	1	2100	G
2	1	2111	U
2	1	2112	G
2	1	2118	U
2	1	2119	A
2	1	2122	U
2	1	2126	A
2	1	2131	U
2	1	2132	U
2	1	2133	G
2	1	2134	A
2	1	2145	C
2	1	2146	C
2	1	2147	A
2	1	2154	A

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Mol	Chain	Res	Type
2	1	2157	G
2	1	2158	A
2	1	2162	G
2	1	2165	C
2	1	2166	U
2	1	2167	U
2	1	2168	G
2	1	2169	A
2	1	2171	A
2	1	2172	U
2	1	2173	A
2	1	2198	A
2	1	2204	G
2	1	2207	C
2	1	2211	A
2	1	2225	A
2	1	2228	G
2	1	2238	G
2	1	2239	G
2	1	2246	G
2	1	2250	G
2	1	2259	U
2	1	2268	A
2	1	2269	G
2	1	2283	C
2	1	2287	A
2	1	2305	U
2	1	2307	G
2	1	2309	A
2	1	2311	A
2	1	2322	A
2	1	2325	G
2	1	2327	A
2	1	2331	G
2	1	2335	A
2	1	2336	A
2	1	2361	G
2	1	2382	G
2	1	2383	G
2	1	2385	C
2	1	2388	A
2	1	2390	U

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Mol	Chain	Res	Type
2	1	2392	A
2	1	2395	C
2	1	2402	U
2	1	2406	A
2	1	2420	C
2	1	2422	C
2	1	2423	U
2	1	2425	A
2	1	2427	C
2	1	2429	G
2	1	2440	C
2	1	2441	U
2	1	2447	G
2	1	2448	A
2	1	2449	U
2	1	2475	C
2	1	2476	A
2	1	2490	G
2	1	2498	C
2	1	2499	C
2	1	2501	C
2	1	2502	G
2	1	2504	U
2	1	2505	G
2	1	2518	A
2	1	2520	C
2	1	2522	U
2	1	2529	G
2	1	2535	G
2	1	2547	A
2	1	2549	G
2	1	2554	U
2	1	2555	U
2	1	2556	C
2	1	2558	C
2	1	2564	A
2	1	2566	A
2	1	2567	G
2	1	2568	U
2	1	2572	A
2	1	2602	A
2	1	2609	U

Continued on next page...

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Mol	Chain	Res	Type
2	1	2610	C
2	1	2613	U
2	1	2615	U
2	1	2621	G
2	1	2629	U
2	1	2646	C
2	1	2656	U
2	1	2663	G
2	1	2682	A
2	1	2685	G
2	1	2689	U
2	1	2690	U
2	1	2691	C
2	1	2714	G
2	1	2716	C
2	1	2718	G
2	1	2727	A
2	1	2733	A
2	1	2744	G
2	1	2748	A
2	1	2755	C
2	1	2756	U
2	1	2759	G
2	1	2765	A
2	1	2771	C
2	1	2776	A
2	1	2777	G
2	1	2778	A
2	1	2779	U
2	1	2791	G
2	1	2794	C
2	1	2799	A
2	1	2800	A
2	1	2801	G
2	1	2807	U
2	1	2818	U
2	1	2820	A
2	1	2821	A
2	1	2823	A
2	1	2835	A
2	1	2866	U
2	1	2867	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	1	2868	A
2	1	2880	C
2	1	2884	U
2	1	2893	A
3	2	2	G
3	2	4	C
3	2	15	A
3	2	24	G
3	2	35	C
3	2	41	G
3	2	44	G
3	2	53	A
3	2	57	A
3	2	89	U
3	2	90	C
3	2	109	A
4	6	4	G
4	6	7	G
4	6	8	U
4	6	9	G
4	6	10	G
4	6	14	A
4	6	16	C
4	6	17(A)	U
4	6	19	G
4	6	20	U
4	6	21	A
4	6	22	G
4	6	35	A
4	6	43	A
4	6	47	U
4	6	59	A
35	4	12	A
35	4	13	A
35	4	14	A
35	4	15	A
35	4	16	A
36	5	2	G
36	5	3	G
36	5	5	G
36	5	6	A
36	5	8	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
36	5	15	G
36	5	16	C
36	5	19	G
36	5	20	U
36	5	21	A
36	5	22	G
36	5	53	G
36	5	59	A
36	5	61	C
36	5	73	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	70	U
1	3	429	U
1	3	1157	A
1	3	1173	U
2	1	889	C
2	1	896	A
2	1	1343	G
2	1	1453	A
2	1	1626	A
2	1	1730	C
2	1	1970	A
2	1	2001	C
2	1	2061	G
2	1	2391	G
35	4	13	A

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

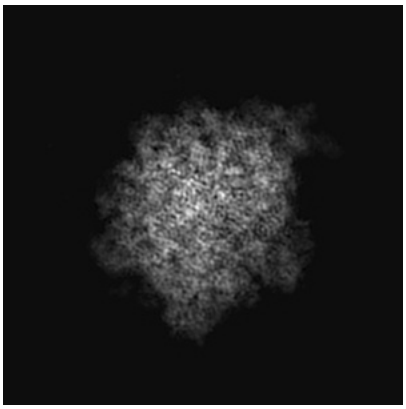
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-25415. These allow visual inspection of the internal detail of the map and identification of artifacts.

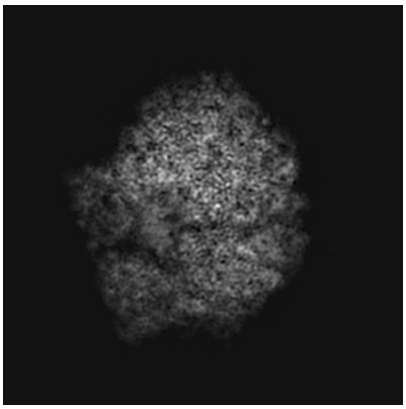
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

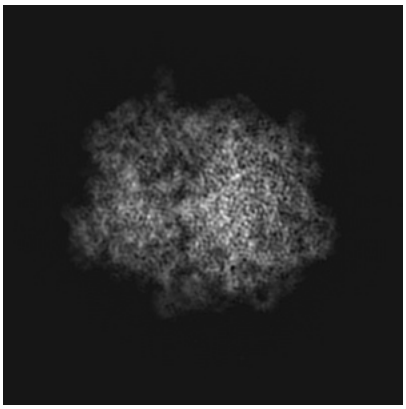
6.1.1 Primary map



X

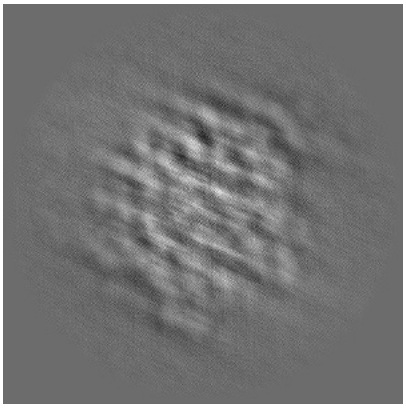


Y

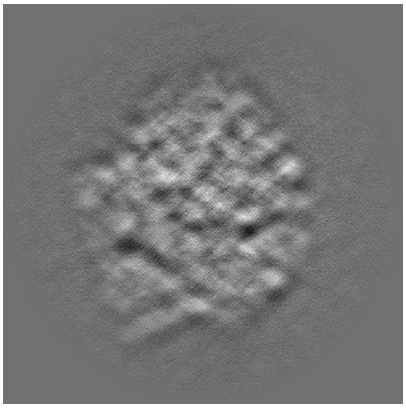


Z

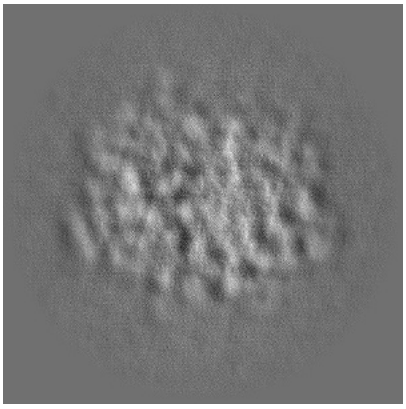
6.1.2 Raw map



X



Y

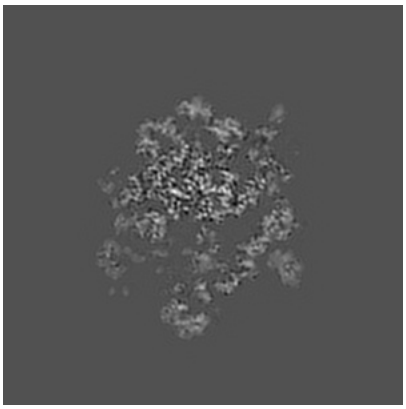


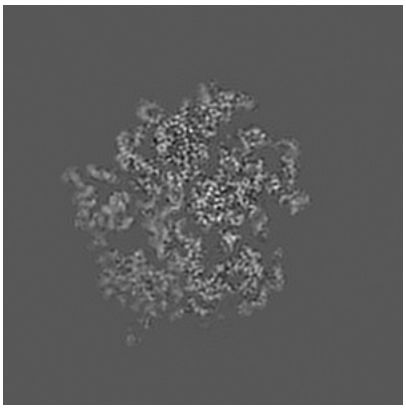
Z

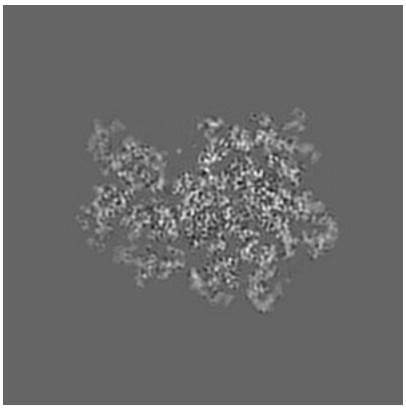
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

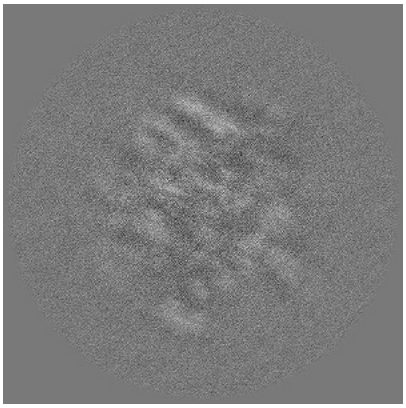
6.2.1 Primary map

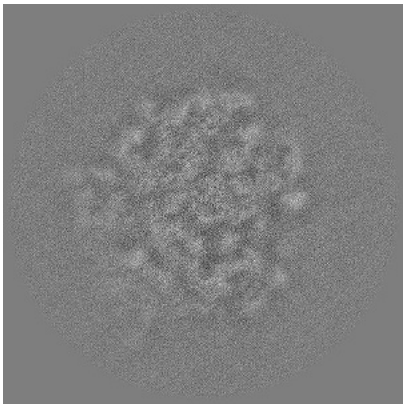

X Index: 224

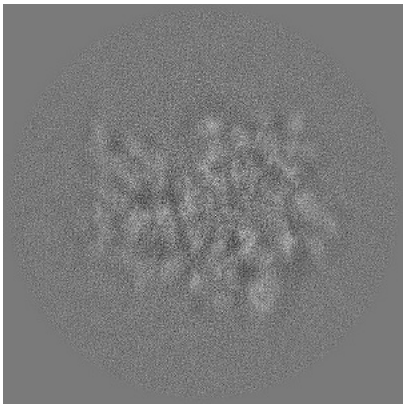

Y Index: 224


Z Index: 224

6.2.2 Raw map


X Index: 224

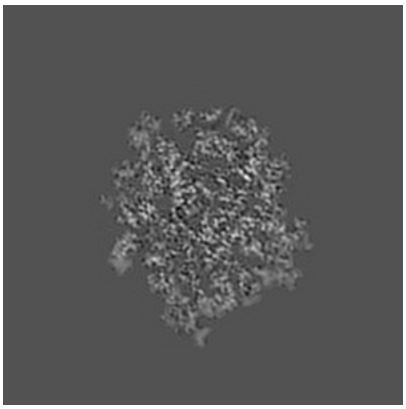

Y Index: 224

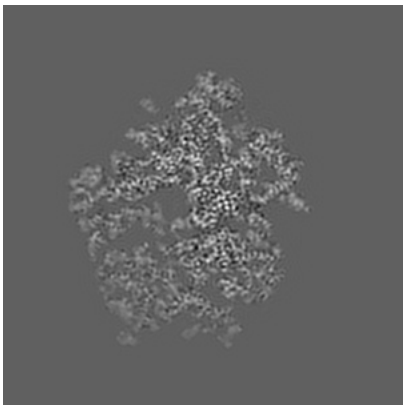

Z Index: 224

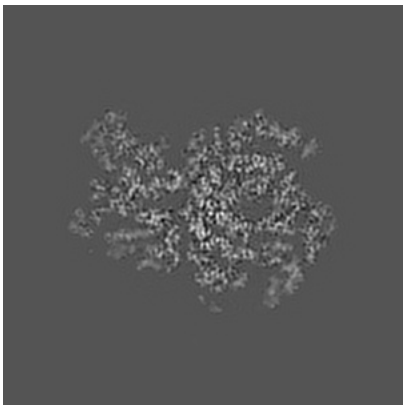
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

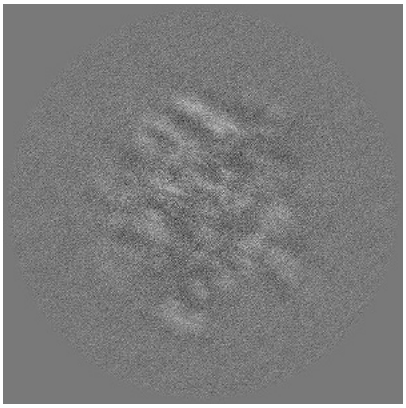
6.3.1 Primary map

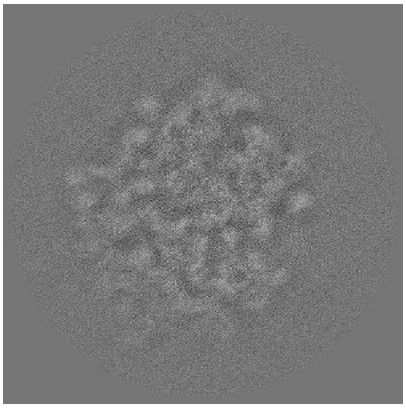

X Index: 255

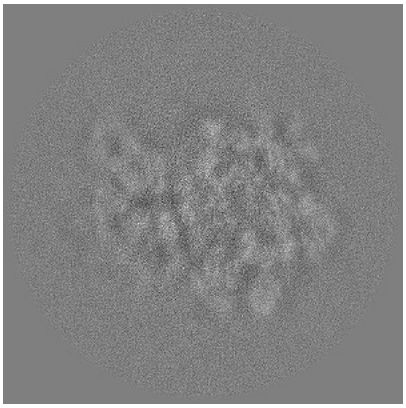

Y Index: 209


Z Index: 238

6.3.2 Raw map


X Index: 224

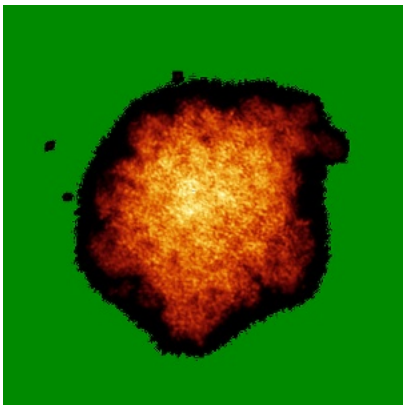

Y Index: 215

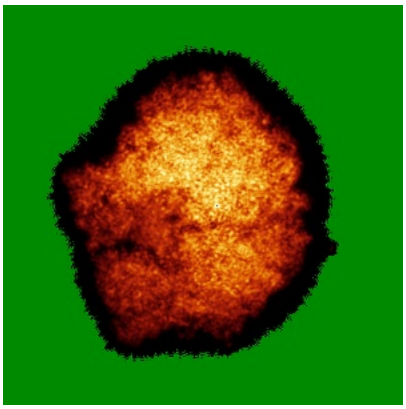

Z Index: 228

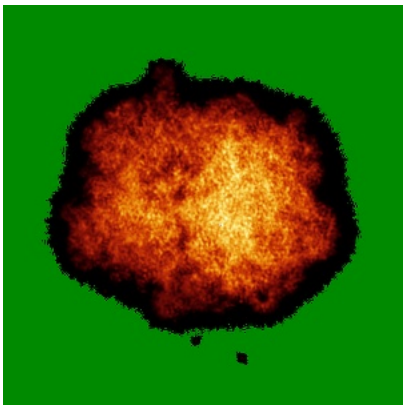
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

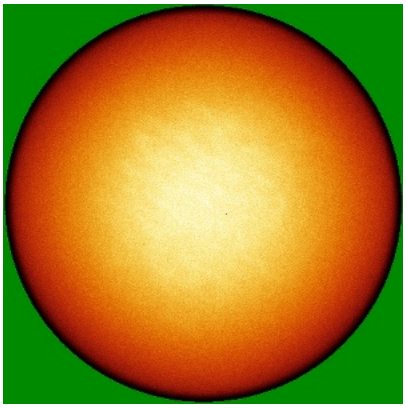
6.4.1 Primary map

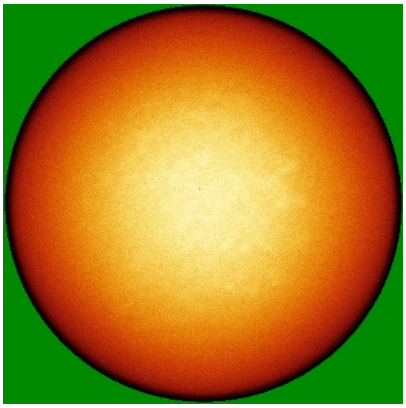

X

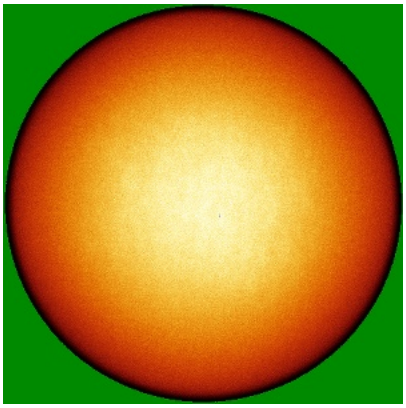

Y


Z

6.4.2 Raw map


X

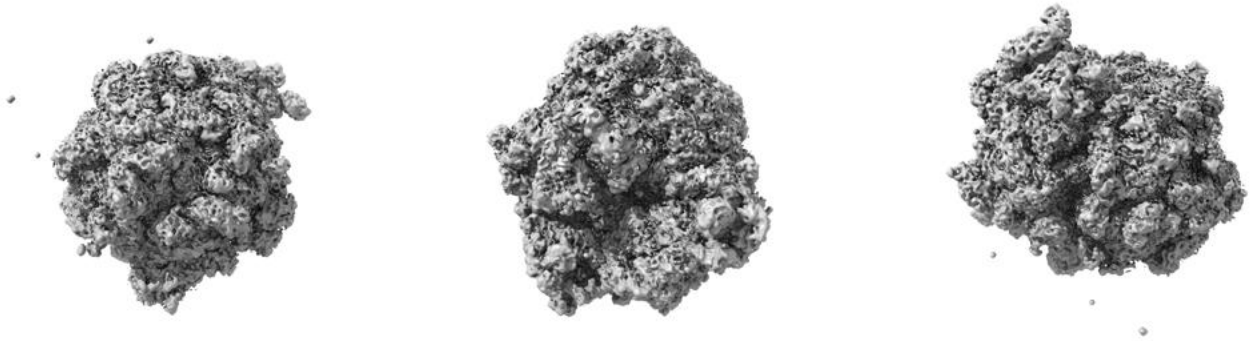

Y


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)

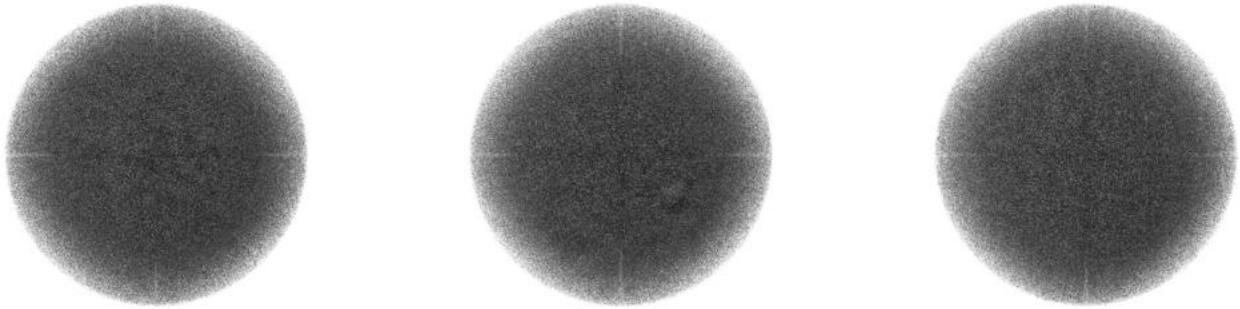
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

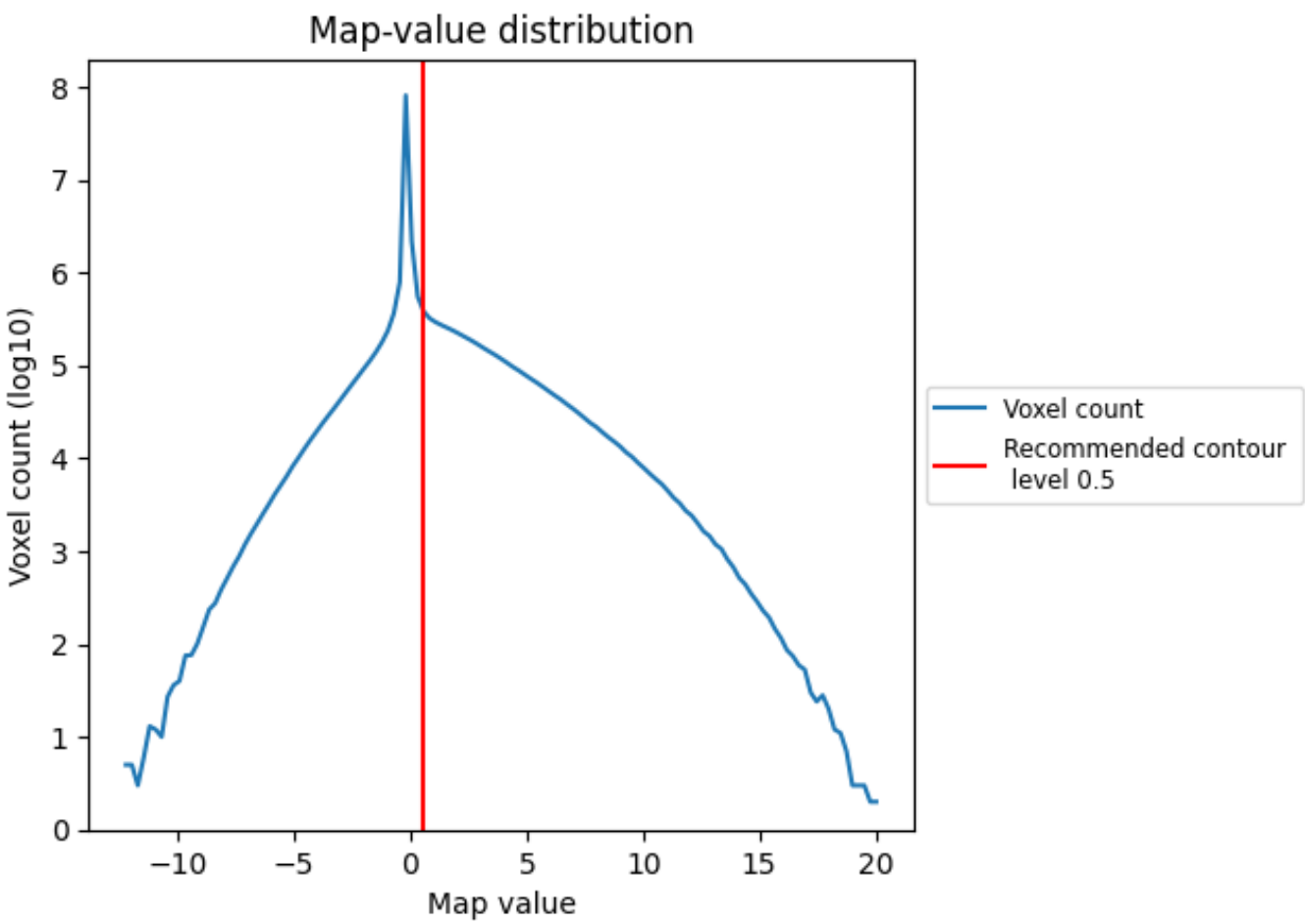
6.6 Mask visualisation (i)

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

7 Map analysis (i)

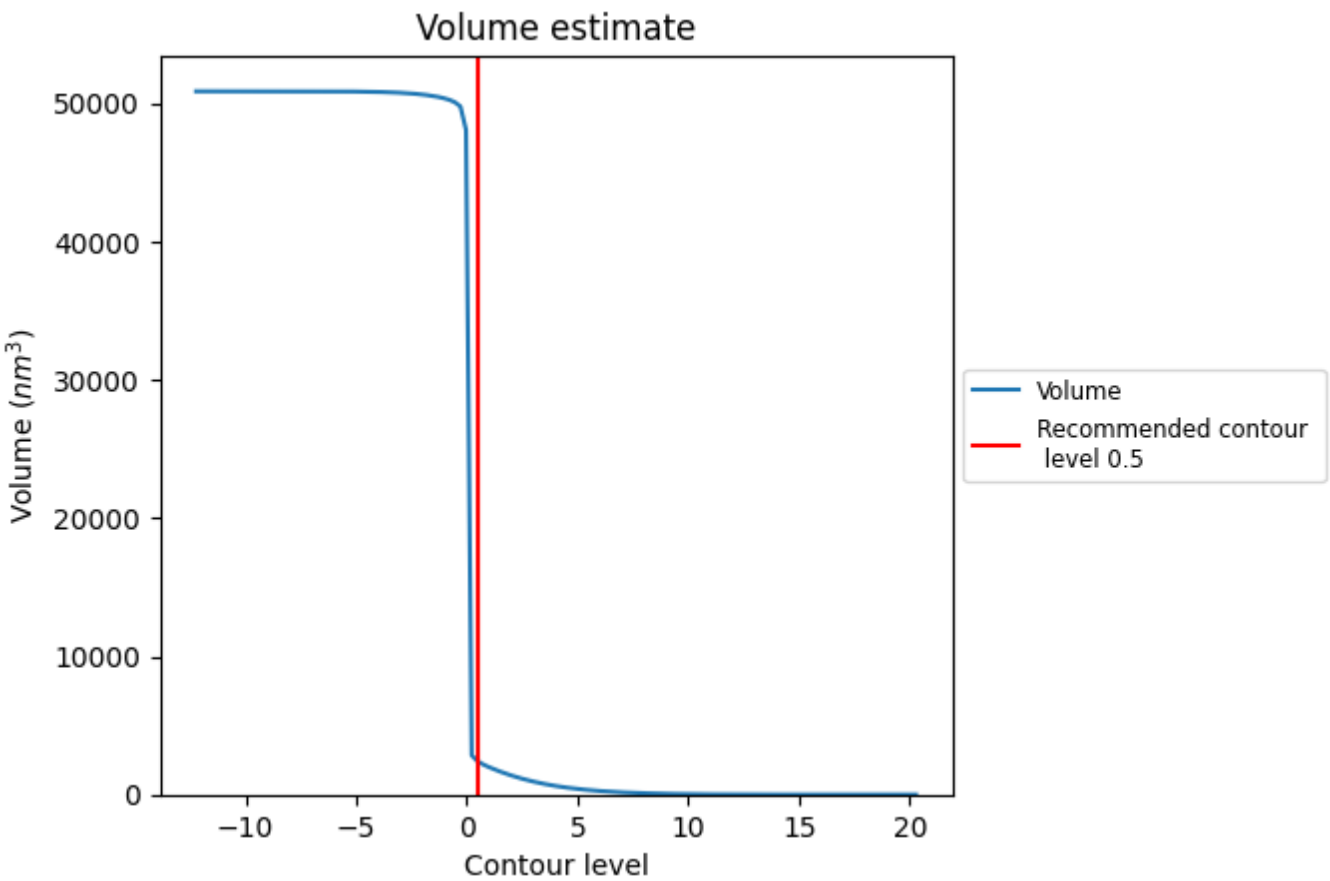
This section contains the results of statistical analysis of the map.

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.

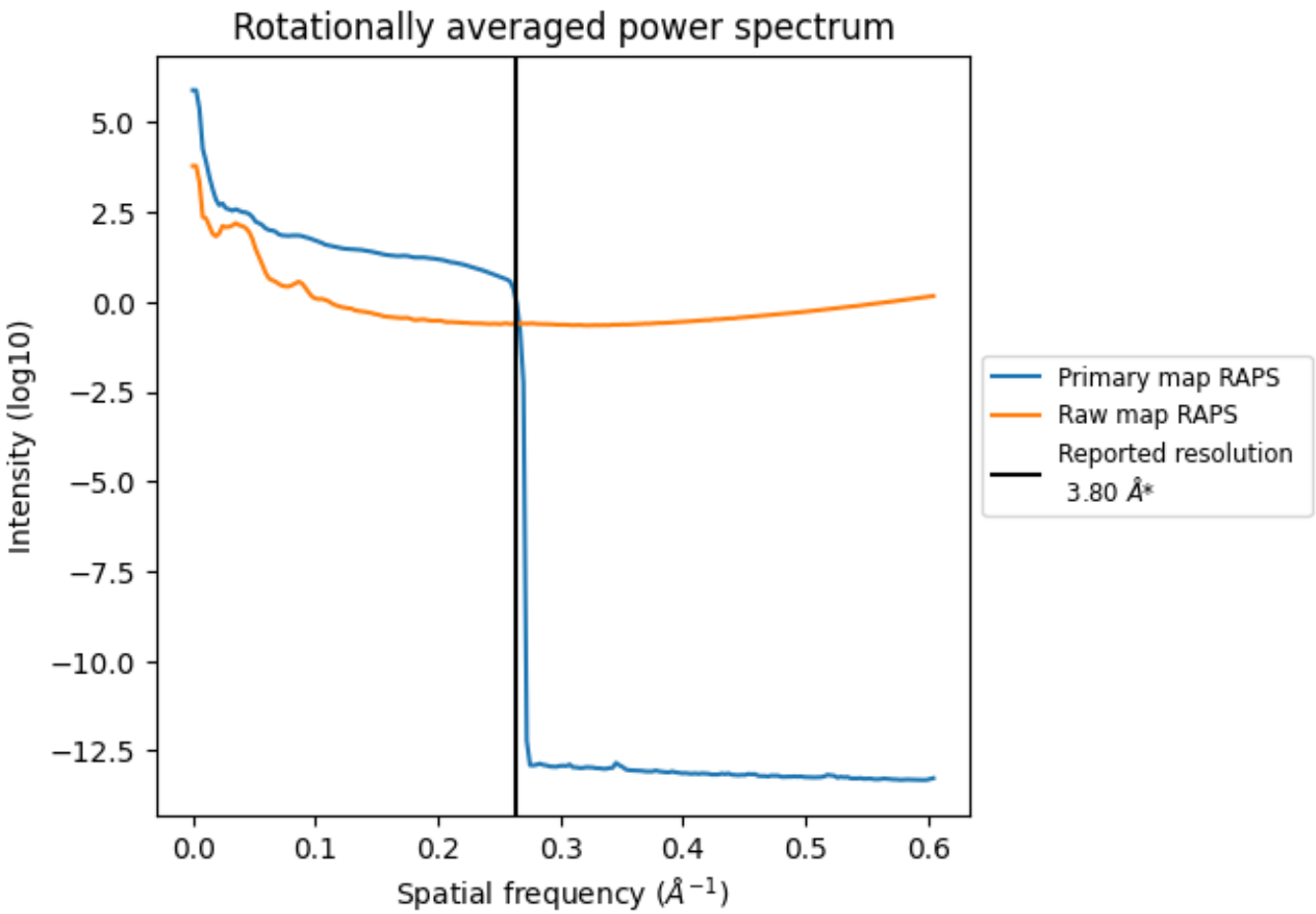
7.2 Volume estimate (i)



The volume at the recommended contour level is 2398 nm^3; this corresponds to an approximate mass of 2166 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)

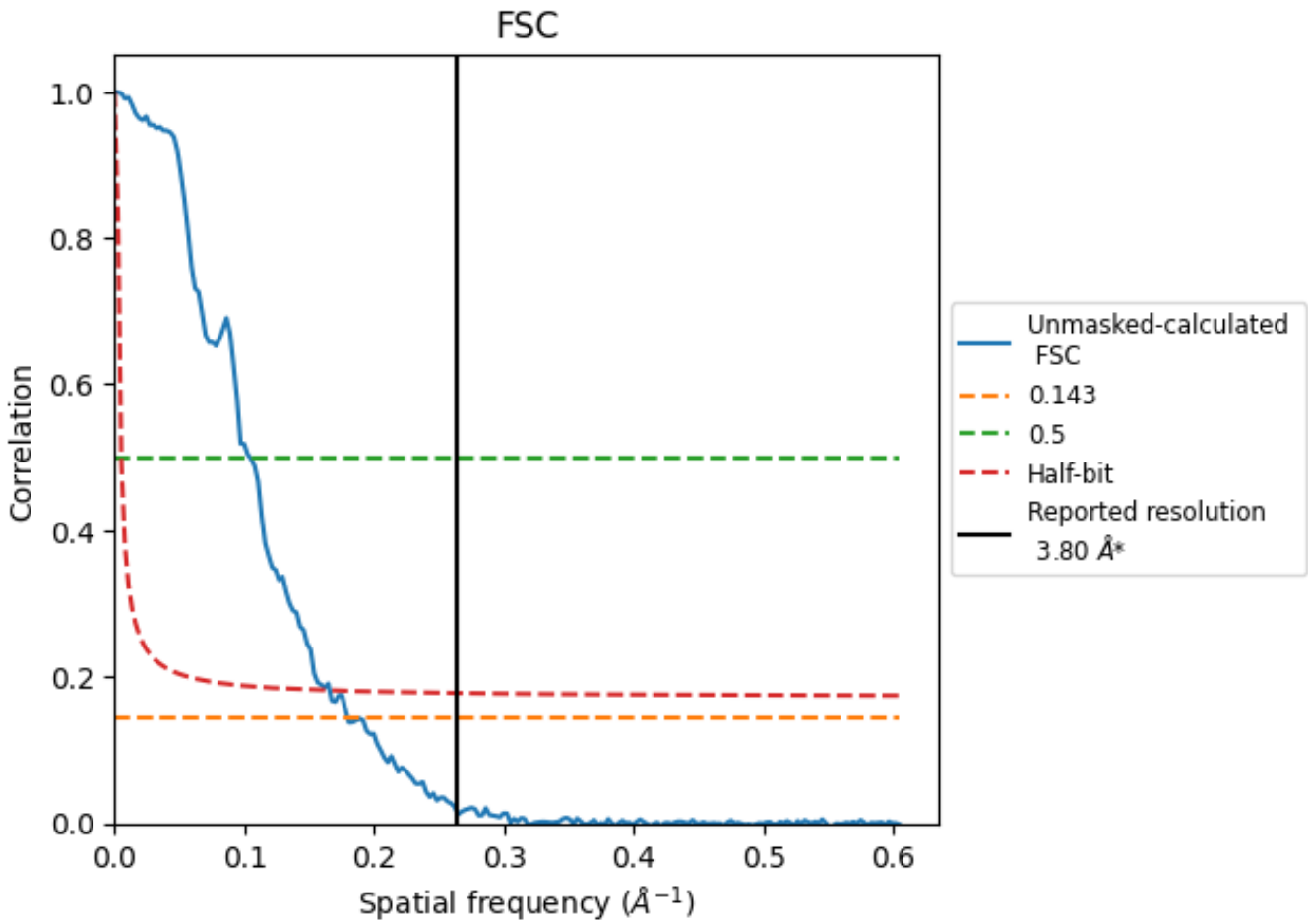


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8 Fourier-Shell correlation (i)

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 (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8.2 Resolution estimates (i)

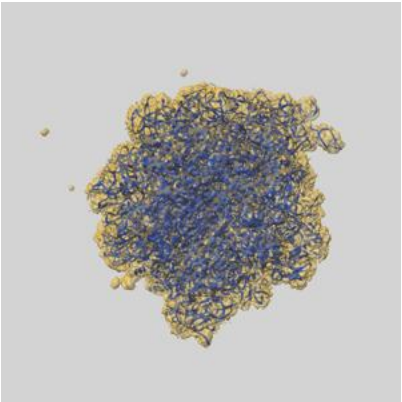
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.56	9.61	6.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.56 differs from the reported value 3.8 by more than 10 %

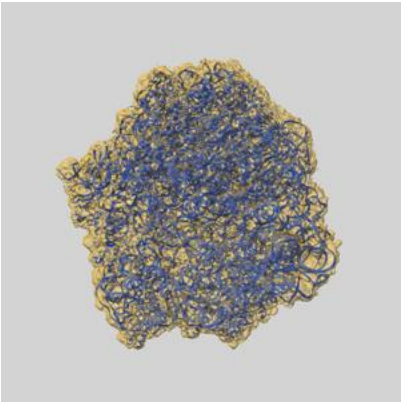
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-25415 and PDB model 7SSW. Per-residue inclusion information can be found in section 3 on page 14.

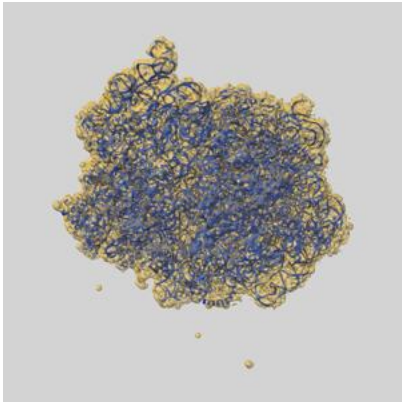
9.1 Map-model overlay (i)



X



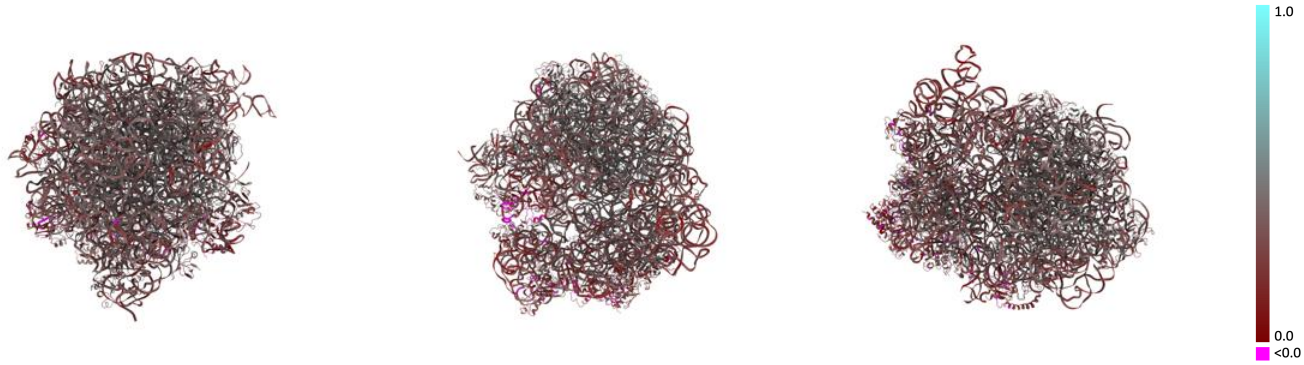
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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.

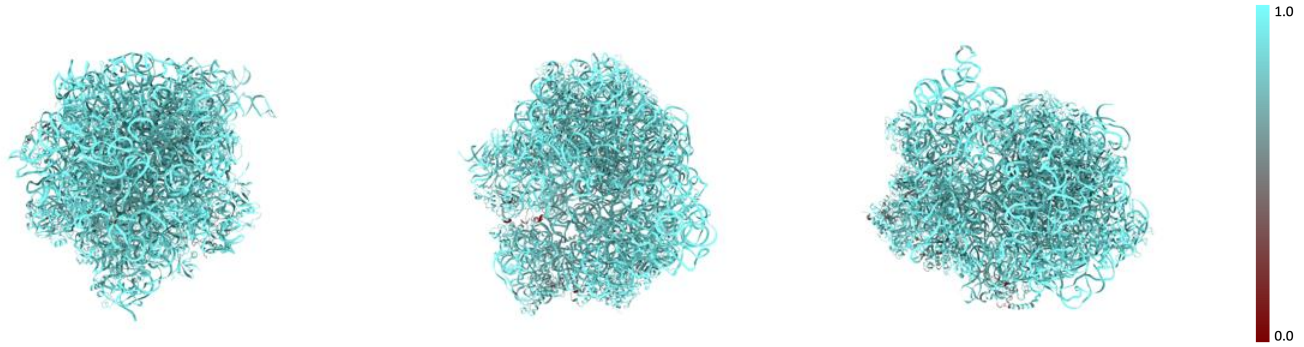
9.2 Q-score mapped to coordinate model (i)



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.

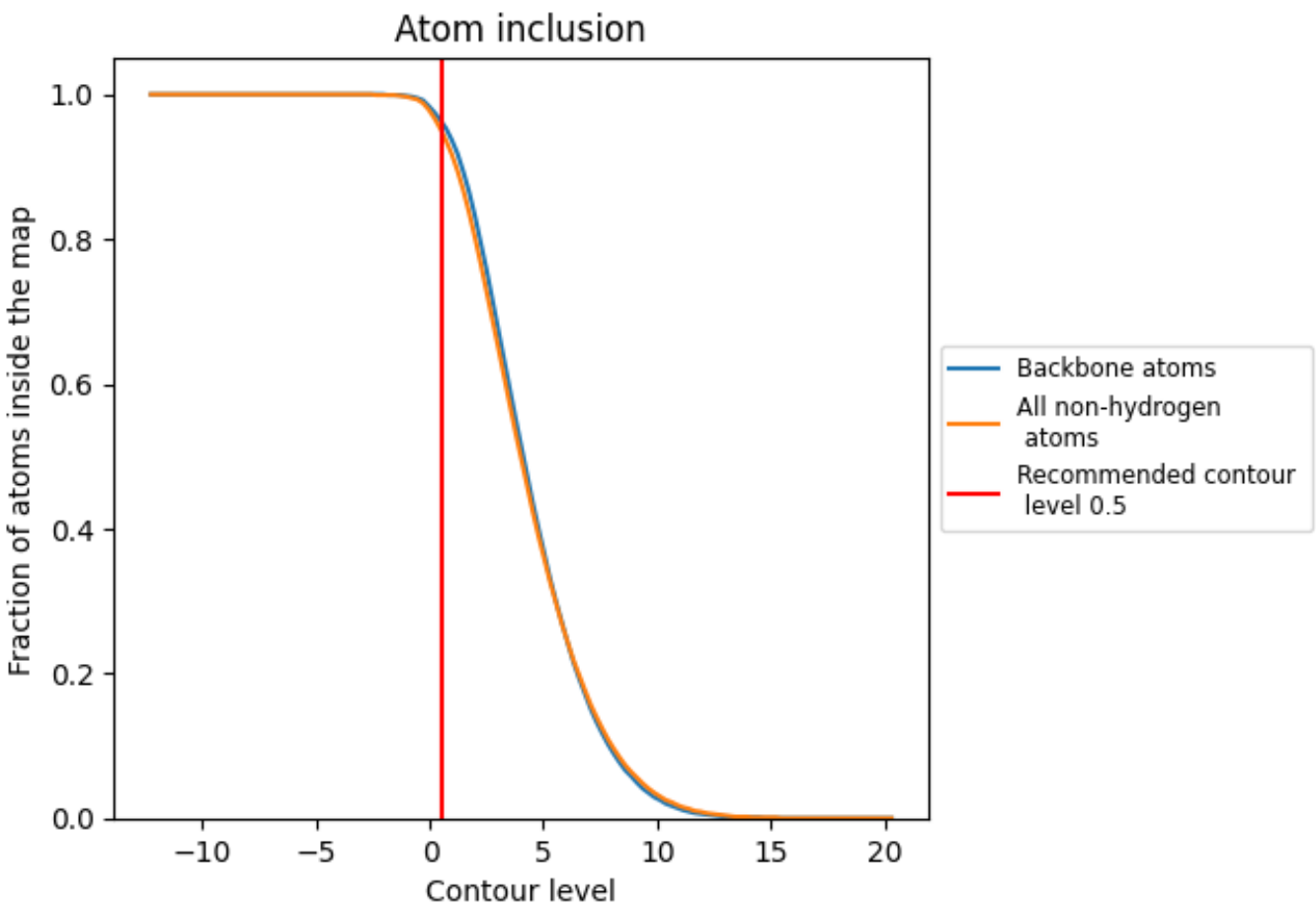
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9510	0.3340
1	0.9740	0.3600
2	0.9830	0.3210
3	0.9590	0.2990
4	0.8140	0.1820
5	0.9480	0.2540
6	0.9400	0.2480
B	0.9490	0.4100
C	0.8580	0.3160
D	0.9610	0.4460
E	0.9490	0.4080
F	0.9620	0.4150
G	0.7880	0.1940
H	0.7490	0.2190
I	0.9220	0.2890
J	0.9520	0.3480
K	0.9510	0.3120
L	0.8070	0.2400
M	0.9250	0.3430
N	0.8840	0.2610
O	0.8320	0.2450
P	0.9600	0.3360
Q	0.9250	0.3340
R	0.8740	0.2500
S	0.9250	0.2820
T	0.9590	0.3580
U	0.9390	0.3280
V	0.9180	0.3250
W	0.9670	0.3470
X	0.9230	0.2950
Y	0.9520	0.3280
Z	0.8820	0.2900
a	0.8750	0.2070
b	0.9600	0.4350
c	0.9660	0.4080

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Chain	Atom inclusion	Q-score
d	0.9430	0.3930
e	0.9180	0.2780
f	0.9550	0.3190
g	0.7000	0.2240
i	0.6610	0.1890
j	0.9680	0.4160
k	0.9570	0.4030
l	0.9510	0.4070
m	0.9560	0.3900
n	0.9640	0.4230
o	0.9690	0.3580
p	0.9620	0.4060
q	0.9570	0.4060
r	0.9570	0.3720
s	0.9510	0.3980
t	0.9490	0.4030
u	0.9520	0.3620
v	0.9610	0.3370
w	0.9480	0.4200
x	0.9480	0.4110
y	0.9720	0.3610
z	0.9540	0.3900