



# wwPDB EM Validation Summary Report ⓘ

Feb 22, 2024 – 03:52 PM EST

PDB ID : 4V7I  
EMDB ID : EMD-1484  
Title : Ribosome-SecY complex.  
Authors : Gumbart, J.C.; Trabuco, L.G.; Schreiner, E.; Villa, E.; Schulten, K.  
Deposited on : 2009-10-21  
Resolution : 9.60 Å(reported)  
Based on initial models : 2I2V, 3BO0

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev70  
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

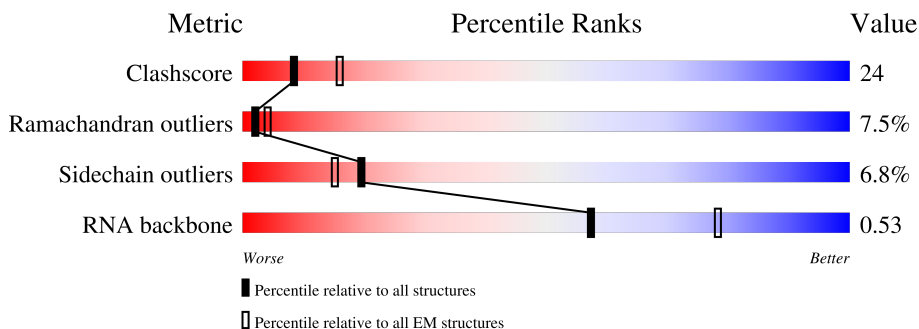
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





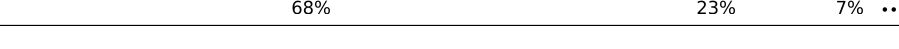
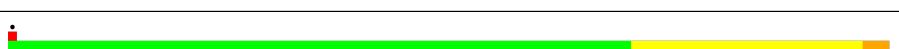



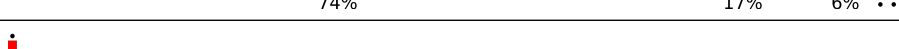



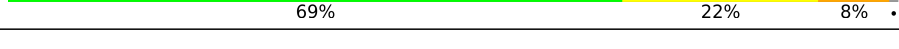

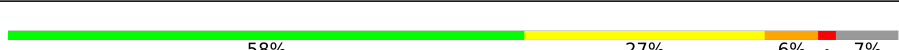


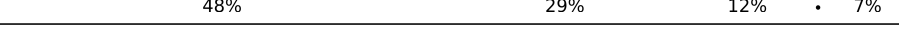







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A7	120	8% (red), 40% (orange), 50% (red), . (grey)
2	A8	2904	10% (yellow), 42% (orange), 48% (red)
3	AA	442	. (red), 87% (green), 9% (yellow), . (grey)
4	AB	65	. (red), 82% (green), 12% (yellow), 6% (orange)
5	AC	53	58% (green), . (grey), 40% (grey)
6	A5	234	6% (red), 77% (green), 21% (yellow), . (grey)
7	A6	273	61% (green), 31% (yellow), 6% (orange), .. (grey)

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Mol	Chain	Length	Quality of chain
8	AD	209	 63% 25% 10% .
9	AE	201	 73% 22% 5%
10	AF	179	 68% 23% 7% ..
11	AG	177	 66% 26% 7% ..
12	AH	149	 70% 26% .
13	AI	142	 74% 20% 6% .
14	AJ	142	 65% 27% 6% .
15	AK	123	 68% 24% 6% ..
16	AL	144	 74% 17% 6% ..
17	AM	136	 55% 35% 9% .
18	AN	127	 60% 28% 5% . 6%
19	AO	117	 79% 18% ..
20	AP	115	 71% 22% . . .
21	AQ	118	 69% 22% 8% .
22	AR	103	 62% 29% 9%
23	AS	110	 66% 25% 6% .
24	AT	100	 58% 27% 6% . 7%
25	AU	104	 66% 24% 5% . .
26	AV	94	 65% 31% . .
27	AW	85	 48% 29% 12% . 7%
28	AX	78	 55% 38% . . .
29	AY	63	 86% 14%
30	AZ	59	 68% 25% . . .
31	A0	57	 65% 25% 9% .
32	A1	55	55% 27% 5% . 9%

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Mol	Chain	Length	Quality of chain
33	A2	46	65% 28% 7%
34	A3	65	63% 26% 6% . .
35	A4	38	71% 18% 11%
36	BA	1542	12% 45% 42% .
37	BB	241	70% 18% . 10%
38	BC	233	67% 17% . 12%
39	BD	206	72% 24% .
40	BE	167	59% 26% 5% . 10%
41	BF	135	41% 27% 5% . 26%
42	BG	179	66% 15% . 16%
43	BH	130	72% 22% 5% . .
44	BI	130	71% 22% . . .
45	BJ	103	69% 22% . 5%
46	BK	129	59% 22% 9% 9%
47	BL	124	. 65% 27% 6% . .
48	BM	118	73% 17% 5% . .
49	BN	101	79% 15% . . .
50	BO	89	70% 24% 6% .
51	BP	82	71% 20% 6% . .
52	BQ	84	60% 29% 6% . 5%
53	BR	75	56% 11% . . 27%
54	BS	92	45% 34% 8% 14%
55	BT	87	74% 20% 5% .
56	BU	71	54% 11% 7% 28%

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 148250 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 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A7	117	2507	1116	459	815	117	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A8	2903	62321	27801	11467	20150	2903	0	0

- Molecule 3 is a protein called PREPROTEIN TRANSLOCASE SECY SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AA	442	3408	2266	547	577	18	0	0

- Molecule 4 is a protein called PREPROTEIN TRANSLOCASE SECE SUBUNIT.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	AB	65	505	332	88	85	0	0

- Molecule 5 is a protein called Preprotein translocase subunit secG.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	AC	32	257	172	42	43	0	0

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A5	234	1733	1081	315	330	7	0	0

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A6	271	2082	1288	423	364	7	0	0

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AF	178	1420	905	251	258	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L6.

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

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called 50S ribosomal protein L11.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AK	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 16 is a protein called 50S ribosomal protein L15.

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

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AN	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

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

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called 50S ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AT	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	AU	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AW	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 28 is a protein called 50S ribosomal protein L28.



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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called 50S ribosomal protein L30.

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

- Molecule 31 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	A1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 33 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	A2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 34 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 35 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 36 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BA	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BC	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BE	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BF	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BG	150	1174	730	226	214	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	BH	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	BI	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	BJ	98	786	493	150	142	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	BK	117	877	540	174	160	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	BL	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	BM	113	876	541	177	155	3	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BP	80	Total	C	N	O	S	0	0
			638	400	126	111	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BQ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
53	BR	55	Total	C	N	O	0	0
			455	288	86	81		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BS	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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

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

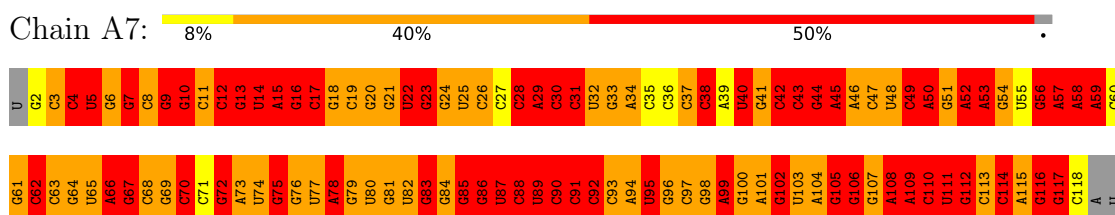
- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	BU	51	425	265	86	73	1	0	0

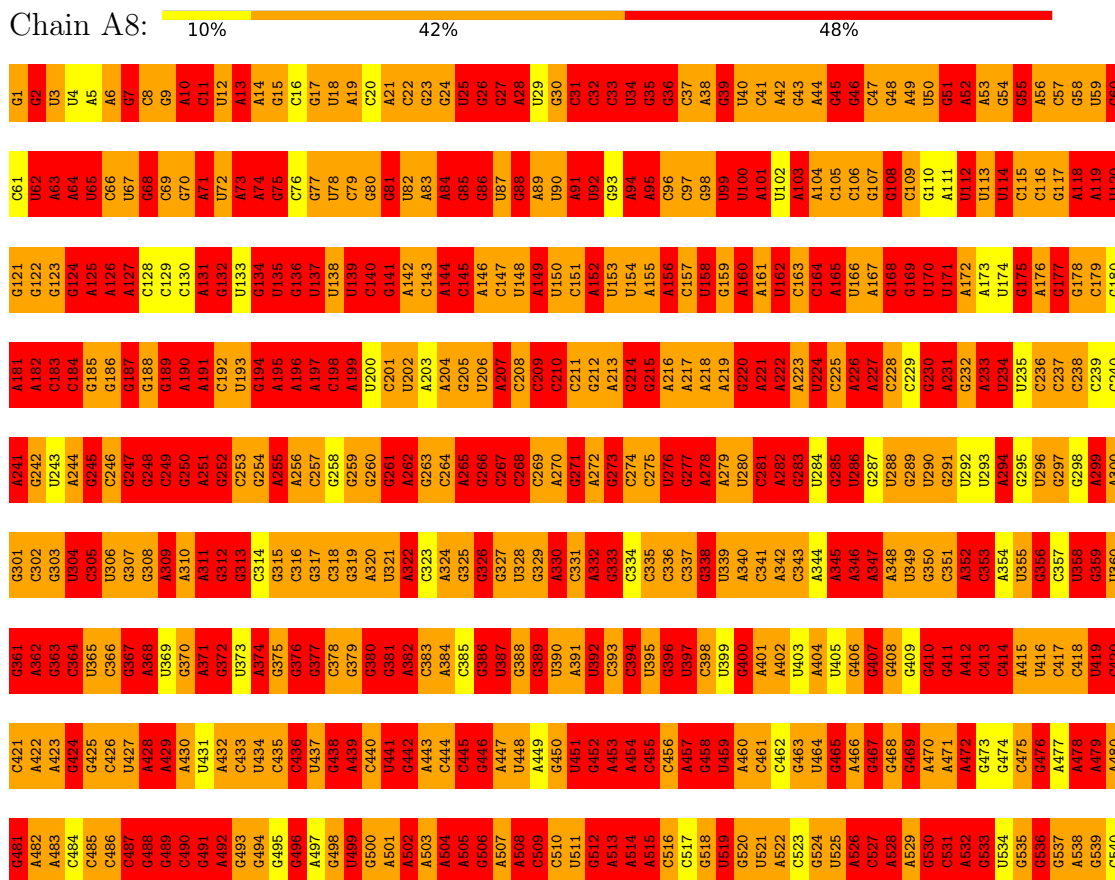
### 3 Residue-property plots

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

- Molecule 1: 5S ribosomal RNA



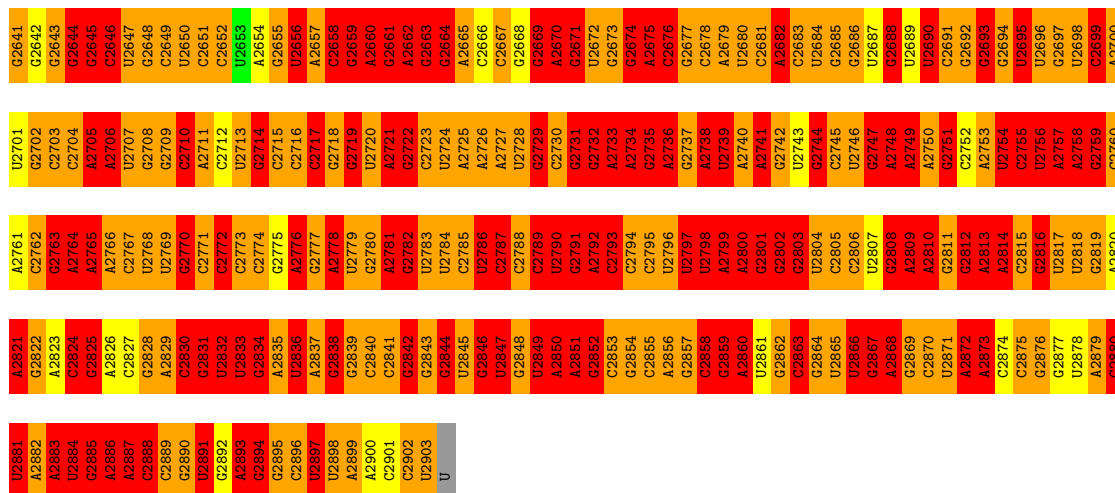
- Molecule 2: 23S ribosomal RNA



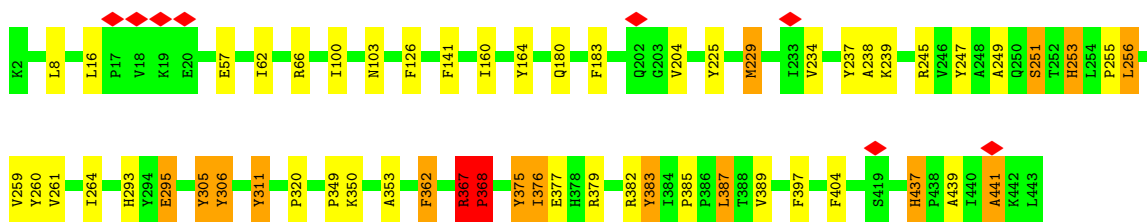
G1561	G1562	G1563	G1564	G1565	G1566	G1567	G1568	G1569	G1570	G1571	G1572	G1573	G1574	G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1585	G1586	G1587	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	G1596	G1597	G1598	G1599	G1600	G1601	G1602	G1603	G1604	G1605	G1606	G1607	G1608	G1609	G1610	G1611	G1612	G1613	G1614	G1615	G1616	G1617	G1618	G1619	G1620																				
G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440																				
G1261	G1262	G1263	G1264	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320																				
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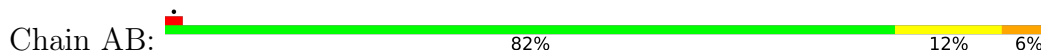




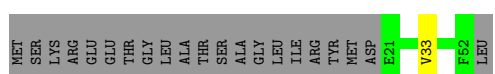
• Molecule 3: PREPROTEIN TRANSLOCASE SECY SUBUNIT



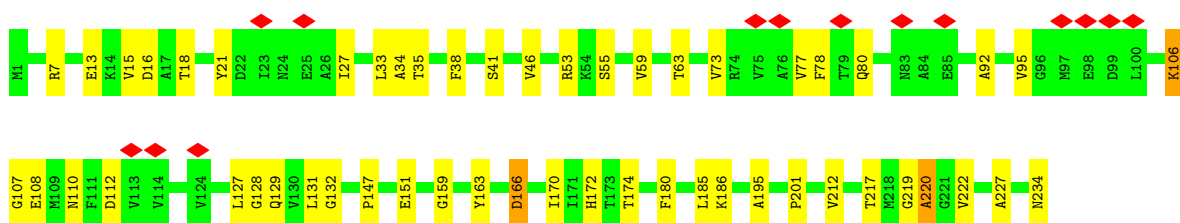
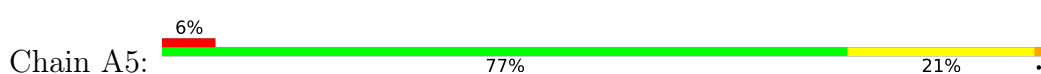
• Molecule 4: PREPROTEIN TRANSLOCASE SECE SUBUNIT



• Molecule 5: Preprotein translocase subunit secG

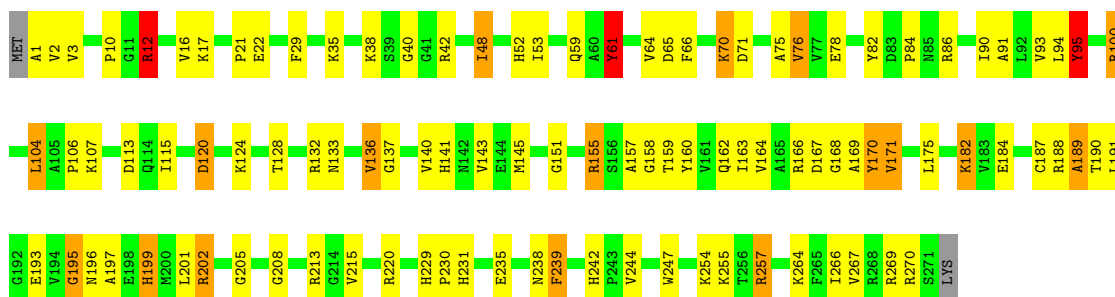


• Molecule 6: 50S ribosomal protein L1



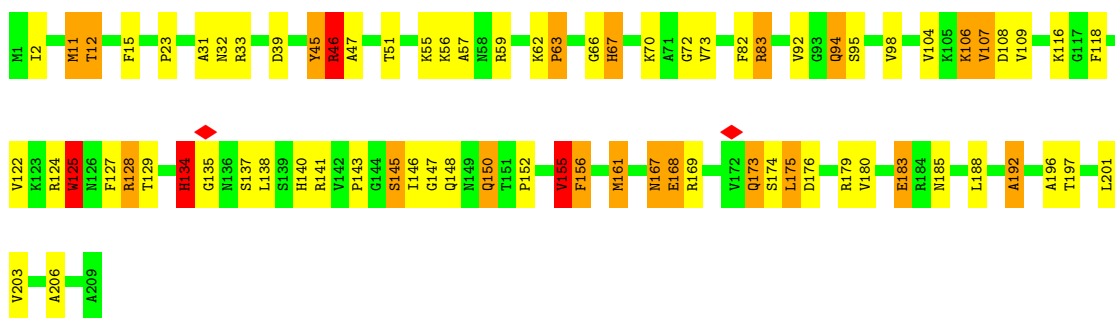
• Molecule 7: 50S ribosomal protein L2

Chain A6:  61% 31% 6% ..




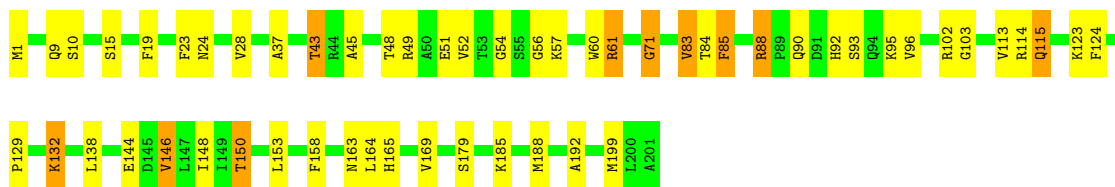
• Molecule 8: 50S ribosomal protein L3

Chain AD:  63% 25% 10% .



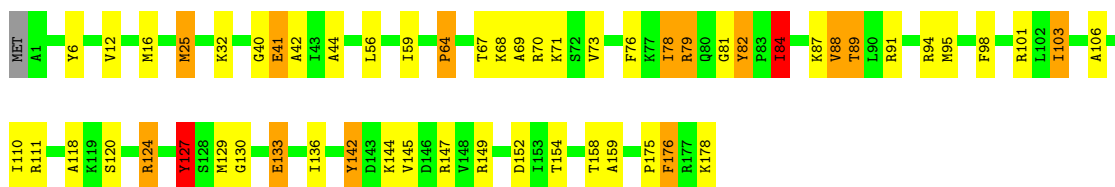
• Molecule 9: 50S ribosomal protein L4

Chain AE:  73% 22% 5%



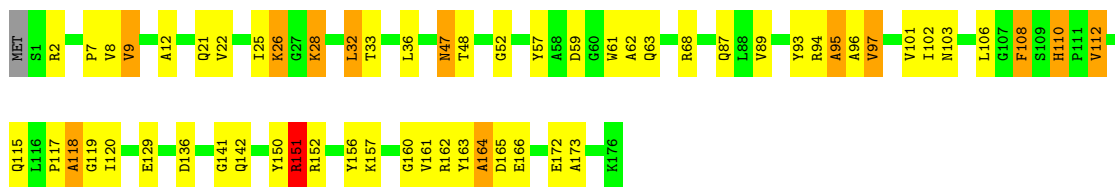
• Molecule 10: 50S ribosomal protein L5

Chain AF:  68% 23% 7% ..



• Molecule 11: 50S ribosomal protein L6

Chain AG:  66% 26% 7% ..



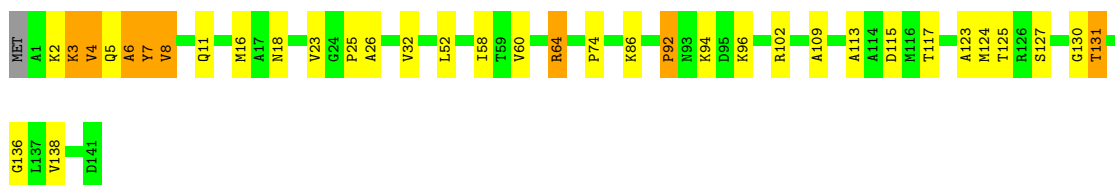
• Molecule 12: 50S ribosomal protein L9

Chain AH:  70% 26% .



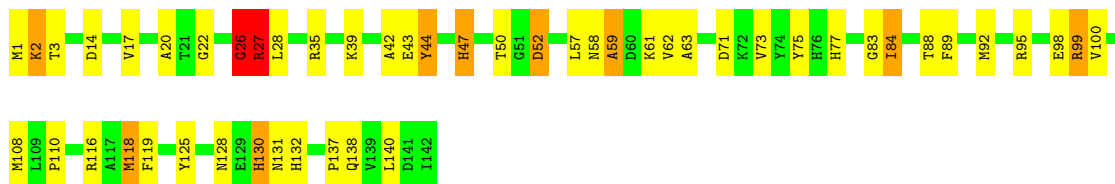
• Molecule 13: 50S ribosomal protein L11

Chain AI:  74% 20% 6% .



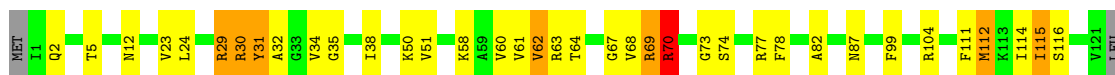
• Molecule 14: 50S ribosomal protein L13

Chain AJ:  65% 27% 6% .




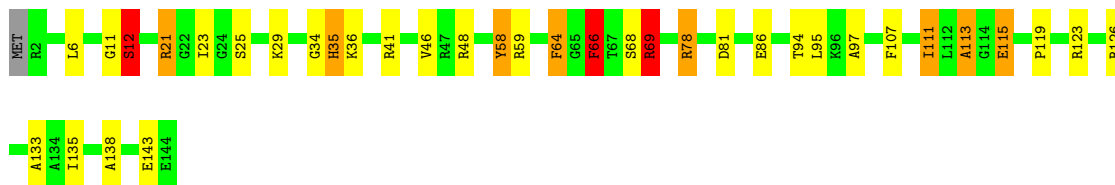
• Molecule 15: 50S ribosomal protein L14

Chain AK:  68% 24% 6% ..

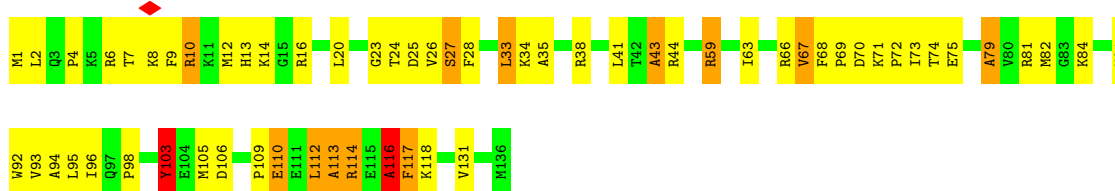


• Molecule 16: 50S ribosomal protein L15

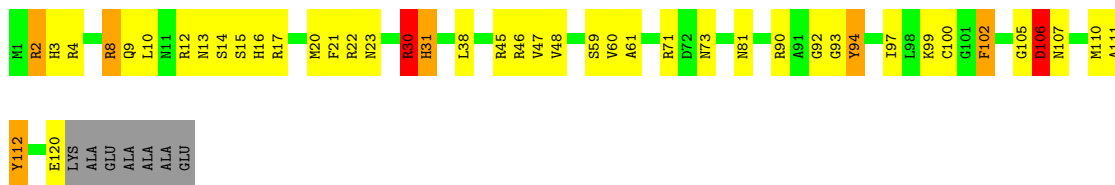
Chain AL:  74% 17% 6% ..



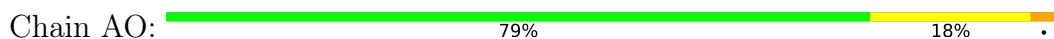
• Molecule 17: 50S ribosomal protein L16



• Molecule 18: 50S ribosomal protein L17



• Molecule 19: 50S ribosomal protein L18



• Molecule 20: 50S ribosomal protein L19



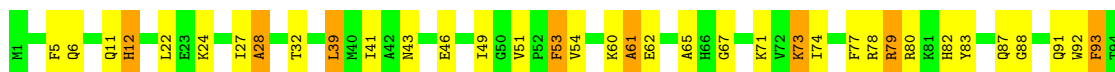
• Molecule 21: 50S ribosomal protein L20





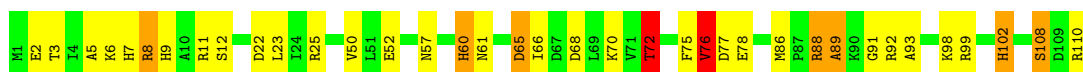
- Molecule 22: 50S ribosomal protein L21

Chain AR: 62% 29% 9%



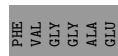
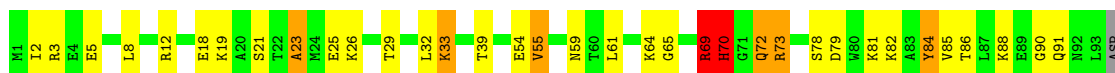
- Molecule 23: 50S ribosomal protein L22

Chain AS: 66% 25% 6%



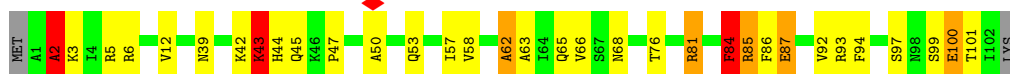
- Molecule 24: 50S ribosomal protein L23

Chain AT: 58% 27% 6% 7%



- Molecule 25: 50S ribosomal protein L24

Chain AU: 66% 24% 5%



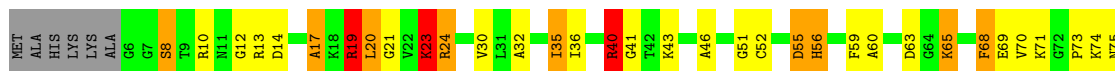
- Molecule 26: 50S ribosomal protein L25

Chain AV: 65% 31%



- Molecule 27: 50S ribosomal protein L27

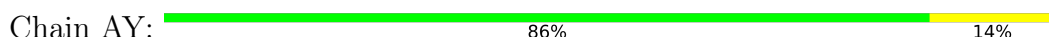
Chain AW: 48% 29% 12% 7%



• Molecule 28: 50S ribosomal protein L28



• Molecule 29: 50S ribosomal protein L29



• Molecule 30: 50S ribosomal protein L30



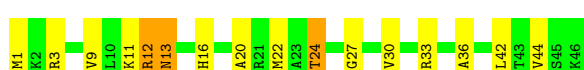
• Molecule 31: 50S ribosomal protein L32



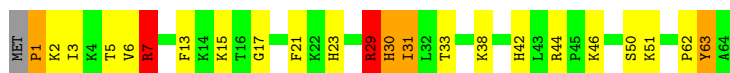
• Molecule 32: 50S ribosomal protein L33



• Molecule 33: 50S ribosomal protein L34



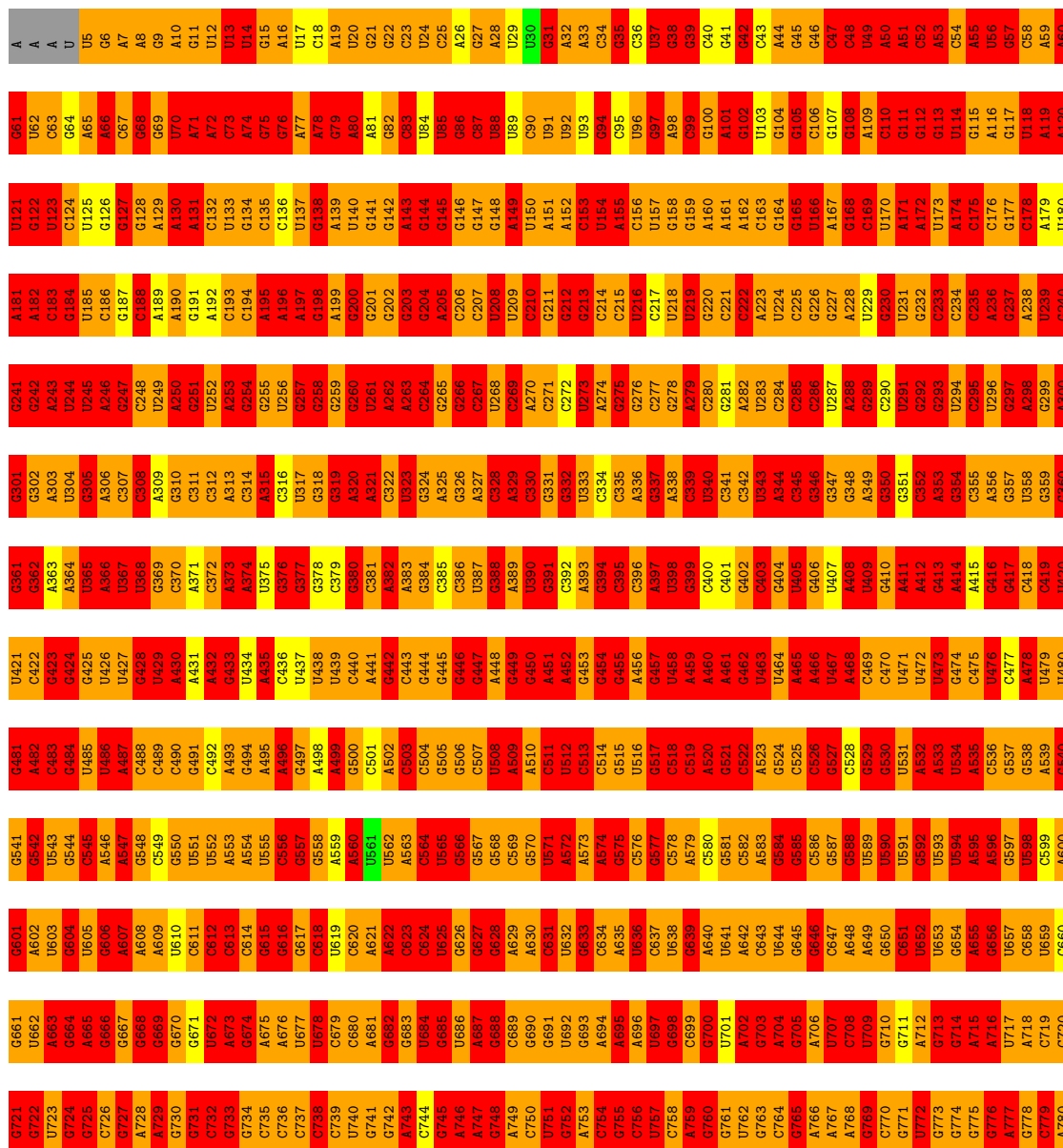
• Molecule 34: 50S ribosomal protein L35



- Molecule 35: 50S ribosomal protein L36



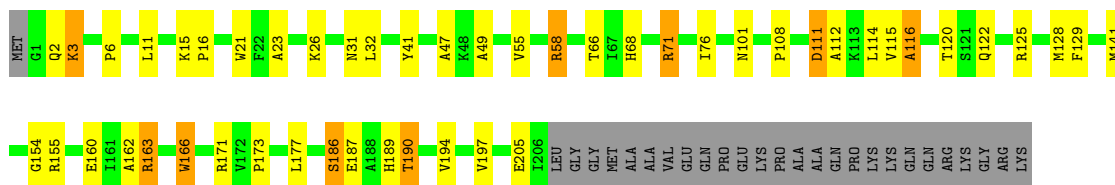
- Molecule 36: 16S ribosomal RNA





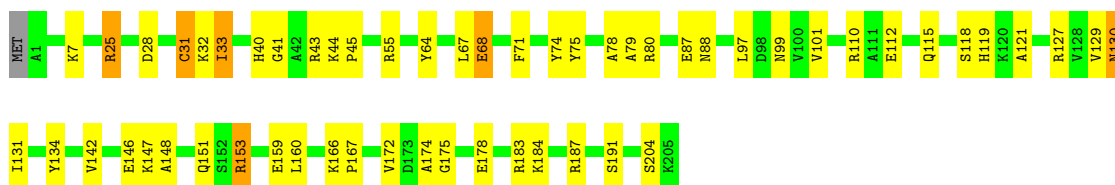


Chain BC:  67% 17% 12%



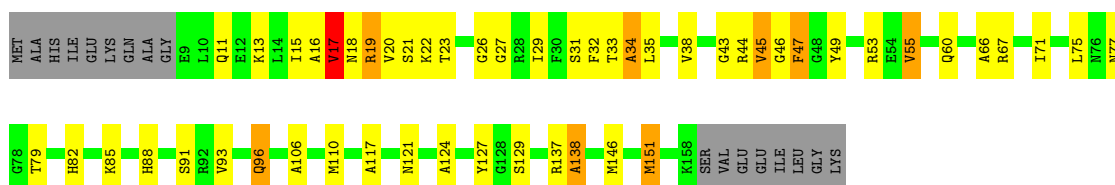
• Molecule 39: 30S ribosomal protein S4

Chain BD:  72% 24%



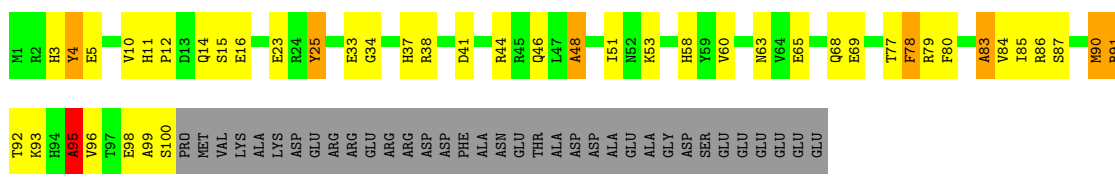
• Molecule 40: 30S ribosomal protein S5

Chain BE:  59% 26% 5% 10%



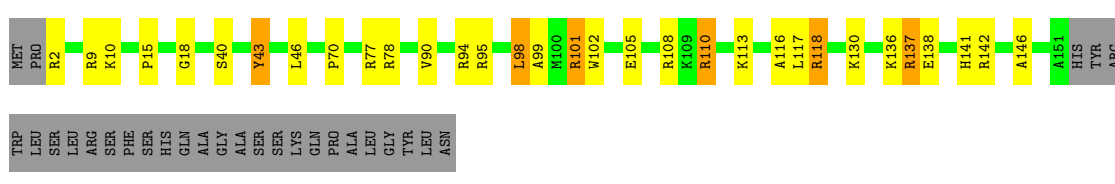
• Molecule 41: 30S ribosomal protein S6

Chain BF:  41% 27% 5% 26%



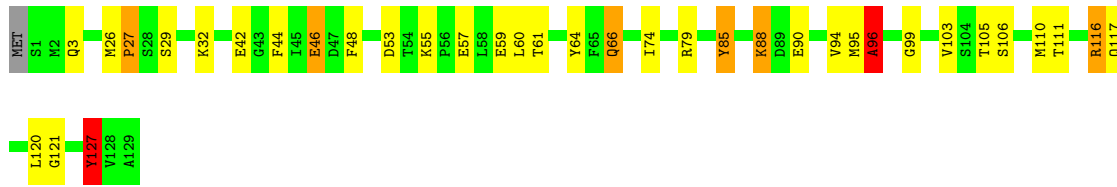
• Molecule 42: 30S ribosomal protein S7

Chain BG:  66% 15% 16%



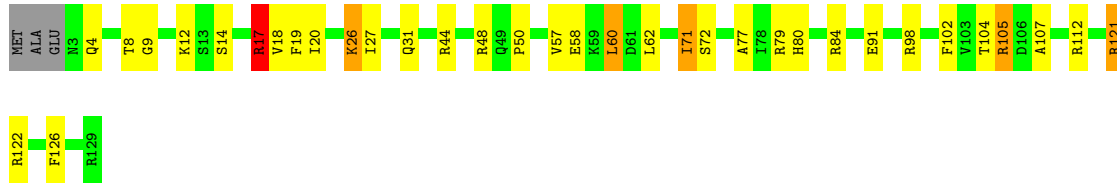
• Molecule 43: 30S ribosomal protein S8

Chain BH: 



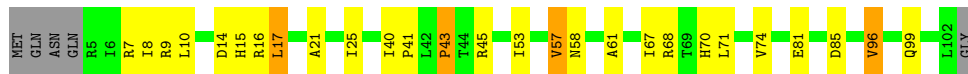
- Molecule 44: 30S ribosomal protein S9

Chain BI: 



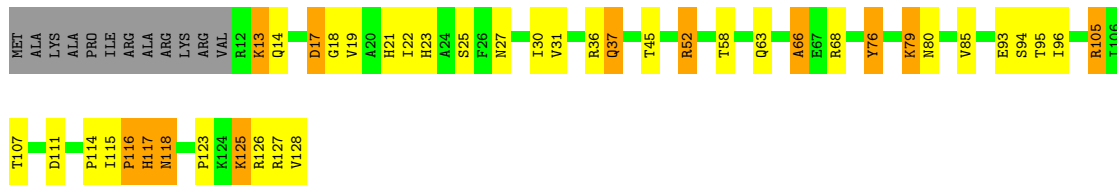
- Molecule 45: 30S ribosomal protein S10

Chain BJ: 



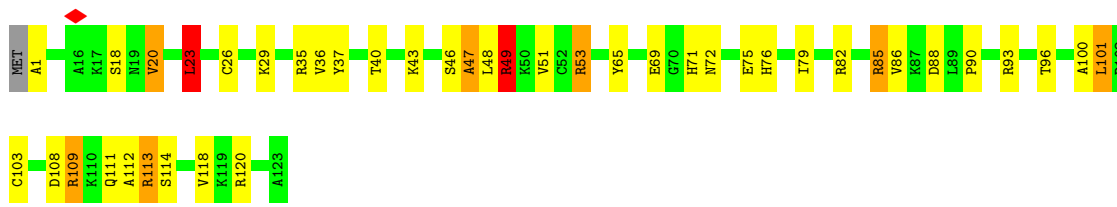
- Molecule 46: 30S ribosomal protein S11

Chain BK: 




- Molecule 47: 30S ribosomal protein S12

Chain BL: 

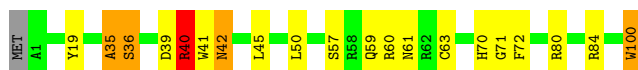
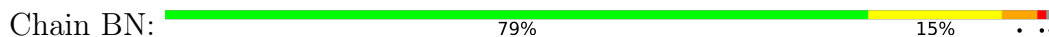


- Molecule 48: 30S ribosomal protein S13

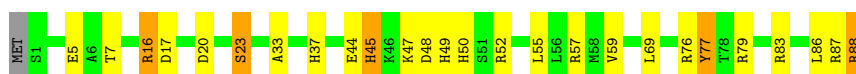
Chain BM: 



- Molecule 49: 30S ribosomal protein S14



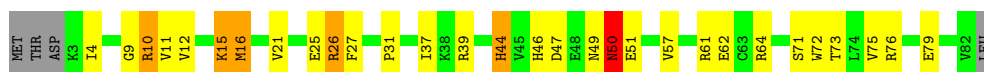
- Molecule 50: 30S ribosomal protein S15



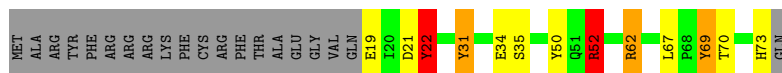
- Molecule 51: 30S ribosomal protein S16



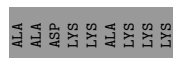
- Molecule 52: 30S ribosomal protein S17




- Molecule 53: 30S ribosomal protein S18



- Molecule 54: 30S ribosomal protein S19



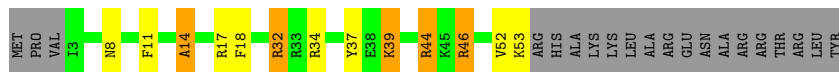
- Molecule 55: 30S ribosomal protein S20

Chain BT:  74% 20% 5%



• Molecule 56: 30S ribosomal protein S21

Chain BU:  54% 11% 7% 28%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39000	Depositor
Resolution determination method	Not provided	
CTF correction method	EMAN- PHASE FLIPPING OF PARTICLES FORM THE SAME MICROGRAPH	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	15	Depositor
Minimum defocus (nm)	-700.00	Depositor
Maximum defocus (nm)	-3000.00	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	10.649	Depositor
Minimum map value	-4.997	Depositor
Average map value	0.150	Depositor
Map value standard deviation	0.868	Depositor
Recommended contour level	0.95	Depositor
Map size (Å)	393.12, 393.12, 393.12	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.73, 2.73, 2.73	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	A7	2.22	139/2803 (5.0%)	3.06	443/4371 (10.1%)
2	A8	2.30	3372/69800 (4.8%)	3.05	10411/108892 (9.6%)
3	AA	0.95	0/3484	1.15	15/4732 (0.3%)
4	AB	0.98	0/514	1.20	1/694 (0.1%)
5	AC	0.98	0/262	1.02	0/354
6	A5	0.98	0/1748	1.20	3/2355 (0.1%)
7	A6	1.15	0/2121	1.35	8/2852 (0.3%)
8	AD	1.10	0/1586	1.41	10/2134 (0.5%)
9	AE	1.05	0/1571	1.28	7/2113 (0.3%)
10	AF	1.11	0/1444	1.37	6/1937 (0.3%)
11	AG	1.09	0/1343	1.41	12/1816 (0.7%)
12	AH	1.05	0/1122	1.36	7/1515 (0.5%)
13	AI	0.96	0/1046	1.24	3/1410 (0.2%)
14	AJ	1.16	1/1152 (0.1%)	1.37	3/1551 (0.2%)
15	AK	1.21	0/939	1.35	4/1258 (0.3%)
16	AL	1.12	0/1054	1.30	7/1403 (0.5%)
17	AM	1.15	0/1093	1.46	12/1460 (0.8%)
18	AN	1.21	0/973	1.43	9/1301 (0.7%)
19	AO	1.16	0/902	1.30	3/1209 (0.2%)
20	AP	1.16	0/929	1.38	5/1242 (0.4%)
21	AQ	1.24	0/960	1.45	8/1278 (0.6%)
22	AR	1.19	0/829	1.43	5/1107 (0.5%)
23	AS	1.11	0/864	1.40	9/1156 (0.8%)
24	AT	1.04	0/744	1.40	5/994 (0.5%)
25	AU	1.05	0/787	1.34	5/1051 (0.5%)
26	AV	1.11	0/766	1.38	4/1025 (0.4%)
27	AW	1.11	0/603	1.37	4/797 (0.5%)
28	AX	1.23	0/635	1.54	6/848 (0.7%)
29	AY	1.08	0/510	1.23	0/677
30	AZ	1.13	0/453	1.34	3/605 (0.5%)
31	A0	1.15	0/450	1.30	2/599 (0.3%)
32	A1	1.03	0/416	1.57	5/554 (0.9%)
33	A2	1.33	0/380	1.51	1/498 (0.2%)
34	A3	1.06	0/513	1.33	2/676 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	A4	1.20	0/303	1.31	1/397 (0.3%)
36	BA	2.16	1315/36762 (3.6%)	2.97	5321/57350 (9.3%)
37	BB	1.01	0/1735	1.19	4/2338 (0.2%)
38	BC	1.04	0/1651	1.24	5/2225 (0.2%)
39	BD	1.09	0/1665	1.25	7/2227 (0.3%)
40	BE	1.08	0/1118	1.32	5/1504 (0.3%)
41	BF	1.11	0/835	1.35	9/1128 (0.8%)
42	BG	1.06	0/1187	1.20	3/1591 (0.2%)
43	BH	1.08	0/989	1.39	5/1326 (0.4%)
44	BI	1.20	0/1034	1.33	4/1375 (0.3%)
45	BJ	1.08	0/796	1.25	2/1077 (0.2%)
46	BK	1.15	0/893	1.36	3/1205 (0.2%)
47	BL	1.21	0/969	1.41	5/1300 (0.4%)
48	BM	1.13	0/884	1.26	6/1181 (0.5%)
49	BN	1.10	0/817	1.34	5/1088 (0.5%)
50	BO	1.19	0/724	1.33	3/966 (0.3%)
51	BP	1.14	0/648	1.29	6/870 (0.7%)
52	BQ	1.09	0/657	1.33	4/881 (0.5%)
53	BR	1.15	0/462	1.41	5/621 (0.8%)
54	BS	1.09	1/652 (0.2%)	1.36	7/877 (0.8%)
55	BT	1.13	0/671	1.30	3/888 (0.3%)
56	BU	1.21	0/430	1.26	2/570 (0.4%)
All	All	1.96	4828/160678 (3.0%)	2.65	16443/239449 (6.9%)

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	A7	0	56
2	A8	0	1380
3	AA	0	12
4	AB	0	2
6	A5	0	3
7	A6	0	18
8	AD	0	9
9	AE	0	6
10	AF	0	5
11	AG	0	6
12	AH	0	2
13	AI	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
14	AJ	0	6
15	AK	0	4
16	AL	0	4
17	AM	0	13
18	AN	0	4
19	AO	0	3
20	AP	0	5
21	AQ	0	7
22	AR	0	4
23	AS	0	2
24	AT	0	3
25	AU	0	4
26	AV	0	1
27	AW	0	1
28	AX	0	2
29	AY	0	2
30	AZ	0	2
31	A0	0	3
32	A1	0	3
33	A2	0	1
34	A3	0	4
35	A4	0	1
36	BA	0	678
37	BB	0	5
38	BC	0	2
39	BD	0	12
40	BE	0	1
41	BF	0	3
42	BG	0	3
43	BH	0	4
44	BI	0	1
45	BJ	0	1
46	BK	0	5
47	BL	0	9
48	BM	0	7
49	BN	0	4
50	BO	0	5
51	BP	0	3
52	BQ	0	1
53	BR	0	4
54	BS	0	2
55	BT	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	BU	0	3
All	All	0	2335

The worst 5 of 4828 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A8	2469	A	N7-C5	-14.86	1.30	1.39
2	A8	1689	A	N7-C5	-14.56	1.30	1.39
2	A8	2412	A	N7-C5	-13.83	1.30	1.39
2	A8	2860	A	N7-C5	-13.77	1.30	1.39
2	A8	633	A	N7-C5	-13.76	1.30	1.39

The worst 5 of 16443 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A8	1723	G	C5-C6-O6	-25.05	113.57	128.60
2	A8	2471	A	O4'-C1'-N9	24.02	127.42	108.20
2	A8	1723	G	N1-C6-O6	23.04	133.72	119.90
2	A8	2468	A	O4'-C1'-N9	21.60	125.48	108.20
2	A8	198	C	C6-N1-C2	-21.54	111.68	120.30

There are no chirality outliers.

5 of 2335 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A7	10	G	Sidechain
1	A7	4	C	Sidechain
1	A7	5	U	Sidechain
1	A7	7	G	Sidechain
1	A7	9	G	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A7	2507	0	1270	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A8	62321	0	31344	3726	0
3	AA	3408	0	3619	13	0
4	AB	505	0	557	1	0
5	AC	257	0	272	1	0
6	A5	1733	0	1824	24	0
7	A6	2082	0	2157	50	0
8	AD	1565	0	1616	37	0
9	AE	1552	0	1619	31	0
10	AF	1420	0	1460	20	0
11	AG	1323	0	1374	22	0
12	AH	1111	0	1148	17	0
13	AI	1032	0	1088	26	0
14	AJ	1129	0	1162	29	0
15	AK	930	0	1003	20	0
16	AL	1045	0	1117	15	0
17	AM	1074	0	1157	24	0
18	AN	960	0	1000	32	0
19	AO	892	0	923	10	0
20	AP	917	0	965	10	0
21	AQ	947	0	1022	15	0
22	AR	816	0	839	17	0
23	AS	857	0	922	22	0
24	AT	738	0	807	14	0
25	AU	779	0	834	16	0
26	AV	753	0	780	23	0
27	AW	596	0	610	29	0
28	AX	625	0	655	19	0
29	AY	509	0	543	5	0
30	AZ	449	0	491	11	0
31	A0	444	0	461	9	0
32	A1	409	0	440	14	0
33	A2	377	0	418	7	0
34	A3	504	0	574	12	0
35	A4	302	0	343	10	0
36	BA	32831	0	16521	1593	0
37	BB	1704	0	1732	17	0
38	BC	1624	0	1699	19	0
39	BD	1643	0	1710	21	0
40	BE	1105	0	1148	22	0
41	BF	817	0	808	21	0
42	BG	1174	0	1230	12	0
43	BH	979	0	1034	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BI	1022	0	1070	17	0
45	BJ	786	0	828	13	0
46	BK	877	0	887	18	0
47	BL	955	0	1019	23	0
48	BM	876	0	937	7	0
49	BN	805	0	847	3	0
50	BO	716	0	742	10	0
51	BP	638	0	656	11	0
52	BQ	648	0	691	10	0
53	BR	455	0	478	6	0
54	BS	637	0	665	25	0
55	BT	665	0	714	7	0
56	BU	425	0	449	4	0
All	All	148250	0	102279	6042	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

The worst 5 of 6042 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A8:1902:C:H1'	7:A6:242:HIS:CE1	2.14	0.83
36:BA:113:G:H1'	36:BA:354:G:H4'	1.61	0.83
2:A8:2121:G:H1	2:A8:2176:A:H61	1.27	0.82
36:BA:68:G:H1'	36:BA:151:A:H61	1.47	0.79
28:AX:18:SER:H	28:AX:22:ASN:H	1.30	0.79

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	440/442 (100%)	383 (87%)	41 (9%)	16 (4%)	3	25
4	AB	63/65 (97%)	55 (87%)	3 (5%)	5 (8%)	1	13
5	AC	30/53 (57%)	29 (97%)	1 (3%)	0	100	100
6	A5	232/234 (99%)	199 (86%)	18 (8%)	15 (6%)	1	16
7	A6	269/273 (98%)	192 (71%)	55 (20%)	22 (8%)	1	12
8	AD	207/209 (99%)	144 (70%)	40 (19%)	23 (11%)	0	7
9	AE	199/201 (99%)	155 (78%)	29 (15%)	15 (8%)	1	13
10	AF	176/179 (98%)	120 (68%)	34 (19%)	22 (12%)	0	5
11	AG	174/177 (98%)	129 (74%)	24 (14%)	21 (12%)	0	6
12	AH	147/149 (99%)	102 (69%)	32 (22%)	13 (9%)	1	11
13	AI	139/142 (98%)	122 (88%)	11 (8%)	6 (4%)	2	22
14	AJ	140/142 (99%)	109 (78%)	22 (16%)	9 (6%)	1	16
15	AK	119/123 (97%)	87 (73%)	26 (22%)	6 (5%)	2	20
16	AL	141/144 (98%)	107 (76%)	18 (13%)	16 (11%)	0	7
17	AM	134/136 (98%)	91 (68%)	31 (23%)	12 (9%)	1	11
18	AN	118/127 (93%)	89 (75%)	21 (18%)	8 (7%)	1	15
19	AO	114/117 (97%)	94 (82%)	17 (15%)	3 (3%)	5	31
20	AP	112/115 (97%)	82 (73%)	20 (18%)	10 (9%)	1	11
21	AQ	115/118 (98%)	87 (76%)	20 (17%)	8 (7%)	1	14
22	AR	101/103 (98%)	84 (83%)	11 (11%)	6 (6%)	1	17
23	AS	108/110 (98%)	85 (79%)	17 (16%)	6 (6%)	2	19
24	AT	91/100 (91%)	60 (66%)	23 (25%)	8 (9%)	1	11
25	AU	100/104 (96%)	67 (67%)	17 (17%)	16 (16%)	0	3
26	AV	92/94 (98%)	73 (79%)	17 (18%)	2 (2%)	6	35
27	AW	77/85 (91%)	48 (62%)	13 (17%)	16 (21%)	0	2
28	AX	75/78 (96%)	49 (65%)	19 (25%)	7 (9%)	0	11
29	AY	61/63 (97%)	41 (67%)	19 (31%)	1 (2%)	9	44
30	AZ	56/59 (95%)	49 (88%)	6 (11%)	1 (2%)	8	40
31	A0	54/57 (95%)	41 (76%)	8 (15%)	5 (9%)	0	11
32	A1	48/55 (87%)	37 (77%)	6 (12%)	5 (10%)	0	8
33	A2	44/46 (96%)	33 (75%)	7 (16%)	4 (9%)	1	11
34	A3	62/65 (95%)	48 (77%)	10 (16%)	4 (6%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	A4	36/38 (95%)	27 (75%)	6 (17%)	3 (8%)	1	12
37	BB	216/241 (90%)	165 (76%)	40 (18%)	11 (5%)	2	19
38	BC	204/233 (88%)	158 (78%)	30 (15%)	16 (8%)	1	13
39	BD	203/206 (98%)	163 (80%)	28 (14%)	12 (6%)	1	17
40	BE	148/167 (89%)	106 (72%)	32 (22%)	10 (7%)	1	15
41	BF	98/135 (73%)	71 (72%)	16 (16%)	11 (11%)	0	7
42	BG	148/179 (83%)	110 (74%)	26 (18%)	12 (8%)	1	12
43	BH	127/130 (98%)	87 (68%)	32 (25%)	8 (6%)	1	17
44	BI	125/130 (96%)	99 (79%)	16 (13%)	10 (8%)	1	12
45	BJ	96/103 (93%)	79 (82%)	9 (9%)	8 (8%)	1	12
46	BK	115/129 (89%)	87 (76%)	15 (13%)	13 (11%)	0	7
47	BL	121/124 (98%)	104 (86%)	13 (11%)	4 (3%)	4	26
48	BM	111/118 (94%)	83 (75%)	18 (16%)	10 (9%)	1	11
49	BN	98/101 (97%)	68 (69%)	21 (21%)	9 (9%)	1	11
50	BO	86/89 (97%)	76 (88%)	7 (8%)	3 (4%)	3	25
51	BP	78/82 (95%)	63 (81%)	9 (12%)	6 (8%)	1	13
52	BQ	78/84 (93%)	58 (74%)	12 (15%)	8 (10%)	0	8
53	BR	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	3	24
54	BS	77/92 (84%)	57 (74%)	16 (21%)	4 (5%)	2	19
55	BT	83/87 (95%)	71 (86%)	8 (10%)	4 (5%)	2	21
56	BU	49/71 (69%)	33 (67%)	11 (22%)	5 (10%)	0	9
All	All	6388/6779 (94%)	4900 (77%)	1008 (16%)	480 (8%)	2	13

5 of 480 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AA	239	LYS
3	AA	349	PRO
6	A5	55	SER
6	A5	59	VAL
7	A6	78	GLU

### 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	
3	AA	362/362 (100%)	341 (94%)	21 (6%)	20	45
4	AB	52/52 (100%)	46 (88%)	6 (12%)	5	21
5	AC	28/45 (62%)	28 (100%)	0	100	100
6	A5	181/181 (100%)	171 (94%)	10 (6%)	21	47
7	A6	216/218 (99%)	200 (93%)	16 (7%)	13	38
8	AD	164/164 (100%)	144 (88%)	20 (12%)	5	20
9	AE	165/165 (100%)	161 (98%)	4 (2%)	49	69
10	AF	149/150 (99%)	135 (91%)	14 (9%)	8	28
11	AG	137/138 (99%)	127 (93%)	10 (7%)	14	39
12	AH	114/114 (100%)	110 (96%)	4 (4%)	36	59
13	AI	109/110 (99%)	100 (92%)	9 (8%)	11	34
14	AJ	116/116 (100%)	106 (91%)	10 (9%)	10	32
15	AK	102/104 (98%)	95 (93%)	7 (7%)	15	40
16	AL	102/103 (99%)	94 (92%)	8 (8%)	12	36
17	AM	109/109 (100%)	97 (89%)	12 (11%)	6	22
18	AN	100/103 (97%)	91 (91%)	9 (9%)	9	30
19	AO	86/87 (99%)	83 (96%)	3 (4%)	36	59
20	AP	99/100 (99%)	94 (95%)	5 (5%)	24	48
21	AQ	89/90 (99%)	81 (91%)	8 (9%)	9	30
22	AR	84/84 (100%)	76 (90%)	8 (10%)	8	27
23	AS	93/93 (100%)	82 (88%)	11 (12%)	5	20
24	AT	80/84 (95%)	72 (90%)	8 (10%)	7	26
25	AU	83/85 (98%)	78 (94%)	5 (6%)	19	44
26	AV	78/78 (100%)	72 (92%)	6 (8%)	13	37
27	AW	59/63 (94%)	51 (86%)	8 (14%)	3	17
28	AX	67/68 (98%)	63 (94%)	4 (6%)	19	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	AY	55/55 (100%)	55 (100%)	0	100	100
30	AZ	48/49 (98%)	46 (96%)	2 (4%)	30	54
31	A0	47/48 (98%)	42 (89%)	5 (11%)	6	24
32	A1	45/49 (92%)	44 (98%)	1 (2%)	52	71
33	A2	38/38 (100%)	34 (90%)	4 (10%)	7	24
34	A3	51/52 (98%)	45 (88%)	6 (12%)	5	20
35	A4	34/34 (100%)	33 (97%)	1 (3%)	42	64
37	BB	180/199 (90%)	173 (96%)	7 (4%)	32	56
38	BC	170/190 (90%)	162 (95%)	8 (5%)	26	51
39	BD	172/173 (99%)	166 (96%)	6 (4%)	36	59
40	BE	113/126 (90%)	103 (91%)	10 (9%)	10	31
41	BF	87/116 (75%)	79 (91%)	8 (9%)	9	29
42	BG	123/147 (84%)	121 (98%)	2 (2%)	62	79
43	BH	104/105 (99%)	96 (92%)	8 (8%)	13	37
44	BI	105/107 (98%)	98 (93%)	7 (7%)	16	41
45	BJ	86/90 (96%)	83 (96%)	3 (4%)	36	59
46	BK	90/99 (91%)	81 (90%)	9 (10%)	7	26
47	BL	103/104 (99%)	93 (90%)	10 (10%)	8	27
48	BM	91/96 (95%)	88 (97%)	3 (3%)	38	61
49	BN	83/84 (99%)	79 (95%)	4 (5%)	25	51
50	BO	76/77 (99%)	73 (96%)	3 (4%)	32	56
51	BP	65/65 (100%)	61 (94%)	4 (6%)	18	43
52	BQ	74/78 (95%)	68 (92%)	6 (8%)	11	35
53	BR	48/65 (74%)	43 (90%)	5 (10%)	7	24
54	BS	70/79 (89%)	67 (96%)	3 (4%)	29	53
55	BT	65/66 (98%)	58 (89%)	7 (11%)	6	23
56	BU	44/61 (72%)	40 (91%)	4 (9%)	9	29
All	All	5291/5518 (96%)	4929 (93%)	362 (7%)	19	41

5 of 362 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	A0	24	VAL

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Mol	Chain	Res	Type
43	BH	26	MET
34	A3	1	PRO
39	BD	31	CYS
44	BI	105	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
31	A0	41	HIS
41	BF	58	HIS
33	A2	16	HIS
38	BC	18	ASN
45	BJ	15	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A7	116/120 (96%)	24 (20%)	4 (3%)
2	A8	2902/2904 (99%)	537 (18%)	109 (3%)
36	BA	1530/1542 (99%)	296 (19%)	51 (3%)
All	All	4548/4566 (99%)	857 (18%)	164 (3%)

5 of 857 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A7	9	G
1	A7	12	C
1	A7	13	G
1	A7	14	U
1	A7	15	A

5 of 164 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	BA	60	A
36	BA	991	U
36	BA	243	A
36	BA	429	U
36	BA	1159	U



## 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.

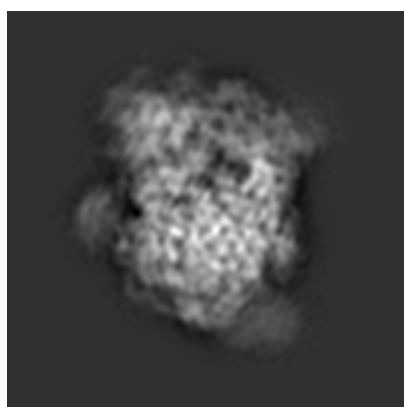
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1484. These allow visual inspection of the internal detail of the map and identification of artifacts.

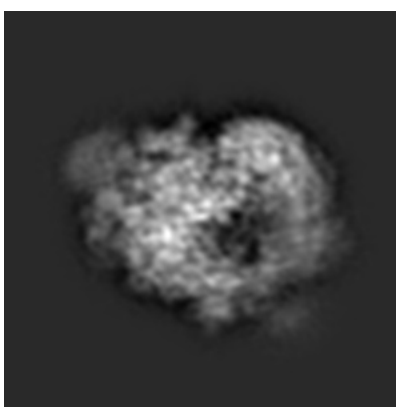
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

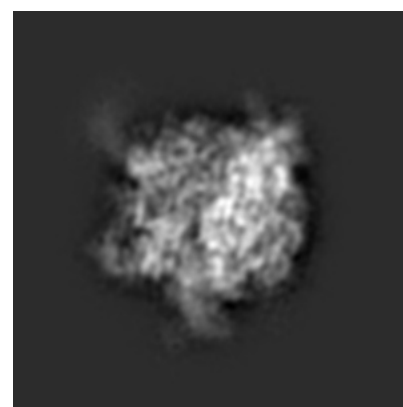
#### 6.1.1 Primary map



X



Y

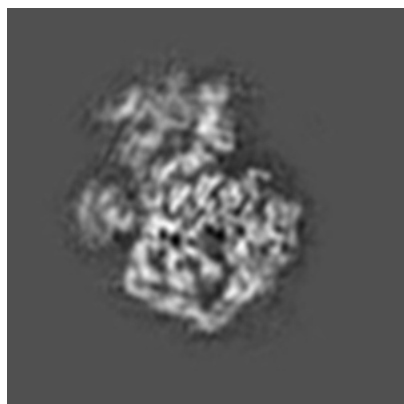


Z

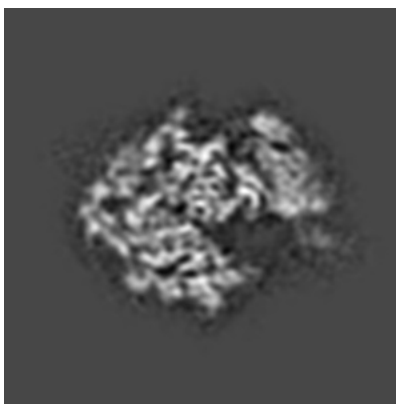
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

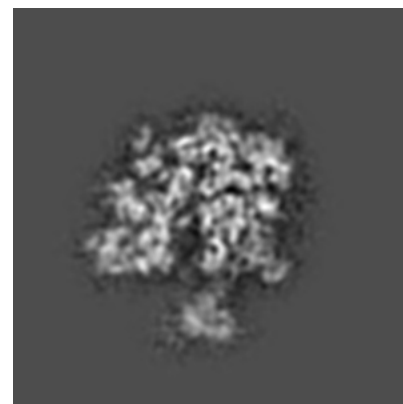
#### 6.2.1 Primary map



X Index: 72



Y Index: 72

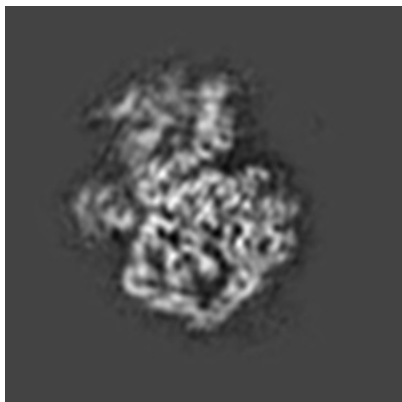


Z Index: 72

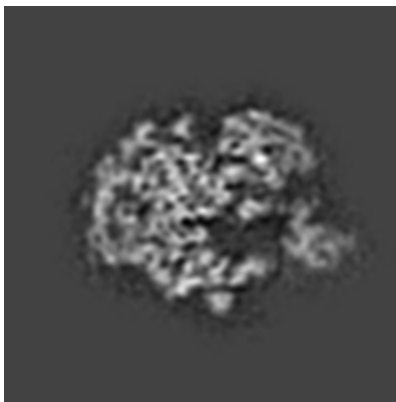
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

### 6.3.1 Primary map



X Index: 73



Y Index: 67

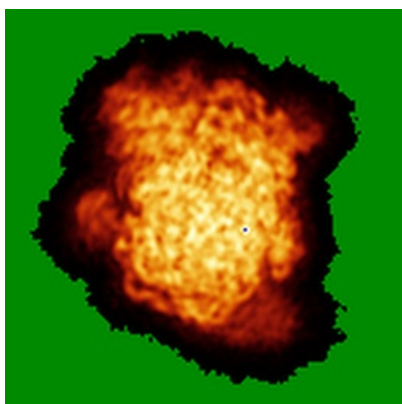


Z Index: 63

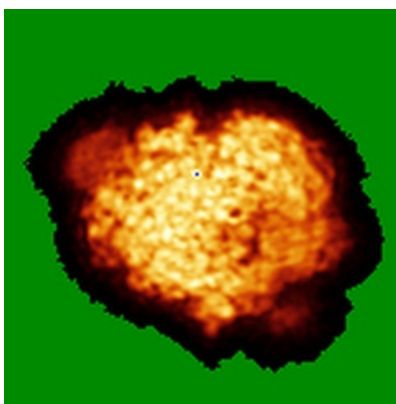
The images above show the largest variance slices of the map in three orthogonal directions.

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

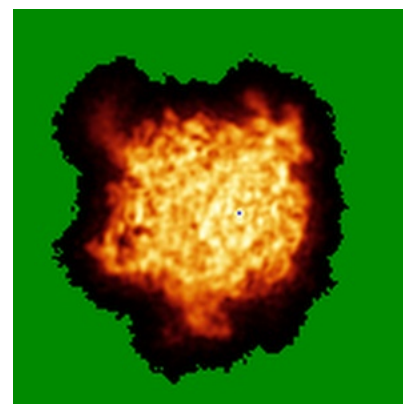
### 6.4.1 Primary map



X



Y

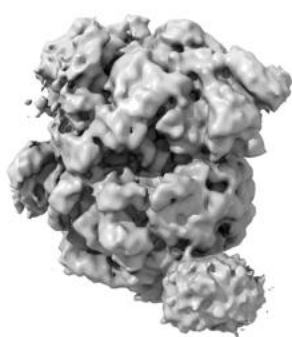


Z

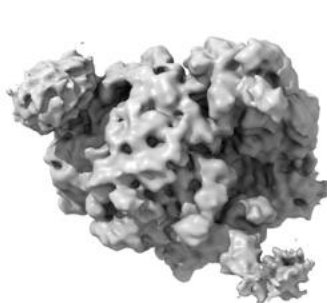
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

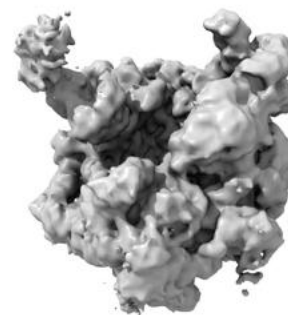
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.95. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

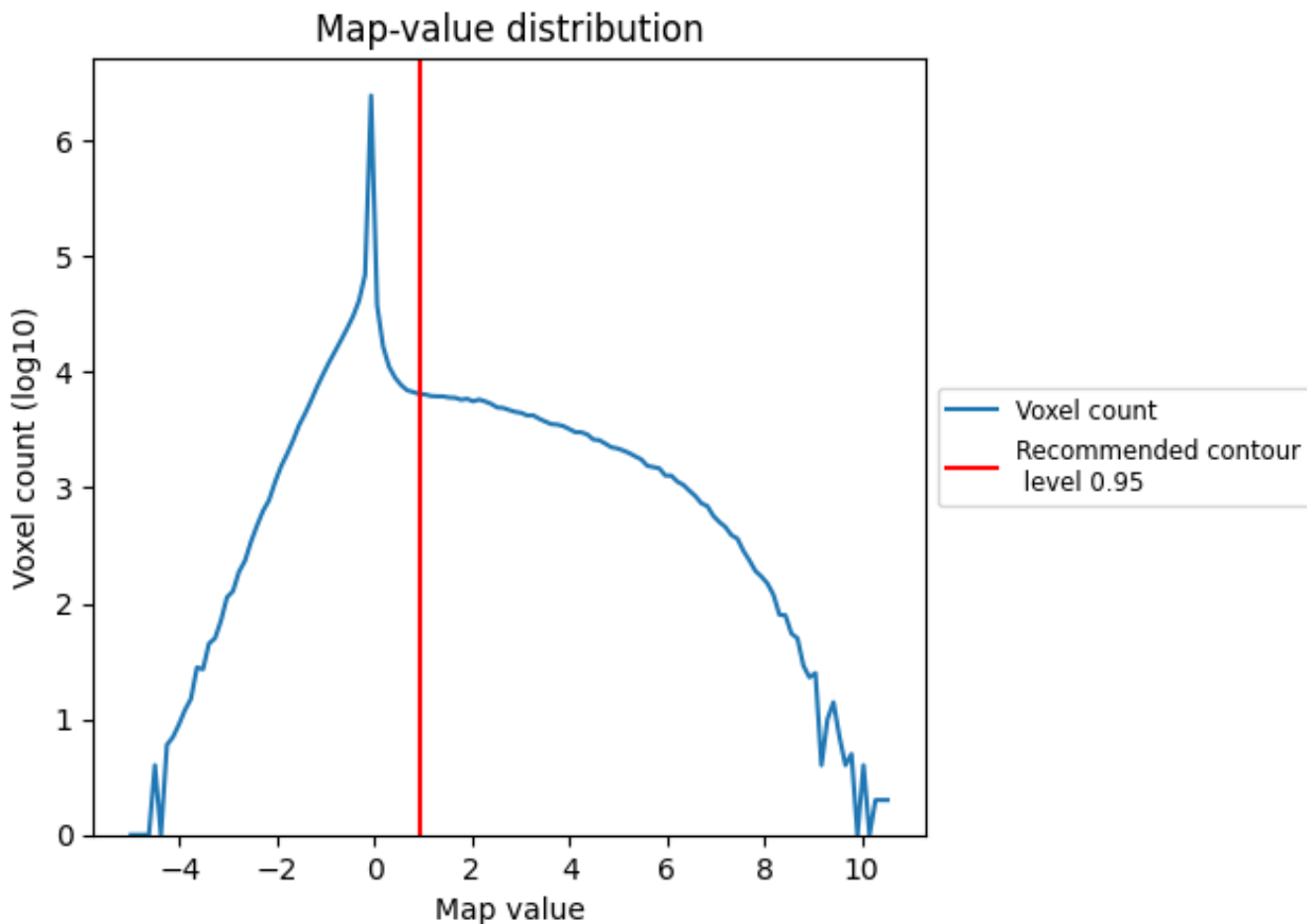
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

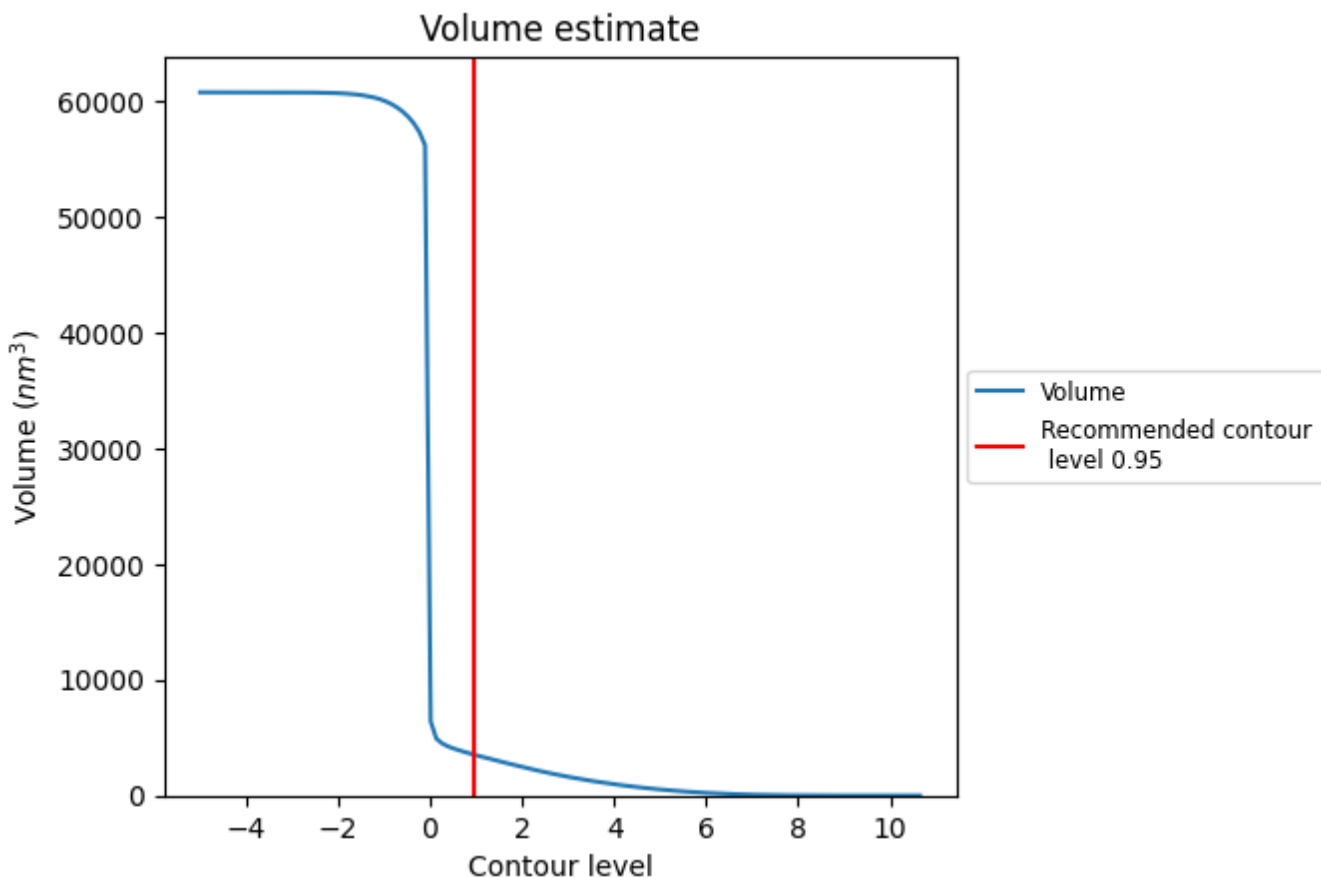
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

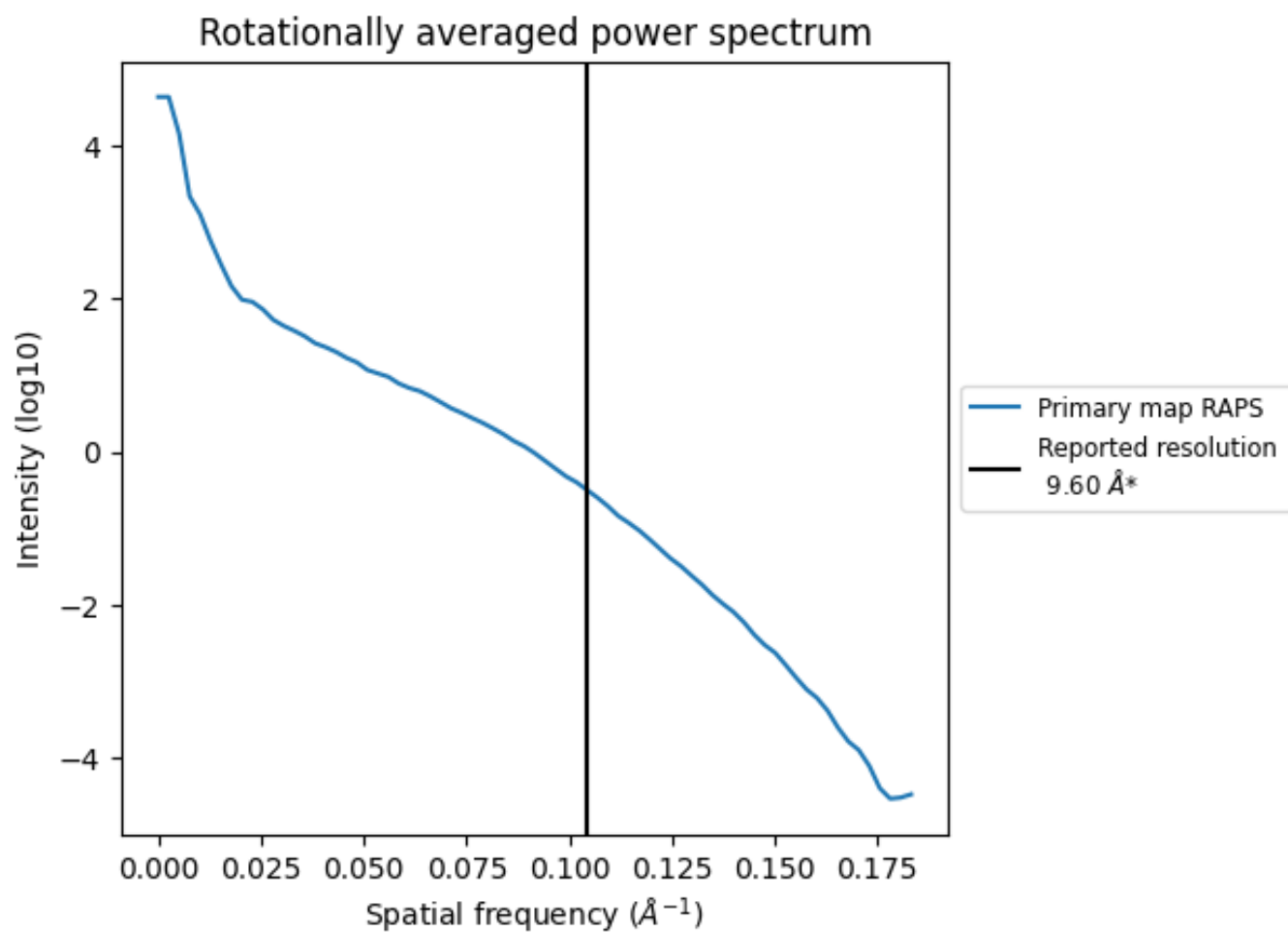
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3544 nm<sup>3</sup>; this corresponds to an approximate mass of 3201 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 0.104 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

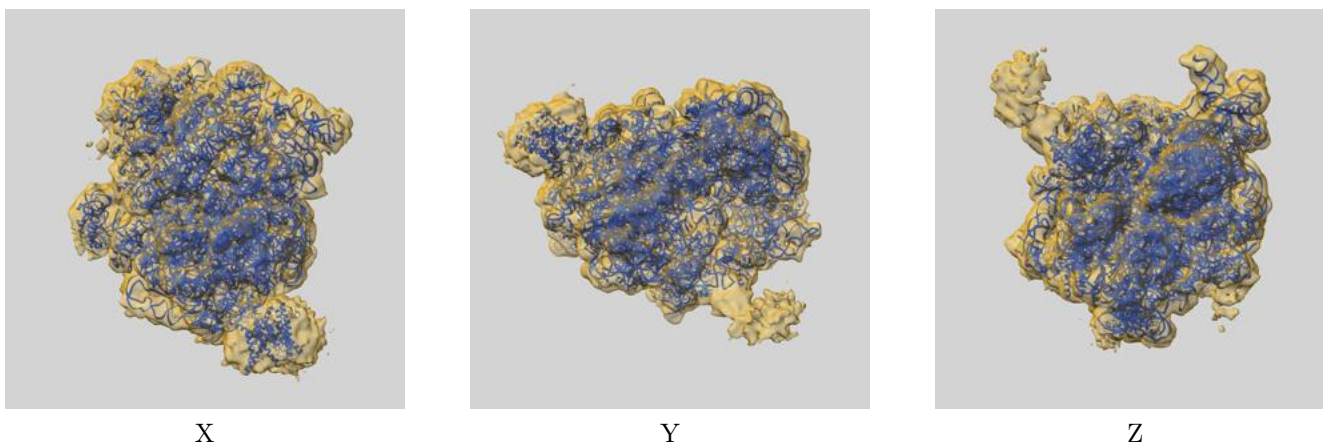
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

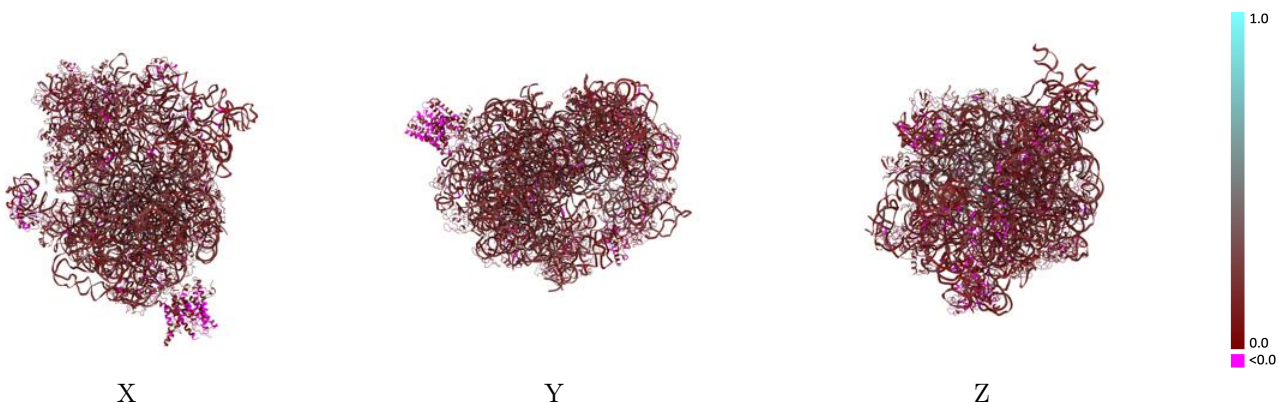
This section contains information regarding the fit between EMDB map EMD-1484 and PDB model 4V7I. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay [i](#)



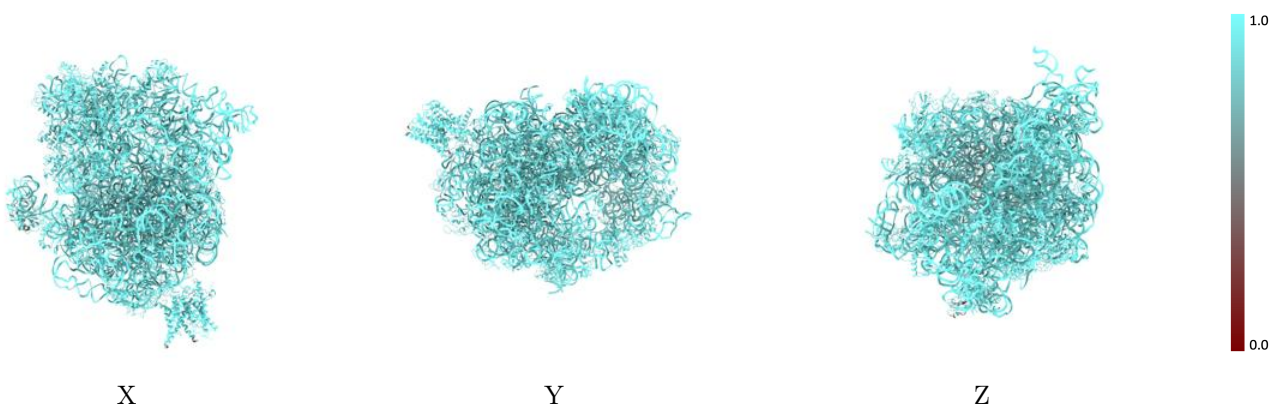
The images above show the 3D surface view of the map at the recommended contour level 0.95 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



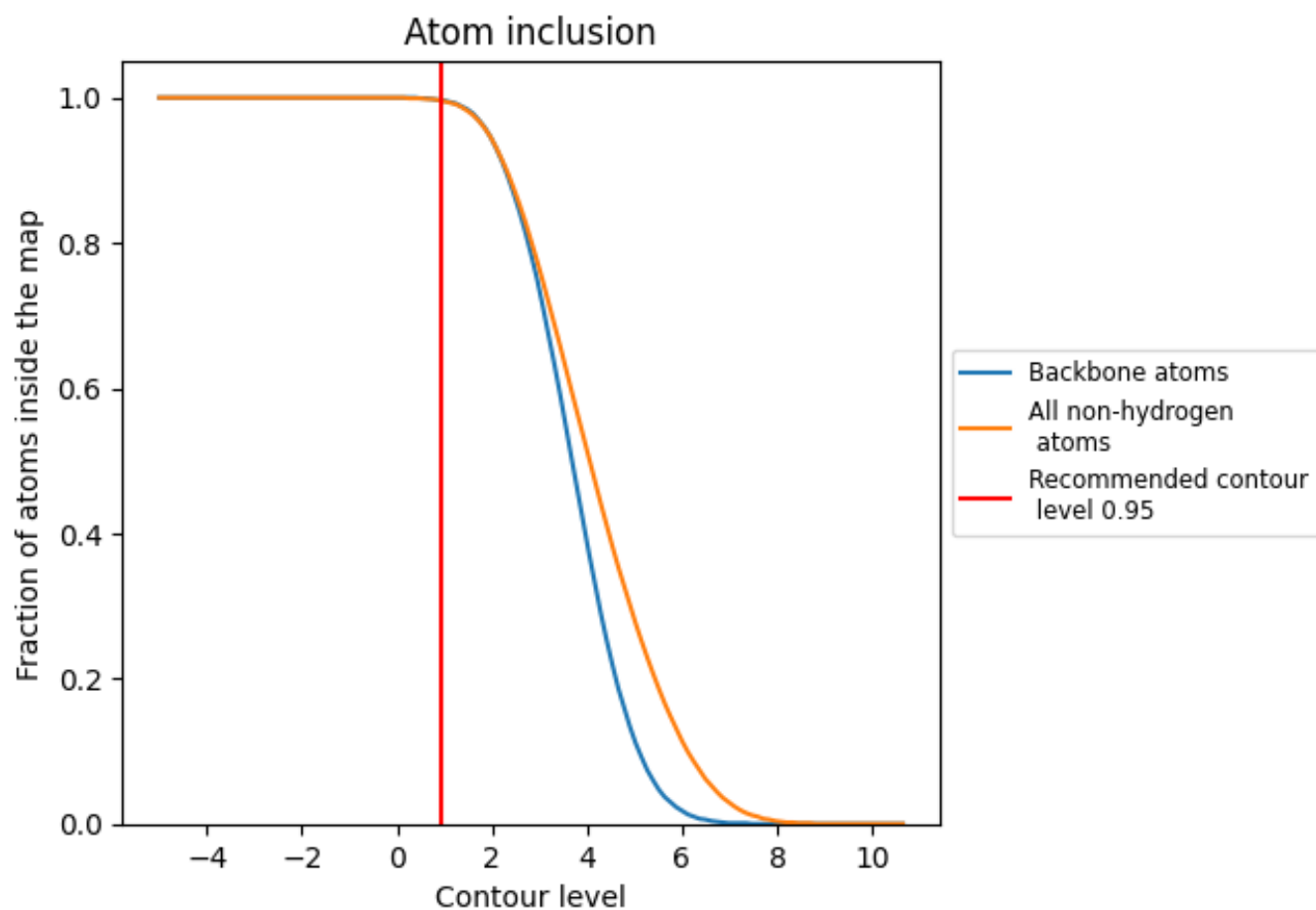
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.95).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.95) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9960	 0.1610
A0	 0.9950	 0.1140
A1	 0.9950	 0.1310
A2	 0.9970	 0.1410
A3	 0.9780	 0.1300
A4	 0.9900	 0.1310
A5	 0.9080	 0.0820
A6	 0.9910	 0.1380
A7	 1.0000	 0.1830
A8	 0.9990	 0.1810
AA	 0.9710	 0.0740
AB	 0.9620	 0.1110
AC	 0.9920	 0.0350
AD	 0.9920	 0.1380
AE	 0.9990	 0.1290
AF	 0.9980	 0.1540
AG	 0.9990	 0.1610
AH	 0.9720	 0.1580
AI	 1.0000	 0.1010
AJ	 0.9890	 0.1590
AK	 0.9740	 0.1580
AL	 0.9940	 0.1270
AM	 0.9850	 0.1460
AN	 0.9980	 0.1410
AO	 0.9980	 0.1320
AP	 0.9930	 0.1520
AQ	 0.9900	 0.1300
AR	 0.9940	 0.1480
AS	 0.9950	 0.1460
AT	 0.9970	 0.1290
AU	 0.9880	 0.1180
AV	 0.9970	 0.1550
AW	 0.9930	 0.1240
AX	 0.9900	 0.1590
AY	 1.0000	 0.1390



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Chain	Atom inclusion	Q-score
AZ	 0.9930	 0.1470
BA	 1.0000	 0.1710
BB	 0.9980	 0.1530
BC	 0.9960	 0.1200
BD	 0.9980	 0.1150
BE	 0.9980	 0.1280
BF	 0.9990	 0.1650
BG	 0.9960	 0.1350
BH	 0.9940	 0.1440
BI	 1.0000	 0.1030
BJ	 0.9970	 0.0880
BK	 0.9980	 0.1390
BL	 0.9860	 0.1320
BM	 0.9950	 0.1580
BN	 0.9970	 0.0940
BO	 0.9940	 0.1470
BP	 1.0000	 0.0910
BQ	 1.0000	 0.1400
BR	 1.0000	 0.1580
BS	 1.0000	 0.0920
BT	 0.9990	 0.1380
BU	 1.0000	 0.1930