



wwPDB EM Validation Summary Report ⓘ

Apr 29, 2024 – 06:38 am BST

PDB ID : 4V5H
EMDB ID : EMD-1657
Title : E.Coli 70s Ribosome Stalled During Translation Of Tnac Leader Peptide.
Authors : Seidelt, B.; Innis, C.A.; Wilson, D.N.; Gartmann, M.; Armache, J.; Villa, E.;
Trabuco, L.G.; Becker, T.; Mielke, T.; Schulten, K.; Steitz, T.A.; Beckmann,
R.
Deposited on : 2009-10-26
Resolution : 5.80 Å(reported)
Based on initial models : 3FIH, 3FIK

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
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

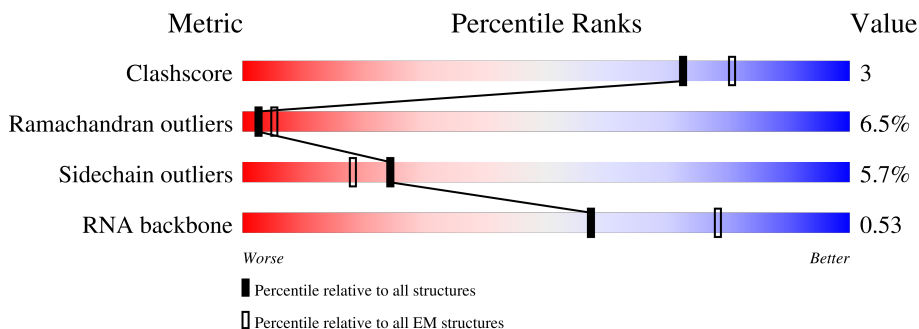
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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)
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 ≥ 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	AA	1530	
2	AB	218	
3	AC	206	
4	AD	205	
5	AE	150	
6	AF	100	
7	AG	150	

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Mol	Chain	Length	Quality of chain
8	AH	129	29% 71% 26%
9	AI	127	38% 59% 33% 7%
10	AJ	98	65% 54% 42%
11	AK	117	30% 70% 26%
12	AL	123	37% 66% 25% 8%
13	AM	113	28% 60% 28% 9%
14	AN	96	27% 64% 27% 9%
15	AO	88	28% 67% 25% 7%
16	AP	80	39% 64% 32%
17	AQ	80	25% 65% 26% 8%
18	AR	55	20% 64% 27% 9%
19	AS	79	25% 59% 30% 10%
20	AT	85	31% 73% 22%
21	AU	51	57% 65% 27% 8%
22	AV	77	26% 58% 29% 13%
23	AX	11	64% 9% 18% 27% 45%
24	AZ	20	55% 80% 20%
25	B0	77	26% 70% 25% 5%
26	B1	63	25% 65% 32%
27	B2	58	22% 76% 24%
28	B3	56	32% 66% 25% 7%
29	B4	50	26% 66% 30%
30	B5	234	99% 77% 20%
31	B6	46	37% 59% 20% 20%
32	B7	64	23% 59% 39%

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Mol	Chain	Length	Quality of chain
33	B8	38	21% 76% 24%
34	BA	117	42% 43% 14%
35	BB	2903	38% 45% 17%
36	BC	271	27% 68% 25% 6%
37	BD	209	20% 67% 23% 8%
38	BE	201	39% 66% 27% 6%
39	BF	178	22% 63% 26% 10%
40	BG	176	14% 72% 22% 6%
41	BH	149	71% 74% 21% 5%
42	BI	141	75% 35% 59% 6%
43	BJ	142	18% 69% 21% 8%
44	BK	121	33% 64% 26% 8%
45	BL	143	30% 67% 29%
46	BM	136	24% 68% 29%
47	BN	120	26% 67% 27% 7%
48	BO	116	20% 74% 22%
49	BP	114	27% 68% 25% 7%
50	BQ	117	22% 60% 31% 7%
51	BR	103	17% 59% 32% 7%
52	BS	110	25% 61% 27% 12%
53	BT	93	37% 56% 39% 5%
54	BU	102	19% 62% 26% 6%
55	BW	94	16% 61% 31% 7%
56	BY	79	32% 63% 27% 6%

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 145960 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 RIBOSOMAL RNA.

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

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AG	150	1174	730	226	214	4	0	0

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AJ	98	786	493	150	142	1	0	0

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AK	117	877	540	174	160	3	0	0

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AM	113	876	541	177	155	3	0	0

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S21.

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

- Molecule 22 is a RNA chain called P-SITE TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0
			1649	733	297	542	77		

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	11	Total	C	N	O	P	0	0
			236	106	46	73	11		

- Molecule 24 is a protein called POLY-ALA NASCENT CHAIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	AZ	20	Total	C	N	O	0	0
			100	60	20	20		

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B1	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	B4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	115	Total	C	N	O	P	0	0
			2464	1097	451	801	115		

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

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

- Molecule 36 is a protein called 50S RIBOSOMAL PROTEIN L2.

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

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L3.

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

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L4.

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

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L5.

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

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BG	175	1316	827	242	245	2	0	0

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L9.

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

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L11.

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

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L13.

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

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BK	121	930	582	179	163	6	0	0

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L15.

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

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L16.

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

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L17.

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

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L18.

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

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L19.

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

- Molecule 50 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BQ	117	947	604	192	151		0	0

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L21.

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

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L23.

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

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	BU	99	755	479	140	136		0	0

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L25.

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

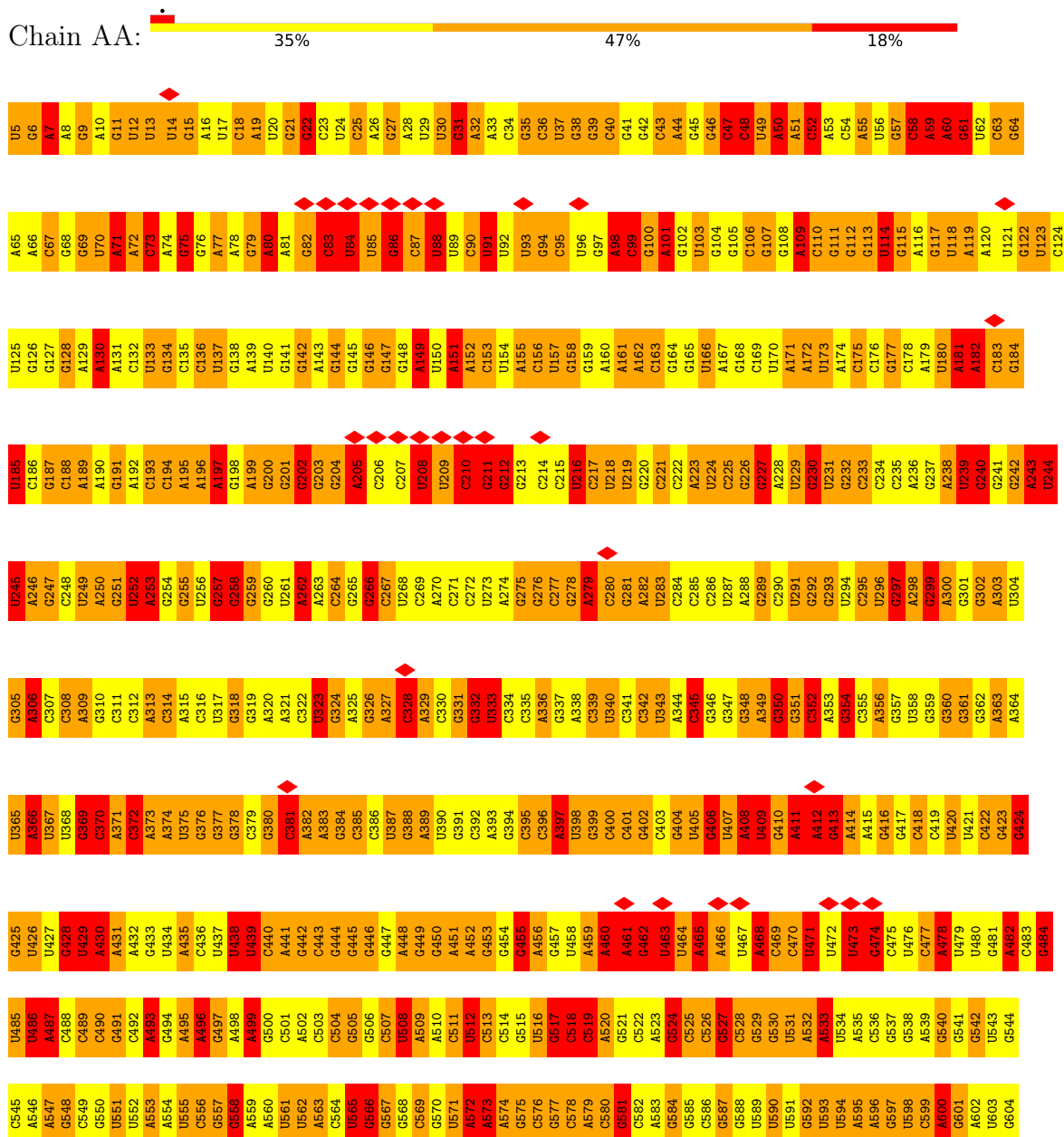
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	BY	79	596	367	120	108	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.

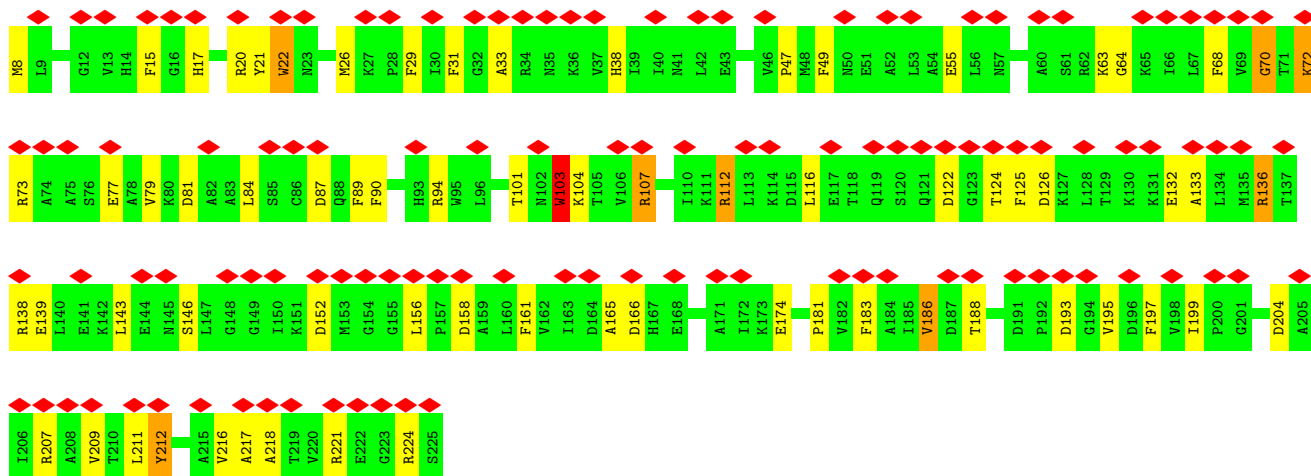
- Molecule 1: 16S RIBOSOMAL RNA



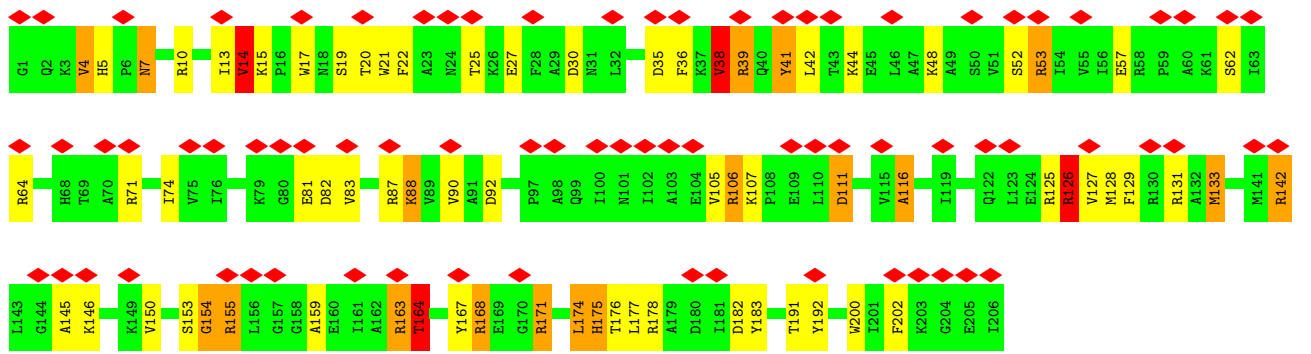
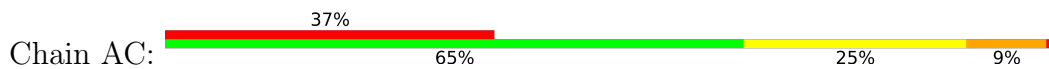
U1445	A1446	A1447	C1448	C1449	U1450	U1451	C1452	G1453	G1454	G1455	A1456	G1457	G1458	G1459	C1460	G1461	C1462	U1463	U1464	A1465	C1466	C1467	A1468	C1469	U1470	U1471	U1472	G1473	U1474	G1475	U1476	U1477	U1478	U1479	A1480	U1481	A1482	A1483	C1484	U1485	G1486	G1487	G1488	G1489	U1490	U1491	A1492	A1493	G1494	U1495	C1496	G1497	U1498	A1499	A1500	C1501	A1502	A1503	G1504
U1205	G1206	G1207	C1208	C1209	U1210	U1211	U1212	C1213	C1214	G1215	U1216	C1217	C1218	U1219	G1220	G1221	G1222	C1223	U1224	A1225	C1226	A1227	C1228	A1229	C1230	G1231	U1232	G1233	C1234	U1235	C1236	U1237	A1238	A1239	U1240	G1241	G1242	C1243	G1244	C1245	U1246	U1247	A1248	G1249	A1250	A1251	A1252	G1253	A1254	G1255	A1256	U1257	G1258	C1259	G1260	A1261	C1262	C1263	U1264
C1265	G1266	C1267	G1268	U1269	G1270	A1271	C1272	C1273	A1274	A1275	G1276	G1277	G1278	G1279	A1280	C1281	U1282	U1283	C1284	U1285	A1286	A1287	A1288	A1289	U1290	U1291	C1292	C1293	G1294	U1295	C1296	G1297	U1298	U1299	G1300	U1301	C1302	C1303	G1304	G1305	A1306	U1307	U1308	G1309	U1310	A1311	G1312	U1313	G1314	U1315	U1316	G1317	C1318	A1319	U1320	U1321	A1322	C1323	A1324
C1325	U1326	C1327	G1328	U1329	U1330	G1331	A1332	C1333	G1334	U1335	C1336	G1337	G1338	A1339	A1340	U1341	C1342	G1343	C1344	U1345	A1346	A1347	U1348	U1349	A1350	U1351	C1352	C1353	U1354	G1355	C1356	U1357	C1358	C1359	A1360	G1361	U1362	A1363	U1364	G1365	C1366	C1367	U1368	C1369	G1370	U1371	U1372	G1373	A1374	U1375	U1376	A1377	C1378	U1379	U1380	U1381	C1382	C1383	G1384
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U1445	A1446	A1447	C1448	C1449	U1450	U1451	C1452	G1453	G1454	G1455	A1456	G1457	G1458	G1459	C1460	G1461	C1462	U1463	U1464	A1465	C1466	C1467	A1468	C1469	U1470	U1471	U1472	G1473	U1474	G1475	U1476	U1477	U1478	U1479	A1480	U1481	A1482	A1483	C1484	U1485	G1486	G1487	G1488	G1489	U1490	U1491	A1492	A1493	G1494	U1495	C1496	G1497	U1498	A1499	A1500	C1501	A1502	A1503	G1504
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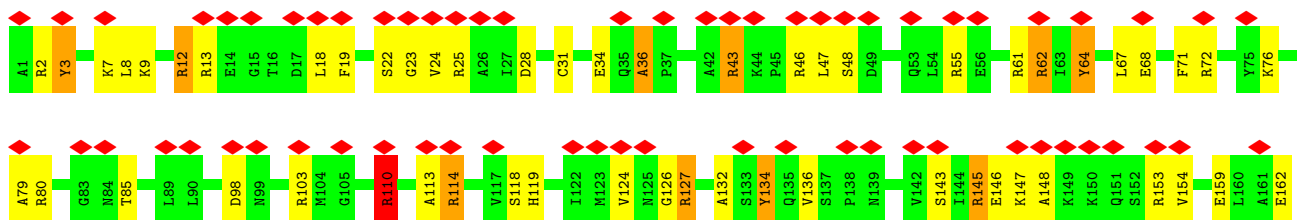
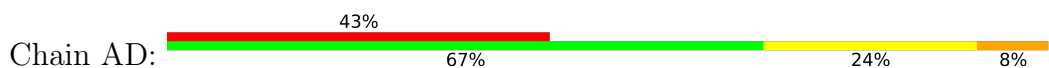
• Molecule 2: 30S RIBOSOMAL PROTEIN S2

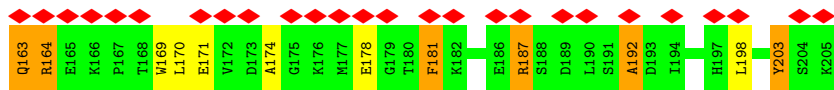


• Molecule 3: 30S RIBOSOMAL PROTEIN S3

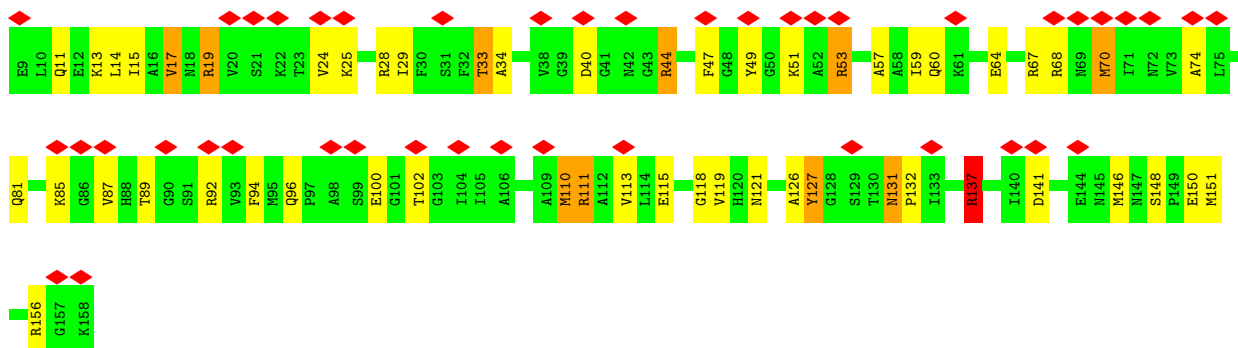


• Molecule 4: 30S RIBOSOMAL PROTEIN S4

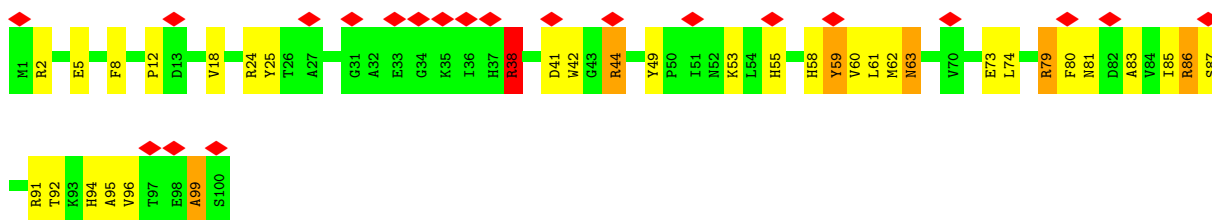




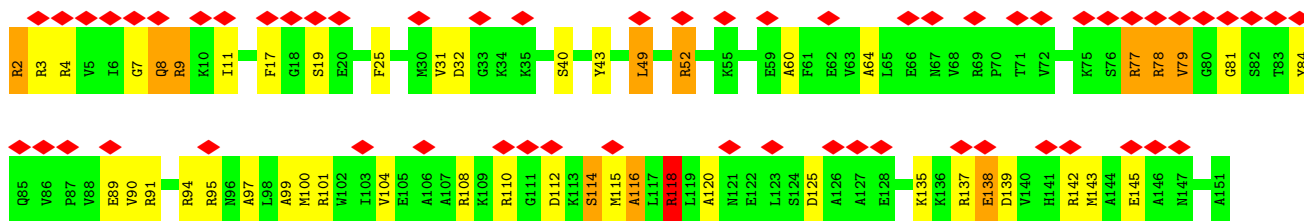
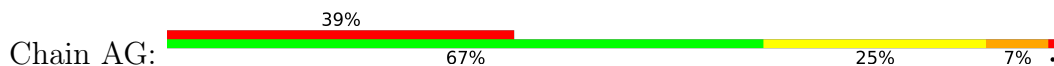
• Molecule 5: 30S RIBOSOMAL PROTEIN S5



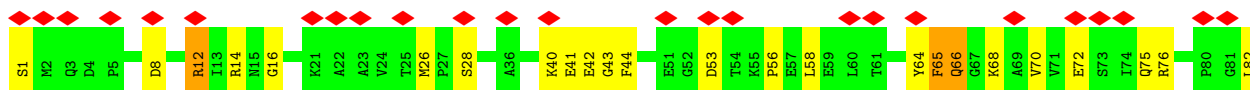
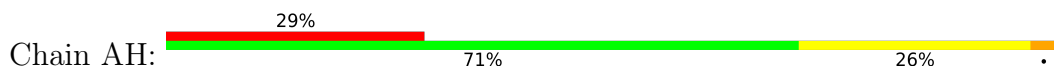
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

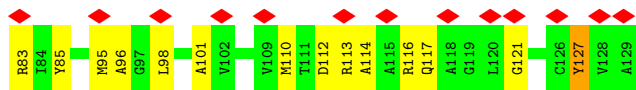


• Molecule 7: 30S RIBOSOMAL PROTEIN S7

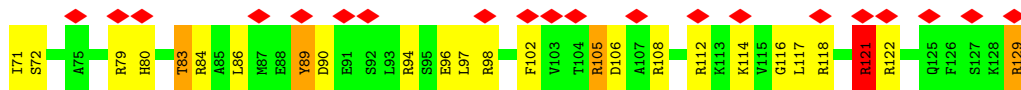
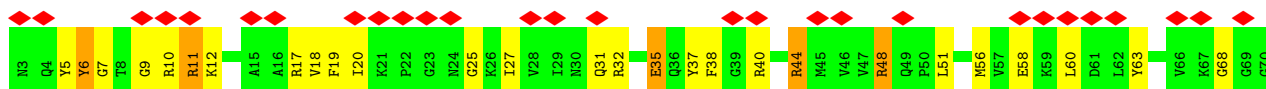
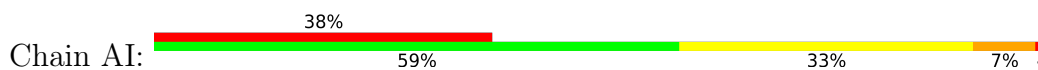


• Molecule 8: 30S RIBOSOMAL PROTEIN S8

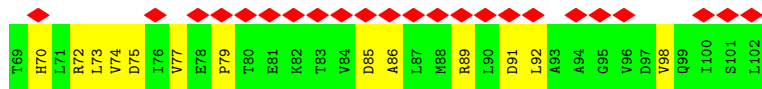




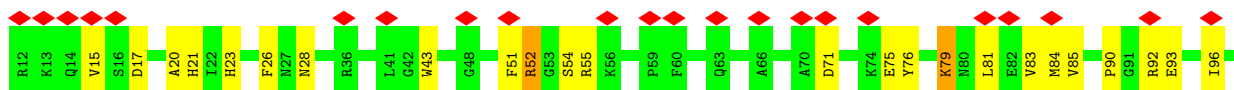
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



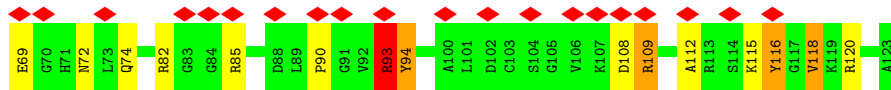
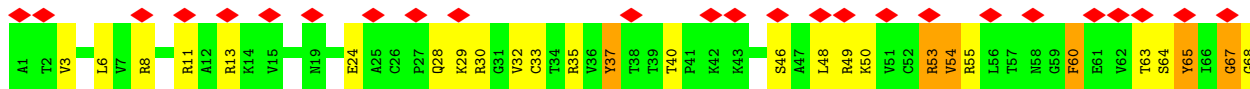
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



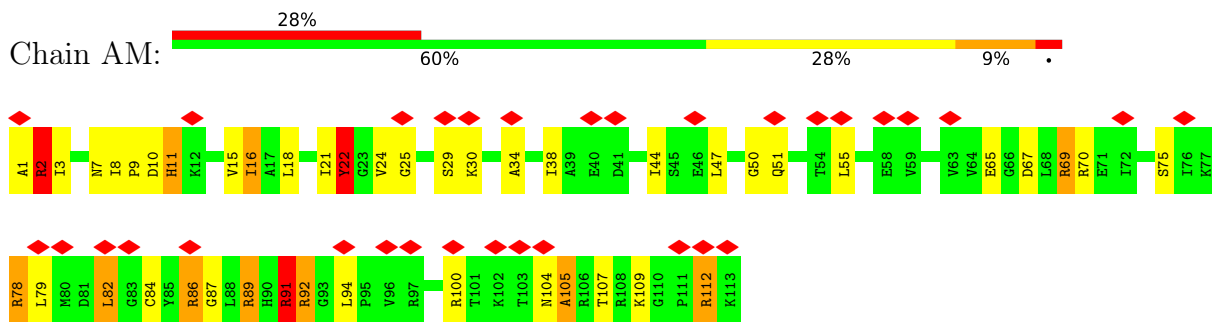
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



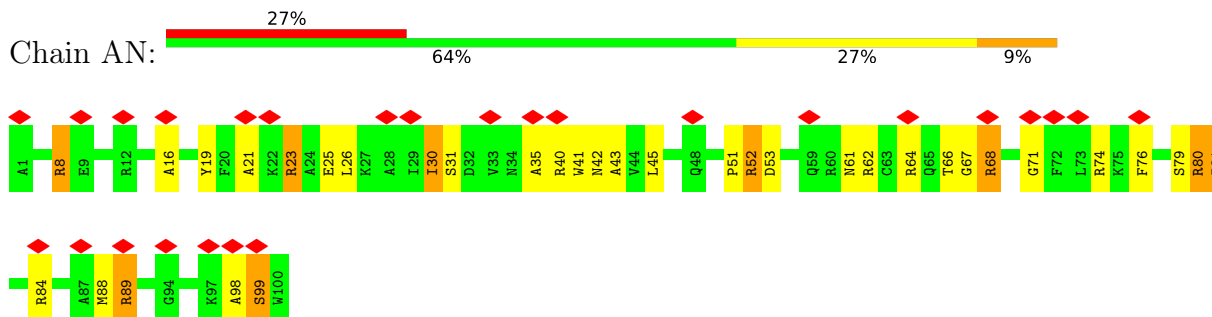
• Molecule 12: 30S RIBOSOMAL PROTEIN S12



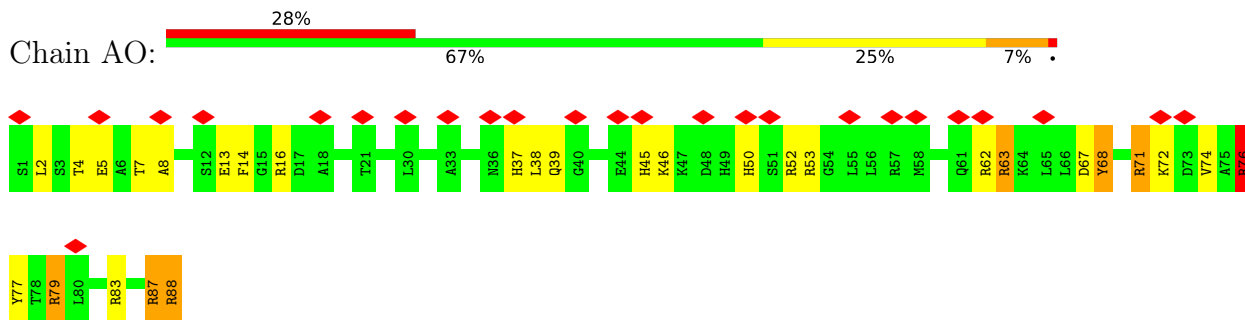
• Molecule 13: 30S RIBOSOMAL PROTEIN S13



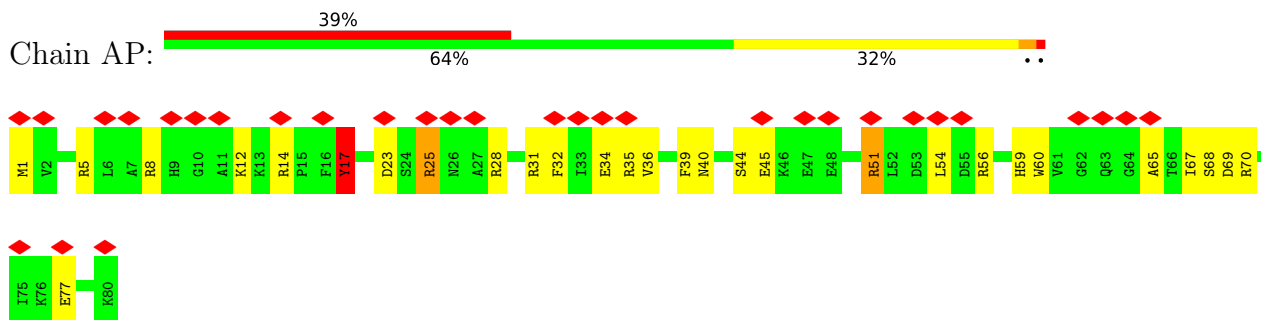
• Molecule 14: 30S RIBOSOMAL PROTEIN S14



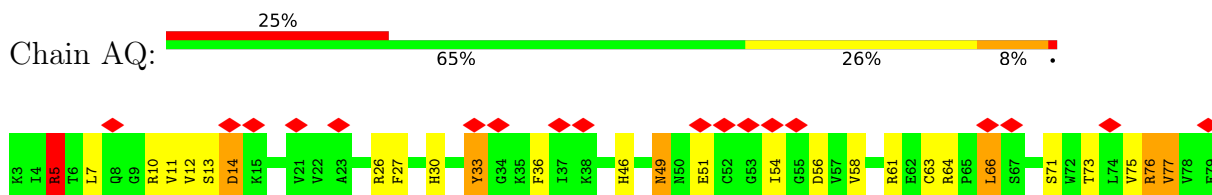
• Molecule 15: 30S RIBOSOMAL PROTEIN S15



• Molecule 16: 30S RIBOSOMAL PROTEIN S16



• Molecule 17: 30S RIBOSOMAL PROTEIN S17

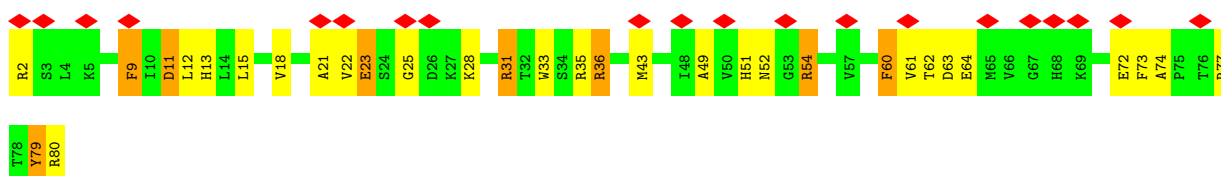




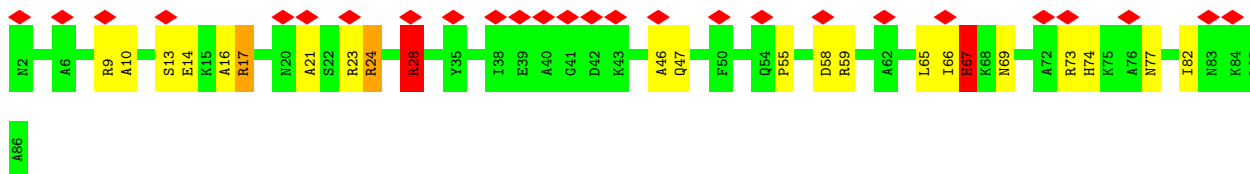
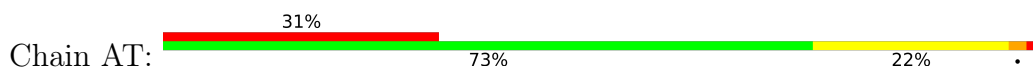
- Molecule 18: 30S RIBOSOMAL PROTEIN S18



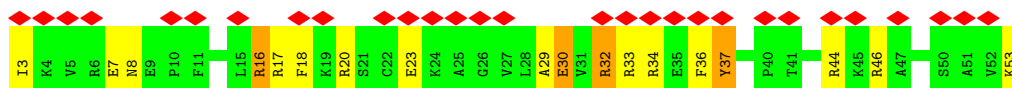
- Molecule 19: 30S RIBOSOMAL PROTEIN S19



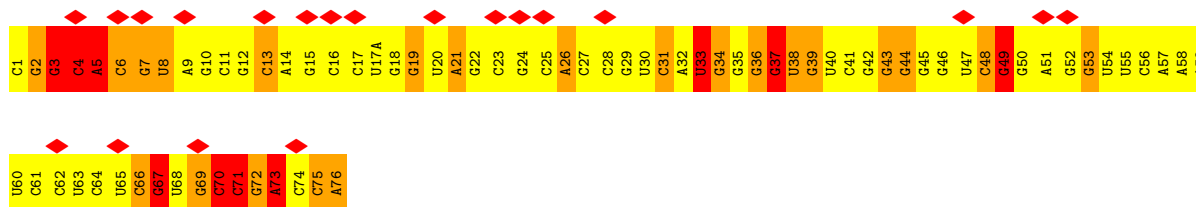
- Molecule 20: 30S RIBOSOMAL PROTEIN S20



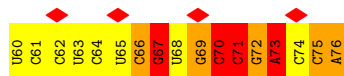
- Molecule 21: 30S RIBOSOMAL PROTEIN S21

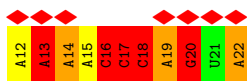
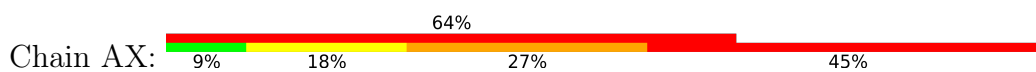


- Molecule 22: P-SITE TRNA

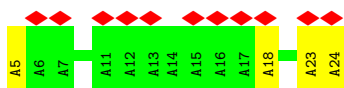
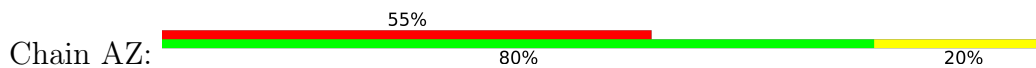


- Molecule 23: MRNA

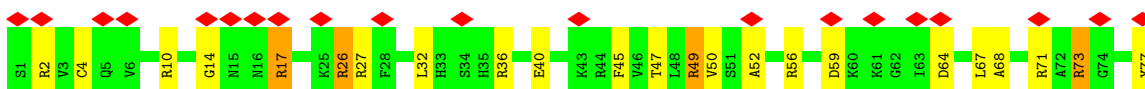
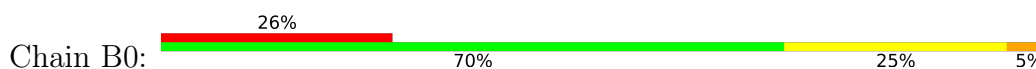




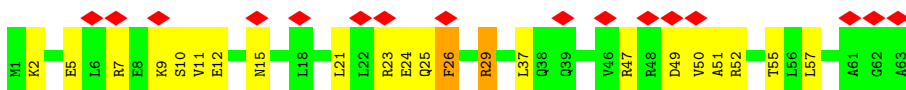
- Molecule 24: POLY-ALA NASCENT CHAIN



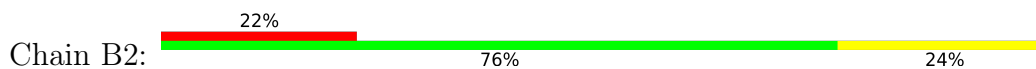
- Molecule 25: 50S RIBOSOMAL PROTEIN L28



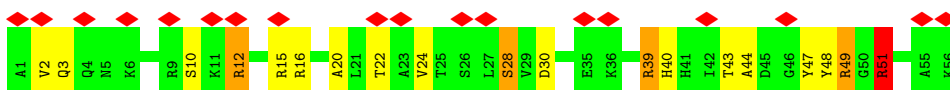
- Molecule 26: 50S RIBOSOMAL PROTEIN L29



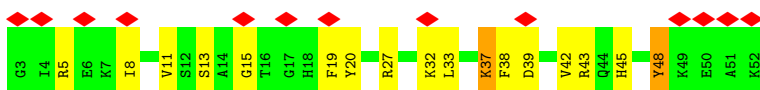
- Molecule 27: 50S RIBOSOMAL PROTEIN L30



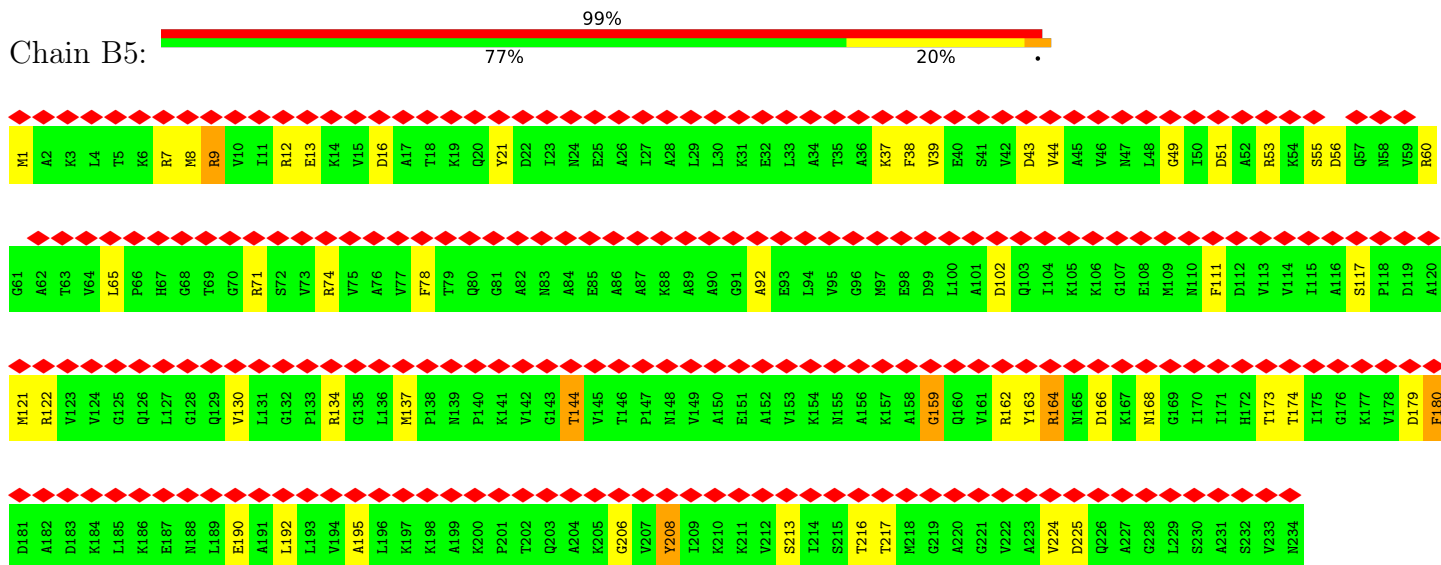
- Molecule 28: 50S RIBOSOMAL PROTEIN L32



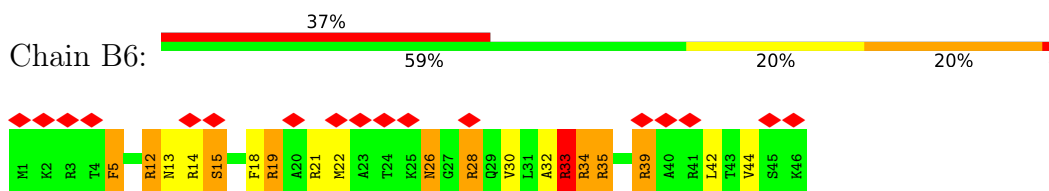
- Molecule 29: 50S RIBOSOMAL PROTEIN L33



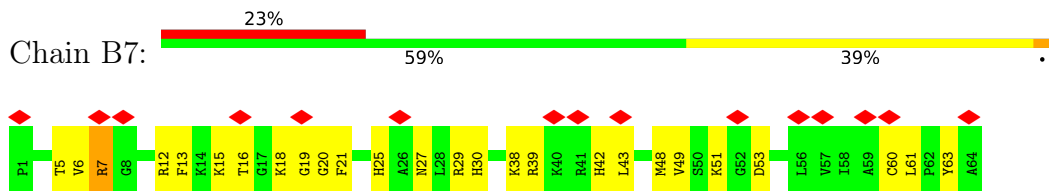
• Molecule 30: 50S RIBOSOMAL PROTEIN L1



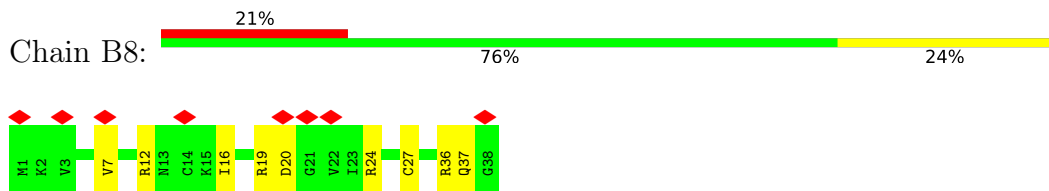
• Molecule 31: 50S RIBOSOMAL PROTEIN L34



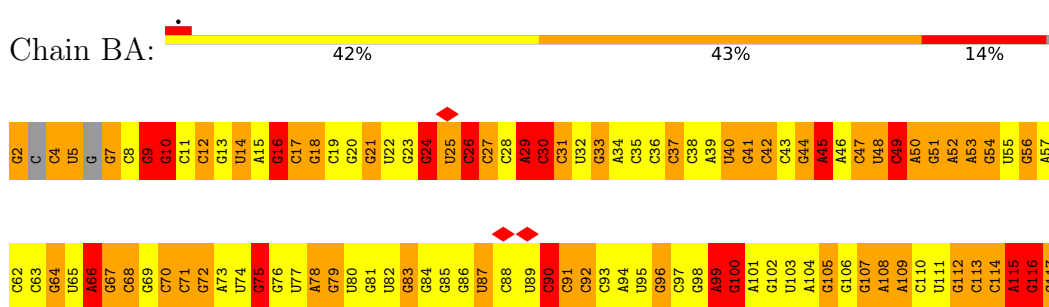
• Molecule 32: 50S RIBOSOMAL PROTEIN L35



• Molecule 33: 50S RIBOSOMAL PROTEIN L36



• Molecule 34: 5S RIBOSOMAL RNA



• Molecule 35: 23S RIBOSOMAL RNA

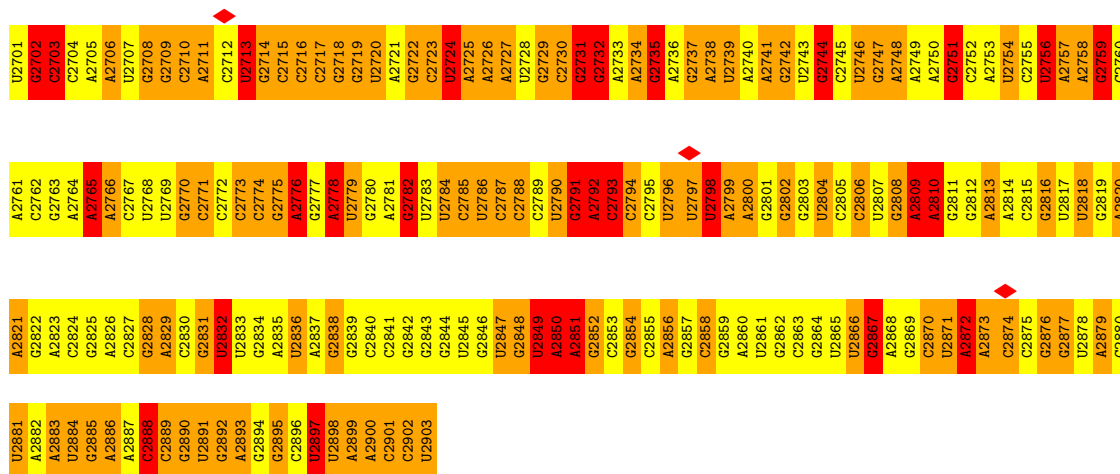
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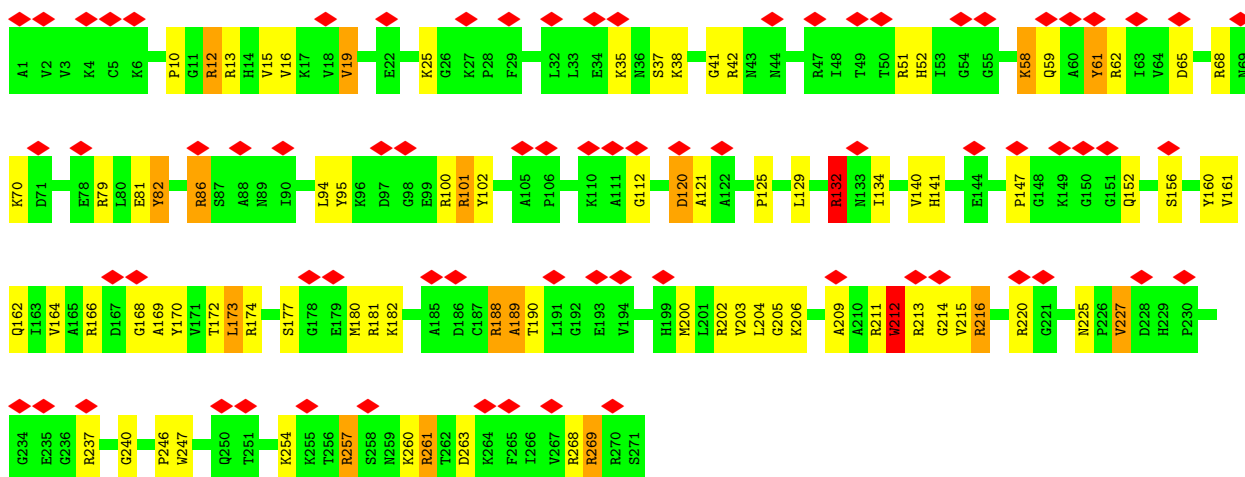
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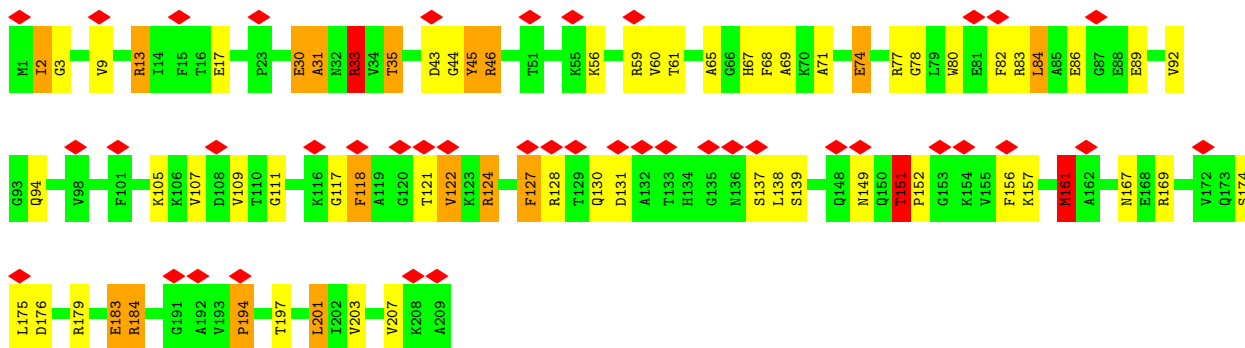
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U2041	A2042	C2043	C2044	C2045	G2046	C2047	G2048	G2049	C2050	U2051	U2052	G2053	A2054	C2055	G2056	G2057	A2058	A2059	A2060	G2061	C2062	C2063	G2064	C2065	C2066	G2067	U2068	C2069	A2070	A2071	U2072	U2073	U2074	U2075	U2076	U2077	U2078	A2081	C2082	C2083	C2084	U2085	U2086	G2087	A2088	C2089	A2090	C2091	G2092	G2093	A2094	C2095	C2096	A2097	U2098	U2099	G2100				
A1981	U1982	G1983	G1984	C1985	U1986	A1987	G1988	G1989	C1990	U1991	G1992	U1993	C1994	U1995	C1996	C1997	A1998	C1999	C2000	C2001	G2002	C2003	G2004	A2005	C2006	U2007	C2008	A2009	G2010	U2011	G2012	A2013	A2014	A2015	U2016	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	A2033	U2034	A2035	C2036	A2037	U2038	U2039	G2040		
G1861	G1862	G1863	U1864	U1865	U1866	G1867	C1868	G1869	C1870	A1871	A1872	G1873	C1874	G1875	A1876	A1877	G1878	C1879	U1880	C1881	U1882	U1883	G1884	A1885	U1886	C1887	U1888	A1889	G1890	A1891	C1892	C1893	A1894	C1895	C1896	G1897	U1898	A1899	G1900	A1901	C1902	G1903	G1904	C1905	U1906	G1907	C1908	C1909	U1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	A1918	A1919	U1979	C1920	
G1921	G1922	U1923	C1924	U1925	U1926	A1927	U1928	G1929	G1930	U1931	A1932	G1933	C1934	U1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942	U1943	U1944	A1885	U1946	U1947	U1948	U1949	G1949	A1950	U1951	A1952	C1953	A1954	U1955	U1956	C1957	U1958	A1959	C1960	C1961	C1962	U1963	G1964	C1965	A1966	G1967	G1968	A1969	U1970	U1971	G1972	G1973	C1974	G1975	U1976	U1977	A1978	U1979	U1979	G1980



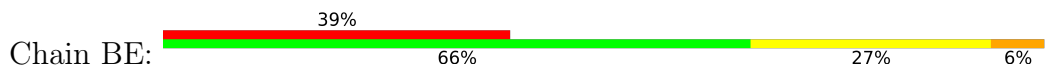
• Molecule 36: 50S RIBOSOMAL PROTEIN L2

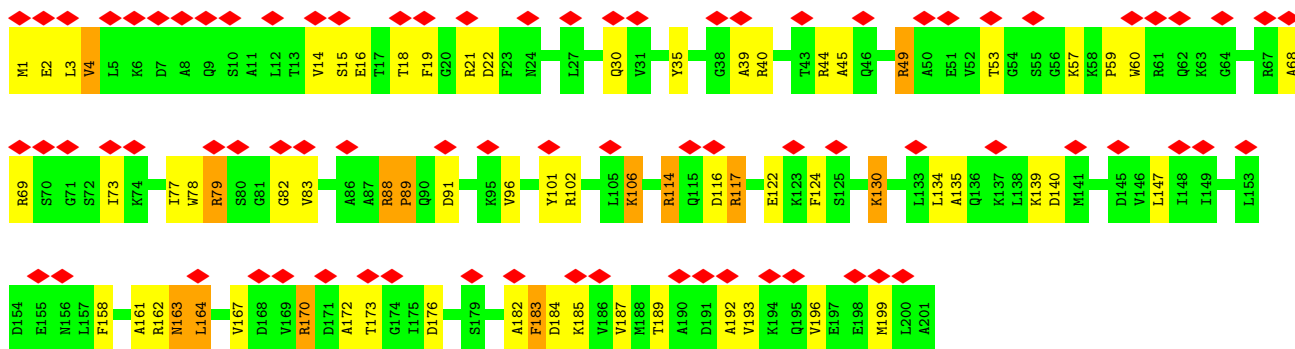


• Molecule 37: 50S RIBOSOMAL PROTEIN L3

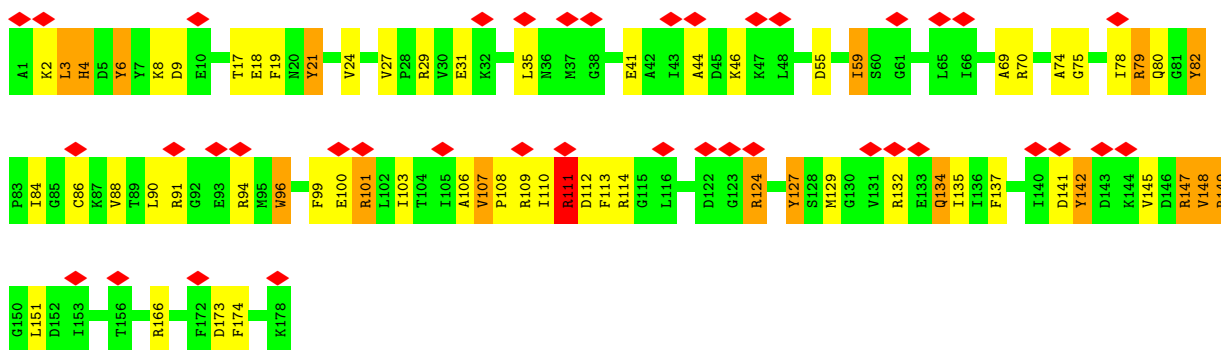


• Molecule 38: 50S RIBOSOMAL PROTEIN L4

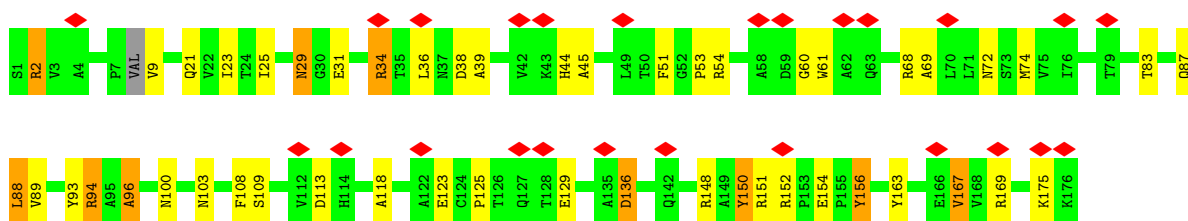
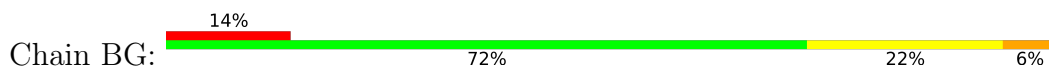




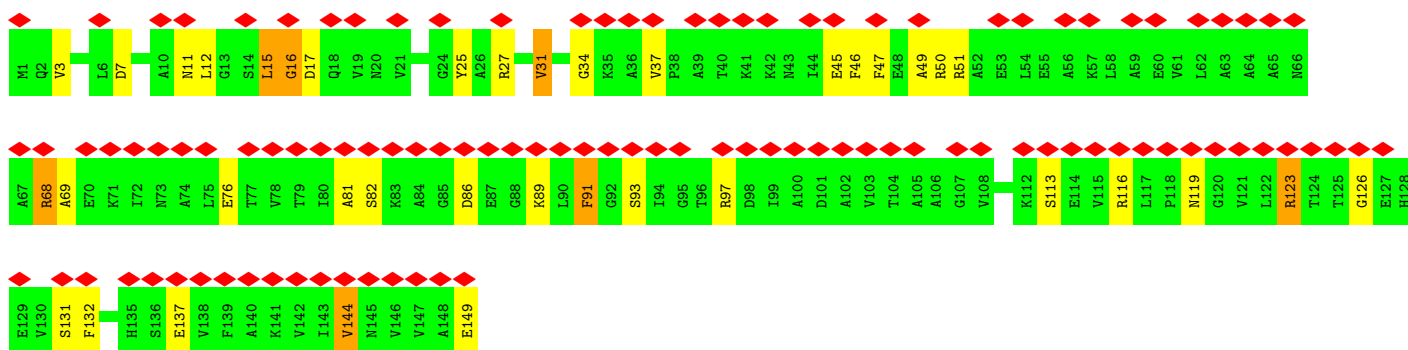
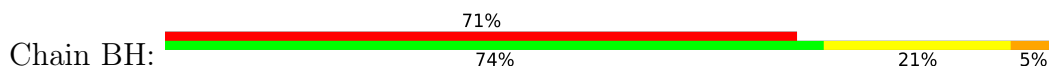
• Molecule 39: 50S RIBOSOMAL PROTEIN L5



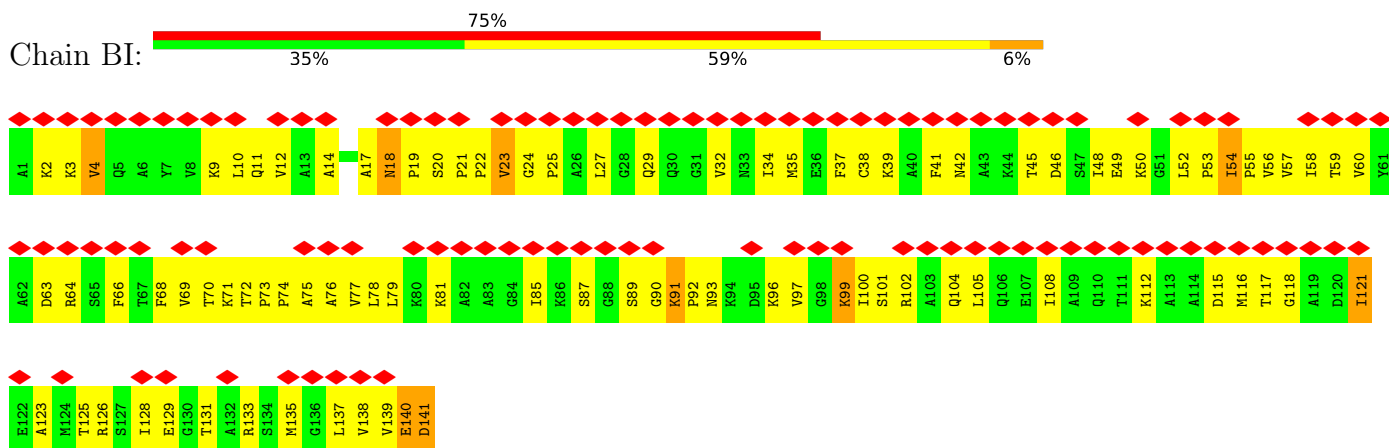
• Molecule 40: 50S RIBOSOMAL PROTEIN L6



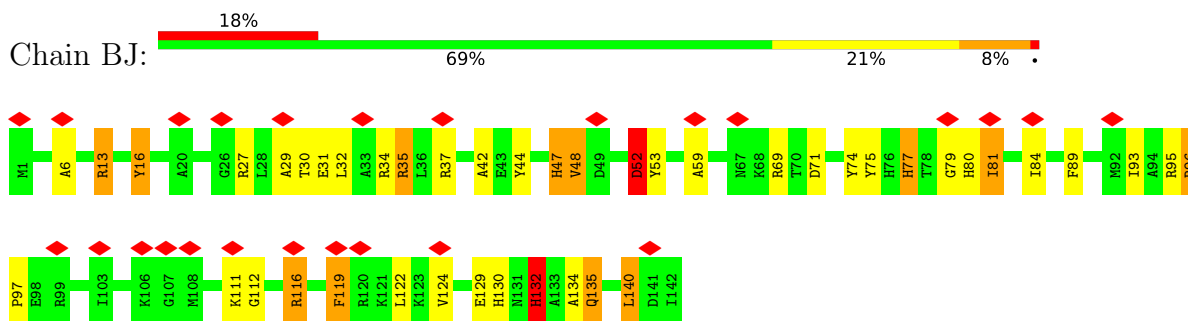
• Molecule 41: 50S RIBOSOMAL PROTEIN L9



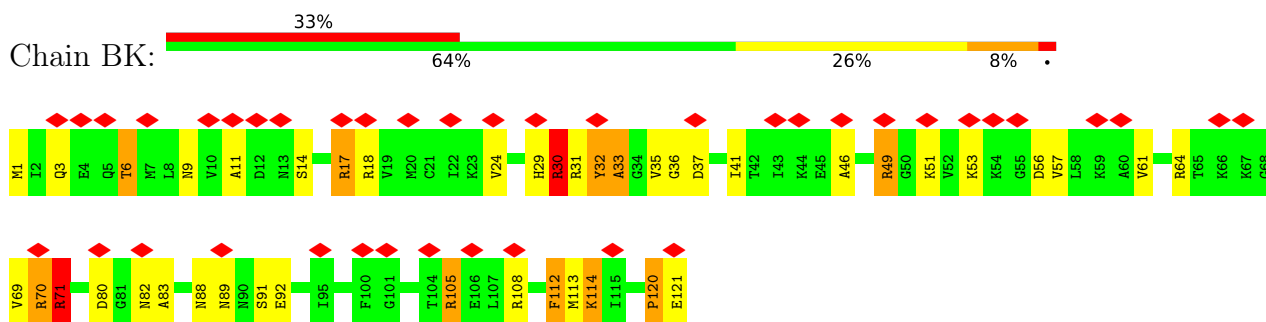
• Molecule 42: 50S RIBOSOMAL PROTEIN L11



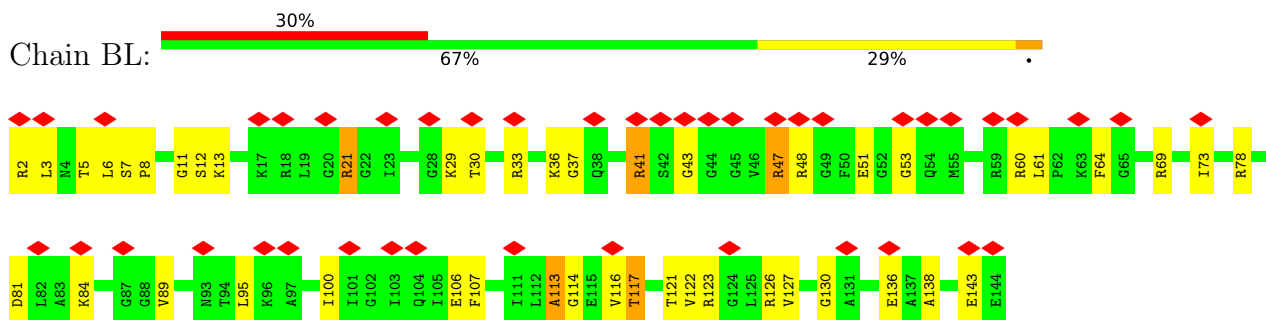
• Molecule 43: 50S RIBOSOMAL PROTEIN L13



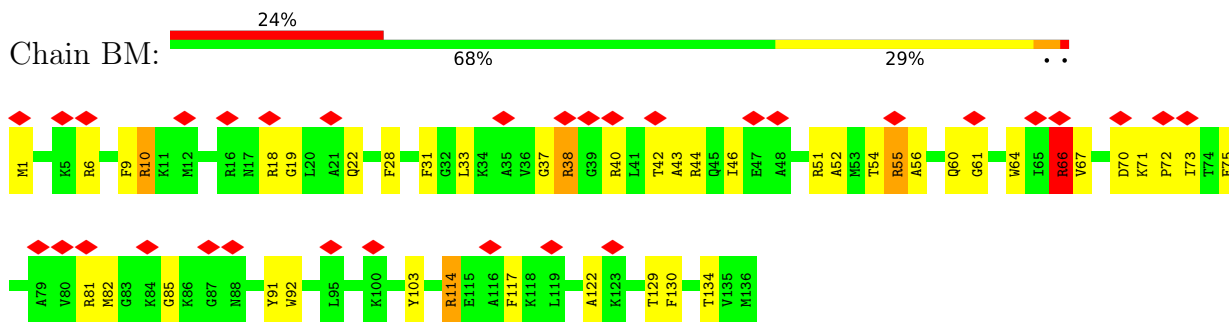
• Molecule 44: 50S RIBOSOMAL PROTEIN L14



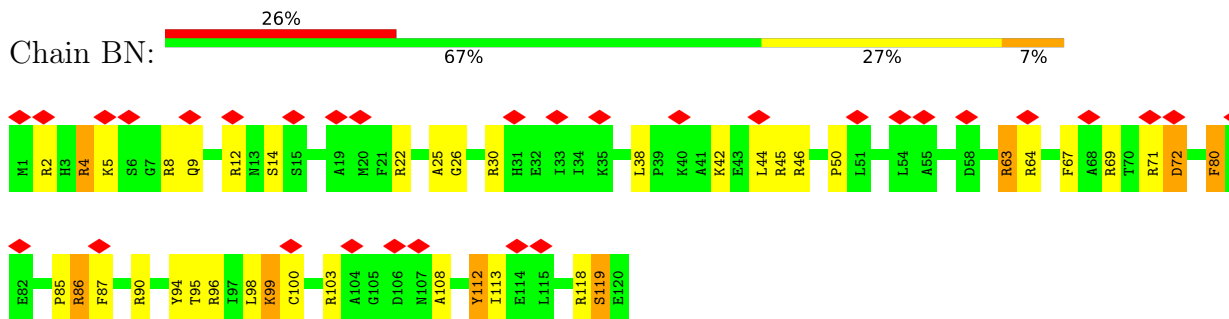
• Molecule 45: 50S RIBOSOMAL PROTEIN L15



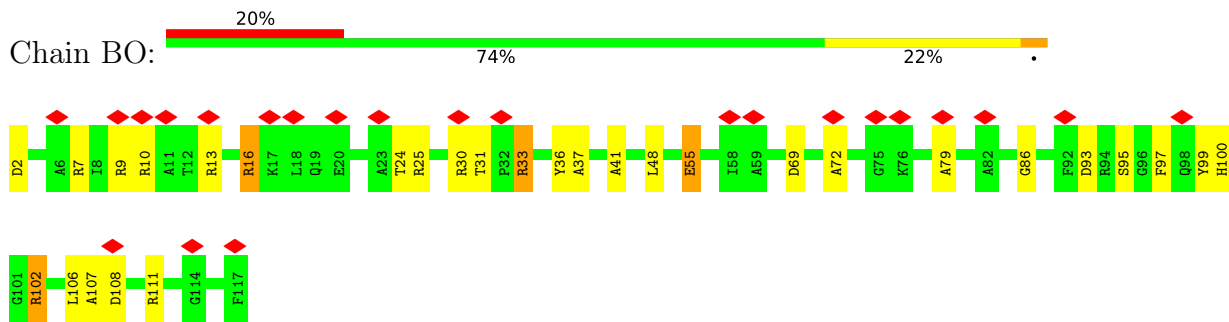
• Molecule 46: 50S RIBOSOMAL PROTEIN L16



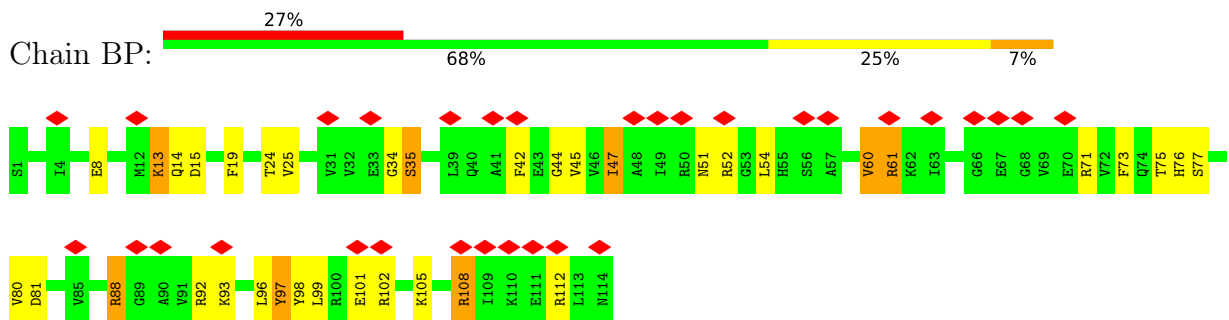
• Molecule 47: 50S RIBOSOMAL PROTEIN L17



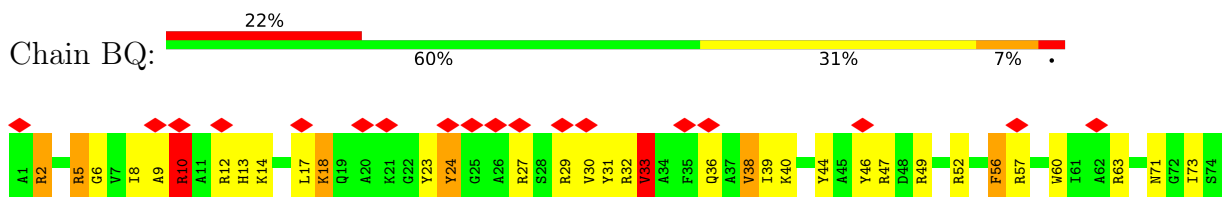
• Molecule 48: 50S RIBOSOMAL PROTEIN L18

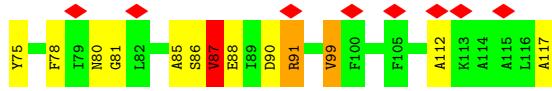


• Molecule 49: 50S RIBOSOMAL PROTEIN L19

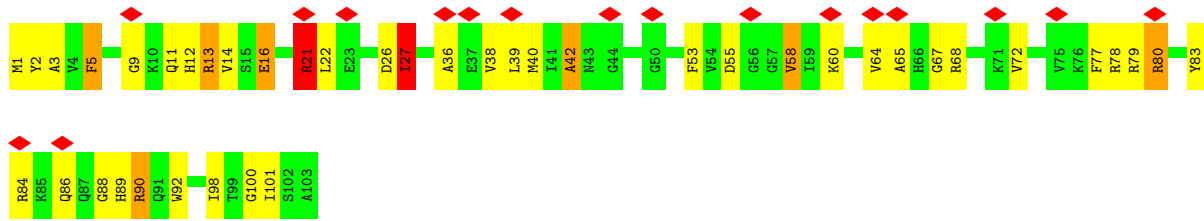


• Molecule 50: 50S RIBOSOMAL PROTEIN L20

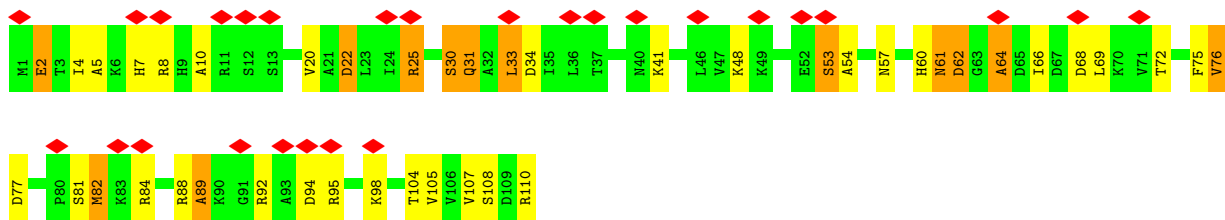




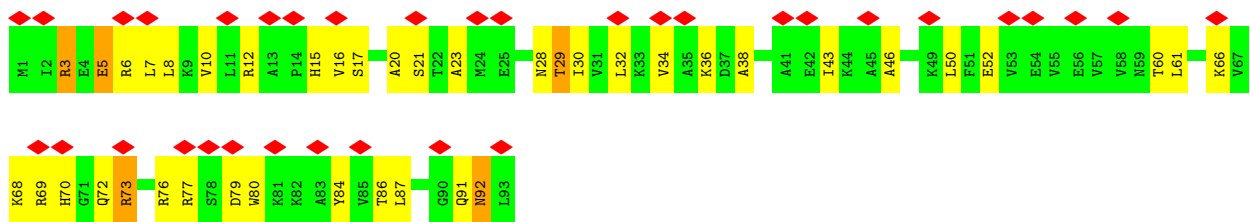
• Molecule 51: 50S RIBOSOMAL PROTEIN L21



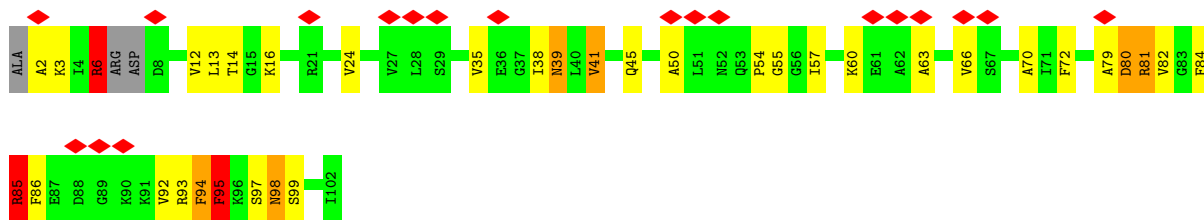
• Molecule 52: 50S RIBOSOMAL PROTEIN L22



• Molecule 53: 50S RIBOSOMAL PROTEIN L23

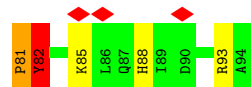
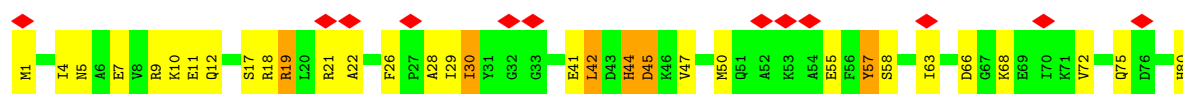


• Molecule 54: 50S RIBOSOMAL PROTEIN L24



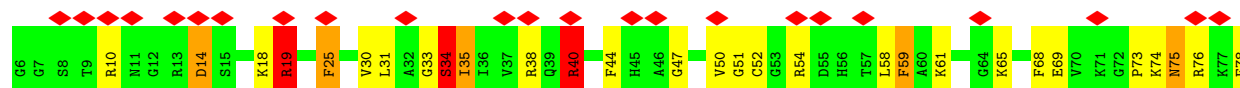
• Molecule 55: 50S RIBOSOMAL PROTEIN L25

Chain BW:  16% 61% 31% 7%



• Molecule 56: 50S RIBOSOMAL PROTEIN L27

Chain BY:  32% 63% 27% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	263000	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP VOLUMES	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	38900	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.760	Depositor
Minimum map value	-0.510	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.12	Depositor
Map size (\AA)	361.62, 363.82498, 361.62	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.23, 1.2375, 1.23	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU

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	AA	3.37	4837/36762 (13.2%)	3.72	8282/57350 (14.4%)
2	AB	1.71	14/1735 (0.8%)	2.05	53/2338 (2.3%)
3	AC	1.73	20/1651 (1.2%)	2.05	55/2225 (2.5%)
4	AD	1.80	24/1665 (1.4%)	2.05	48/2227 (2.2%)
5	AE	1.73	17/1118 (1.5%)	1.97	27/1504 (1.8%)
6	AF	1.77	7/835 (0.8%)	1.96	17/1128 (1.5%)
7	AG	1.82	18/1187 (1.5%)	2.01	40/1591 (2.5%)
8	AH	1.79	10/989 (1.0%)	2.07	29/1326 (2.2%)
9	AI	1.97	21/1034 (2.0%)	2.09	33/1375 (2.4%)
10	AJ	1.78	11/796 (1.4%)	1.89	15/1077 (1.4%)
11	AK	1.75	7/893 (0.8%)	1.96	18/1205 (1.5%)
12	AL	1.85	13/969 (1.3%)	1.98	28/1300 (2.2%)
13	AM	1.73	12/884 (1.4%)	2.02	28/1181 (2.4%)
14	AN	1.80	6/785 (0.8%)	1.92	19/1043 (1.8%)
15	AO	1.77	11/724 (1.5%)	1.90	24/966 (2.5%)
16	AP	1.84	9/648 (1.4%)	2.16	26/870 (3.0%)
17	AQ	1.73	4/657 (0.6%)	1.93	18/881 (2.0%)
18	AR	1.74	6/462 (1.3%)	2.28	16/621 (2.6%)
19	AS	1.78	8/652 (1.2%)	2.15	26/877 (3.0%)
20	AT	1.66	4/671 (0.6%)	1.93	17/888 (1.9%)
21	AU	1.82	6/430 (1.4%)	2.16	13/570 (2.3%)
22	AV	2.38	76/1820 (4.2%)	2.84	256/2836 (9.0%)
23	AX	1.81	4/264 (1.5%)	2.14	19/407 (4.7%)
24	AZ	1.97	1/99 (1.0%)	1.94	5/137 (3.6%)
25	B0	1.75	7/635 (1.1%)	2.27	19/848 (2.2%)
26	B1	1.72	5/510 (1.0%)	1.94	14/677 (2.1%)
27	B2	1.75	4/453 (0.9%)	1.86	10/605 (1.7%)
28	B3	1.82	6/450 (1.3%)	2.19	16/599 (2.7%)
29	B4	1.63	4/416 (1.0%)	2.02	13/554 (2.3%)
30	B5	1.56	11/1748 (0.6%)	1.95	40/2355 (1.7%)
31	B6	1.85	4/380 (1.1%)	2.31	17/498 (3.4%)
32	B7	1.68	4/513 (0.8%)	2.03	12/676 (1.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B8	1.83	4/303 (1.3%)	2.01	7/397 (1.8%)
34	BA	3.34	356/2753 (12.9%)	3.78	615/4288 (14.3%)
35	BB	3.39	9308/69800 (13.3%)	3.73	15832/108892 (14.5%)
36	BC	1.81	24/2121 (1.1%)	2.05	60/2852 (2.1%)
37	BD	1.77	16/1586 (1.0%)	2.01	31/2134 (1.5%)
38	BE	1.69	8/1571 (0.5%)	1.97	41/2113 (1.9%)
39	BF	1.73	14/1444 (1.0%)	2.17	40/1937 (2.1%)
40	BG	1.76	13/1335 (1.0%)	2.04	28/1803 (1.6%)
41	BH	1.74	11/1122 (1.0%)	2.05	35/1515 (2.3%)
42	BI	0.62	2/1046 (0.2%)	0.56	1/1410 (0.1%)
43	BJ	1.77	12/1152 (1.0%)	2.04	30/1551 (1.9%)
44	BK	1.76	13/939 (1.4%)	1.99	23/1257 (1.8%)
45	BL	1.78	10/1054 (0.9%)	1.94	28/1403 (2.0%)
46	BM	1.83	9/1093 (0.8%)	2.07	30/1460 (2.1%)
47	BN	1.76	12/973 (1.2%)	2.22	32/1301 (2.5%)
48	BO	1.79	15/902 (1.7%)	2.02	24/1209 (2.0%)
49	BP	1.68	5/929 (0.5%)	2.03	20/1242 (1.6%)
50	BQ	1.89	15/960 (1.6%)	2.11	29/1278 (2.3%)
51	BR	1.80	11/829 (1.3%)	2.03	23/1107 (2.1%)
52	BS	1.71	7/864 (0.8%)	2.16	34/1156 (2.9%)
53	BT	1.69	5/744 (0.7%)	1.99	18/994 (1.8%)
54	BU	1.73	3/761 (0.4%)	2.02	25/1013 (2.5%)
55	BW	1.79	13/766 (1.7%)	2.05	18/1025 (1.8%)
56	BY	1.73	3/603 (0.5%)	2.11	23/797 (2.9%)
All	All	2.98	15080/158485 (9.5%)	3.34	26300/236869 (11.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	740
2	AB	0	5
3	AC	0	7
4	AD	0	11
5	AE	0	5
6	AF	0	3
7	AG	0	3
8	AH	0	3
9	AI	0	7
10	AJ	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	AK	0	3
12	AL	0	5
13	AM	0	9
14	AN	0	3
15	AO	0	6
16	AP	0	4
17	AQ	0	1
18	AR	0	5
19	AS	0	4
20	AT	0	3
22	AV	0	13
23	AX	0	4
25	B0	0	4
26	B1	0	1
28	B3	0	2
29	B4	0	3
30	B5	0	6
31	B6	0	3
32	B7	0	1
34	BA	0	50
35	BB	0	1343
36	BC	0	8
37	BD	0	6
38	BE	0	5
39	BF	0	10
40	BG	0	3
41	BH	0	1
43	BJ	0	4
44	BK	0	5
45	BL	0	1
46	BM	0	3
47	BN	0	5
48	BO	0	2
49	BP	0	5
50	BQ	0	5
51	BR	0	3
52	BS	0	1
53	BT	0	1
54	BU	0	2
55	BW	0	4
56	BY	0	5
All	All	0	2342

The worst 5 of 15080 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BB	1403	A	N9-C4	21.34	1.50	1.37
35	BB	1301	A	N7-C5	-20.38	1.27	1.39
1	AA	930	C	N1-C6	19.80	1.49	1.37
1	AA	816	A	N7-C5	-19.29	1.27	1.39
35	BB	1821	A	N9-C4	19.18	1.49	1.37

The worst 5 of 26300 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	753	A	N1-C6-N6	30.52	136.91	118.60
35	BB	666	A	N1-C6-N6	26.10	134.26	118.60
35	BB	533	G	N1-C6-O6	25.90	135.44	119.90
1	AA	242	G	C5-C6-O6	-25.60	113.24	128.60
35	BB	1014	A	N1-C6-N6	25.57	133.94	118.60

There are no chirality outliers.

5 of 2342 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	12	U	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	Sidechain
1	AA	7	A	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	AA	32831	0	16502	183	0
2	AB	1704	0	1732	3	0
3	AC	1624	0	1699	12	0
4	AD	1643	0	1710	5	0
5	AE	1105	0	1148	6	0
6	AF	817	0	808	7	0
7	AG	1174	0	1230	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AH	979	0	1034	1	0
9	AI	1022	0	1070	9	0
10	AJ	786	0	828	3	0
11	AK	877	0	887	9	0
12	AL	955	0	1019	2	0
13	AM	876	0	937	7	0
14	AN	774	0	827	2	0
15	AO	716	0	742	3	0
16	AP	638	0	656	0	0
17	AQ	648	0	691	4	0
18	AR	455	0	478	1	0
19	AS	637	0	665	5	0
20	AT	665	0	714	4	0
21	AU	425	0	449	2	0
22	AV	1649	0	832	21	0
23	AX	236	0	121	10	0
24	AZ	100	0	99	0	0
25	B0	625	0	655	1	0
26	B1	509	0	543	1	0
27	B2	449	0	491	1	0
28	B3	444	0	461	3	0
29	B4	409	0	440	0	0
30	B5	1733	0	1824	4	0
31	B6	377	0	418	3	0
32	B7	504	0	574	5	0
33	B8	302	0	343	0	0
34	BA	2464	0	1246	8	0
35	BB	62321	0	31294	336	0
36	BC	2082	0	2157	14	0
37	BD	1565	0	1616	8	0
38	BE	1552	0	1619	9	0
39	BF	1420	0	1460	9	0
40	BG	1316	0	1364	4	0
41	BH	1111	0	1148	1	0
42	BI	1032	0	1088	118	0
43	BJ	1129	0	1162	8	0
44	BK	930	0	1003	6	0
45	BL	1045	0	1117	6	0
46	BM	1074	0	1157	4	0
47	BN	960	0	1000	2	0
48	BO	892	0	923	2	0
49	BP	917	0	965	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	BQ	947	0	1022	8	0
51	BR	816	0	839	8	0
52	BS	857	0	922	3	0
53	BT	738	0	807	5	0
54	BU	755	0	807	10	0
55	BW	753	0	780	5	0
56	BY	596	0	610	1	0
All	All	145960	0	98733	840	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 3.

The worst 5 of 840 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)
22:AV:35:G:N2	23:AX:18:C:C2	2.08	1.22
42:BI:11:GLN:HG2	42:BI:55:PRO:HB3	1.51	0.91
42:BI:140:GLU:O	42:BI:141:ASP:OXT	1.91	0.89
42:BI:27:LEU:HD23	42:BI:27:LEU:H	1.43	0.82
42:BI:121:ILE:HD13	42:BI:121:ILE:H	1.44	0.82

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	
2	AB	216/218 (99%)	159 (74%)	41 (19%)	16 (7%)	1	13
3	AC	204/206 (99%)	158 (78%)	31 (15%)	15 (7%)	1	13
4	AD	203/205 (99%)	160 (79%)	34 (17%)	9 (4%)	2	22
5	AE	148/150 (99%)	110 (74%)	27 (18%)	11 (7%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AF	98/100 (98%)	73 (74%)	18 (18%)	7 (7%)	1	14
7	AG	148/150 (99%)	109 (74%)	33 (22%)	6 (4%)	3	22
8	AH	127/129 (98%)	94 (74%)	27 (21%)	6 (5%)	2	21
9	AI	125/127 (98%)	99 (79%)	21 (17%)	5 (4%)	3	23
10	AJ	96/98 (98%)	71 (74%)	14 (15%)	11 (12%)	0	6
11	AK	115/117 (98%)	96 (84%)	14 (12%)	5 (4%)	2	22
12	AL	121/123 (98%)	100 (83%)	12 (10%)	9 (7%)	1	13
13	AM	111/113 (98%)	80 (72%)	19 (17%)	12 (11%)	0	7
14	AN	92/96 (96%)	57 (62%)	22 (24%)	13 (14%)	0	4
15	AO	86/88 (98%)	73 (85%)	11 (13%)	2 (2%)	6	33
16	AP	78/80 (98%)	62 (80%)	10 (13%)	6 (8%)	1	12
17	AQ	78/80 (98%)	65 (83%)	7 (9%)	6 (8%)	1	12
18	AR	53/55 (96%)	42 (79%)	8 (15%)	3 (6%)	1	17
19	AS	77/79 (98%)	61 (79%)	13 (17%)	3 (4%)	3	23
20	AT	83/85 (98%)	68 (82%)	13 (16%)	2 (2%)	6	33
21	AU	49/51 (96%)	41 (84%)	5 (10%)	3 (6%)	1	16
24	AZ	18/20 (90%)	16 (89%)	1 (6%)	1 (6%)	2	18
25	B0	75/77 (97%)	52 (69%)	20 (27%)	3 (4%)	3	23
26	B1	61/63 (97%)	45 (74%)	14 (23%)	2 (3%)	4	26
27	B2	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
28	B3	54/56 (96%)	42 (78%)	9 (17%)	3 (6%)	2	18
29	B4	48/50 (96%)	39 (81%)	7 (15%)	2 (4%)	3	22
30	B5	232/234 (99%)	190 (82%)	37 (16%)	5 (2%)	6	35
31	B6	44/46 (96%)	29 (66%)	11 (25%)	4 (9%)	1	10
32	B7	62/64 (97%)	52 (84%)	5 (8%)	5 (8%)	1	12
33	B8	36/38 (95%)	30 (83%)	4 (11%)	2 (6%)	2	18
36	BC	269/271 (99%)	209 (78%)	47 (18%)	13 (5%)	2	20
37	BD	207/209 (99%)	149 (72%)	37 (18%)	21 (10%)	0	9
38	BE	199/201 (99%)	161 (81%)	23 (12%)	15 (8%)	1	13
39	BF	176/178 (99%)	131 (74%)	26 (15%)	19 (11%)	0	7
40	BG	171/176 (97%)	134 (78%)	28 (16%)	9 (5%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BH	147/149 (99%)	111 (76%)	31 (21%)	5 (3%)	3	26
42	BI	139/141 (99%)	113 (81%)	21 (15%)	5 (4%)	3	25
43	BJ	140/142 (99%)	106 (76%)	24 (17%)	10 (7%)	1	14
44	BK	119/121 (98%)	95 (80%)	14 (12%)	10 (8%)	1	11
45	BL	141/143 (99%)	115 (82%)	16 (11%)	10 (7%)	1	14
46	BM	134/136 (98%)	105 (78%)	21 (16%)	8 (6%)	1	16
47	BN	118/120 (98%)	96 (81%)	16 (14%)	6 (5%)	2	19
48	BO	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	8	40
49	BP	112/114 (98%)	85 (76%)	19 (17%)	8 (7%)	1	14
50	BQ	115/117 (98%)	84 (73%)	21 (18%)	10 (9%)	1	11
51	BR	101/103 (98%)	80 (79%)	13 (13%)	8 (8%)	1	12
52	BS	108/110 (98%)	76 (70%)	21 (19%)	11 (10%)	0	8
53	BT	91/93 (98%)	60 (66%)	25 (28%)	6 (7%)	1	15
54	BU	94/102 (92%)	71 (76%)	16 (17%)	7 (7%)	1	13
55	BW	92/94 (98%)	76 (83%)	10 (11%)	6 (6%)	1	15
56	BY	77/79 (98%)	46 (60%)	18 (23%)	13 (17%)	0	3
All	All	5858/5971 (98%)	4523 (77%)	956 (16%)	379 (6%)	2	15

5 of 379 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	17	TRP
3	AC	116	ALA
5	AE	11	GLN
5	AE	17	VAL
9	AI	58	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	
2	AB	180/180 (100%)	171 (95%)	9 (5%)	24	49
3	AC	170/170 (100%)	158 (93%)	12 (7%)	14	39
4	AD	172/172 (100%)	165 (96%)	7 (4%)	30	55
5	AE	113/113 (100%)	103 (91%)	10 (9%)	10	31
6	AF	87/87 (100%)	85 (98%)	2 (2%)	50	70
7	AG	123/123 (100%)	120 (98%)	3 (2%)	49	69
8	AH	104/104 (100%)	99 (95%)	5 (5%)	25	51
9	AI	105/105 (100%)	100 (95%)	5 (5%)	25	51
10	AJ	86/86 (100%)	81 (94%)	5 (6%)	20	45
11	AK	90/90 (100%)	86 (96%)	4 (4%)	28	53
12	AL	103/103 (100%)	98 (95%)	5 (5%)	25	50
13	AM	91/91 (100%)	89 (98%)	2 (2%)	52	71
14	AN	79/79 (100%)	76 (96%)	3 (4%)	33	57
15	AO	76/76 (100%)	69 (91%)	7 (9%)	9	29
16	AP	65/65 (100%)	62 (95%)	3 (5%)	27	52
17	AQ	74/74 (100%)	68 (92%)	6 (8%)	11	35
18	AR	48/48 (100%)	44 (92%)	4 (8%)	11	34
19	AS	70/70 (100%)	64 (91%)	6 (9%)	10	32
20	AT	65/65 (100%)	64 (98%)	1 (2%)	65	80
21	AU	44/44 (100%)	38 (86%)	6 (14%)	3	17
25	B0	67/67 (100%)	65 (97%)	2 (3%)	41	63
26	B1	55/55 (100%)	50 (91%)	5 (9%)	9	30
27	B2	48/48 (100%)	47 (98%)	1 (2%)	53	72
28	B3	47/47 (100%)	46 (98%)	1 (2%)	53	72
29	B4	45/45 (100%)	42 (93%)	3 (7%)	16	40
30	B5	181/181 (100%)	175 (97%)	6 (3%)	38	61
31	B6	38/38 (100%)	33 (87%)	5 (13%)	4	18
32	B7	51/51 (100%)	48 (94%)	3 (6%)	19	45
33	B8	34/34 (100%)	34 (100%)	0	100	100
36	BC	216/216 (100%)	204 (94%)	12 (6%)	21	46
37	BD	164/164 (100%)	146 (89%)	18 (11%)	6	22
38	BE	165/165 (100%)	157 (95%)	8 (5%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BF	149/149 (100%)	143 (96%)	6 (4%)	31	55
40	BG	136/137 (99%)	125 (92%)	11 (8%)	11	35
41	BH	114/114 (100%)	110 (96%)	4 (4%)	36	59
42	BI	109/109 (100%)	104 (95%)	5 (5%)	27	52
43	BJ	116/116 (100%)	112 (97%)	4 (3%)	37	60
44	BK	102/102 (100%)	92 (90%)	10 (10%)	8	26
45	BL	102/102 (100%)	98 (96%)	4 (4%)	32	56
46	BM	109/109 (100%)	104 (95%)	5 (5%)	27	52
47	BN	100/100 (100%)	96 (96%)	4 (4%)	31	55
48	BO	86/86 (100%)	84 (98%)	2 (2%)	50	70
49	BP	99/99 (100%)	96 (97%)	3 (3%)	41	63
50	BQ	89/89 (100%)	83 (93%)	6 (7%)	16	40
51	BR	84/84 (100%)	76 (90%)	8 (10%)	8	28
52	BS	93/93 (100%)	87 (94%)	6 (6%)	17	42
53	BT	80/80 (100%)	68 (85%)	12 (15%)	3	15
54	BU	81/83 (98%)	76 (94%)	5 (6%)	18	43
55	BW	78/78 (100%)	73 (94%)	5 (6%)	17	42
56	BY	59/59 (100%)	54 (92%)	5 (8%)	10	33
All	All	4842/4845 (100%)	4568 (94%)	274 (6%)	24	45

5 of 274 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	BQ	40	LYS
51	BR	78	ARG
54	BU	14	THR
19	AS	60	PHE
19	AS	22	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
43	BJ	40	HIS
51	BR	91	GLN
43	BJ	80	HIS

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Mol	Chain	Res	Type
49	BP	76	HIS
54	BU	39	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1529/1530 (99%)	269 (17%)	34 (2%)
22	AV	76/77 (98%)	15 (19%)	0
23	AX	10/11 (90%)	8 (80%)	0
34	BA	112/117 (95%)	16 (14%)	2 (1%)
35	BB	2902/2903 (99%)	471 (16%)	56 (1%)
All	All	4629/4638 (99%)	779 (16%)	92 (1%)

5 of 779 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	A
1	AA	9	G
1	AA	15	G
1	AA	31	G
1	AA	32	A

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BB	1332	G
35	BB	2131	U
35	BB	1459	G
35	BB	1808	A
35	BB	2145	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	5MU	AV	54	22	18,21,23	0.64	0	26,30,35	0.71	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	5MU	AV	54	22	-	0/7/25/26	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	AV	54	5MU	O4'-C1'-N1	2.42	113.90	108.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	BU	1
14	AN	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BU	4:ILE	C	6:ARG	N	4.65
1	AN	35:ALA	C	40:ARG	N	4.56

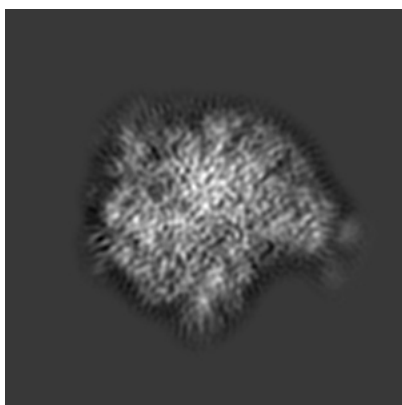
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1657. These allow visual inspection of the internal detail of the map and identification of artifacts.

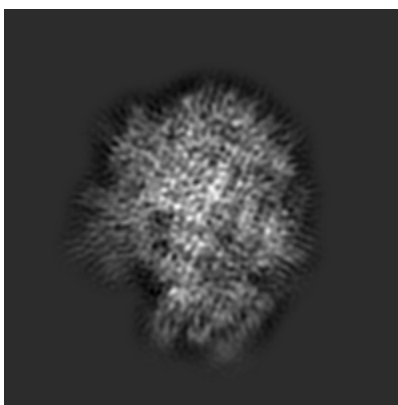
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

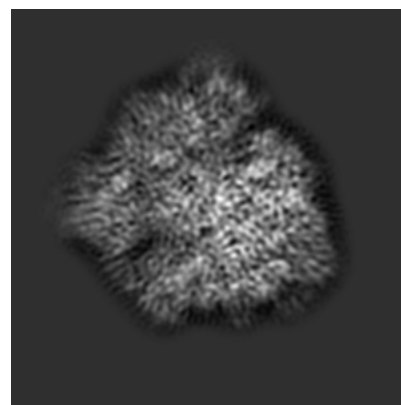
6.1.1 Primary map



X



Y

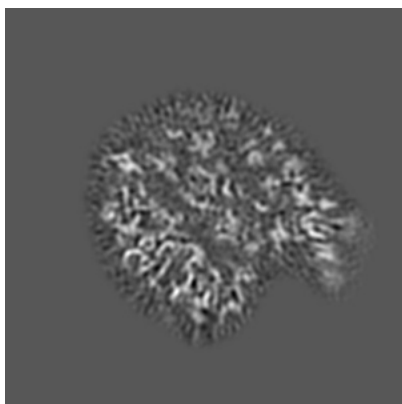


Z

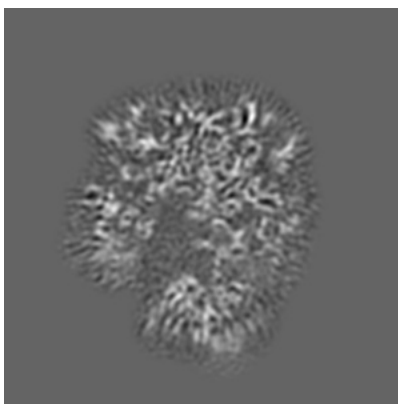
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

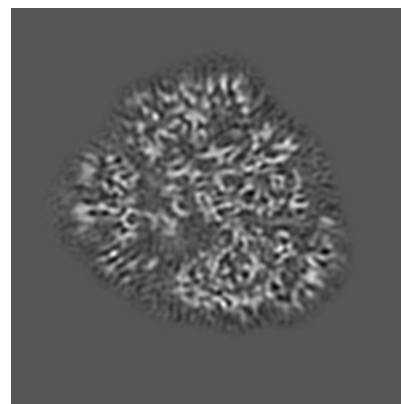
6.2.1 Primary map



X Index: 147



Y Index: 147

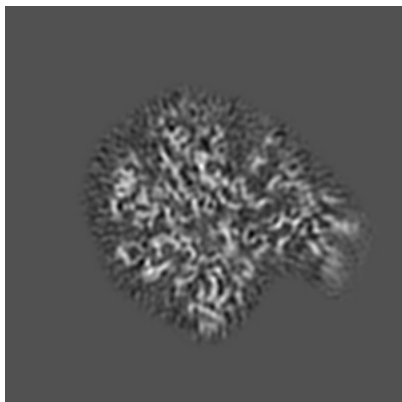


Z Index: 147

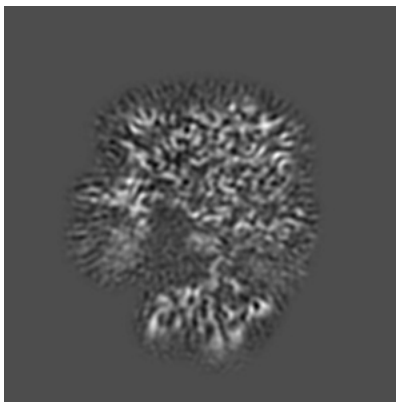
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

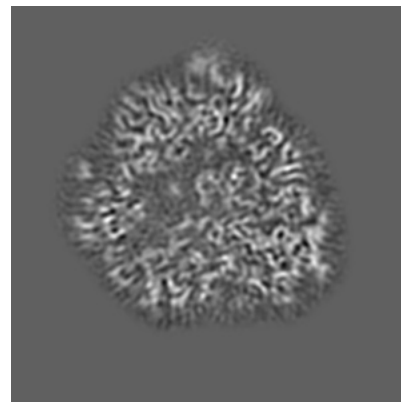
6.3.1 Primary map



X Index: 152



Y Index: 155



Z Index: 136

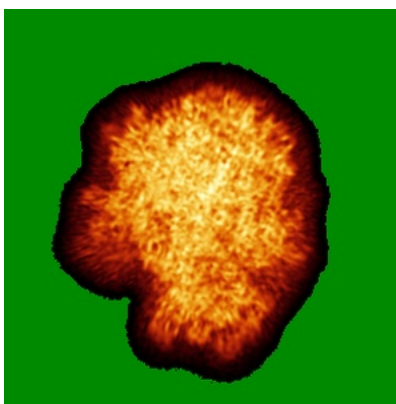
The images above show the largest variance slices of the map in three orthogonal directions.

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

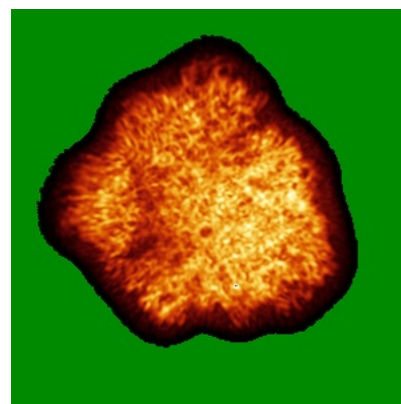
6.4.1 Primary map



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](#)

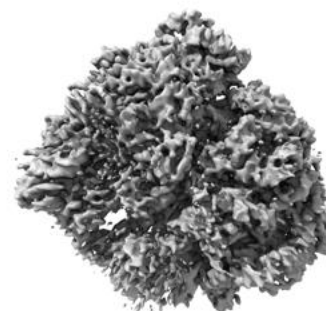
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

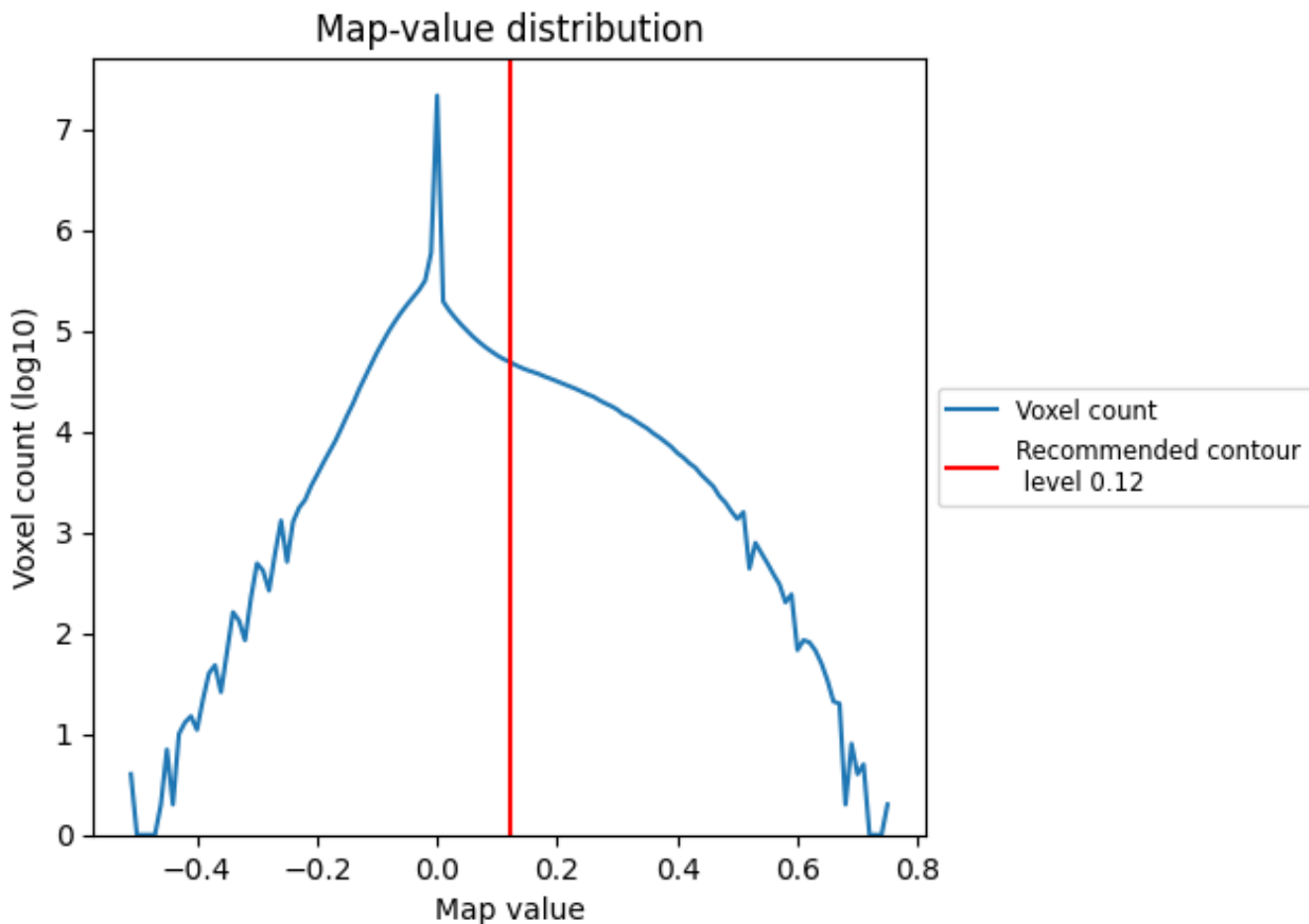
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

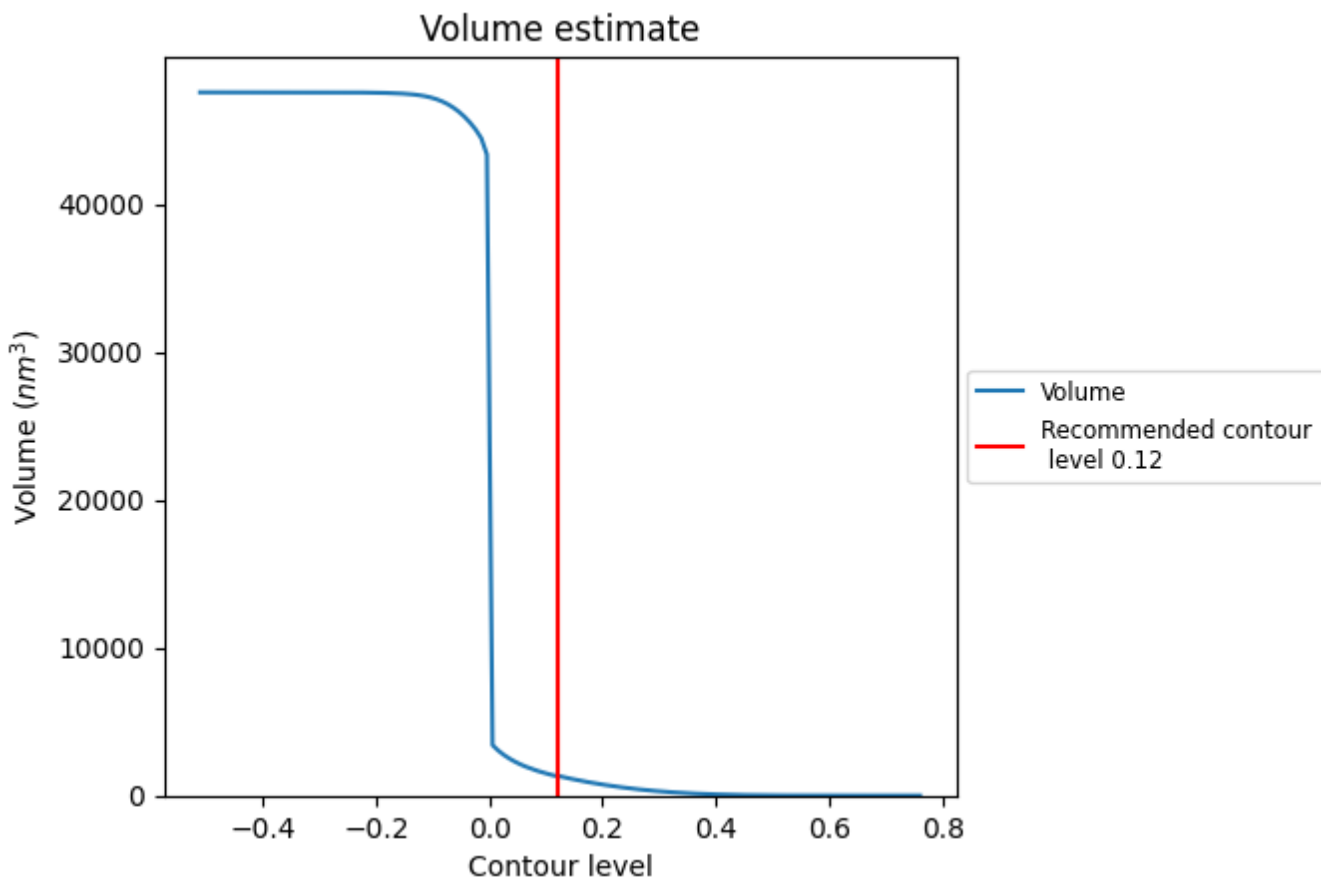
This section contains the results of statistical analysis of the map.

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.

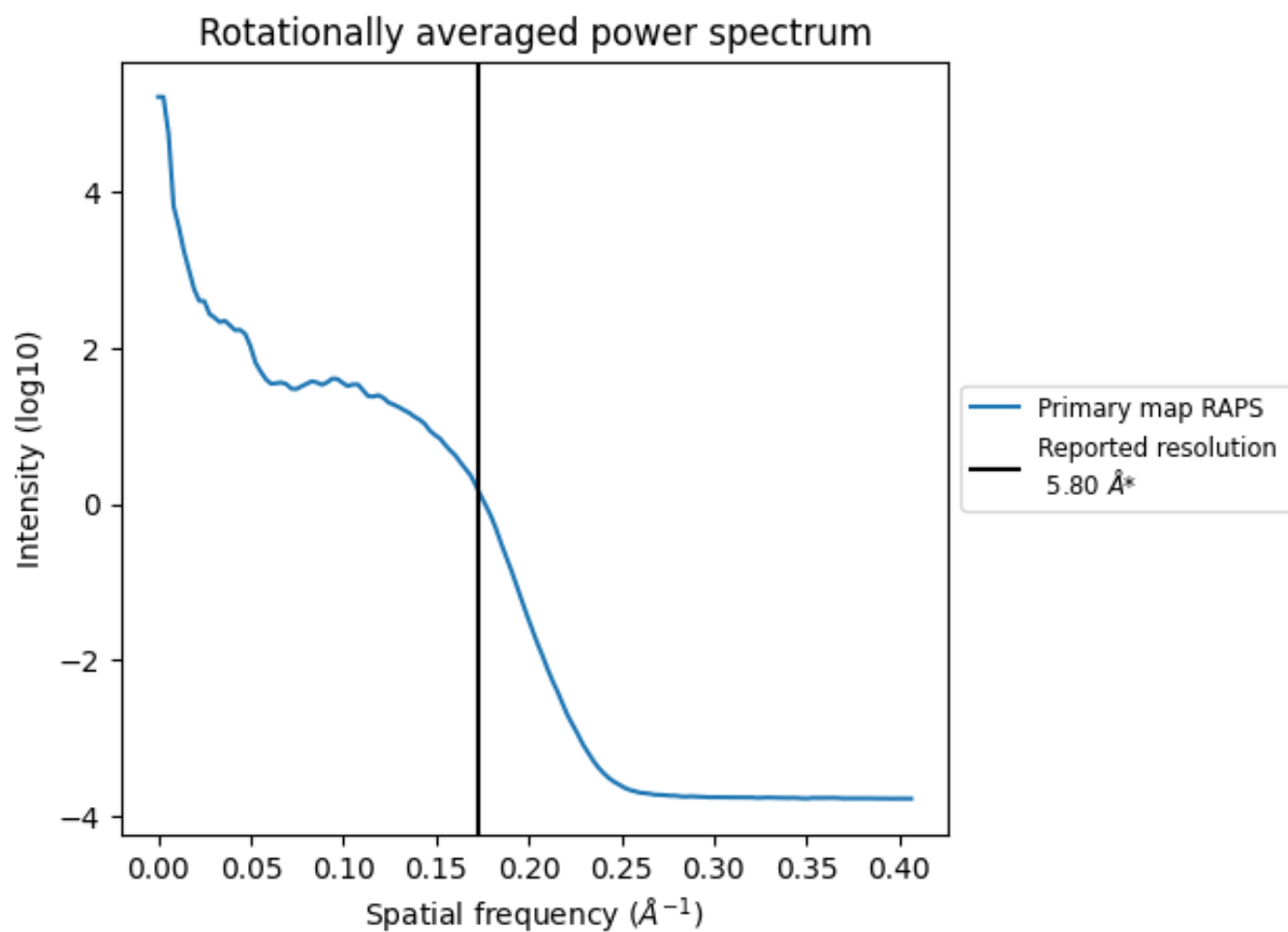
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1327 nm³; this corresponds to an approximate mass of 1198 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 0.172\AA^{-1}

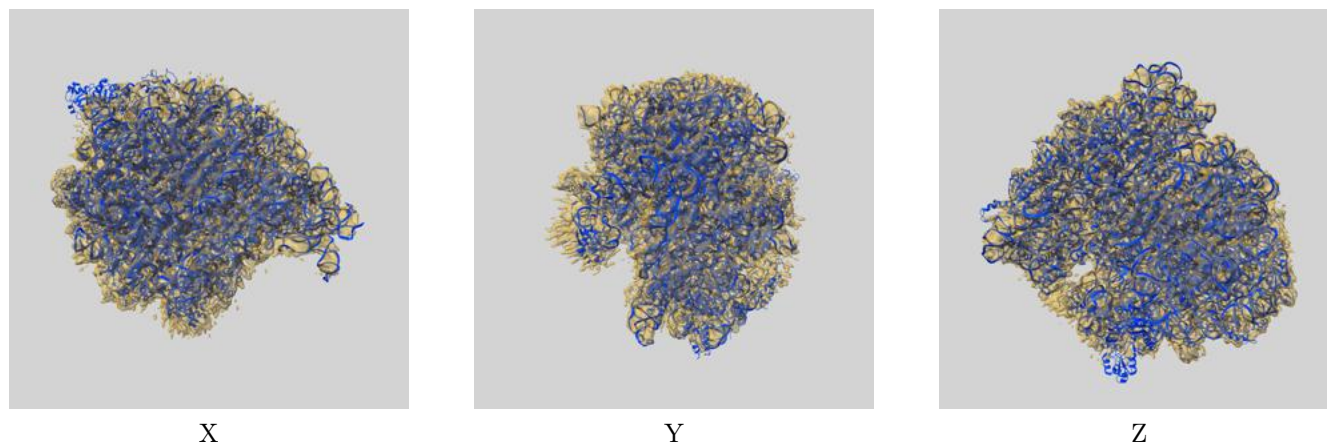
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

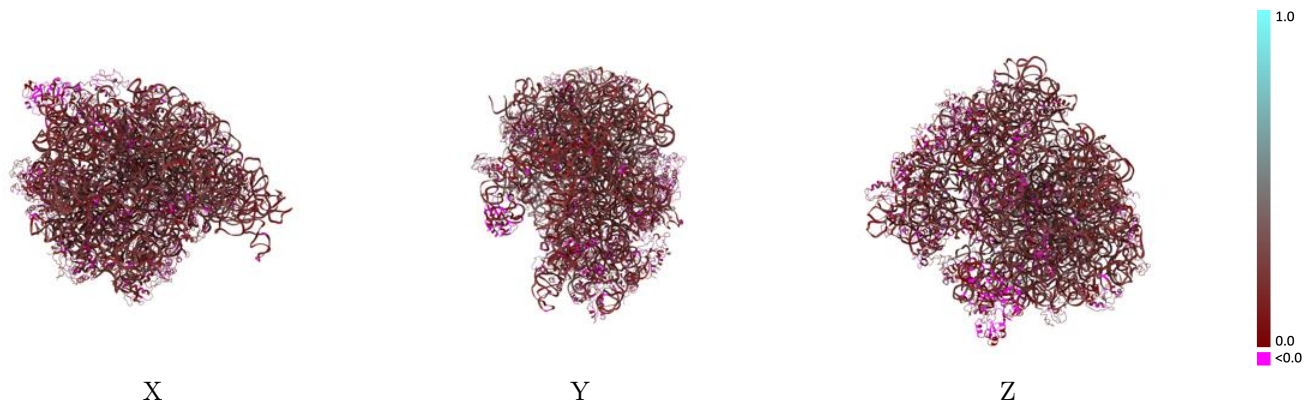
This section contains information regarding the fit between EMDB map EMD-1657 and PDB model 4V5H. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



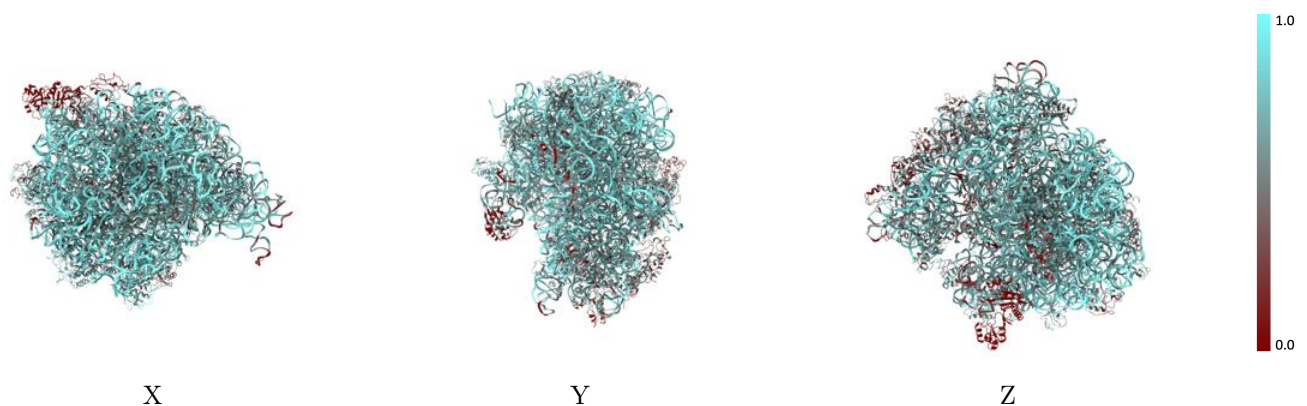
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



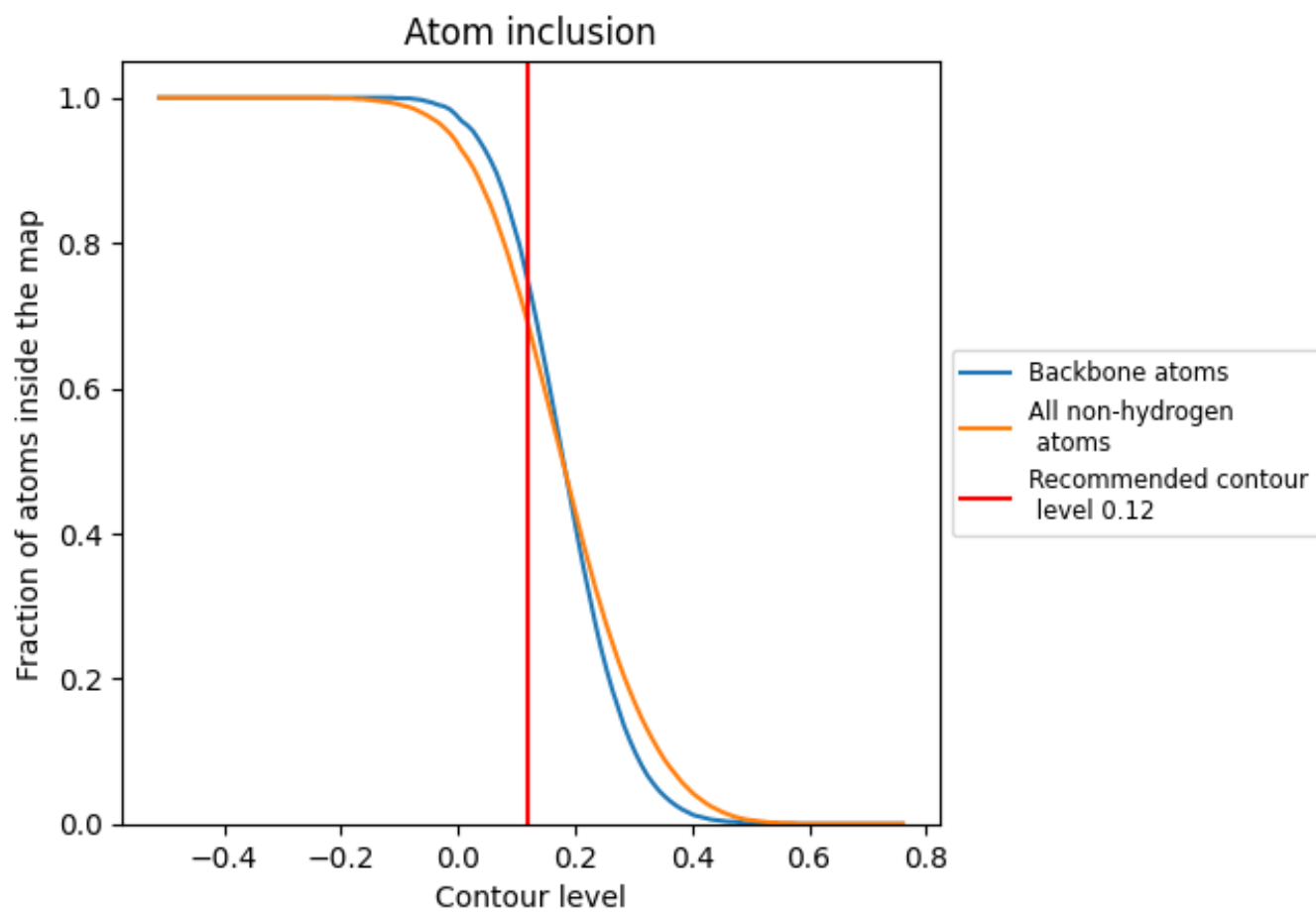
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6880	 0.1890
AA	 0.7560	 0.2050
AB	 0.3910	 0.1500
AC	 0.4960	 0.1420
AD	 0.4610	 0.1350
AE	 0.5320	 0.1500
AF	 0.6060	 0.1760
AG	 0.4700	 0.1610
AH	 0.5290	 0.1450
AI	 0.4710	 0.1220
AJ	 0.3250	 0.1070
AK	 0.5430	 0.1610
AL	 0.5160	 0.1630
AM	 0.5490	 0.1550
AN	 0.5610	 0.1400
AO	 0.5640	 0.1650
AP	 0.5310	 0.1390
AQ	 0.5680	 0.1720
AR	 0.5870	 0.1720
AS	 0.5860	 0.1570
AT	 0.5280	 0.1460
AU	 0.3500	 0.1570
AV	 0.5620	 0.1430
AX	 0.2630	 0.1480
AZ	 0.4900	 0.3070
B0	 0.5410	 0.1620
B1	 0.5510	 0.1390
B2	 0.5810	 0.1740
B3	 0.5650	 0.1600
B4	 0.5760	 0.1680
B5	 0.0180	 -0.0010
B6	 0.4650	 0.1340
B7	 0.5580	 0.1530
B8	 0.5620	 0.1810
BA	 0.8170	 0.2140



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Chain	Atom inclusion	Q-score
BB	 0.7850	 0.2140
BC	 0.5570	 0.1700
BD	 0.5980	 0.1590
BE	 0.4930	 0.1400
BF	 0.5940	 0.1600
BG	 0.6720	 0.1850
BH	 0.2460	 0.1340
BI	 0.2170	 0.0320
BJ	 0.6080	 0.1750
BK	 0.5070	 0.1660
BL	 0.5340	 0.1610
BM	 0.5540	 0.1740
BN	 0.5570	 0.1360
BO	 0.6230	 0.1600
BP	 0.5640	 0.1720
BQ	 0.5560	 0.1160
BR	 0.6200	 0.1840
BS	 0.5420	 0.1360
BT	 0.5230	 0.1380
BU	 0.5570	 0.1560
BW	 0.6440	 0.1700
BY	 0.5190	 0.1080