



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:48 AM UTC

PDB ID : 4V5H / pdb_00004v5h
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 : 3FIK, 3FIH

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

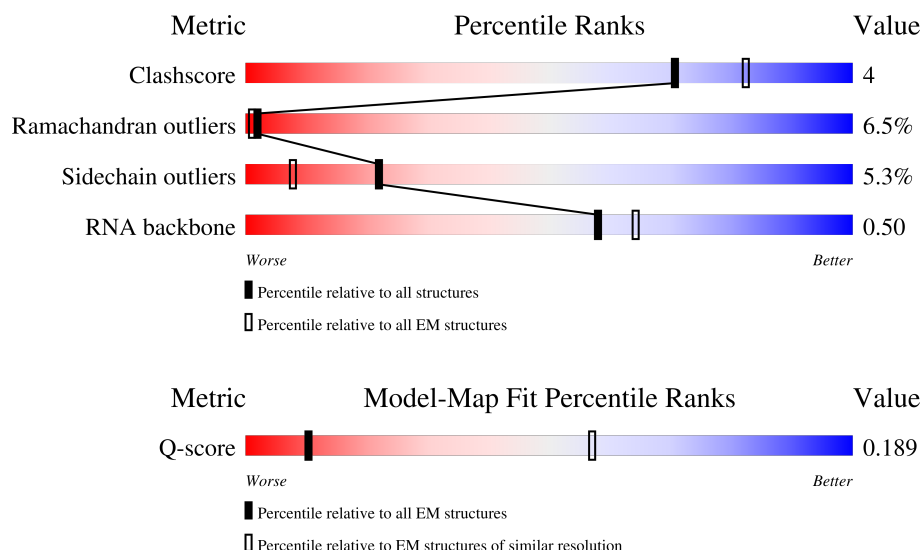
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	511 (5.30 - 6.30)

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	

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Mol	Chain	Length	Quality of chain
4	AD	205	
5	AE	150	
6	AF	100	
7	AG	150	
8	AH	129	
9	AI	127	
10	AJ	98	
11	AK	117	
12	AL	123	
13	AM	113	
14	AN	96	
15	AO	88	
16	AP	80	
17	AQ	80	
18	AR	55	
19	AS	79	
20	AT	85	
21	AU	51	
22	AV	77	
23	AX	11	
24	AZ	20	
25	B0	77	
26	B1	63	
27	B2	58	
28	B3	56	

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Mol	Chain	Length	Quality of chain
29	B4	50	
30	B5	234	
31	B6	46	
32	B7	64	
33	B8	38	
34	BA	117	
35	BB	2903	
36	BC	271	
37	BD	209	
38	BE	201	
39	BF	178	
40	BG	176	
41	BH	149	
42	BI	141	
43	BJ	142	
44	BK	121	
45	BL	143	
46	BM	136	
47	BN	120	
48	BO	116	
49	BP	114	
50	BQ	117	
51	BR	103	
52	BS	110	
53	BT	93	

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Mol	Chain	Length	Quality of chain
54	BU	102	19% 31% 56% 7%
55	BW	94	16% 35% 51% 12%
56	BY	79	32% 33% 51% 13%

2 Entry composition

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
1	AA	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
35	BB	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

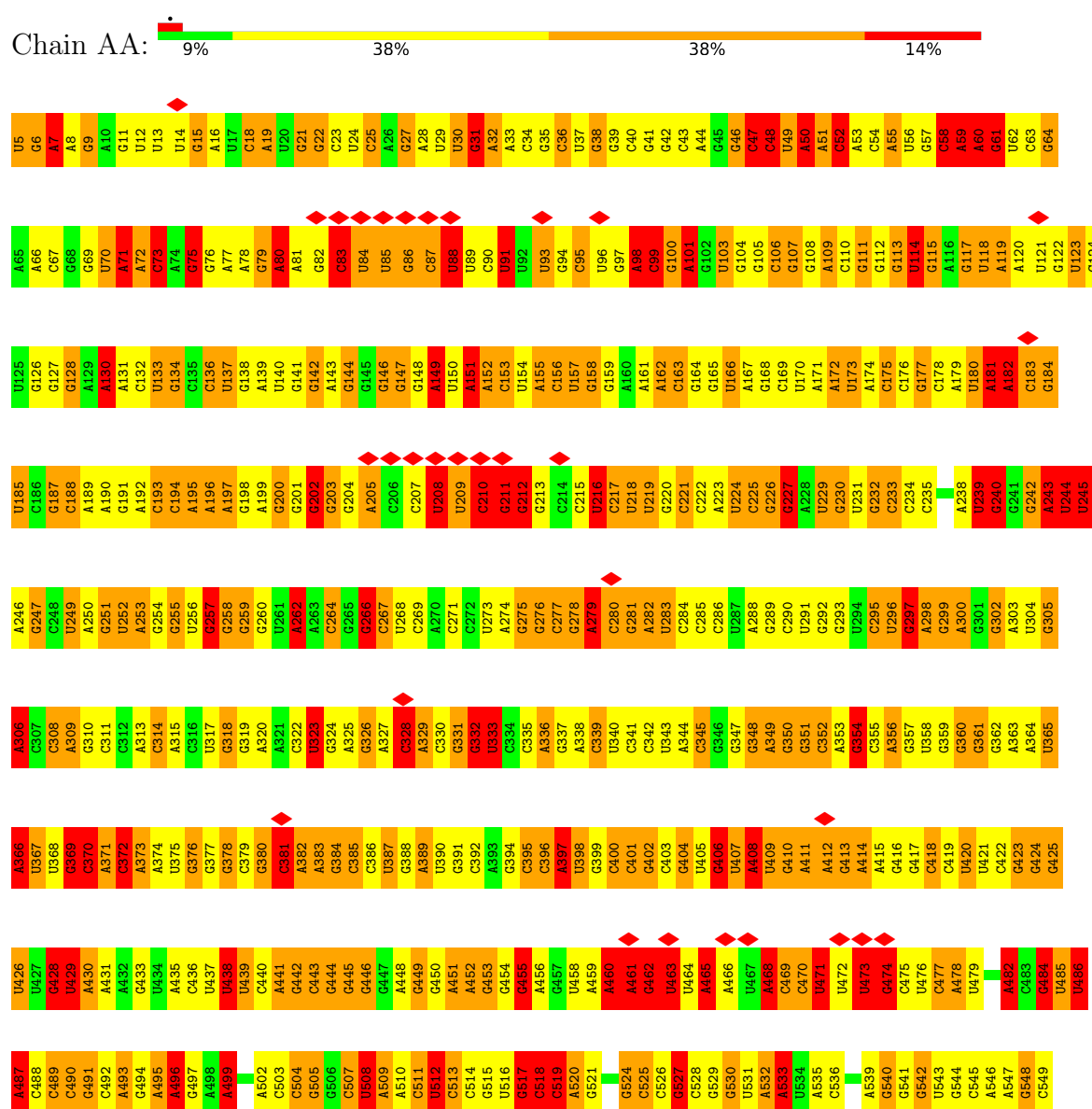
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L27.

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

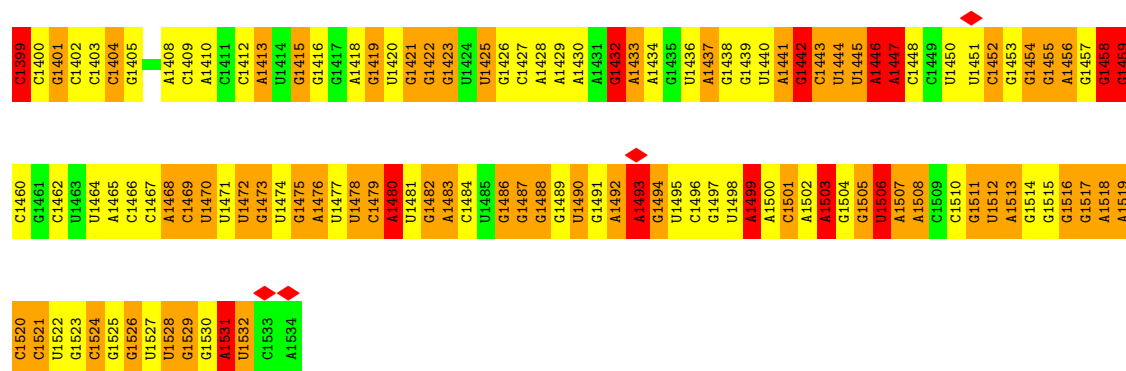
3 Residue-property plots

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.

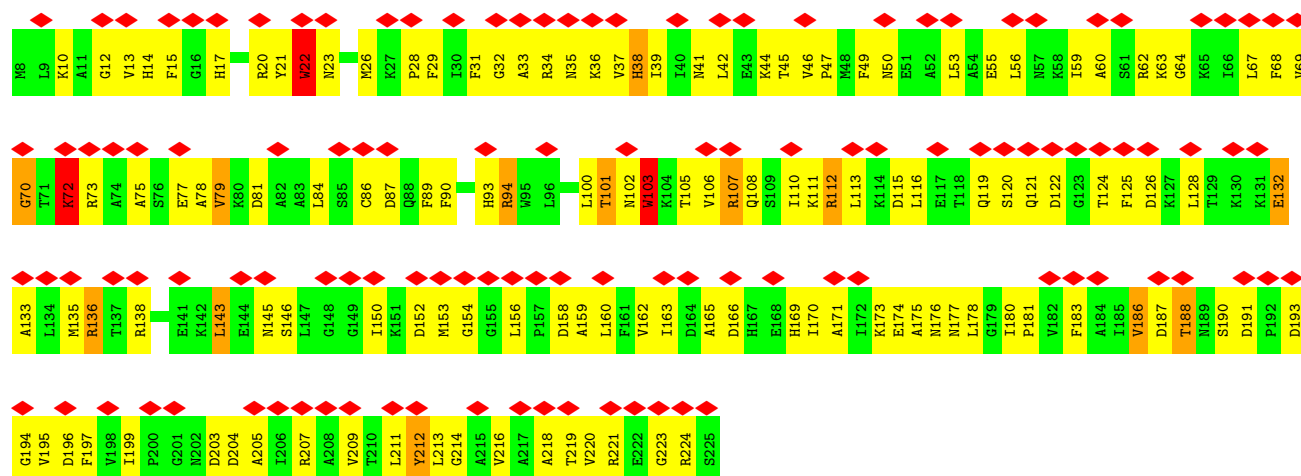
• Molecule 1: 16S RIBOSOMAL RNA



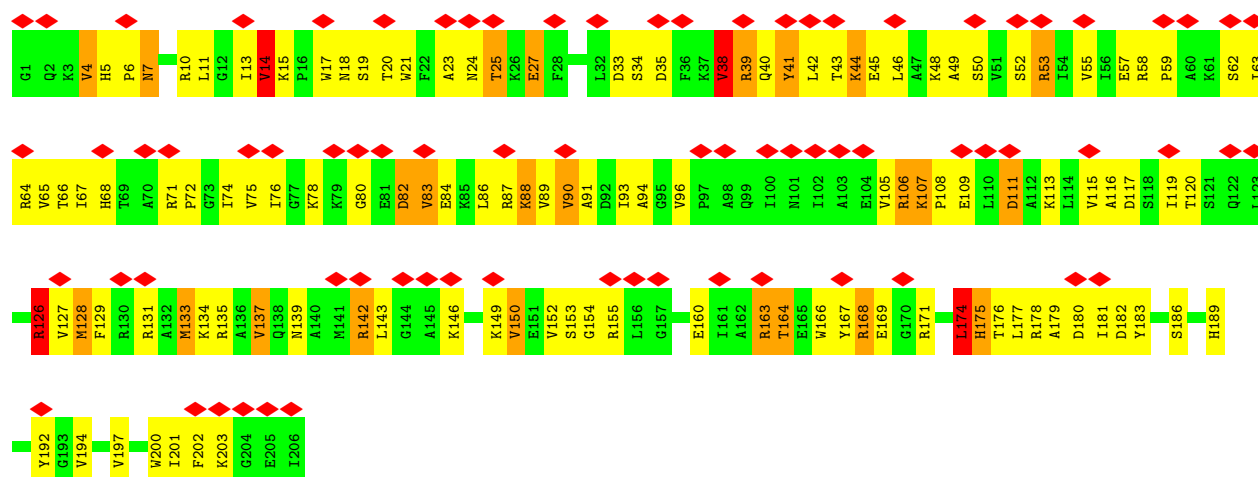
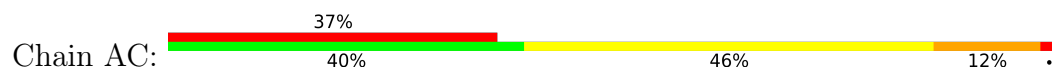
G1338	G1339	A1340	U1341	C1342	G1343	C1344	U1345	A1346	G1347	U1348	A1349	C1352	G1353	U1354	G1355	G1356	A1357	C1358	G1359	A1360	G1361	A1362	A1363	U1364	G1365	G1366	G1367	A1368	G1369	C1370	G1371	G1372	A1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	C1382	C1383	C1384	G1385	G1386	G1387	C1388	C1389	U1390	U1391	G1392	U1393	A1394	C1395	A1396	G1397	A1398																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G1278	G1279	A1280	C1281	C1282	U1283	C1284	A1285	U1286	A1287	A1288	G1289	U1290	G1291	C1292	C1293	G1294	U1295	G1296	G1297	A1298	A1299	G1300	U1301	C1302	C1303	G1304	G1305	G1306	A1307	U1308	G1309	G1310	A1311	G1312	U1313	C1314	U1315	G1316	G1317	A1318	A1319	C1320	U1321	C1322	A1323	G1324	C1325	U1326	C1327	C1328	A1329	G1330	G1331	A1332	U1333	G1334	A1335	C1336	U1337	G1338	G1339	A1340	C1341	U1342	G1343	G1344	C1345	U1346	G1347	A1348	C1349	U1350	G1351	A1352	C1353	U1354	G1355	A1356	C1357	U1358	A1359	G1360	C1361	U1362	G1363	A1364	G1365	G1366	G1367	A1368	C1369	C1370	G1371	G1372	A1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	C1382	C1383	C1384	G1385	G1386	G1387	C1388	C1389	U1390	U1391	G1392	U1393	A1394	C1395	A1396	G1397	A1398																																																																																																																																																																																																																																																																																																																																																																																																																																				
G1215	A1216	C1217	C1218	U1219	G1220	G1221	G1222	C1223	U1224	A1225	C1226	A1227	U1228	C1229	G1230	G1231	A1236	C1237	A1238	U1239	A1240	G1241	C1242	G1243	C1244	C1245	A1246	U1247	A1248	C1249	A1250	A1251	G1252	U1253	A1254	G1255	A1256	A1257	G1258	C1259	G1260	A1261	C1262	U1263	G1264	C1265	G1266	C1267	G1268	U1269	G1270	A1271	G1272	A1273	A1274	U1275	C1276	G1277	A1278	C1279	U1280	A1281	G1282	C1283	U1284	A1285	U1286	A1287	A1288	G1289	U1290	G1291	C1292	C1293	G1294	U1295	G1296	G1297	A1298	A1299	G1300	U1301	C1302	C1303	G1304	G1305	G1306	A1307	U1308	G1309	G1310	A1311	G1312	U1313	C1314	U1315	G1316	G1317	A1318	A1319	C1320	U1321	C1322	A1323	G1324	C1325	U1326	C1327	C1328	A1329	G1330	G1331	A1332	U1333	G1334	A1335	C1336	U1337	G1338	G1339	A1340	C1341	U1342	G1343	G1344	C1345	U1346	G1347	A1348	C1349	U1350	G1351	A1352	C1353	U1354	G1355	A1356	C1357	U1358	A1359	G1360	C1361	U1362	G1363	A1364	G1365	G1366	G1367	A1368	C1369	C1370	G1371	G1372	A1373	A1374	A1375	U1376	A1377	C1378	G1379	U1380	U1381	C1382	C1383	C1384	G1385	G1386	G1387	C1388	C1389	U1390	U1391	G1392	U1393	A1394	C1395	A1396	G1397	A1398																																																																																																																																																																																																																																																																																																																																																																									
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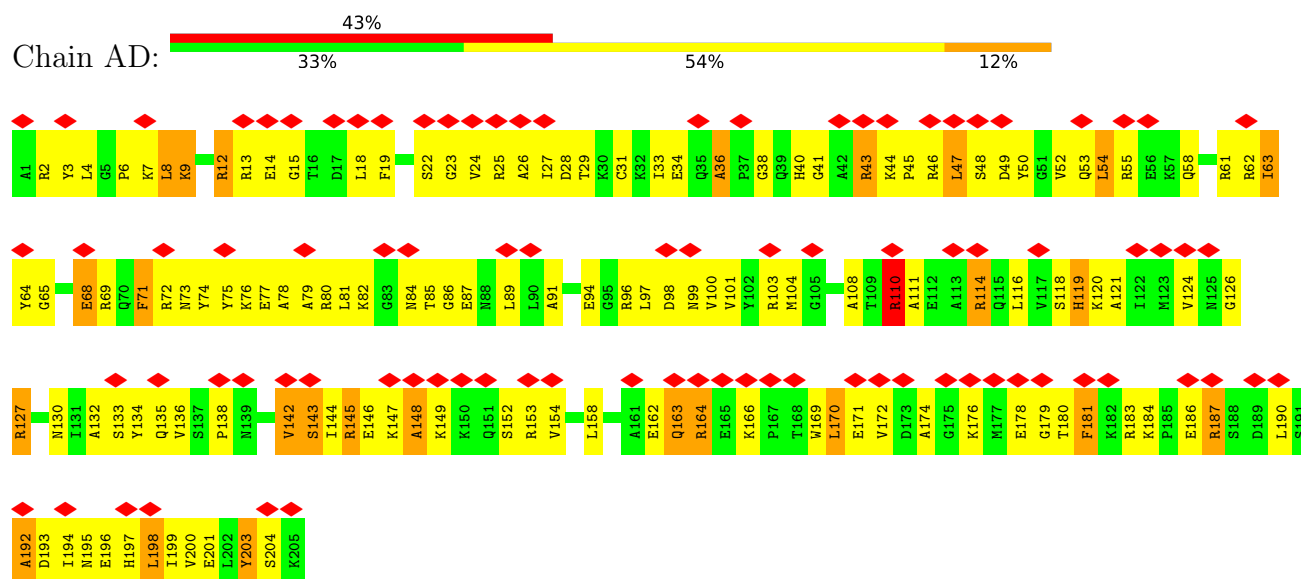
• Molecule 2: 30S RIBOSOMAL PROTEIN S2



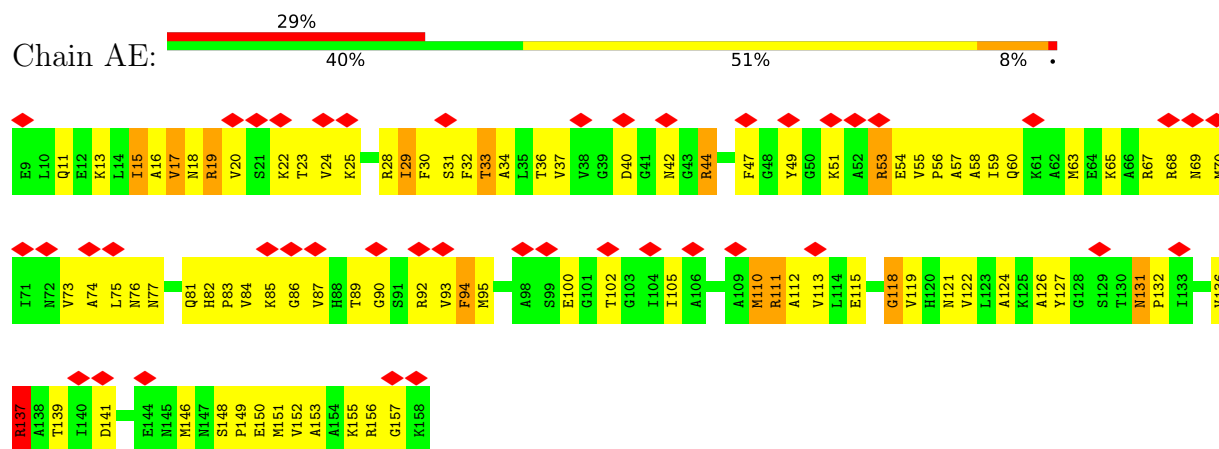
• Molecule 3: 30S RIBOSOMAL PROTEIN S3



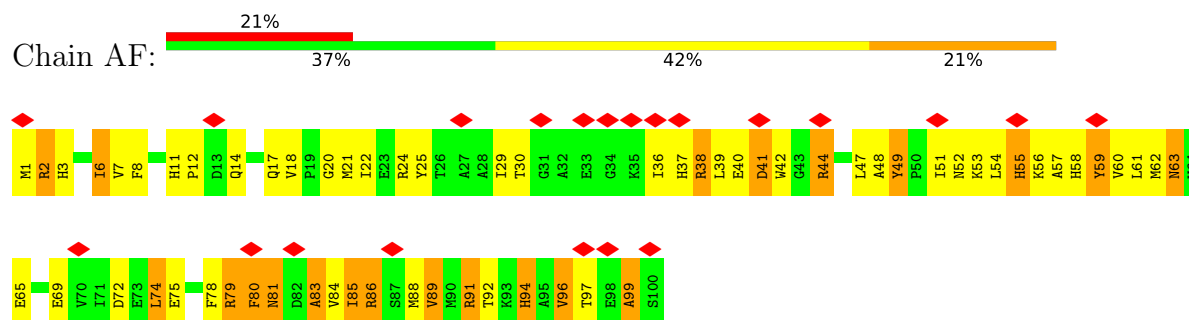
• Molecule 4: 30S RIBOSOMAL PROTEIN S4



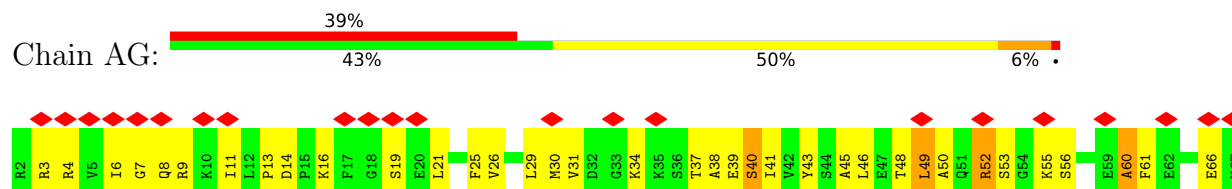
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

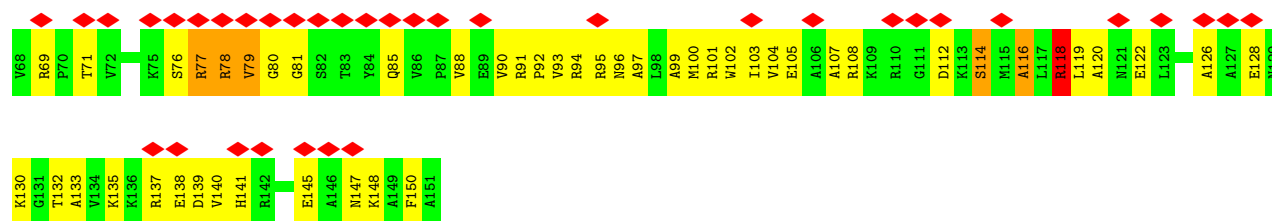


• Molecule 6: 30S RIBOSOMAL PROTEIN S6

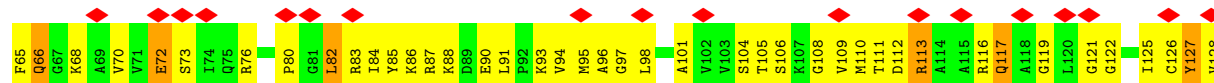
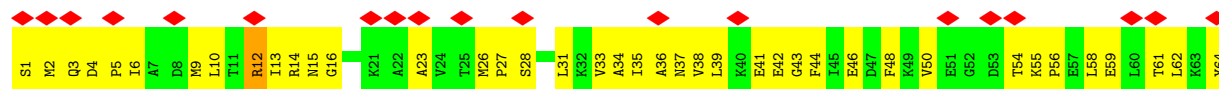


• Molecule 7: 30S RIBOSOMAL PROTEIN S7

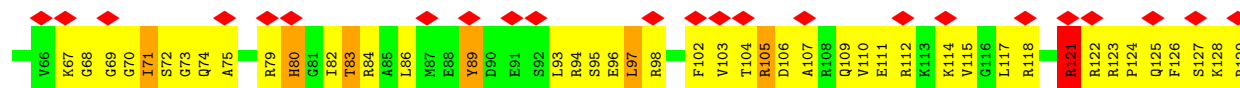
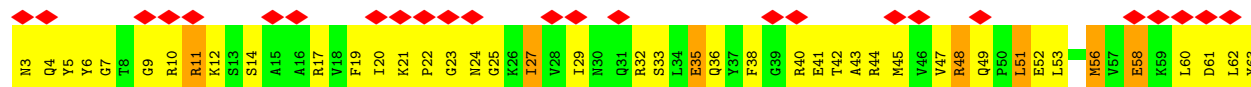




• Molecule 8: 30S RIBOSOMAL PROTEIN S8



• Molecule 9: 30S RIBOSOMAL PROTEIN S9

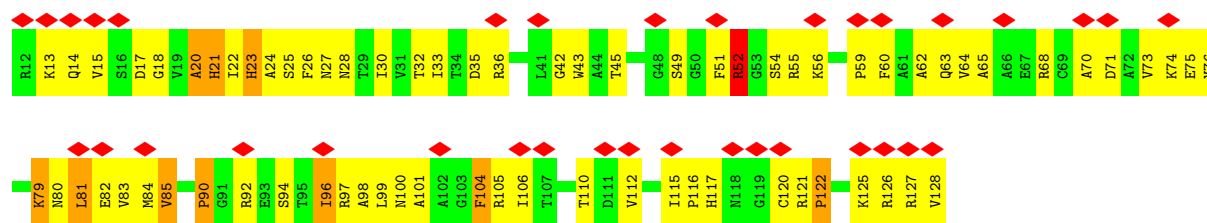


• Molecule 10: 30S RIBOSOMAL PROTEIN S10

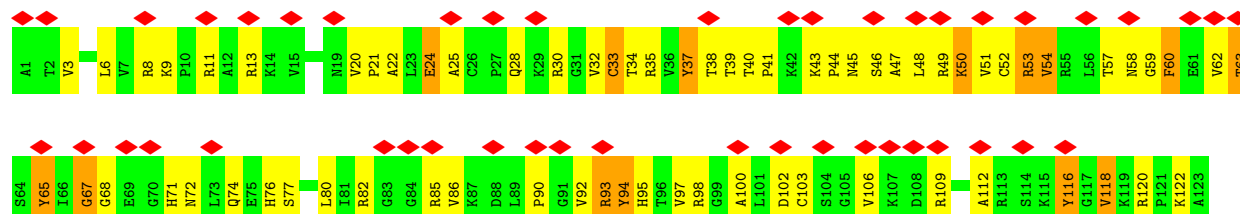
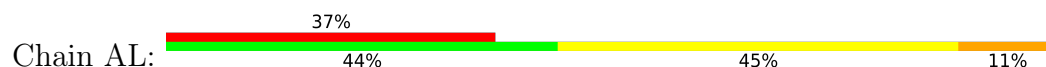


• Molecule 11: 30S RIBOSOMAL PROTEIN S11

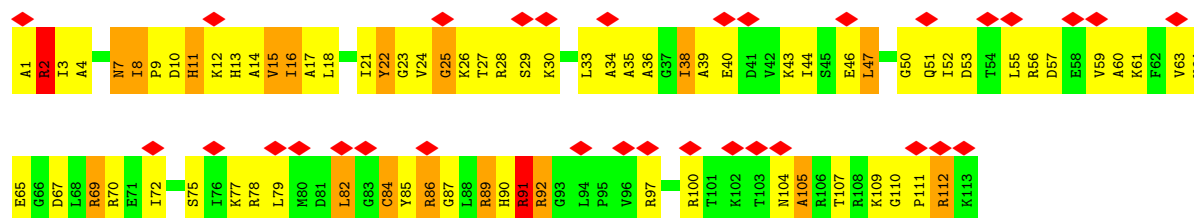




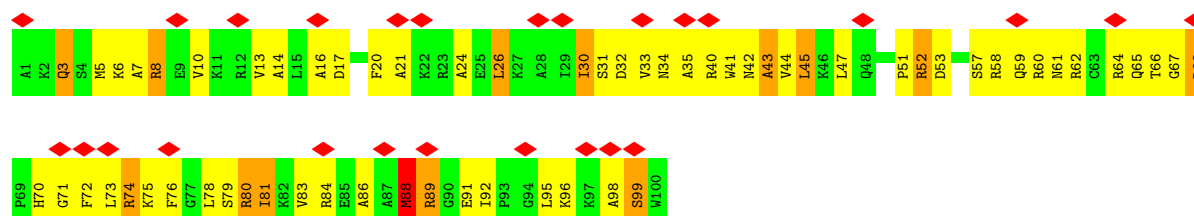
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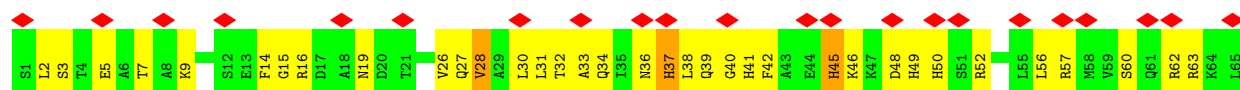
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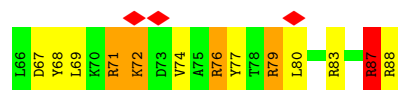


• Molecule 14: 30S RIBOSOMAL PROTEIN S14

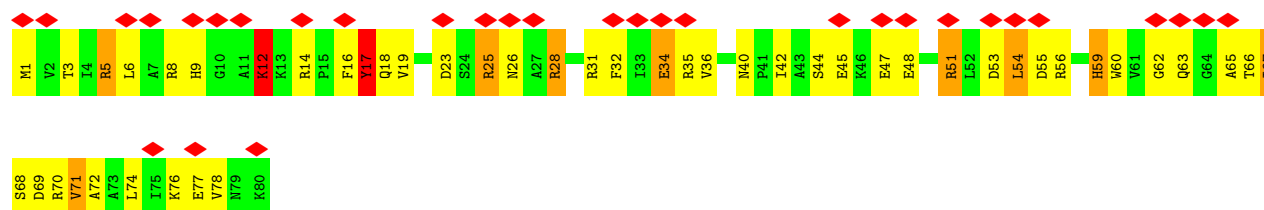
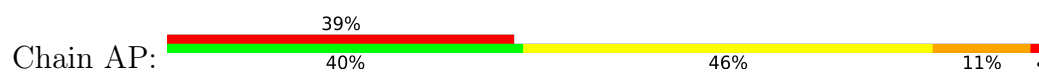


• Molecule 15: 30S RIBOSOMAL PROTEIN S15

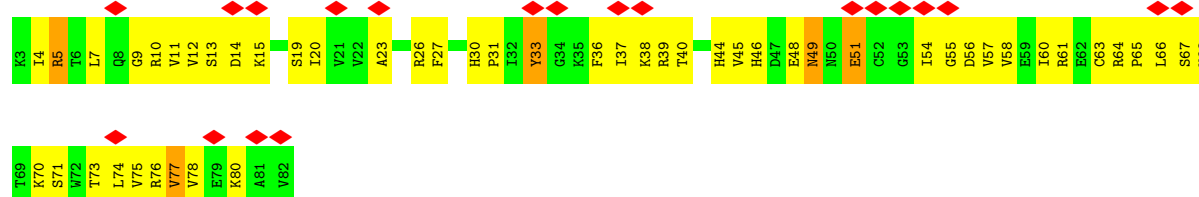




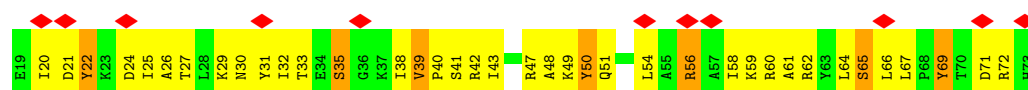
• Molecule 16: 30S RIBOSOMAL PROTEIN S16



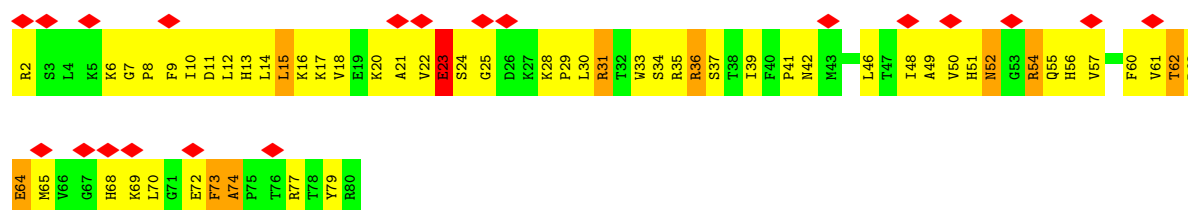
• Molecule 17: 30S RIBOSOMAL PROTEIN S17



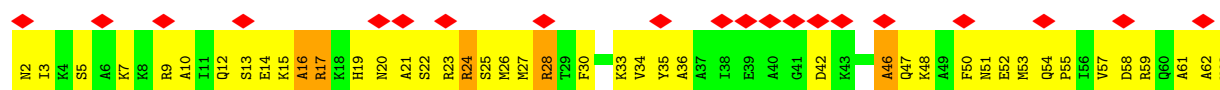
• Molecule 18: 30S RIBOSOMAL PROTEIN S18

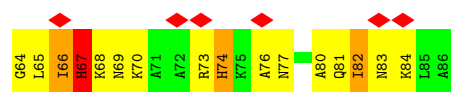


• Molecule 19: 30S RIBOSOMAL PROTEIN S19

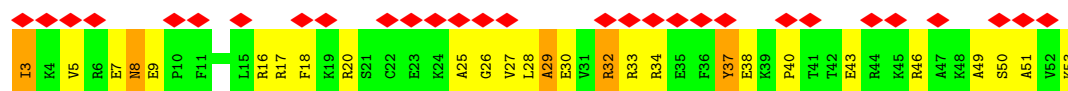


• Molecule 20: 30S RIBOSOMAL PROTEIN S20

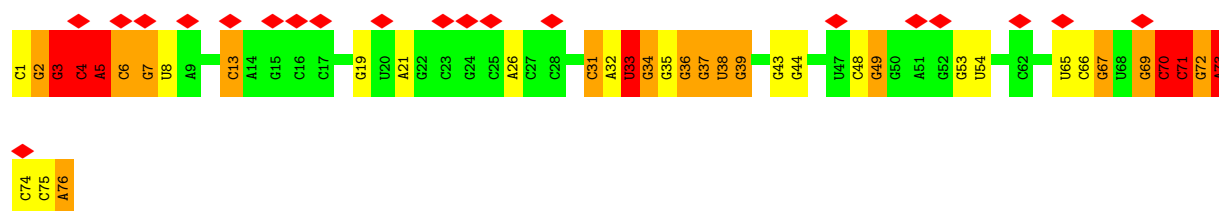




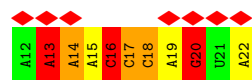
- Molecule 21: 30S RIBOSOMAL PROTEIN S21



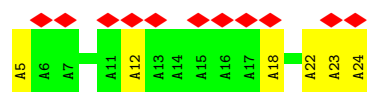
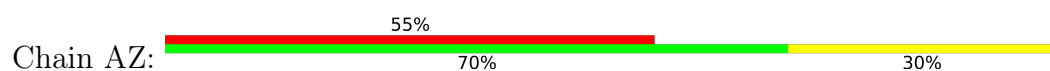
- Molecule 22: P-SITE TRNA



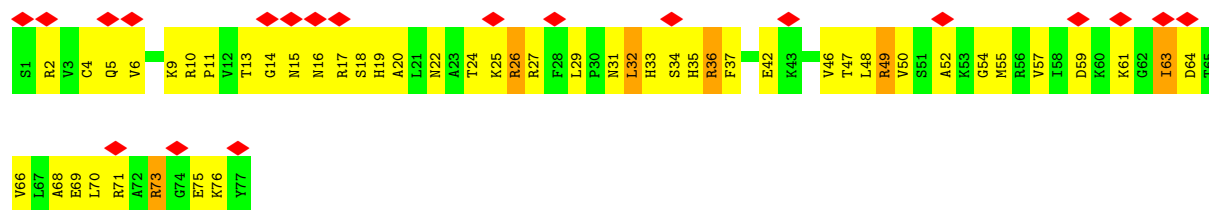
- Molecule 23: MRNA



- Molecule 24: POLY-ALA NASCENT CHAIN

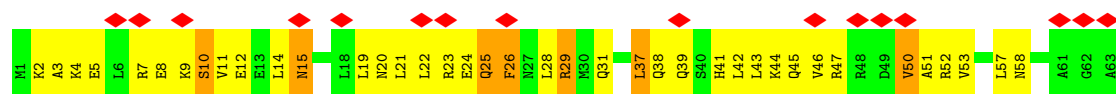


- Molecule 25: 50S RIBOSOMAL PROTEIN L28

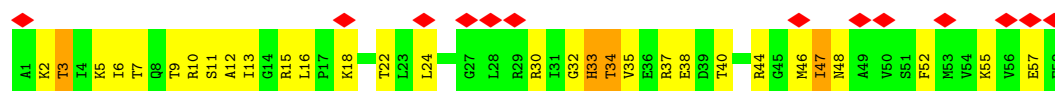


- Molecule 26: 50S RIBOSOMAL PROTEIN L29





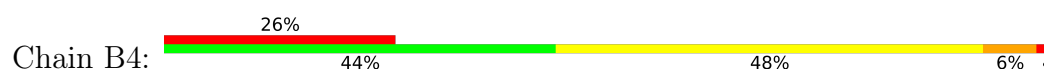
• Molecule 27: 50S RIBOSOMAL PROTEIN L30



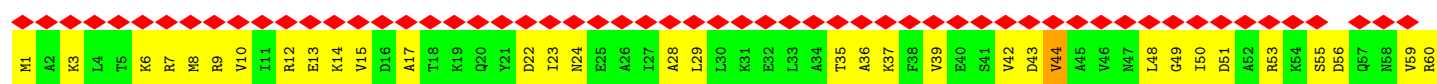
• Molecule 28: 50S RIBOSOMAL PROTEIN L32



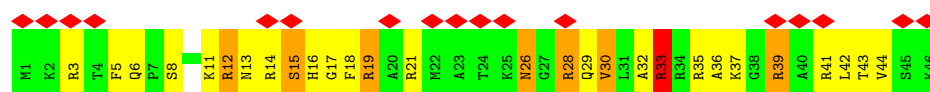
• Molecule 29: 50S RIBOSOMAL PROTEIN L33



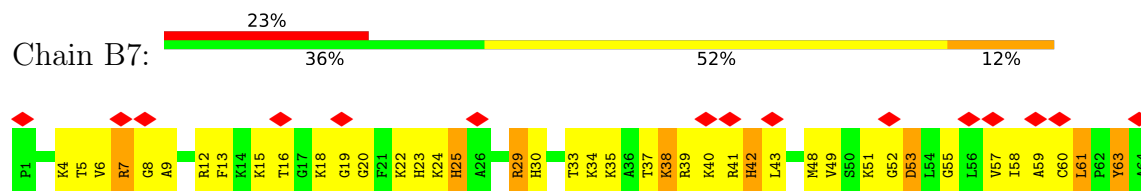
• Molecule 30: 50S RIBOSOMAL PROTEIN L1



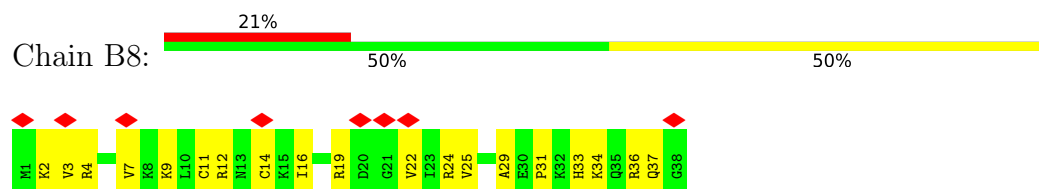
• Molecule 31: 50S RIBOSOMAL PROTEIN L34



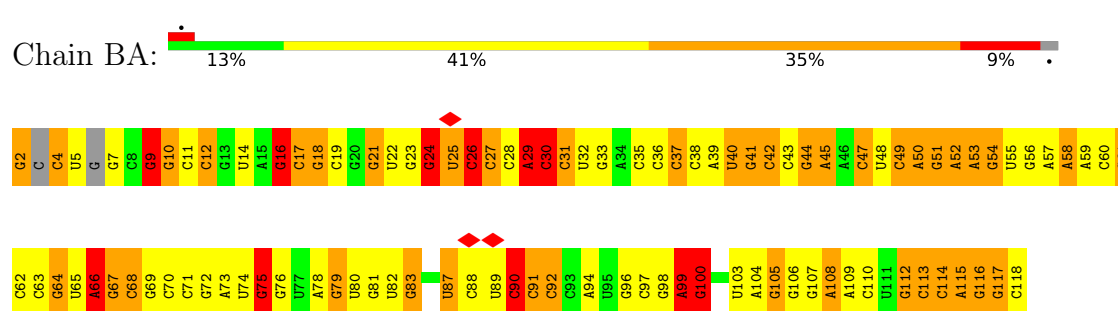
- Molecule 32: 50S RIBOSOMAL PROTEIN L35



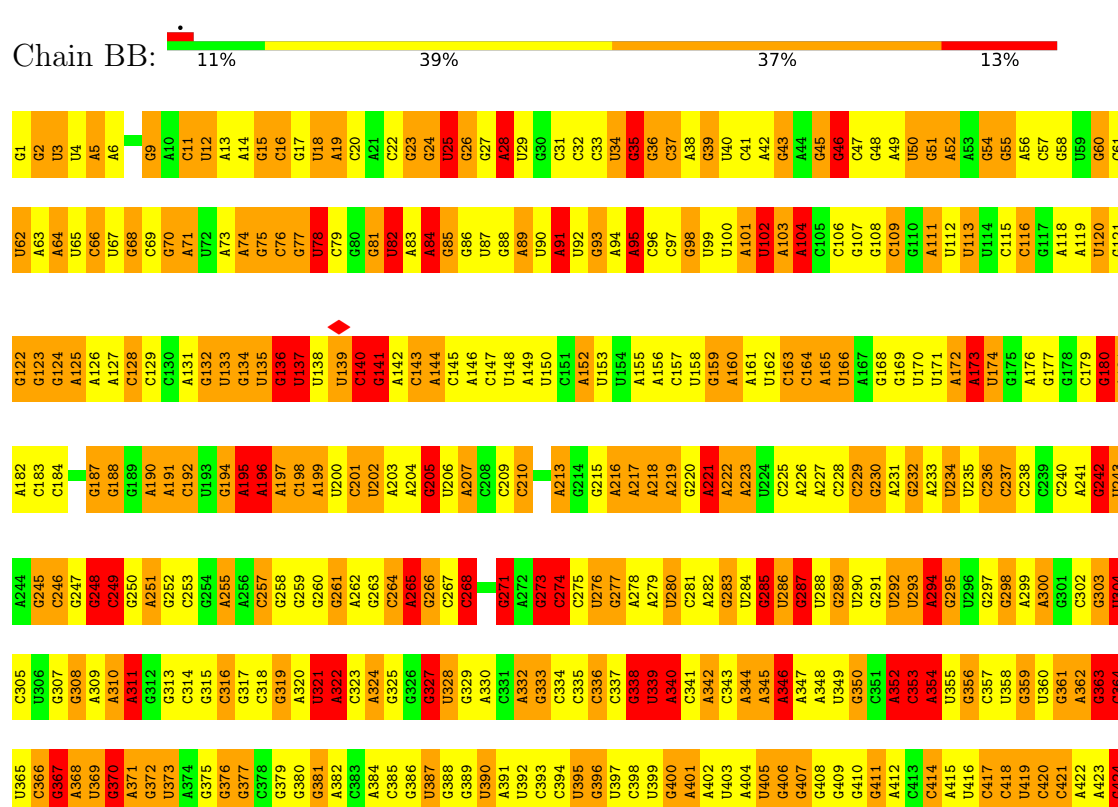
- Molecule 33: 50S RIBOSOMAL PROTEIN L36



- Molecule 34: 5S RIBOSOMAL RNA

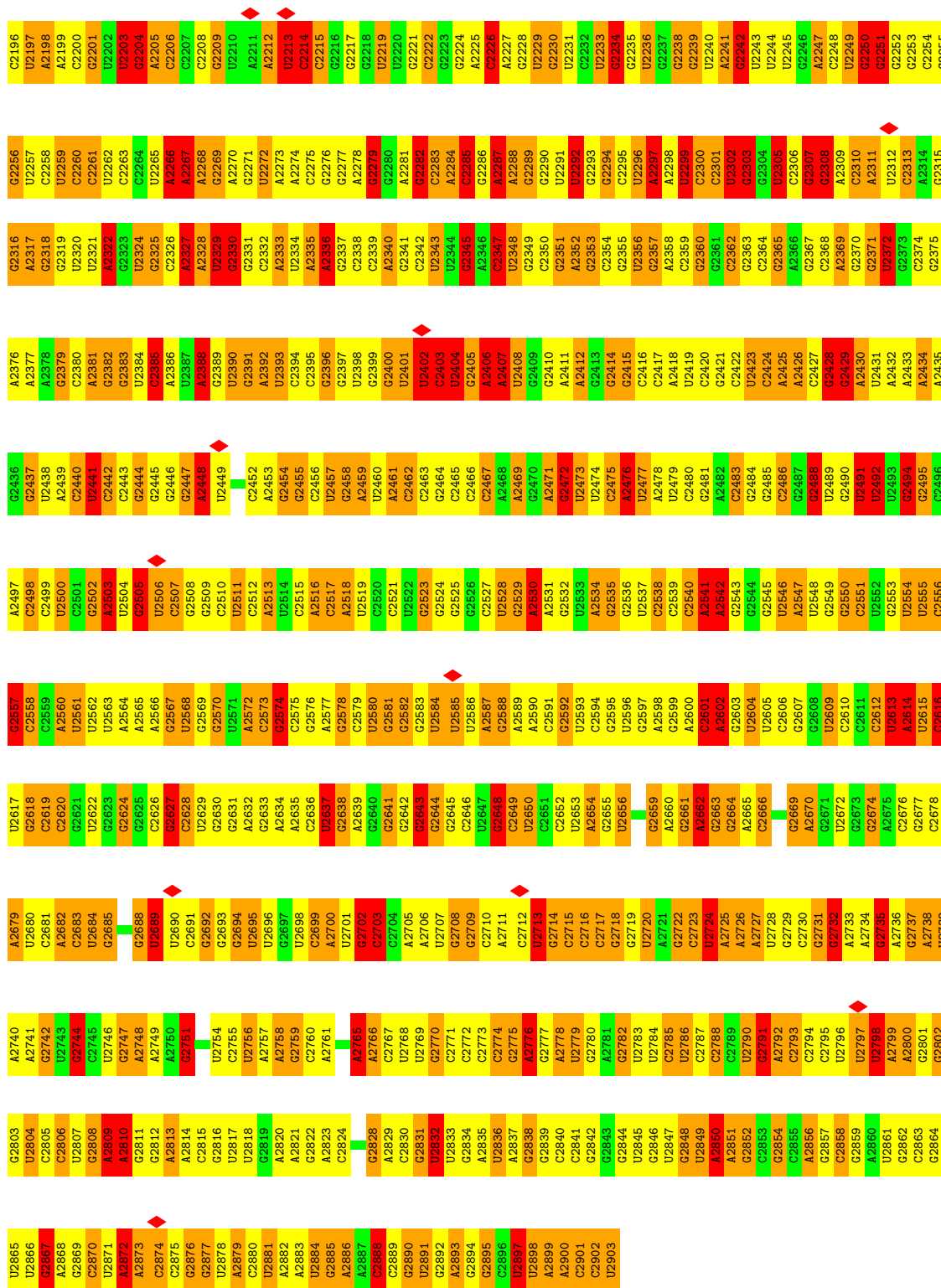


- Molecule 35: 23S RIBOSOMAL RNA

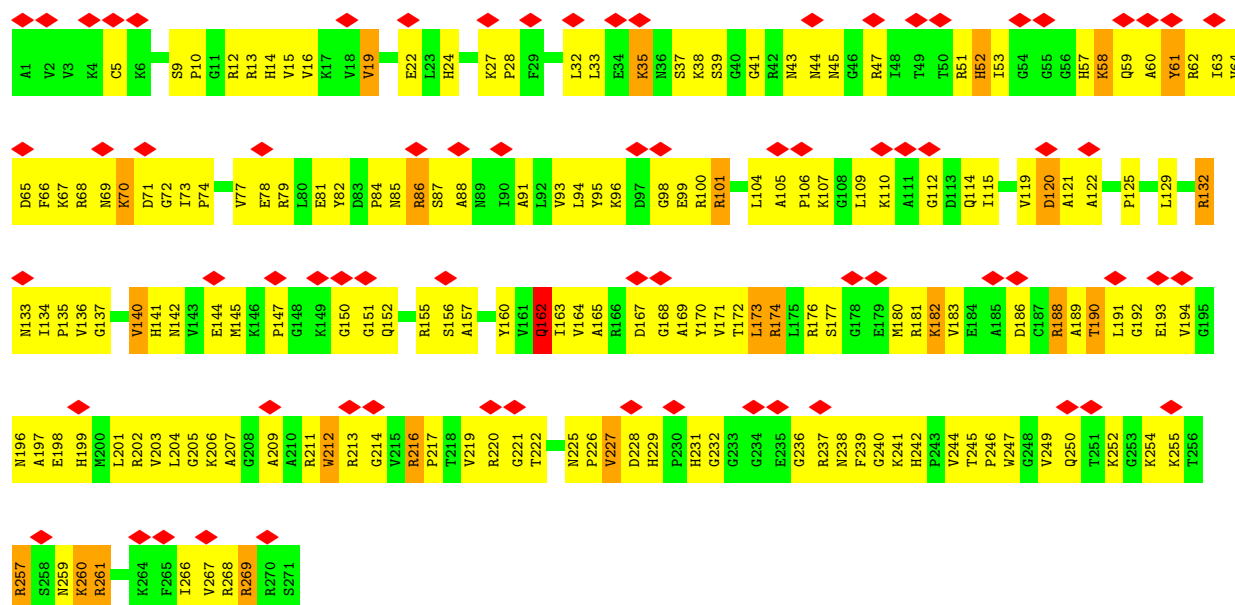


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G1283	G1221	C1158	G1098	G1038	G977	C915	C854	A794	C673	A613	G553	G489	U427
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C1290	G1228	U1105	G1105	A1046	A984	G922	G861	U741	C680	G620	C560	G496	C436
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G1300	G1239	A1175	G1115	G1055	C996	U934	U871	A751	C690	G630	G570	G506	C445
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A1320	A1260	G1195	C1134	A1073	U1015	G954	C890	G771	G711	C650	A590	G530	G467
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				A1095			C912						

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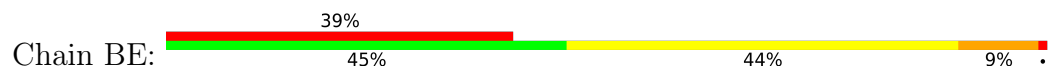
• Molecule 36: 50S RIBOSOMAL PROTEIN L2



• Molecule 37: 50S RIBOSOMAL PROTEIN L3

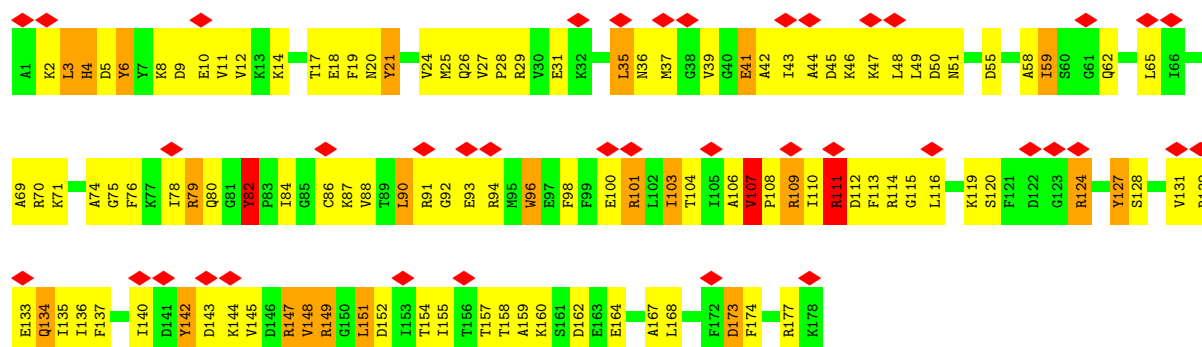


• Molecule 38: 50S RIBOSOMAL PROTEIN L4

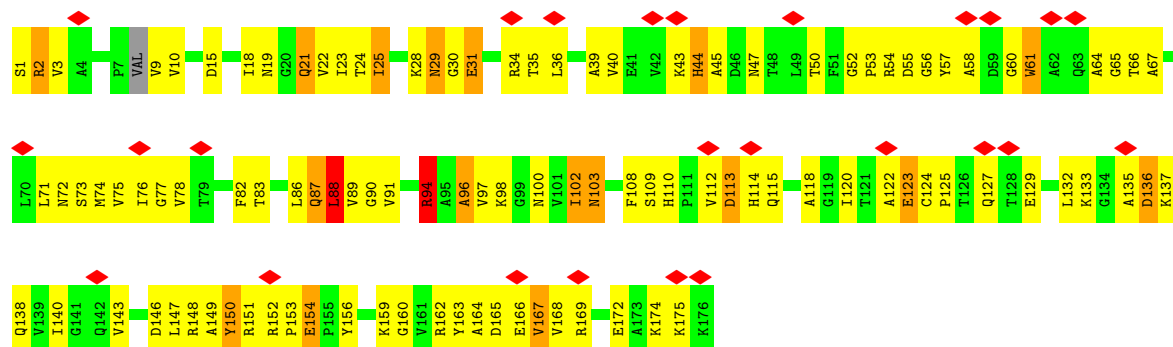




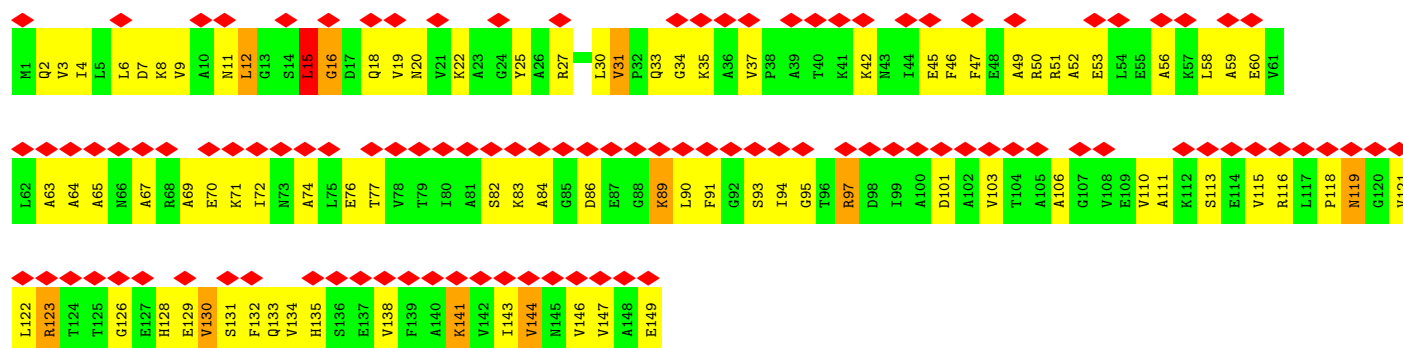
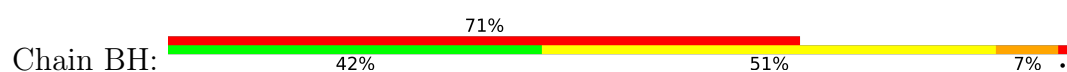
• Molecule 39: 50S RIBOSOMAL PROTEIN L5



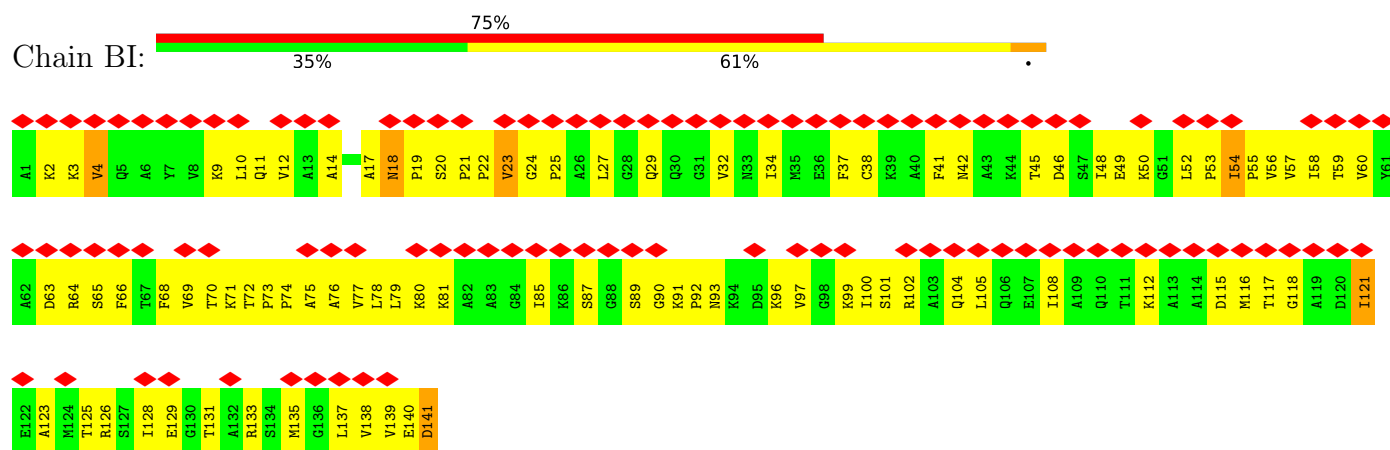
• Molecule 40: 50S RIBOSOMAL PROTEIN L6



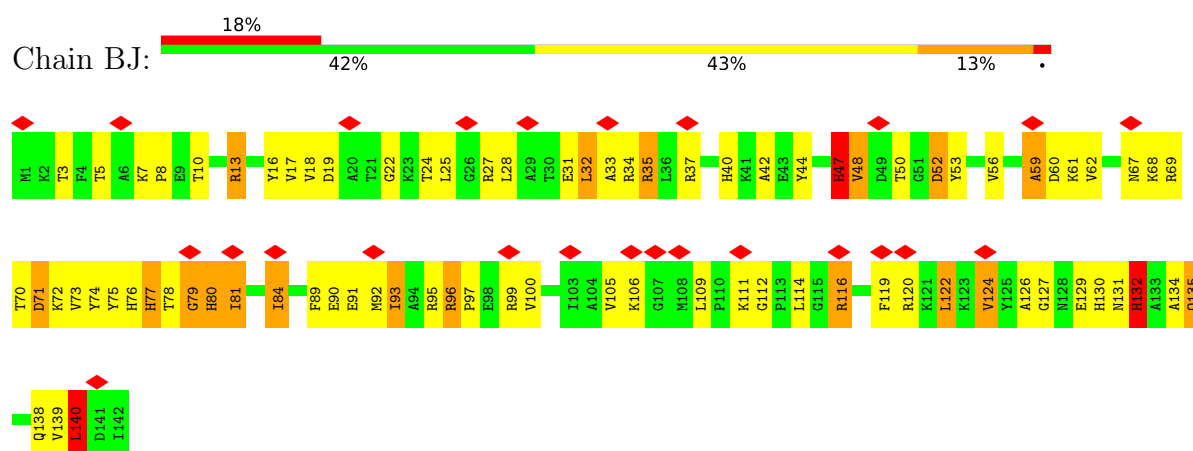
• Molecule 41: 50S RIBOSOMAL PROTEIN L9



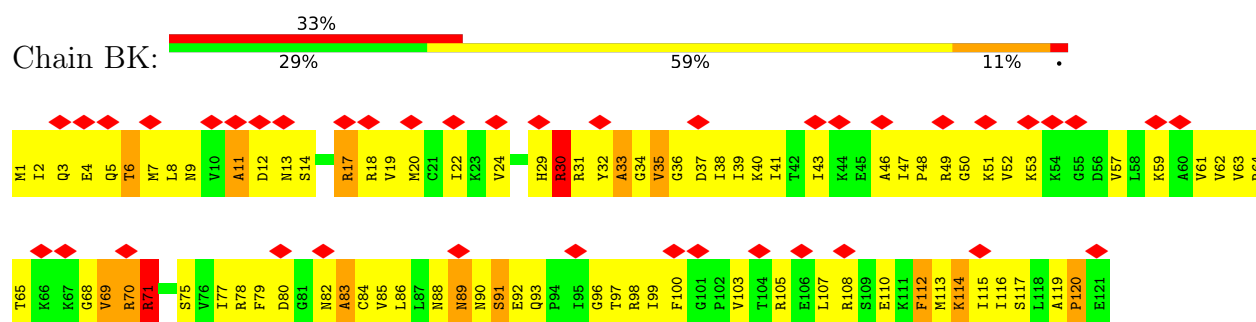
• Molecule 42: 50S RIBOSOMAL PROTEIN L11



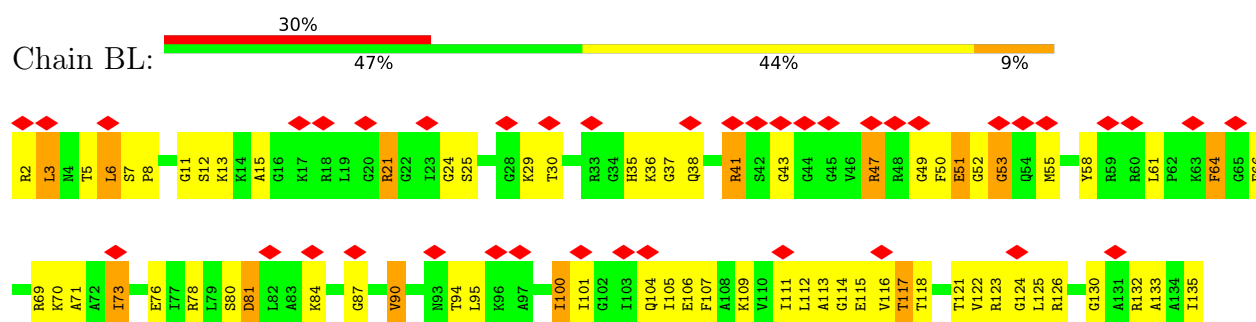
• Molecule 43: 50S RIBOSOMAL PROTEIN L13



• Molecule 44: 50S RIBOSOMAL PROTEIN L14

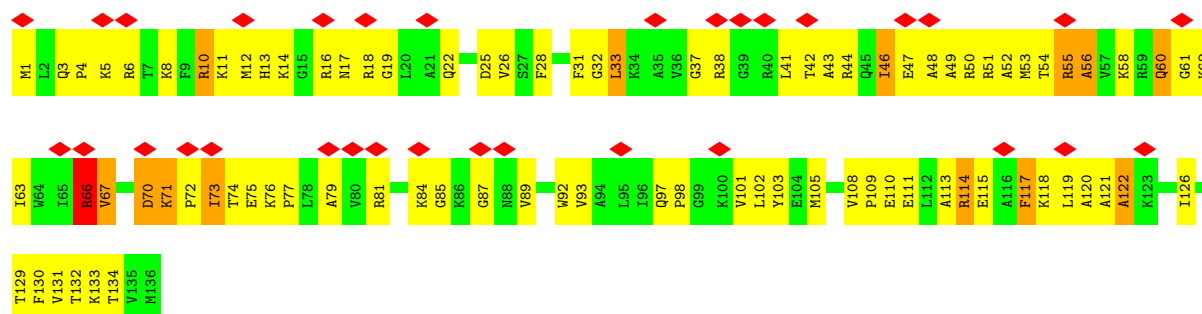


• Molecule 45: 50S RIBOSOMAL PROTEIN L15

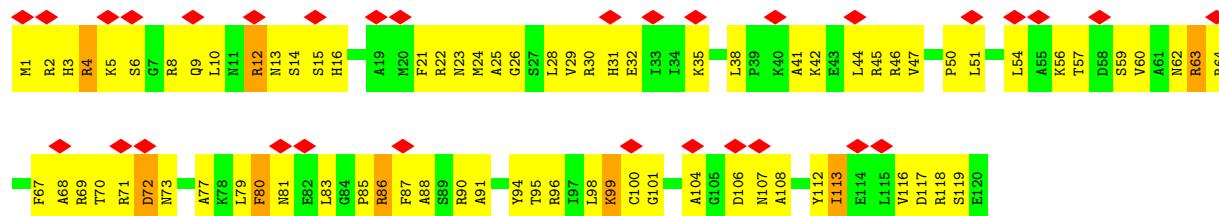




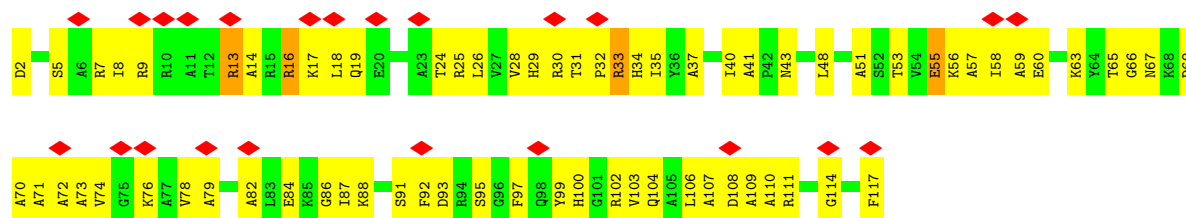
• Molecule 46: 50S RIBOSOMAL PROTEIN L16



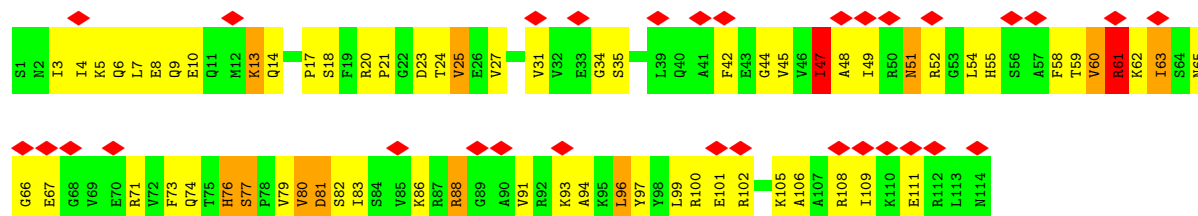
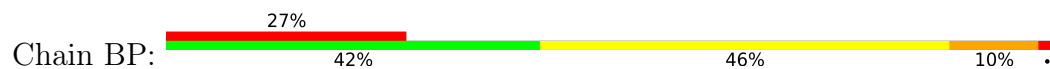
• Molecule 47: 50S RIBOSOMAL PROTEIN L17

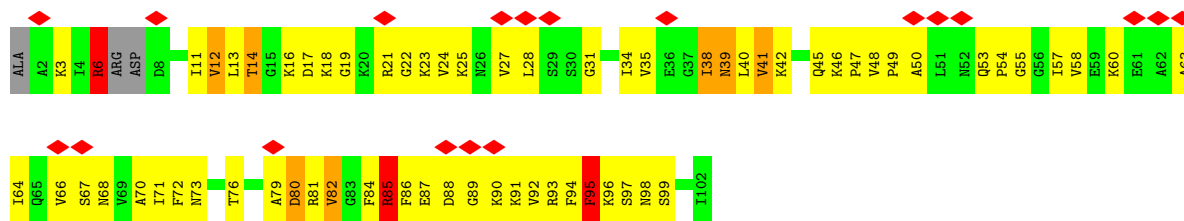


• Molecule 48: 50S RIBOSOMAL PROTEIN L18



• Molecule 49: 50S RIBOSOMAL PROTEIN L19

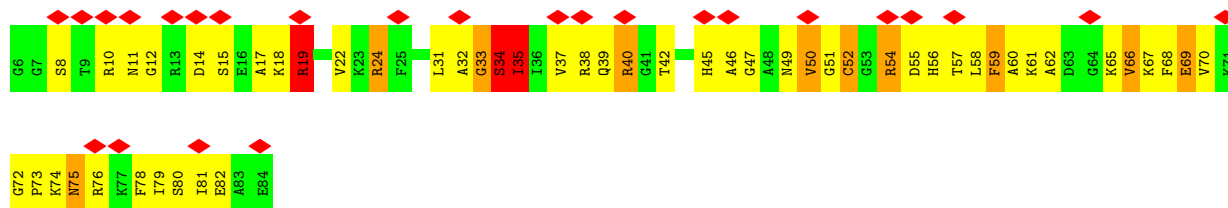




• Molecule 55: 50S RIBOSOMAL PROTEIN L25



• Molecule 56: 50S RIBOSOMAL PROTEIN L27



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 ($\text{\AA}$)	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 ($\text{\AA}$)	1.23, 1.2375, 1.23	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1.98	658/36762 (1.8%)	1.85	1280/57350 (2.2%)
2	AB	2.29	75/1735 (4.3%)	2.55	130/2338 (5.6%)
3	AC	2.28	61/1651 (3.7%)	2.48	105/2225 (4.7%)
4	AD	2.30	68/1665 (4.1%)	2.52	145/2227 (6.5%)
5	AE	2.26	44/1118 (3.9%)	2.45	72/1504 (4.8%)
6	AF	2.36	36/835 (4.3%)	2.43	56/1128 (5.0%)
7	AG	2.36	49/1187 (4.1%)	2.50	78/1591 (4.9%)
8	AH	2.36	47/989 (4.8%)	2.54	73/1326 (5.5%)
9	AI	2.45	57/1034 (5.5%)	2.50	69/1375 (5.0%)
10	AJ	2.43	36/796 (4.5%)	2.44	57/1077 (5.3%)
11	AK	2.39	45/893 (5.0%)	2.65	71/1205 (5.9%)
12	AL	2.45	46/969 (4.7%)	2.43	62/1300 (4.8%)
13	AM	2.29	34/884 (3.8%)	2.48	70/1181 (5.9%)
14	AN	2.33	31/785 (3.9%)	2.47	50/1043 (4.8%)
15	AO	2.36	27/724 (3.7%)	2.54	50/966 (5.2%)
16	AP	2.41	40/648 (6.2%)	2.49	45/870 (5.2%)
17	AQ	2.30	22/657 (3.3%)	2.34	33/881 (3.7%)
18	AR	2.28	18/462 (3.9%)	2.53	39/621 (6.3%)
19	AS	2.41	40/652 (6.1%)	2.57	48/877 (5.5%)
20	AT	2.27	31/671 (4.6%)	2.74	67/888 (7.5%)
21	AU	2.31	17/430 (4.0%)	2.32	25/570 (4.4%)
22	AV	1.39	12/1820 (0.7%)	1.46	31/2836 (1.1%)
23	AX	1.34	1/264 (0.4%)	1.34	1/407 (0.2%)
24	AZ	2.55	4/99 (4.0%)	2.40	7/137 (5.1%)
25	B0	2.34	24/635 (3.8%)	2.62	54/848 (6.4%)
26	B1	2.30	26/510 (5.1%)	2.55	40/677 (5.9%)
27	B2	2.35	17/453 (3.8%)	2.32	23/605 (3.8%)
28	B3	2.40	25/450 (5.6%)	2.59	30/599 (5.0%)
29	B4	2.16	8/416 (1.9%)	2.43	28/554 (5.1%)
30	B5	2.17	61/1748 (3.5%)	2.41	111/2355 (4.7%)
31	B6	2.46	17/380 (4.5%)	2.59	28/498 (5.6%)
32	B7	2.28	19/513 (3.7%)	2.47	33/676 (4.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B8	2.52	15/303 (5.0%)	2.35	10/397 (2.5%)
34	BA	1.94	38/2753 (1.4%)	1.84	87/4288 (2.0%)
35	BB	1.99	1362/69800 (2.0%)	1.85	2359/108892 (2.2%)
36	BC	2.43	97/2121 (4.6%)	2.47	149/2852 (5.2%)
37	BD	2.36	78/1586 (4.9%)	2.44	102/2134 (4.8%)
38	BE	2.29	57/1571 (3.6%)	2.47	99/2113 (4.7%)
39	BF	2.29	60/1444 (4.2%)	2.53	103/1937 (5.3%)
40	BG	2.39	59/1335 (4.4%)	2.47	89/1803 (4.9%)
41	BH	2.35	53/1122 (4.7%)	2.57	80/1515 (5.3%)
42	BI	0.69	2/1046 (0.2%)	0.92	0/1410
43	BJ	2.40	50/1152 (4.3%)	2.52	83/1551 (5.4%)
44	BK	2.39	46/939 (4.9%)	2.43	65/1257 (5.2%)
45	BL	2.29	32/1054 (3.0%)	2.35	61/1403 (4.3%)
46	BM	2.43	52/1093 (4.8%)	2.43	64/1460 (4.4%)
47	BN	2.40	49/973 (5.0%)	2.51	77/1301 (5.9%)
48	BO	2.37	37/902 (4.1%)	2.50	63/1209 (5.2%)
49	BP	2.23	29/929 (3.1%)	2.59	67/1242 (5.4%)
50	BQ	2.37	37/960 (3.9%)	2.59	82/1278 (6.4%)
51	BR	2.39	42/829 (5.1%)	2.43	54/1107 (4.9%)
52	BS	2.41	42/864 (4.9%)	2.58	72/1156 (6.2%)
53	BT	2.24	25/744 (3.4%)	2.52	52/994 (5.2%)
54	BU	2.39	39/761 (5.1%)	2.47	48/1013 (4.7%)
55	BW	2.35	32/766 (4.2%)	2.58	55/1025 (5.4%)
56	BY	2.31	25/603 (4.1%)	2.51	39/797 (4.9%)
All	All	2.09	4054/158485 (2.6%)	2.03	6971/236869 (2.9%)

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	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 4054 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	B6	6	GLN	CA-C	-12.83	1.42	1.52
45	BL	138	ALA	C-N	12.29	1.46	1.33
11	AK	122	PRO	CA-C	-11.74	1.44	1.52
24	AZ	24	ALA	C-O	-11.58	1.00	1.23
42	BI	141	ASP	C-O	-11.57	1.00	1.23

The worst 5 of 6971 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	85	U	P-O3'-C3'	18.67	148.21	120.20
35	BB	2132	U	P-O3'-C3'	17.26	146.10	120.20
35	BB	2585	U	P-O3'-C3'	15.81	143.91	120.20
30	B5	168	ASN	CA-CB-CG	-14.26	98.34	112.60
11	AK	122	PRO	N-CA-CB	-14.24	95.81	103.22

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	182	0
2	AB	1704	0	1732	3	0
3	AC	1624	0	1699	13	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	2	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	4	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	2	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	3	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	335	0
36	BC	2082	0	2157	15	0
37	BD	1565	0	1616	9	0
38	BE	1552	0	1619	9	0
39	BF	1420	0	1460	10	0
40	BG	1316	0	1364	6	0
41	BH	1111	0	1148	1	0
42	BI	1032	0	1088	126	0
43	BJ	1129	0	1162	9	0
44	BK	930	0	1003	7	0
45	BL	1045	0	1117	7	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	9	0
51	BR	816	0	839	9	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	861	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 4.

The worst 5 of 861 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	10
3	AC	204/206 (99%)	158 (78%)	31 (15%)	15 (7%)	1	10
4	AD	203/205 (99%)	160 (79%)	34 (17%)	9 (4%)	2	16
5	AE	148/150 (99%)	110 (74%)	27 (18%)	11 (7%)	1	10

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BH	147/149 (99%)	111 (76%)	31 (21%)	5 (3%)	3	20
42	BI	139/141 (99%)	113 (81%)	21 (15%)	5 (4%)	2	20
43	BJ	140/142 (99%)	106 (76%)	24 (17%)	10 (7%)	1	10
44	BK	119/121 (98%)	95 (80%)	14 (12%)	10 (8%)	0	8
45	BL	141/143 (99%)	115 (82%)	16 (11%)	10 (7%)	1	10
46	BM	134/136 (98%)	105 (78%)	21 (16%)	8 (6%)	1	12
47	BN	118/120 (98%)	96 (81%)	16 (14%)	6 (5%)	1	14
48	BO	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	6	34
49	BP	112/114 (98%)	85 (76%)	19 (17%)	8 (7%)	1	10
50	BQ	115/117 (98%)	84 (73%)	21 (18%)	10 (9%)	0	8
51	BR	101/103 (98%)	80 (79%)	13 (13%)	8 (8%)	1	9
52	BS	108/110 (98%)	76 (70%)	21 (19%)	11 (10%)	0	6
53	BT	91/93 (98%)	60 (66%)	25 (28%)	6 (7%)	1	11
54	BU	94/102 (92%)	71 (76%)	16 (17%)	7 (7%)	1	10
55	BW	92/94 (98%)	76 (83%)	10 (11%)	6 (6%)	1	12
56	BY	77/79 (98%)	46 (60%)	18 (23%)	13 (17%)	0	2
All	All	5858/5971 (98%)	4523 (77%)	956 (16%)	379 (6%)	2	12

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 ⓘ

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%)	22	42
3	AC	170/170 (100%)	158 (93%)	12 (7%)	13	35
4	AD	172/172 (100%)	161 (94%)	11 (6%)	16	37
5	AE	113/113 (100%)	107 (95%)	6 (5%)	20	41
6	AF	87/87 (100%)	83 (95%)	4 (5%)	24	45
7	AG	123/123 (100%)	122 (99%)	1 (1%)	73	79
8	AH	104/104 (100%)	101 (97%)	3 (3%)	37	57
9	AI	105/105 (100%)	101 (96%)	4 (4%)	29	50
10	AJ	86/86 (100%)	81 (94%)	5 (6%)	18	39
11	AK	90/90 (100%)	87 (97%)	3 (3%)	33	55
12	AL	103/103 (100%)	100 (97%)	3 (3%)	37	57
13	AM	91/91 (100%)	87 (96%)	4 (4%)	25	46
14	AN	79/79 (100%)	75 (95%)	4 (5%)	21	42
15	AO	76/76 (100%)	71 (93%)	5 (7%)	15	36
16	AP	65/65 (100%)	60 (92%)	5 (8%)	12	32
17	AQ	74/74 (100%)	71 (96%)	3 (4%)	27	48
18	AR	48/48 (100%)	46 (96%)	2 (4%)	26	48
19	AS	70/70 (100%)	67 (96%)	3 (4%)	26	47
20	AT	65/65 (100%)	62 (95%)	3 (5%)	24	45
21	AU	44/44 (100%)	39 (89%)	5 (11%)	5	18
25	B0	67/67 (100%)	64 (96%)	3 (4%)	24	46
26	B1	55/55 (100%)	50 (91%)	5 (9%)	9	27
27	B2	48/48 (100%)	46 (96%)	2 (4%)	26	48
28	B3	47/47 (100%)	46 (98%)	1 (2%)	47	65
29	B4	45/45 (100%)	42 (93%)	3 (7%)	15	36
30	B5	181/181 (100%)	173 (96%)	8 (4%)	25	46
31	B6	38/38 (100%)	36 (95%)	2 (5%)	20	41
32	B7	51/51 (100%)	50 (98%)	1 (2%)	48	66
33	B8	34/34 (100%)	34 (100%)	0	100	100
36	BC	216/216 (100%)	207 (96%)	9 (4%)	26	48
37	BD	164/164 (100%)	147 (90%)	17 (10%)	7	22
38	BE	165/165 (100%)	157 (95%)	8 (5%)	23	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BF	149/149 (100%)	143 (96%)	6 (4%)	28	49
40	BG	136/137 (99%)	126 (93%)	10 (7%)	13	33
41	BH	114/114 (100%)	107 (94%)	7 (6%)	17	38
42	BI	109/109 (100%)	107 (98%)	2 (2%)	51	67
43	BJ	116/116 (100%)	112 (97%)	4 (3%)	32	54
44	BK	102/102 (100%)	95 (93%)	7 (7%)	14	36
45	BL	102/102 (100%)	97 (95%)	5 (5%)	22	43
46	BM	109/109 (100%)	104 (95%)	5 (5%)	24	45
47	BN	100/100 (100%)	97 (97%)	3 (3%)	36	57
48	BO	86/86 (100%)	84 (98%)	2 (2%)	44	63
49	BP	99/99 (100%)	94 (95%)	5 (5%)	21	42
50	BQ	89/89 (100%)	81 (91%)	8 (9%)	9	27
51	BR	84/84 (100%)	77 (92%)	7 (8%)	10	30
52	BS	93/93 (100%)	88 (95%)	5 (5%)	20	41
53	BT	80/80 (100%)	70 (88%)	10 (12%)	4	16
54	BU	81/83 (98%)	78 (96%)	3 (4%)	30	51
55	BW	78/78 (100%)	73 (94%)	5 (6%)	16	37
56	BY	59/59 (100%)	52 (88%)	7 (12%)	5	17
All	All	4842/4845 (100%)	4587 (95%)	255 (5%)	22	41

5 of 255 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	B5	207	VAL
51	BR	64	VAL
37	BD	183	GLU
51	BR	21	ARG
53	BT	34	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 153 such sidechains are listed below:

Mol	Chain	Res	Type
43	BJ	77	HIS
53	BT	70	HIS
44	BK	29	HIS

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Mol	Chain	Res	Type
49	BP	65	ASN
55	BW	5	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1529/1530 (99%)	270 (17%)	34 (2%)
22	AV	76/77 (98%)	15 (19%)	0
23	AX	10/11 (90%)	8 (80%)	0
34	BA	112/117 (95%)	17 (15%)	2 (1%)
35	BB	2902/2903 (99%)	472 (16%)	56 (1%)
All	All	4629/4638 (99%)	782 (16%)	92 (1%)

5 of 782 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 ⓘ

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	0.65	0	25,30,35	0.74	1 (4%)

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	2.45	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 oligosaccharides 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

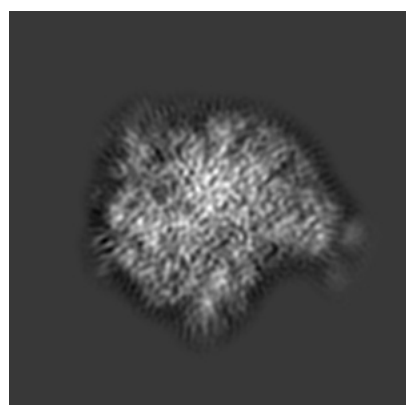
6 Map visualisation [i](#)

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.

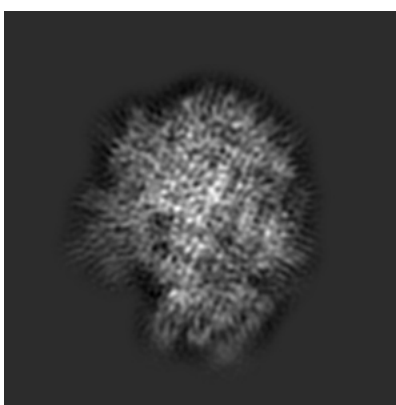
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

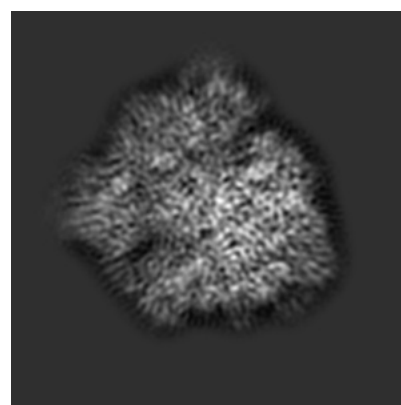
6.1.1 Primary map



X



Y

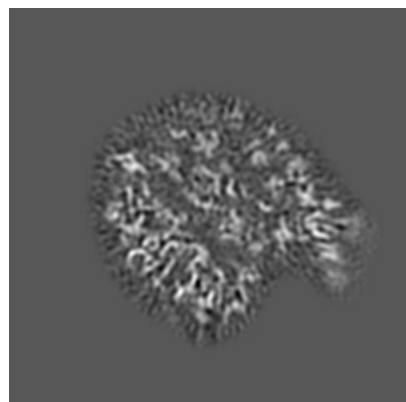


Z

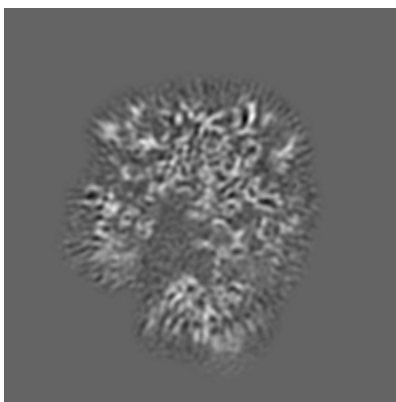
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

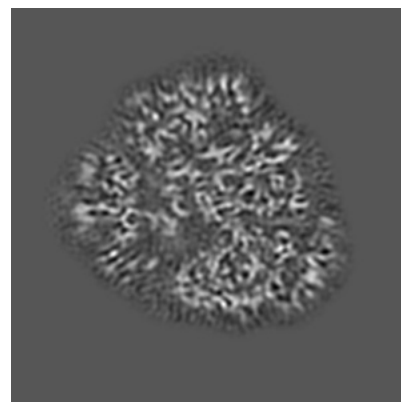
6.2.1 Primary map



X Index: 147



Y Index: 147

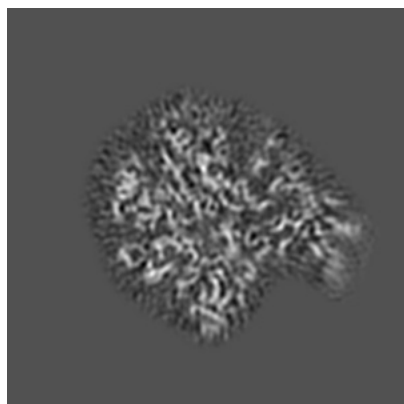


Z Index: 147

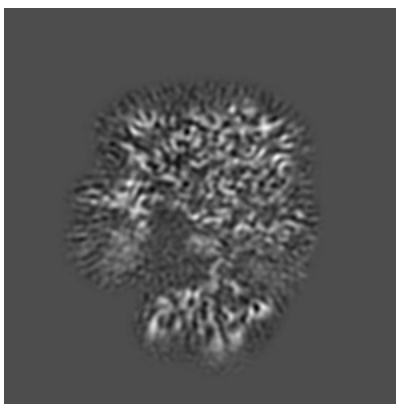
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

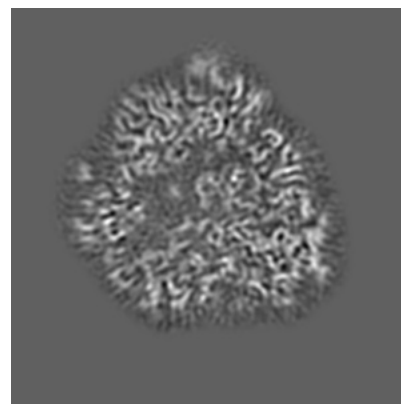
6.3.1 Primary map



X Index: 152



Y Index: 155

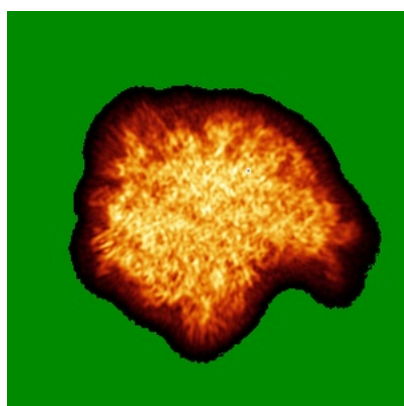


Z Index: 136

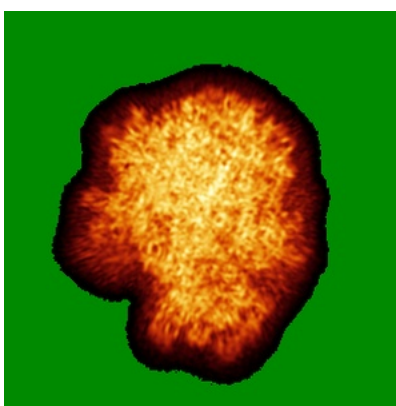
The images above show the largest variance slices of the map in three orthogonal directions.

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

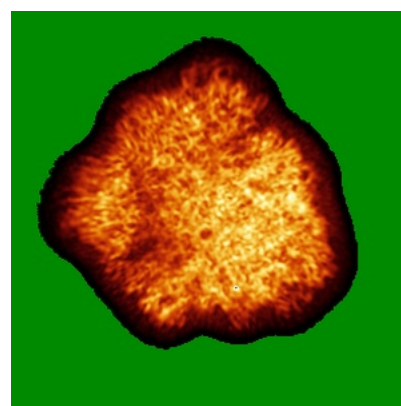
6.4.1 Primary map



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

This section was not generated.

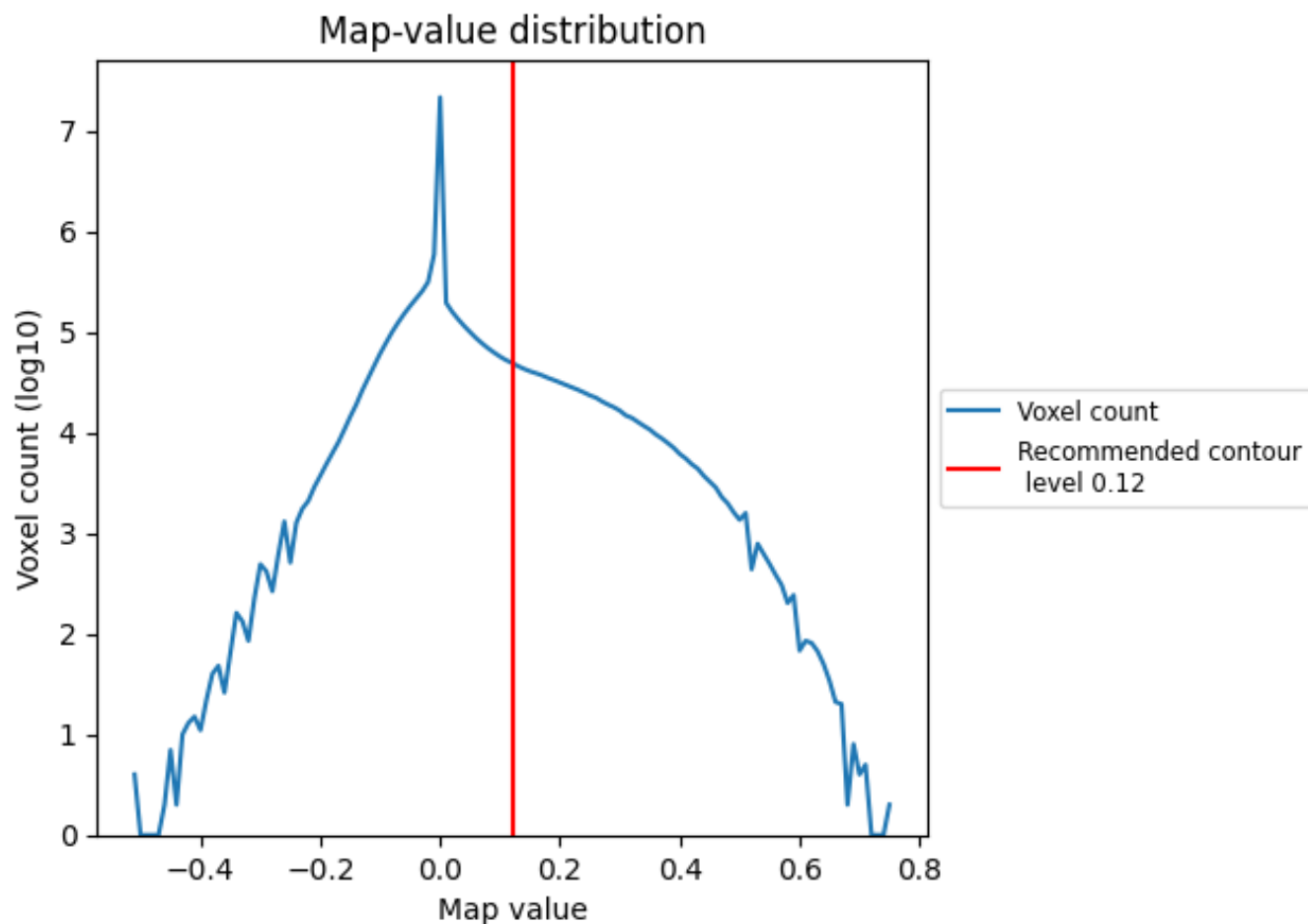
6.6 Mask visualisation

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

7 Map analysis [i](#)

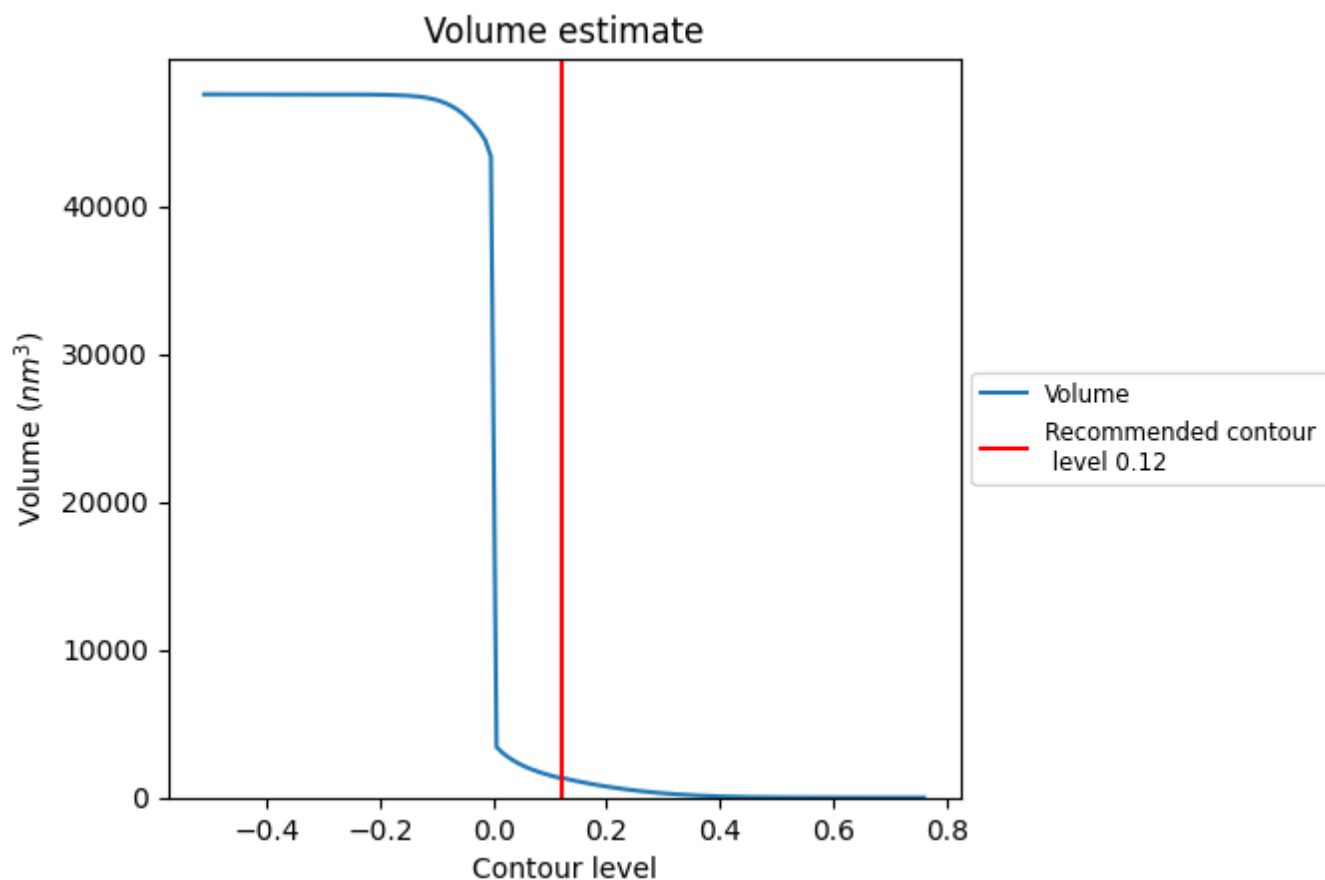
This section contains the results of statistical analysis of the map.

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.

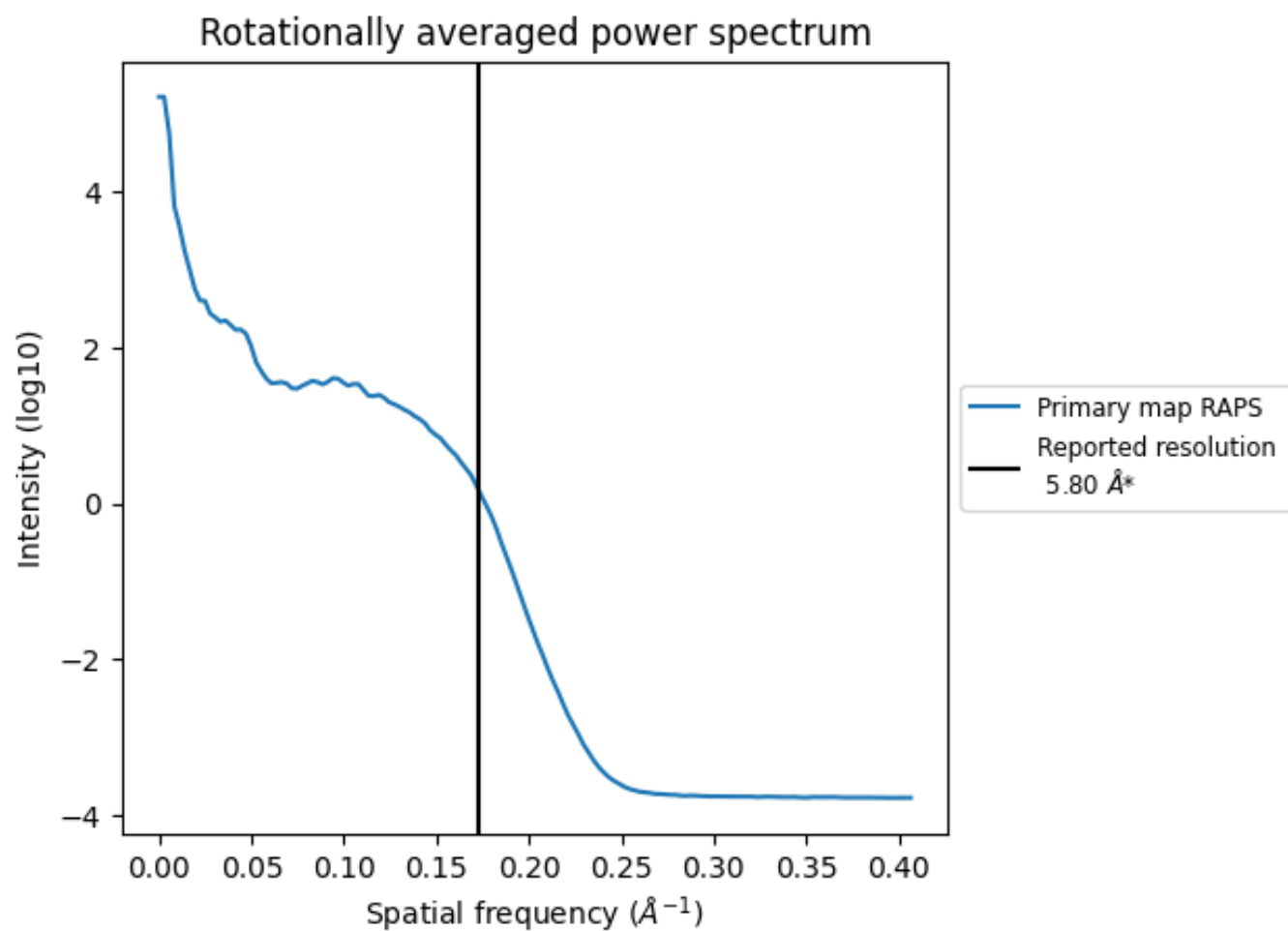
7.2 Volume estimate [i](#)



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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.172 Å⁻¹

8 Fourier-Shell correlation

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

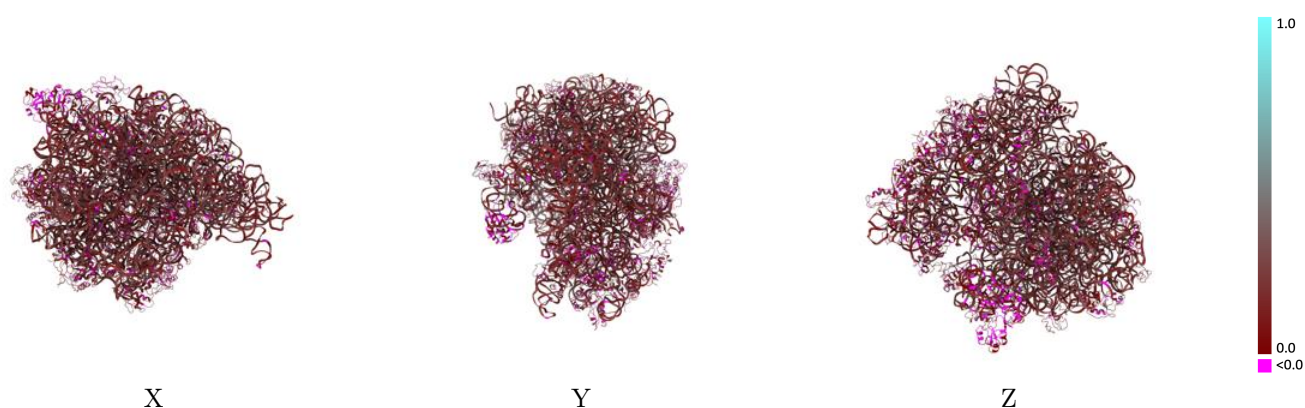
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1657 and PDB model 4V5H. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

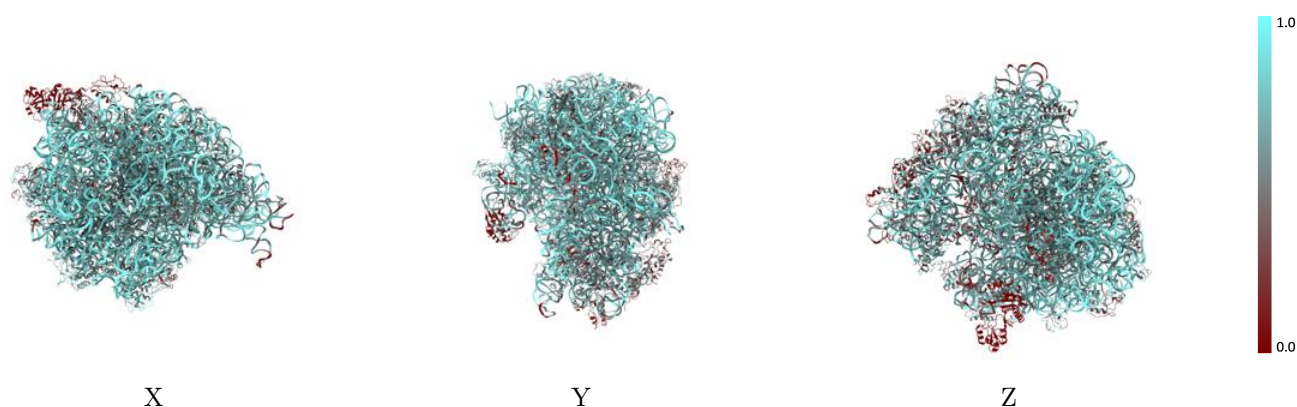
This section was not generated.

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



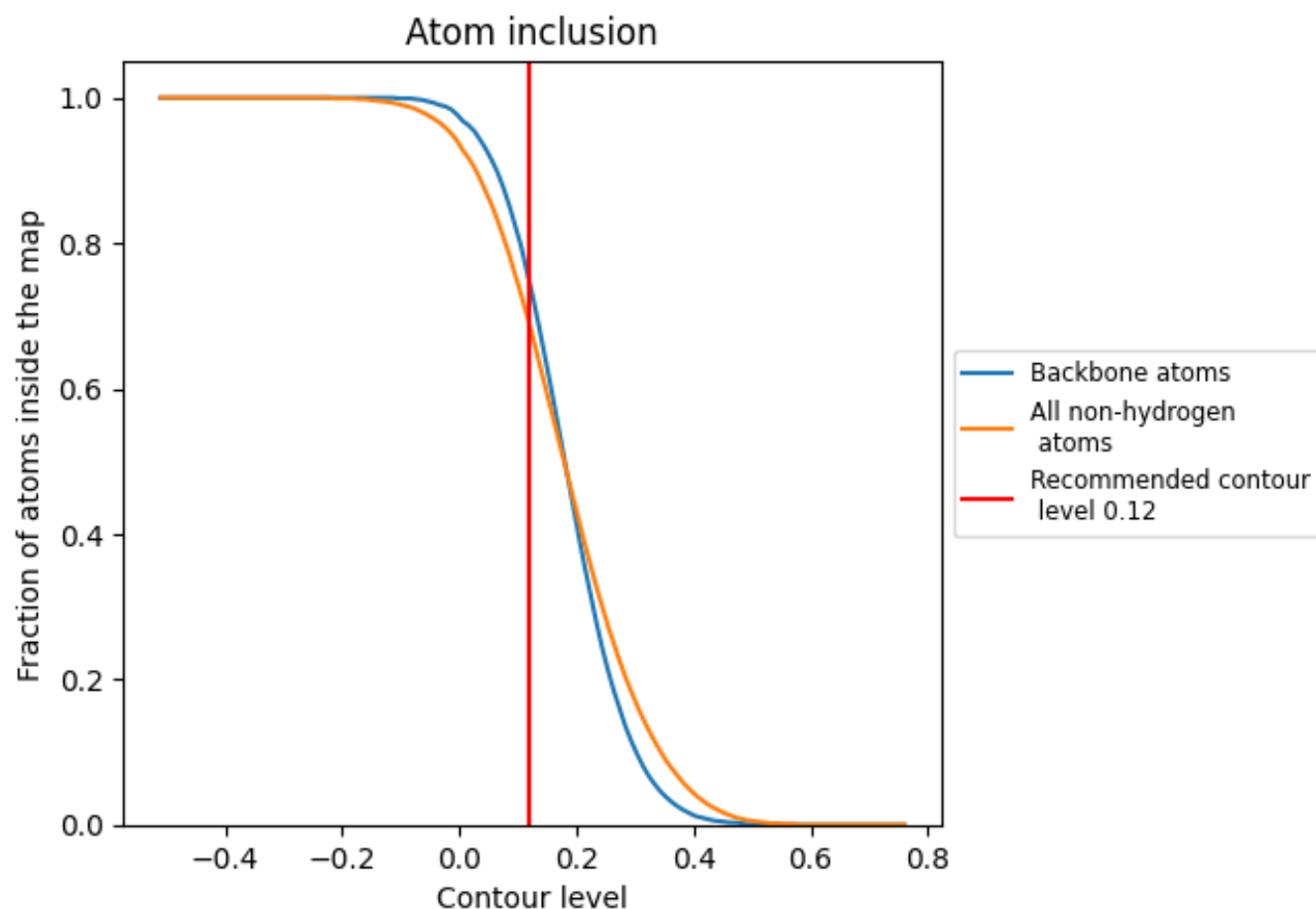
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 -0.0020
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