



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:01 PM UTC

PDB ID : 5APN / pdb_00005apn
EMDB ID : EMD-3152
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and N-terminally tagged Rei1
Authors : Greber, B.J.; Gerhardy, S.; Leitner, A.; Leibundgut, M.; Salem, M.; Boehringer, D.; Leulliot, N.; Aebersold, R.; Panse, V.G.; Ban, V.
Deposited on : 2015-09-17
Resolution : 3.91 Å(reported)

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

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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

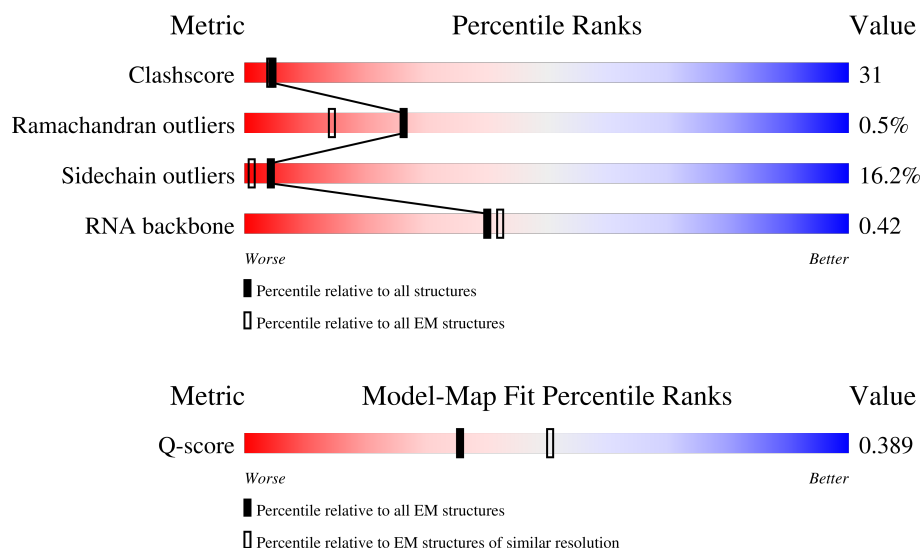
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.91 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.



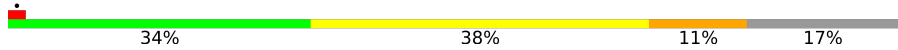
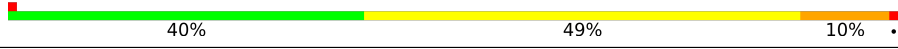
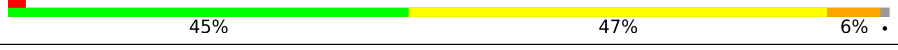
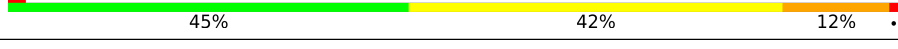
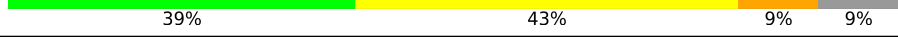
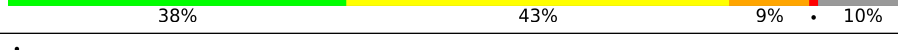
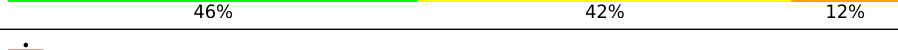
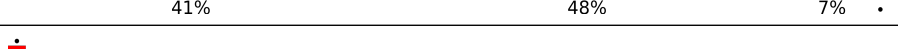
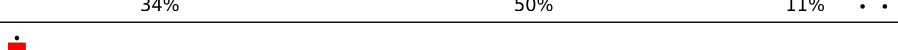
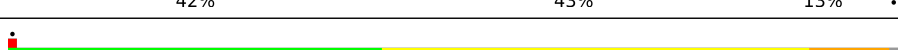
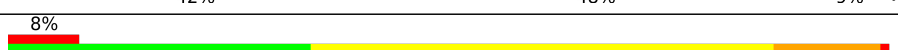
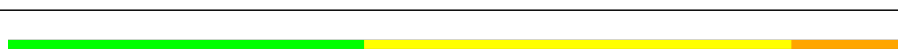
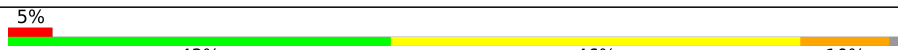
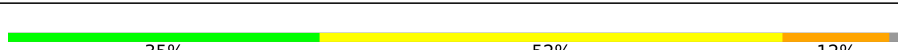
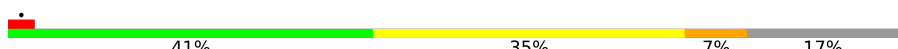
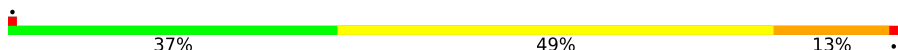
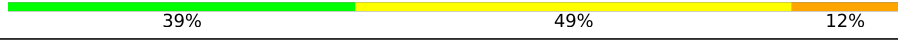
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	5	3396	
2	7	121	
3	8	158	

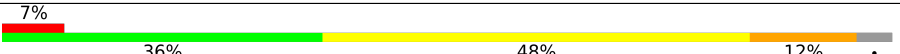
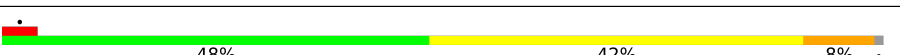
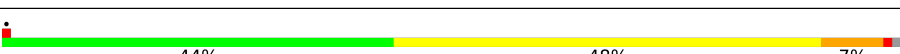
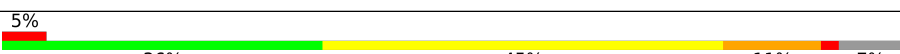
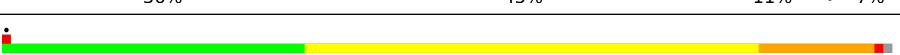
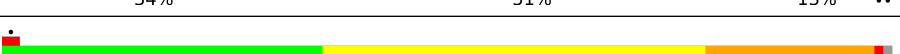
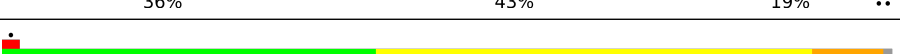
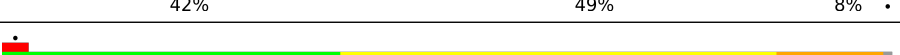
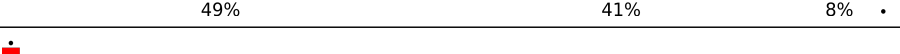
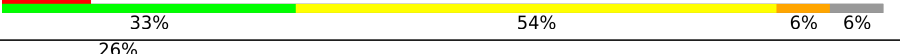
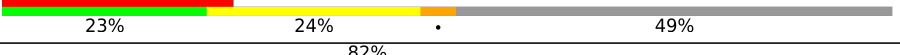
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Mol	Chain	Length	Quality of chain
4	A	254	
5	B	387	
6	C	362	
7	D	297	
8	E	176	
9	F	244	
10	G	256	
11	H	191	
12	I	221	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	155	
26	X	142	
27	Y	127	
28	Z	136	

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Mol	Chain	Length	Quality of chain
29	a	149	
30	b	59	
31	c	105	
32	d	113	
33	e	130	
34	f	107	
35	g	121	
36	h	120	
37	i	100	
38	j	88	
39	k	78	
40	l	51	
41	m	128	
42	o	106	
43	p	92	
44	q	312	
45	x	616	
46	y	414	
47	z	85	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 129324 atoms, of which 3 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3112	Total	C	N	O	P	0	0
			66537	29736	11996	21694	3111		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	212	Total	C	N	O	S	0	0
			1630	1021	325	283	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	175	Total	C	N	O	S	0	0
			1355	877	242	235	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	M	137	Total	C	N	O	S	0
			1059	678	200	179	2	0

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	N	203	Total	C	N	O	S	0
			1720	1077	361	281	1	0

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	O	197	Total	C	N	O	S	0
			1555	1003	289	262	1	0

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	183	Total	C	N	O		0
			1442	896	287	259		0

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	Q	185	Total	C	N	O	S	0
			1441	908	290	241	2	0

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	156	Total	C	N	O		0
			1258	781	265	212		0

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	102	Total	C	N	O		0	0
			808	524	132	152			

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	129	Total	C	N	O	S	0	0
			1034	655	207	171	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	120	Total	C	N	O	S	0	0
			962	618	169	172	3		

- Molecule 45 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	579	Total	C	N	O	S	0	0
			4477	2823	772	867	15		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-22	MET	-	initiating methionine	UNP Q03862
x	-21	GLY	-	expression tag	UNP Q03862
x	-20	SER	-	expression tag	UNP Q03862
x	-19	SER	-	expression tag	UNP Q03862
x	-18	HIS	-	expression tag	UNP Q03862
x	-17	HIS	-	expression tag	UNP Q03862
x	-16	HIS	-	expression tag	UNP Q03862
x	-15	HIS	-	expression tag	UNP Q03862
x	-14	HIS	-	expression tag	UNP Q03862
x	-13	HIS	-	expression tag	UNP Q03862
x	-12	SER	-	expression tag	UNP Q03862
x	-11	SER	-	expression tag	UNP Q03862
x	-10	GLY	-	expression tag	UNP Q03862
x	-9	LEU	-	expression tag	UNP Q03862
x	-8	VAL	-	expression tag	UNP Q03862
x	-7	PRO	-	expression tag	UNP Q03862
x	-6	ARG	-	expression tag	UNP Q03862
x	-5	GLY	-	expression tag	UNP Q03862
x	-4	SER	-	expression tag	UNP Q03862

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Chain	Residue	Modelled	Actual	Comment	Reference
x	-3	HIS	-	expression tag	UNP Q03862
x	-2	MET	-	expression tag	UNP Q03862
x	-1	LEU	-	expression tag	UNP Q03862
x	0	GLU	-	expression tag	UNP Q03862

- Molecule 46 is a protein called Cytoplasmic 60S subunit biogenesis factor REI1.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	y	211	Total	C	H	N	O	S	0	0
			1727	1095	3	307	314	8		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	-20	HIS	-	expression tag	UNP P38344
y	-19	HIS	-	expression tag	UNP P38344
y	-18	HIS	-	expression tag	UNP P38344
y	-17	HIS	-	expression tag	UNP P38344
y	-16	HIS	-	expression tag	UNP P38344
y	-15	HIS	-	expression tag	UNP P38344
y	-14	ASP	-	expression tag	UNP P38344
y	-13	TYR	-	expression tag	UNP P38344
y	-12	ASP	-	expression tag	UNP P38344
y	-11	ILE	-	expression tag	UNP P38344
y	-10	PRO	-	expression tag	UNP P38344
y	-9	THR	-	expression tag	UNP P38344
y	-8	THR	-	expression tag	UNP P38344
y	-7	GLU	-	expression tag	UNP P38344
y	-6	ASN	-	expression tag	UNP P38344
y	-5	LEU	-	expression tag	UNP P38344
y	-4	TYR	-	expression tag	UNP P38344
y	-3	PHE	-	expression tag	UNP P38344
y	-2	GLN	-	expression tag	UNP P38344
y	-1	GLY	-	expression tag	UNP P38344
y	0	ALA	-	expression tag	UNP P38344

- Molecule 47 is a protein called ALB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	z	85	Total	C	N	O	0	0
			510	340	85	85		

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	5	259	Total 259	Mg 259	0
48	7	6	Total 6	Mg 6	0
48	8	7	Total 7	Mg 7	0
48	B	1	Total 1	Mg 1	0
48	C	2	Total 2	Mg 2	0
48	N	1	Total 1	Mg 1	0
48	P	1	Total 1	Mg 1	0
48	V	1	Total 1	Mg 1	0
48	a	2	Total 2	Mg 2	0

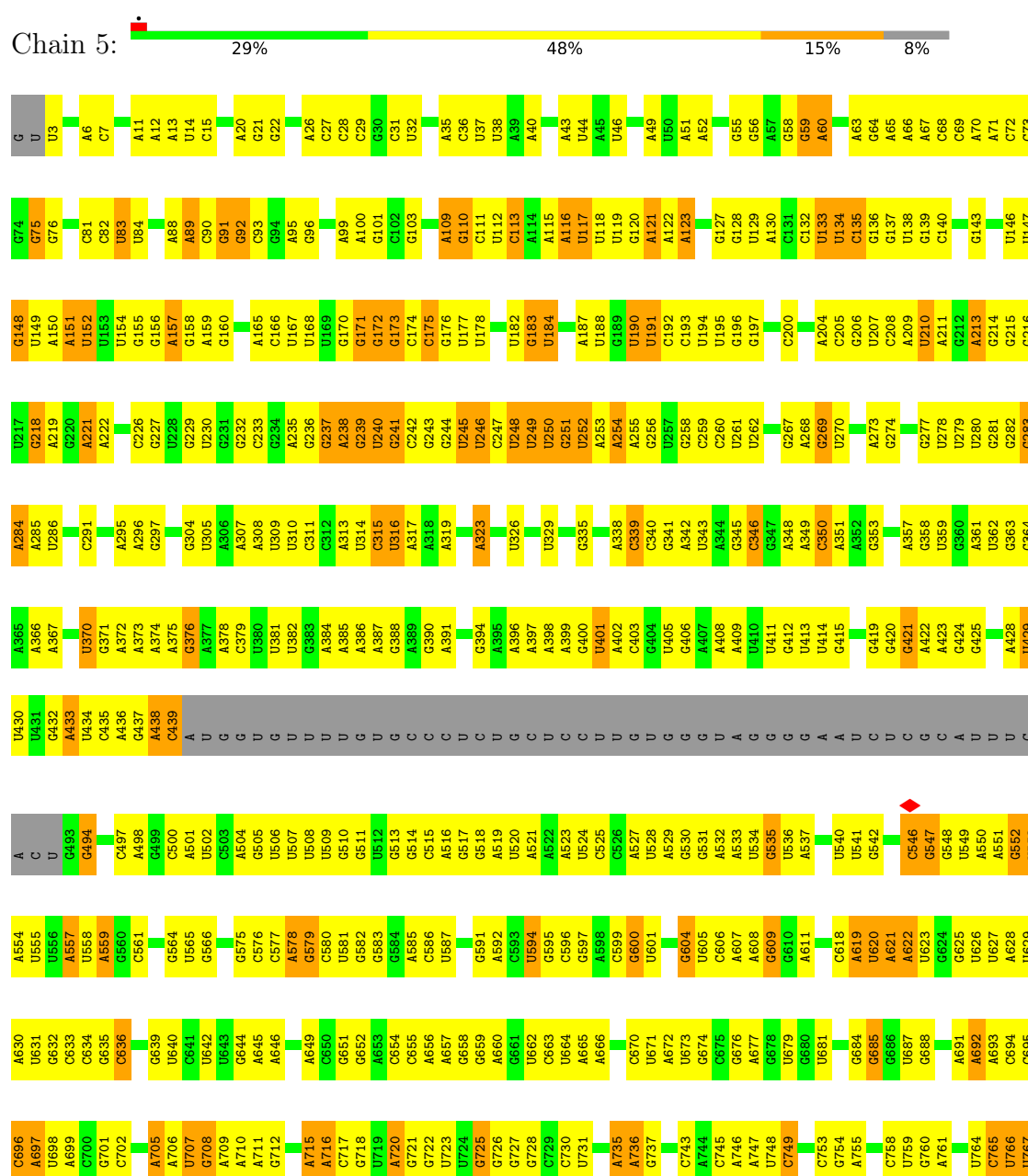
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	p	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0

3 Residue-property plots

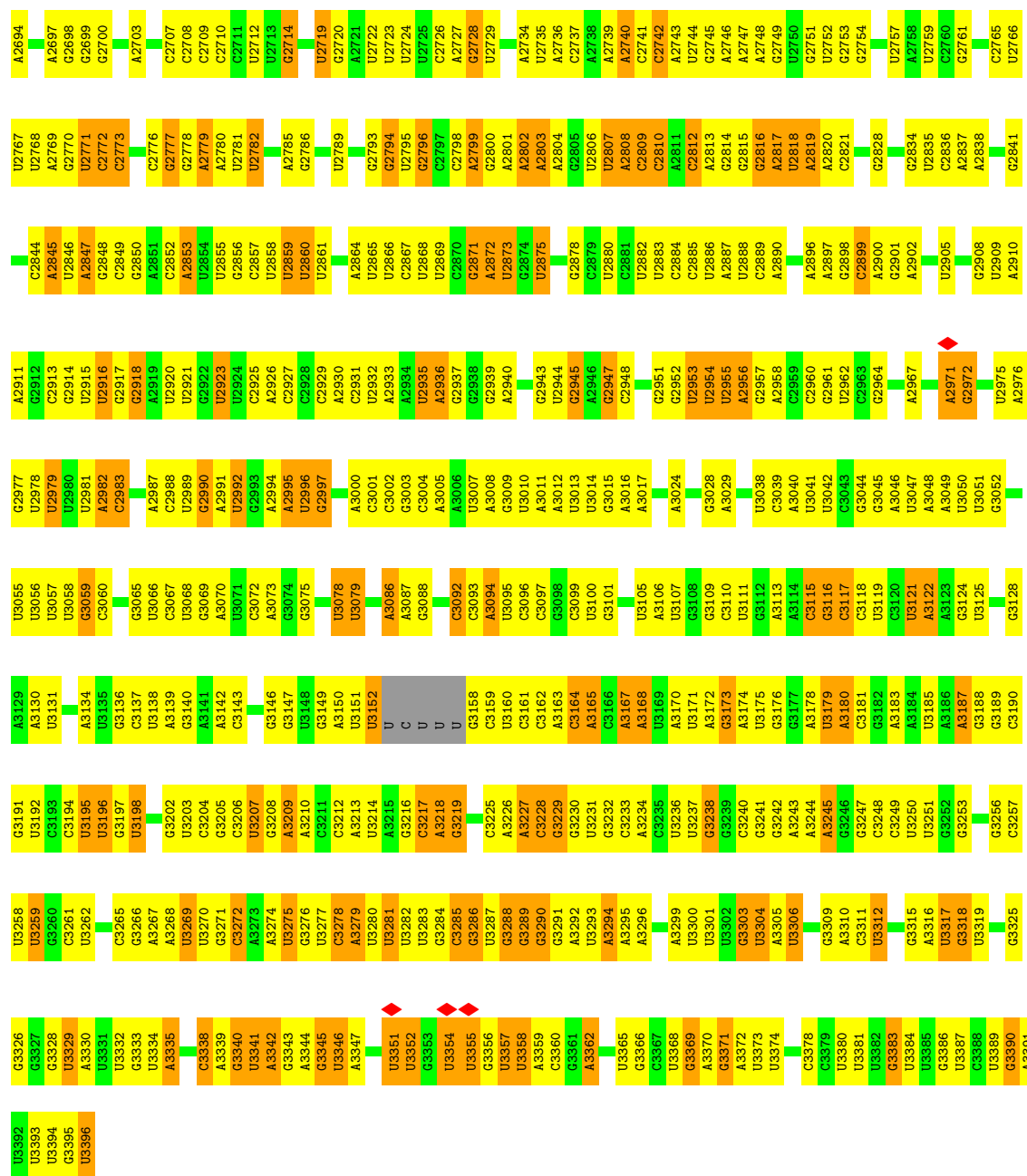
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

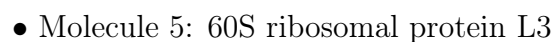
• Molecule 1: 25S rRNA



C1660	A1593	A1524	A1456	G1380	U1309	U1241	G1171	A1103	C	A970	U905	A836	C768
G1661	A1594	G1525	U1457	A1361	G1312	U1242	G1172	G1104	C	G371	A906	A837	G769
C1662	U1595	U1526	U1458	G1362	G1313	G1243		A1105	U	A972	G907	G838	G770
	C1596	G1363	C1459	G1363	G1314	A1244	C1176	U1108		A973	G908	C839	A771
	C1597	U1532	A1460	U1384	C1314	A1245	G1177	U1109	G1036	G974	G909	G840	U772
G1668	U1598	U1533	A1461	C1365	C1315	A1246	G1178	U1110	C1037	C975	G910	A841	
C1669	G1599	A1534	A1462	A1386	C1316	U1247	A1179	U1111	C1038	U976	C911	G842	
C1670	A1600	A1535	U1463	G1367	A1317	C1248	A1180	U1112	U1039	C977	G912	G843	U776
C1671	G1536	U1388	G1464	U1388	A1318		A1181			G978	G913	G844	U777
			A1465			A1252	C1182	G1115	A1047	U979	A914	G845	
A1676	A1605	A1539	G1466	G1392	G1323	U1253	C1183	G1116	A1048	A980	A915	A846	A780
G1677	U1540	U1540	A1467	C1284	U1325	G1254	A1184	G1117	C1049	U981	G916	A847	G781
A1678	U1607	G1541	A1468	G1395	U1326	C1255		C1118	A1050	A982	A917	A848	
A1679	C1608	G1542	C1469	C1396	A1326	G1256	A1190	C1119	U1051	A983	C918	C849	A784
G1680	C1609	G1543	U1470	C1397	C1327	C1257	U1191	C1120	U1052	U985	A921	U850	G785
U1681	G1610	U1471	U1471	U1398	C1328	C1257	C1192	U1121	A1053	U986	G922	G851	G786
A1682		U1472	A1473	A1399	U1329	U1258	A1193	U1122	U1054	U987	C923	G852	G787
A1683		G1473	G1473	C1400	A1330	G1259	G1194	U1123	A1055	U988	G924	G853	G788
U1684		A1474	A1474	G1405	U1331	G1261	A1195	U1125	U1056	A989	A925	G856	U790
C1685		A1475	A1475	A1406	A1332	G1262		G1126	A1057	U990	A926	G857	A791
U1686		G1476	G1476	A1407	C1333	A1263	A1200	G1127	U1058	A996	C927	A858	U792
U1687		A1477	A1477	G1408	U1334	G1264	C1201	U1128	G1059	A997	C928	G859	C793
U1688		C1478	G1478		C1335	U1265	A1202	U1129	G1066	A998	A929	G860	U794
U1689		U1479	U1479	C1411	U1336	G1266	G1203	A1130	U1067	G999	U930	G861	G795
C1690		G1480	G1480		A1337		A1204	G1131	C1068	U1000	U931		U796
U1691		A1481	A1481		C1338		A1205	C1132	A1064	A996	G934	G869	
U1692				C1416	C1339	U1269	A1206	G1133	A1065	A997	U935	G870	U797
U1692			U1484	G1417	G1340	A1270	C1207	G1134	G1066	A998	A936	G871	G798
C1693			G1488	A1418	U1341	C1271	U1208		U1067	G999	G937	C873	G799
				G1561		G1272	G1209	U1138	C1068	U1000	C938	U874	G800
C1698					G1345		G1210	G1139		G1001	U939		A801
U1702	U1629	C1562	A1491	C1423	G1346	U1276	U1211	G1140	G1072	A1002	G940	C877	C802
U1703	C1630	U1563	G1492	C1424	U1347	C1277	G1212	A1143	U1073	A1003	G941	C878	C803
	A1632	G1565	U1493		U1348	A1278	G1213		U1074	U1004	U942	U879	C804
C1710	C1633	U1566	G1494	U1427	G1349	C1279		A1144	U1075	G1005	U943	G880	G805
C1711	G1634	U1567	U1495	U1428	A1350	C1280	A1217	G1145	C1076	A1006	C944	C881	A806
G1712	G1635	U1568	C1496	G1429	U1351	G1281	U1218	C1146	U1077	U1007	C945	A882	A807
G1713	U1636	U1569	G1497	U1430	A1352	G1282	C1219	G1147	U1078	U1008	U946	A883	A808
A1714	A1637	U1570	A1498	G1431	U1353	C1283	C1219	G1148	U1079	A1009	G947	A884	
A1715	U1638	A1571	G1499	C1432	G1354	C1284	U1220	G1149	A1080	G1010	C948	U885	G815
U1716	C1639	U1572	G1500	A1433	A1355	U1285	A1221	A1150	U1081	C949	C949	C886	G816
U1717	G1640	U1573	U1501	G1434	U1356	G1286	G1222	U1151	U1082	G950	G950	G887	A817
G1718	U1641	C1574	G1502	U1435	G1357	A1286	C1224	G1152	G1083	A951	A951	A888	C818
G1719	A1642	U1575	A1503	U1436	U1357		A1225	A1153	A1084	A952	A952	U889	U819
U1720	A1643	G1576	A1504	C1437	C1358	A1290	A1226		U1085	C953	G953	C890	
U1721	C1644	U1577	U1438	G1437	C1359	A1291	G1227	G1157	C1086		U956		G822
U1722	U1645	G1577	U1439	U1440	U1361	A1294	C1228	A1158	G1089	C		G891	G823
A1723	C1578	C1578	G1440	G1441	G1362	G1295	G1229	A1159	G	G		U892	C824
U1724	G1646	U1579	G1510	G1441	A1363	C1296	G1230	C1160	G1090	G		C893	U825
C1725	A1648	A1580	U1511	U1442	C1364	C1297	A1231	G1161		G		G894	G826
G1726	U1649	C1581	G1512	G1443	G1365	C1298	C1232	U1162	A1093	U	U960	A895	A827
C1727	G1650	C1582	G1513	U1444	A1366	C1299	G1233	U1163	U1094	C	A962	A896	G828
U1651	U1651	A1583	G1517	U1445		G1300	C1234	G1164	U1096	G	G964	U897	U829
		U1584	U1518	A1446	A1369	A1301	G1235	A1165	U1096	A	A	U899	A830
A1654	G1655	C1585	G1519	U1447	G1370	A1302	U1236	G1166	G1097	A	U966	G900	G831
G1730	A1656	U1587	G1520	U1448	G1371	A1303	G1237	U1167	A1098	A		G901	G832
	C1657	A1588	G1521	U1449	C1372	U1305	C1238	U1168	U1099	U	A967	G902	G833
U1737	G1658	U1589	U1522	A1452	A1373	G1306	C1239	U1169	U1000	G		U903	U834
A1741	U1659	G1590	U1523		G1374	G1307	A1240	A1170		A		A904	G835

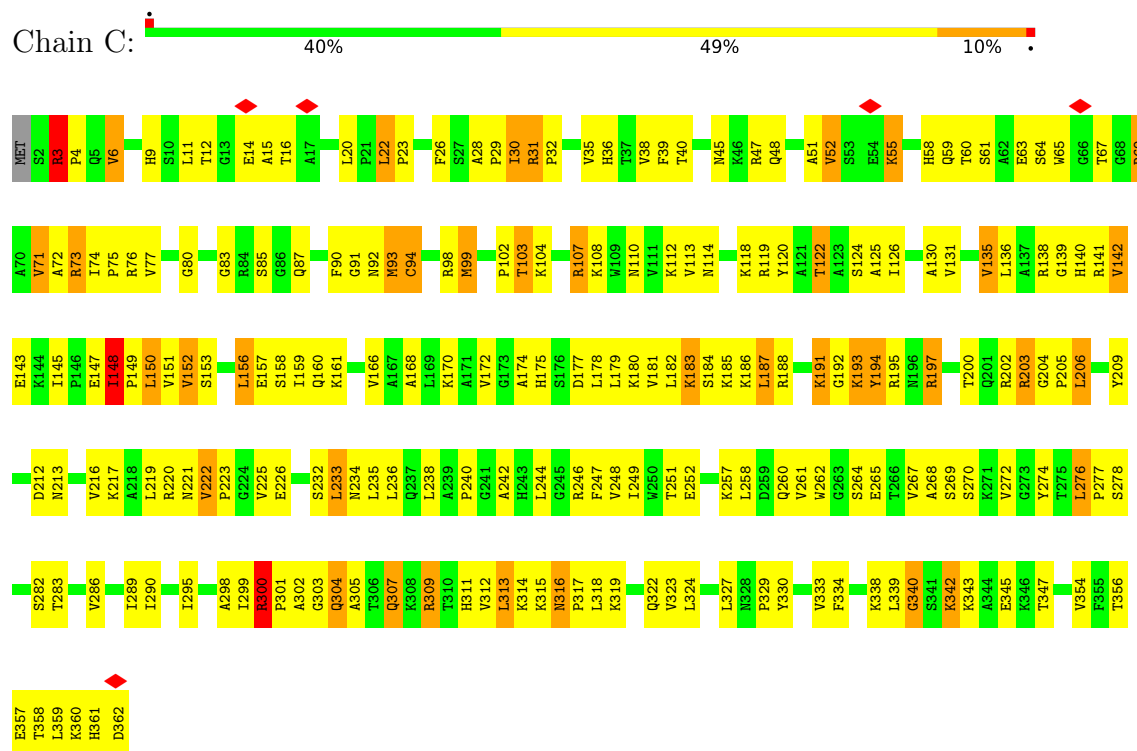
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A2628	C2556	U2433	U2294	A2233	A2166	A2024	P5P	Y5P	A1886	G1811	G1743
A2629	A2557	U2434	A2295	G2234	G2169	A2025	P5P	Y5P	A1887	A1812	
C2630	C2558	G2435	A2296		G2170	A2093	P5P	Y5P	U1888	G1813	U1746
U2631	U2559	U2436	U2297	C2237	G2171	C2094	P5P	Y5P	G1889	A1814	G1747
G2632	C2560	G2437	U2298	G2238	U2175	G2095	P5P	Y5P	U1890	A1815	
U2633	A2561	A2438	A2299	G2239	U2176	A2096	P5P	Y5P	A1891	A1816	A1750
U2634	A2562	A2439		G2240	U2177	U2097	P5P	Y5P	G1892	G1751	
A2635	G2563	G	C2304	U2241	U2178	C2098	P5P	Y5P	A1893	A1817	
A2636		A	G2305	U2242	G2177	A2099	P5P	Y5P	U1894	U1818	
A2637	A2566	A	G2306	A2243	A2178	A2100	P5P	Y5P	A1895	U1819	
G2638	C2567	A	G2307	A2244	G2179	C2101	P5P	Y5P	A1896	U1820	
A2639	A2568	C	C2308	A2245	G2180	U2102	P5P	Y5P	G1897	C1756	
U2640	U2570	A	A2309	G2246	C2181	U2103	P5P	Y5P	G1898		
U2641	C2571	U	G2310	G2247	A2182		P5P	Y5P	G1899		
A2642	U2572	C	U2311	G2248	A2183	A2107	P5P	Y5P		G1825	
	G2573	A	G2312	G2249	U2184	C2108	P5P	Y5P	G1906	G1829	
G2645	U2574	A	A2313	G	U2185	U2109	P5P	Y5P	G1907	G1830	
G2646	C2575	G	G2314	G2249	U2186	G2110	P5P	Y5P	A1909	G1833	
U2650	C2582	G	G2315	G	U2190	U2111	P5P	Y5P	G1919	G1838	
G2651	G2583	U	G2316	G	U2191	U2112	P5P	Y5P	U1920	A1839	
C2652	U2584	U	A2317	A	C2192	A2113	P5P	Y5P	U1921	C1767	
C2653	G2585	G		A	U2193	C2114	P5P	Y5P	C1926	U1768	
C2654	G2586	U	A2321	U	U2196	A2117	P5P	Y5P	G1927	G1770	
U2655	U2587	A		A	C2197		P5P	Y5P	G1928	C1771	
A2656	A2588	A	G2328	C	A2198	G2121	P5P	Y5P	G1929	U1772	
	G2589	U	U2329	A	G2199	G2122	P5P	Y5P	G1935	C1844	
G2660	A2590	A	A2332	U	U2200	G2123	P5P	Y5P	G1939	C1845	
G2661	A2591	A	C2333	A	G2201	A2124	P5P	Y5P	U1944	C1846	
G2662	A2592	G	C2334	U	U2205	A2125	P5P	Y5P	A1945	A1847	
C2663	G2593	U	U2335	G	U2206	C2132	P5P	Y5P	A1946	G1848	
G2664	C2594	G	U2336	U	C2202	U2128	P5P	Y5P	G1947	U1783	
U2665	G2595	G	A2403	C	U2203	U2129	P5P	Y5P	U1948	U1785	
G2666	U2596	G	A2404	C	C2204	G2130	P5P	Y5P	G1949	G1786	
A2667	G2597	A	C2407	U	U2206	A2131	P5P	Y5P	U1950	C1788	
U2668	U2598	G	U2408	U	A2207	C2136	P5P	Y5P	G1951	A1869	
G2669	U2599	C	U2409	U	A2208	U2137	P5P	Y5P	U1951	G1861	
G2670	C2600	U	U2410	U	U2209	U2141	P5P	Y5P	U1951	U1862	
A2673	A2601	U	U2411	U	U2210	U2142	P5P	Y5P	Y5P1987	C1792	
A2674	G2602	C	A2412	C	U2211	A2143	P5P	Y5P	Y5P1988	C1793	
C2675	U2603	G	C2415	A	U2212	A2144	P5P	Y5P	Y5P1989	A1864	
A2676	C2604	C	U2416	C	A2213	U2147	P5P	Y5P	Y5P1990	A1865	
G2677	G2605	G	U2417	U	A2214	A2148	P5P	Y5P	Y5P1991	C1866	
	C2606	C	G2418	G	A2215	A2149	P5P	Y5P	Y5P1992		
A2680	G2607	G	U2419	U	G2216	G2150	P5P	Y5P	Y5P1993	U1873	
U2681	C2608	A	C2420	C	A2219	C2151	P5P	Y5P	Y5P1994	A1798	
C2682	U2610	U	U2421	A	A2220	U2153	P5P	Y5P	Y5P1995	A1799	
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C2684	U2612	U	C2423	A	A2222	A2158	P5P	Y5P	Y5P1995	U1877	
C2685	U2613	G	U2424	C	A2223	A2159	P5P	Y5P	Y5P1995	A1874	
A2686	G2614	A	A2425	U	A2224	G2160	P5P	Y5P	Y5P1995	A1879	
G2687	U2615	A	G2426	C	U2225		P5P	Y5P	Y5P1995	U1880	
U2688	C2616	U	U2427	C	U2226		P5P	Y5P	Y5P1995	A1881	
A2689	U2617	U	U2428	A	U2227		P5P	Y5P	Y5P1995	G1882	
G2690	G2618	C	G2429	C	U2228		P5P	Y5P	Y5P1995	A1883	
A2691		A	C2430	A	A2229		P5P	Y5P	Y5P1995	G1884	
	G2624		C2431	U	C2230		P5P	Y5P	Y5P1995		
					C2231		P5P	Y5P	Y5P1995		
					U2292		P5P	Y5P	Y5P1995		



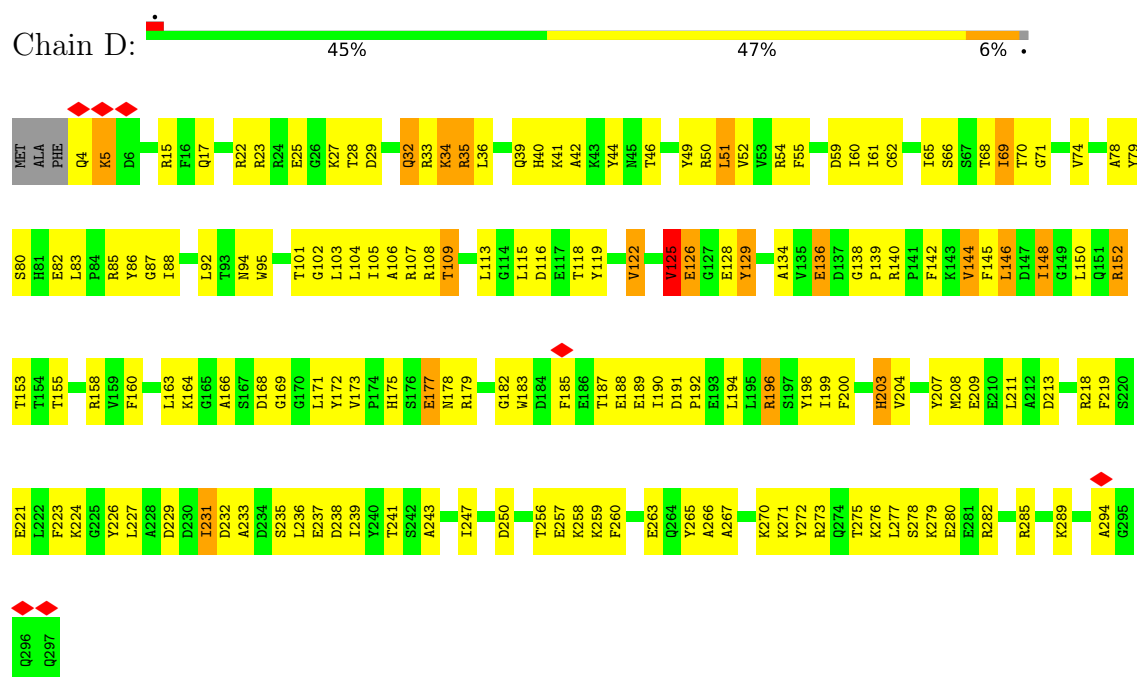




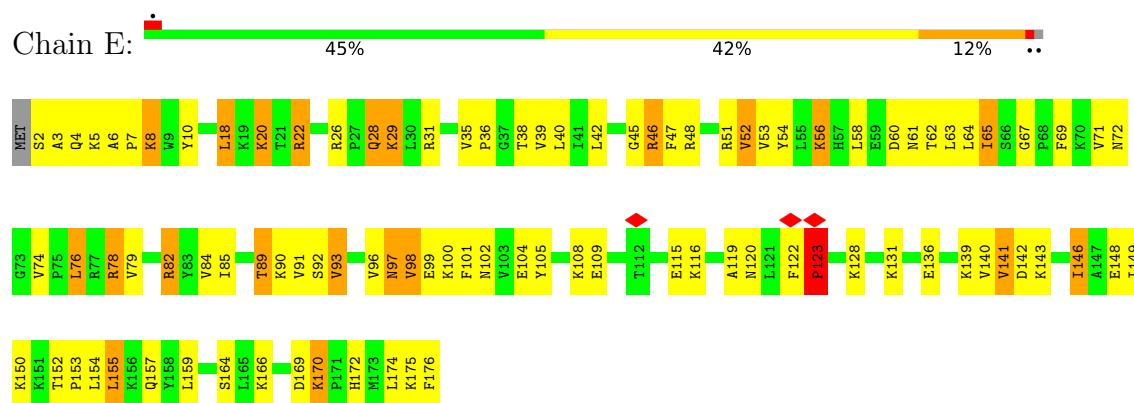
• Molecule 6: 60S ribosomal protein L4-A



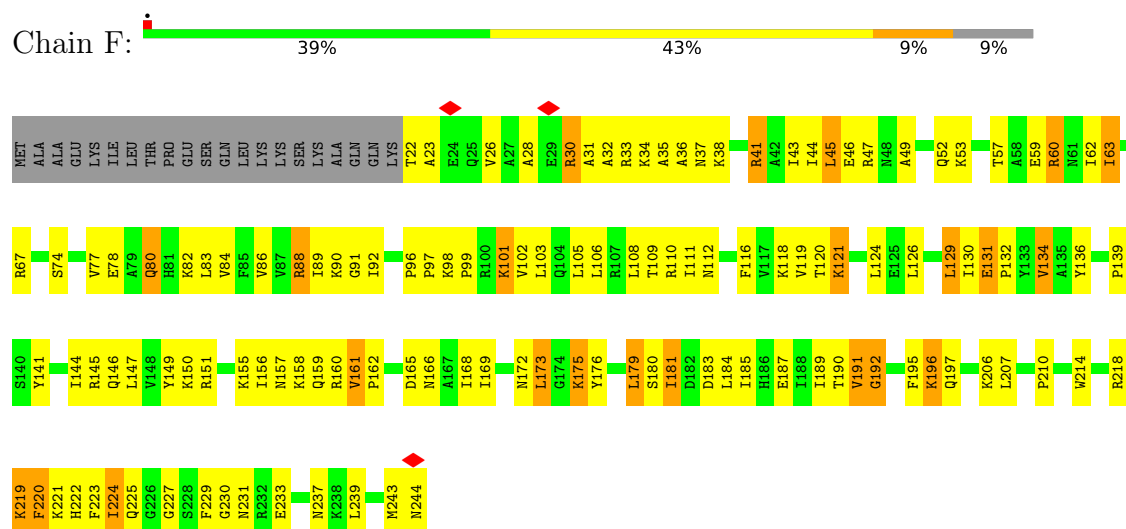
• Molecule 7: 60S ribosomal protein L5



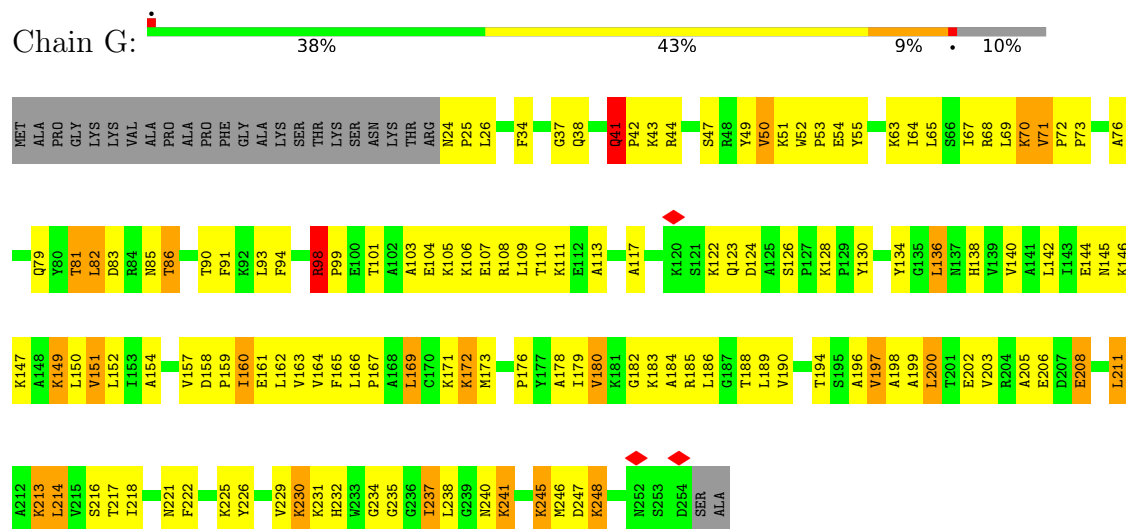
• Molecule 8: 60S ribosomal protein L6-A



- Molecule 9: 60S ribosomal protein L7-A



- Molecule 10: 60S ribosomal protein L8-A

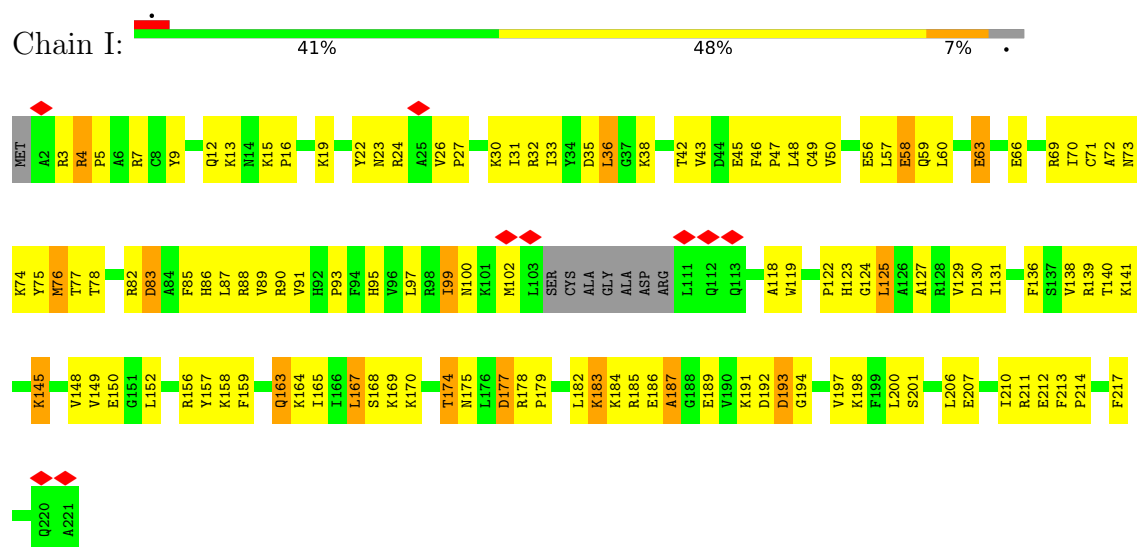


- Molecule 11: 60S ribosomal protein L9-A





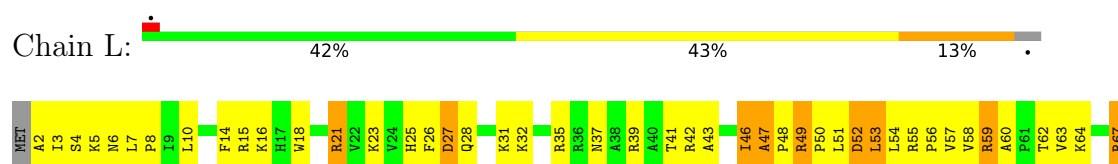
• Molecule 12: 60S ribosomal protein L10

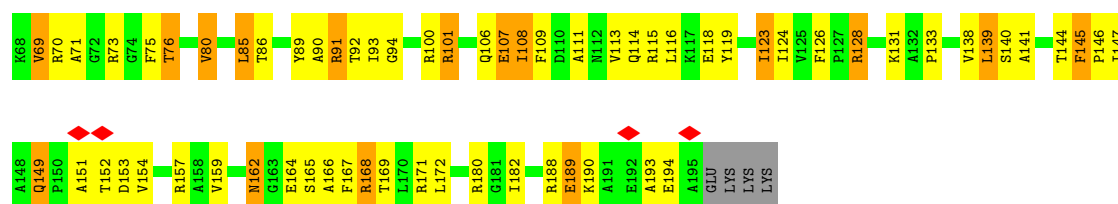


• Molecule 13: 60S ribosomal protein L11-A

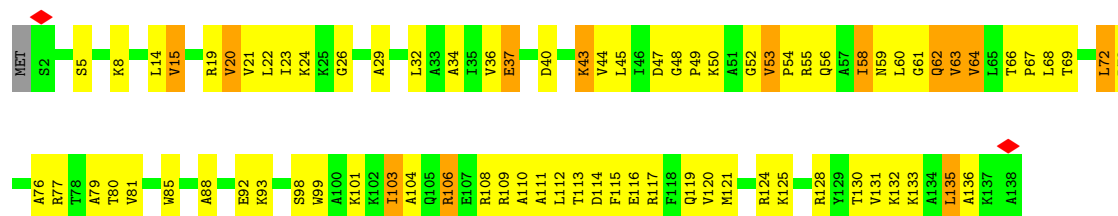


• Molecule 14: 60S ribosomal protein L13-A

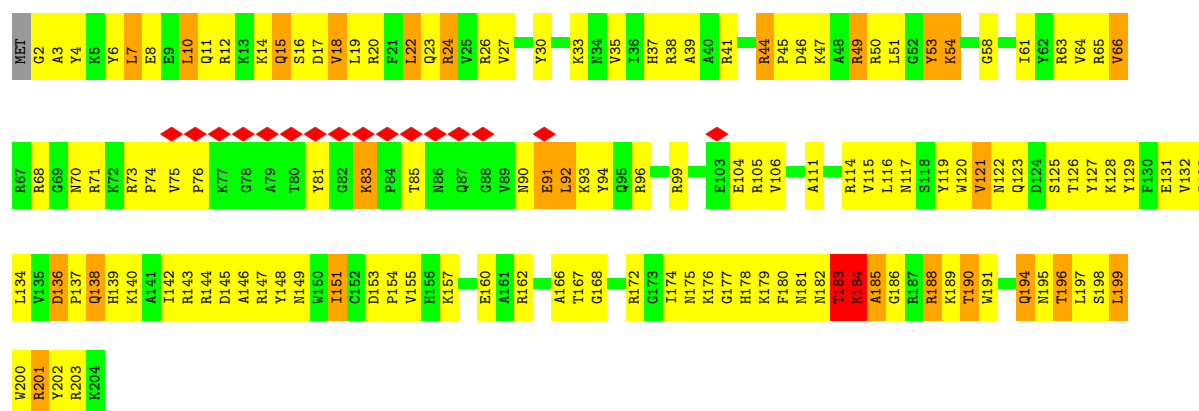




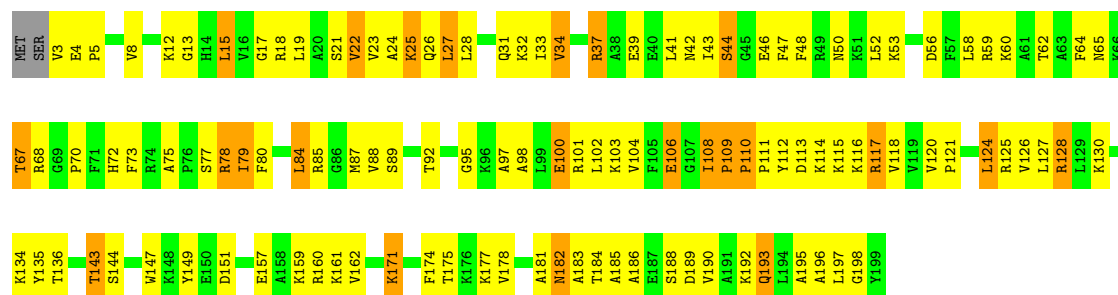
• Molecule 15: 60S ribosomal protein L14-A



• Molecule 16: 60S ribosomal protein L15-A

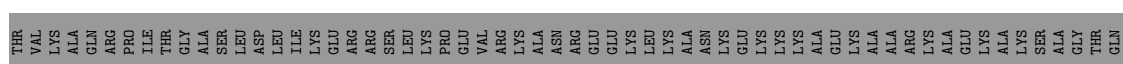


• Molecule 17: 60S ribosomal protein L16-A



• Molecule 18: 60S ribosomal protein L17-A





SER
SER
LYS
PHE
SER
LYS
GLN
GLN
ALA
LYS
GLY
ALA
PHE
GLN
LYS
VAL
GLY
ALA
ALA
THR
SER
ARG

• Molecule 26: 60S ribosomal protein L25

Chain X:  39% 34% 12% 15%

MET
ALA
PRO
SER
ALA
LYS
ALA
THR
ALA
LYS
LYS
VAL
VAL
LYS
GLY
THR
ASN
GLY
LYS
LYS
A23
L24
R27
T28
T31
F32
R33
L34
P35
K36
T37
L38
K39
L40
A43
P44
K45
K49
A50
V51
P52
H53
Y54
K55
R56
L57
K61
V62
I63
E64
Q65
P66
I67

T68
S69
E70
T71
A72
M73
K74
D78
G79
N80
I81
L82
V83
F84
Y93
K96
K97
A98
V99
K100
E101
L102
Y103
E104
V105
D106
V107
L108
K109
V110
N111
T112
R115
K121
R125
L126
T127
D128
Y129
D130
D131
A132
L133
I134
I135
A136
N137
Y141
I142

• Molecule 27: 60S ribosomal protein L26-A

Chain Y:  39% 49% 12%

MET
A2
K3
Q4
S5
V8
S9
S10
D11
R12
R13
K14
K17
A18
A22
P23
S24
S25
Q26
R27
R28
L31
S32
A33
P34
L35
S36
K37
E38
L39
R40
A41
G42
Y43
G44
L45
L48
P49
I50
R51
R52
D53
D54
E55
V56
V58
V59
R60
Q66
E67
I70

Y74
R75
L76
K77
F78
A79
V80
Q81
R82
D83
K84
R85
T86
K89
V90
N91
S94
V95
P96
I97
N98
L99
H100
K103
L104
V105
I106
T107
K108
L109
H110
L111
D112
K113
D114
R115
K116
A117
L118
I119
Q120
R121
K122
K125
L126
E127

• Molecule 28: 60S ribosomal protein L27-A

Chain Z:  35% 51% 12% ..

MET
A2
K3
V10
A11
V12
V13
V14
R15
G16
R17
Y18
K21
K22
V23
V24
I25
V26
K27
H28
H29
K34
S35
H36
P37
F38
Q39
H40
A41
L42
I46
E47
R48
Y49
P50
L51
K52
V53
T54
H57
K61
K64
R65
T66
K67
T68
K69
P70
F71
I72
K73
V74
V75

N76
Y77
N78
H79
L80
L81
P82
T83
R84
W85
T86
L87
D88
V89
E90
K93
S94
V95
V96
S97
T98
E99
T100
F101
E102
Q103
P104
S105
Q106
S107
R107
E108
A109
A110
K111
K112
V113
V114
K115
K116
A117
K118
F118
E119
E120
R121
H122
Q123
A124
G125
K126
N127
K128
P129
H130
F130
F131
S132
K133
L134
R135
F136

• Molecule 29: 60S ribosomal protein L28

Chain a:  39% 50% 10%

MET
P2
S3
R4
F5
T6
K7
T8
R9
H11
K10
R12
G13
H14
V15
S16
A17
G18
K19
G20
R21
I22
G23
K24
H25
R26
K27
H28
P29
G30
G31
R32
G33
M34
A35
G36
H40
H41
R42
I43
M44
M45
D46
G51
G57
M58
R59
Y60
F61
H62
K63
Q64
Q65
A66
H67
F68
W69

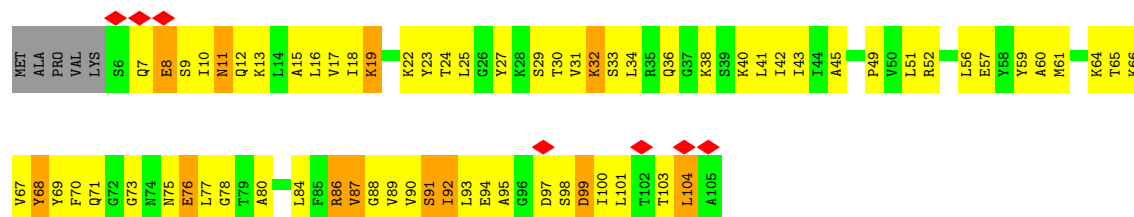
K70
P71
V72
L73
N74
L75
D76
K77
L78
W79
T80
L81
I82
P83
E84
D85
K86
L91
K96
E97
T98
A99
P100
V101
I102
G108
Y109
G110
K111
I112
L113
K115
G116
R117
I118
P119
N120
V121
P122
V123
I124
V125
K126
A127
R128
F129
V130
S131
K132
L133
A134
F135
A136
K137
I138

V144
L147
I148
A149

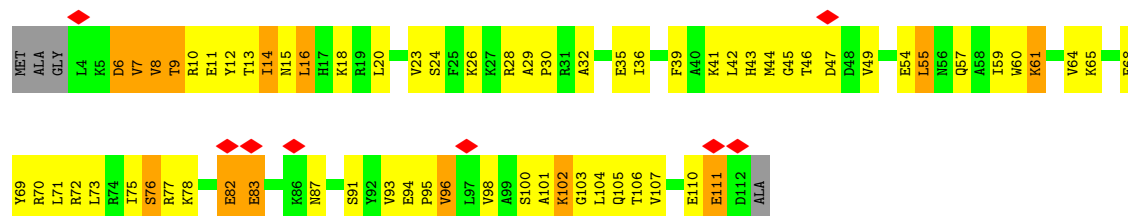
• Molecule 30: 60S ribosomal protein L29



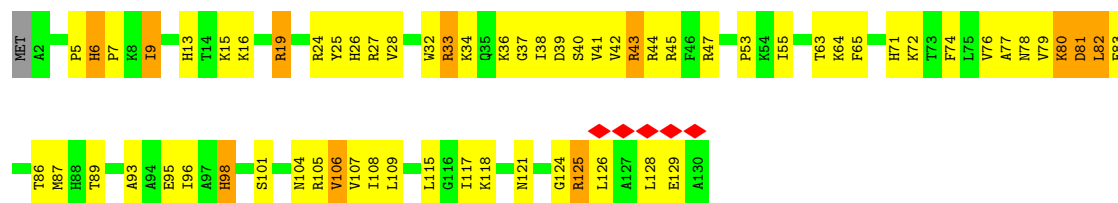
• Molecule 31: 60S ribosomal protein L30



• Molecule 32: 60S ribosomal protein L31-A



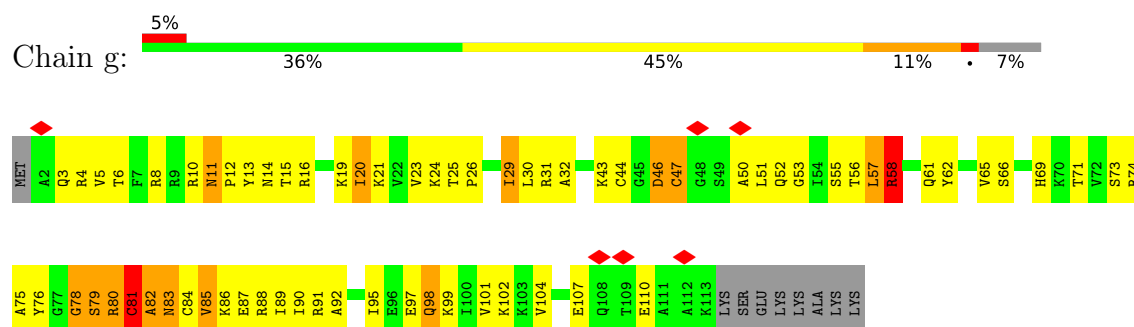
• Molecule 33: 60S ribosomal protein L32



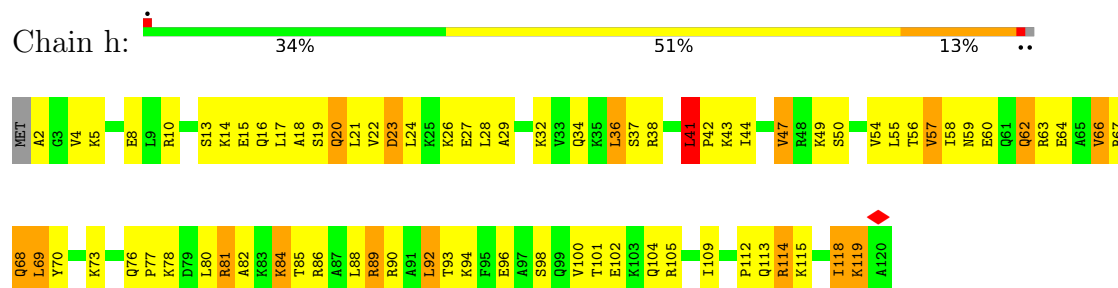
• Molecule 34: 60S ribosomal protein L33-A



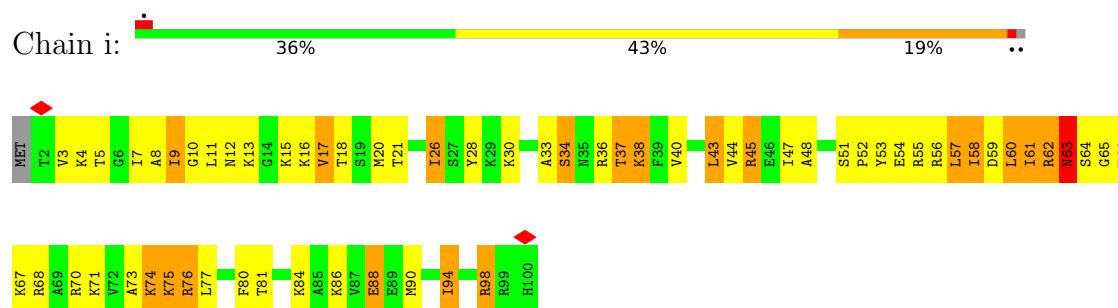
• Molecule 35: 60S ribosomal protein L34-A



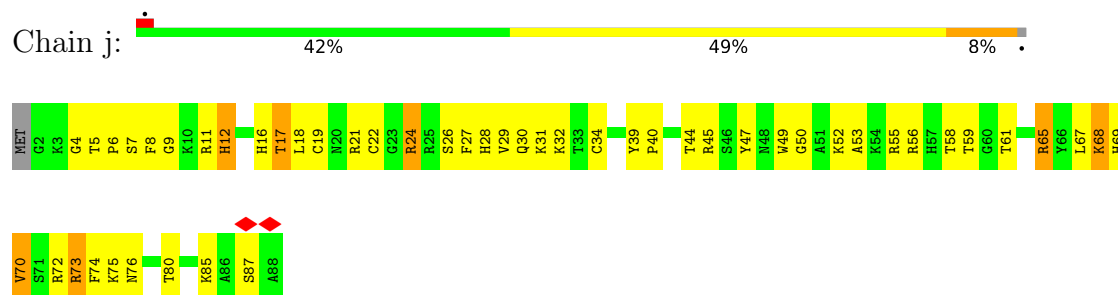
- Molecule 36: 60S ribosomal protein L35-A



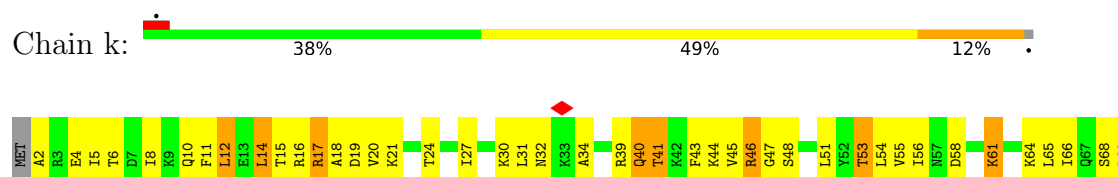
- Molecule 37: 60S ribosomal protein L36-A



- Molecule 38: 60S ribosomal protein L37-A

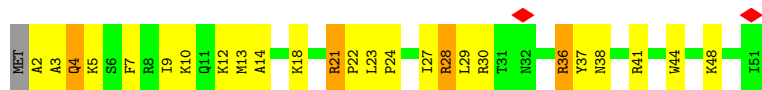


- Molecule 39: 60S ribosomal protein L38

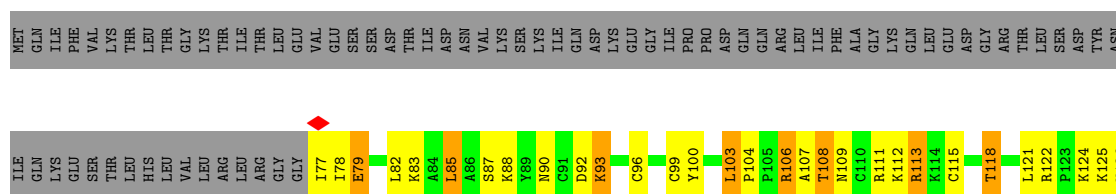
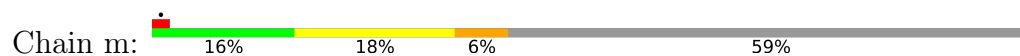




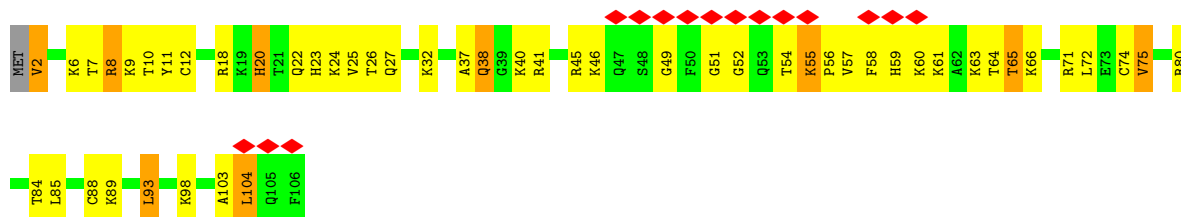
- Molecule 40: 60S ribosomal protein L39



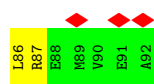
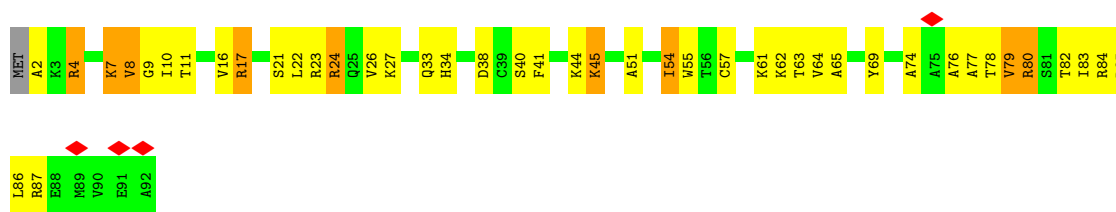
- Molecule 41: Ubiquitin-60S ribosomal protein L40



- Molecule 42: 60S ribosomal protein L42-A



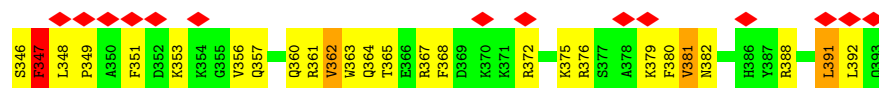
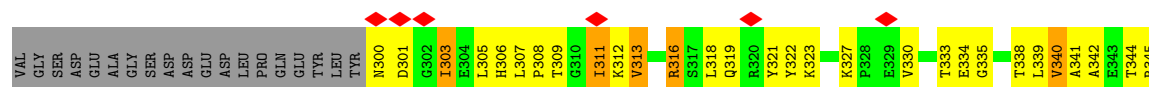
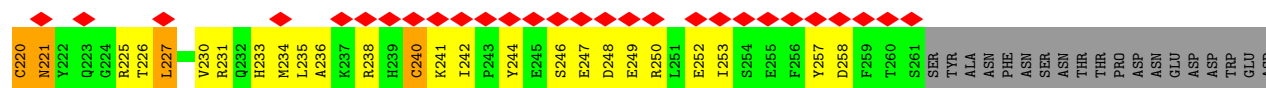
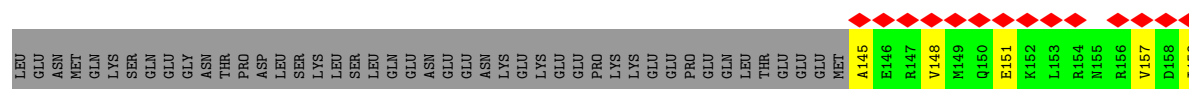
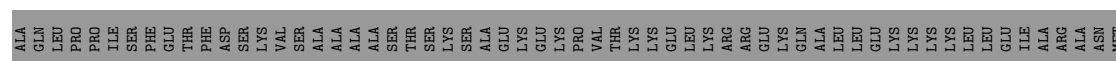
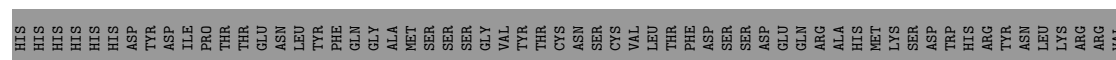
- Molecule 43: 60S ribosomal protein L43-A



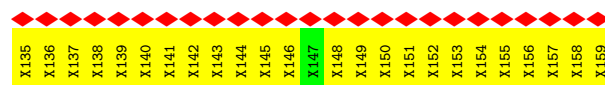
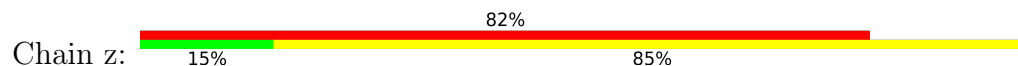
- Molecule 44: 60S acidic ribosomal protein P0



- Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1



- Molecule 47: ALB1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22040	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100720	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.352	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	Depositor
Map size ($\text{\AA}$)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: P5P, Y5P, MG, ZN

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	5	0.24	0/74039	0.39	1/115426 (0.0%)
2	7	0.18	0/2883	0.29	0/4491
3	8	0.25	0/3746	0.41	0/5832
4	A	0.44	0/1662	0.94	5/2236 (0.2%)
5	B	0.46	0/3146	0.90	8/4228 (0.2%)
6	C	0.49	0/2800	0.98	13/3790 (0.3%)
7	D	0.41	0/2408	0.86	2/3248 (0.1%)
8	E	0.46	0/1377	0.97	6/1851 (0.3%)
9	F	0.46	0/1828	0.92	6/2461 (0.2%)
10	G	0.47	0/1795	0.96	9/2429 (0.4%)
11	H	0.43	0/1539	0.87	3/2073 (0.1%)
12	I	0.44	0/1758	0.92	4/2358 (0.2%)
13	J	0.42	0/1374	0.89	5/1842 (0.3%)
14	L	0.47	0/1573	1.01	7/2113 (0.3%)
15	M	0.44	0/1074	0.90	0/1446
16	N	0.54	0/1757	0.95	5/2354 (0.2%)
17	O	0.48	0/1585	0.96	7/2128 (0.3%)
18	P	0.52	0/1465	0.93	3/1968 (0.2%)
19	Q	0.45	0/1465	0.93	5/1965 (0.3%)
20	R	0.43	0/1275	0.80	0/1702
21	S	0.46	0/1473	0.89	7/1980 (0.4%)
22	T	0.42	0/1300	0.85	1/1743 (0.1%)
23	U	0.42	0/825	0.88	1/1120 (0.1%)
24	V	0.43	0/1018	0.93	3/1369 (0.2%)
25	W	0.41	0/533	0.83	0/707
26	X	0.44	0/974	1.01	2/1314 (0.2%)
27	Y	0.43	0/1004	0.91	4/1341 (0.3%)
28	Z	0.44	0/1118	1.01	4/1497 (0.3%)
29	a	0.50	0/1204	0.95	6/1612 (0.4%)
30	b	0.44	0/473	1.00	3/629 (0.5%)
31	c	0.44	0/775	0.86	0/1040
32	d	0.44	0/897	0.99	2/1205 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.49	0/1055	0.88	2/1413 (0.1%)
34	f	0.48	0/868	0.95	5/1168 (0.4%)
35	g	0.44	0/890	1.02	7/1189 (0.6%)
36	h	0.46	0/974	1.00	6/1297 (0.5%)
37	i	0.43	0/777	0.85	0/1033
38	j	0.48	0/696	0.91	0/923
39	k	0.43	0/614	0.94	3/822 (0.4%)
40	l	0.50	0/443	0.86	0/588
41	m	0.47	0/423	1.06	4/562 (0.7%)
42	o	0.46	0/860	0.97	4/1136 (0.4%)
43	p	0.44	0/701	0.86	2/934 (0.2%)
44	q	0.84	0/977	0.98	3/1313 (0.2%)
45	x	0.48	0/4557	0.93	10/6189 (0.2%)
46	y	0.57	0/1759	0.90	1/2363 (0.0%)
All	All	0.35	0/137737	0.65	169/202428 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	C	0	2
13	J	0	1
16	N	0	2
28	Z	0	1
32	d	0	2
35	g	0	1
45	x	0	2
46	y	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 169 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	O	109	PRO	CA-C-N	10.69	131.39	120.38
17	O	109	PRO	C-N-CA	10.69	131.39	120.38
35	g	11	ASN	CA-C-N	9.88	129.54	119.56
35	g	11	ASN	C-N-CA	9.88	129.54	119.56
26	X	43	ALA	CA-C-N	9.84	129.20	118.97

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	148	ILE	Peptide
6	C	197	ARG	Peptide
13	J	9	MET	Peptide
16	N	183	THR	Peptide
16	N	184	LYS	Peptide

5.2 Too-close contacts

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	5	66537	0	33464	2452	0
2	7	2579	0	1303	103	0
3	8	3353	0	1695	149	0
4	A	1630	0	1682	154	0
5	B	3075	0	3142	292	0
6	C	2748	0	2859	266	0
7	D	2359	0	2311	166	0
8	E	1355	0	1413	116	0
9	F	1791	0	1869	143	0
10	G	1763	0	1819	160	0
11	H	1518	0	1587	118	0
12	I	1722	0	1755	129	0
13	J	1353	0	1383	141	0
14	L	1548	0	1613	165	0
15	M	1059	0	1154	80	0
16	N	1720	0	1779	179	0
17	O	1555	0	1659	119	0
18	P	1442	0	1485	116	0
19	Q	1441	0	1543	139	0
20	R	1258	0	1342	95	0
21	S	1437	0	1475	110	0
22	T	1276	0	1323	105	0
23	U	808	0	822	70	0
24	V	1003	0	1048	87	0
25	W	521	0	551	24	0
26	X	959	0	1023	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	Y	993	0	1081	79	0
28	Z	1092	0	1155	93	0
29	a	1173	0	1215	110	0
30	b	462	0	491	38	0
31	c	767	0	816	96	0
32	d	883	0	918	84	0
33	e	1034	0	1101	50	0
34	f	850	0	880	77	0
35	g	880	0	945	75	0
36	h	965	0	1067	97	0
37	i	770	0	846	89	0
38	j	681	0	683	57	0
39	k	608	0	671	53	0
40	l	436	0	475	34	0
41	m	417	0	455	25	0
42	o	847	0	914	77	0
43	p	694	0	734	61	0
44	q	962	0	989	143	0
45	x	4477	0	4559	463	0
46	y	1724	3	1681	150	0
47	z	510	0	517	111	0
48	5	259	0	0	0	0
48	7	6	0	0	0	0
48	8	7	0	0	0	0
48	B	1	0	0	0	0
48	C	2	0	0	0	0
48	N	1	0	0	0	0
48	P	1	0	0	0	0
48	V	1	0	0	0	0
48	a	2	0	0	0	0
49	j	1	0	0	0	0
49	m	1	0	0	0	0
49	o	1	0	0	0	0
49	p	1	0	0	0	0
49	y	2	0	0	0	0
All	All	129321	3	95292	6807	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 31.

The worst 5 of 6807 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)
36:h:114:ARG:HH11	36:h:114:ARG:HG3	1.08	1.16
17:O:128:ARG:HH11	17:O:128:ARG:HG3	1.11	1.14
10:G:162:LEU:HD23	16:N:7:LEU:HD11	1.30	1.13
30:b:32:LEU:HD13	30:b:35:VAL:HG21	1.15	1.13
14:L:91:ARG:HH11	14:L:91:ARG:HG3	1.15	1.11

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	
4	A	210/254 (83%)	193 (92%)	17 (8%)	0	100	100
5	B	384/387 (99%)	359 (94%)	25 (6%)	0	100	100
6	C	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	21	56
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	18	53
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	7	35
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	24	59
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	14	47
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	24	59
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100
13	J	167/174 (96%)	143 (86%)	19 (11%)	5 (3%)	3	26
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	12	44
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	12	44
17	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	173 (94%)	9 (5%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	R	154/189 (82%)	148 (96%)	6 (4%)	0	100	100
21	S	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	T	157/160 (98%)	153 (98%)	2 (1%)	2 (1%)	9	40
23	U	100/121 (83%)	95 (95%)	5 (5%)	0	100	100
24	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
25	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
26	X	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	16	50
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	5	30
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	18	53
30	b	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
31	c	98/105 (93%)	91 (93%)	7 (7%)	0	100	100
32	d	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	14	47
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	50
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	6	34
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	3	25
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	9	40
40	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	m	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
42	o	103/106 (97%)	96 (93%)	7 (7%)	0	100	100
43	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
44	q	116/312 (37%)	109 (94%)	7 (6%)	0	100	100
45	x	577/616 (94%)	540 (94%)	37 (6%)	0	100	100
46	y	207/414 (50%)	192 (93%)	15 (7%)	0	100	100
All	All	6982/7900 (88%)	6509 (93%)	437 (6%)	36 (0%)	26	59

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL

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Mol	Chain	Res	Type
13	J	10	ARG
13	J	95	ASN
16	N	184	LYS
13	J	115	LYS

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	
4	A	166/196 (85%)	132 (80%)	34 (20%)	1	8
5	B	319/323 (99%)	267 (84%)	52 (16%)	2	14
6	C	288/289 (100%)	233 (81%)	55 (19%)	1	10
7	D	243/245 (99%)	214 (88%)	29 (12%)	5	21
8	E	136/153 (89%)	115 (85%)	21 (15%)	2	15
9	F	187/205 (91%)	157 (84%)	30 (16%)	2	14
10	G	177/208 (85%)	145 (82%)	32 (18%)	2	11
11	H	171/171 (100%)	137 (80%)	34 (20%)	1	9
12	I	179/187 (96%)	155 (87%)	24 (13%)	4	18
13	J	147/150 (98%)	120 (82%)	27 (18%)	1	11
14	L	154/159 (97%)	126 (82%)	28 (18%)	2	11
15	M	108/109 (99%)	89 (82%)	19 (18%)	2	12
16	N	175/176 (99%)	145 (83%)	30 (17%)	2	13
17	O	160/162 (99%)	129 (81%)	31 (19%)	1	9
18	P	145/146 (99%)	124 (86%)	21 (14%)	3	16
19	Q	150/151 (99%)	122 (81%)	28 (19%)	1	10
20	R	129/154 (84%)	108 (84%)	21 (16%)	2	14
21	S	155/156 (99%)	124 (80%)	31 (20%)	1	9
22	T	136/137 (99%)	106 (78%)	30 (22%)	1	6
23	U	89/107 (83%)	77 (86%)	12 (14%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	V	104/105 (99%)	91 (88%)	13 (12%)	4	20
25	W	55/129 (43%)	51 (93%)	4 (7%)	13	38
26	X	104/118 (88%)	82 (79%)	22 (21%)	1	7
27	Y	109/110 (99%)	85 (78%)	24 (22%)	1	6
28	Z	115/116 (99%)	96 (84%)	19 (16%)	2	13
29	a	118/119 (99%)	103 (87%)	15 (13%)	4	20
30	b	46/47 (98%)	39 (85%)	7 (15%)	3	15
31	c	84/88 (96%)	70 (83%)	14 (17%)	2	13
32	d	94/97 (97%)	78 (83%)	16 (17%)	2	13
33	e	110/111 (99%)	93 (84%)	17 (16%)	2	15
34	f	90/91 (99%)	80 (89%)	10 (11%)	6	23
35	g	95/103 (92%)	80 (84%)	15 (16%)	2	15
36	h	103/105 (98%)	84 (82%)	19 (18%)	1	11
37	i	80/82 (98%)	55 (69%)	25 (31%)	0	2
38	j	70/71 (99%)	59 (84%)	11 (16%)	2	15
39	k	67/69 (97%)	56 (84%)	11 (16%)	2	13
40	l	45/46 (98%)	37 (82%)	8 (18%)	2	12
41	m	47/116 (40%)	37 (79%)	10 (21%)	1	6
42	o	90/91 (99%)	77 (86%)	13 (14%)	3	17
43	p	71/72 (99%)	61 (86%)	10 (14%)	3	17
44	q	105/254 (41%)	91 (87%)	14 (13%)	4	18
45	x	508/540 (94%)	455 (90%)	53 (10%)	7	25
46	y	182/378 (48%)	165 (91%)	17 (9%)	8	29
All	All	5906/6642 (89%)	4950 (84%)	956 (16%)	4	14

5 of 956 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	P	119	VAL
45	x	5	ILE
22	T	141	VAL
44	q	55	LYS
46	y	303	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
20	R	7	GLN
45	x	447	HIS
27	Y	66	GLN
45	x	429	ASN
46	y	239	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3102/3396 (91%)	666 (21%)	79 (2%)
2	7	120/121 (99%)	13 (10%)	0
3	8	157/158 (99%)	42 (26%)	6 (3%)
All	All	3379/3675 (91%)	721 (21%)	85 (2%)

5 of 721 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	21	G
1	5	22	G
1	5	26	A

5 of 85 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2662	G
1	5	3228	C
1	5	2772	C
1	5	3078	U
1	5	3317	U

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

20 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	Y5P	5	1994	1	14,19,20	4.35	2 (14%)	18,26,29	1.10	1 (5%)
1	P5P	5	2024	1	20,23,24	0.74	1 (5%)	27,33,36	0.73	1 (3%)
1	P5P	5	2020	1	20,23,24	0.73	1 (5%)	27,33,36	0.74	1 (3%)
1	P5P	5	2021	1	20,23,24	0.66	1 (5%)	27,33,36	0.70	1 (3%)
1	Y5P	5	1990	1	14,19,20	4.32	2 (14%)	18,26,29	1.10	1 (5%)
1	P5P	5	2019	1	20,23,24	0.68	1 (5%)	27,33,36	0.74	1 (3%)
1	P5P	5	2016	1	20,23,24	0.74	1 (5%)	27,33,36	0.73	1 (3%)
1	Y5P	5	1986	1	14,19,20	4.35	2 (14%)	18,26,29	1.06	1 (5%)
1	P5P	5	2017	1	20,23,24	0.64	1 (5%)	27,33,36	0.71	1 (3%)
1	P5P	5	2025	1	20,23,24	0.65	1 (5%)	27,33,36	0.70	1 (3%)
1	P5P	5	2018	1	20,23,24	0.71	1 (5%)	27,33,36	0.74	1 (3%)
1	Y5P	5	1987	1	14,19,20	4.17	2 (14%)	18,26,29	1.05	1 (5%)
1	P5P	5	2022	1	20,23,24	0.75	1 (5%)	27,33,36	0.74	1 (3%)
1	Y5P	5	1993	1	14,19,20	4.39	2 (14%)	18,26,29	1.04	1 (5%)
1	Y5P	5	1995	1	14,19,20	4.21	2 (14%)	18,26,29	1.00	1 (5%)
1	Y5P	5	1991	1	14,19,20	4.22	2 (14%)	18,26,29	1.03	1 (5%)
1	P5P	5	2023	1	20,23,24	0.65	1 (5%)	27,33,36	0.75	1 (3%)
1	Y5P	5	1988	1	14,19,20	4.35	2 (14%)	18,26,29	1.06	1 (5%)
1	Y5P	5	1992	1	14,19,20	4.44	2 (14%)	18,26,29	1.08	1 (5%)
1	Y5P	5	1989	1	14,19,20	4.21	2 (14%)	18,26,29	1.01	1 (5%)

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
1	Y5P	5	1994	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2024	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2020	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2021	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1990	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2019	1	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	P5P	5	2016	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1986	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2017	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2025	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2018	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1987	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2022	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1993	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1995	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1991	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2023	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1988	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1992	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1989	1	-	1/7/33/34	0/2/2/2

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1992	Y5P	C2-N3	14.52	1.38	1.27
1	5	1986	Y5P	C2-N3	14.12	1.38	1.27
1	5	1988	Y5P	C2-N3	14.05	1.38	1.27
1	5	1993	Y5P	C2-N3	14.04	1.38	1.27
1	5	1994	Y5P	C2-N3	13.97	1.38	1.27

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1994	Y5P	N1-C2-N3	-3.99	114.34	125.39
1	5	1986	Y5P	N1-C2-N3	-3.97	114.38	125.39
1	5	1992	Y5P	N1-C2-N3	-3.94	114.47	125.39
1	5	1990	Y5P	N1-C2-N3	-3.92	114.52	125.39
1	5	1988	Y5P	N1-C2-N3	-3.87	114.67	125.39

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	5	1987	Y5P	O4'-C1'-N1-C2
1	5	1989	Y5P	O4'-C1'-N1-C2
1	5	1990	Y5P	O4'-C1'-N1-C2
1	5	1991	Y5P	O4'-C1'-N1-C2
1	5	1993	Y5P	O4'-C1'-N1-C2

There are no ring outliers.

13 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	5	1994	Y5P	1	0
1	5	2024	P5P	1	0
1	5	1990	Y5P	3	0
1	5	2017	P5P	1	0
1	5	2018	P5P	1	0
1	5	1987	Y5P	1	0
1	5	2022	P5P	1	0
1	5	1993	Y5P	1	0
1	5	1991	Y5P	1	0
1	5	2023	P5P	1	0
1	5	1988	Y5P	1	0
1	5	1992	Y5P	1	0
1	5	1989	Y5P	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 286 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	2
47	z	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1953:G	O3'	1986:Y5P	P	107.33
1	5	2025:P5P	O3'	2093:A	P	105.65
1	z	107:UNK	C	115:UNK	N	20.22
1	z	127:UNK	C	131:UNK	N	9.70

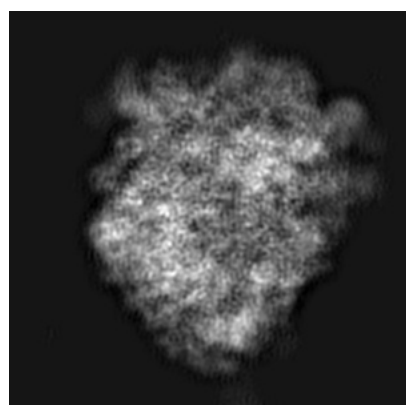
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3152. These allow visual inspection of the internal detail of the map and identification of artifacts.

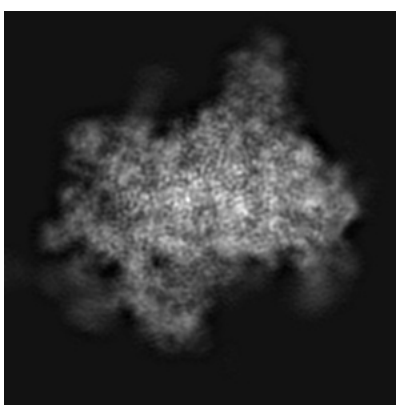
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

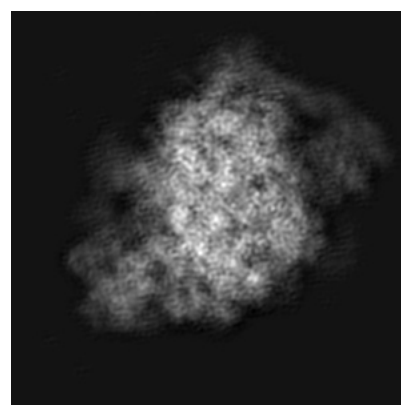
6.1.1 Primary map



X



Y

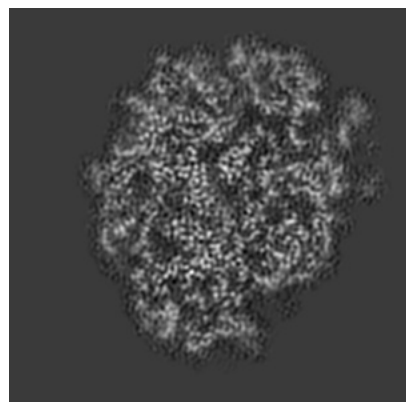


Z

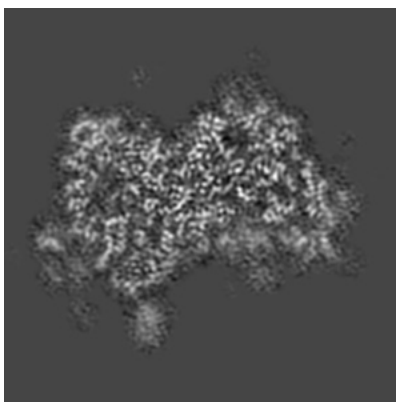
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

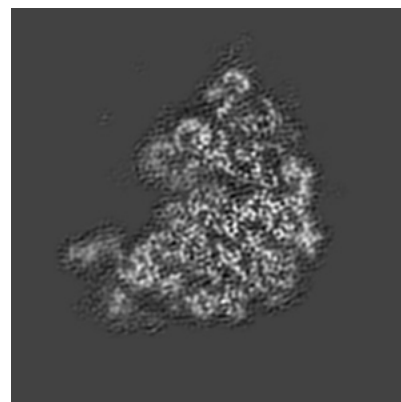
6.2.1 Primary map



X Index: 108



Y Index: 108

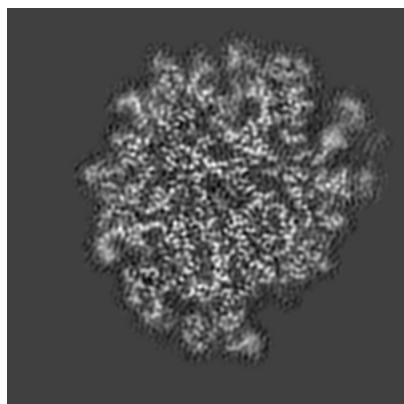


Z Index: 108

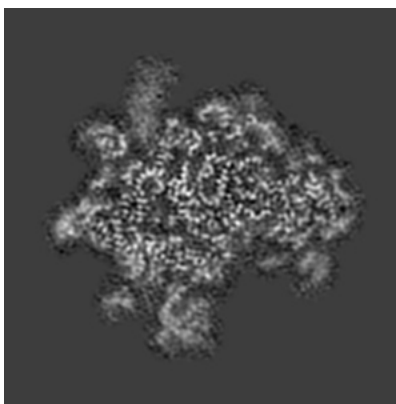
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

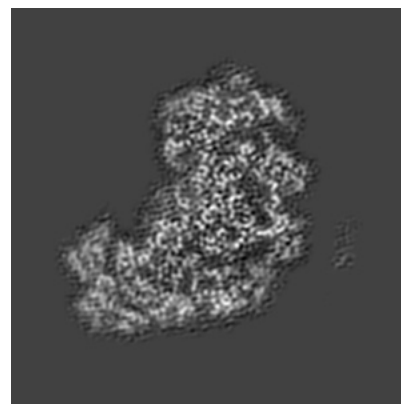
6.3.1 Primary map



X Index: 113



Y Index: 87

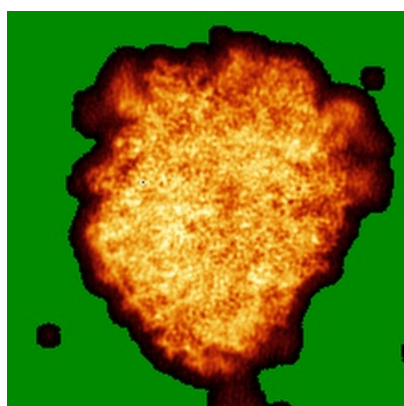


Z Index: 94

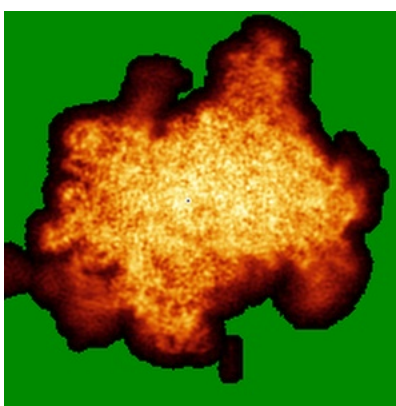
The images above show the largest variance slices of the map in three orthogonal directions.

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

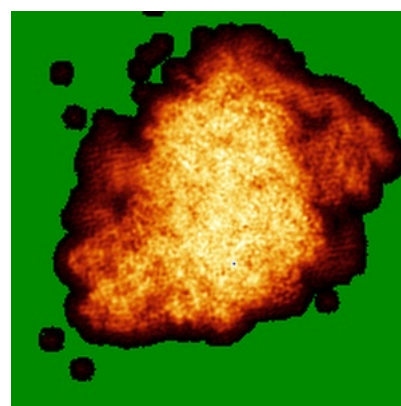
6.4.1 Primary map



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 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

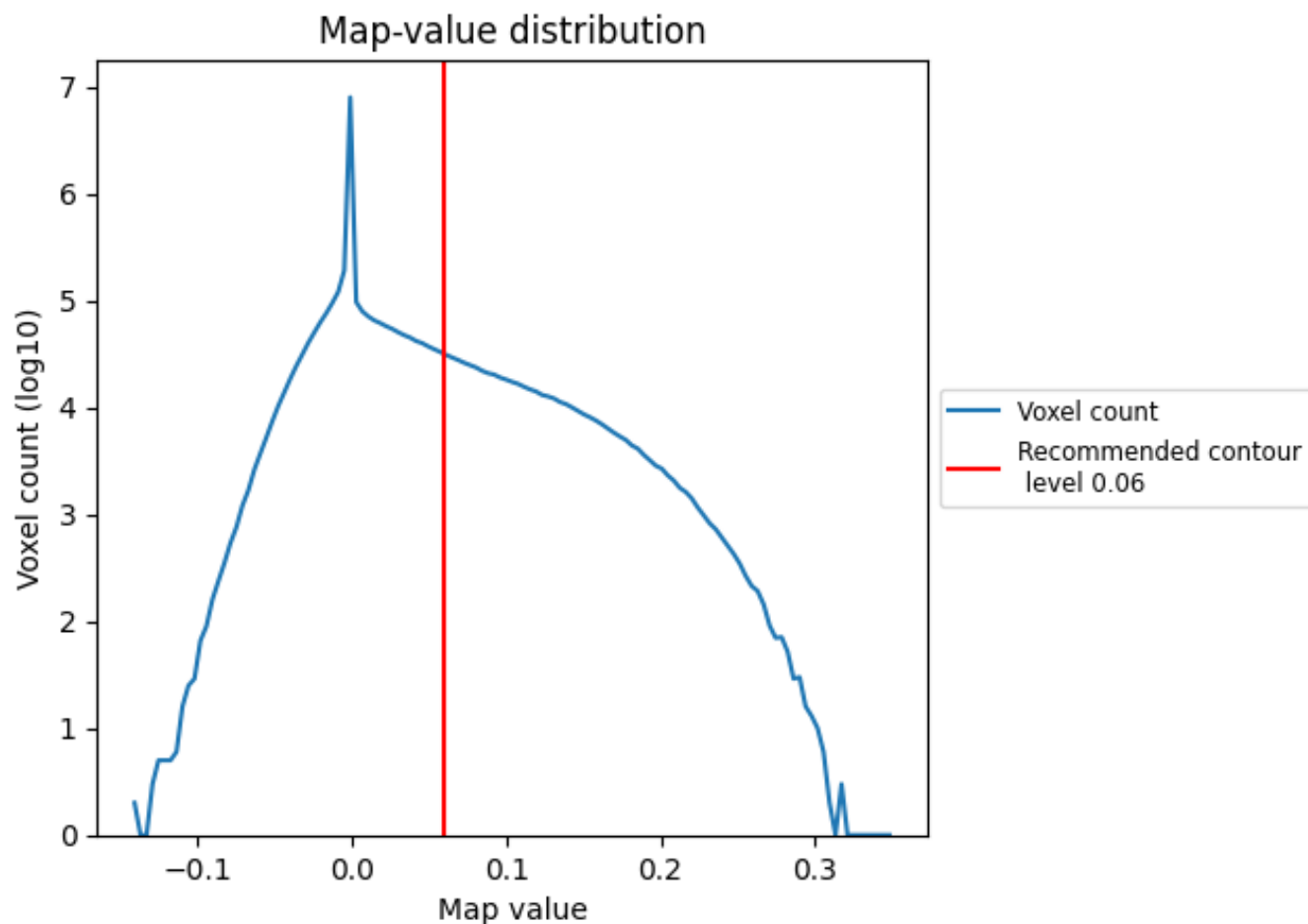
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

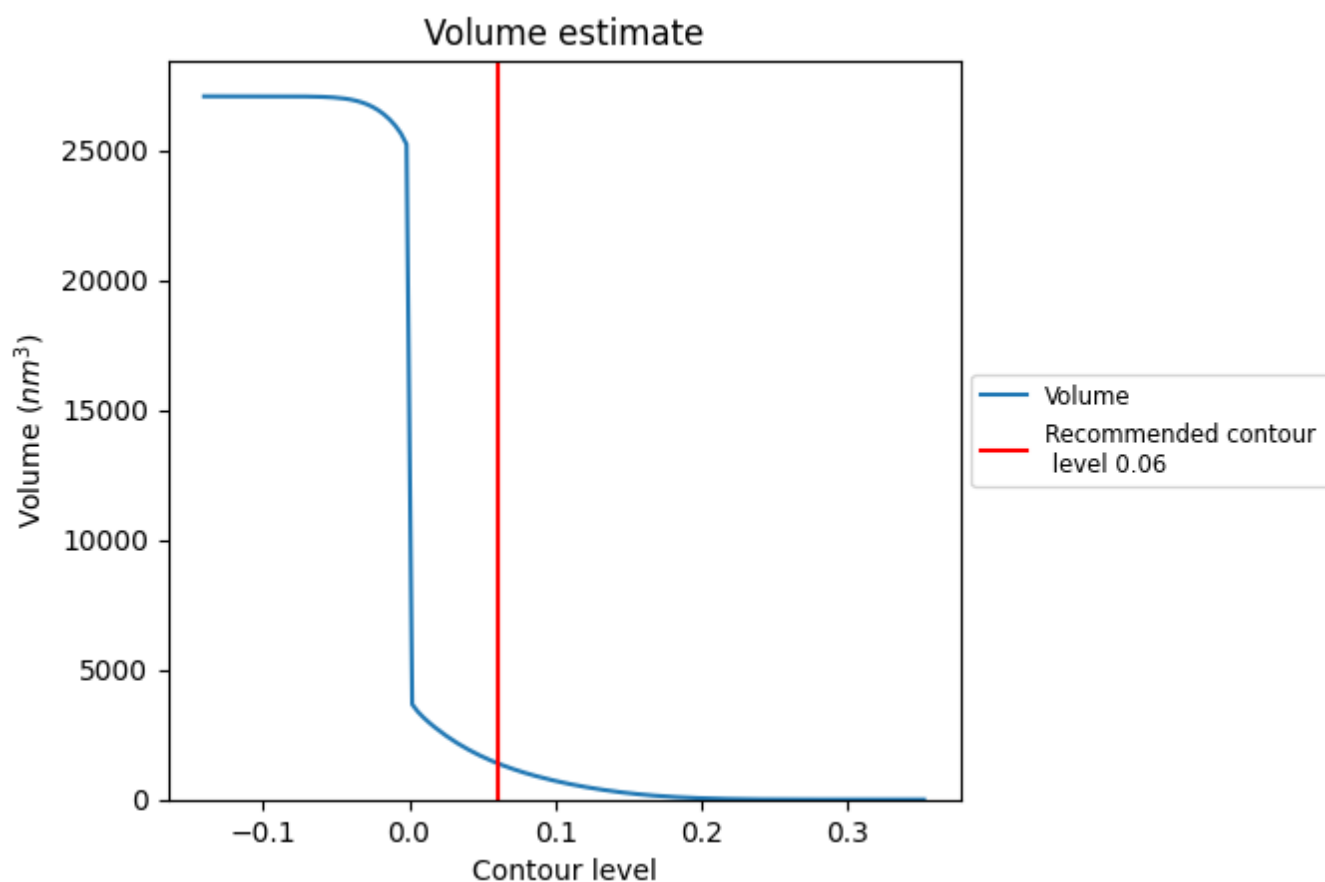
This section contains the results of statistical analysis of the map.

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.

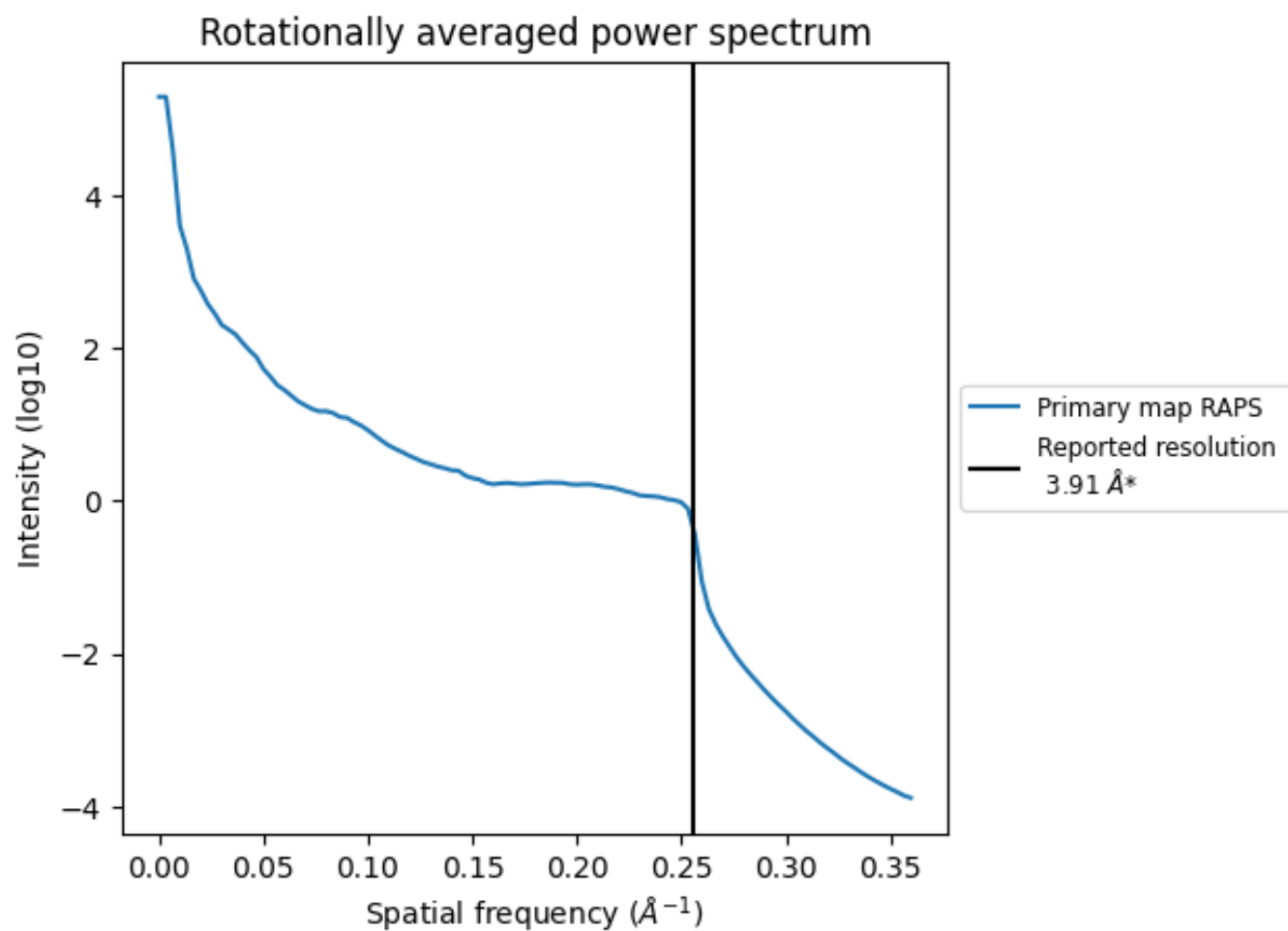
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1406 nm³; this corresponds to an approximate mass of 1270 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 0.256 Å⁻¹

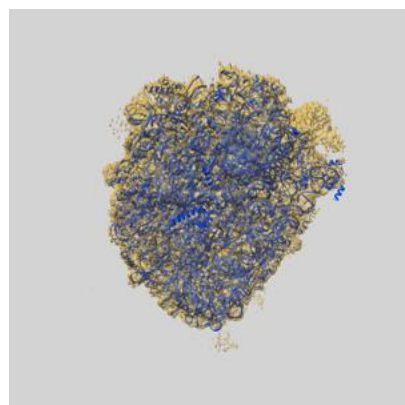
8 Fourier-Shell correlation

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

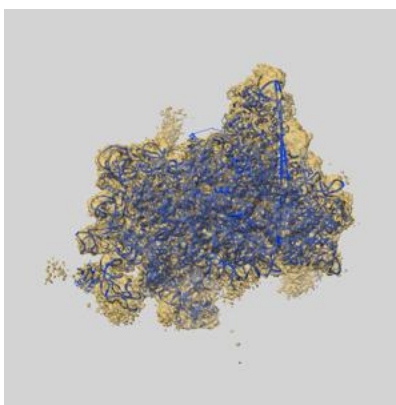
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3152 and PDB model 5APN. Per-residue inclusion information can be found in section 3 on page 14.

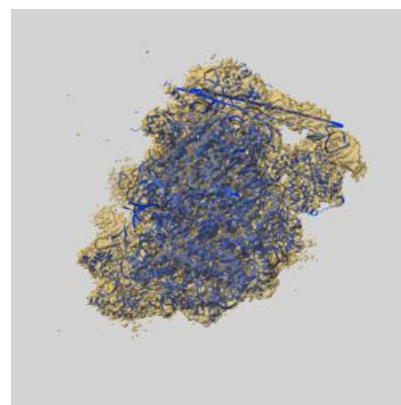
9.1 Map-model overlay [i](#)



X



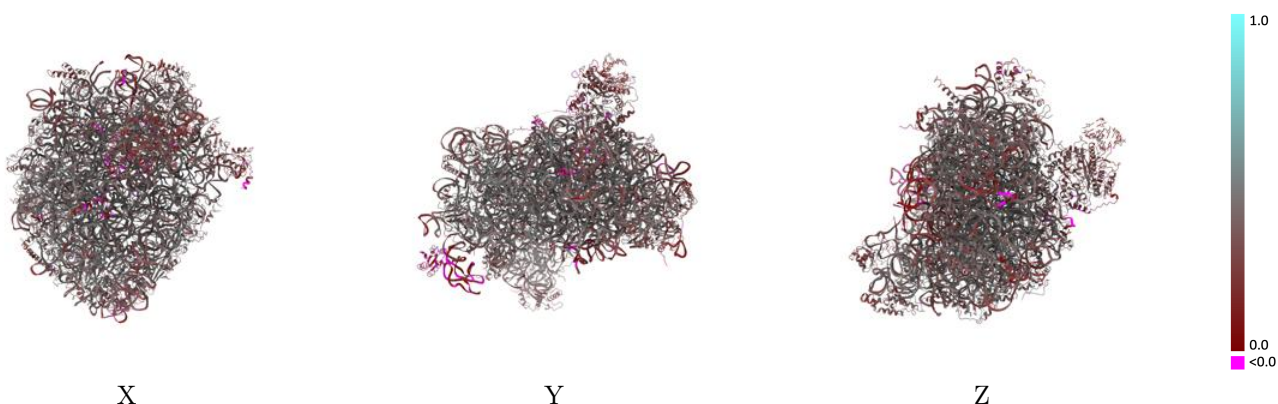
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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](#)

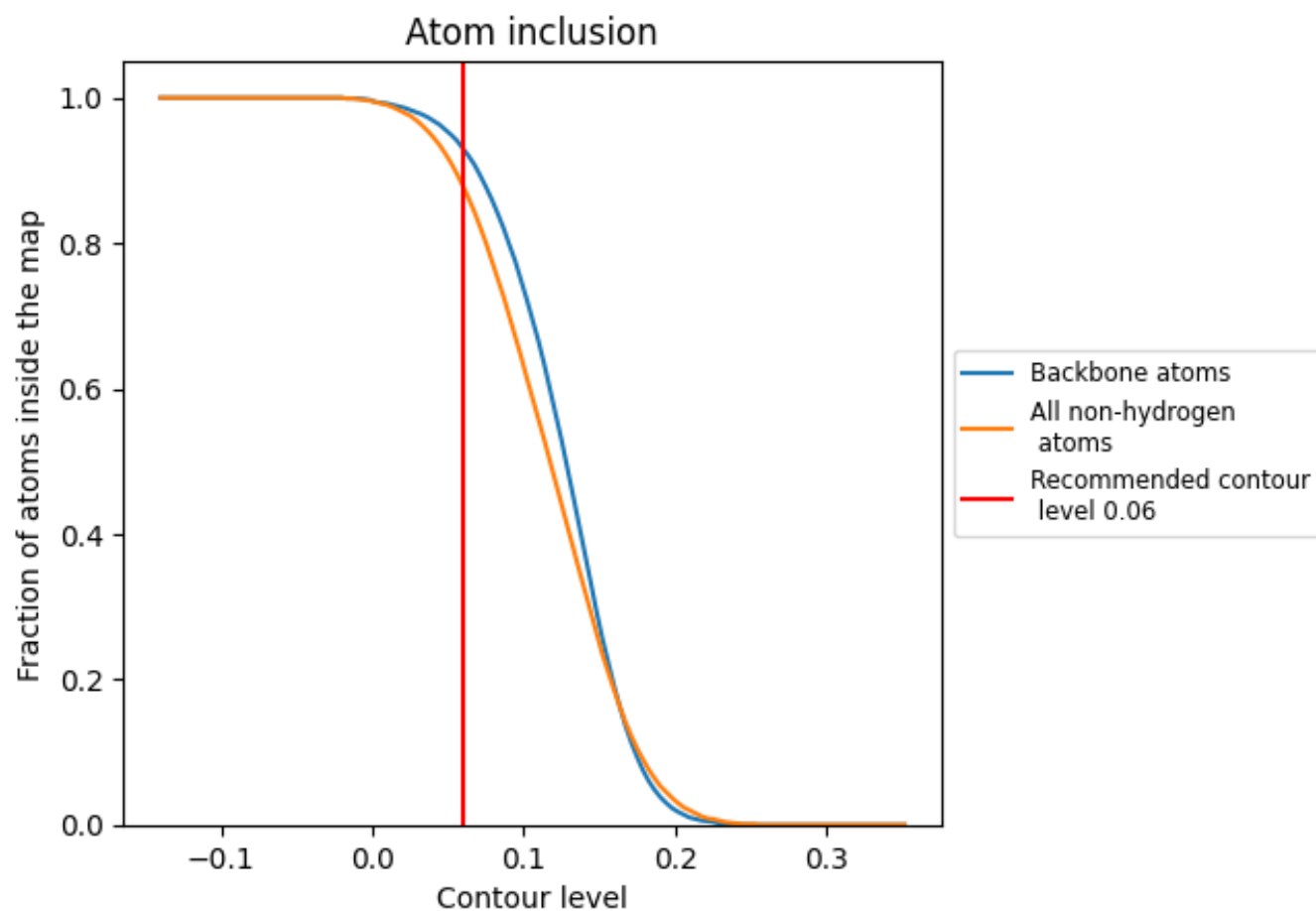


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8780	 0.3890
5	 0.9420	 0.3900
7	 0.9870	 0.3860
8	 0.9580	 0.4110
A	 0.8140	 0.4210
B	 0.8650	 0.4260
C	 0.8610	 0.4350
D	 0.8470	 0.3440
E	 0.8500	 0.3920
F	 0.8400	 0.4230
G	 0.8500	 0.3660
H	 0.8500	 0.4020
I	 0.8290	 0.4030
J	 0.8310	 0.3050
L	 0.8480	 0.4110
M	 0.8670	 0.4080
N	 0.7920	 0.4200
O	 0.8620	 0.4310
P	 0.8190	 0.4360
Q	 0.8510	 0.4350
R	 0.8300	 0.4090
S	 0.8570	 0.4310
T	 0.8350	 0.4310
U	 0.7800	 0.3730
V	 0.8170	 0.4070
W	 0.8300	 0.4050
X	 0.8070	 0.4340
Y	 0.8460	 0.4160
Z	 0.8500	 0.3590
a	 0.8690	 0.4330
b	 0.7810	 0.4000
c	 0.7620	 0.3400
d	 0.7760	 0.4280
e	 0.8150	 0.4370
f	 0.8560	 0.4520



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Chain	Atom inclusion	Q-score
g	 0.7940	 0.4070
h	 0.8330	 0.3990
i	 0.7840	 0.3800
j	 0.8490	 0.4430
k	 0.7900	 0.3690
l	 0.7830	 0.4430
m	 0.8190	 0.3980
o	 0.7230	 0.3430
p	 0.8000	 0.3950
q	 0.1230	 0.0770
x	 0.7050	 0.3040
y	 0.4140	 0.2860
z	 0.1510	 0.0910