



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:09 PM UTC

PDB ID : 4V7I / pdb_00004v7i
EMDB ID : EMD-1484
Title : Ribosome-SecY complex.
Authors : Gumbart, J.C.; Trabuco, L.G.; Schreiner, E.; Villa, E.; Schulten, K.
Deposited on : 2009-10-21
Resolution : 9.60 Å(reported)
Based on initial models : 3BO0, 2I2V

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
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

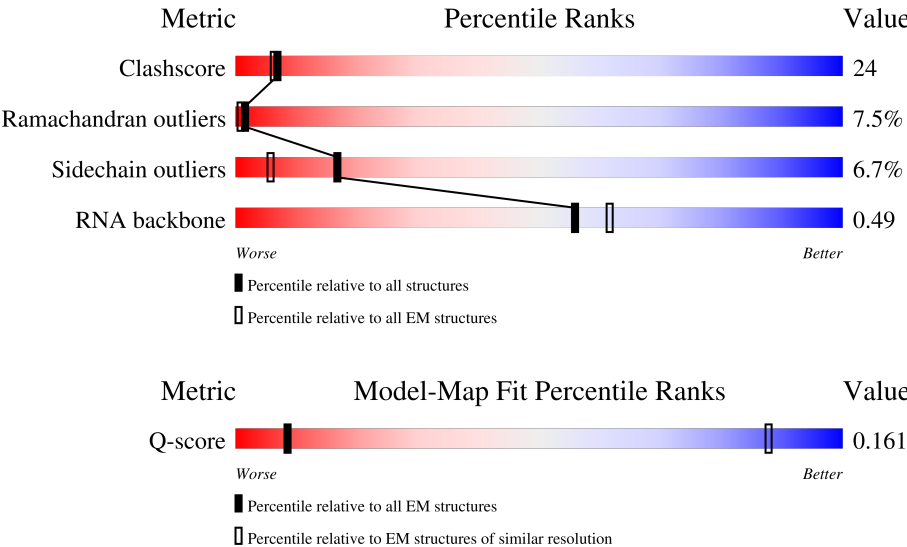
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.60 Å.

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



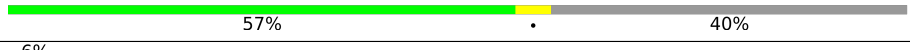
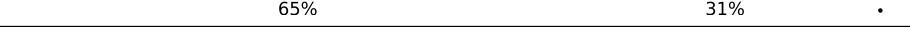
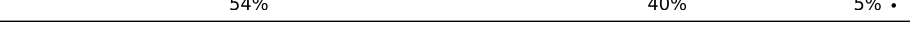
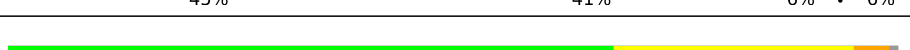
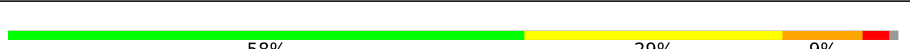
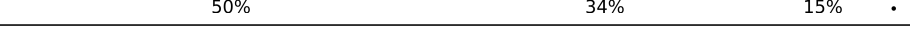
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	185 (9.10 - 10.10)

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	A7	120	27% 38% 28%
2	A8	2904	5% 24% 39% 32%
3	AA	442	81% 15%

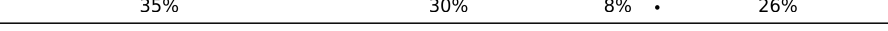
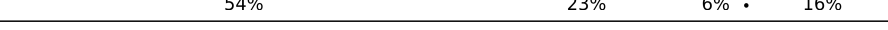
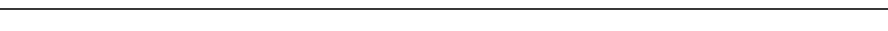
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Mol	Chain	Length	Quality of chain
4	AB	65	
5	AC	53	
6	A5	234	
7	A6	273	
8	AD	209	
9	AE	201	
10	AF	179	
11	AG	177	
12	AH	149	
13	AI	142	
14	AJ	142	
15	AK	123	
16	AL	144	
17	AM	136	
18	AN	127	
19	AO	117	
20	AP	115	
21	AQ	118	
22	AR	103	
23	AS	110	
24	AT	100	
25	AU	104	
26	AV	94	
27	AW	85	
28	AX	78	

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Mol	Chain	Length	Quality of chain
29	AY	63	
30	AZ	59	
31	A0	57	
32	A1	55	
33	A2	46	
34	A3	65	
35	A4	38	
36	BA	1542	
37	BB	241	
38	BC	233	
39	BD	206	
40	BE	167	
41	BF	135	
42	BG	179	
43	BH	130	
44	BI	130	
45	BJ	103	
46	BK	129	
47	BL	124	
48	BM	118	
49	BN	101	
50	BO	89	
51	BP	82	
52	BQ	84	
53	BR	75	

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Mol	Chain	Length	Quality of chain
54	BS	92	 41% 26% 16% • 14%
55	BT	87	 48% 38% 9% • •
56	BU	71	 45% 24% • 28%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 148250 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5S ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

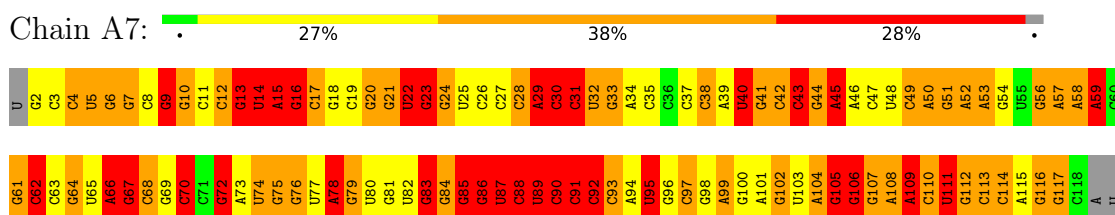
- Molecule 56 is a protein called 30S ribosomal protein S21.

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

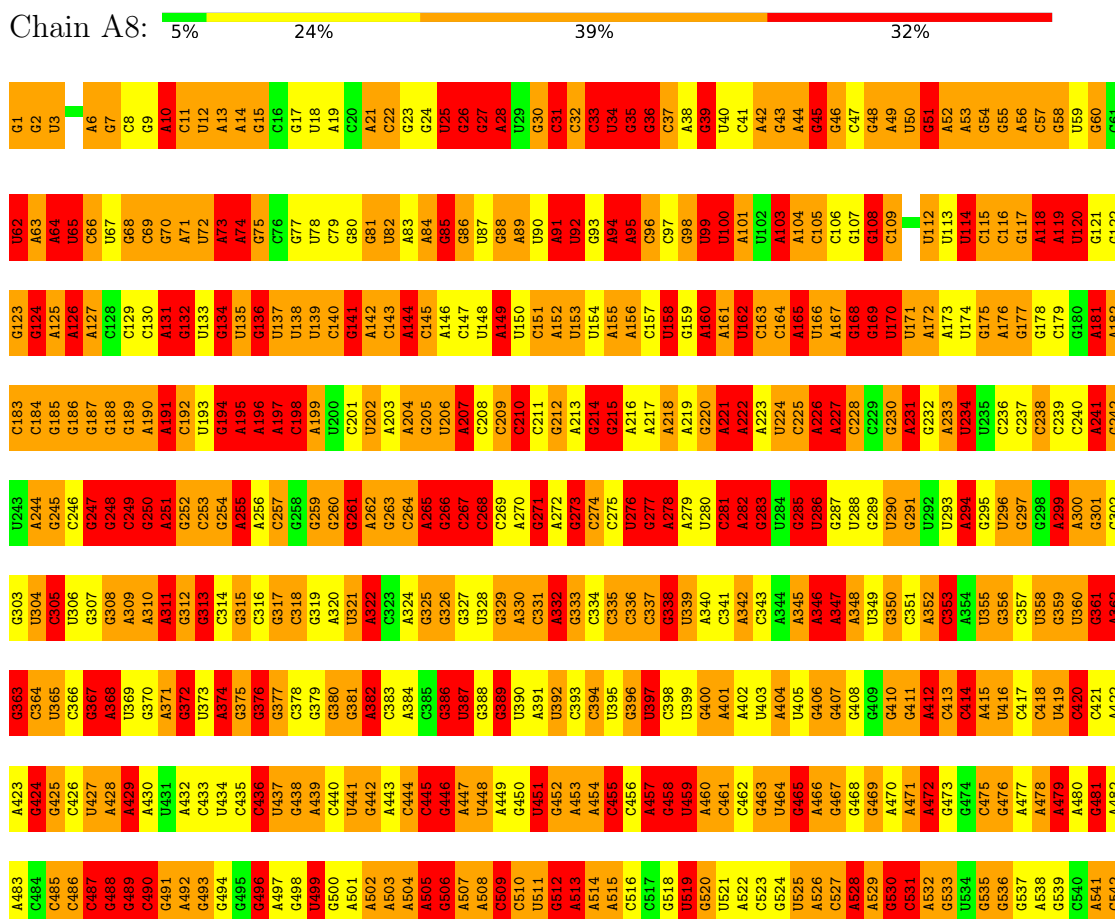
3 Residue-property plots

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

• Molecule 1: 5S ribosomal RNA

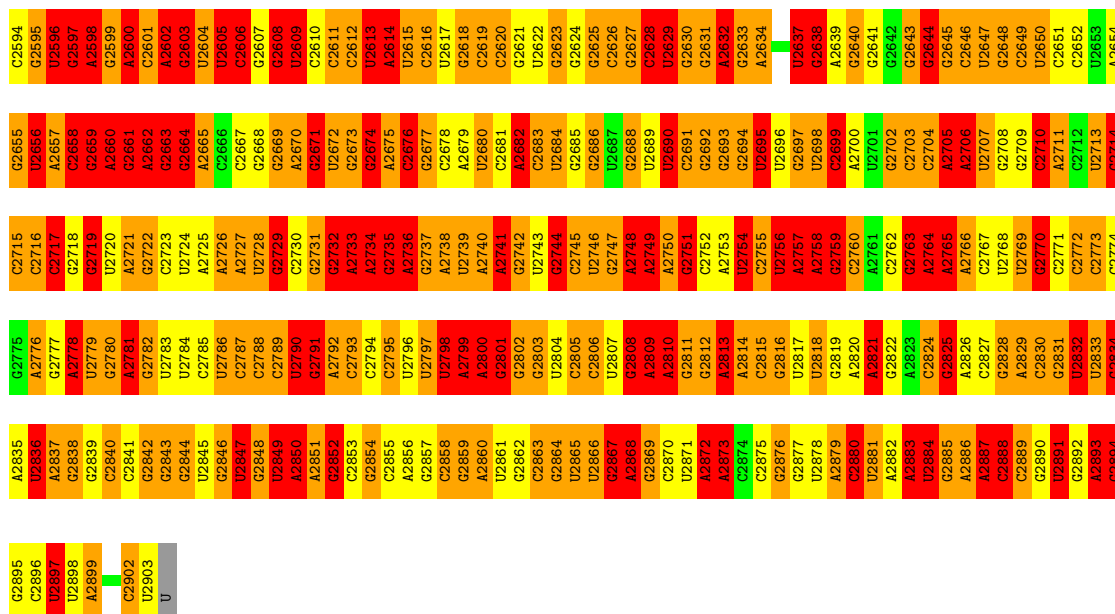


• Molecule 2: 23S ribosomal RNA

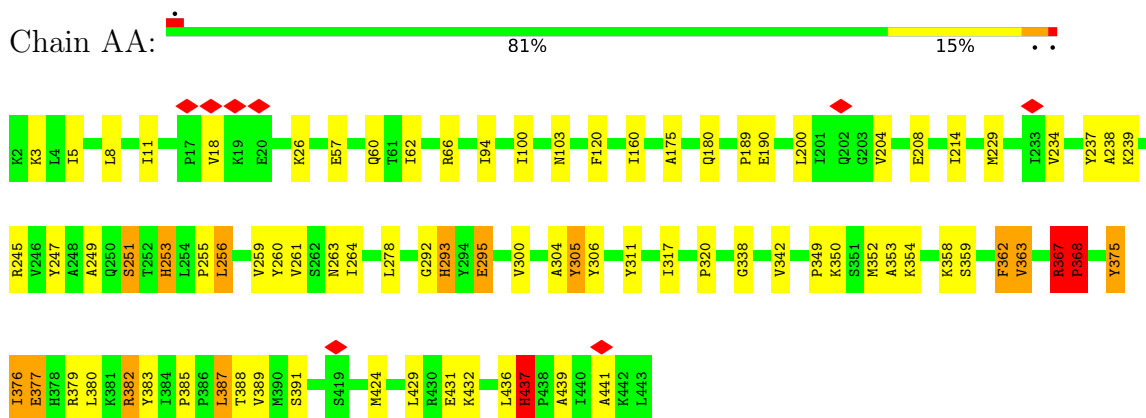


U1513	C1451	U1391	G1331	G1271	G1211	G1149	A1089	A1028	U967	U896	U846	G784	U724	G663	A603	G543
G1514	G1452	A1392	G1332	A1272	G1212	C1150	A1090	A1028	C968	G907	U847	G785	G725	G664	G604	C544
A1515	A1453	A1393	G1333	A1273	A1213	C1151	G1091	C1030	G969	C908	C848	G786	G726	U685	G605	U545
C1516	C1454	U1394	G1334	A1274	A1214	C1152	G1092	G1031	U970	A909	A849	C787	A727	U686	U606	U546
G1517	G1455	A1395	G1335	A1275	G1215	C1153	G1093	A1032	G971	G910	U850	A788	G728	U687	U607	A547
C1518	C1456	U1396	A1336	A1276	G1216	C1154	U1094	U1033	A972	A911	C851	A789	G729	A688	A608	G548
U1519	U1457	U1397	G1337	G1277	U1217	A1155	A1095	G1034	A973	C912	U852	U790	A730	G669	A609	G549
U1520	U1458	C1398	G1338	G1278	G1218	A1156	A1096	U1035	A974	U913	C853	C791	C731	G670	C610	C550
G1521	G1459	U1399	U1219	G1279	U1219	G1157	A1097	U1036	A975	U914	C854	A792	G732	C671	C611	G551
A1522	A1460	U1400	G1340	G1280	G1220	C1158	A1098	G1037	C976	C915	G855	A793	G733	G612	A612	U552
U1523	C1461	G1401	G1341	G1281	C1221	U1159	G1099	G1038	G977	G916	C856	A794	A734	A613	A613	G553
G1524	U1462	U1402	A1342	U1282	U1222	G1160	C1100	A1039	A978	A917	G857	C795	A735	U614	U614	U554
A1525	A1463	A1403	G1343	U1283	G1223	C1161	U1101	A1040	A979	A918	G858	G796	G736	A615	A615	G555
C1526	U1466	C1404	U1344	A1284	U1224	G1162	C1102	G1041	A980	U919	C859	G797	C737	A616	A616	A556
G1527	U1467	U1405	G1345	A1285	G1225	G1163	A1103	G1042	U981	A920	U860	G798	G738	G617	G617	C557
A1528	U1468	U1406	G1346	A1286	A1226	C1164	C1104	A861	C982	C921	U861	G799	A739	C678	C678	U558
G1529	A1469	G1407	A1347	A1287	G1227	A1165	U105	A893	C983	C922	G862	G799	G740	C680	G619	G559
U1530	A1470	G1408	G1348	U1288	G1228	G1166	G1106	C1045	A984	G923	A863	G801	U741	G681	G620	C560
C1531	G1471	U1409	C1349	C1289	C1229	C1167	G1107	A1046	C985	G924	G864	A802	A742	G682	A621	G561
A1532	C1472	G1410	C1350	C1290	A1230	G1168	U1108	G1047	C986	A925	C865	U803	A743	U683	G622	U562
G1533	G1473	U1411	C1351	C1291	U1231	A1169	C1109	A1048	C987	G926	A866	U804	U744	U683	G623	A563
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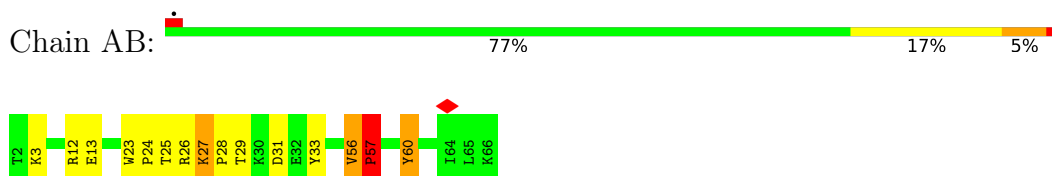
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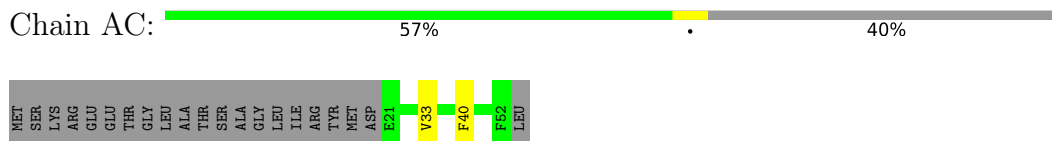
• Molecule 3: PREPROTEIN TRANSLOCASE SECY SUBUNIT



• Molecule 4: PREPROTEIN TRANSLOCASE SECE SUBUNIT

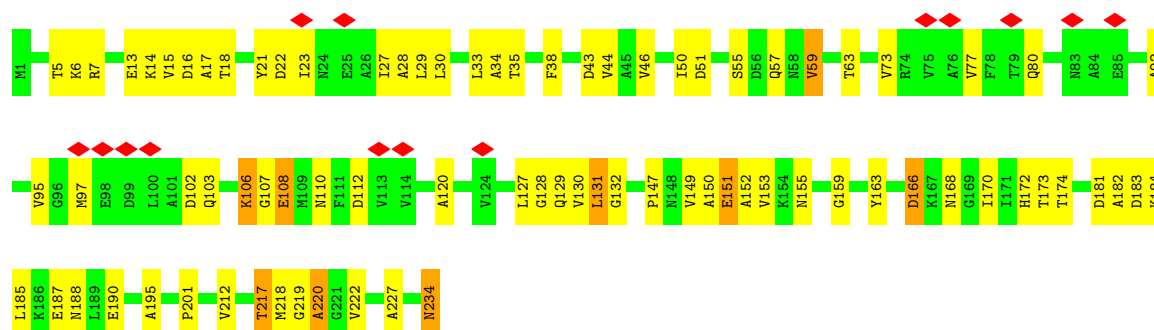


• Molecule 5: Preprotein translocase subunit secG



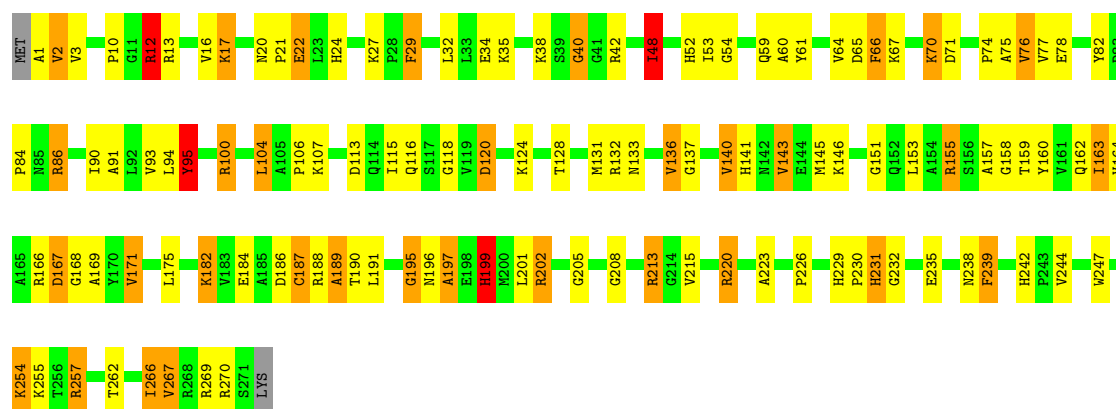
• Molecule 6: 50S ribosomal protein L1





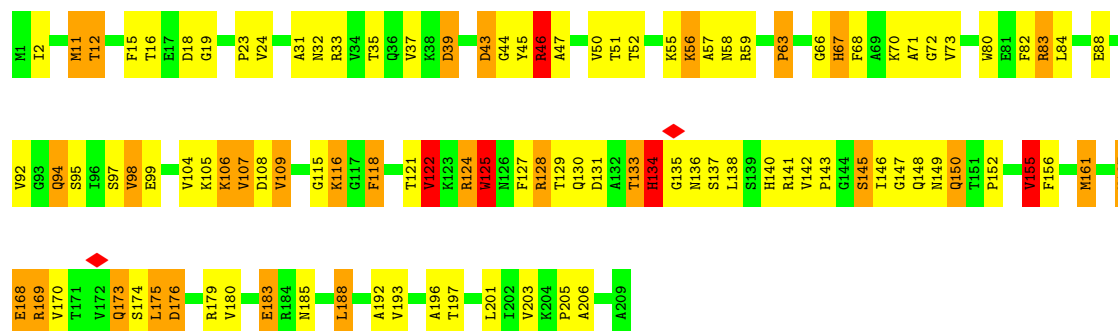
• Molecule 7: 50S ribosomal protein L2

Chain A6: 55% 31% 12% ..



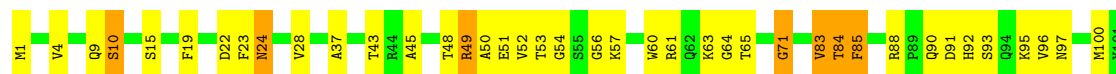
• Molecule 8: 50S ribosomal protein L3

Chain AD: 49% 34% 14% .



• Molecule 9: 50S ribosomal protein L4

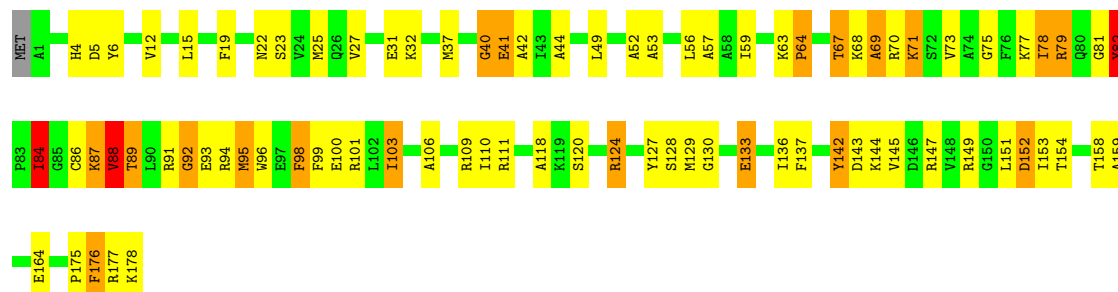
Chain AE: 63% 31% 6%





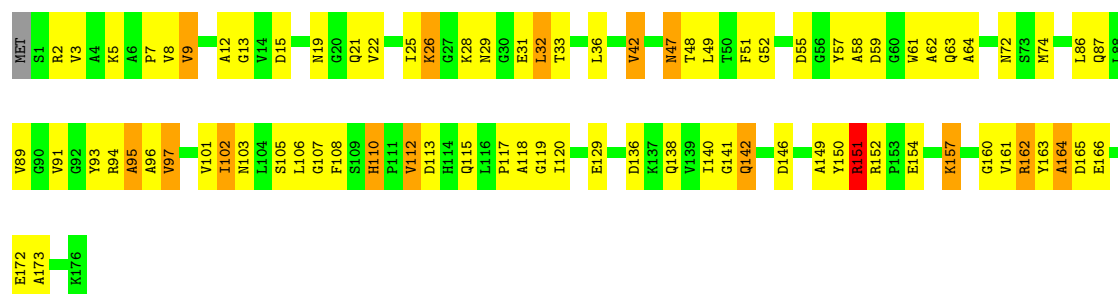
• Molecule 10: 50S ribosomal protein L5

Chain AF: 53% 35% 11% ..



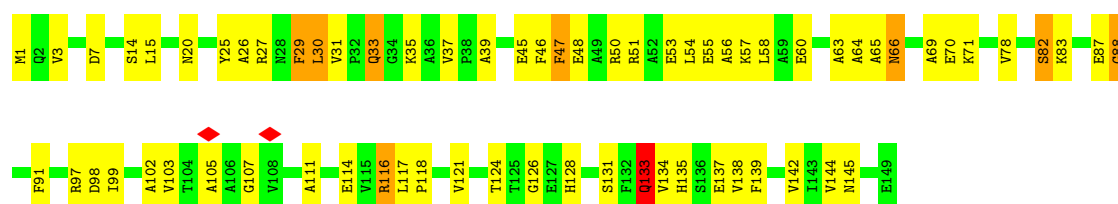
• Molecule 11: 50S ribosomal protein L6

Chain AG: 53% 38% 8% ..



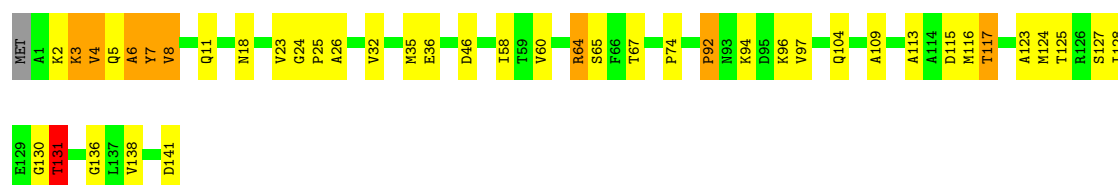
• Molecule 12: 50S ribosomal protein L9

Chain AH: 54% 40% 5% ..

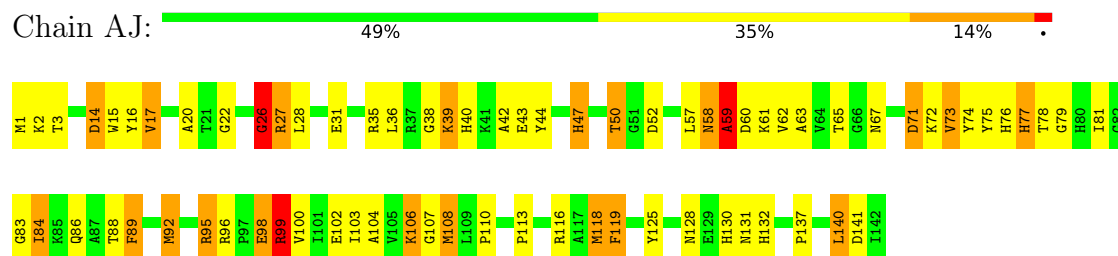


• Molecule 13: 50S ribosomal protein L11

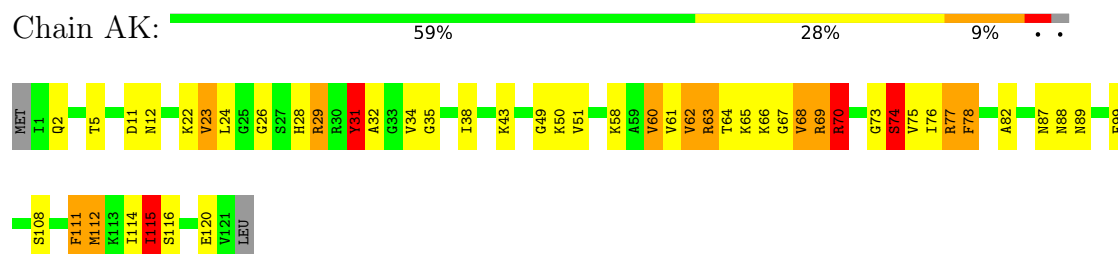
Chain AI: 69% 24% 6% ..



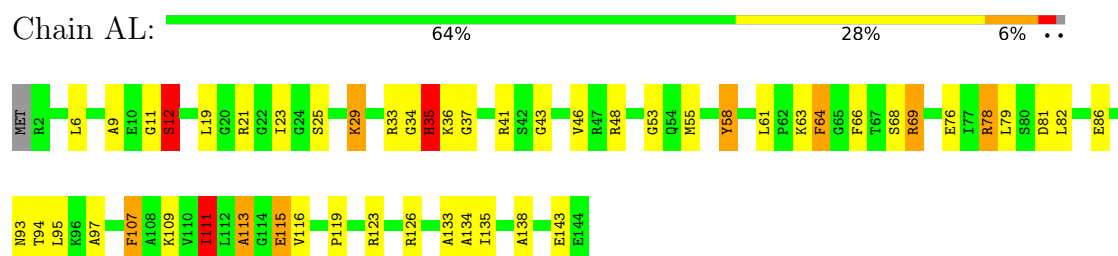
- Molecule 14: 50S ribosomal protein L13



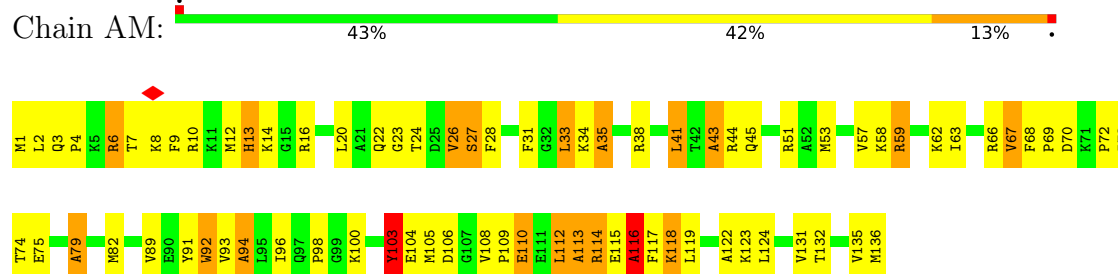
- Molecule 15: 50S ribosomal protein L14



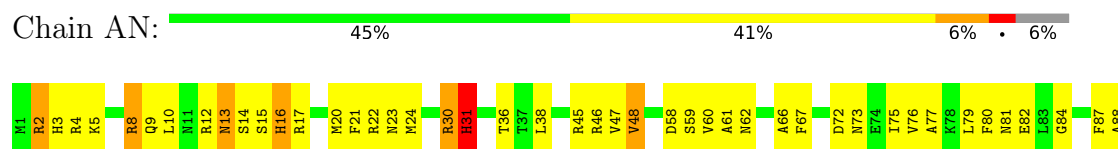
- Molecule 16: 50S ribosomal protein L15

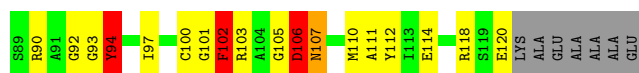


- Molecule 17: 50S ribosomal protein L16



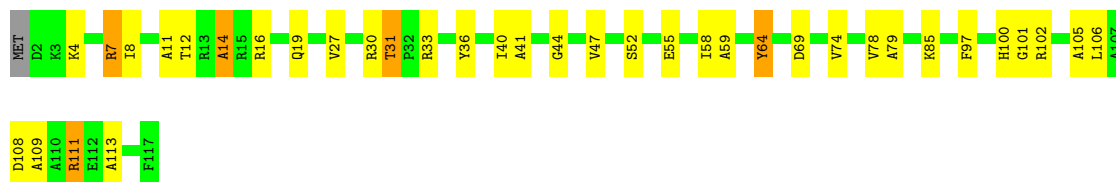
- Molecule 18: 50S ribosomal protein L17





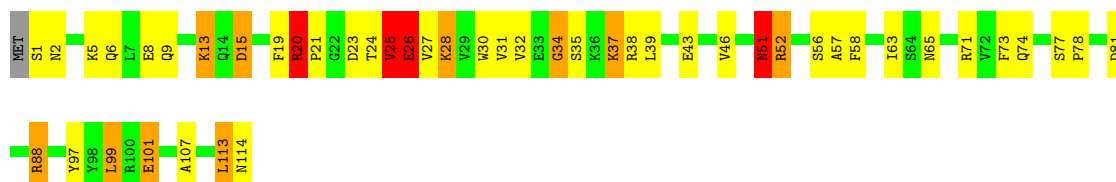
- Molecule 19: 50S ribosomal protein L18

Chain AO: 68% 27% ..



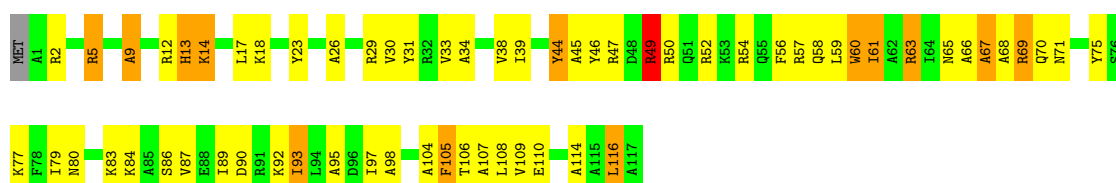
- Molecule 20: 50S ribosomal protein L19

Chain AP: 58% 29% 9% ..



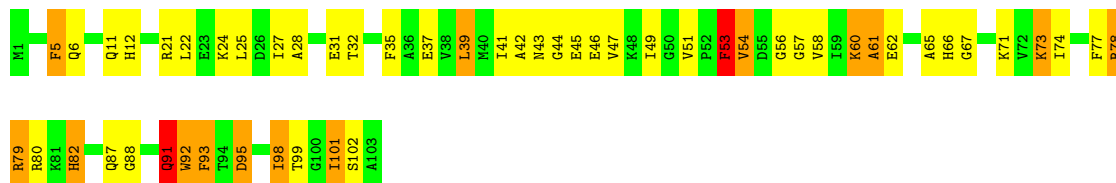
- Molecule 21: 50S ribosomal protein L20

Chain AQ: 46% 42% 11% ..



- Molecule 22: 50S ribosomal protein L21

Chain AR: 49% 36% 14% .



- Molecule 23: 50S ribosomal protein L22

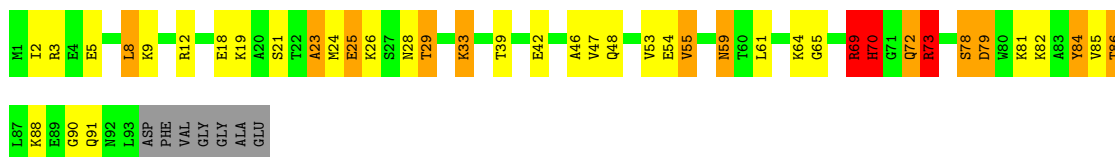
Chain AS: 50% 34% 15% .





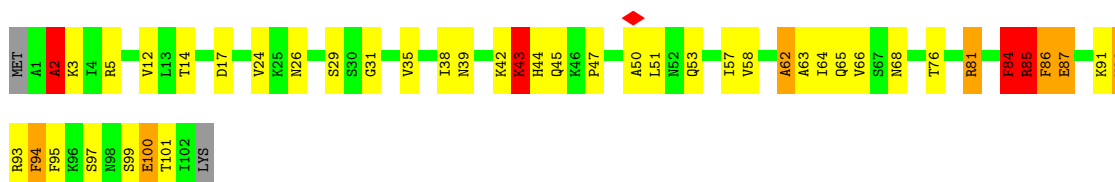
• Molecule 24: 50S ribosomal protein L23

Chain AT: 51% 27% 12% 7%



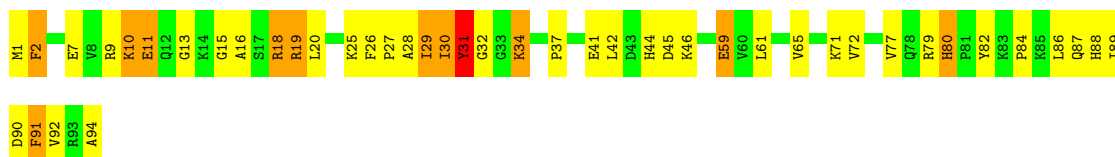
• Molecule 25: 50S ribosomal protein L24

Chain AU: 56% 32% 7%



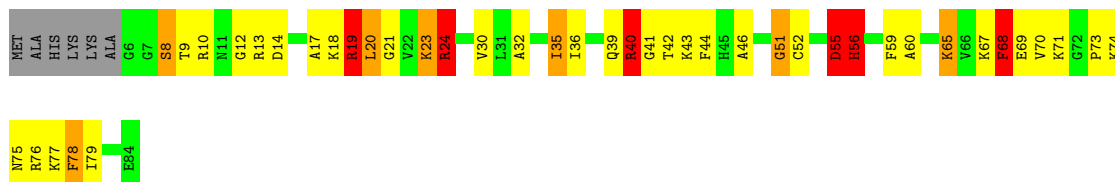
• Molecule 26: 50S ribosomal protein L25

Chain AV: 52% 35% 12%



• Molecule 27: 50S ribosomal protein L27

Chain AW: 42% 35% 8% 7% 7%



• Molecule 28: 50S ribosomal protein L28

Chain AX: 37% 42% 18% 2%





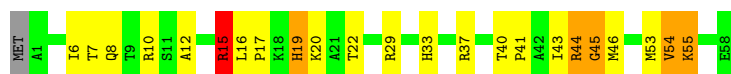
- Molecule 29: 50S ribosomal protein L29

Chain AY: 68% 25% 6%



- Molecule 30: 50S ribosomal protein L30

Chain AZ: 59% 29% 8% ..



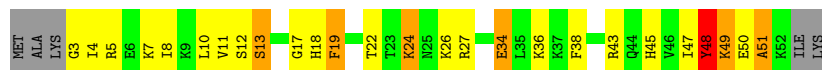
- Molecule 31: 50S ribosomal protein L32

Chain A0: 53% 33% 12% .



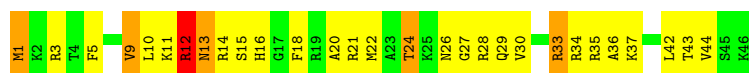
- Molecule 32: 50S ribosomal protein L33

Chain A1: 44% 35% 11% . 9%



- Molecule 33: 50S ribosomal protein L34

Chain A2: 37% 50% 11% .



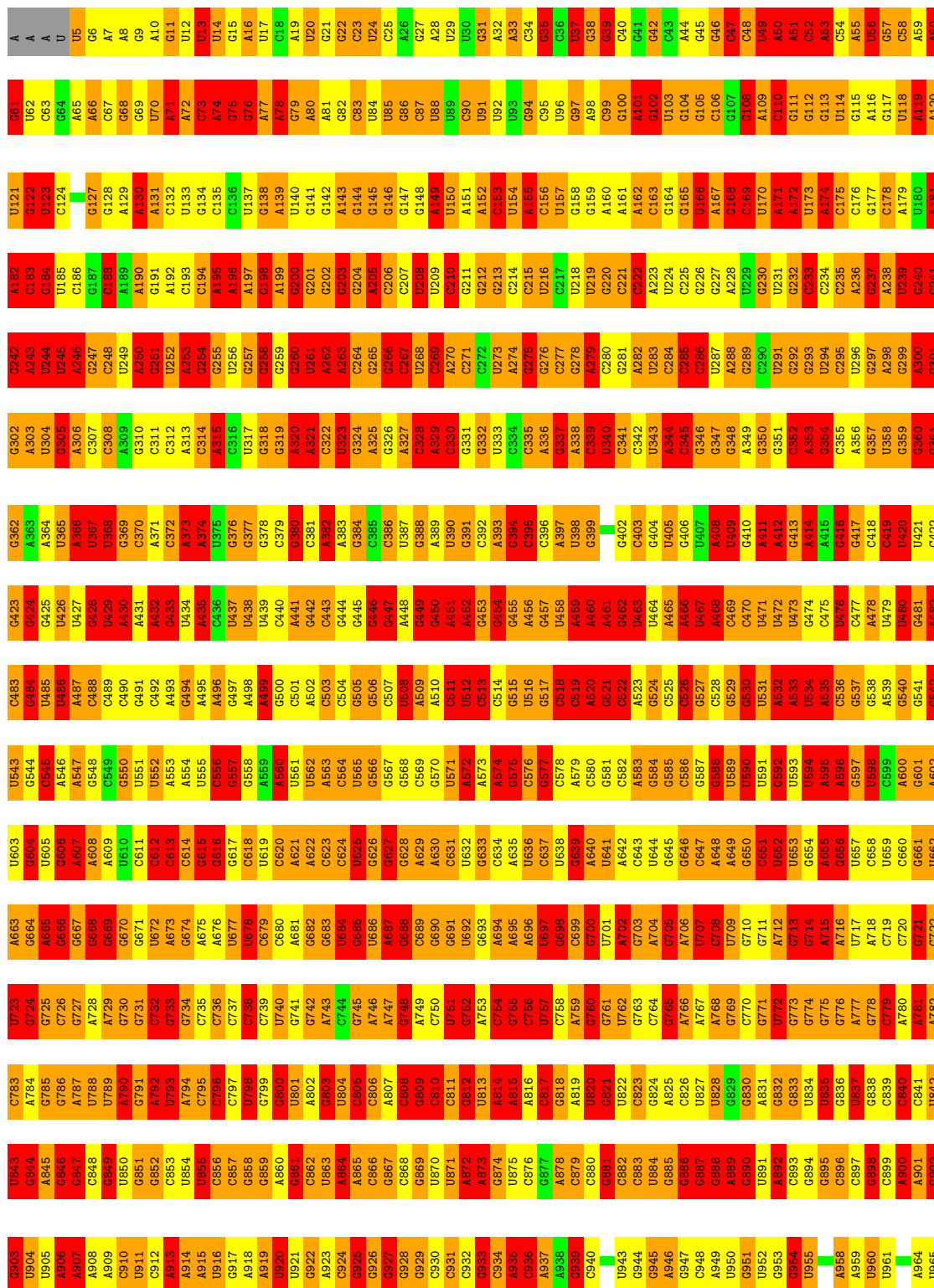
- Molecule 34: 50S ribosomal protein L35

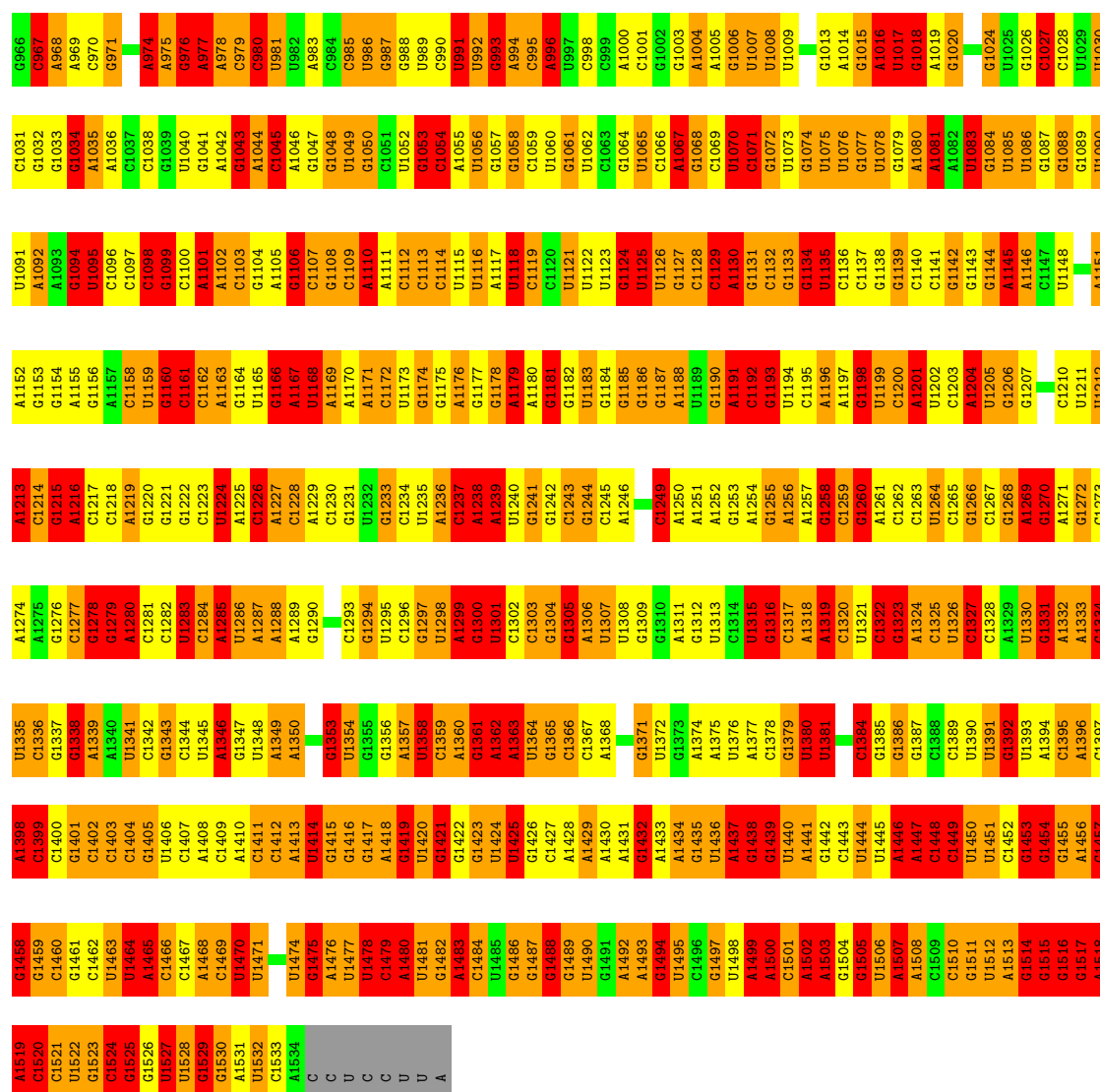
Chain A3: 54% 31% 12% ..



- Molecule 35: 50S ribosomal protein L36

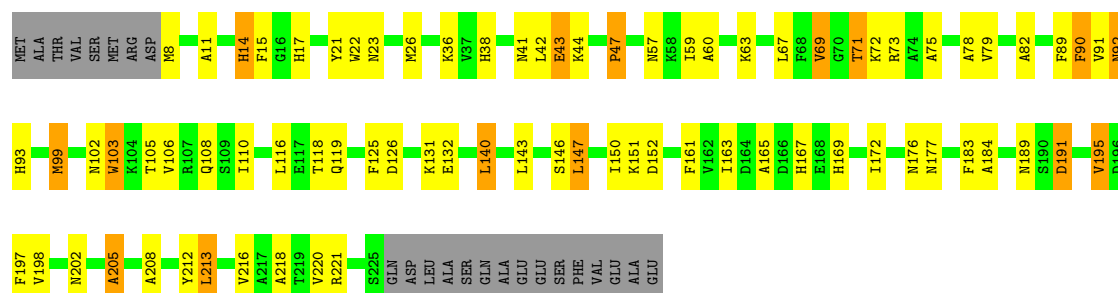
Chain A4: 63% 26% 8% .





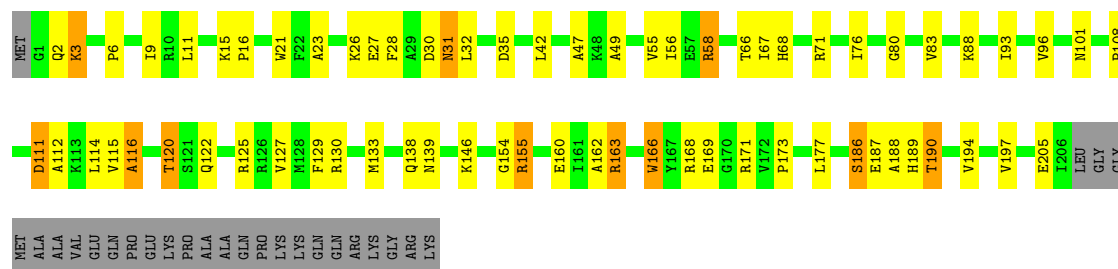
• Molecule 37: 30S ribosomal protein S2

Chain BB: 58% 27% 6% 10%



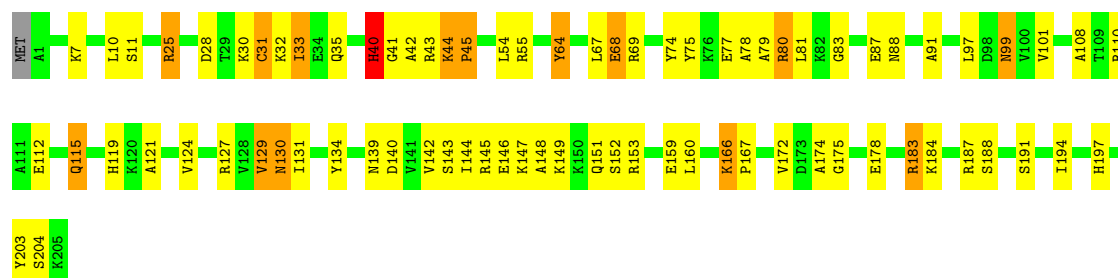
• Molecule 38: 30S ribosomal protein S3

Chain BC: 59% 24% 5% 12%



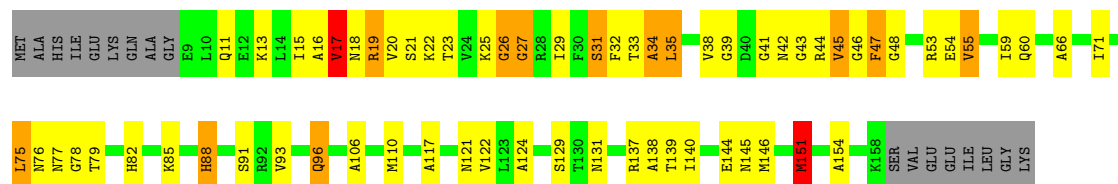
- Molecule 39: 30S ribosomal protein S4

Chain BD: 62% 31% 7%



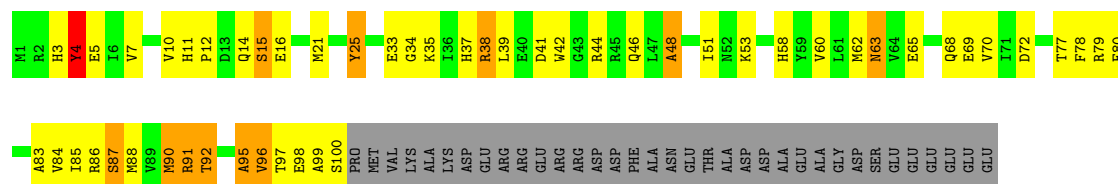
- Molecule 40: 30S ribosomal protein S5

Chain BE: 51% 31% 7% • 10%



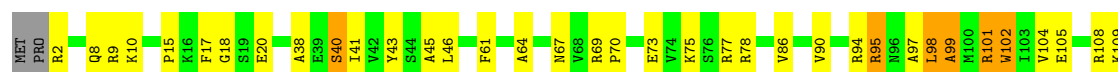
- Molecule 41: 30S ribosomal protein S6

Chain BF: 35% 30% 8% • 26%



- Molecule 42: 30S ribosomal protein S7

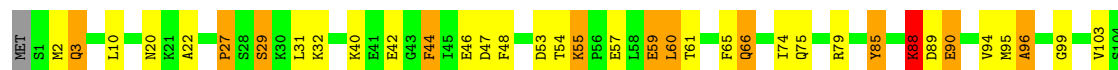
Chain BG: 54% 23% 6% • 16%





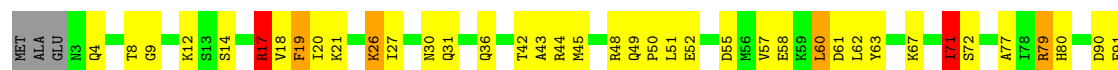
- Molecule 43: 30S ribosomal protein S8

Chain BH: 61% 27% 11% ..



- Molecule 44: 30S ribosomal protein S9

Chain BI: 58% 34% 5% ..



- Molecule 45: 30S ribosomal protein S10

Chain BJ: 64% 24% 6% • 5%



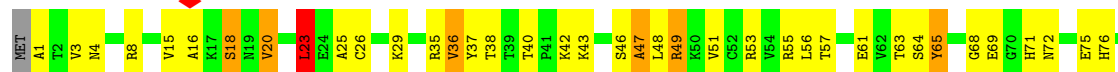
- Molecule 46: 30S ribosomal protein S11

Chain BK: 48% 24% 17% • 9%



- Molecule 47: 30S ribosomal protein S12

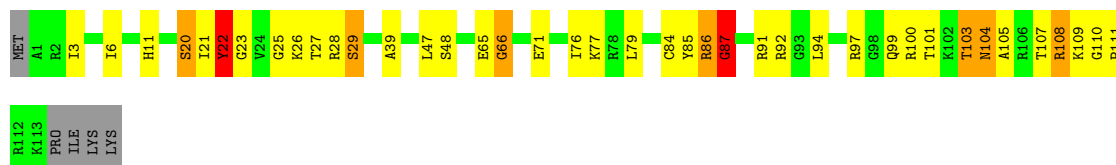
Chain BL: 49% 40% 10% ..





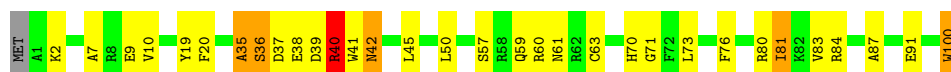
- Molecule 48: 30S ribosomal protein S13

Chain BM: 62% 26% 6% . .



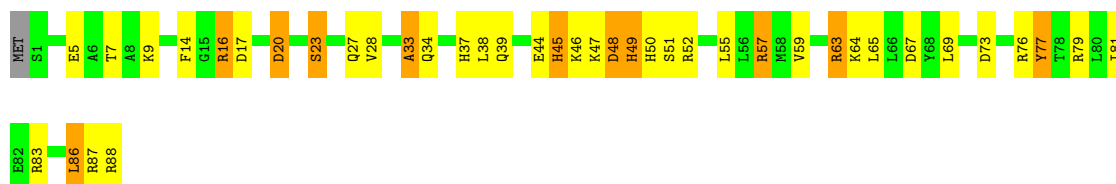
- Molecule 49: 30S ribosomal protein S14

Chain BN: 67% 26% 5% . .



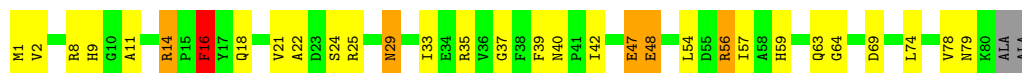
- Molecule 50: 30S ribosomal protein S15

Chain BO: 53% 34% 12% .



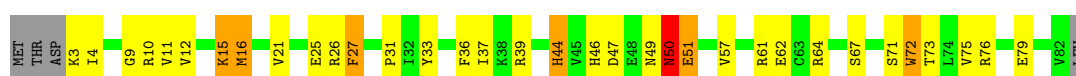
- Molecule 51: 30S ribosomal protein S16

Chain BP: 60% 30% 6% . .



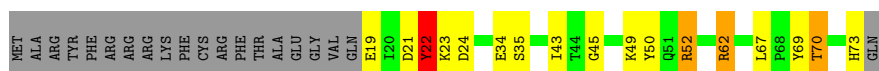
- Molecule 52: 30S ribosomal protein S17

Chain BQ: 55% 32% 7% . 5%

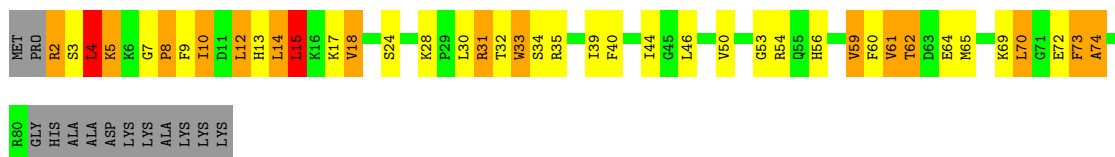


- Molecule 53: 30S ribosomal protein S18

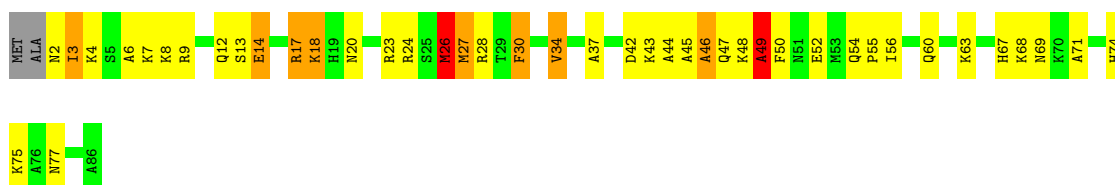
Chain BR: 51% 17% . . 27%



- Molecule 54: 30S ribosomal protein S19



- Molecule 55: 30S ribosomal protein S20



- Molecule 56: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39000	Depositor
Resolution determination method	Not provided	
CTF correction method	EMAN- PHASE FLIPPING OF PARTICLES FORM THE SAME MICROGRAPH	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	-700.00	Depositor
Maximum defocus (nm)	-3000.00	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	10.649	Depositor
Minimum map value	-4.997	Depositor
Average map value	0.150	Depositor
Map value standard deviation	0.868	Depositor
Recommended contour level	0.95	Depositor
Map size (Å)	393.12, 393.12, 393.12	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.73, 2.73, 2.73	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A7	1.41	13/2803 (0.5%)	1.80	88/4371 (2.0%)
2	A8	1.47	412/69800 (0.6%)	1.82	2289/108892 (2.1%)
3	AA	1.28	1/3484 (0.0%)	1.76	62/4732 (1.3%)
4	AB	1.35	0/514	1.78	11/694 (1.6%)
5	AC	1.28	0/262	1.61	1/354 (0.3%)
6	A5	1.35	2/1748 (0.1%)	1.81	52/2355 (2.2%)
7	A6	1.60	8/2121 (0.4%)	1.82	42/2852 (1.5%)
8	AD	1.59	8/1586 (0.5%)	1.86	50/2134 (2.3%)
9	AE	1.49	3/1571 (0.2%)	1.77	30/2113 (1.4%)
10	AF	1.56	6/1444 (0.4%)	1.89	56/1937 (2.9%)
11	AG	1.57	2/1343 (0.1%)	1.84	36/1816 (2.0%)
12	AH	1.54	3/1122 (0.3%)	1.93	47/1515 (3.1%)
13	AI	1.37	1/1046 (0.1%)	1.80	17/1410 (1.2%)
14	AJ	1.69	14/1152 (1.2%)	1.93	38/1551 (2.5%)
15	AK	1.73	4/939 (0.4%)	1.79	23/1258 (1.8%)
16	AL	1.49	0/1054	1.74	26/1403 (1.9%)
17	AM	1.61	9/1093 (0.8%)	1.90	33/1460 (2.3%)
18	AN	1.65	2/973 (0.2%)	1.99	41/1301 (3.2%)
19	AO	1.60	0/902	1.88	24/1209 (2.0%)
20	AP	1.64	3/929 (0.3%)	1.85	27/1242 (2.2%)
21	AQ	1.73	6/960 (0.6%)	2.07	46/1278 (3.6%)
22	AR	1.74	5/829 (0.6%)	1.87	29/1107 (2.6%)
23	AS	1.64	4/864 (0.5%)	1.98	42/1156 (3.6%)
24	AT	1.49	1/744 (0.1%)	1.89	23/994 (2.3%)
25	AU	1.52	3/787 (0.4%)	1.77	26/1051 (2.5%)
26	AV	1.65	5/766 (0.7%)	1.93	23/1025 (2.2%)
27	AW	1.53	1/603 (0.2%)	1.82	20/797 (2.5%)
28	AX	1.77	6/635 (0.9%)	2.15	40/848 (4.7%)
29	AY	1.51	1/510 (0.2%)	1.81	16/677 (2.4%)
30	AZ	1.63	3/453 (0.7%)	1.95	13/605 (2.1%)
31	A0	1.60	1/450 (0.2%)	1.89	12/599 (2.0%)
32	A1	1.51	1/416 (0.2%)	1.93	13/554 (2.3%)
33	A2	1.77	0/380	2.19	22/498 (4.4%)
34	A3	1.48	0/513	1.88	13/676 (1.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	A4	1.69	2/303 (0.7%)	1.78	4/397 (1.0%)
36	BA	1.36	151/36762 (0.4%)	1.74	1041/57350 (1.8%)
37	BB	1.45	4/1735 (0.2%)	1.78	44/2338 (1.9%)
38	BC	1.43	0/1651	1.74	35/2225 (1.6%)
39	BD	1.47	2/1665 (0.1%)	1.81	41/2227 (1.8%)
40	BE	1.53	3/1118 (0.3%)	1.79	22/1504 (1.5%)
41	BF	1.61	5/835 (0.6%)	1.88	24/1128 (2.1%)
42	BG	1.43	2/1187 (0.2%)	1.86	47/1591 (3.0%)
43	BH	1.56	3/989 (0.3%)	1.88	24/1326 (1.8%)
44	BI	1.56	2/1034 (0.2%)	1.79	32/1375 (2.3%)
45	BJ	1.49	1/796 (0.1%)	1.71	12/1077 (1.1%)
46	BK	1.59	3/893 (0.3%)	2.02	36/1205 (3.0%)
47	BL	1.72	10/969 (1.0%)	1.95	32/1300 (2.5%)
48	BM	1.49	2/884 (0.2%)	1.92	29/1181 (2.5%)
49	BN	1.38	1/817 (0.1%)	1.92	28/1088 (2.6%)
50	BO	1.70	1/724 (0.1%)	2.12	38/966 (3.9%)
51	BP	1.51	1/648 (0.2%)	1.76	16/870 (1.8%)
52	BQ	1.60	3/657 (0.5%)	1.74	11/881 (1.2%)
53	BR	1.56	0/462	1.97	10/621 (1.6%)
54	BS	1.49	3/652 (0.5%)	1.91	23/877 (2.6%)
55	BT	1.63	2/671 (0.3%)	2.00	34/888 (3.8%)
56	BU	1.57	0/430	1.80	10/570 (1.8%)
All	All	1.47	729/160678 (0.5%)	1.81	4924/239449 (2.1%)

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

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

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

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

The worst 5 of 729 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A8	204	A	O3'-P	-8.25	1.48	1.61
20	AP	51	ASN	CA-C	-8.13	1.41	1.52
36	BA	577	G	P-O5'	-8.04	1.47	1.59
10	AF	77	LYS	CA-C	-7.80	1.49	1.53
2	A8	479	A	Cl'-N9	-7.77	1.35	1.47

The worst 5 of 4924 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A8	2283	C	P-O5'-C5'	17.12	146.58	120.90
2	A8	984	A	P-O5'-C5'	16.80	146.10	120.90
36	BA	49	U	P-O3'-C3'	16.57	145.05	120.20
2	A8	1275	A	P-O3'-C3'	15.66	143.68	120.20
12	AH	134	VAL	N-CA-C	-15.58	96.83	111.48

There are no chirality outliers.

5 of 2335 planarity outliers are listed below:

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

5.2 Too-close contacts

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

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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A8	62321	0	31344	3730	0
3	AA	3408	0	3619	13	0
4	AB	505	0	557	1	0
5	AC	257	0	272	1	0
6	A5	1733	0	1824	26	0
7	A6	2082	0	2157	51	0
8	AD	1565	0	1616	40	0
9	AE	1552	0	1619	32	0
10	AF	1420	0	1460	21	0
11	AG	1323	0	1374	23	0
12	AH	1111	0	1148	17	0
13	AI	1032	0	1088	26	0
14	AJ	1129	0	1162	30	0
15	AK	930	0	1003	21	0
16	AL	1045	0	1117	17	0
17	AM	1074	0	1157	26	0
18	AN	960	0	1000	33	0
19	AO	892	0	923	10	0
20	AP	917	0	965	11	0
21	AQ	947	0	1022	16	0
22	AR	816	0	839	19	0
23	AS	857	0	922	24	0
24	AT	738	0	807	14	0
25	AU	779	0	834	16	0
26	AV	753	0	780	25	0
27	AW	596	0	610	28	0
28	AX	625	0	655	19	0
29	AY	509	0	543	6	0
30	AZ	449	0	491	12	0
31	A0	444	0	461	9	0
32	A1	409	0	440	15	0
33	A2	377	0	418	9	0
34	A3	504	0	574	12	0
35	A4	302	0	343	10	0
36	BA	32831	0	16521	1591	0
37	BB	1704	0	1732	19	0
38	BC	1624	0	1699	21	0
39	BD	1643	0	1710	22	0
40	BE	1105	0	1148	23	0
41	BF	817	0	808	22	0
42	BG	1174	0	1230	12	0
43	BH	979	0	1034	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BI	1022	0	1070	17	0
45	BJ	786	0	828	13	0
46	BK	877	0	887	18	0
47	BL	955	0	1019	23	0
48	BM	876	0	937	8	0
49	BN	805	0	847	4	0
50	BO	716	0	742	11	0
51	BP	638	0	656	11	0
52	BQ	648	0	691	11	0
53	BR	455	0	478	6	0
54	BS	637	0	665	26	0
55	BT	665	0	714	9	0
56	BU	425	0	449	4	0
All	All	148250	0	102279	6072	0

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

The worst 5 of 6072 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	440/442 (100%)	383 (87%)	41 (9%)	16 (4%)	2	20
4	AB	63/65 (97%)	55 (87%)	3 (5%)	5 (8%)	1	10
5	AC	30/53 (57%)	29 (97%)	1 (3%)	0	100	100
6	A5	232/234 (99%)	199 (86%)	18 (8%)	15 (6%)	1	12
7	A6	269/273 (98%)	192 (71%)	55 (20%)	22 (8%)	0	9
8	AD	207/209 (99%)	144 (70%)	40 (19%)	23 (11%)	0	5
9	AE	199/201 (99%)	155 (78%)	29 (15%)	15 (8%)	1	10
10	AF	176/179 (98%)	120 (68%)	34 (19%)	22 (12%)	0	4
11	AG	174/177 (98%)	129 (74%)	24 (14%)	21 (12%)	0	4
12	AH	147/149 (99%)	102 (69%)	32 (22%)	13 (9%)	0	8
13	AI	139/142 (98%)	122 (88%)	11 (8%)	6 (4%)	2	17
14	AJ	140/142 (99%)	109 (78%)	22 (16%)	9 (6%)	1	12
15	AK	119/123 (97%)	87 (73%)	26 (22%)	6 (5%)	1	16
16	AL	141/144 (98%)	107 (76%)	18 (13%)	16 (11%)	0	5
17	AM	134/136 (98%)	91 (68%)	31 (23%)	12 (9%)	0	8
18	AN	118/127 (93%)	89 (75%)	21 (18%)	8 (7%)	1	11
19	AO	114/117 (97%)	94 (82%)	17 (15%)	3 (3%)	4	25
20	AP	112/115 (97%)	82 (73%)	20 (18%)	10 (9%)	0	8
21	AQ	115/118 (98%)	87 (76%)	20 (17%)	8 (7%)	1	11
22	AR	101/103 (98%)	84 (83%)	11 (11%)	6 (6%)	1	13
23	AS	108/110 (98%)	85 (79%)	17 (16%)	6 (6%)	1	14
24	AT	91/100 (91%)	60 (66%)	23 (25%)	8 (9%)	0	8
25	AU	100/104 (96%)	67 (67%)	17 (17%)	16 (16%)	0	2
26	AV	92/94 (98%)	73 (79%)	17 (18%)	2 (2%)	5	29
27	AW	77/85 (91%)	48 (62%)	13 (17%)	16 (21%)	0	2
28	AX	75/78 (96%)	49 (65%)	19 (25%)	7 (9%)	0	8
29	AY	61/63 (97%)	41 (67%)	19 (31%)	1 (2%)	7	38
30	AZ	56/59 (95%)	49 (88%)	6 (11%)	1 (2%)	6	34
31	A0	54/57 (95%)	41 (76%)	8 (15%)	5 (9%)	0	8
32	A1	48/55 (87%)	37 (77%)	6 (12%)	5 (10%)	0	6
33	A2	44/46 (96%)	33 (75%)	7 (16%)	4 (9%)	0	8
34	A3	62/65 (95%)	48 (77%)	10 (16%)	4 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	A4	36/38 (95%)	27 (75%)	6 (17%)	3 (8%)	0	9
37	BB	216/241 (90%)	165 (76%)	40 (18%)	11 (5%)	1	15
38	BC	204/233 (88%)	158 (78%)	30 (15%)	16 (8%)	1	10
39	BD	203/206 (98%)	163 (80%)	28 (14%)	12 (6%)	1	13
40	BE	148/167 (89%)	106 (72%)	32 (22%)	10 (7%)	1	11
41	BF	98/135 (73%)	71 (72%)	16 (16%)	11 (11%)	0	5
42	BG	148/179 (83%)	110 (74%)	26 (18%)	12 (8%)	1	9
43	BH	127/130 (98%)	87 (68%)	32 (25%)	8 (6%)	1	13
44	BI	125/130 (96%)	99 (79%)	16 (13%)	10 (8%)	1	9
45	BJ	96/103 (93%)	79 (82%)	9 (9%)	8 (8%)	0	9
46	BK	115/129 (89%)	87 (76%)	15 (13%)	13 (11%)	0	5
47	BL	121/124 (98%)	104 (86%)	13 (11%)	4 (3%)	3	21
48	BM	111/118 (94%)	83 (75%)	18 (16%)	10 (9%)	0	8
49	BN	98/101 (97%)	68 (69%)	21 (21%)	9 (9%)	0	8
50	BO	86/89 (97%)	76 (88%)	7 (8%)	3 (4%)	3	20
51	BP	78/82 (95%)	63 (81%)	9 (12%)	6 (8%)	1	10
52	BQ	78/84 (93%)	58 (74%)	12 (15%)	8 (10%)	0	6
53	BR	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	2	19
54	BS	77/92 (84%)	57 (74%)	16 (21%)	4 (5%)	1	15
55	BT	83/87 (95%)	71 (86%)	8 (10%)	4 (5%)	2	16
56	BU	49/71 (69%)	33 (67%)	11 (22%)	5 (10%)	0	7
All	All	6388/6779 (94%)	4900 (77%)	1008 (16%)	480 (8%)	1	10

5 of 480 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AA	362/362 (100%)	343 (95%)	19 (5%)	21	42
4	AB	52/52 (100%)	48 (92%)	4 (8%)	12	32
5	AC	28/45 (62%)	28 (100%)	0	100	100
6	A5	181/181 (100%)	173 (96%)	8 (4%)	25	47
7	A6	216/218 (99%)	199 (92%)	17 (8%)	11	32
8	AD	164/164 (100%)	142 (87%)	22 (13%)	4	14
9	AE	165/165 (100%)	160 (97%)	5 (3%)	36	57
10	AF	149/150 (99%)	135 (91%)	14 (9%)	8	26
11	AG	137/138 (99%)	127 (93%)	10 (7%)	13	34
12	AH	114/114 (100%)	108 (95%)	6 (5%)	20	41
13	AI	109/110 (99%)	101 (93%)	8 (7%)	13	34
14	AJ	116/116 (100%)	106 (91%)	10 (9%)	10	29
15	AK	102/104 (98%)	93 (91%)	9 (9%)	9	28
16	AL	102/103 (99%)	94 (92%)	8 (8%)	11	32
17	AM	109/109 (100%)	100 (92%)	9 (8%)	10	30
18	AN	100/103 (97%)	94 (94%)	6 (6%)	17	39
19	AO	86/87 (99%)	83 (96%)	3 (4%)	32	53
20	AP	99/100 (99%)	90 (91%)	9 (9%)	9	27
21	AQ	89/90 (99%)	82 (92%)	7 (8%)	11	32
22	AR	84/84 (100%)	77 (92%)	7 (8%)	10	30
23	AS	93/93 (100%)	83 (89%)	10 (11%)	6	21
24	AT	80/84 (95%)	73 (91%)	7 (9%)	9	28
25	AU	83/85 (98%)	78 (94%)	5 (6%)	17	39
26	AV	78/78 (100%)	69 (88%)	9 (12%)	5	18
27	AW	59/63 (94%)	53 (90%)	6 (10%)	7	23
28	AX	67/68 (98%)	64 (96%)	3 (4%)	24	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	AY	55/55 (100%)	55 (100%)	0	100	100
30	AZ	48/49 (98%)	45 (94%)	3 (6%)	16	37
31	A0	47/48 (98%)	44 (94%)	3 (6%)	16	37
32	A1	45/49 (92%)	43 (96%)	2 (4%)	25	47
33	A2	38/38 (100%)	34 (90%)	4 (10%)	6	21
34	A3	51/52 (98%)	46 (90%)	5 (10%)	7	24
35	A4	34/34 (100%)	32 (94%)	2 (6%)	18	39
37	BB	180/199 (90%)	174 (97%)	6 (3%)	33	55
38	BC	170/190 (90%)	162 (95%)	8 (5%)	23	45
39	BD	172/173 (99%)	163 (95%)	9 (5%)	21	42
40	BE	113/126 (90%)	103 (91%)	10 (9%)	9	28
41	BF	87/116 (75%)	81 (93%)	6 (7%)	14	36
42	BG	123/147 (84%)	121 (98%)	2 (2%)	55	70
43	BH	104/105 (99%)	94 (90%)	10 (10%)	8	25
44	BI	105/107 (98%)	99 (94%)	6 (6%)	18	40
45	BJ	86/90 (96%)	82 (95%)	4 (5%)	23	45
46	BK	90/99 (91%)	79 (88%)	11 (12%)	5	17
47	BL	103/104 (99%)	96 (93%)	7 (7%)	14	36
48	BM	91/96 (95%)	87 (96%)	4 (4%)	25	47
49	BN	83/84 (99%)	79 (95%)	4 (5%)	23	44
50	BO	76/77 (99%)	73 (96%)	3 (4%)	28	49
51	BP	65/65 (100%)	62 (95%)	3 (5%)	24	45
52	BQ	74/78 (95%)	69 (93%)	5 (7%)	14	36
53	BR	48/65 (74%)	45 (94%)	3 (6%)	16	37
54	BS	70/79 (89%)	64 (91%)	6 (9%)	10	29
55	BT	65/66 (98%)	57 (88%)	8 (12%)	4	17
56	BU	44/61 (72%)	43 (98%)	1 (2%)	44	64
All	All	5291/5518 (96%)	4935 (93%)	356 (7%)	17	36

5 of 356 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	A2	13	ASN

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Mol	Chain	Res	Type
43	BH	79	ARG
35	A4	4	ARG
39	BD	129	VAL
45	BJ	99	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
24	AT	70	HIS
54	BS	13	HIS
32	A1	45	HIS
51	BP	29	ASN
48	BM	11	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A7	116/120 (96%)	24 (20%)	4 (3%)
2	A8	2902/2904 (99%)	543 (18%)	109 (3%)
36	BA	1530/1542 (99%)	299 (19%)	51 (3%)
All	All	4548/4566 (99%)	866 (19%)	164 (3%)

5 of 866 RNA backbone outliers are listed below:

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

5 of 164 RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no 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 [i](#)

There are no chain breaks in this entry.

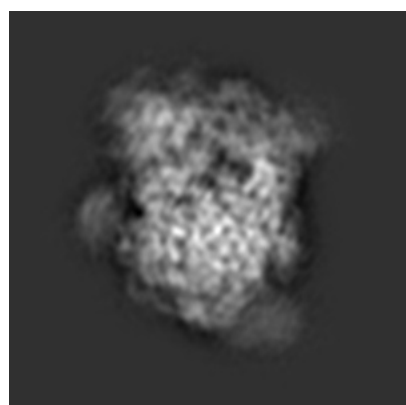
6 Map visualisation [i](#)

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

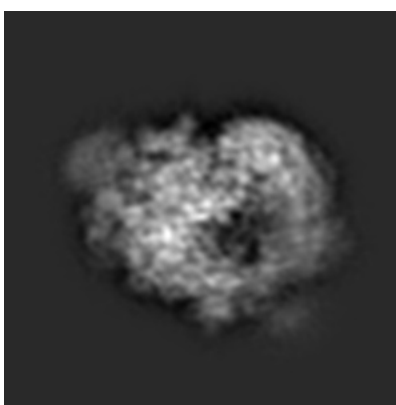
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

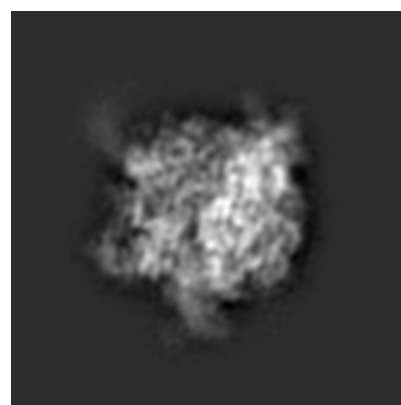
6.1.1 Primary map



X



Y

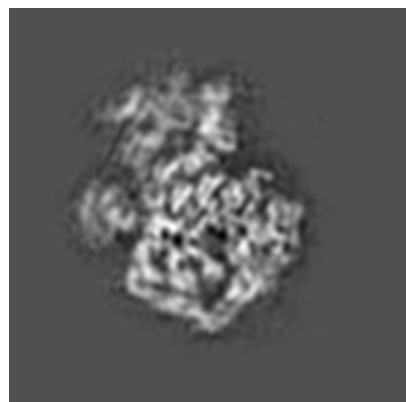


Z

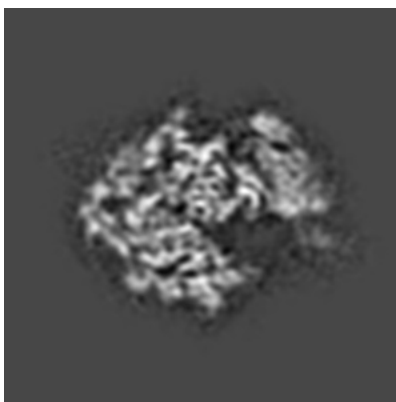
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

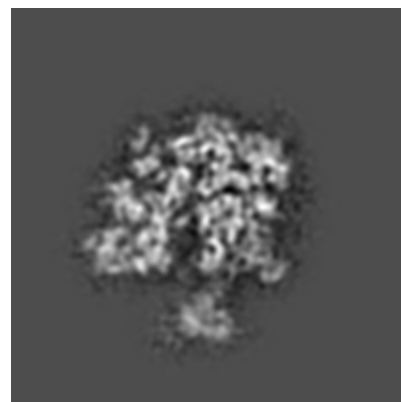
6.2.1 Primary map



X Index: 72



Y Index: 72

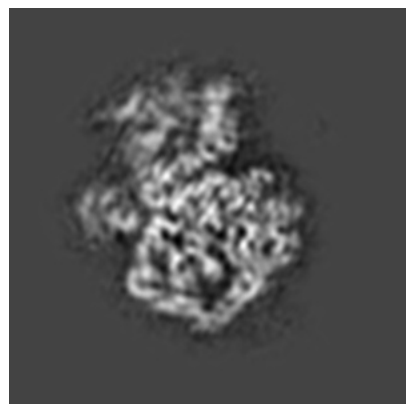


Z Index: 72

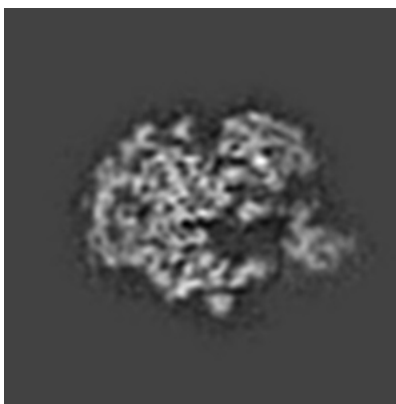
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 73



Y Index: 67

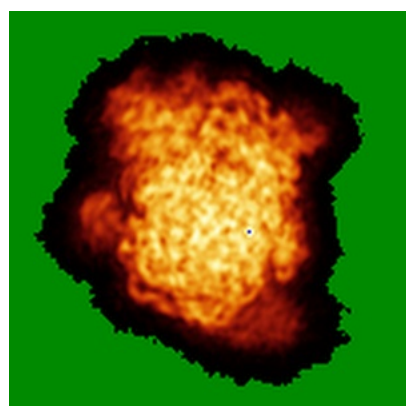


Z Index: 63

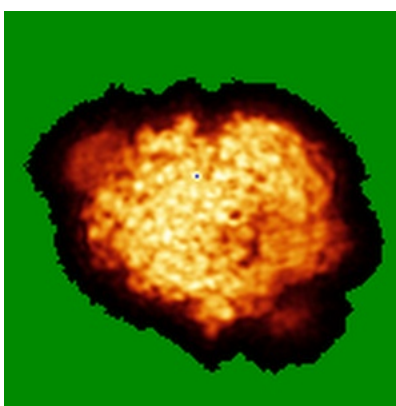
The images above show the largest variance slices of the map in three orthogonal directions.

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

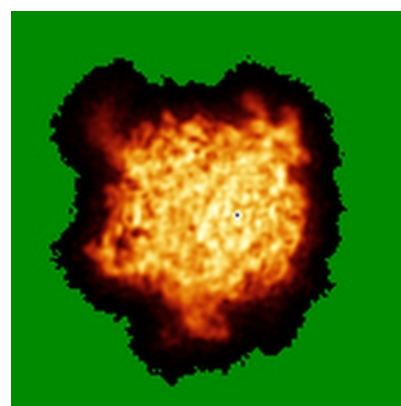
6.4.1 Primary map



X



Y



Z

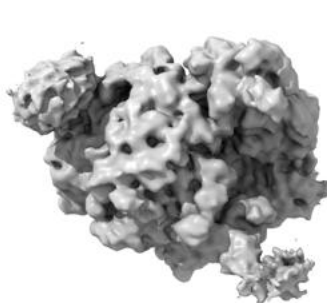
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

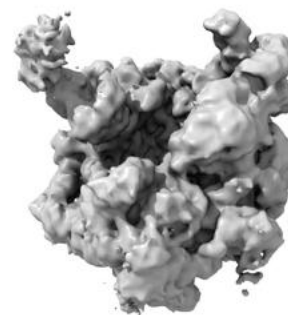
6.5.1 Primary map



X



Y



Z

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

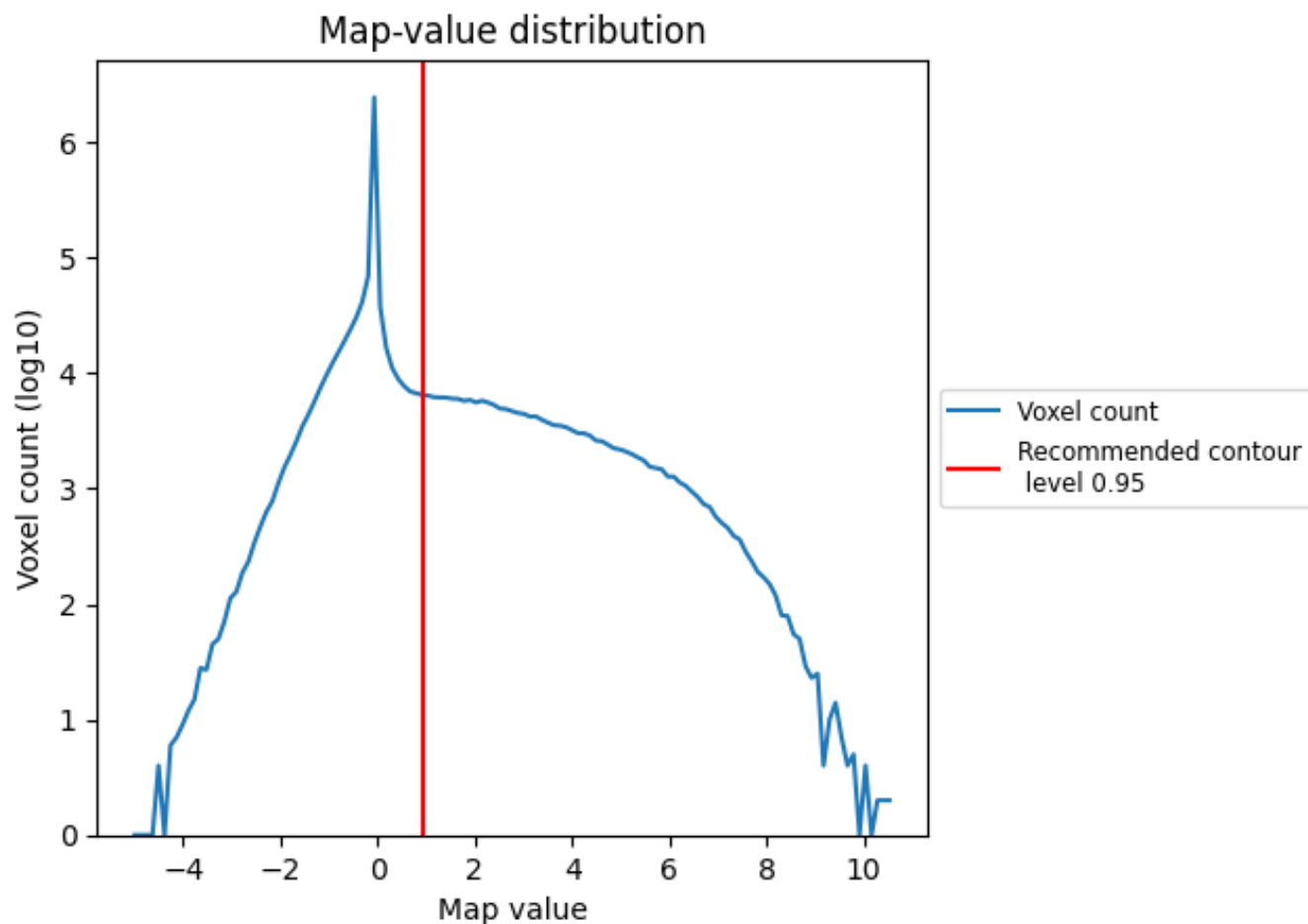
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

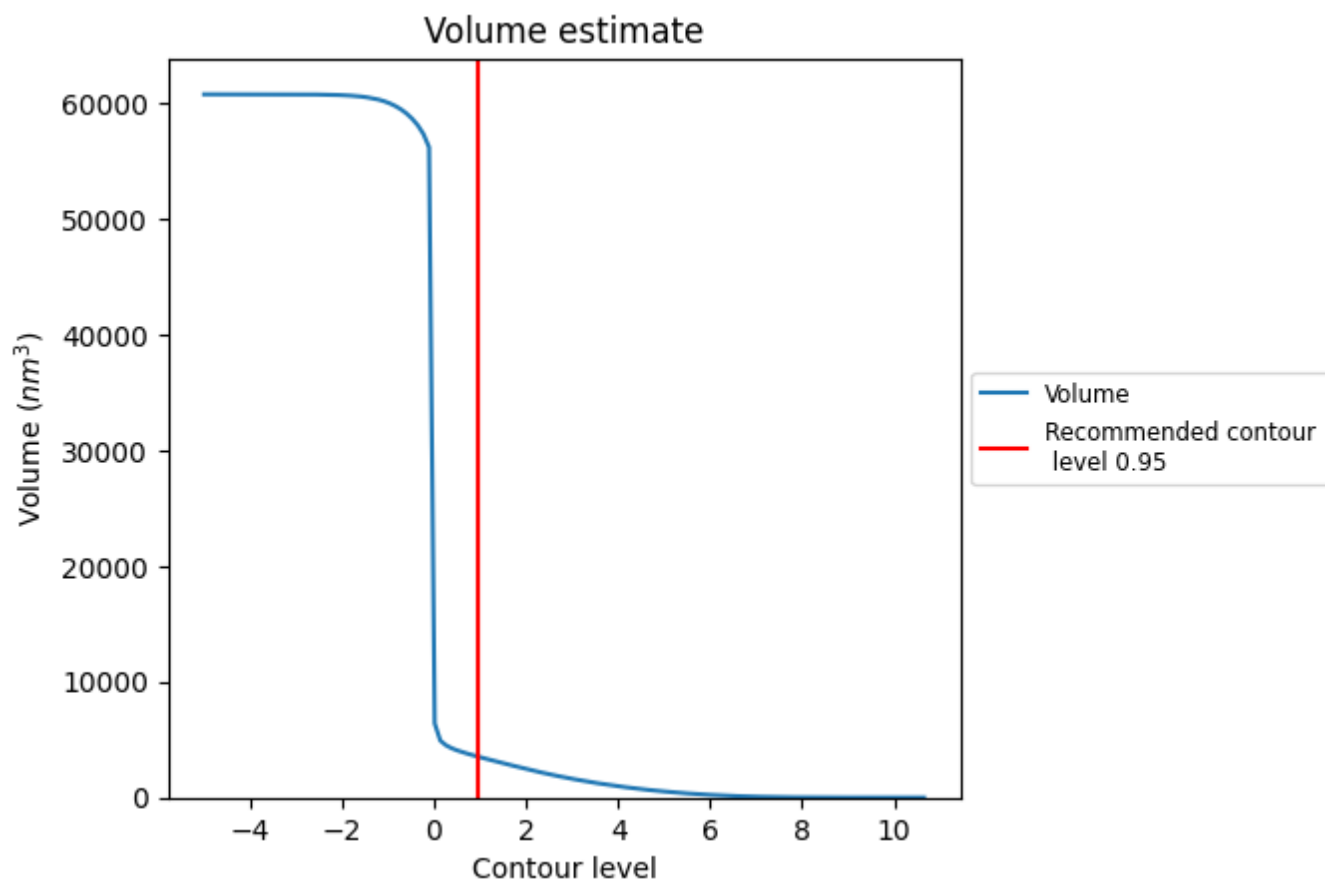
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

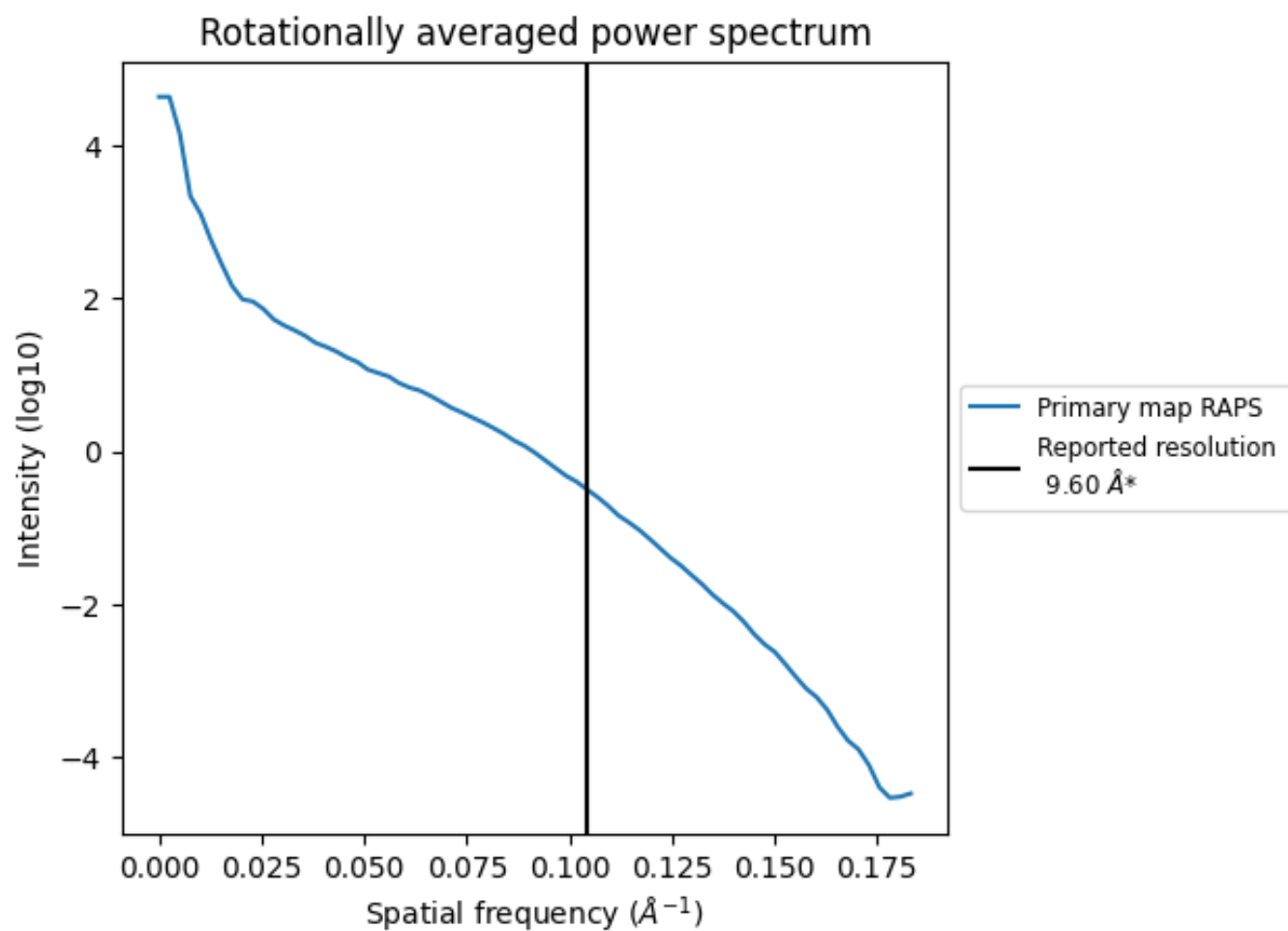
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3544 nm³; this corresponds to an approximate mass of 3201 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.104 Å⁻¹

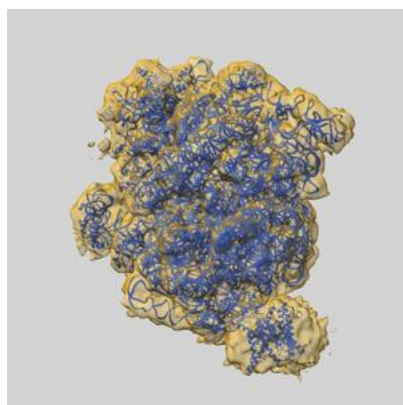
8 Fourier-Shell correlation

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

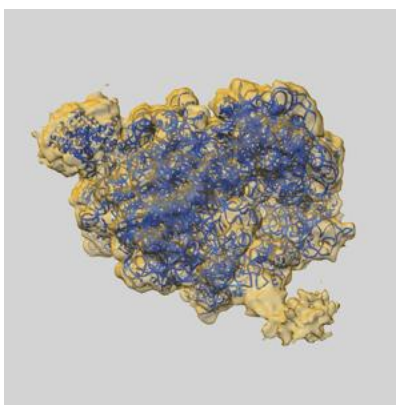
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1484 and PDB model 4V7I. Per-residue inclusion information can be found in section 3 on page 15.

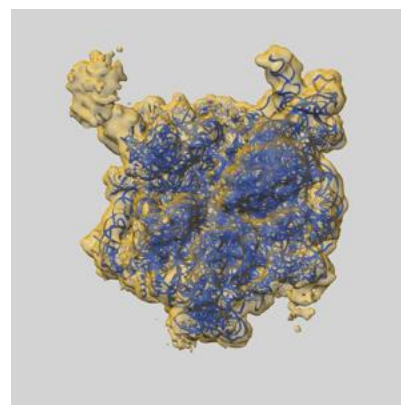
9.1 Map-model overlay [i](#)



X



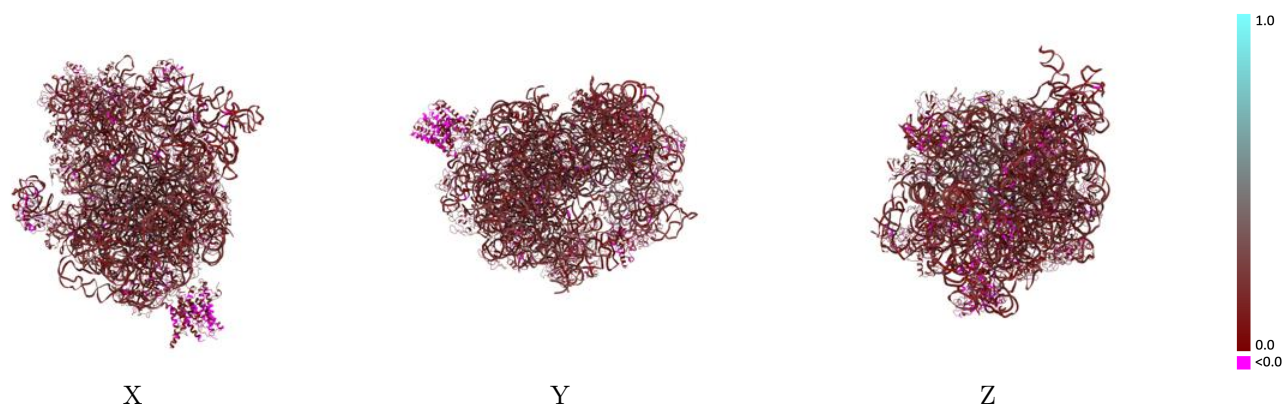
Y



Z

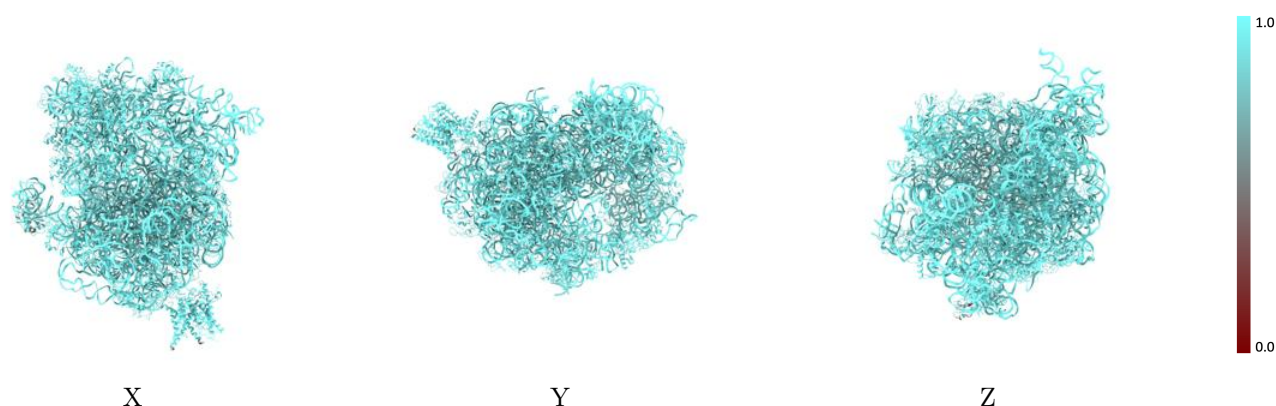
The images above show the 3D surface view of the map at the recommended contour level 0.95 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



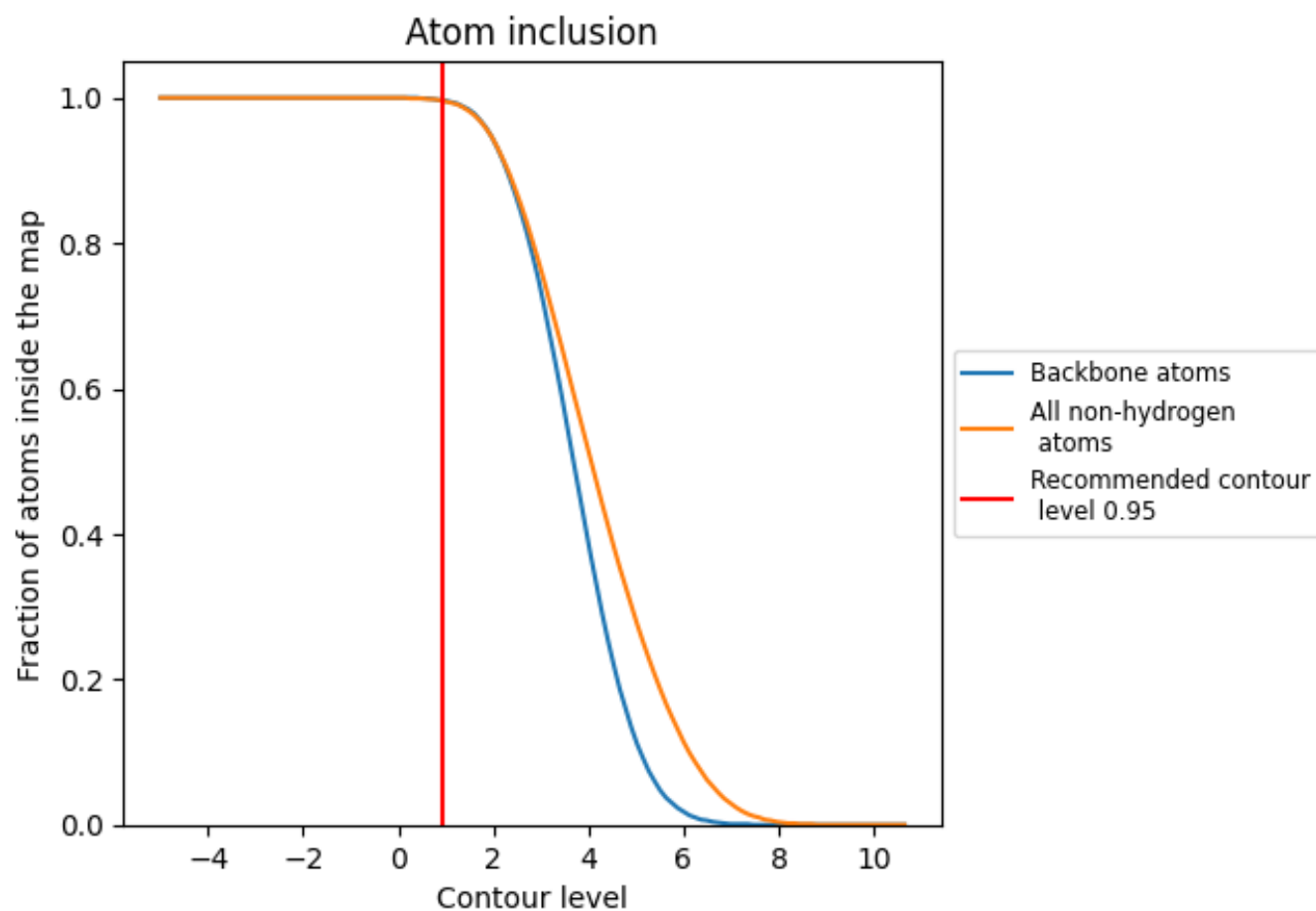
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.95).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.95) and Q-score for the entire model and for each chain.

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



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