wwPDB EM Validation Summary Report

Mar 8, 2026 – 12:14 AM UTC

PDB ID	:	7QG8 / pdb_00007qg8
EMDB ID	:	EMD-13952
Title	:	Structure of the collided E. coli disome - VemP-stalled 70S ribosome
Authors	:	Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2021-12-07
Resolution	:	3.97 Å(reported)

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:

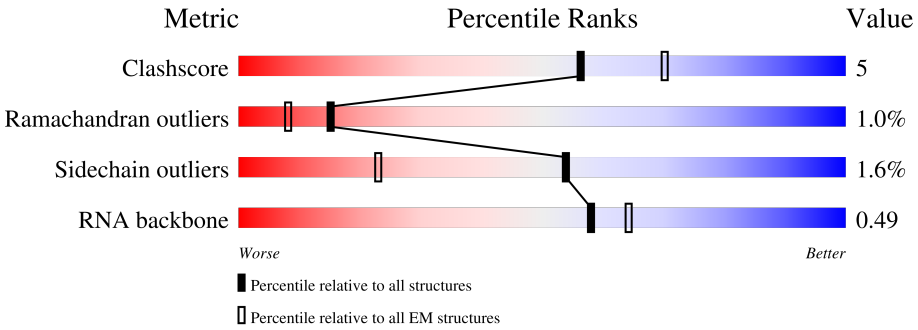
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

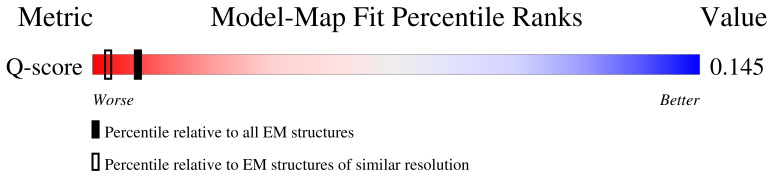
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.97 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	7578 (3.47 - 4.47)

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 <=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	A	73	14% 66% 30%
2	s	179	17% 79%
3	M	75	68% 24% 7%

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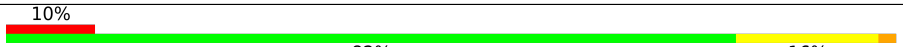
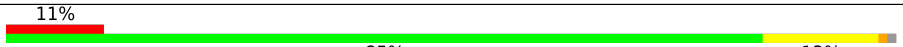
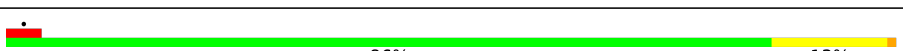
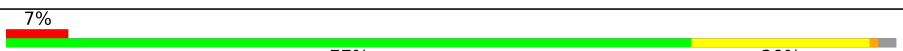
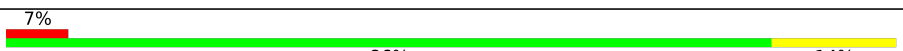
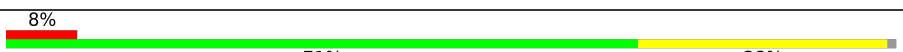
Mol	Chain	Length	Quality of chain
4	O	120	
5	P	273	
6	Q	209	
7	R	201	
8	S	179	
9	T	177	
10	U	149	
11	V	142	
12	W	142	
13	X	123	
14	Y	144	
15	Z	136	
16	a	127	
17	b	117	
18	c	115	
19	d	118	
20	e	103	
21	f	110	
22	g	100	
23	h	104	
24	i	94	
25	j	85	
26	k	78	
27	l	63	
28	m	59	

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Mol	Chain	Length	Quality of chain
29	n	57	5% 70% 23% 5%
30	o	55	5% 64% 24% 9%
31	p	46	59% 35% 7%
32	q	65	82% 14%
33	r	55	51% 11% 7% 31%
34	N	2903	64% 28% 7%
35	L	70	31% 56% 23% 21%
36	C	223	53% 39% 21% 40%
37	0	1539	68% 26% 5%
38	1	239	25% 72% 18% 9%
39	2	218	27% 76% 17% 6%
40	3	206	15% 82% 17%
41	4	162	65% 23% 7%
42	5	131	28% 56% 16% 5% 24%
43	6	156	20% 76% 15% 8%
44	7	130	7% 89% 10%
45	8	130	10% 68% 28%
46	9	103	33% 67% 26% 5%
47	D	129	36% 68% 22% 9%
48	E	124	80% 15%
49	F	118	31% 72% 22%
50	G	101	31% 79% 15% 5%
51	H	89	8% 88% 11%
52	I	82	9% 77% 20%
53	J	84	7% 80% 13% 5%

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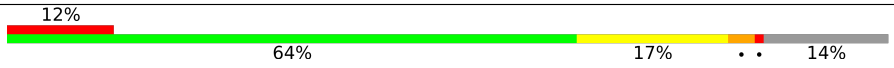
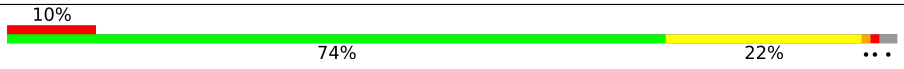
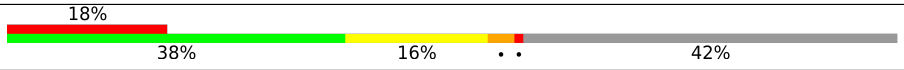
Mol	Chain	Length	Quality of chain
54	K	75	
55	t	92	
56	u	87	
57	v	88	

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 147108 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 A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	73	Total	C	N	O	P	0	0
			1561	695	279	514	73		

- Molecule 2 is a protein called VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	37	Total	C	N	O	S	0	0
			316	198	58	58	2		

- Molecule 3 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	75	Total	C	N	O	P	0	0
			1594	711	281	527	75		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	X	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	variant	UNP P0AG44

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	c	114	Total	C	N	O	S	0	0
			915	573	179	162	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	e	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	variant	UNP P0ADZ0

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	75	Total	C	N	O	S	0	0
			568	353	113	101	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	3	UNK	HIS	variant	UNP P0A7L8

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	k	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	l	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

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

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	p	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	q	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	r	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 34 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	2897	Total	C	N	O	P	1	0
			62215	27754	11448	20115	2898		

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	55	Total	C	N	O	S	0	0
			419	258	76	79	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	variant	UNP P0A7M9

- Molecule 36 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	C	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 37 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	0	1532	Total	C	N	O	P	0	0
			32873	14661	6031	10649	1532		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	variant	UNP P0A7W1

- Molecule 42 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	101	SER	PRO	variant	UNP P02358

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	6	144	Total	C	N	O	S	0	0
			1129	705	213	207	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	78	HIS	ARG	variant	UNP P02359

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	variant	UNP P0A7X3

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	D	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	5	ALA	PRO	variant	UNP P0A7R9

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	E	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	F	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	VAL	MET	variant	UNP P0A7S9

- Molecule 50 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	G	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	40	ALA	ASP	variant	UNP P0AG59

- Molecule 51 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	H	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	I	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 53 is a protein called 30S ribosomal protein S17.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	2	ALA	THR	variant	UNP P0AG63

- Molecule 54 is a protein called 30S ribosomal protein S18.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	15	THR	ALA	variant	UNP P0A7T7
K	19	VAL	GLN	variant	UNP P0A7T7

- Molecule 55 is a protein called 30S ribosomal protein S19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	82	TYR	GLY	variant	UNP P0A7U3
t	83	TYR	HIS	variant	UNP P0A7U3

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	u	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	1	LEU	MET	variant	UNP P0A7U7

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	51	Total	C	N	O	S	0	0
			421	263	86	71	1		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
58	A	2	Total Mg 2 2	0

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
59	A	1	Total K 1 1	0

- Molecule 60 is water.

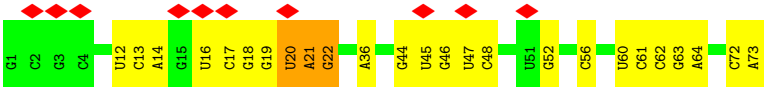
Mol	Chain	Residues	Atoms	AltConf
60	A	9	Total O 9 9	0

3 Residue-property plots (i)

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.

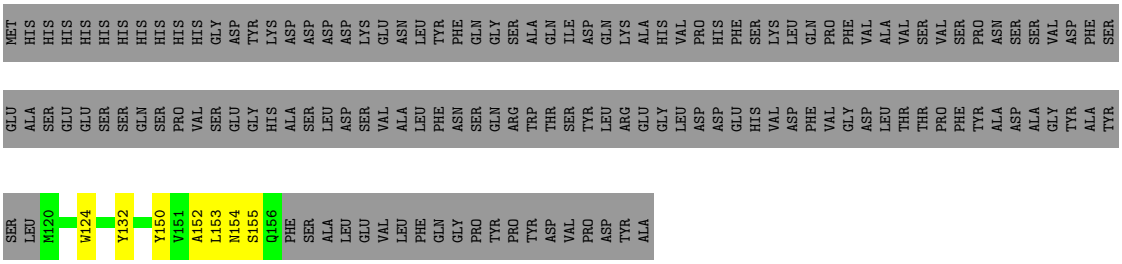
- Molecule 1: A-site tRNA

Chain A:



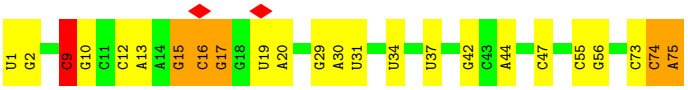
- Molecule 2: VemP nascent chain

Chain s:



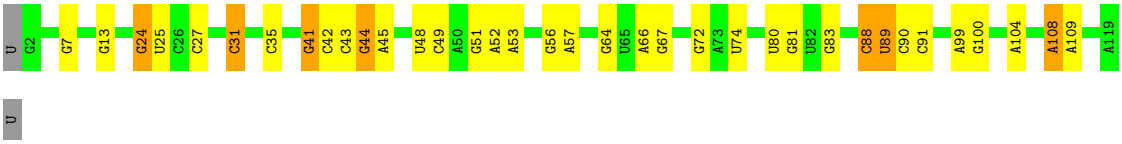
- Molecule 3: P-site tRNA

Chain M:



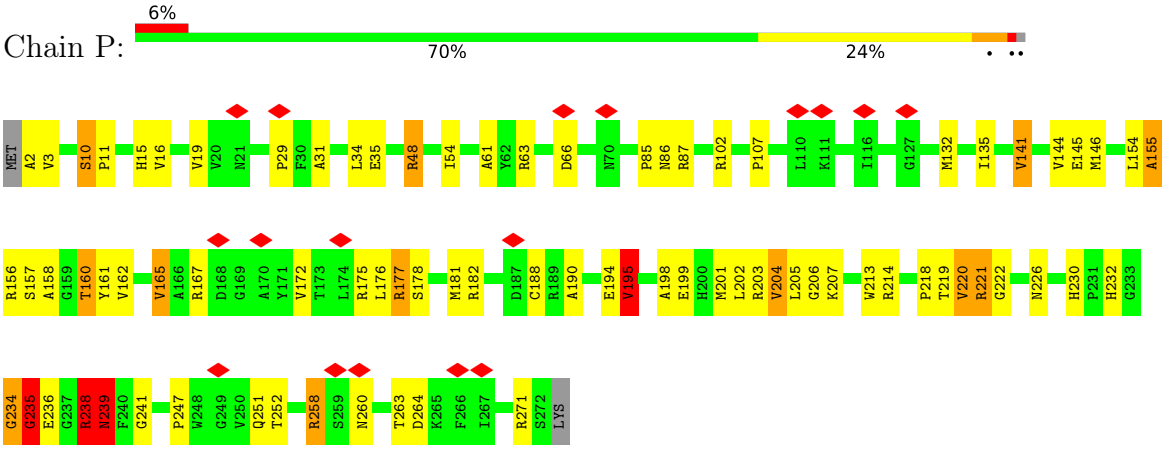
- Molecule 4: 5S rRNA

Chain O:



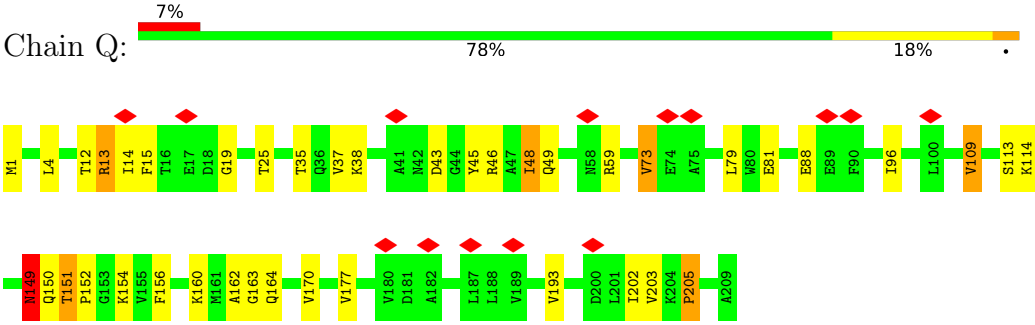
- Molecule 5: 50S ribosomal protein L2

Chain P:



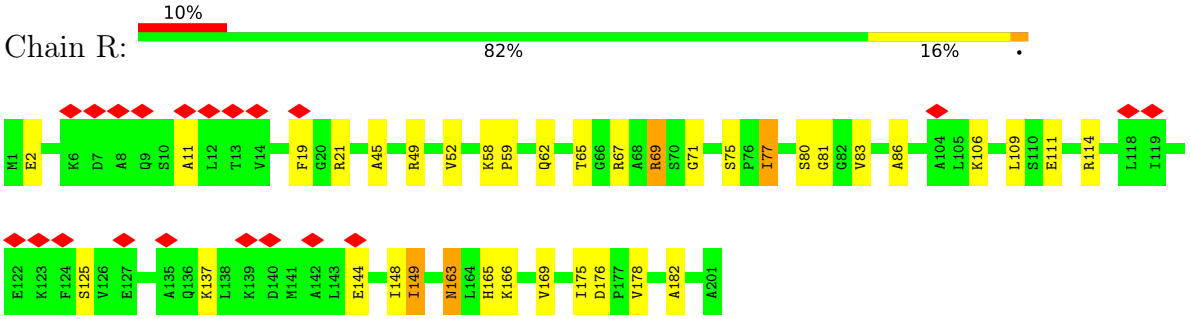
- Molecule 6: 50S ribosomal protein L3

Chain Q:



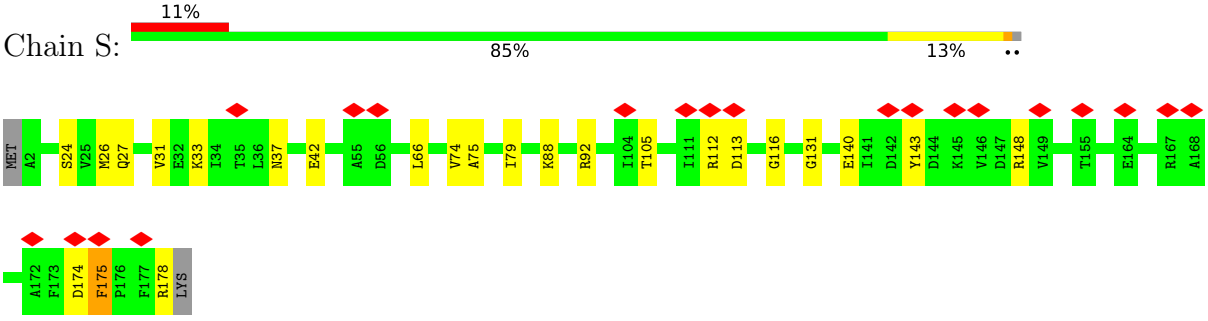
- Molecule 7: 50S ribosomal protein L4

Chain R:



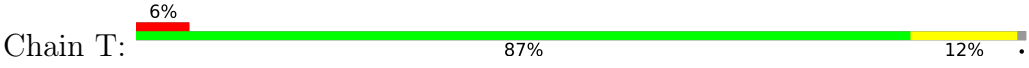
- Molecule 8: 50S ribosomal protein L5

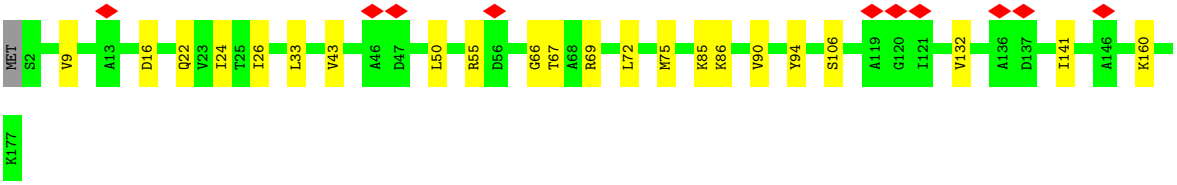
Chain S:



- Molecule 9: 50S ribosomal protein L6

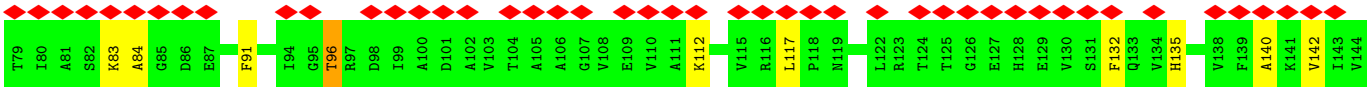
Chain T:

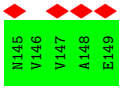




• Molecule 10: 50S ribosomal protein L9

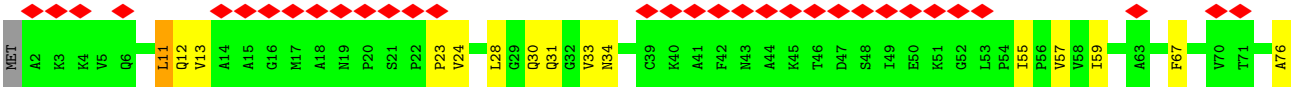
Chain U:





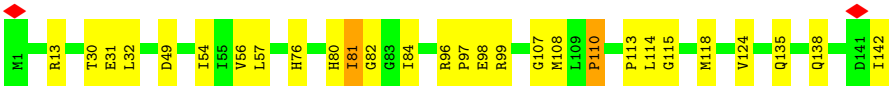
• Molecule 11: 50S ribosomal protein L11

Chain V:



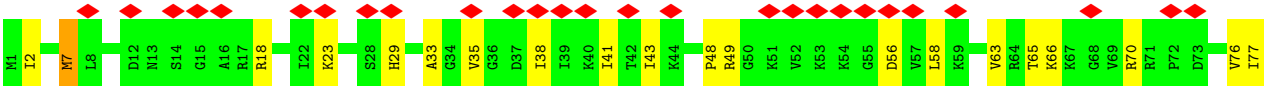
• Molecule 12: 50S ribosomal protein L13

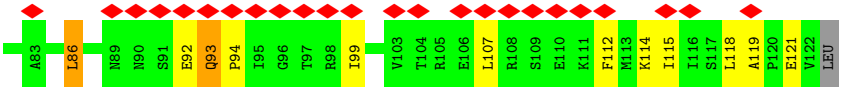
Chain W:



• Molecule 13: 50S ribosomal protein L14

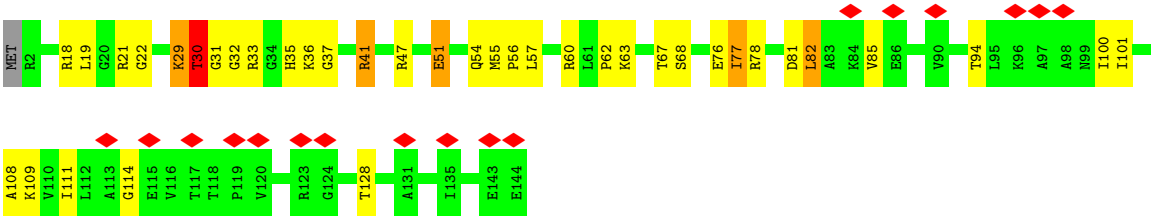
Chain X:





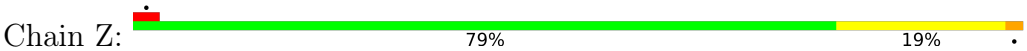
• Molecule 14: 50S ribosomal protein L15

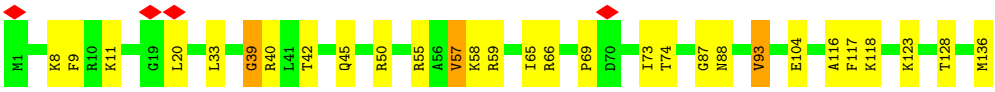
Chain Y:



• Molecule 15: 50S ribosomal protein L16

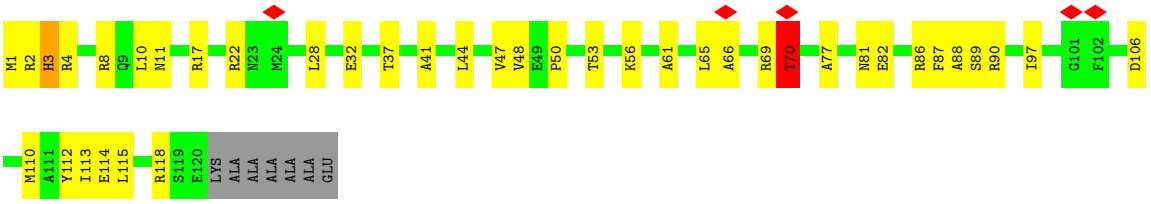
Chain Z:





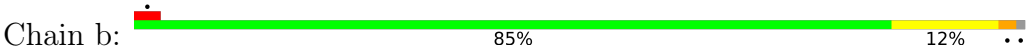
• Molecule 16: 50S ribosomal protein L17

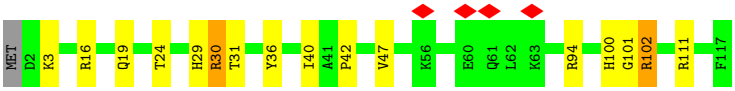
Chain a:



• Molecule 17: 50S ribosomal protein L18

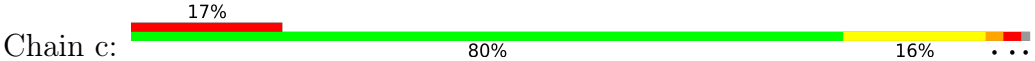
Chain b:

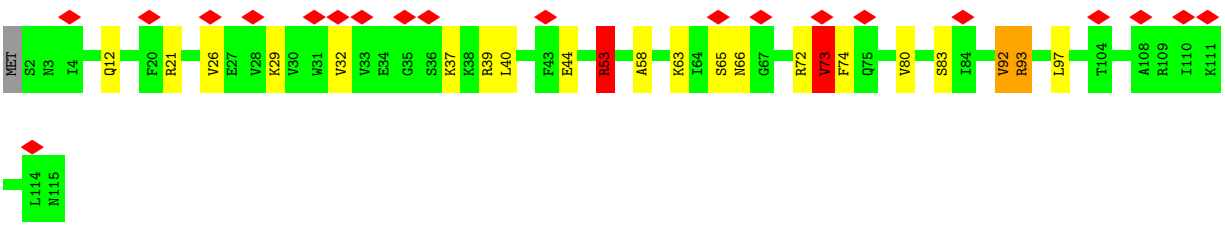




• Molecule 18: 50S ribosomal protein L19

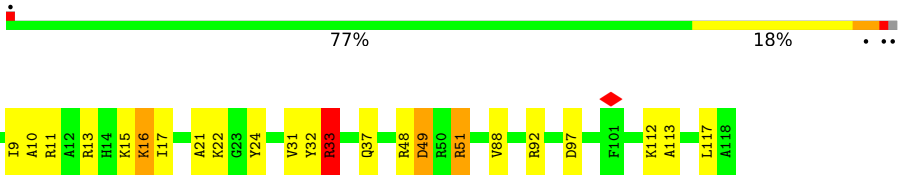
Chain c:





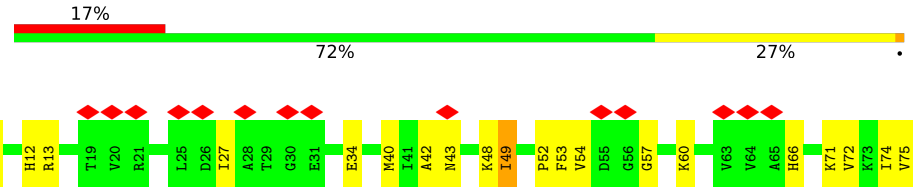
• Molecule 19: 50S ribosomal protein L20

Chain d:



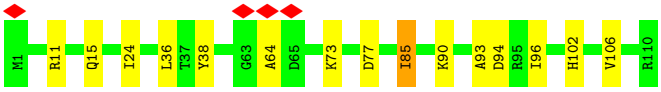
• Molecule 20: 50S ribosomal protein L21

Chain e:



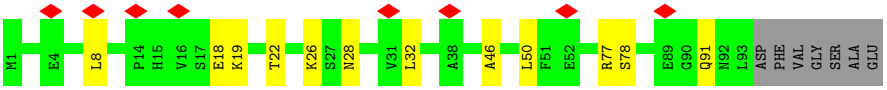
• Molecule 21: 50S ribosomal protein L22

Chain f:



• Molecule 22: 50S ribosomal protein L23

Chain g:

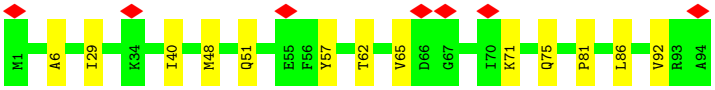


• Molecule 23: 50S ribosomal protein L24

Chain h:

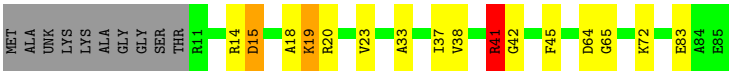
• Molecule 24: 50S ribosomal protein L25

Chain i:



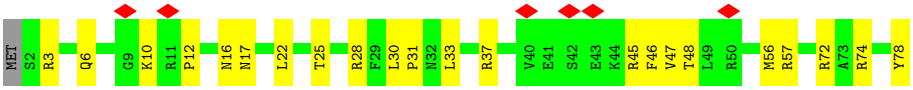
• Molecule 25: 50S ribosomal protein L27

Chain j:



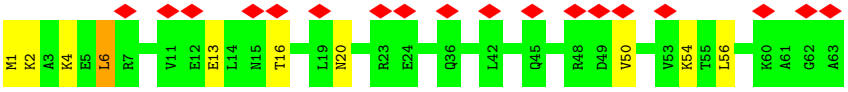
• Molecule 26: 50S ribosomal protein L28

Chain k:



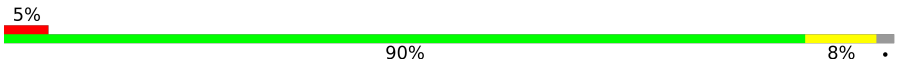
• Molecule 27: 50S ribosomal protein L29

Chain l:



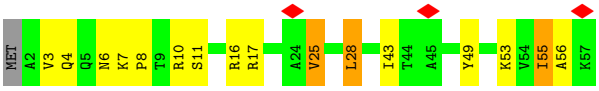
• Molecule 28: 50S ribosomal protein L30

Chain m:



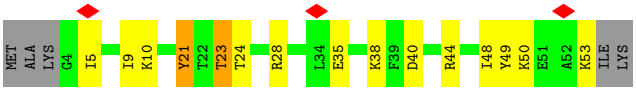
• Molecule 29: 50S ribosomal protein L32

Chain n:



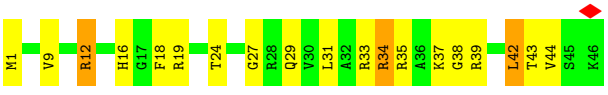
• Molecule 30: 50S ribosomal protein L33

Chain o:



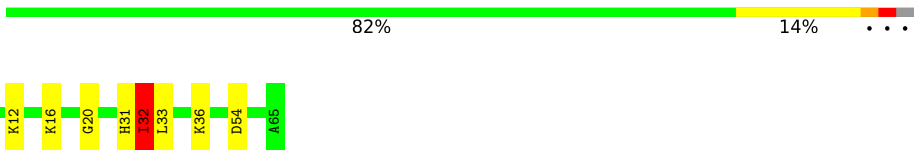
• Molecule 31: 50S ribosomal protein L34

Chain p:



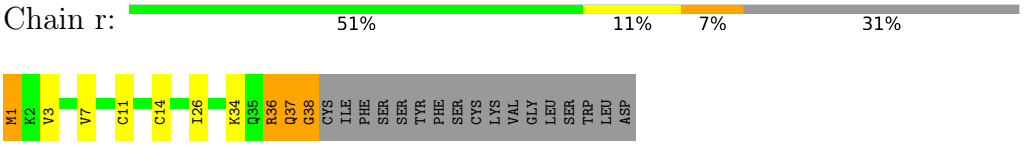
• Molecule 32: 50S ribosomal protein L35

Chain q:



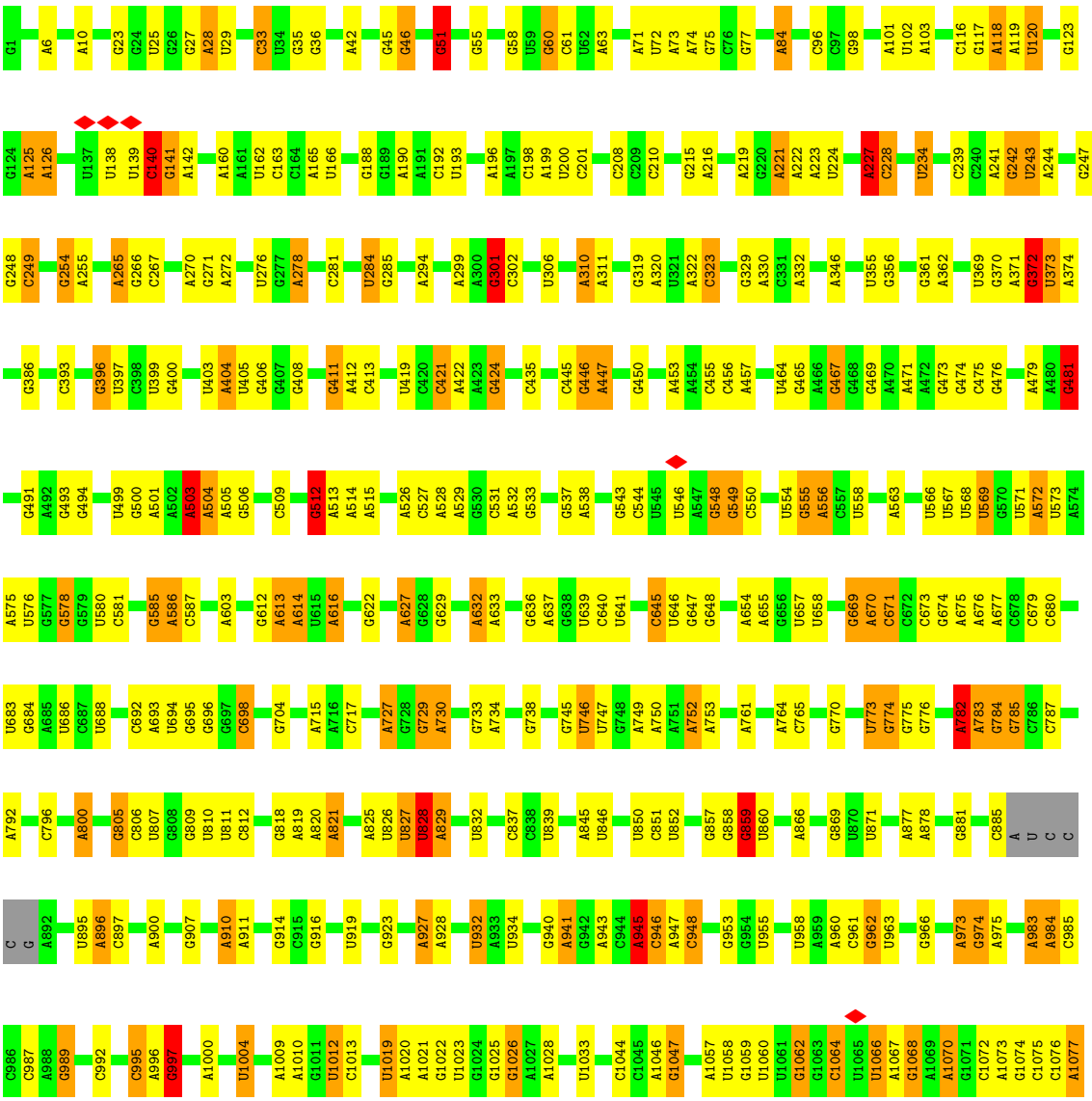
• Molecule 33: 50S ribosomal protein L36

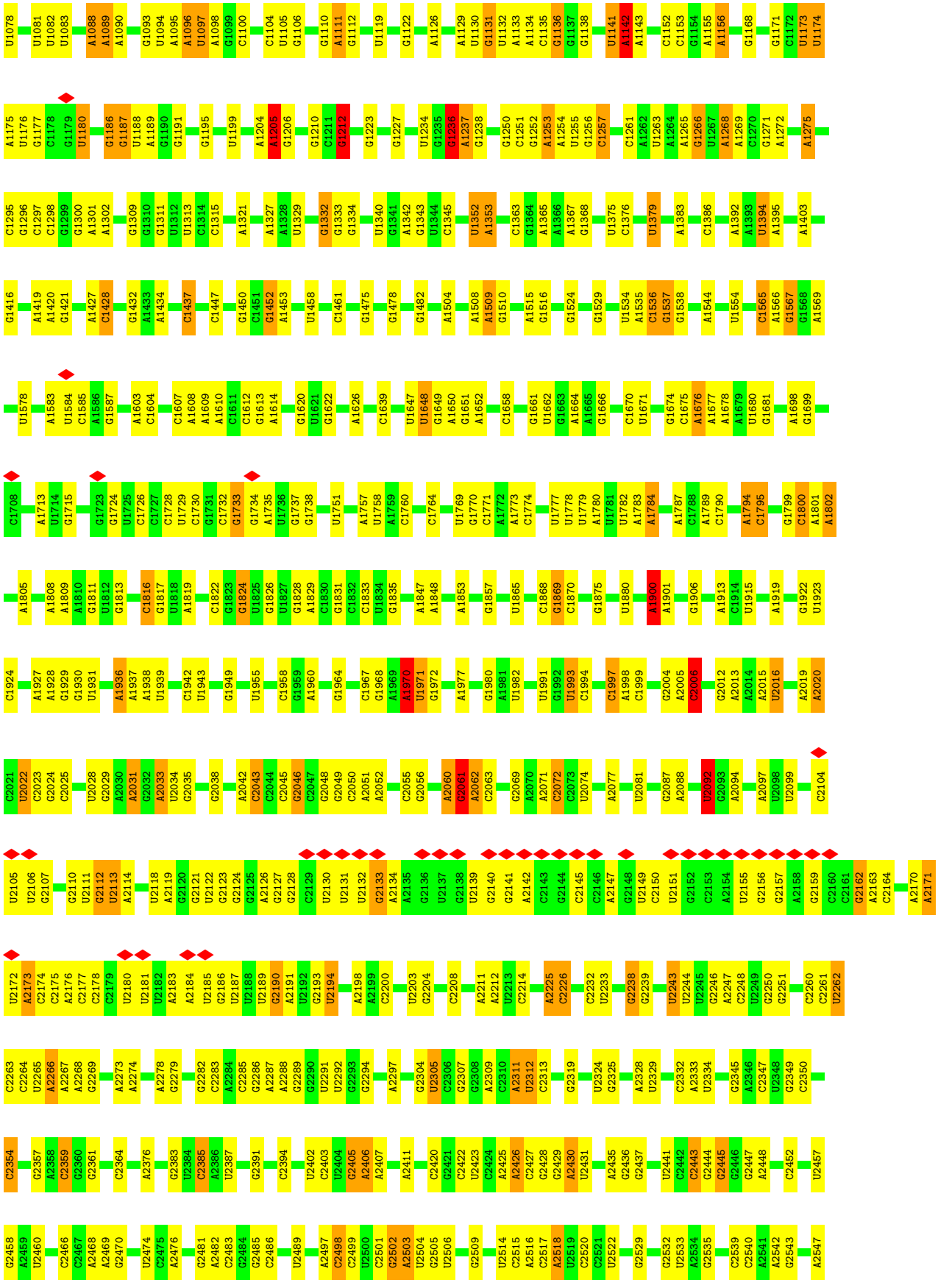
Chain r:



• Molecule 34: 23S rRNA

Chain N:




U1078 U1081 U1082 U1083 A1088 A1089 A1090 G1093 U1094 A1095 A1096 U1097 A1098 G1099 C1100 C1104 U1105 G1106 G1110 A1111 G1112 U1119 G1122 A1126 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 G1138 U1141 A1142 A1143 C1152 C1153 G1154 A1155 A1156 G1168 G1171 C1172 U1173 U1174
A1175 U1176 G1177 C1178 G1179 U1180 G1186 G1187 U1188 A1189 G1190 G1191 G1195 U1199 A1204 A1205 G1206 G1210 C1211 G1212 G1223 G1227 U1234 G1235 G1236 A1237 G1238 G1250 C1251 G1252 A1253 A1254 U1255 G1256 C1257 C1261 A1262 U1263 A1264 A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 A1275
C1295 G1296 C1297 C1298 G1299 G1300 A1301 A1302 G1309 G1310 G1311 U1312 U1313 C1314 C1315 A1321 A1327 A1328 U1329 G1332 G1333 G1334 U1340 G1341 A1342 G1343 U1344 C1345 U1352 A1353 C1363 G1364 A1365 A1366 A1367 G1368 U1375 C1376 U1379 A1383 C1386 A1392 A1393 U1394 A1395 A1403
G1416 A1419 A1420 G1421 A1427 C1428 G1432 A1433 A1434 C1437 C1447 C1450 C1451 G1452 A1453 U1458 C1461 G1475 G1478 G1482 A1504 A1508 A1509 G1510 A1515 G1516 G1524 G1529 U1534 A1535 C1536 G1537 G1538 A1544 U1554 C1565 A1566 G1567 G1568 A1569
U1578 A1583 U1584 C1585 A1586 G1587 A1603 C1604 C1607 A1608 A1609 A1610 C1611 C1612 G1613 A1614 G1620 U1621 G1622 A1626 C1639 U1647 U1648 G1649 A1650 G1651 A1652 C1658 G1661 U1662 G1663 A1664 A1665 G1666 C1670 U1671 G1674 C1675 A1676 A1677 A1678 A1679 U1680 G1681 A1698 G1699
C1708 A1713 U1714 G1715 G1723 G1724 U1725 C1726 C1727 C1728 U1729 C1730 G1731 C1732 G1733 G1734 A1735 U1736 G1737 G1738 U1751 A1757 U1758 A1759 C1760 C1764 U1769 G1770 C1771 A1772 A1773 C1774 U1777 U1778 U1779 A1780 U1781 U1782 A1783 A1784 A1787 C1788 A1789 C1790 A1794 C1795 G1799 C1800 A1801 A1802
A1805 A1808 A1809 A1810 G1811 U1812 G1813 C1816 G1817 U1818 A1819 C1822 G1823 G1824 U1825 G1826 U1827 G1828 A1829 G1830 G1831 C1832 C1833 U1834 G1835 A1847 A1848 A1863 G1857 U1865 C1868 G1869 C1870 G1875 U1880 A1900 A1901 G1906 A1913 C1914 U1915 A1919 G1922 U1923
C1924 A1927 A1928 G1929 G1930 U1931 A1936 A1937 A1938 U1939 C1942 U1943 G1949 U1955 C1958 G1959 A1960 G1964 C1967 G1968 A1969 A1970 U1971 G1972 A1977 G1980 A1981 U1982 U1991 G1992 U1993 C1994 C1997 A1998 C1999 G2004 A2005 C2006 G2012 A2013 A2014 A2015 U2016 A2019 A2020
C2021 U2022 C2023 G2024 C2025 U2028 G2029 A2030 A2031 G2032 A2033 U2034 G2035 G2038 A2042 C2043 C2044 C2045 G2046 C2047 G2048 G2049 C2050 A2051 A2052 C2055 G2056 A2060 G2061 A2062 C2063 G2069 A2070 A2071 C2072 C2073 U2074 A2077 U2081 G2087 A2088 U2092 G2093 A2094 A2097 U2098 U2099 C2104
U2105 U2106 G2107 G2110 U2111 G2112 U2113 A2114 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135 G2136 U2137 G2138 U2139 G2140 G2141 A2142 C2143 G2144 C2145 C2146 A2147 G2148 U2149 C2150 U2151 G2152 C2153 A2154 U2155 G2156 C2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 A2170 A2171
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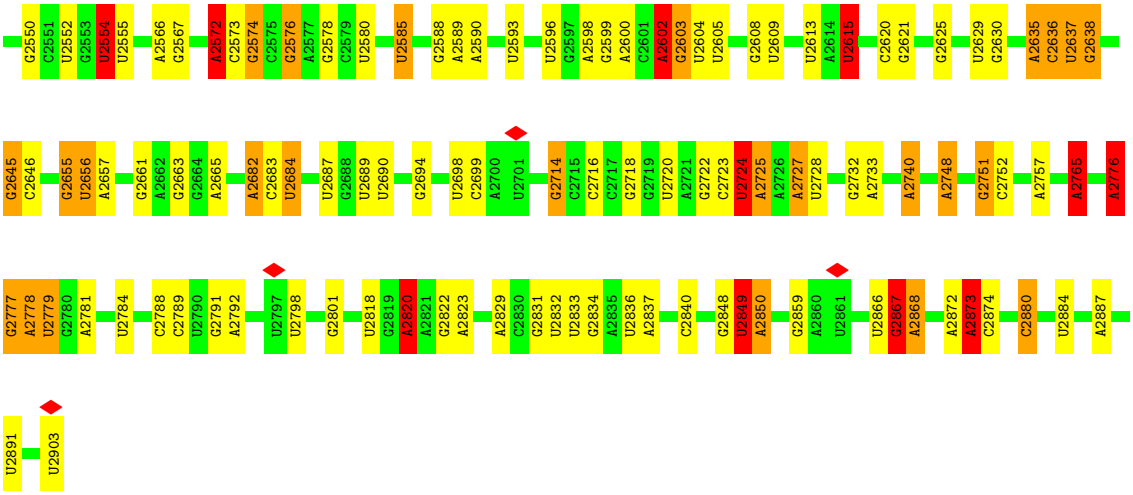
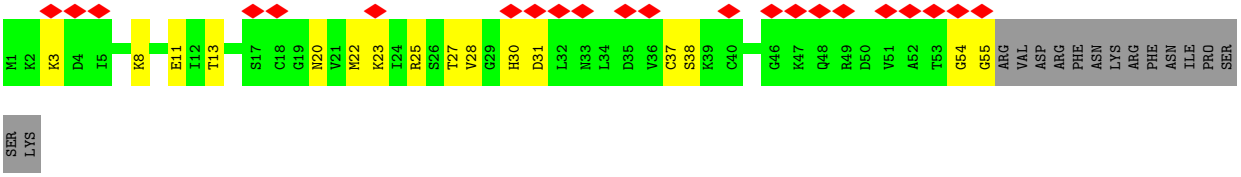
C2263 C2264 U2265 A2266 A2267 A2268 G2269 A2273 A2274 A2278 G2279 G2282 C2283 A2284 C2285 G2286 A2287 A2288 G2289 G2290 U2291 U2292 G2293 G2294 A2297 G2304 U2305 C2306 G2307 G2308 A2309 C2310 A2311 U2312 C2313 G2319 U2324 G2325 A2328 U2329 C2332 A2333 U2334 G2345 A2346 C2347 U2348 G2349 C2350
C2354 G2357 A2358 C2359 G2360 G2361 C2364 A2376 G2383 U2384 C2385 A2386 U2387 G2391 C2394 U2402 C2403 U2404 G2405 A2406 A2407 A2411 C2420 G2421 C2422 U2423 C2424 A2425 A2426 C2427 G2428 G2429 A2430 U2431 A2435 G2436 G2437 U2441 C2442 C2443 G2444 G2445 G2446 G2447 A2448 C2452 U2457
G2458 A2459 U2460 C2466 C2467 A2468 A2469 G2470 U2474 C2475 A2476 G2481 A2482 C2483 G2484 G2485 C2486 U2489 A2497 C2498 C2499 U2500 C2501 G2502 A2503 U2504 G2505 U2506 G2509 U2514 C2515 A2516 C2517 A2518 U2519 C2520 C2521 U2522 G2529 G2532 U2533 A2534 G2535 C2539 C2540 A2541 A2542 G2543 A2547



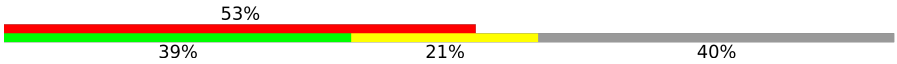
• Molecule 35: 50S ribosomal protein L31

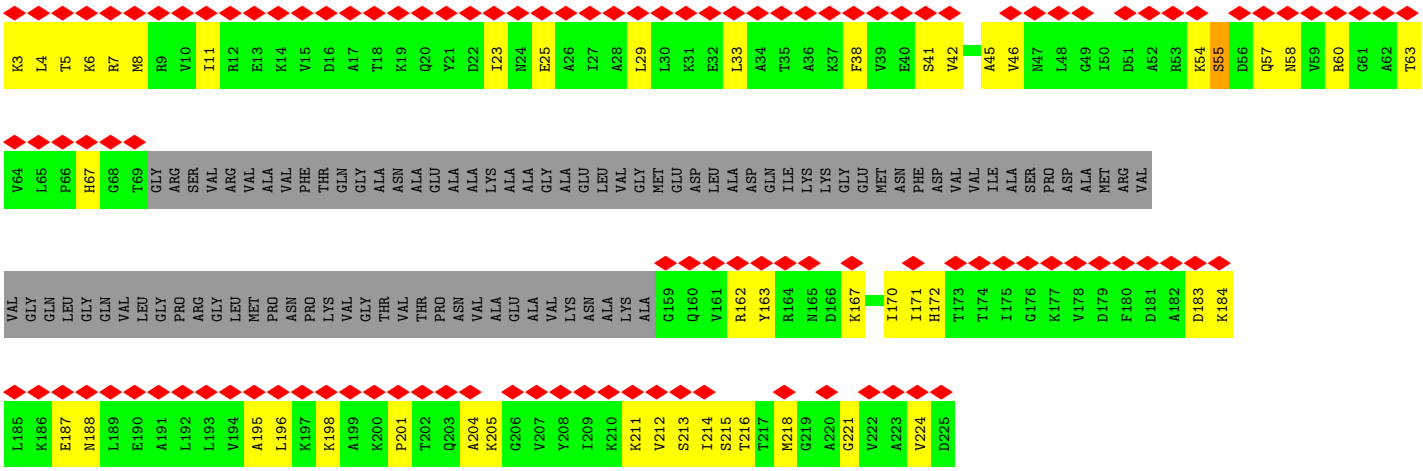
Chain L:



• Molecule 36: 50S ribosomal protein L1

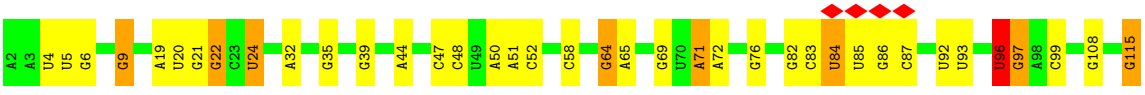
Chain C:

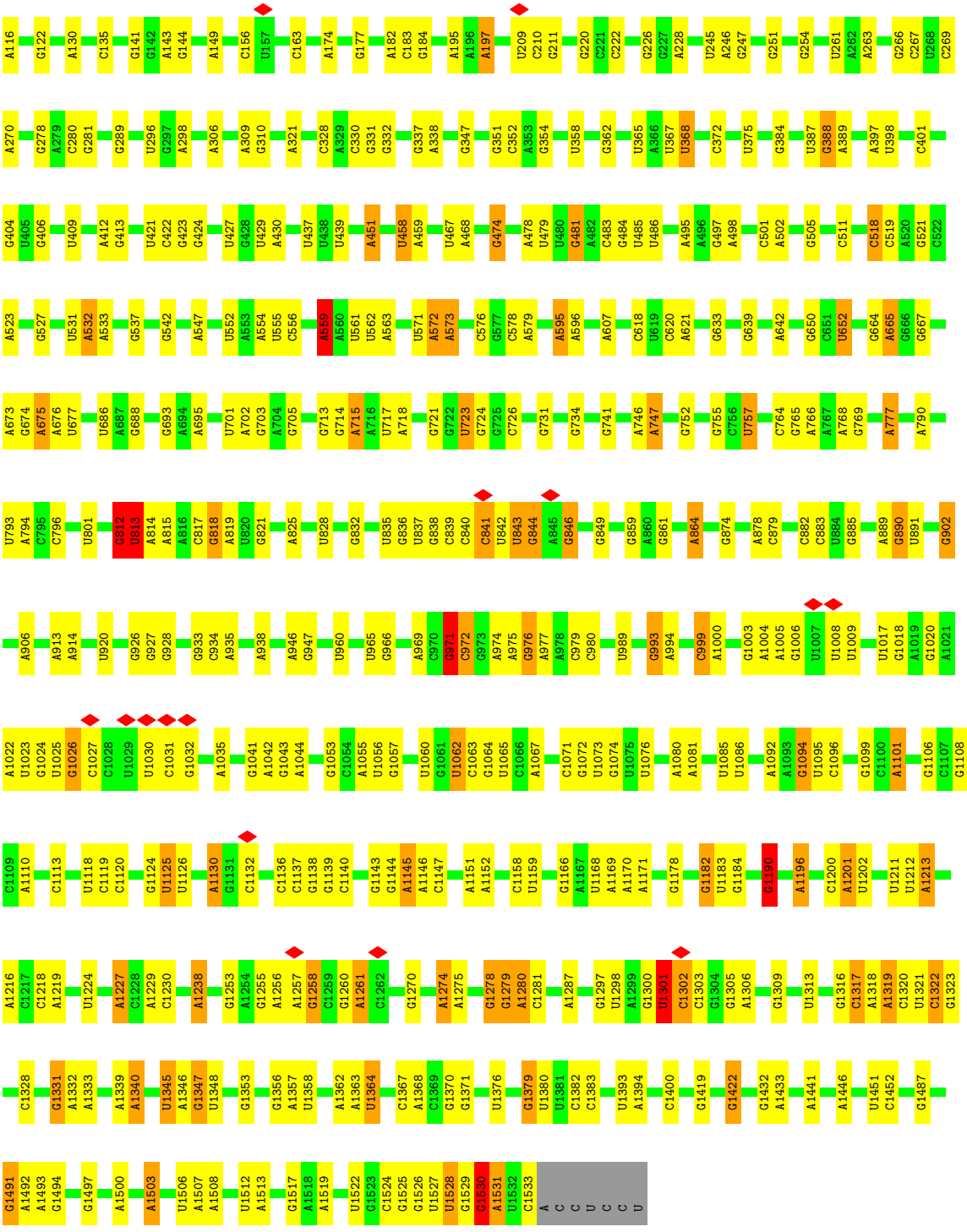




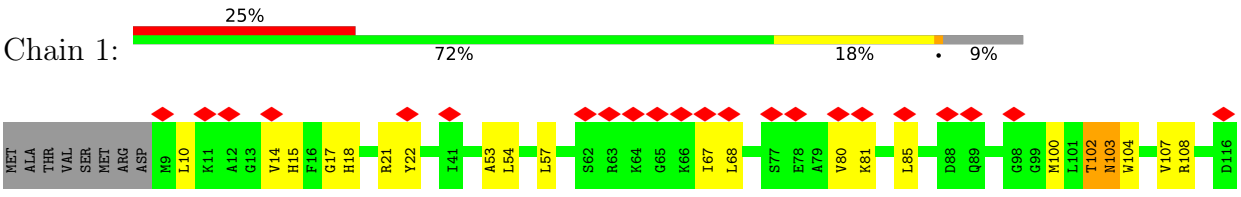
• Molecule 37: 16S rRNA

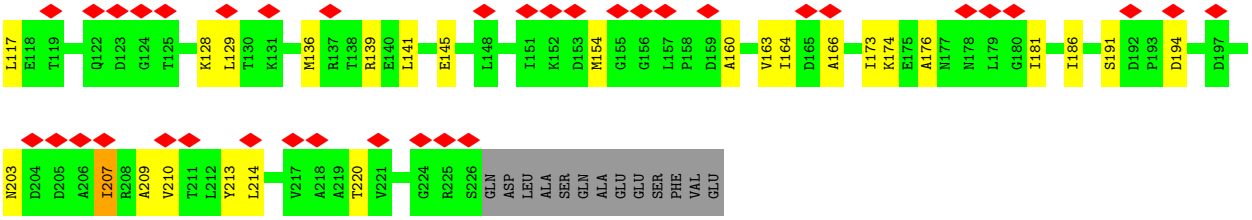
Chain 0:



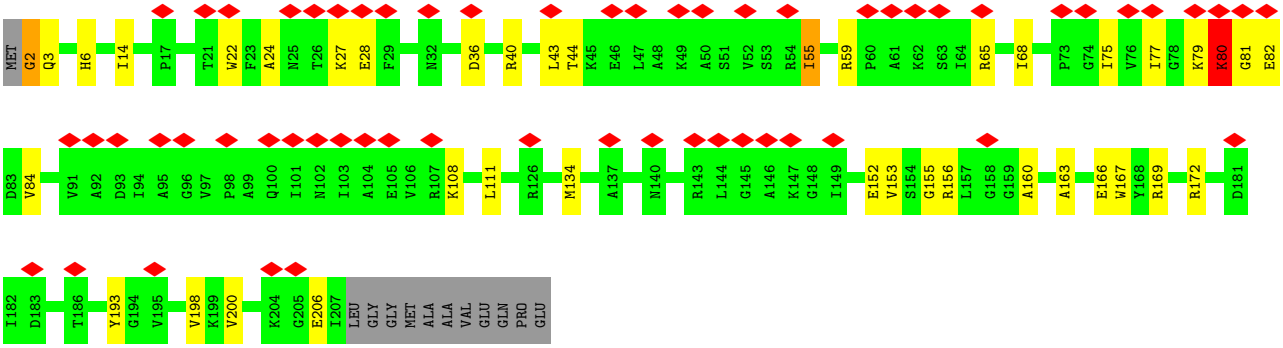


• Molecule 38: 30S ribosomal protein S2

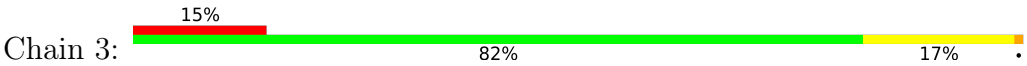


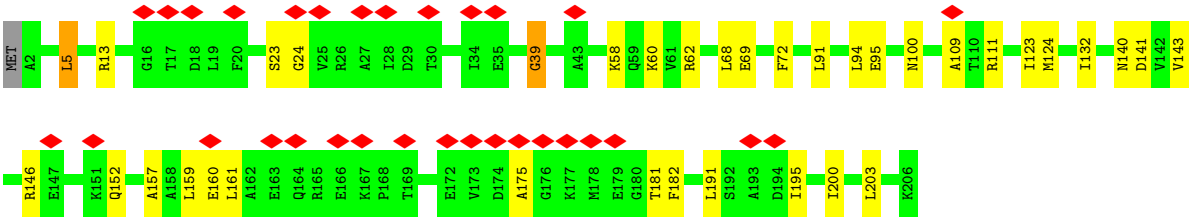


• Molecule 39: 30S ribosomal protein S3

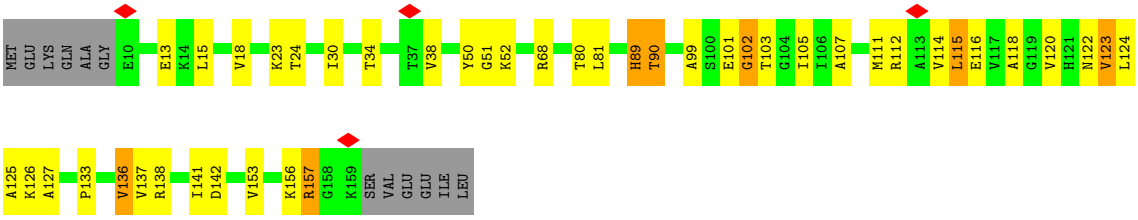


• Molecule 40: 30S ribosomal protein S4

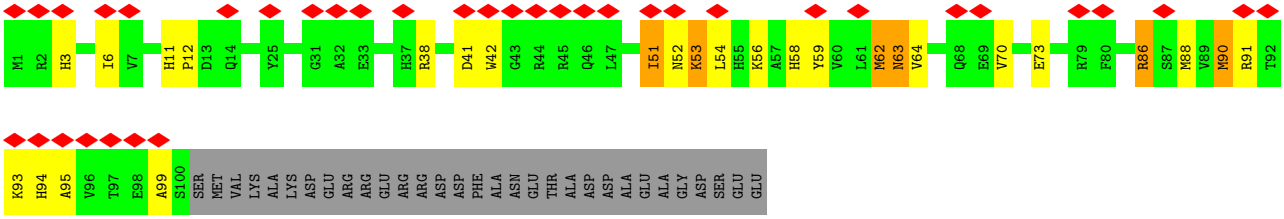




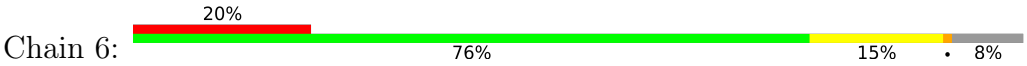
• Molecule 41: 30S ribosomal protein S5

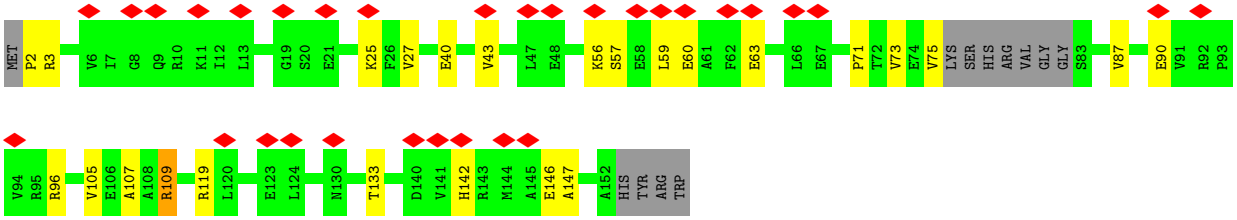


• Molecule 42: 30S ribosomal protein S6, non-modified isoform

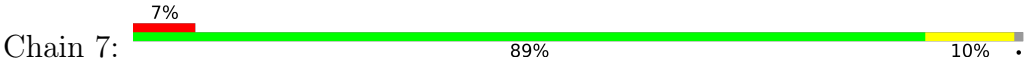


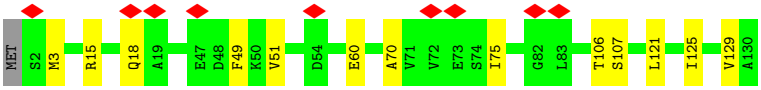
• Molecule 43: 30S ribosomal protein S7





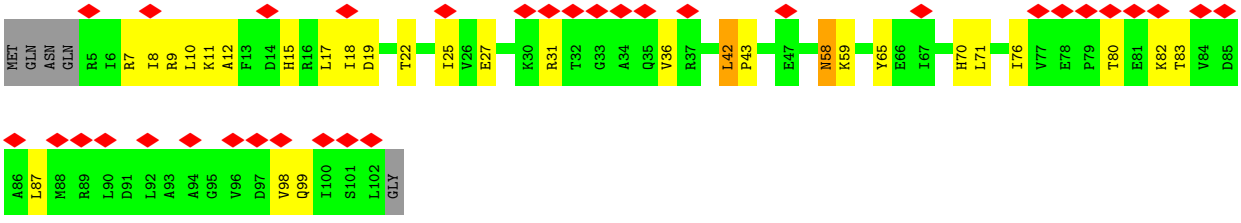
• Molecule 44: 30S ribosomal protein S8





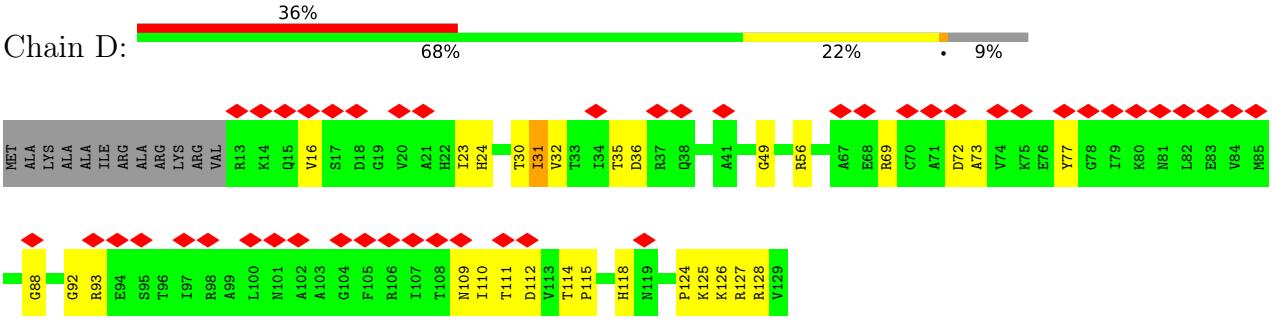
• Molecule 45: 30S ribosomal protein S9

• Molecule 46: 30S ribosomal protein S10



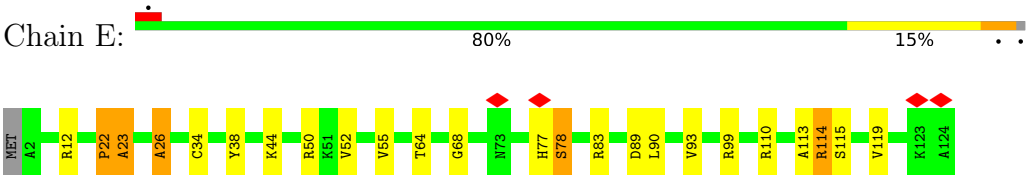
• Molecule 47: 30S ribosomal protein S11

Chain D:



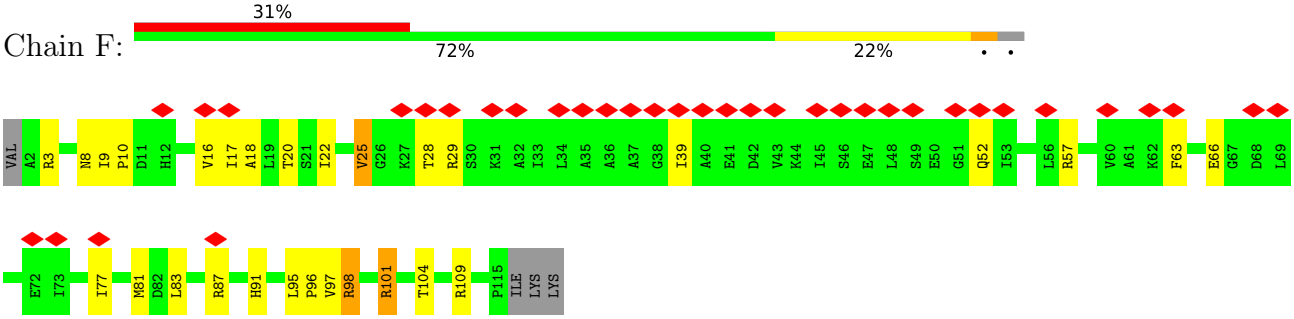
• Molecule 48: 30S ribosomal protein S12

Chain E:



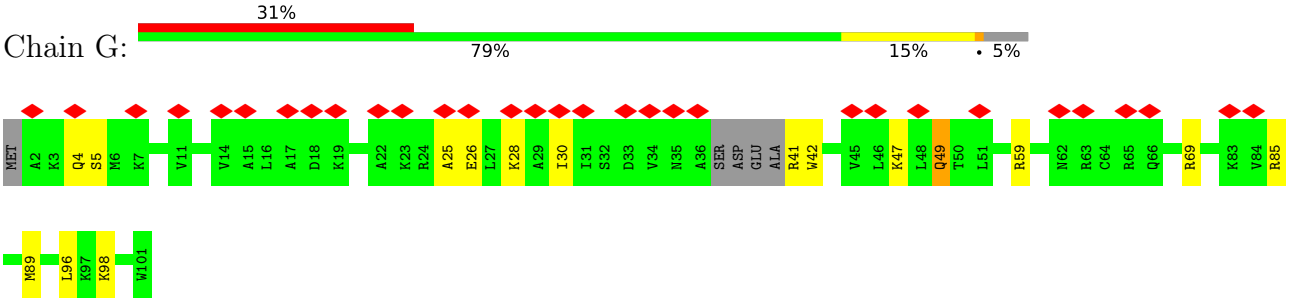
• Molecule 49: 30S ribosomal protein S13

Chain F:



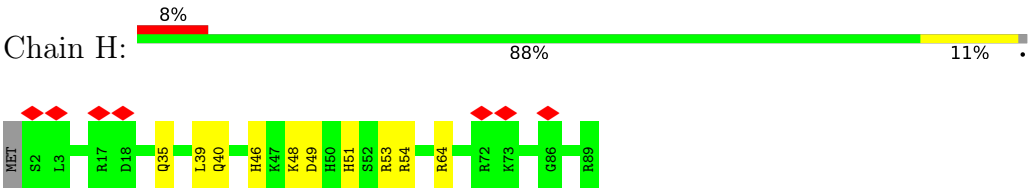
• Molecule 50: 30S ribosomal protein S14

Chain G:



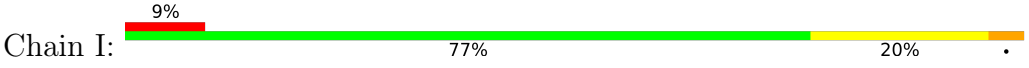
• Molecule 51: 30S ribosomal protein S15

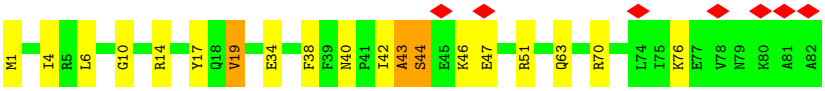
Chain H:



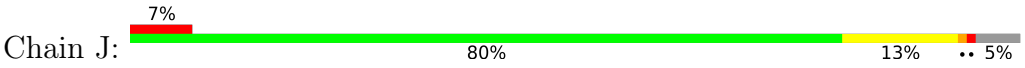
• Molecule 52: 30S ribosomal protein S16

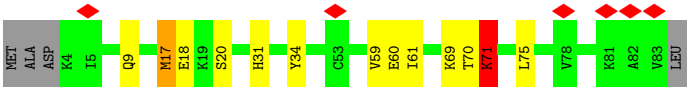
Chain I:



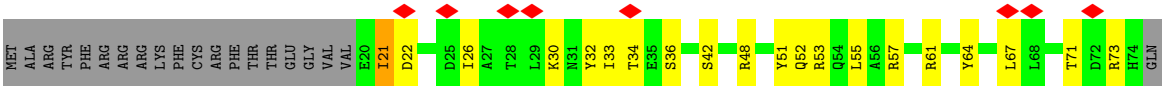


• Molecule 53: 30S ribosomal protein S17

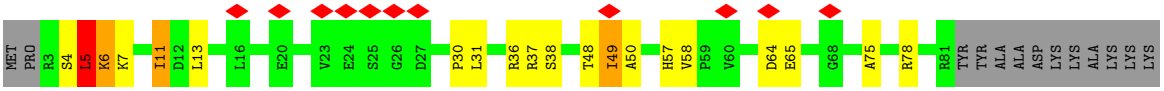




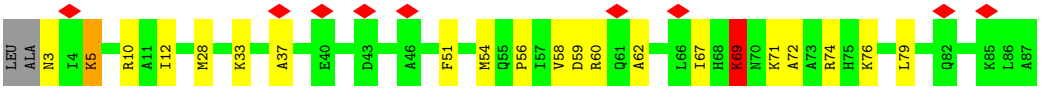
• Molecule 54: 30S ribosomal protein S18



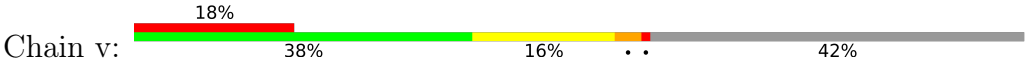
• Molecule 55: 30S ribosomal protein S19

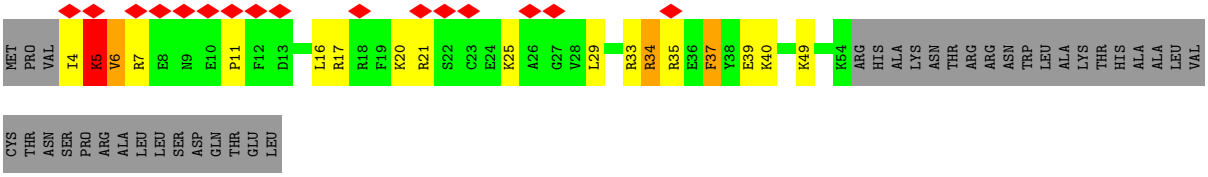


• Molecule 56: 30S ribosomal protein S20



• Molecule 57: 30S ribosomal protein S21





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75081	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.540	Depositor
Minimum map value	-0.736	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	654.0, 654.0, 654.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	A	0.51	0/1744	0.72	0/2716
2	s	0.96	1/326 (0.3%)	0.92	0/441
3	M	0.51	0/1779	0.77	3/2768 (0.1%)
4	O	0.65	1/2828 (0.0%)	0.83	7/4410 (0.2%)
5	P	1.72	39/2121 (1.8%)	1.42	17/2852 (0.6%)
6	Q	1.54	14/1585 (0.9%)	1.29	10/2134 (0.5%)
7	R	1.21	8/1571 (0.5%)	1.09	5/2113 (0.2%)
8	S	0.84	0/1434	0.89	0/1926
9	T	0.83	0/1342	0.86	0/1816
10	U	0.68	1/1122 (0.1%)	1.02	3/1515 (0.2%)
11	V	0.77	0/1045	0.74	0/1410
12	W	1.42	10/1151 (0.9%)	1.10	0/1551
13	X	1.53	8/947 (0.8%)	1.28	4/1268 (0.3%)
14	Y	1.65	14/1053 (1.3%)	1.44	7/1403 (0.5%)
15	Z	1.42	4/1092 (0.4%)	1.20	2/1460 (0.1%)
16	a	1.65	11/973 (1.1%)	1.35	5/1301 (0.4%)
17	b	1.05	2/901 (0.2%)	1.04	5/1209 (0.4%)
18	c	1.38	4/927 (0.4%)	1.21	4/1240 (0.3%)
19	d	1.57	7/959 (0.7%)	1.32	7/1278 (0.5%)
20	e	1.39	6/828 (0.7%)	1.21	1/1107 (0.1%)
21	f	1.33	2/864 (0.2%)	1.14	1/1156 (0.1%)
22	g	1.22	0/744	1.10	0/994
23	h	1.00	1/787 (0.1%)	1.06	0/1051
24	i	0.96	0/765	0.90	0/1025
25	j	1.50	5/575 (0.9%)	1.38	6/762 (0.8%)
26	k	1.35	1/634 (0.2%)	1.16	2/848 (0.2%)
27	l	0.89	0/509	1.00	0/677
28	m	1.18	0/452	1.14	1/605 (0.2%)
29	n	1.48	2/449 (0.4%)	1.40	6/599 (1.0%)
30	o	1.45	5/416 (1.2%)	1.02	0/554
31	p	1.73	5/379 (1.3%)	1.61	5/498 (1.0%)
32	q	1.50	0/512	1.35	2/676 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	r	1.43	3/302 (1.0%)	1.34	3/397 (0.8%)
34	N	0.95	271/69681 (0.4%)	0.95	171/108706 (0.2%)
35	L	0.78	0/426	0.90	1/570 (0.2%)
36	C	0.32	0/1034	0.81	1/1387 (0.1%)
37	0	0.76	28/36809 (0.1%)	0.85	49/57423 (0.1%)
38	1	1.02	1/1735 (0.1%)	0.99	2/2338 (0.1%)
39	2	1.08	4/1651 (0.2%)	0.97	3/2225 (0.1%)
40	3	0.95	2/1664 (0.1%)	1.03	2/2227 (0.1%)
41	4	1.53	6/1118 (0.5%)	1.35	7/1504 (0.5%)
42	5	1.16	5/835 (0.6%)	1.14	3/1128 (0.3%)
43	6	0.83	0/1142	0.86	1/1532 (0.1%)
44	7	1.15	1/988 (0.1%)	1.04	0/1326
45	8	1.09	1/1033 (0.1%)	1.13	2/1375 (0.1%)
46	9	0.95	1/796 (0.1%)	1.02	2/1077 (0.2%)
47	D	1.11	0/892	1.12	3/1205 (0.2%)
48	E	1.37	6/968 (0.6%)	1.25	3/1300 (0.2%)
49	F	1.09	1/892 (0.1%)	1.07	0/1193
50	G	1.10	0/784	1.14	1/1043 (0.1%)
51	H	1.20	2/717 (0.3%)	1.03	1/959 (0.1%)
52	I	1.18	3/658 (0.5%)	1.19	5/884 (0.6%)
53	J	1.08	1/657 (0.2%)	1.06	1/881 (0.1%)
54	K	1.20	0/462	1.15	1/621 (0.2%)
55	t	1.02	1/652 (0.2%)	1.00	1/877 (0.1%)
56	u	1.19	2/670 (0.3%)	1.20	2/888 (0.2%)
57	v	1.24	5/426 (1.2%)	1.27	3/565 (0.5%)
All	All	0.99	495/159806 (0.3%)	0.97	371/238994 (0.2%)

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
5	P	0	3
6	Q	0	1
8	S	0	2
10	U	0	1
11	V	0	1
14	Y	0	2
15	Z	0	2
23	h	0	1
32	q	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	6
37	0	0	5
38	1	0	3
39	2	0	2
41	4	0	5
42	5	0	2
45	8	0	4
47	D	0	1
48	E	0	2
53	J	0	2
55	t	0	1
56	u	0	1
57	v	0	1
All	All	0	49

The worst 5 of 495 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	2502	G	P-OP2	14.12	1.77	1.49
34	N	1156	A	P-OP2	12.93	1.74	1.49
34	N	1333	G	P-OP2	10.88	1.70	1.49
34	N	783	A	P-OP2	10.82	1.70	1.49
41	4	127	ALA	C-O	-10.60	1.10	1.23

The worst 5 of 371 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	73	C	O3'-P-O5'	18.16	131.23	104.00
6	Q	151	THR	CA-C-N	12.76	134.27	119.47
6	Q	151	THR	C-N-CA	12.76	134.27	119.47
34	N	1936	A	C4'-C3'-O3'	-11.05	96.42	113.00
34	N	2725	A	C3'-C2'-O2'	-10.56	94.86	110.70

There are no chirality outliers.

5 of 49 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	P	195	VAL	Peptide
5	P	234	GLY	Peptide
5	P	238	ARG	Peptide
6	Q	151	THR	Peptide

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Mol	Chain	Res	Type	Group
8	S	174	ASP	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1561	0	788	14	0
2	s	316	0	283	7	0
3	M	1594	0	809	65	0
4	O	2529	0	1281	13	0
5	P	2082	0	2154	39	0
6	Q	1564	0	1616	24	0
7	R	1552	0	1619	21	0
8	S	1410	0	1444	27	0
9	T	1322	0	1371	13	0
10	U	1111	0	1148	28	0
11	V	1031	0	1085	22	0
12	W	1128	0	1162	15	0
13	X	938	0	1012	17	0
14	Y	1044	0	1117	18	0
15	Z	1073	0	1157	16	0
16	a	960	0	1000	16	0
17	b	891	0	923	10	0
18	c	915	0	958	14	0
19	d	946	0	1019	23	0
20	e	815	0	839	18	0
21	f	857	0	922	10	0
22	g	738	0	807	6	0
23	h	779	0	831	11	0
24	i	752	0	780	9	0
25	j	568	0	581	10	0
26	k	624	0	652	11	0
27	l	508	0	543	7	0
28	m	448	0	488	3	0
29	n	443	0	458	12	0
30	o	409	0	440	6	0
31	p	376	0	418	17	0
32	q	503	0	572	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	r	301	0	341	8	0
34	N	62215	0	31275	411	0
35	L	419	0	418	12	0
36	C	1027	0	1091	43	0
37	0	32873	0	16532	180	0
38	1	1704	0	1732	28	0
39	2	1624	0	1696	24	0
40	3	1642	0	1707	22	0
41	4	1105	0	1148	19	0
42	5	817	0	808	14	0
43	6	1129	0	1178	16	0
44	7	978	0	1031	6	0
45	8	1021	0	1070	23	0
46	9	786	0	828	21	0
47	D	876	0	887	23	0
48	E	954	0	1016	17	0
49	F	883	0	941	20	0
50	G	773	0	824	12	0
51	H	709	0	728	12	0
52	I	648	0	666	11	0
53	J	648	0	691	5	0
54	K	455	0	478	12	0
55	t	637	0	665	11	0
56	u	664	0	714	15	0
57	v	421	0	445	15	0
58	A	2	0	0	0	0
59	A	1	0	0	0	0
60	A	9	0	0	0	0
All	All	147108	0	99187	1167	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 5.

The worst 5 of 1167 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)
3:M:75:A:H5”	34:N:2602:A:C5	1.40	1.55
34:N:306:U:H3	34:N:310:A:N6	1.15	1.40
37:0:1238:A:N6	37:0:1301:U:H3	1.22	1.37
3:M:75:A:H3’	34:N:2602:A:N6	1.36	1.37
10:U:43:ASN:HB3	10:U:47:PHE:CE2	1.62	1.32

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	s	35/179 (20%)	32 (91%)	3 (9%)	0	100 100
5	P	269/273 (98%)	247 (92%)	18 (7%)	4 (2%)	8 38
6	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	24 60
7	R	199/201 (99%)	191 (96%)	8 (4%)	0	100 100
8	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	21 57
9	T	174/177 (98%)	165 (95%)	9 (5%)	0	100 100
10	U	147/149 (99%)	125 (85%)	19 (13%)	3 (2%)	6 33
11	V	139/142 (98%)	112 (81%)	27 (19%)	0	100 100
12	W	140/142 (99%)	136 (97%)	4 (3%)	0	100 100
13	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	7 36
14	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	4 28
15	Z	134/136 (98%)	119 (89%)	10 (8%)	5 (4%)	2 23
16	a	118/127 (93%)	102 (86%)	14 (12%)	2 (2%)	7 36
17	b	114/117 (97%)	108 (95%)	6 (5%)	0	100 100
18	c	112/115 (97%)	104 (93%)	8 (7%)	0	100 100
19	d	115/118 (98%)	115 (100%)	0	0	100 100
20	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12 45
21	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14 48
22	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	5 31
23	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	6 33
24	i	92/94 (98%)	89 (97%)	3 (3%)	0	100 100
25	j	73/85 (86%)	71 (97%)	2 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	9	41
27	l	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
28	m	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
29	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	34
30	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
31	p	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
32	q	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	37
33	r	36/55 (66%)	35 (97%)	1 (3%)	0	100	100
35	L	53/70 (76%)	45 (85%)	7 (13%)	1 (2%)	6	34
36	C	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
38	1	216/239 (90%)	187 (87%)	28 (13%)	1 (0%)	24	60
39	2	204/218 (94%)	186 (91%)	16 (8%)	2 (1%)	12	45
40	3	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
41	4	148/162 (91%)	116 (78%)	30 (20%)	2 (1%)	9	39
42	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1	16
43	6	140/156 (90%)	130 (93%)	10 (7%)	0	100	100
44	7	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	7	37
46	9	96/103 (93%)	84 (88%)	9 (9%)	3 (3%)	3	26
47	D	115/129 (89%)	102 (89%)	13 (11%)	0	100	100
48	E	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	7	36
49	F	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	14	48
50	G	92/101 (91%)	77 (84%)	14 (15%)	1 (1%)	11	44
51	H	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
52	I	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	9	41
53	J	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	2	22
54	K	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	6	34
55	t	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
56	u	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	42
57	v	49/88 (56%)	41 (84%)	7 (14%)	1 (2%)	6	33
All	All	5826/6442 (90%)	5264 (90%)	503 (9%)	59 (1%)	15	45

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	P	239	ASN
10	U	72	ILE
14	Y	36	LYS
15	Z	58	LYS
20	e	53	PHE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	s	34/158 (22%)	34 (100%)	0	100	100
5	P	216/218 (99%)	213 (99%)	3 (1%)	59	71
6	Q	164/164 (100%)	159 (97%)	5 (3%)	36	57
7	R	165/165 (100%)	162 (98%)	3 (2%)	51	67
8	S	148/150 (99%)	147 (99%)	1 (1%)	76	79
9	T	137/138 (99%)	137 (100%)	0	100	100
10	U	114/114 (100%)	109 (96%)	5 (4%)	25	48
11	V	109/110 (99%)	109 (100%)	0	100	100
12	W	116/116 (100%)	115 (99%)	1 (1%)	70	76
13	X	103/104 (99%)	101 (98%)	2 (2%)	50	67
14	Y	102/103 (99%)	100 (98%)	2 (2%)	48	66
15	Z	109/109 (100%)	108 (99%)	1 (1%)	70	76
16	a	100/102 (98%)	98 (98%)	2 (2%)	48	66
17	b	86/87 (99%)	85 (99%)	1 (1%)	63	73
18	c	98/100 (98%)	94 (96%)	4 (4%)	27	49
19	d	89/90 (99%)	87 (98%)	2 (2%)	45	64
20	e	84/84 (100%)	83 (99%)	1 (1%)	63	73
21	f	93/93 (100%)	93 (100%)	0	100	100
22	g	80/85 (94%)	79 (99%)	1 (1%)	61	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	h	83/85 (98%)	81 (98%)	2 (2%)	43	63
24	i	78/78 (100%)	77 (99%)	1 (1%)	61	72
25	j	56/62 (90%)	55 (98%)	1 (2%)	51	67
26	k	67/68 (98%)	67 (100%)	0	100	100
27	l	55/55 (100%)	54 (98%)	1 (2%)	51	67
28	m	48/49 (98%)	48 (100%)	0	100	100
29	n	47/48 (98%)	46 (98%)	1 (2%)	47	65
30	o	45/49 (92%)	45 (100%)	0	100	100
31	p	38/38 (100%)	38 (100%)	0	100	100
32	q	51/52 (98%)	49 (96%)	2 (4%)	28	50
33	r	34/50 (68%)	33 (97%)	1 (3%)	37	58
35	L	48/63 (76%)	48 (100%)	0	100	100
36	C	110/174 (63%)	109 (99%)	1 (1%)	70	76
38	1	180/198 (91%)	179 (99%)	1 (1%)	78	81
39	2	170/178 (96%)	167 (98%)	3 (2%)	51	67
40	3	172/173 (99%)	170 (99%)	2 (1%)	63	73
41	4	113/123 (92%)	107 (95%)	6 (5%)	20	44
42	5	87/112 (78%)	87 (100%)	0	100	100
43	6	119/129 (92%)	118 (99%)	1 (1%)	73	77
44	7	104/105 (99%)	101 (97%)	3 (3%)	37	58
45	8	105/107 (98%)	104 (99%)	1 (1%)	68	76
46	9	86/90 (96%)	85 (99%)	1 (1%)	63	73
47	D	90/98 (92%)	89 (99%)	1 (1%)	65	74
48	E	103/104 (99%)	103 (100%)	0	100	100
49	F	92/96 (96%)	90 (98%)	2 (2%)	45	64
50	G	79/83 (95%)	79 (100%)	0	100	100
51	H	75/77 (97%)	75 (100%)	0	100	100
52	I	65/65 (100%)	64 (98%)	1 (2%)	57	70
53	J	74/77 (96%)	73 (99%)	1 (1%)	59	71
54	K	48/66 (73%)	47 (98%)	1 (2%)	47	65
55	t	70/80 (88%)	66 (94%)	4 (6%)	18	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
56	u	65/66 (98%)	65 (100%)	0	100 100
57	v	43/76 (57%)	37 (86%)	6 (14%)	3 17
All	All	4847/5264 (92%)	4769 (98%)	78 (2%)	54 70

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	7	51	VAL
55	t	58	VAL
44	7	125	ILE
52	I	19	VAL
57	v	16	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
50	G	66	GLN
51	H	37	ASN
56	u	20	HIS
19	d	37	GLN
18	c	52	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	72/73 (98%)	20 (27%)	8 (11%)
3	M	74/75 (98%)	11 (14%)	0
34	N	2894/2903 (99%)	521 (18%)	34 (1%)
37	0	1531/1539 (99%)	277 (18%)	22 (1%)
4	O	117/120 (97%)	21 (17%)	1 (0%)
All	All	4688/4710 (99%)	850 (18%)	65 (1%)

5 of 850 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	C
1	A	14	A
1	A	16	U
1	A	17	C

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Mol	Chain	Res	Type
1	A	18	G

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
37	0	1190	G
37	0	1300	G
34	N	784	G
34	N	774	G
37	0	1345	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)

Of 3 ligands modelled in this entry, 3 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)

There are no chain breaks in this entry.

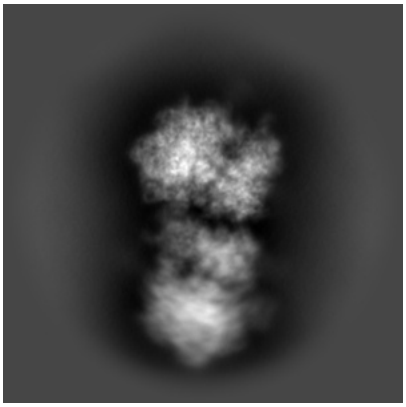
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13952. These allow visual inspection of the internal detail of the map and identification of artifacts.

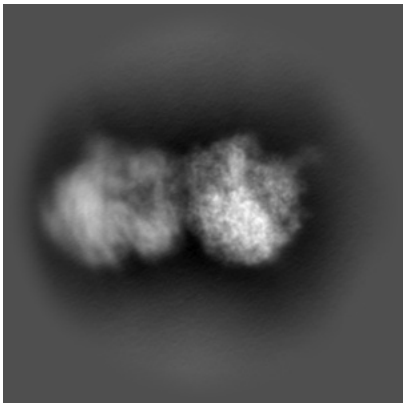
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

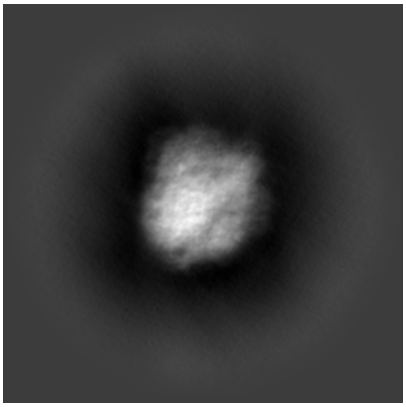
6.1.1 Primary map



X



Y

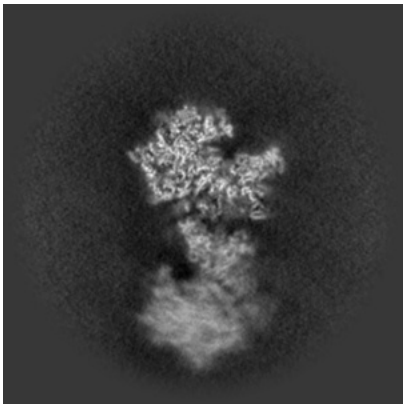


Z

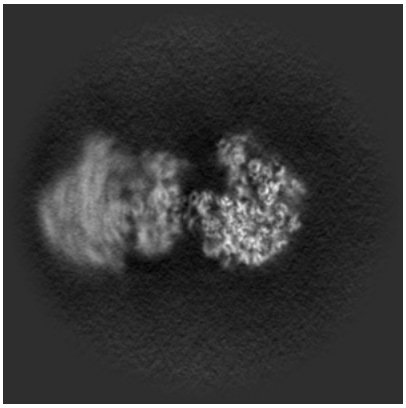
The images above show the map projected in three orthogonal directions.

6.2 Central slices

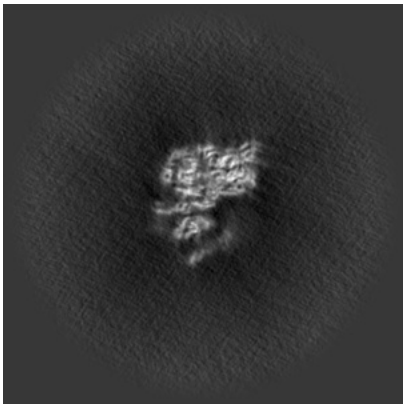
6.2.1 Primary map



X Index: 300



Y Index: 300

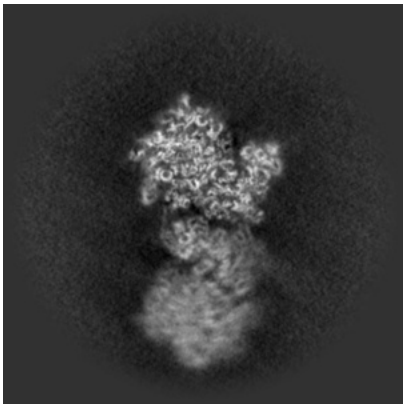


Z Index: 300

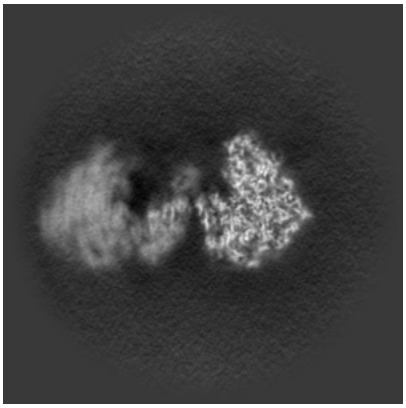
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

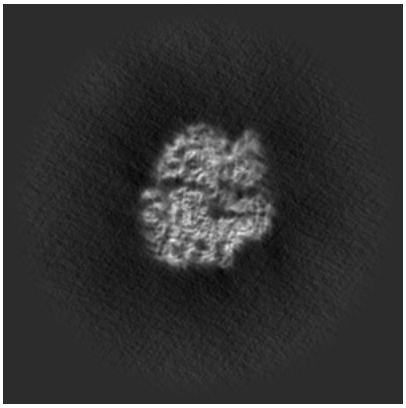
6.3.1 Primary map



X Index: 282



Y Index: 275

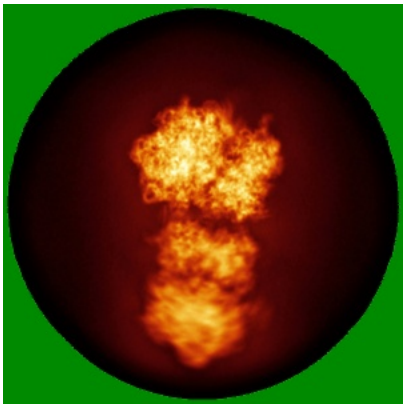


Z Index: 348

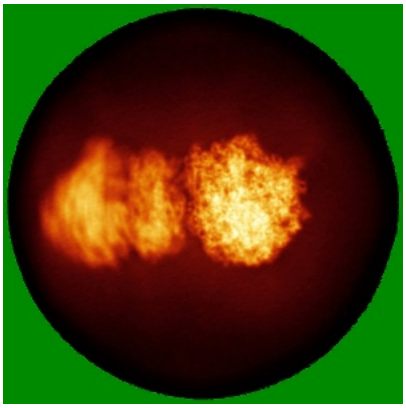
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

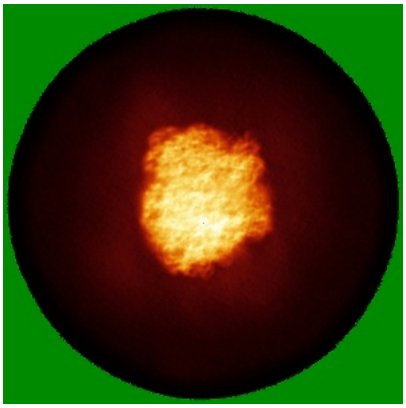
6.4.1 Primary map



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)

This section was not generated.

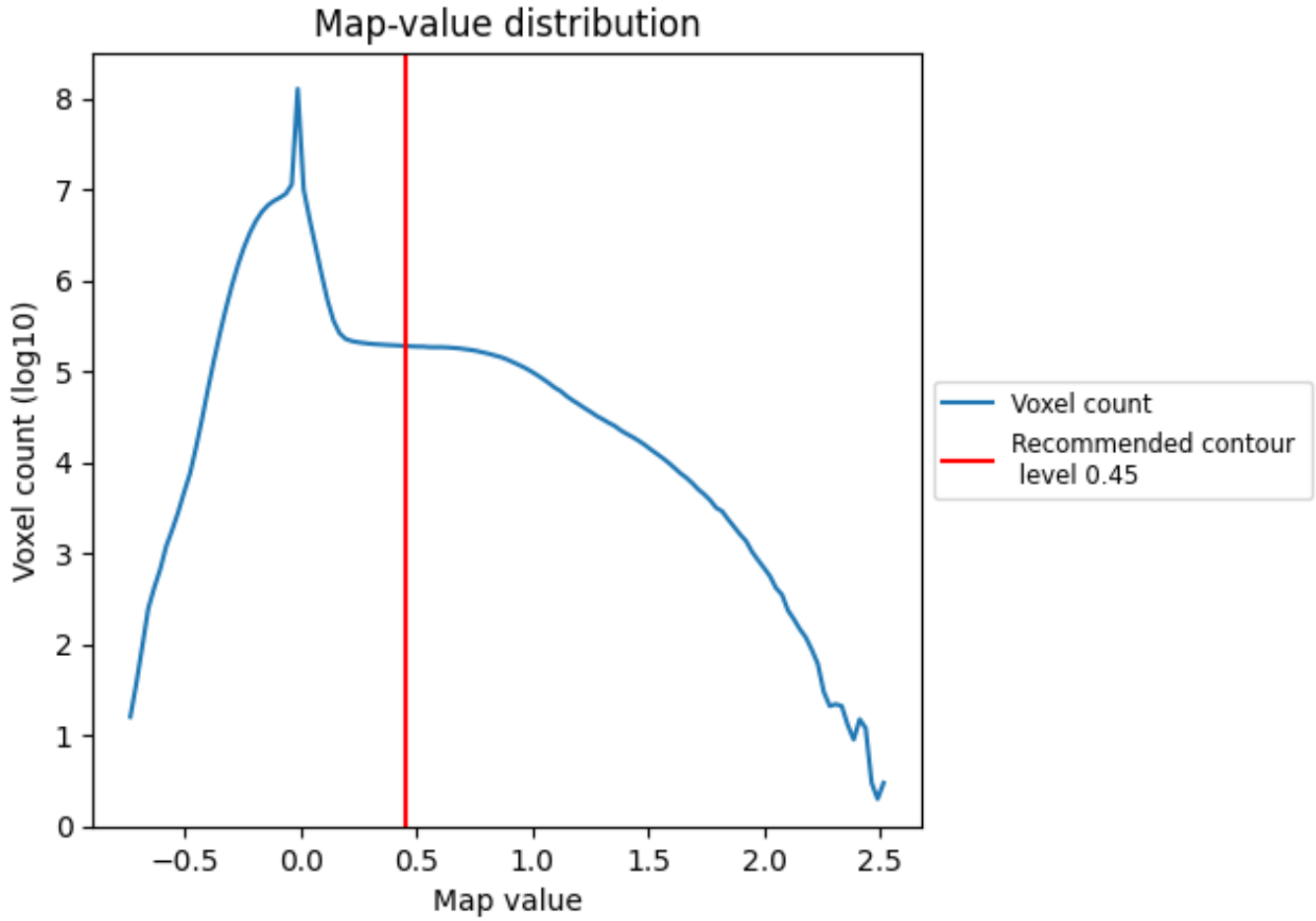
6.6 Mask visualisation (i)

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

7 Map analysis

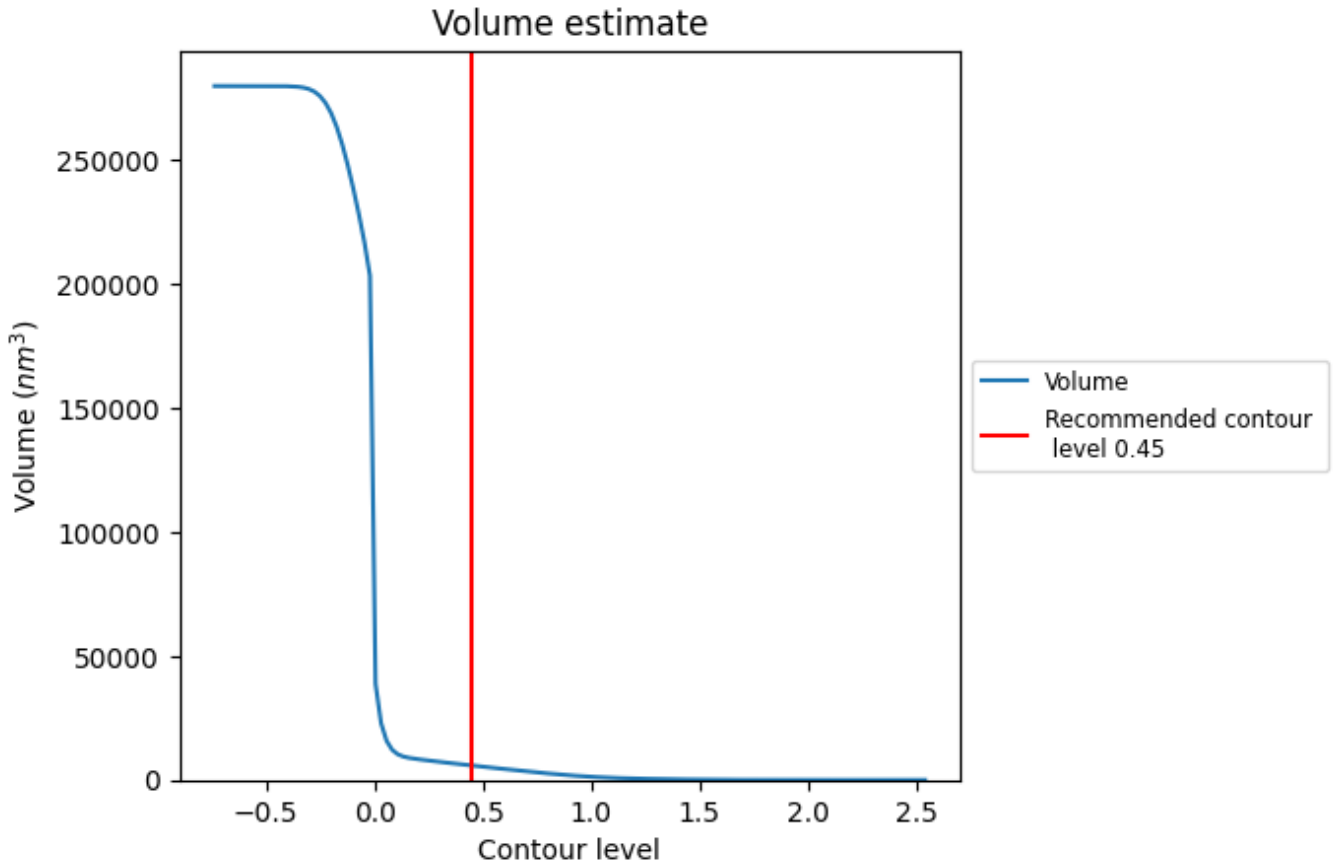
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

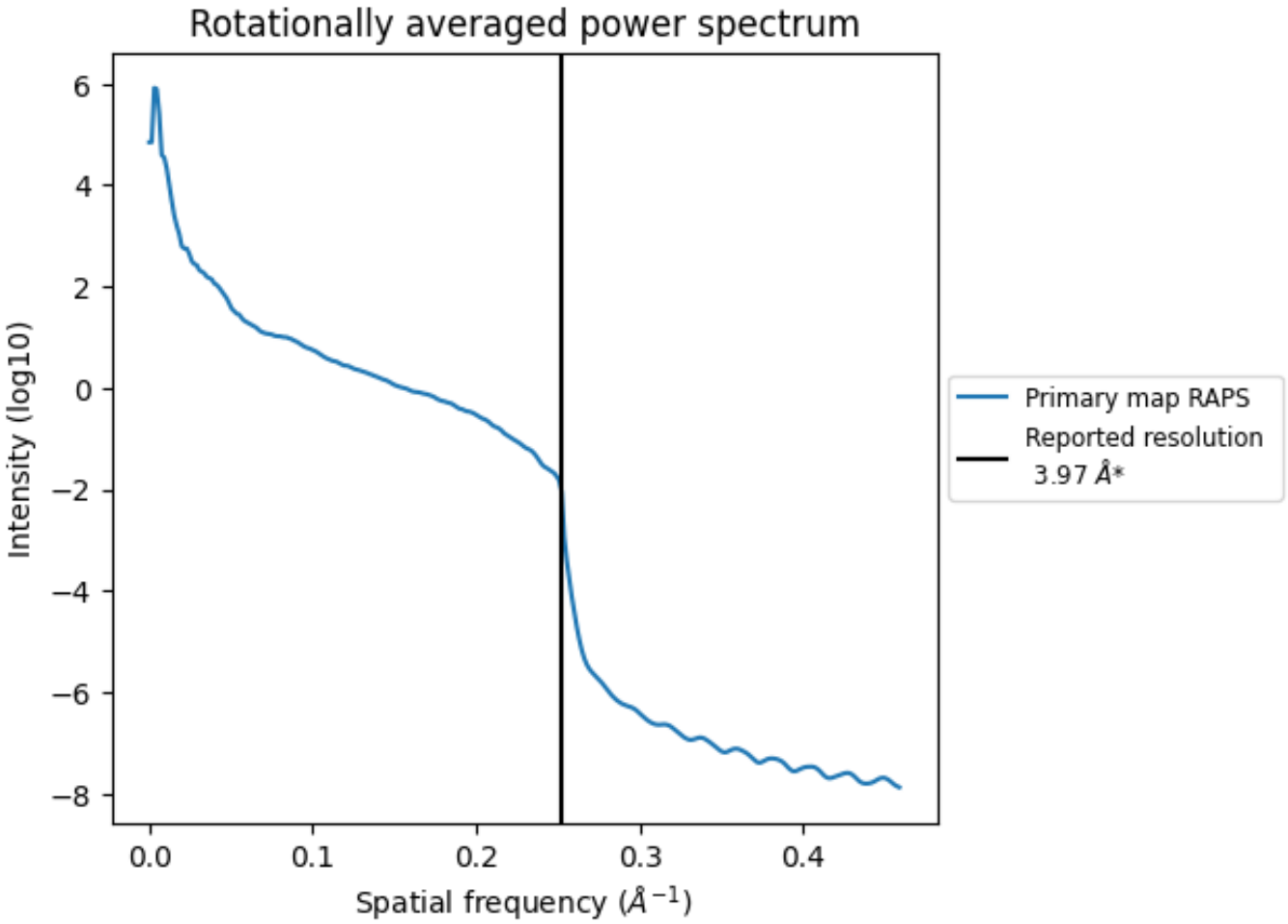
7.2 Volume estimate (i)



The volume at the recommended contour level is 5826 nm^3; this corresponds to an approximate mass of 5263 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.252 Å^{-1}

8 Fourier-Shell correlation (i)

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

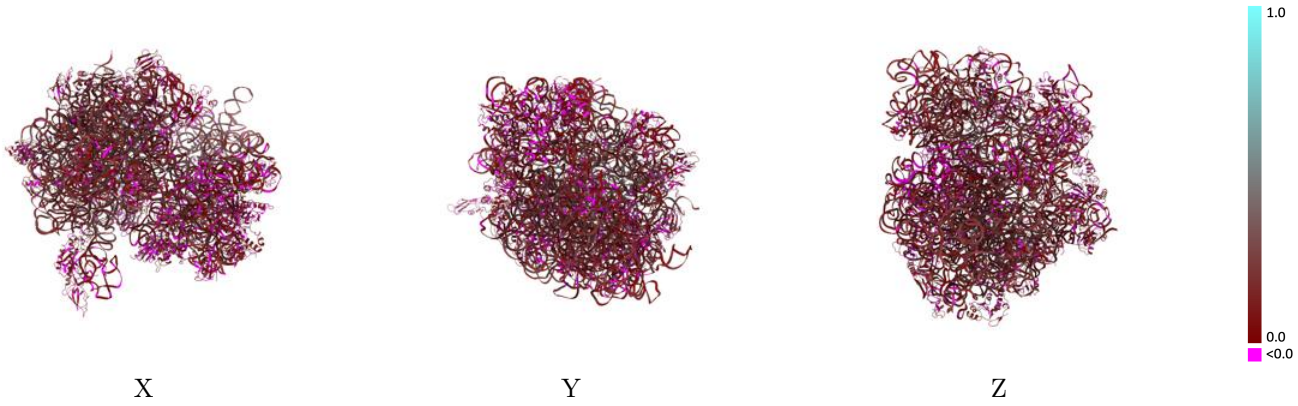
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13952 and PDB model 7QG8. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay

This section was not generated.

9.2 Q-score mapped to coordinate model

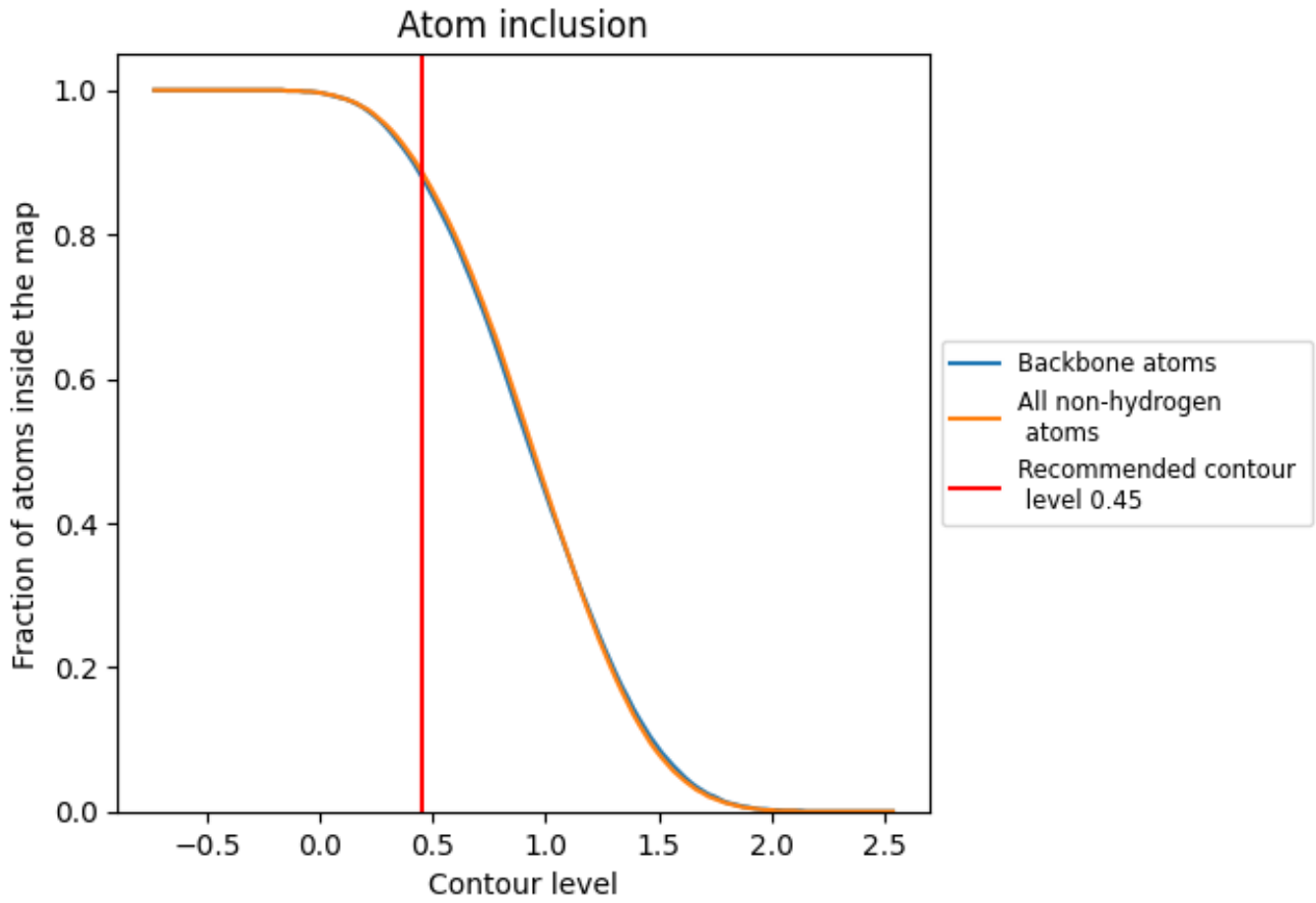


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model

This section was not generated.

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 89% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8870	0.1450
0	0.9490	0.1580
1	0.5930	0.1110
2	0.6140	0.0610
3	0.7810	0.1020
4	0.9050	0.1390
5	0.5230	0.1150
6	0.6800	0.0780
7	0.8020	0.1190
8	0.8100	0.0840
9	0.5700	0.0820
A	0.7540	0.1560
C	0.0970	0.0690
D	0.5490	0.0490
E	0.8960	0.0910
F	0.6170	0.0710
G	0.6480	0.0470
H	0.8100	0.1300
I	0.8750	0.1250
J	0.8260	0.0380
K	0.6810	0.1310
L	0.5070	0.1250
M	0.9150	0.1840
N	0.9560	0.1680
O	0.9550	0.1550
P	0.8630	0.0740
Q	0.8170	0.0790
R	0.7890	0.1310
S	0.7900	0.0960
T	0.8470	0.1070
U	0.3990	0.1080
V	0.5640	0.0520
W	0.9230	0.1590
X	0.5170	0.0200
Y	0.8110	0.1500

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Chain	Atom inclusion	Q-score
Z	0.8730	0.1730
a	0.9130	0.0930
b	0.8500	0.1160
c	0.7270	0.0160
d	0.9130	0.1470
e	0.7430	0.1710
f	0.8900	0.1250
g	0.7700	0.0810
h	0.8570	0.1110
i	0.8560	0.1420
j	0.9820	0.1180
k	0.7880	0.1460
l	0.6030	0.1020
m	0.8900	0.1580
n	0.8500	0.0900
o	0.8700	0.1480
p	0.9660	0.1100
q	0.9740	0.1670
r	0.9490	0.1150
s	0.9480	0.1080
t	0.7970	0.0600
u	0.7810	0.1080
v	0.5870	0.1390