



## wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 01:46 pm GMT

PDB ID : 5MMM  
EMDB ID : EMD-3533  
Title : Structure of the 70S chloroplast ribosome  
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.  
Deposited on : 2016-12-11  
Resolution : 3.40 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](mailto: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>.

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

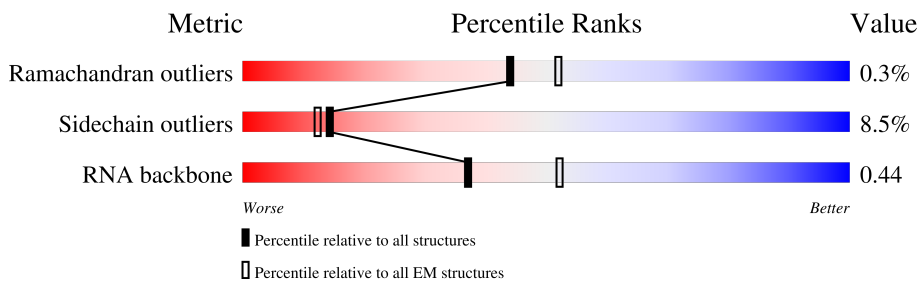
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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.





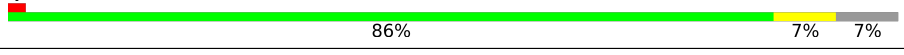



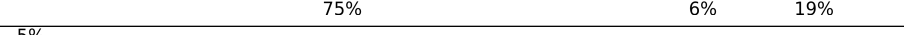



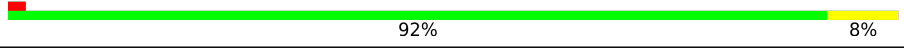

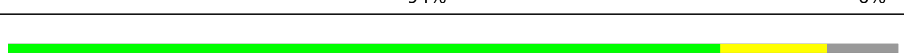


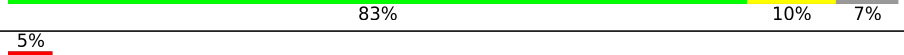

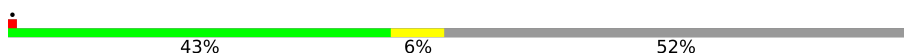


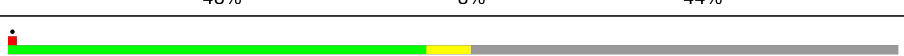




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	0	130	
2	1	57	
3	2	66	
4	3	152	
5	4	159	
6	5	37	
7	6	142	
8	7	116	


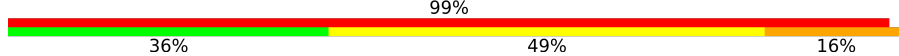
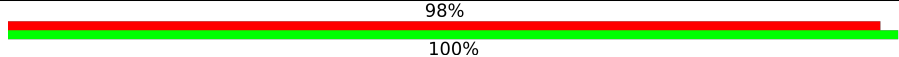
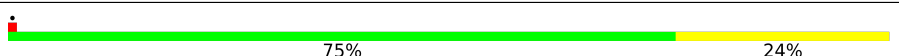
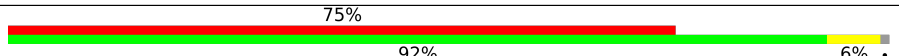
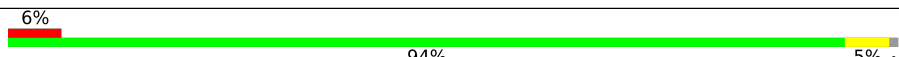
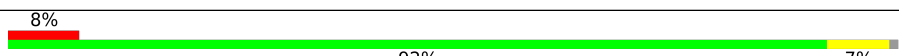
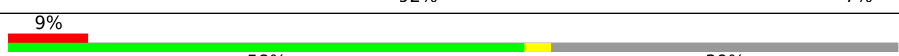


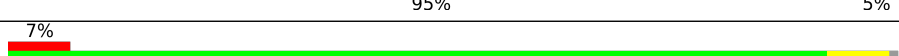
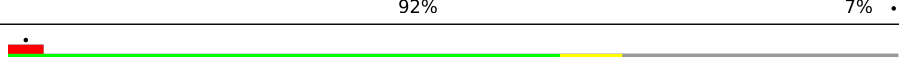


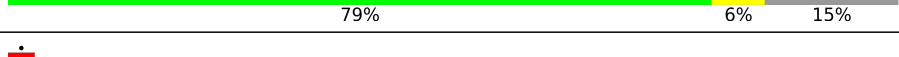
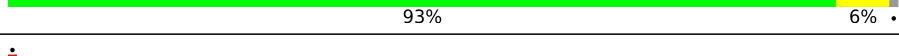

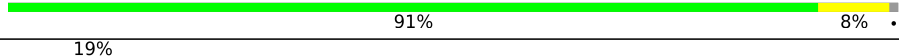

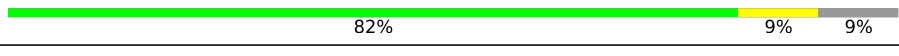

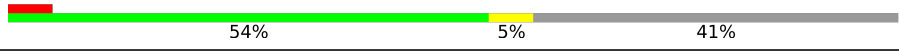



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Mol	Chain	Length	Quality of chain
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	
29	U	198	
30	V	192	
31	W	106	
32	X	194	
33	Y	148	

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Mol	Chain	Length	Quality of chain
34	Z	168	
35	z	76	
36	8	174	
37	a	1491	
38	b	236	
39	c	218	
40	d	201	
41	e	308	
42	f	211	
43	g	155	
44	h	134	
45	i	208	
46	j	195	
47	k	138	
48	l	123	
49	m	172	
50	n	100	
51	o	90	
52	p	88	
53	q	165	
54	r	101	
55	s	92	
56	t	183	
57	u	180	
58	v	260	

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Mol	Chain	Length	Quality of chain
59	w	179	37% 46% 54%
60	x	101	40% 60%
61	y	302	37% 62%

## 2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 152465 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 protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	66	536	338	94	102	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	1	48	396	261	75	60	0	0

- Molecule 3 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	60	489	304	98	83	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	60	467	282	107	75	3	0	0

- Molecule 5 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	72	588	370	124	93	1	0	0

- Molecule 6 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	37	305	186	70	45	4	0	0

- Molecule 7 is a protein called plastid ribosomal protein cL37, PSRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	49	422	268	92	57	5	0	0

- Molecule 8 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	46	368	237	71	59	1	0	0

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	A	2798	60083	26804	11116	19365	2798	0	0

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	B	121	2584	1154	466	843	121	0	0

- Molecule 11 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	253	1952	1209	401	336	6	0	0

- Molecule 12 is a protein called plastid ribosomal protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D	221	1686	1066	308	301	11	0	0

- Molecule 13 is a protein called plastid ribosomal protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	212	1676	1061	312	300	3	0	0

- Molecule 14 is a protein called plastid ribosomal protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	193	1454	923	255	268	8	0	0

- Molecule 15 is a protein called plastid ribosomal protein uL6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	178	1391	878	256	253	4	0	0

- Molecule 16 is a protein called plastid ribosomal protein bL9c.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	H	48	382	251	69	62	0	0

- Molecule 17 is a protein called plastid ribosomal protein uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	137	1106	711	186	203	6	0	0

- Molecule 18 is a protein called 50S ribosomal protein L11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	133	977	624	161	186	6	0	0

- Molecule 19 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	203	1648	1047	307	289	5	0	0

- Molecule 20 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	121	942	588	179	170	5	0	0

- Molecule 21 is a protein called plastid ribosomal protein uL15c.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M	185	1410	879	280	245	6	0	0

- Molecule 22 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	N	135	1075	677	218	174	6	0	0

- Molecule 23 is a protein called plastid ribosomal protein uL14c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O	116	944	592	193	155	4	0	0

- Molecule 24 is a protein called plastid ribosomal protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	P	122	962	598	186	173	5	0	0

- Molecule 25 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Q	118	953	611	186	155	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	R	119	1029	652	213	162	2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	S	170	1310	844	227	239	0	0

- Molecule 28 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	172	Total	C	N	O	S	0	0
			1395	892	257	237	9		

- Molecule 29 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	96	Total	C	N	O	S	0	0
			776	503	135	136	2		

- Molecule 30 is a protein called plastid ribosomal protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	134	Total	C	N	O	S	0	0
			1078	677	203	195	3		

- Molecule 31 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 32 is a protein called plastid ribosomal protein bL27c.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	109	Total	C	N	O	0	0
			888	560	175	153		

- Molecule 33 is a protein called plastid ribosomal protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	S	0	0
			634	402	128	103	1		

- Molecule 34 is a protein called plastid ribosomal protein uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	101	Total	C	N	O	S	0	0
			846	529	167	147	3		

- Molecule 35 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	z	76	1623	723	290	534	76	0	0

- Molecule 36 is a protein called plastid ribosomal protein bS1c.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	8	174	870	522	174	174	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	a	1484	31868	14208	5881	10295	1484	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	b	233	1844	1163	339	329	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	c	216	1736	1108	313	309	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	d	199	1633	1032	319	278	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	e	187	1331	826	259	240	6	0	0

- Molecule 42 is a protein called plastid ribosomal protein bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	f	113	911	583	152	172	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	g	154	1210	753	244	210	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	h	133	1079	679	210	185	5	0	0

- Molecule 45 is a protein called plastid ribosomal protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	i	144	1119	712	211	195	1	0	0

- Molecule 46 is a protein called plastid ribosomal protein uS10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	j	99	805	517	144	139	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	k	117	882	546	181	150	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	l	122	959	599	197	161	2	0	0

- Molecule 49 is a protein called plastid ribosomal protein uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	m	110	Total	C	N	O	S	0	0
			904	556	182	161	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	n	99	Total	C	N	O	S	0	0
			820	507	174	136	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	o	75	Total	C	N	O	S	0	0
			635	404	123	107	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 53 is a protein called plastid ribosomal protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	q	86	Total	C	N	O	S	0	0
			693	434	136	119	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	60	Total	C	N	O	S	0	0
			490	308	96	85	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	s	78	Total	C	N	O	S	0	0
			631	406	119	104	2		

- Molecule 56 is a protein called plastid ribosomal protein bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	t	107	Total	C	N	O	S	0	0
			853	528	173	151	1		

- Molecule 57 is a protein called plastid ribosomal protein bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	65	Total	C	N	O	S	0	0
			568	339	127	100	2		

- Molecule 58 is a protein called 30S ribosomal protein 2, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	v	80	Total	C	N	O	0	0
			613	388	104	121		

- Molecule 59 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	w	82	Total	C	N	O	S	0	0
			686	454	113	116	3		

- Molecule 60 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	x	40	Total	C	N	O	0	0
			309	192	69	48		

- Molecule 61 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	y	116	Total	C	N	O	S	0	0
			919	567	181	169	2		

- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	2	1	Total	Zn	0
			1	1	
62	5	1	Total	Zn	0
			1	1	

- Molecule 63 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
63	4	1	Total Mg 1 1	0
63	6	1	Total Mg 1 1	0
63	7	1	Total Mg 1 1	0
63	A	511	Total Mg 511 511	0
63	B	15	Total Mg 15 15	0
63	C	1	Total Mg 1 1	0
63	D	1	Total Mg 1 1	0
63	E	1	Total Mg 1 1	0
63	F	1	Total Mg 1 1	0
63	H	1	Total Mg 1 1	0
63	M	2	Total Mg 2 2	0
63	P	1	Total Mg 1 1	0
63	R	1	Total Mg 1 1	0
63	S	1	Total Mg 1 1	0
63	T	1	Total Mg 1 1	0
63	U	1	Total Mg 1 1	0
63	V	1	Total Mg 1 1	0
63	W	14	Total Mg 14 14	0
63	a	219	Total Mg 219 219	0
63	k	1	Total Mg 1 1	0
63	l	1	Total Mg 1 1	0
63	n	1	Total Mg 1 1	0

*Continued on next page...*

*Continued from previous page...*

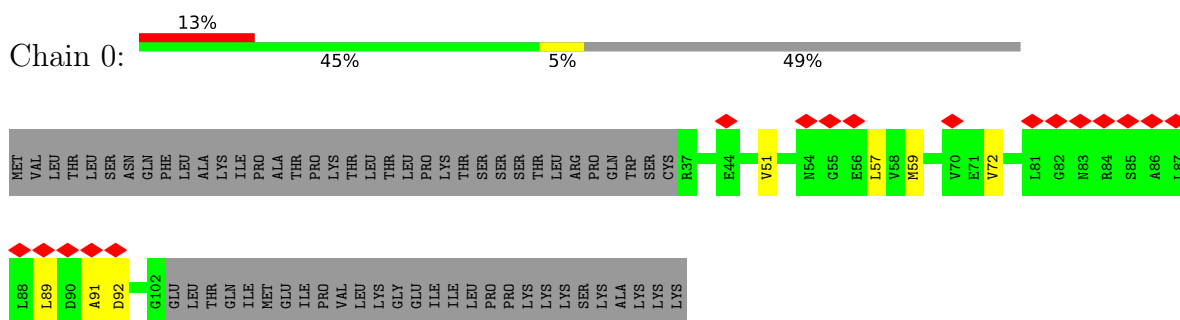
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
63	x	1	1	1	0



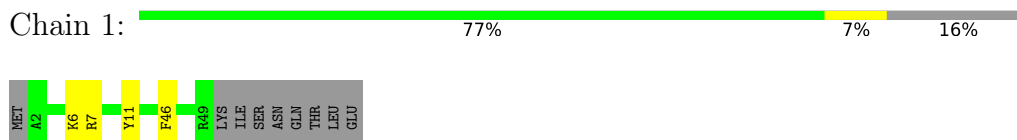
### 3 Residue-property plots [i](#)

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.

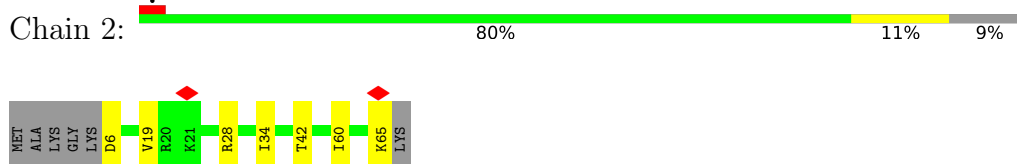
- Molecule 1: 50S ribosomal protein L31



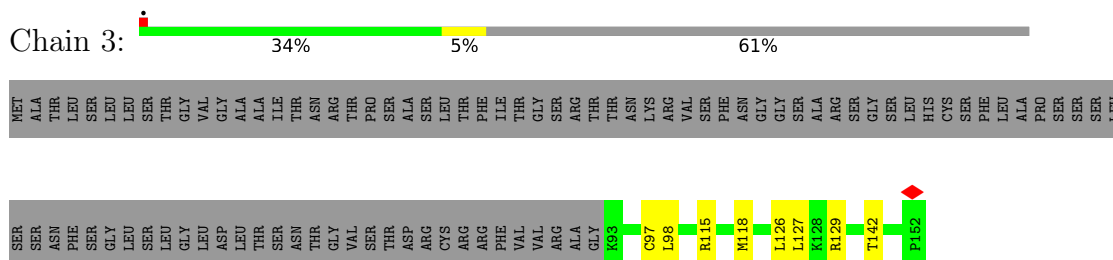
- Molecule 2: 50S ribosomal protein L32, chloroplastic



- Molecule 3: 50S ribosomal protein L33, chloroplastic

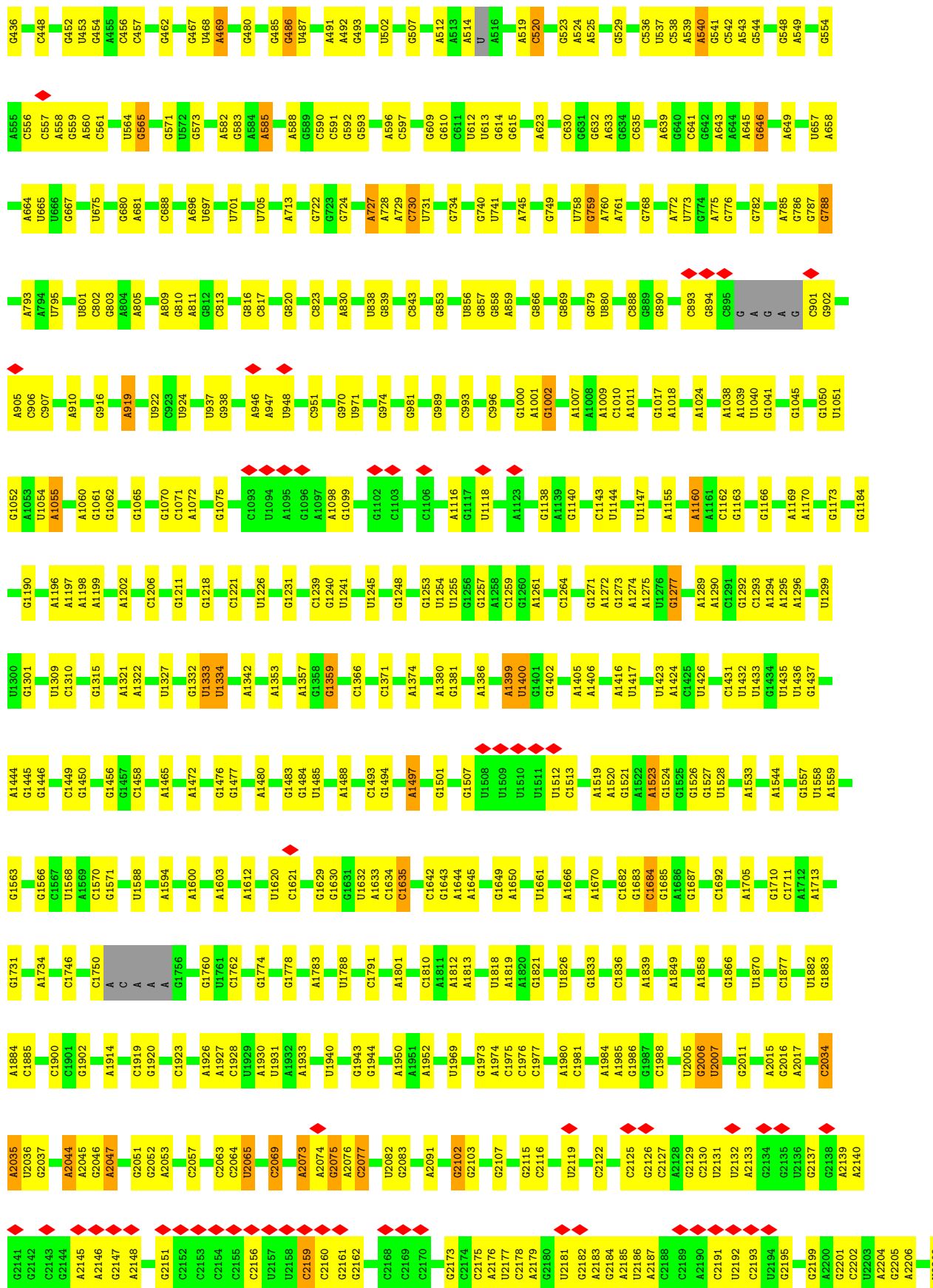


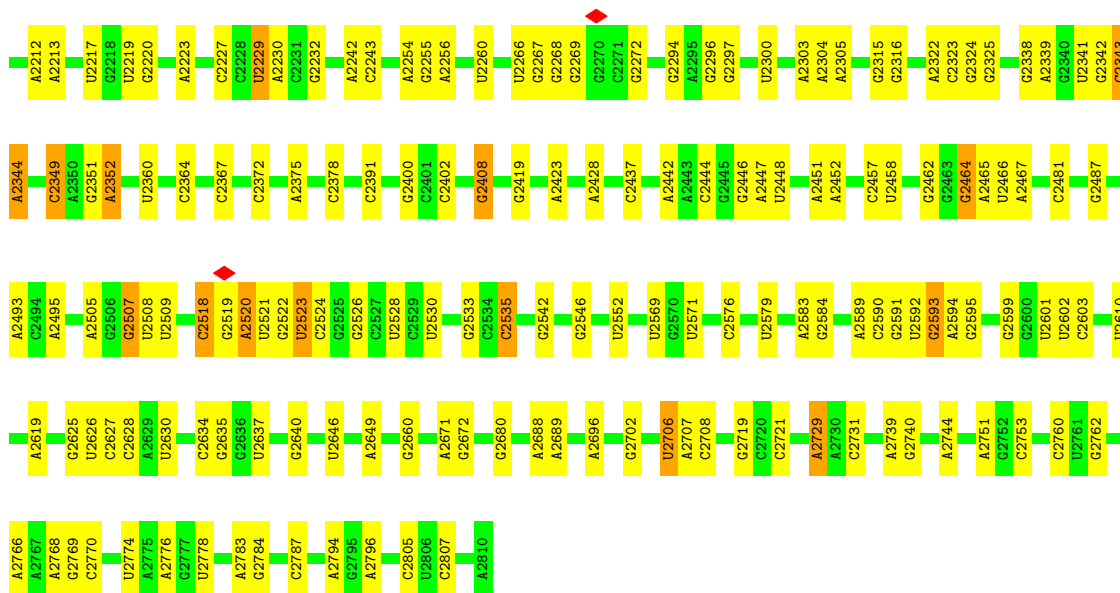
- Molecule 4: 50S ribosomal protein L34, chloroplastic



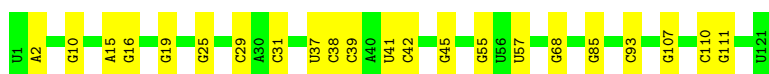
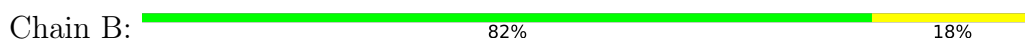
- Molecule 5: 50S ribosomal protein L35, chloroplastic



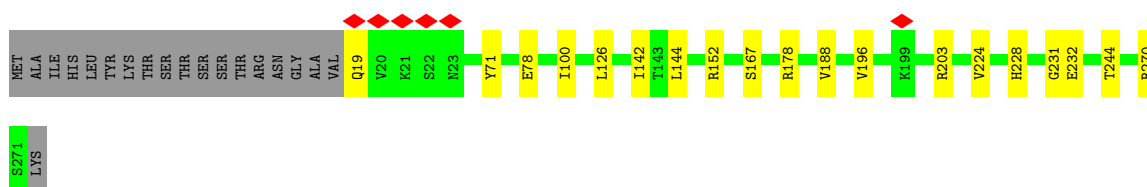
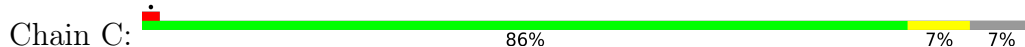




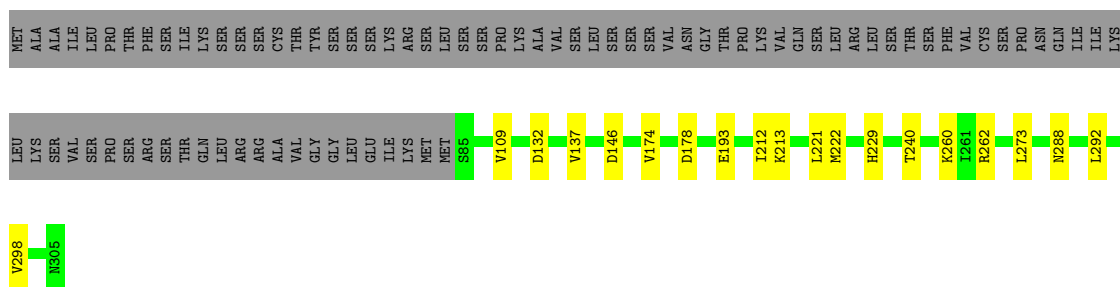
● Molecule 10: 5S ribosomal RNA



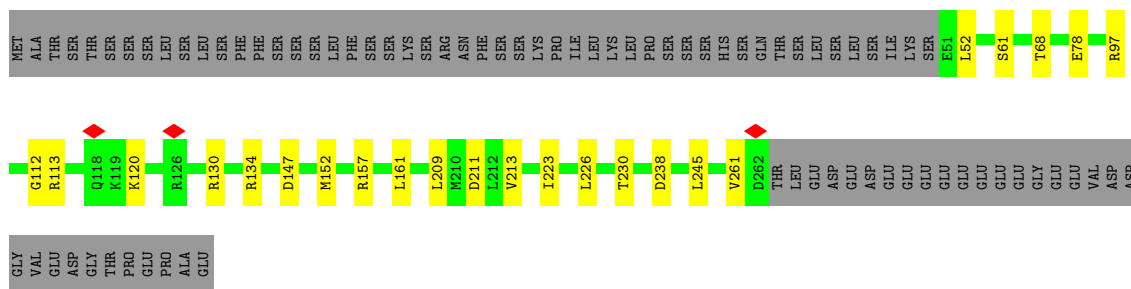
● Molecule 11: 50S ribosomal protein L2, chloroplastic



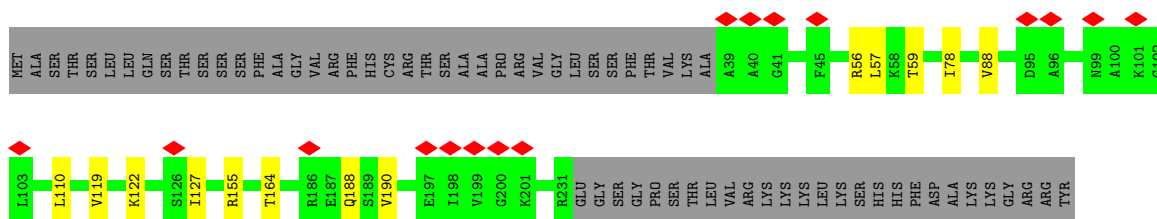
● Molecule 12: plastid ribosomal protein uL3c



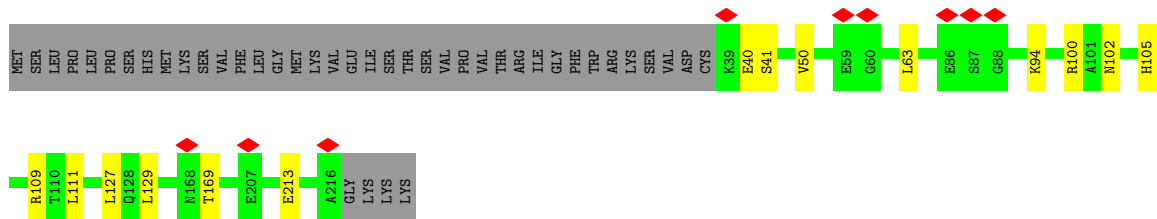
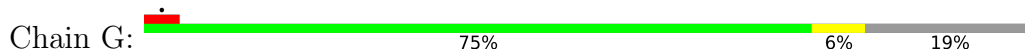
● Molecule 13: plastid ribosomal protein uL4c



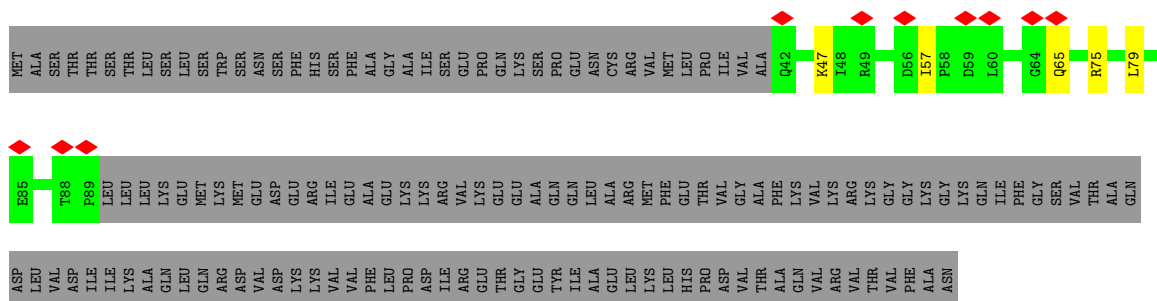
• Molecule 14: plastid ribosomal protein uL5c



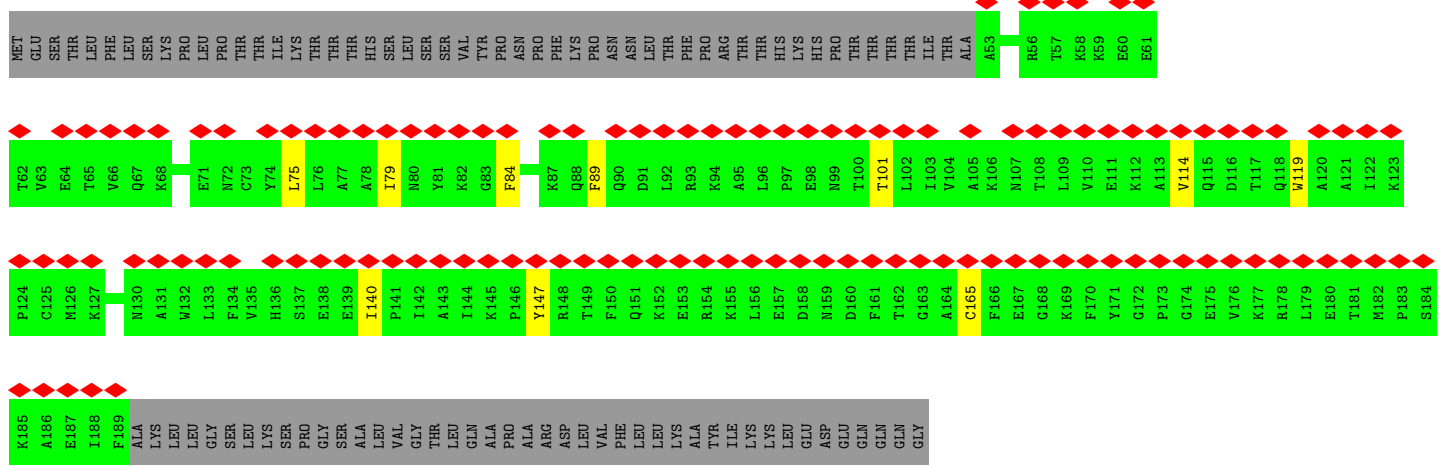
• Molecule 15: plastid ribosomal protein uL6c



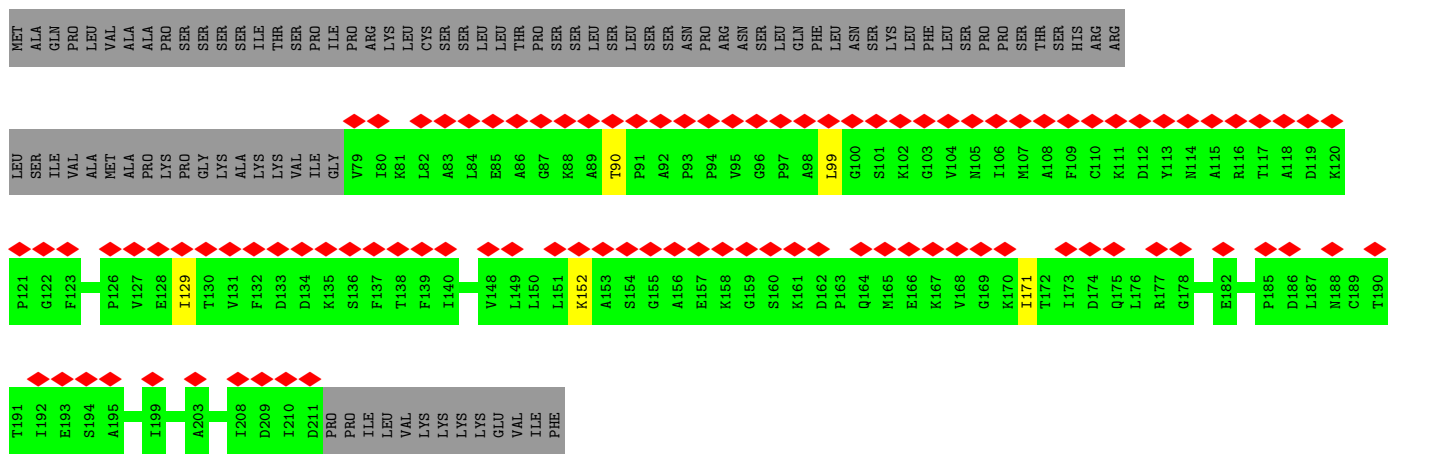
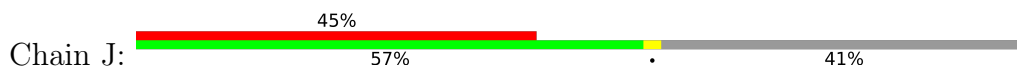
• Molecule 16: plastid ribosomal protein bL9c



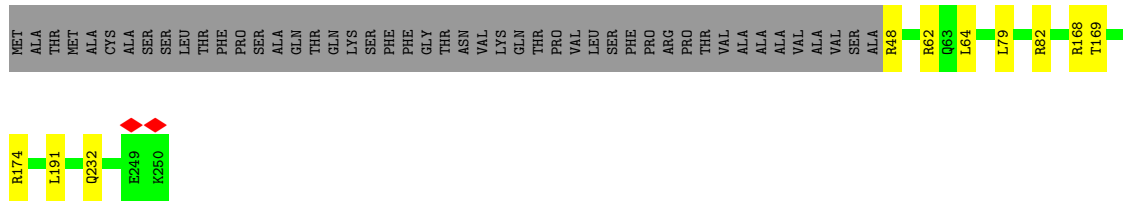
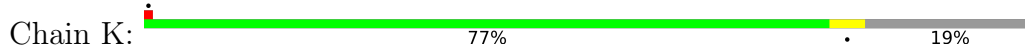
• Molecule 17: plastid ribosomal protein uL10c



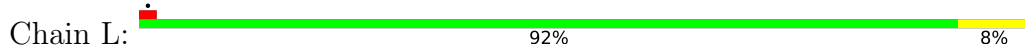
• Molecule 18: 50S ribosomal protein L11, chloroplastic

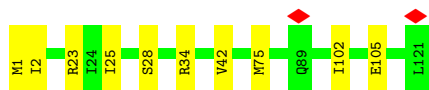


• Molecule 19: 50S ribosomal protein L13, chloroplastic

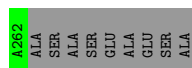
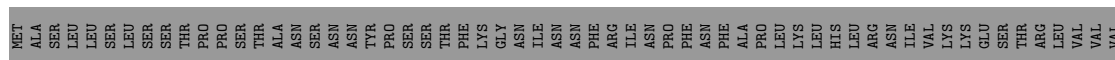


• Molecule 20: 50S ribosomal protein L14, chloroplastic

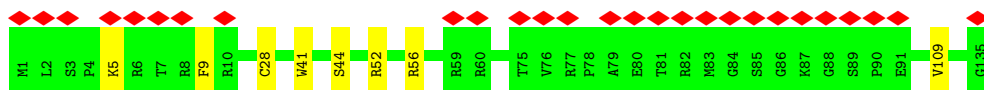




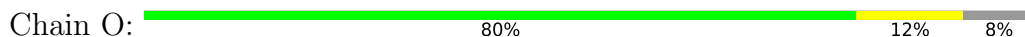
• Molecule 21: plastid ribosomal protein uL15c



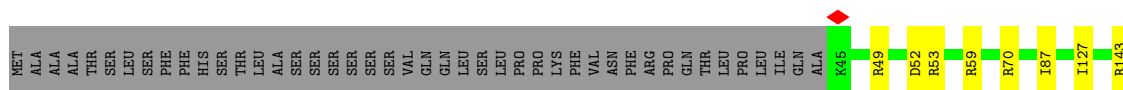
• Molecule 22: 50S ribosomal protein L16, chloroplastic



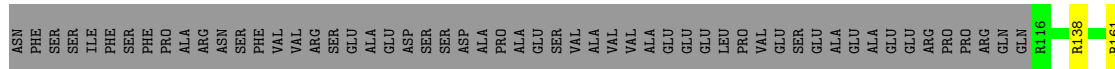
• Molecule 23: plastid ribosomal protein uL14c



• Molecule 24: plastid ribosomal protein uL18c

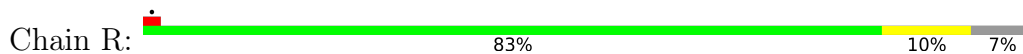


• Molecule 25: 50S ribosomal protein L19, chloroplastic





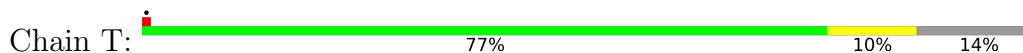
- Molecule 26: 50S ribosomal protein L20, chloroplastic



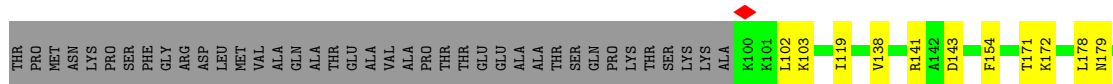
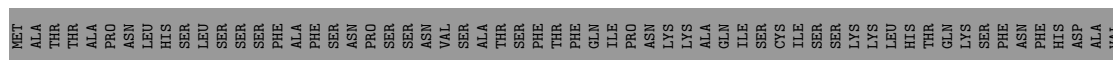
- Molecule 27: 50S ribosomal protein L21, chloroplastic



- Molecule 28: 50S ribosomal protein L22, chloroplastic



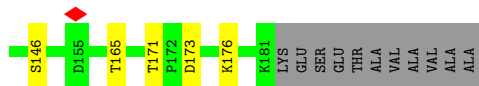
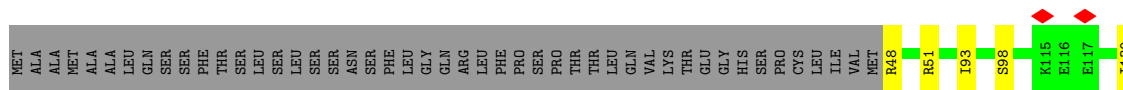
- Molecule 29: 50S ribosomal protein L23, chloroplastic



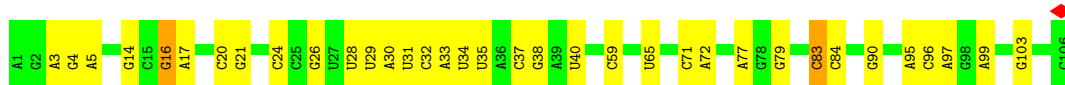
- Molecule 30: plastid ribosomal protein uL24c



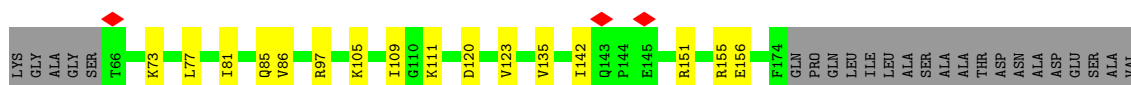
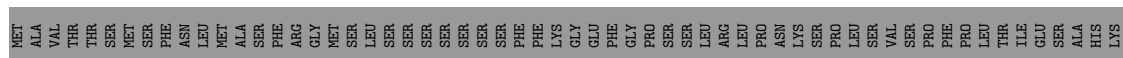




• Molecule 31: 4.5S ribosomal RNA

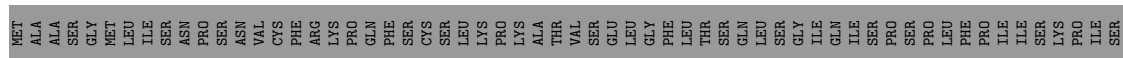


• Molecule 32: plastid ribosomal protein bL27c

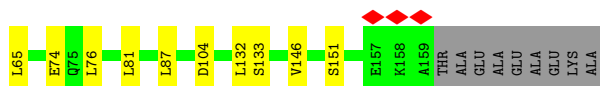
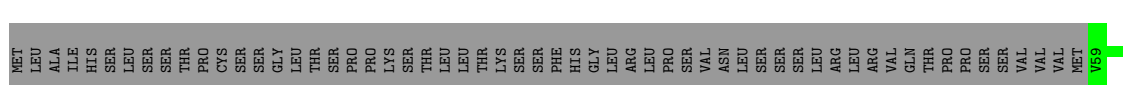


CYS

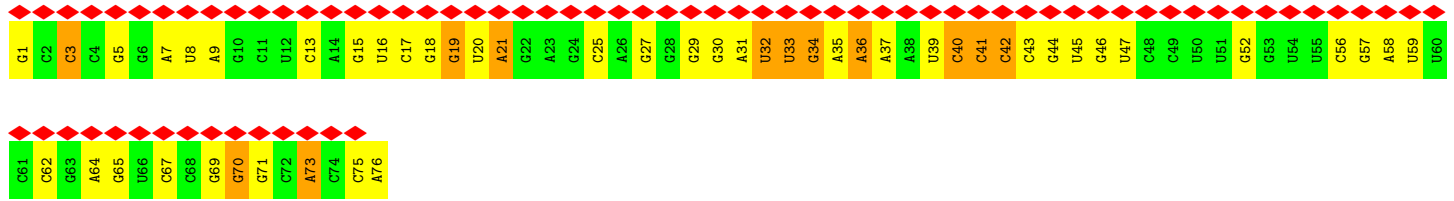
• Molecule 33: plastid ribosomal protein bL28c



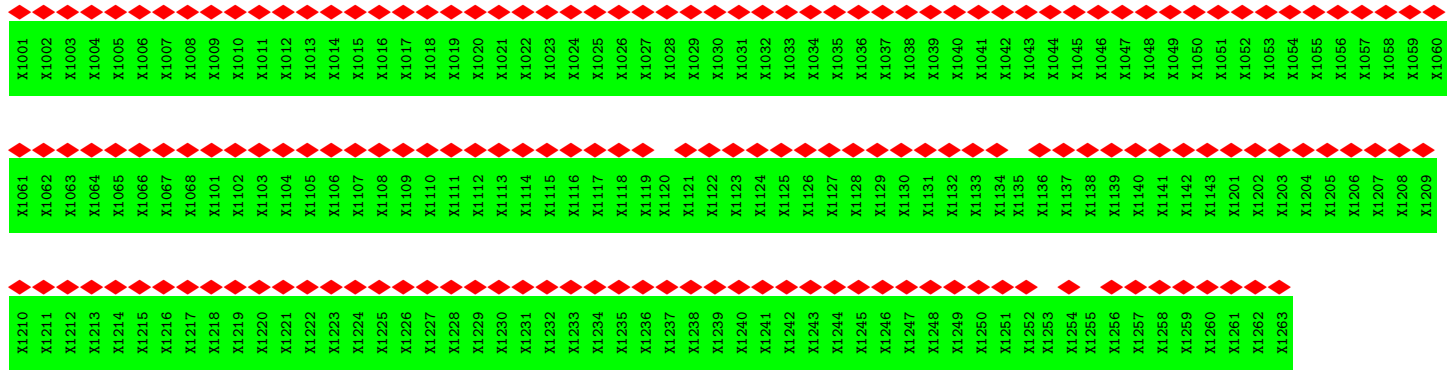
• Molecule 34: plastid ribosomal protein uL29c



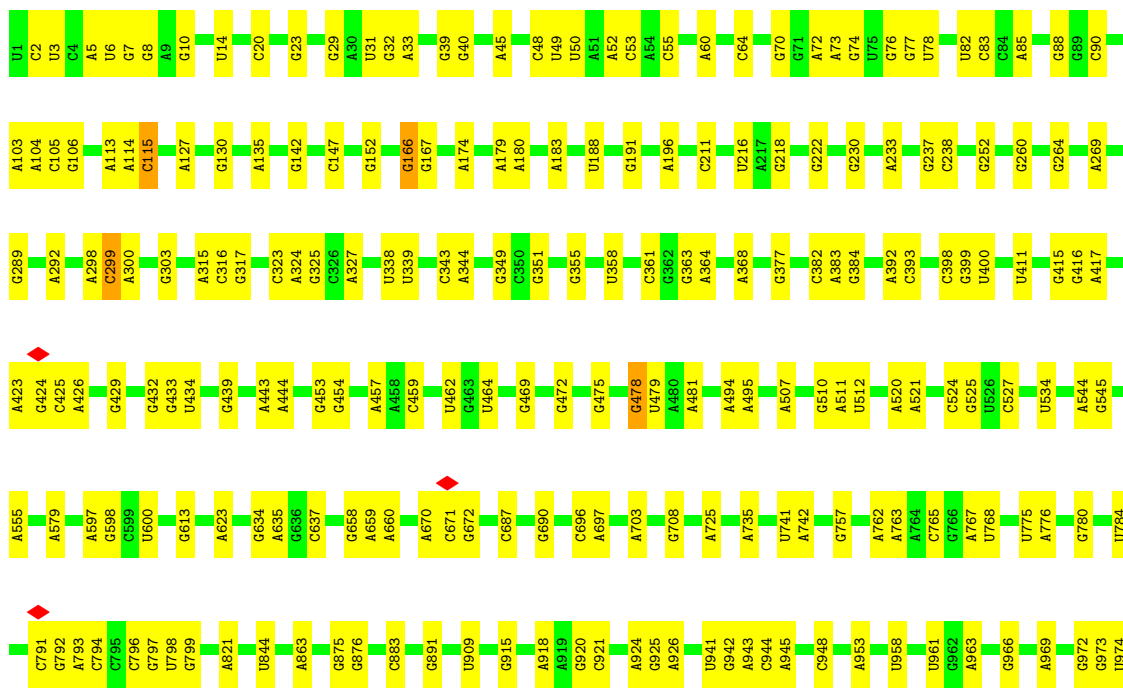
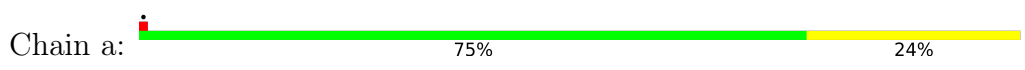
• Molecule 35: tRNA-Phe

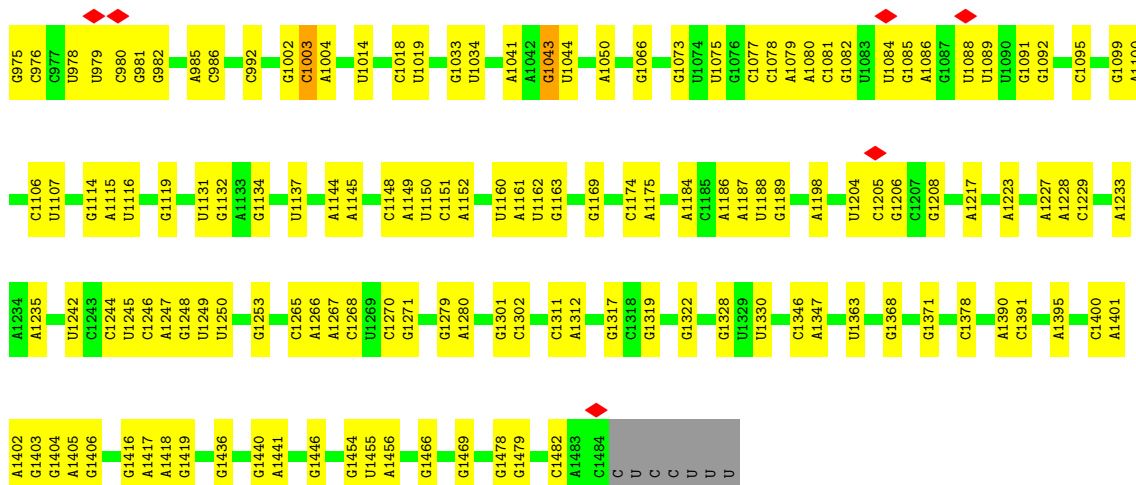


• Molecule 36: plastid ribosomal protein bS1c

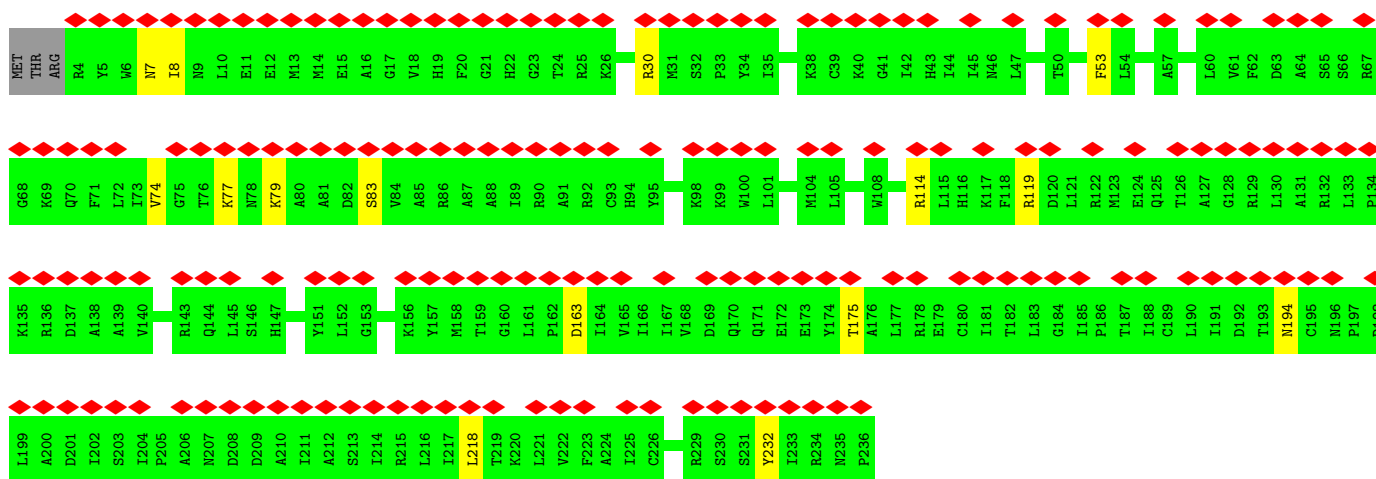
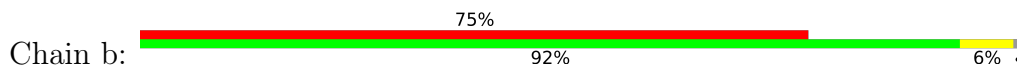


• Molecule 37: 16S ribosomal RNA

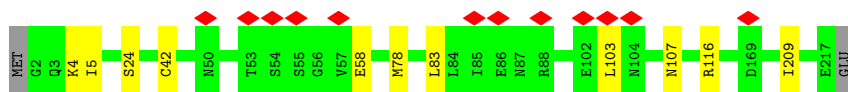
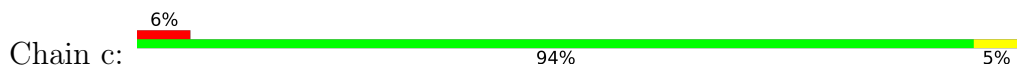




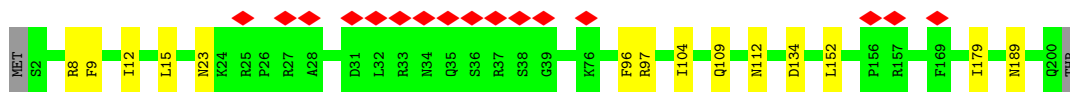
• Molecule 38: 30S ribosomal protein S2, chloroplastic



• Molecule 39: 30S ribosomal protein S3, chloroplastic



• Molecule 40: 30S ribosomal protein S4, chloroplastic

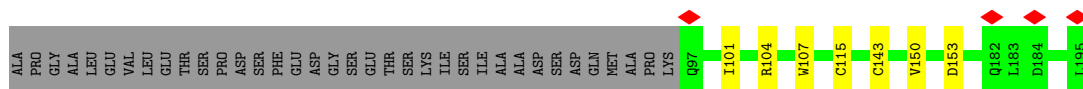


• Molecule 41: 30S ribosomal protein S5, chloroplastic

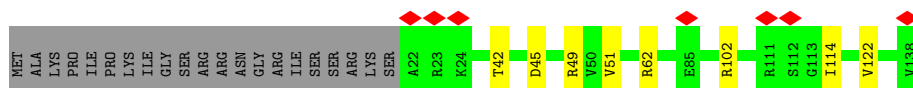
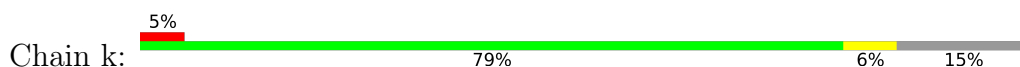




- Molecule 46: plastid ribosomal protein uS10c



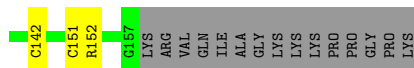
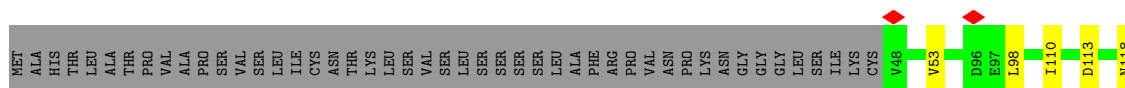
- Molecule 47: 30S ribosomal protein S11, chloroplastic



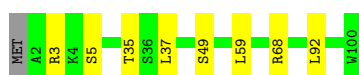
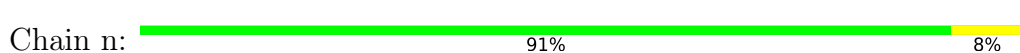
- Molecule 48: 30S ribosomal protein S12, chloroplastic



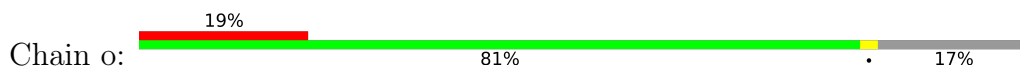
- Molecule 49: plastid ribosomal protein uS13c

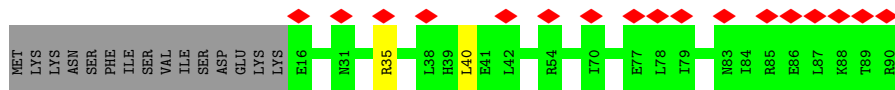


- Molecule 50: 30S ribosomal protein S14, chloroplastic

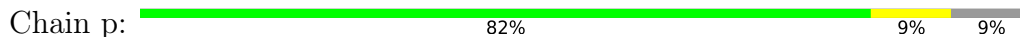


- Molecule 51: 30S ribosomal protein S15, chloroplastic

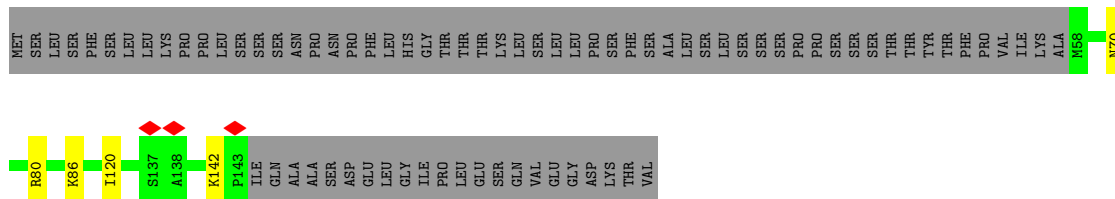




• Molecule 52: 30S ribosomal protein S16, chloroplactic



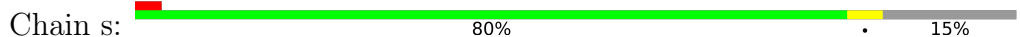
• Molecule 53: plastid ribosomal protein uS17c



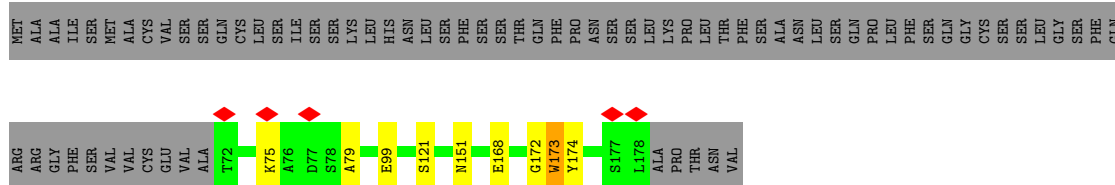
• Molecule 54: 30S ribosomal protein S18, chloroplactic



• Molecule 55: 30S ribosomal protein S19 alpha, chloroplactic



• Molecule 56: plastid ribosomal protein bS20c



• Molecule 57: plastid ribosomal protein bS21c





ASP  
PRO  
SER  
GLN  
LYS  
GLU  
ASP

- Molecule 61: Ribosome-binding factor PSRP1, chloroplastic



MET  
ALA  
THR  
LEU  
CYS  
THR  
SER  
ALA  
ILE  
ASN  
MET  
ASN  
PRO  
ASN  
LEU  
THR  
ASN  
SER  
LEU  
SER  
ASN  
SER  
ILE  
ASN  
LEU  
SER  
THR  
PRO  
THR  
ASN  
LEU  
SER  
PHE  
THR  
ASN  
CYS  
SER  
LEU  
GLY  
LEU  
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LYS  
SER  
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GLN  
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SER  
ARG  
ASN  
LYS

PRO  
ASN  
VAL  
VAL  
CYS  
MET  
SER  
W66  
D69  
G70  
R82  
N83  
R91  
R119  
D122  
L123  
R140  
R145  
H181  
M182  
K183  
GLY  
PHE  
ASN  
ARG  
SER  
LYS  
VAL  
ARG  
ASP  
PRO  
GLU  
PRO  
VAL  
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THR  
ARG  
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ALA  
PRO  
ALA  
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TYR  
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ASN  
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ASP  
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ASP  
PHE  
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PHE  
ARG  
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GLU  
GLU  
THR  
GLY  
ASP  
ILE  
ASN  
ILE  
LEU  
TYR  
LYS  
ARG  
LYS  
GLU  
GLY  
GLY  
TYR  
ALA  
GLY

LEU  
ILE  
PRO  
LYS  
ASP  
GLY  
LYS  
THR  
GLU  
LYS  
LEU  
GLU  
SER  
LEU  
PRO  
VAL  
GLN  
THR  
ASP  
LYS  
GLN  
PRO  
SER  
PHE  
ALA  
GLU



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	140583	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 ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.481	Depositor
Minimum map value	-0.179	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.06	Depositor
Map size ( $\text{\AA}$ )	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.39, 1.39, 1.39	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.65	0/548	0.88	1/737 (0.1%)
2	1	0.61	0/405	0.71	0/537
3	2	0.47	0/497	0.74	1/664 (0.2%)
4	3	0.55	0/470	0.71	0/619
5	4	0.57	0/594	0.67	0/784
6	5	0.38	0/307	0.54	0/403
7	6	0.46	0/425	0.77	0/551
8	7	0.43	0/382	0.57	0/520
9	A	0.82	39/67297 (0.1%)	1.21	253/104984 (0.2%)
10	B	0.49	0/2890	1.01	3/4503 (0.1%)
11	C	0.49	0/1986	0.69	2/2666 (0.1%)
12	D	0.54	0/1713	0.70	0/2291
13	E	0.54	0/1707	0.77	1/2298 (0.0%)
14	F	0.39	0/1475	0.60	1/1990 (0.1%)
15	G	0.39	0/1412	0.57	0/1898
16	H	0.41	0/386	0.59	0/514
17	I	0.54	0/1129	0.56	0/1521
18	J	0.56	0/992	0.58	0/1343
19	K	0.50	0/1688	0.63	0/2279
20	L	0.48	0/951	0.63	0/1282
21	M	0.50	0/1430	0.69	0/1896
22	N	0.45	0/1097	0.61	0/1471
23	O	0.55	0/959	0.72	0/1280
24	P	0.40	0/978	0.57	0/1311
25	Q	0.57	0/967	0.69	0/1299
26	R	0.60	0/1046	0.72	0/1395
27	S	0.48	0/1339	0.69	3/1826 (0.2%)
28	T	0.50	0/1420	0.63	0/1900
29	U	0.50	0/787	0.69	0/1056
30	V	0.42	0/1093	0.61	0/1457
31	W	0.74	0/2551	1.18	4/3977 (0.1%)
32	X	0.45	0/905	0.60	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Y	0.46	0/644	0.62	0/856
34	Z	0.41	0/854	0.56	0/1131
35	z	1.35	7/1813 (0.4%)	1.93	81/2823 (2.9%)
37	a	0.57	0/35687	1.00	35/55680 (0.1%)
38	b	0.40	0/1878	0.55	0/2538
39	c	0.39	0/1763	0.58	0/2370
40	d	0.37	0/1661	0.57	0/2230
41	e	0.44	0/1345	0.61	0/1817
42	f	0.34	0/929	0.54	0/1255
43	g	0.37	0/1226	0.53	0/1641
44	h	0.37	0/1094	0.57	0/1467
45	i	0.37	0/1138	0.60	0/1526
46	j	0.42	0/822	0.58	0/1111
47	k	0.35	0/896	0.59	0/1206
48	l	0.45	0/975	0.60	0/1312
49	m	0.37	0/912	0.61	0/1219
50	n	0.39	0/836	0.55	0/1116
51	o	0.38	0/642	0.49	0/852
52	p	0.39	0/674	0.62	0/902
53	q	0.37	0/707	0.55	0/949
54	r	0.37	0/494	0.56	0/660
55	s	0.40	0/646	0.61	0/870
56	t	0.41	0/862	0.63	1/1151 (0.1%)
57	u	0.34	0/572	0.47	0/754
58	v	0.58	0/621	0.49	0/833
59	w	0.58	0/707	0.55	0/962
60	x	0.46	0/317	0.62	0/418
61	y	0.40	0/930	0.71	2/1243 (0.2%)
All	All	0.67	46/163471 (0.0%)	1.03	388/243348 (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
13	E	0	1
21	M	0	1
38	b	0	1
41	e	0	1
56	t	0	2
All	All	0	6

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	z	1	G	OP3-P	-10.61	1.48	1.61
9	A	1272	A	N3-C4	-8.41	1.29	1.34
9	A	1272	A	N9-C4	-7.74	1.33	1.37
9	A	727	A	N3-C4	7.72	1.39	1.34
9	A	830	A	N3-C4	-7.35	1.30	1.34

The worst 5 of 388 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	727	A	N1-C2-N3	-17.96	120.32	129.30
35	z	34	G	N1-C2-N2	-13.39	104.15	116.20
9	A	1272	A	C2-N3-C4	-12.32	104.44	110.60
61	y	140	ARG	NE-CZ-NH2	-11.37	114.62	120.30
9	A	727	A	C6-N1-C2	10.68	125.01	118.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	E	134	ARG	Peptide
21	M	104	ALA	Peptide
38	b	74	VAL	Peptide
41	e	144	LYS	Peptide
56	t	75	LYS	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	
1	0	64/130 (49%)	56 (88%)	5 (8%)	3 (5%)	2	15
2	1	46/57 (81%)	45 (98%)	1 (2%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	7	30
8	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
11	C	251/272 (92%)	235 (94%)	15 (6%)	1 (0%)	34	67
12	D	219/305 (72%)	206 (94%)	12 (6%)	1 (0%)	29	61
13	E	210/293 (72%)	196 (93%)	14 (7%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	165 (94%)	11 (6%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100
19	K	201/250 (80%)	193 (96%)	8 (4%)	0	100	100
20	L	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
21	M	183/271 (68%)	168 (92%)	13 (7%)	2 (1%)	14	44
22	N	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
23	O	114/126 (90%)	108 (95%)	6 (5%)	0	100	100
24	P	120/166 (72%)	113 (94%)	7 (6%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	158 (94%)	8 (5%)	2 (1%)	13	41
28	T	170/199 (85%)	162 (95%)	7 (4%)	1 (1%)	25	57
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	123 (93%)	9 (7%)	0	100	100
32	X	107/194 (55%)	96 (90%)	11 (10%)	0	100	100
33	Y	75/148 (51%)	73 (97%)	2 (3%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	15	46
38	b	231/236 (98%)	221 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	c	214/218 (98%)	201 (94%)	13 (6%)	0	100	100
40	d	197/201 (98%)	186 (94%)	11 (6%)	0	100	100
41	e	185/308 (60%)	182 (98%)	3 (2%)	0	100	100
42	f	111/211 (53%)	106 (96%)	4 (4%)	1 (1%)	17	49
43	g	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
44	h	131/134 (98%)	127 (97%)	2 (2%)	2 (2%)	10	36
45	i	142/208 (68%)	136 (96%)	6 (4%)	0	100	100
46	j	97/195 (50%)	93 (96%)	3 (3%)	1 (1%)	15	46
47	k	115/138 (83%)	108 (94%)	7 (6%)	0	100	100
48	l	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
49	m	108/172 (63%)	101 (94%)	6 (6%)	1 (1%)	17	49
50	n	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
51	o	73/90 (81%)	72 (99%)	1 (1%)	0	100	100
52	p	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
53	q	84/165 (51%)	78 (93%)	6 (7%)	0	100	100
54	r	58/101 (57%)	55 (95%)	3 (5%)	0	100	100
55	s	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
56	t	105/183 (57%)	100 (95%)	3 (3%)	2 (2%)	8	31
57	u	63/180 (35%)	62 (98%)	1 (2%)	0	100	100
58	v	78/260 (30%)	76 (97%)	2 (3%)	0	100	100
59	w	80/179 (45%)	78 (98%)	2 (2%)	0	100	100
60	x	38/101 (38%)	37 (97%)	1 (3%)	0	100	100
61	y	114/302 (38%)	106 (93%)	8 (7%)	0	100	100
All	All	6476/9784 (66%)	6138 (95%)	319 (5%)	19 (0%)	44	72

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	92	ASP
27	S	78	PRO
49	m	53	VAL
56	t	174	TYR
11	C	232	GLU

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	57/117 (49%)	54 (95%)	3 (5%)	22	52
2	1	41/50 (82%)	37 (90%)	4 (10%)	8	28
3	2	56/60 (93%)	50 (89%)	6 (11%)	6	24
4	3	50/125 (40%)	42 (84%)	8 (16%)	2	10
5	4	62/140 (44%)	52 (84%)	10 (16%)	2	10
6	5	34/34 (100%)	30 (88%)	4 (12%)	5	19
7	6	46/124 (37%)	42 (91%)	4 (9%)	10	34
8	7	40/96 (42%)	33 (82%)	7 (18%)	2	7
11	C	201/217 (93%)	185 (92%)	16 (8%)	12	38
12	D	182/259 (70%)	164 (90%)	18 (10%)	8	27
13	E	179/255 (70%)	158 (88%)	21 (12%)	5	20
14	F	152/214 (71%)	140 (92%)	12 (8%)	12	39
15	G	151/190 (80%)	137 (91%)	14 (9%)	9	31
16	H	42/170 (25%)	37 (88%)	5 (12%)	5	19
17	I	119/204 (58%)	109 (92%)	10 (8%)	11	36
18	J	106/189 (56%)	101 (95%)	5 (5%)	26	57
19	K	176/213 (83%)	166 (94%)	10 (6%)	20	50
20	L	101/101 (100%)	91 (90%)	10 (10%)	8	27
21	M	141/215 (66%)	123 (87%)	18 (13%)	4	16
22	N	108/108 (100%)	100 (93%)	8 (7%)	13	42
23	O	96/103 (93%)	81 (84%)	15 (16%)	2	11
24	P	100/139 (72%)	90 (90%)	10 (10%)	7	27
25	Q	104/207 (50%)	94 (90%)	10 (10%)	8	29
26	R	106/115 (92%)	93 (88%)	13 (12%)	4	17
27	S	137/223 (61%)	131 (96%)	6 (4%)	28	58
28	T	152/176 (86%)	134 (88%)	18 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	U	85/171 (50%)	74 (87%)	11 (13%)	4	16
30	V	121/169 (72%)	111 (92%)	10 (8%)	11	36
32	X	92/163 (56%)	76 (83%)	16 (17%)	2	7
33	Y	67/130 (52%)	59 (88%)	8 (12%)	5	19
34	Z	93/153 (61%)	84 (90%)	9 (10%)	8	28
38	b	198/201 (98%)	184 (93%)	14 (7%)	14	44
39	c	186/188 (99%)	175 (94%)	11 (6%)	19	49
40	d	178/180 (99%)	164 (92%)	14 (8%)	12	39
41	e	121/255 (48%)	113 (93%)	8 (7%)	16	46
42	f	100/186 (54%)	94 (94%)	6 (6%)	19	49
43	g	125/126 (99%)	118 (94%)	7 (6%)	21	51
44	h	116/117 (99%)	108 (93%)	8 (7%)	15	45
45	i	114/169 (68%)	99 (87%)	15 (13%)	4	15
46	j	91/173 (53%)	85 (93%)	6 (7%)	16	46
47	k	91/109 (84%)	83 (91%)	8 (9%)	10	33
48	l	105/106 (99%)	98 (93%)	7 (7%)	16	46
49	m	99/151 (66%)	92 (93%)	7 (7%)	14	44
50	n	89/90 (99%)	81 (91%)	8 (9%)	9	32
51	o	70/85 (82%)	68 (97%)	2 (3%)	42	69
52	p	71/79 (90%)	63 (89%)	8 (11%)	6	21
53	q	77/149 (52%)	72 (94%)	5 (6%)	17	46
54	r	56/96 (58%)	51 (91%)	5 (9%)	9	33
55	s	68/81 (84%)	64 (94%)	4 (6%)	19	49
56	t	89/156 (57%)	84 (94%)	5 (6%)	21	51
57	u	59/160 (37%)	55 (93%)	4 (7%)	16	45
58	v	67/225 (30%)	67 (100%)	0	100	100
59	w	76/162 (47%)	76 (100%)	0	100	100
60	x	30/85 (35%)	30 (100%)	0	100	100
61	y	104/275 (38%)	99 (95%)	5 (5%)	25	56
All	All	5577/8434 (66%)	5101 (92%)	476 (8%)	14	35

5 of 476 residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
26	R	48	ARG
52	p	28	ARG
32	X	73	LYS
51	o	35	ARG
61	y	122	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
49	m	87	ASN
57	u	140	ASN
50	n	48	GLN
52	p	13	GLN
61	y	89	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	20 (16%)	0
31	W	105/106 (99%)	34 (32%)	1 (0%)
35	z	75/76 (98%)	22 (29%)	0
37	a	1483/1491 (99%)	349 (23%)	0
9	A	2794/2810 (99%)	658 (23%)	8 (0%)
All	All	4577/4604 (99%)	1083 (23%)	9 (0%)

5 of 1083 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	8	G
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	2602	U
31	W	77	A
9	A	795	U
9	A	1520	A

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Mol	Chain	Res	Type
9	A	2035	A

#### 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 monosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

Of 781 ligands modelled in this entry, 781 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	1068:UNK	C	1101:UNK	N	66.30
1	8	1143:UNK	C	1201:UNK	N	11.98

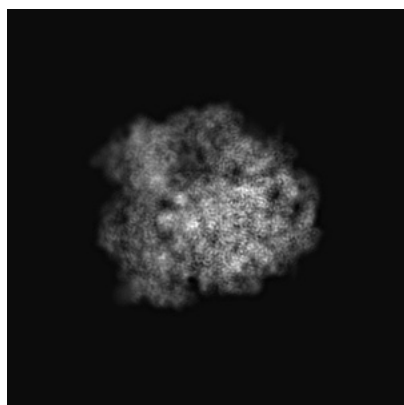
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3533. These allow visual inspection of the internal detail of the map and identification of artifacts.

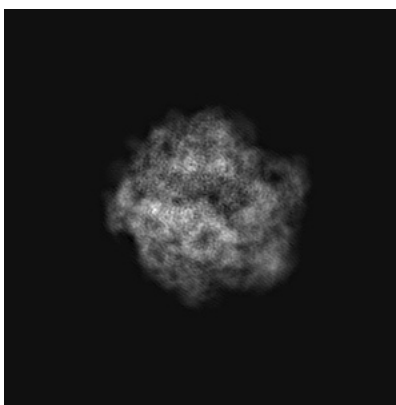
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

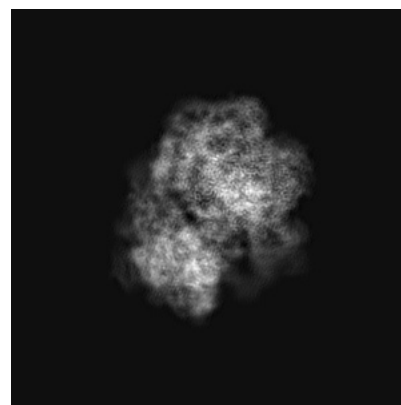
#### 6.1.1 Primary map



X



Y

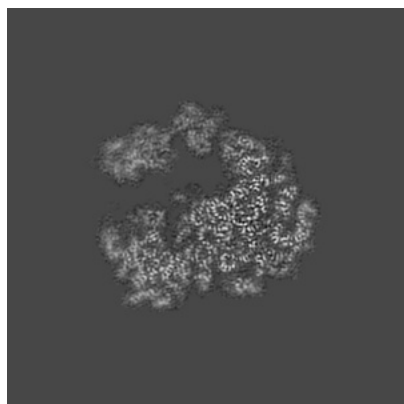


Z

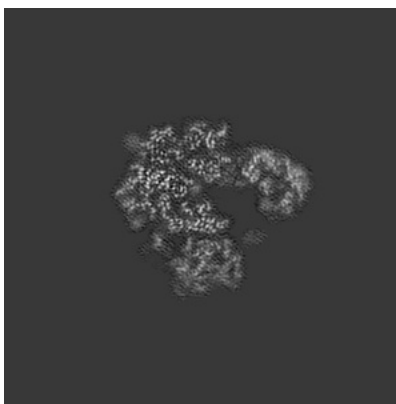
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

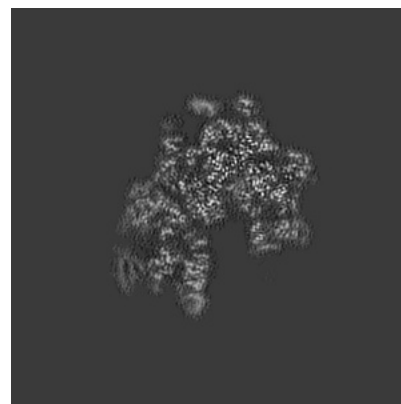
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

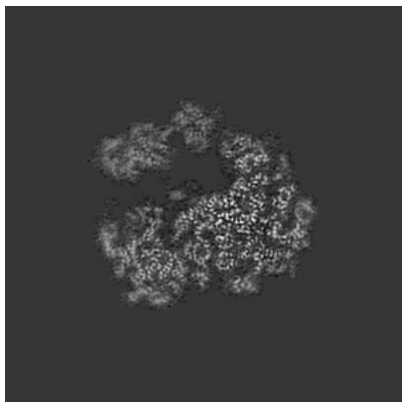


Z Index: 160

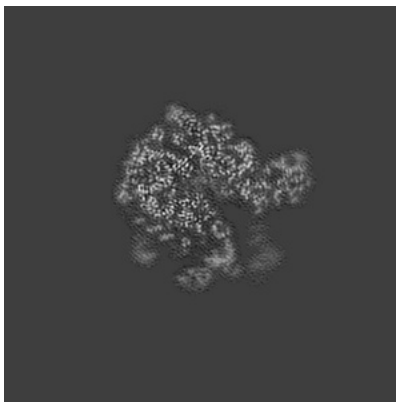
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

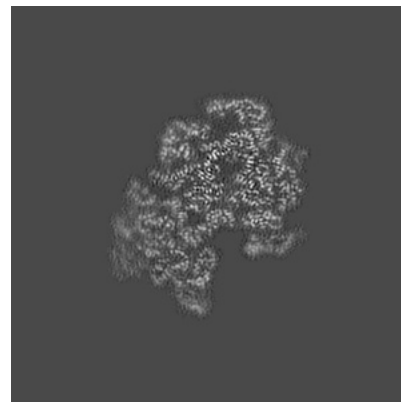
### 6.3.1 Primary map



X Index: 159



Y Index: 173



Z Index: 148

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

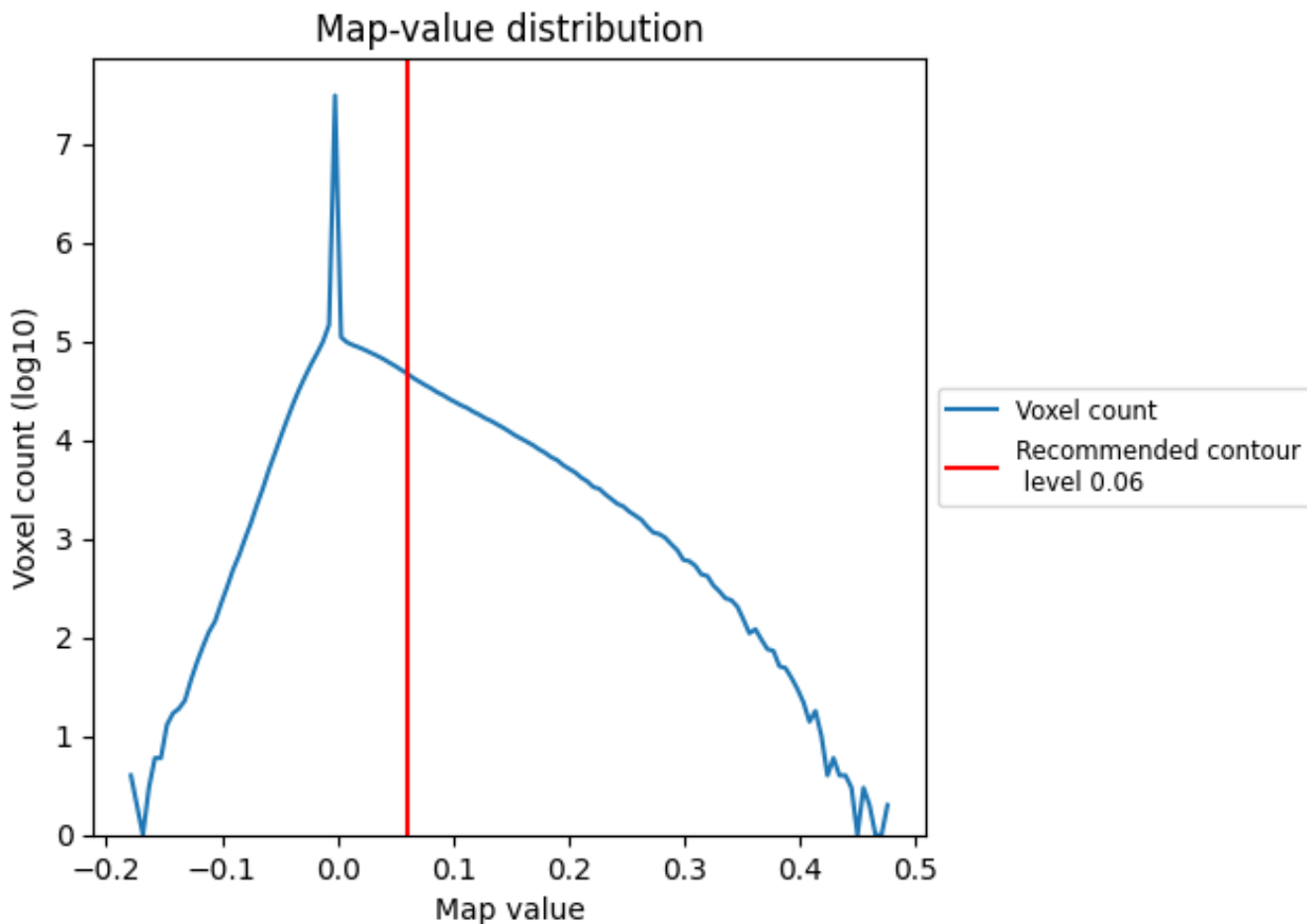
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

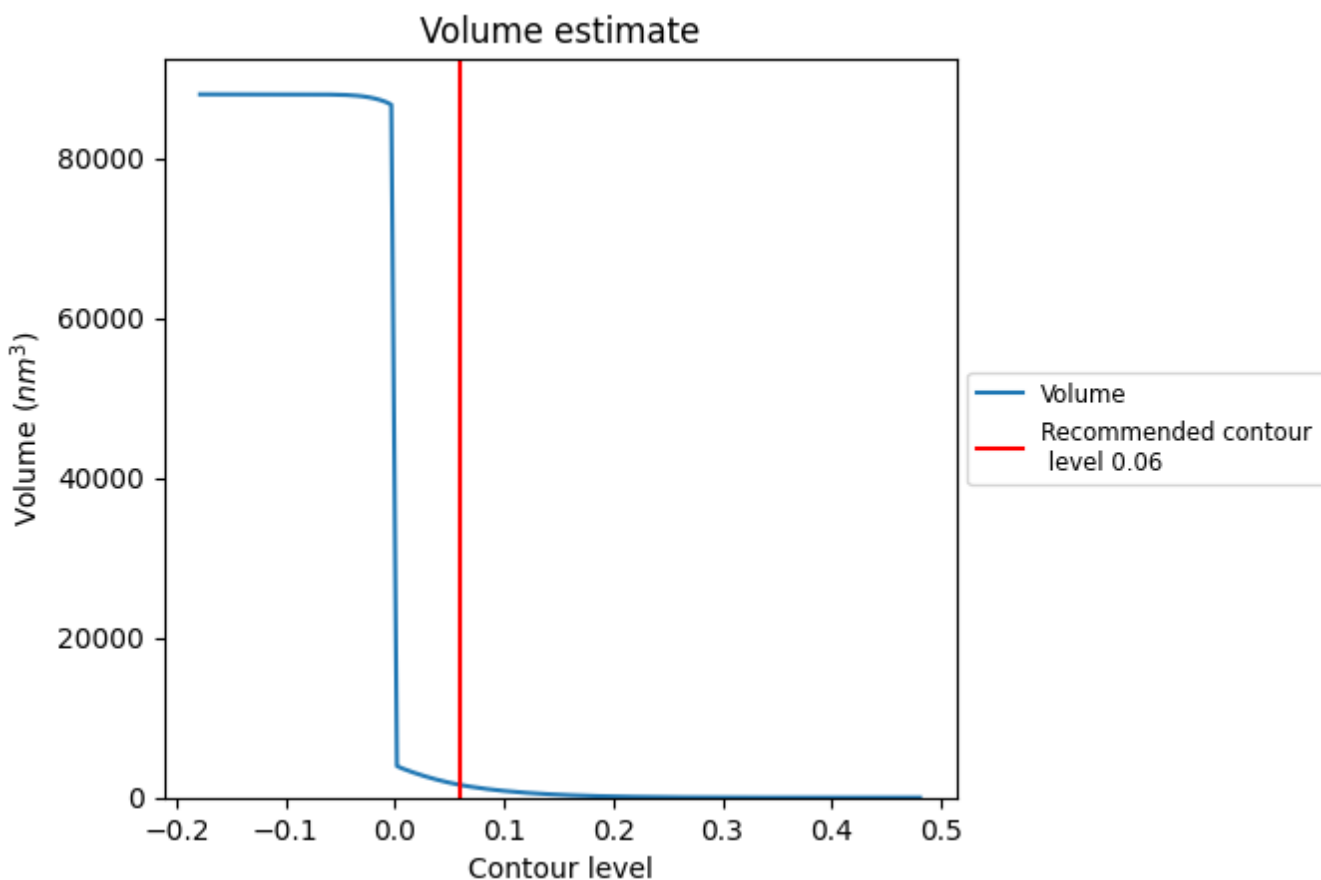
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

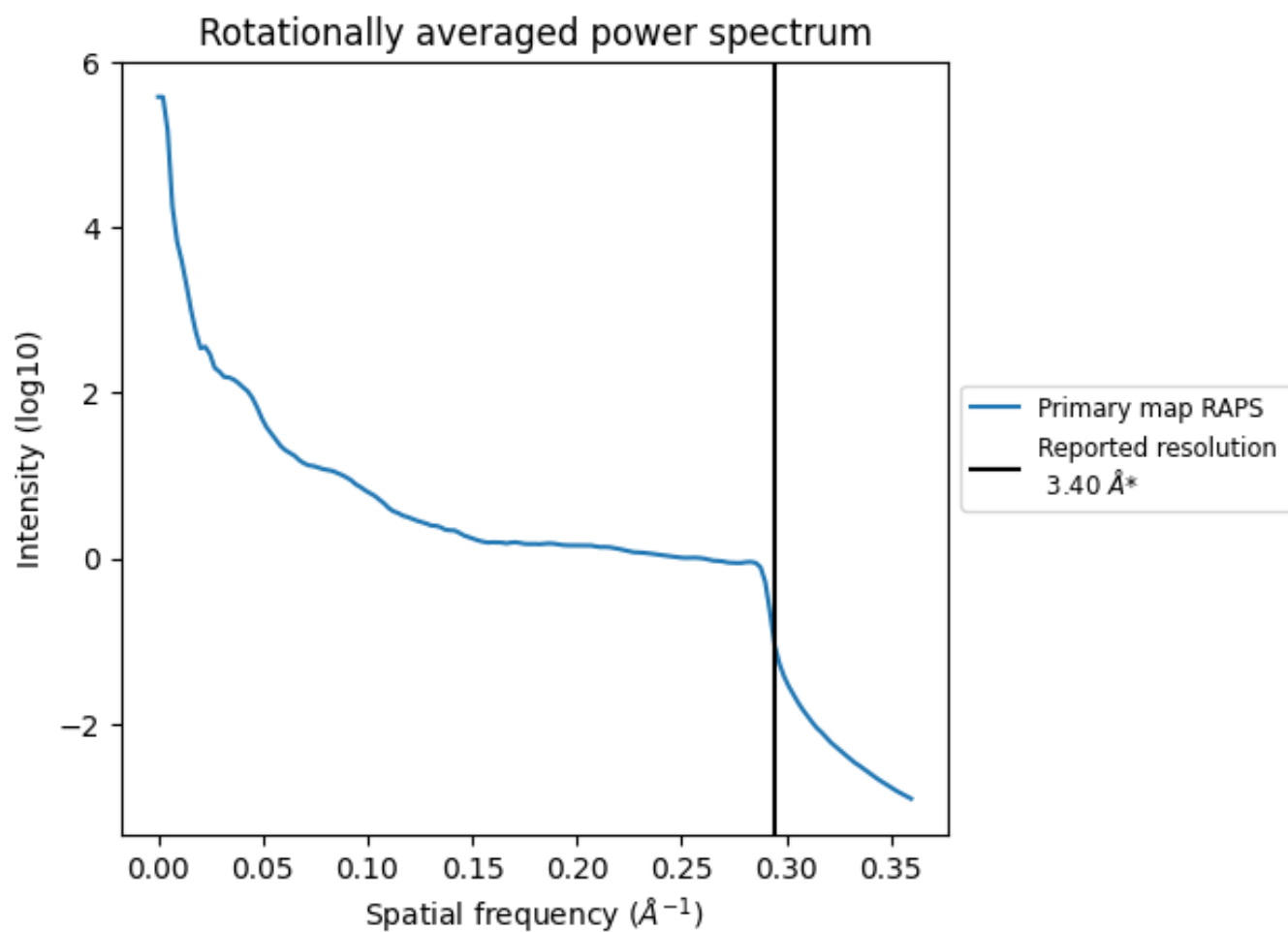
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1578 nm<sup>3</sup>; this corresponds to an approximate mass of 1425 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](#)



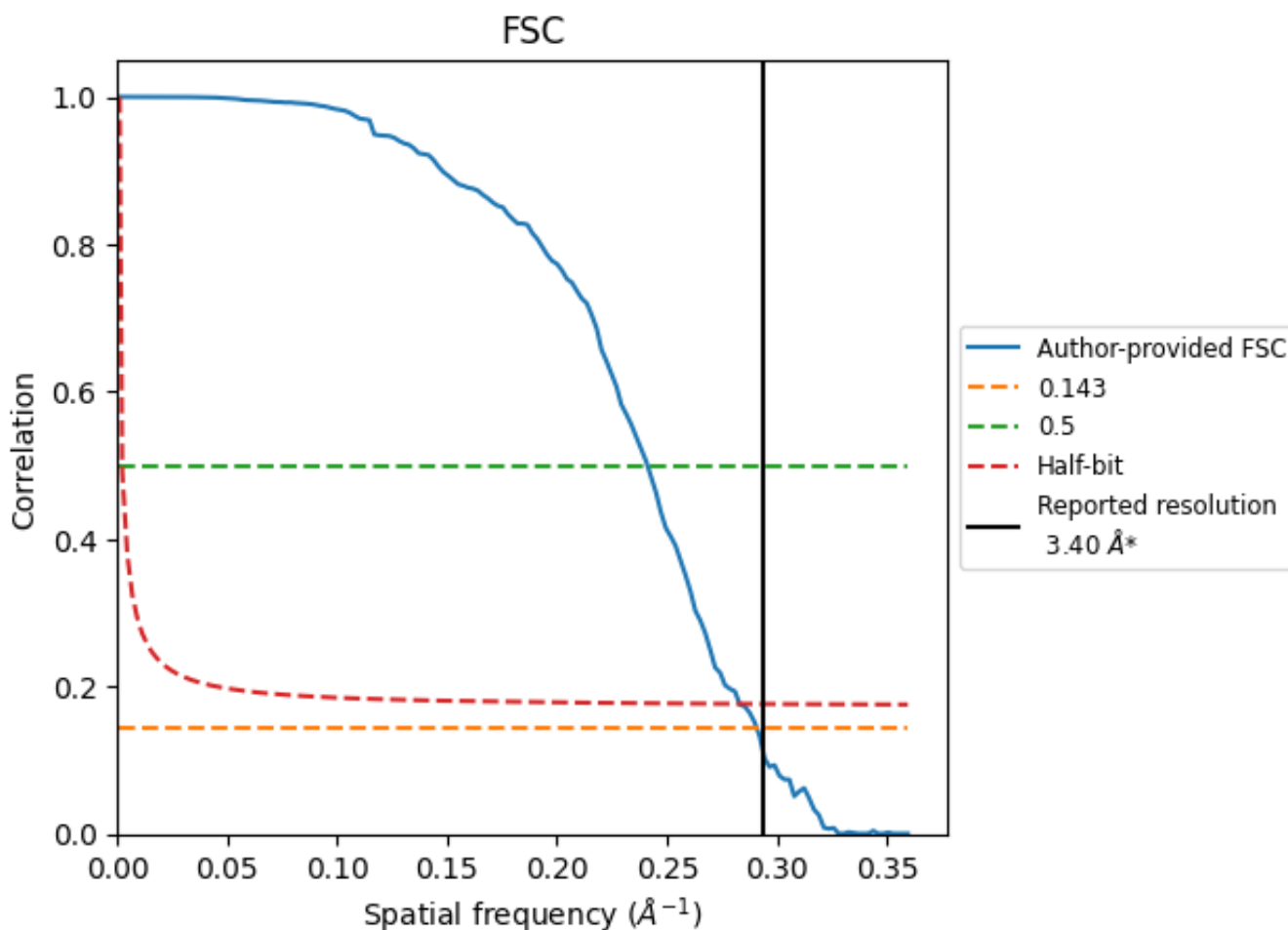
\*Reported resolution corresponds to spatial frequency of  $0.294 \text{\AA}^{-1}$



## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.294 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

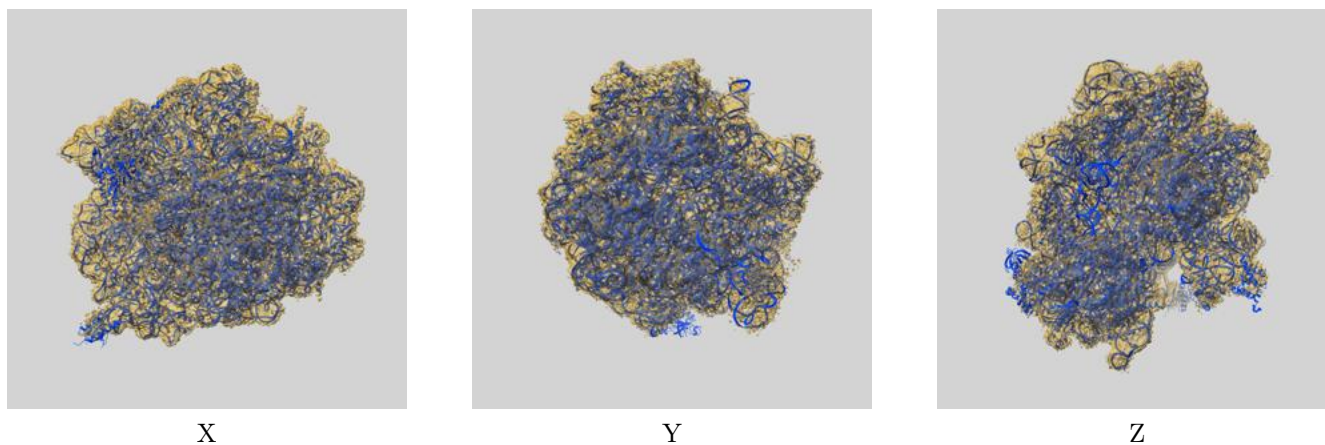
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	4.15	3.53
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

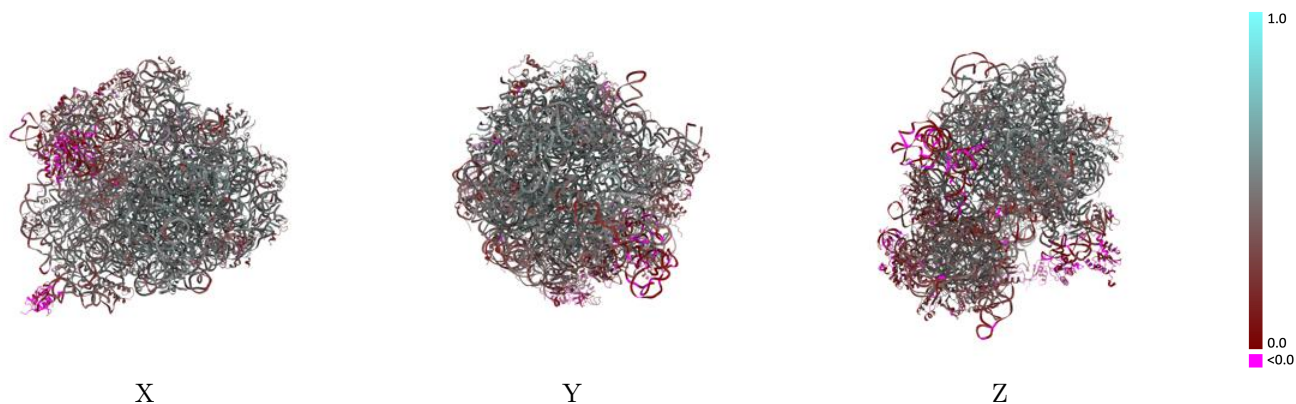
This section contains information regarding the fit between EMDB map EMD-3533 and PDB model 5MMM. Per-residue inclusion information can be found in section 3 on page 17.

### 9.1 Map-model overlay [i](#)



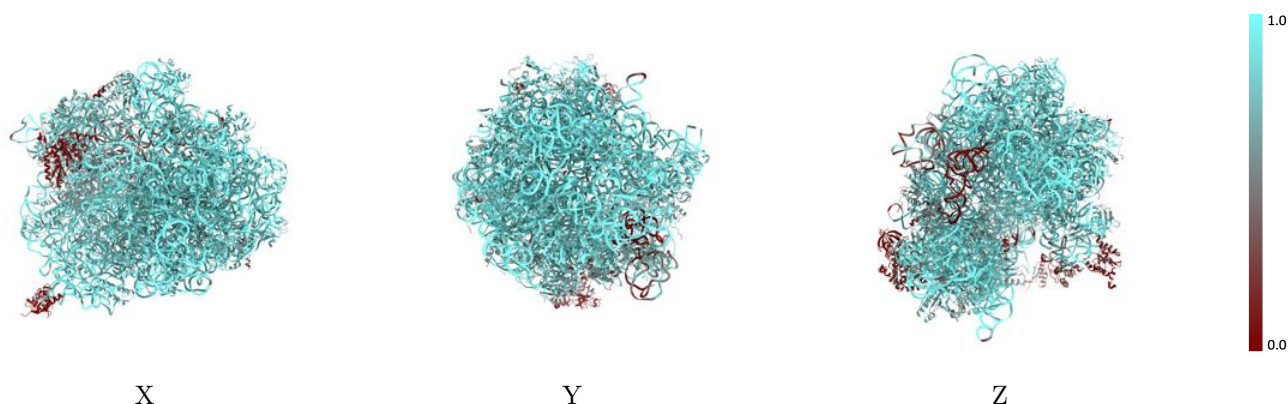
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



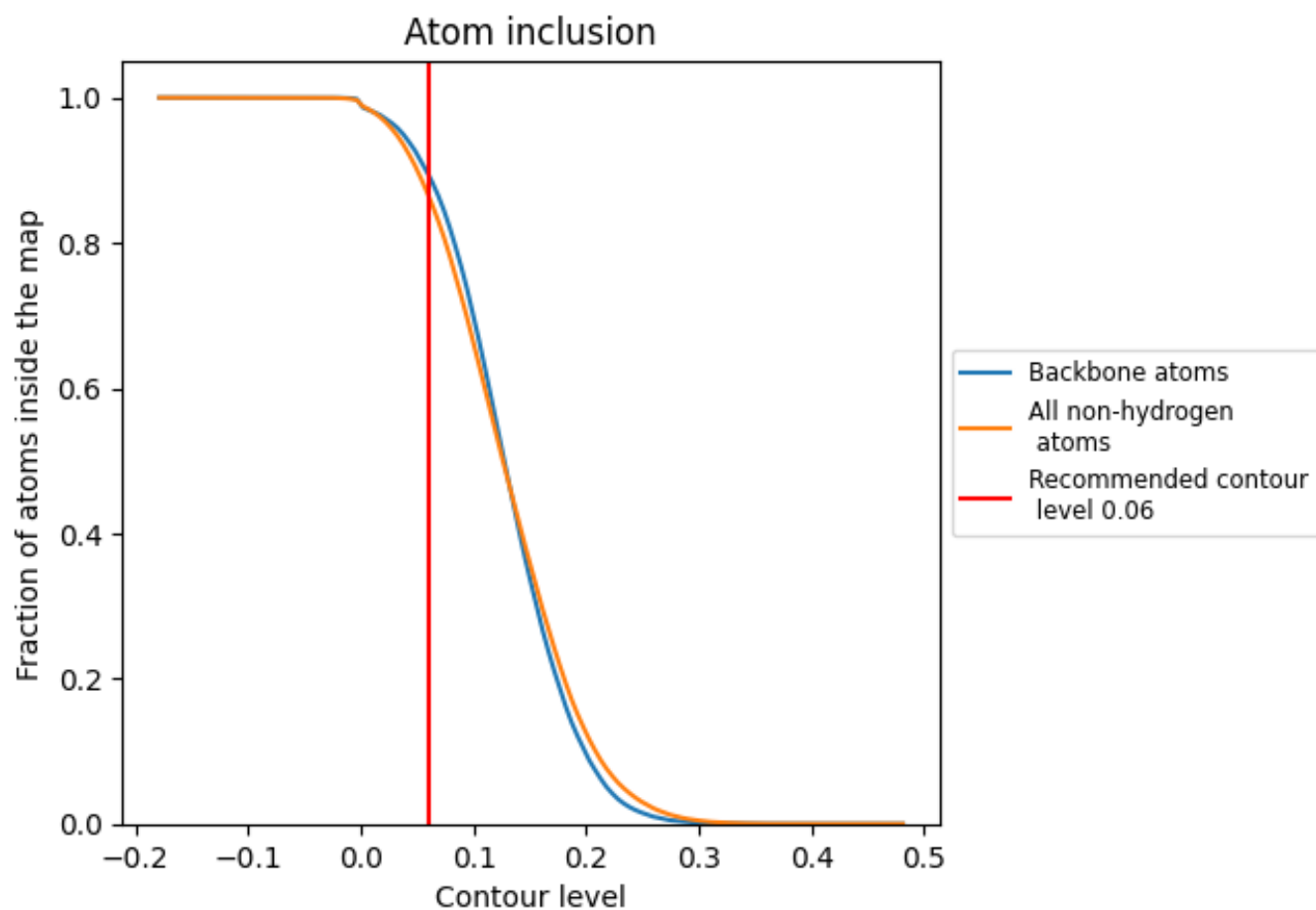
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.06).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary























































The table lists the average atom inclusion at the recommended contour level (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8655	 0.4060
0	 0.5679	 0.1880
1	 0.8880	 0.4900
2	 0.8351	 0.4440
3	 0.8736	 0.5230
4	 0.8820	 0.5190
5	 0.8414	 0.4480
6	 0.7956	 0.4120
7	 0.8939	 0.4790
8	 0.0621	 0.0550
A	 0.9471	 0.4530
B	 0.9781	 0.4150
C	 0.8453	 0.4740
D	 0.8890	 0.4860
E	 0.8676	 0.4720
F	 0.7497	 0.3180
G	 0.7994	 0.3340
H	 0.5703	 0.3640
I	 0.1376	 0.0550
J	 0.2474	 0.0420
K	 0.8777	 0.4710
L	 0.8162	 0.4730
M	 0.8821	 0.4570
N	 0.6394	 0.3880
O	 0.9050	 0.4980
P	 0.8781	 0.4120
Q	 0.8477	 0.4600
R	 0.8988	 0.4970
S	 0.8359	 0.4410
T	 0.8375	 0.4460
U	 0.8200	 0.4390
V	 0.8266	 0.4310
W	 0.9747	 0.4680
X	 0.8789	 0.4610
Y	 0.8553	 0.4770



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Chain	Atom inclusion	Q-score
Z	 0.7993	 0.3890
a	 0.9670	 0.4080
b	 0.2828	 0.1970
c	 0.7353	 0.3250
d	 0.7814	 0.3520
e	 0.7446	 0.3810
f	 0.7001	 0.2920
g	 0.5709	 0.2520
h	 0.7478	 0.3400
i	 0.7888	 0.3030
j	 0.7802	 0.3140
k	 0.7793	 0.3370
l	 0.7976	 0.4510
m	 0.7592	 0.2780
n	 0.8295	 0.3360
o	 0.5635	 0.3050
p	 0.8547	 0.3850
q	 0.8027	 0.3690
r	 0.7611	 0.3150
s	 0.7528	 0.3000
t	 0.8083	 0.3470
u	 0.4496	 0.2220
v	 0.0033	 -0.0100
w	 0.1541	 0.0210
x	 0.8467	 0.3380
y	 0.6372	 0.3190
z	 0.0425	 0.0540