



wwPDB EM Validation Summary Report ⓘ

Jun 22, 2026 – 10:20 PM EDT

PDB ID : 8VFT / pdb_00008vft
EMDB ID : EMD-43189
Title : Translating 80S rabbit ribosome stalled by emetine with eEF2
Authors : Murray, J.; Shao, S.
Deposited on : 2023-12-22
Resolution : 3.30 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:

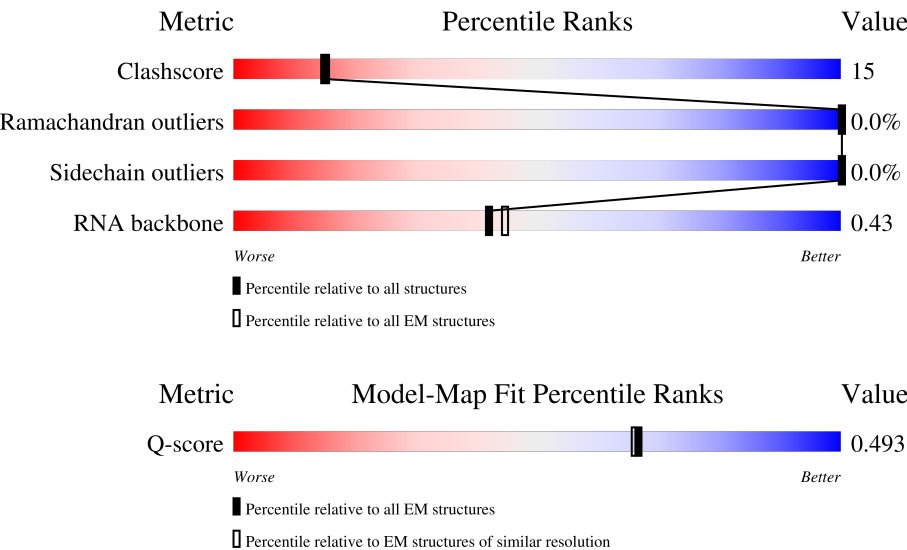
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.30 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	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	67% 30%
2	B	403	10% 64% 33%
3	C	425	7% 56% 29% 15%

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	245	
28	c	115	

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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	93	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	318	
44	t	165	
45	5	3543	
46	7	120	
47	8	156	
48	v	858	
49	9	1869	
50	AA	295	
51	BB	264	
52	CC	293	
53	DD	243	

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Mol	Chain	Length	Quality of chain
54	EE	263	
55	FF	204	
56	GG	249	
57	HH	194	
58	II	208	
59	JJ	194	
60	KK	165	
61	LL	158	
62	MM	132	
63	NN	151	
64	OO	168	
65	PP	145	
66	QQ	146	
67	RR	135	
68	SS	152	
69	TT	145	
70	UU	119	
71	VV	83	
72	WW	130	
73	XX	143	
74	YY	130	
75	ZZ	125	
76	aa	115	
77	bb	84	
78	cc	69	

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Mol	Chain	Length	Quality of chain
79	dd	56	
80	ee	133	
81	ff	156	
82	gg	317	
83	3	75	
84	w	6	
85	2	76	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 220911 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	0
			1891	1185	388	312	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	289	Total	C	N	O	S	0	0
			2361	1495	431	421	14		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	215	Total	C	N	O	S	0	0
			1726	1110	327	286	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1768	1127	341	296	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	208	Total	C	N	O	S	0	0
			1691	1072	327	279	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	167	Total	C	N	O	S	0	0
			1336	846	249	235	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	198	Total	C	N	O	S	0	0
			1621	1046	317	253	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	179	Total	C	N	O	S	0	0
			1502	930	327	236	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3

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Chain	Residue	Modelled	Actual	Comment	Reference
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	98	Total	C	N	O	S	0	0
			800	514	139	145	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	116	Total	C	N	O	S	0	0
			949	606	178	164	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	94	Total	C	N	O	S	0	0
			732	464	130	132	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	100	Total	C	N	O	S	0	0
			833	530	163	138	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	49	Total	C	N	O	S	0	0
			438	280	95	62	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	51	Total	C	N	O	S	0	0
			421	260	89	66	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3529	Total	C	N	O	P	0	0
			75712	33770	13864	24549	3529		

- Molecule 46 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 47 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 48 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	835	Total	C	N	O	S	0	0
			6516	4144	1117	1211	44		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	847	GLY	-	insertion	UNP P55823

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	9	1698	Total	C	N	O	P	0	0
			36291	16217	6509	11868	1697		

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 51 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 53 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 55 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 62 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	PP	117	Total	C	N	O	S	0	0
			975	622	181	165	7		

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 72 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	XX	138	Total	C	N	O	S	0	0
			1069	676	210	180	3		

- Molecule 74 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8
aa	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 77 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 80 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ee	34	Total	C	N	O	S	0	0
			289	175	70	43	1		

- Molecule 81 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	74	Total	C	N	O	P	0	0
			1573	703	279	518	73		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	w	6	Total	C	N	O	P	0	0
			120	54	12	48	6		

- Molecule 85 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	2	74	Total	C	N	O	P	0	0
			1577	705	286	513	73		

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	2	Total 2	Mg 2	0
86	I	2	Total 2	Mg 2	0
86	P	1	Total 1	Mg 1	0
86	V	1	Total 1	Mg 1	0
86	a	1	Total 1	Mg 1	0
86	e	1	Total 1	Mg 1	0
86	f	1	Total 1	Mg 1	0
86	g	1	Total 1	Mg 1	0
86	o	1	Total 1	Mg 1	0
86	5	198	Total 198	Mg 198	0
86	7	5	Total 5	Mg 5	0
86	8	1	Total 1	Mg 1	0
86	9	56	Total 56	Mg 56	0
86	QQ	1	Total 1	Mg 1	0
86	TT	1	Total 1	Mg 1	0
86	aa	1	Total 1	Mg 1	0
86	w	1	Total 1	Mg 1	0
86	2	1	Total 1	Mg 1	0

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

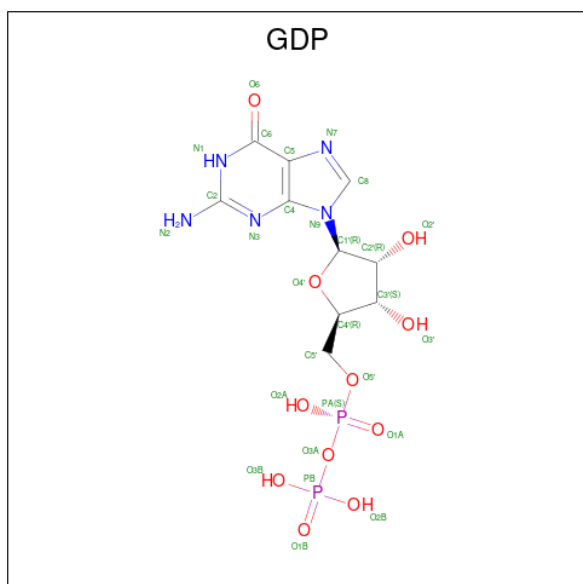
Mol	Chain	Residues	Atoms		AltConf
87	g	1	Total 1	Zn 1	0
87	j	1	Total 1	Zn 1	0

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Mol	Chain	Residues	Atoms		AltConf
87	m	1	Total	Zn	0
			1	1	
87	o	1	Total	Zn	0
			1	1	
87	p	1	Total	Zn	0
			1	1	
87	aa	1	Total	Zn	0
			1	1	
87	dd	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
88	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

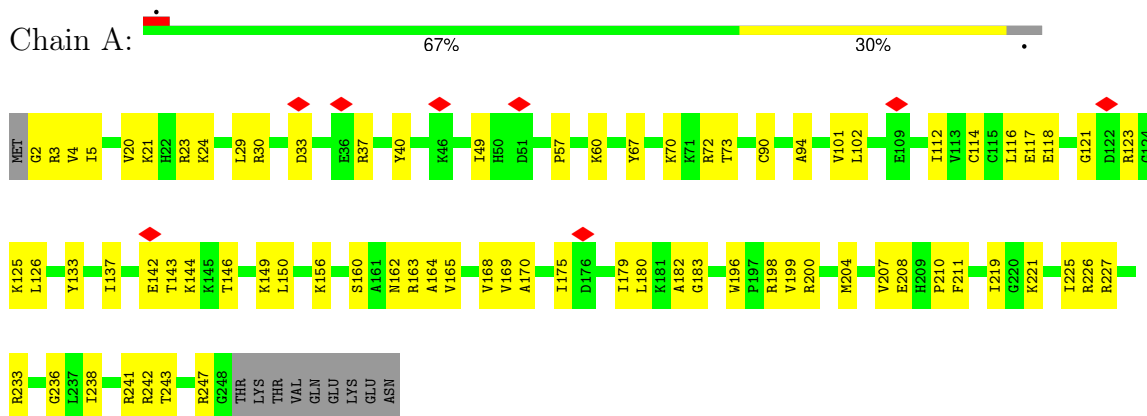
- Molecule 89 is emetine (CCD ID: 34G) (formula: $C_{29}H_{40}N_2O_4$).



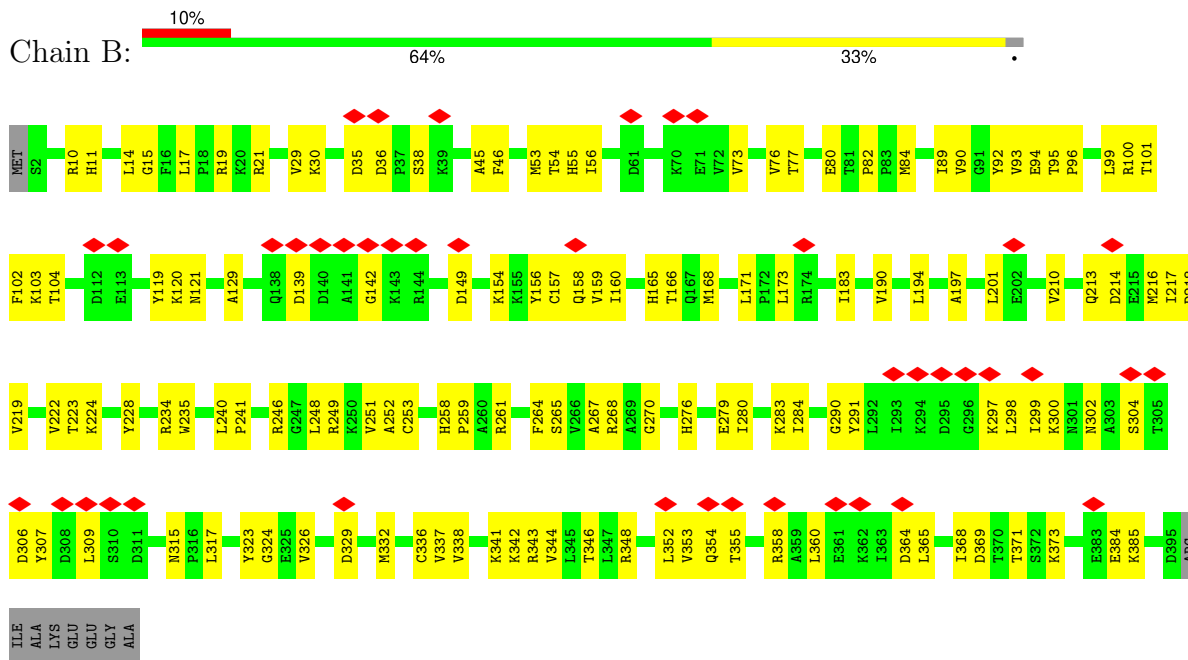
3 Residue-property plots

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

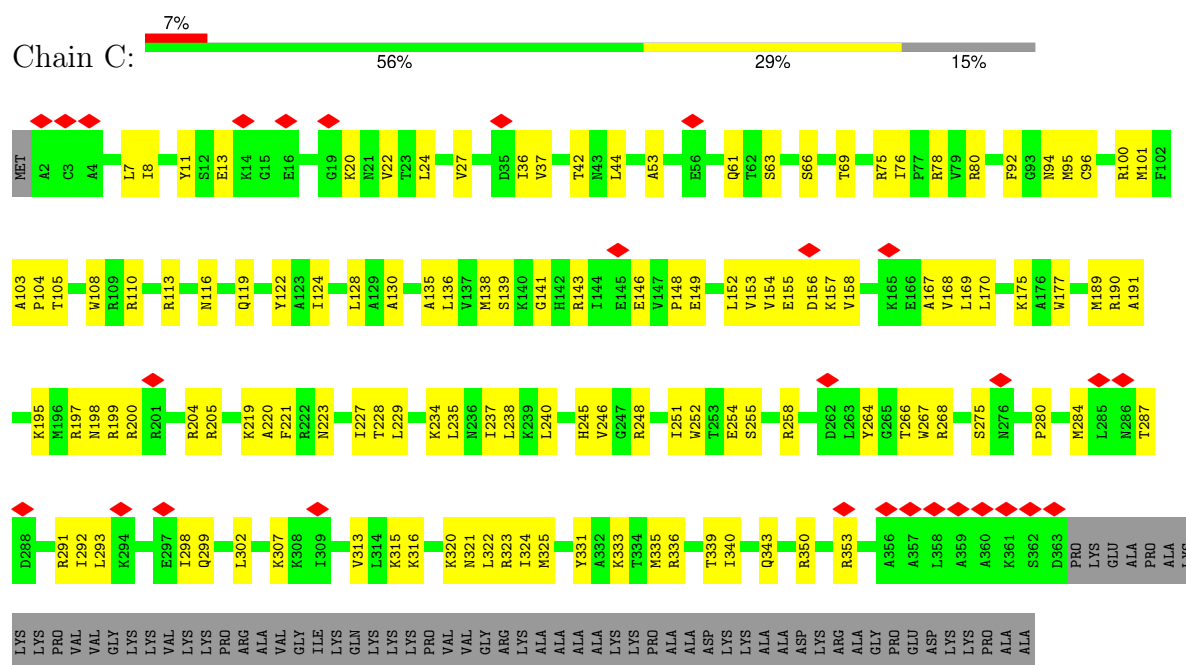
• Molecule 1: uL2



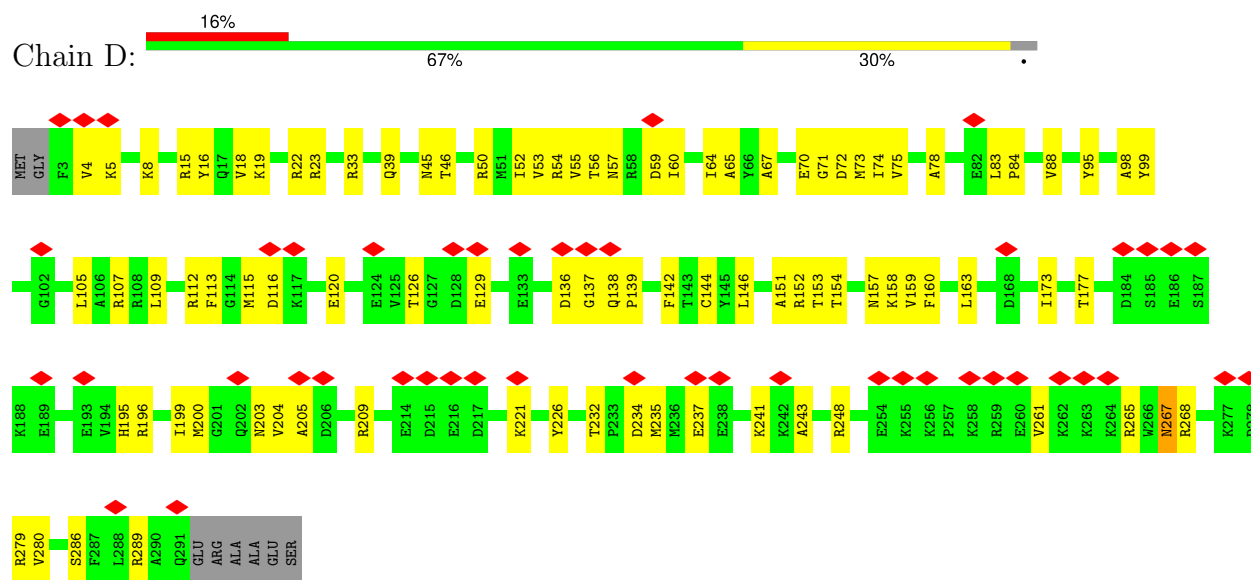
• Molecule 2: uL3



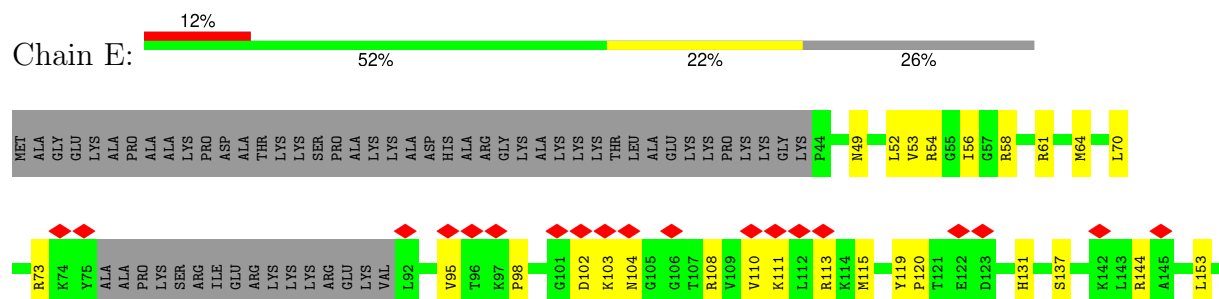
• Molecule 3: uL4

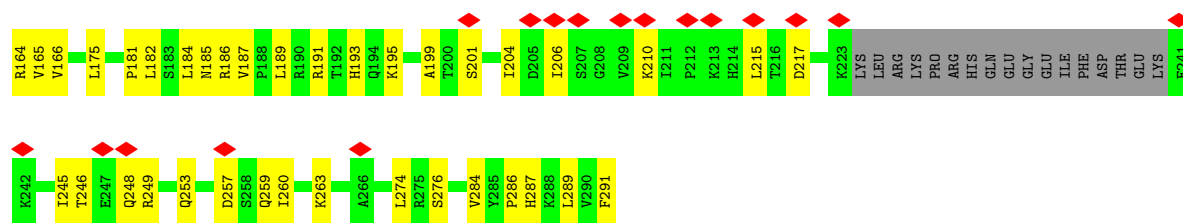


• Molecule 4: uL18



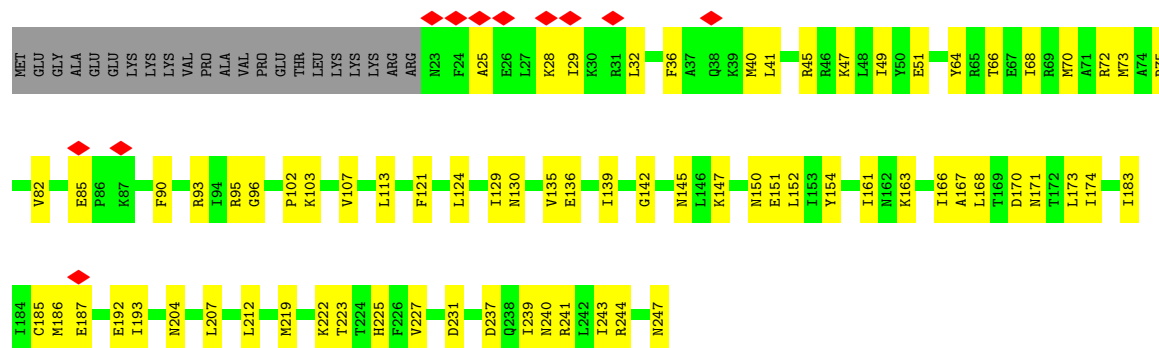
• Molecule 5: eL6





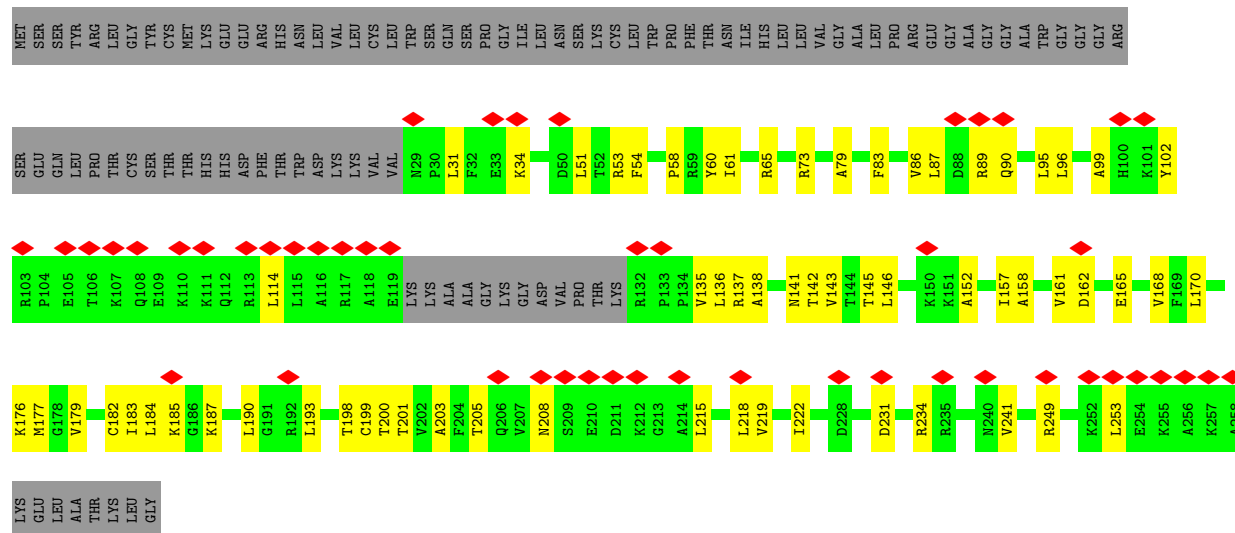
• Molecule 6: uL30

Chain F: 62% 30% 9%



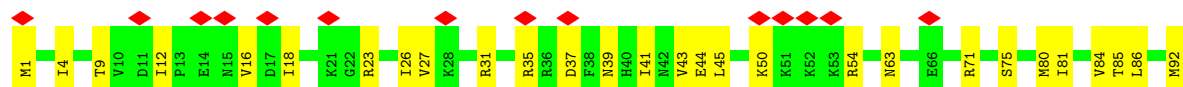
• Molecule 7: eL8

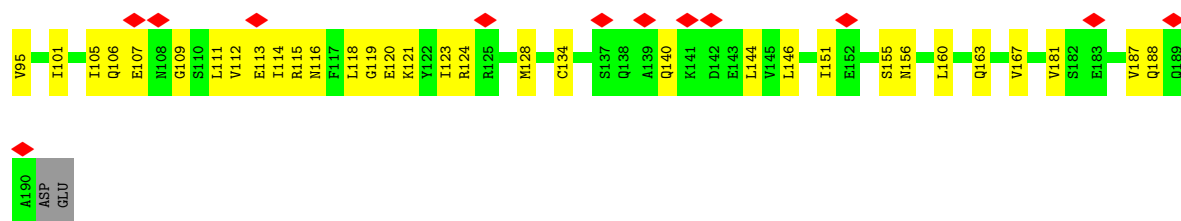
Chain G: 15% 48% 20% 32%



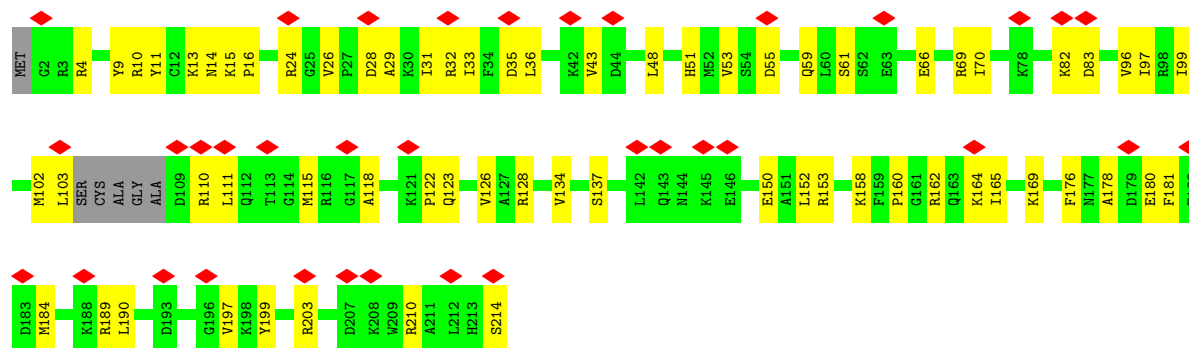
• Molecule 8: uL6

Chain H: 14% 68% 31%

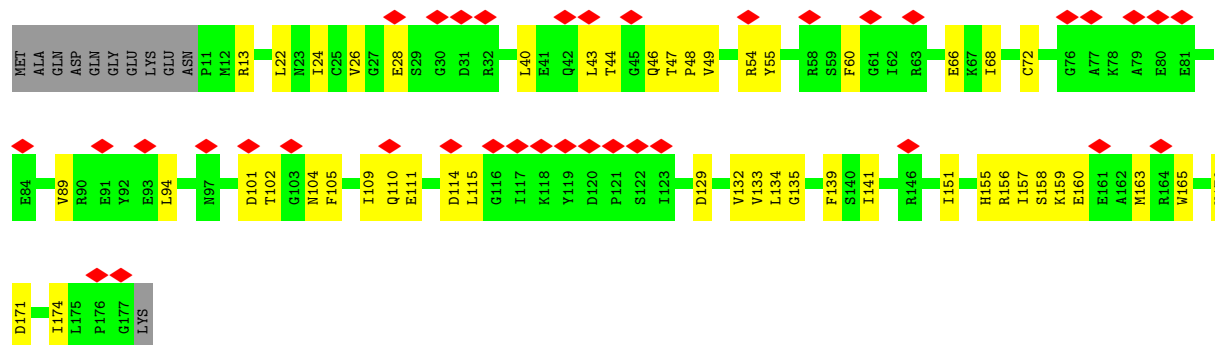




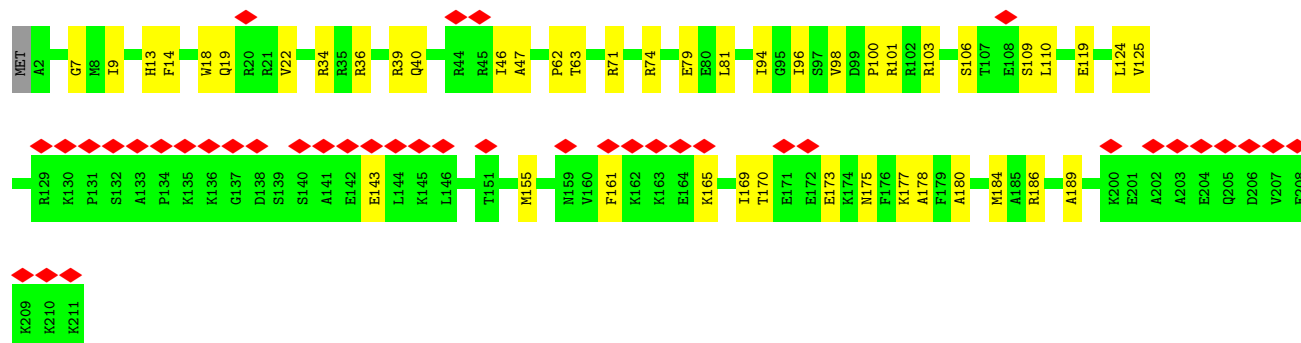
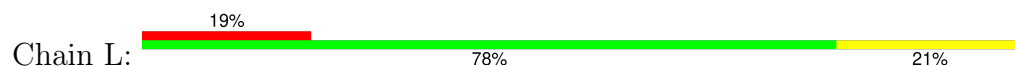
• Molecule 9: uL16



• Molecule 10: uL5



• Molecule 11: eL13



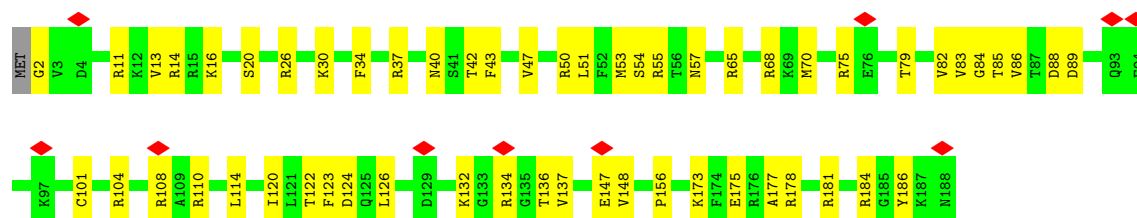
Protein	Protein Type	Protein Size (aa)	Protein Weight (kDa)	Protein pI	Protein Charge	Protein Stability	Protein Solubility	Protein Localization	Protein Function	Protein Interactions	Protein Mutations	Protein Variants	Protein Annotations
Met	Met	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
V2	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
R5	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
F6	GLN	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
V7	LYS	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
F8	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
R11	PRO	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
F17	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
L24	GLN	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
I27	LYS	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
V28	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
D29	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
V30	GLY	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
I31	GLN	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
D32	LYS	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
Q33	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
N34	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
R35	GLN	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
A36	PRO	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
L37	PRO	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
V38	LYS	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
L43	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
R46	GLN	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
R47	GLY	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
Q48	LYS	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
A49	PRO	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
F52	PRO	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
K53	ALA	22	2.2	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5
C54	GLN	22	2.2										

R204	L113	R114	V115	Y119	D124	S125	T126	Y127	E131	V132	I135	D136	F137	F138	H139	K140	A141	I142	R143	R144	D147	T148	I151	V155	H156	K157	H158	R159	E160	M161	R162	S166	K170	S171	R172	H176	K179	F180	H181	I184	V192	R193	R194	R195	N196	L200
	G2	A3	Y4	K5	Q8	E9	L10	W11	R12	D17	V18	M19	L23	R24	V25	R26	R31	Q32	L33	L36	H37	R38	R44	R49	R50	V60	T64	R65	V66	R67	R73	Y81	L92	K93	R96	Q99	S100	E103	E104	R105	A106	G107	R108			

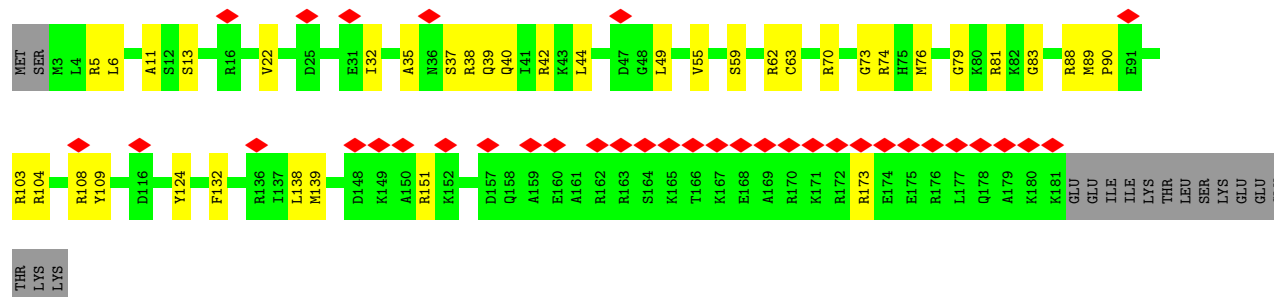
[illegible]

Figure 1: Schematic representation of the 120 amino acid residues of the protein. The protein is represented as a horizontal bar divided into segments. The segments are color-coded: yellow for residues 1-10, 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80, 81-90, 91-100, 101-110, 111-120. The segments are labeled with residue numbers. The segments are color-coded: yellow for residues 1-10, 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80, 81-90, 91-100, 101-110, 111-120. The segments are labeled with residue numbers. The segments are color-coded: yellow for residues 1-10, 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80, 81-90, 91-100, 101-110, 111-120. The segments are labeled with residue numbers.

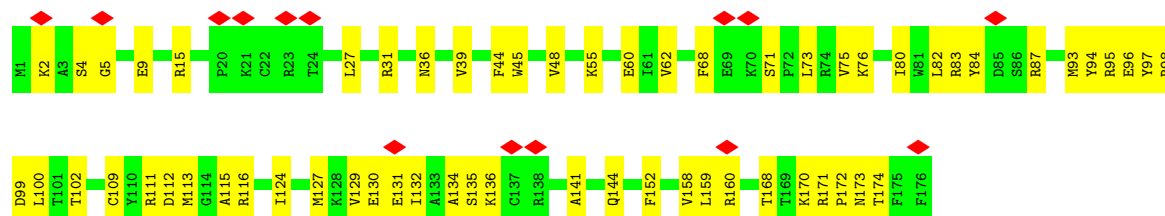
WORLDWIDE
PDB
PROTEIN DATA BANK



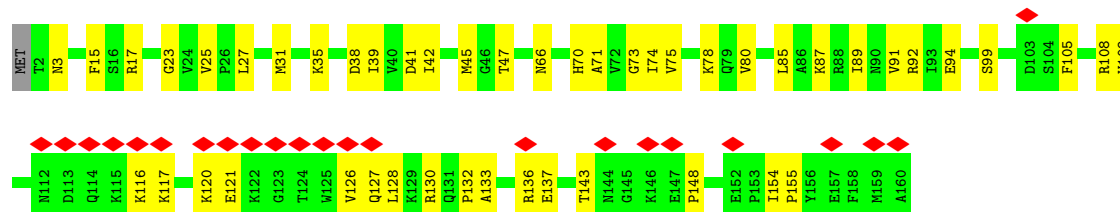
• Molecule 17: eL19



• Molecule 18: eL20



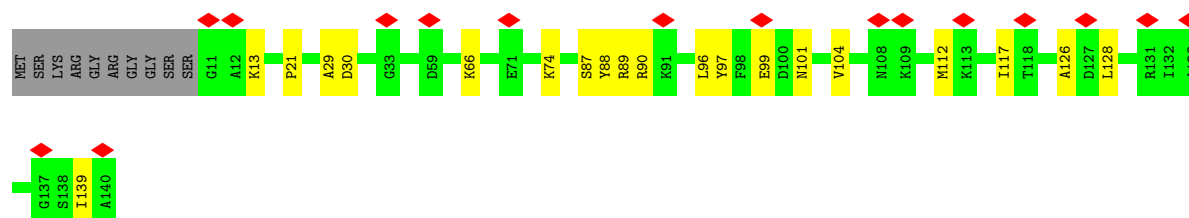
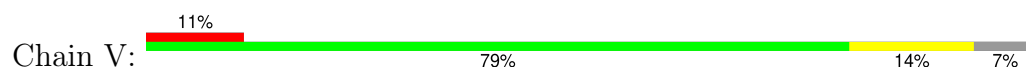
• Molecule 19: eL21



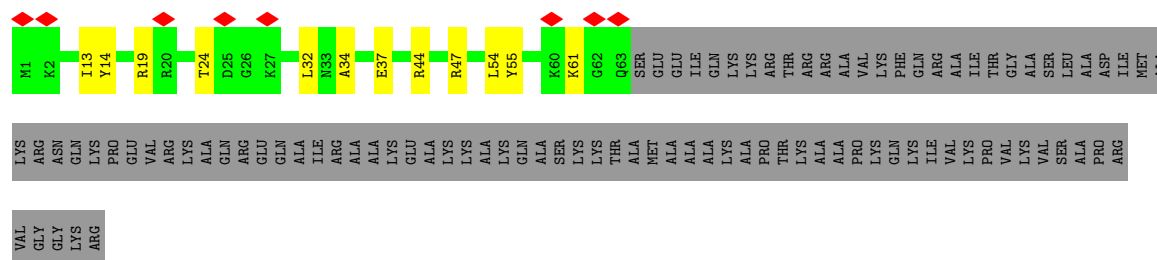
• Molecule 20: eL22



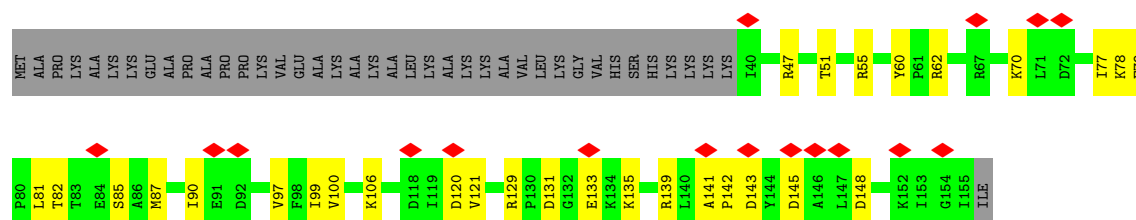
- Molecule 21: uL14



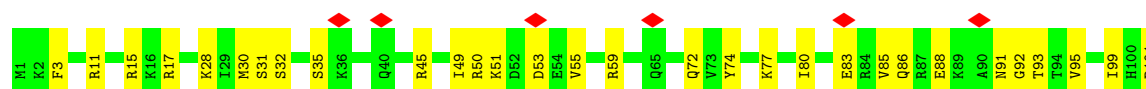
- Molecule 22: eL24

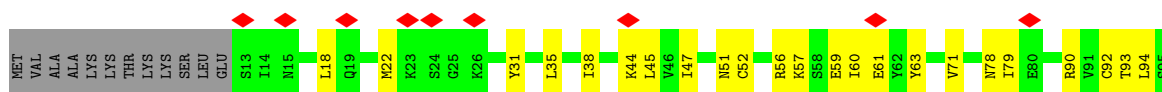


- Molecule 23: uL23



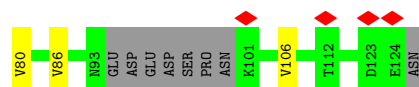
- Molecule 24: uL24

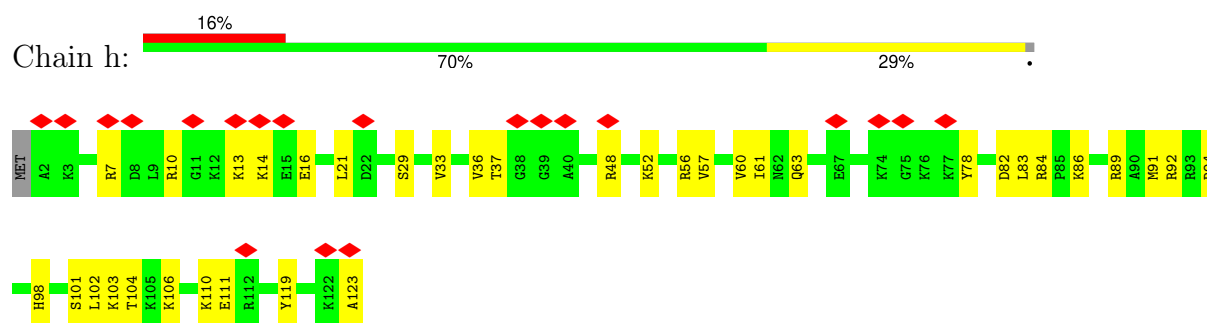




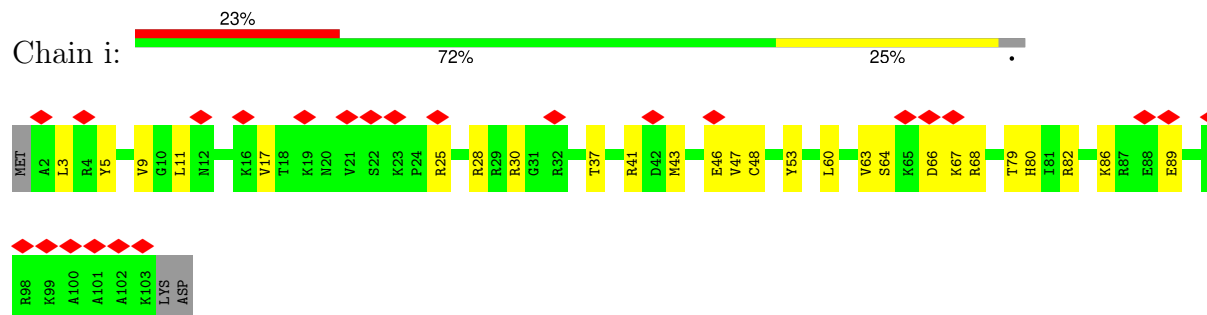


• Molecule 29: eL31

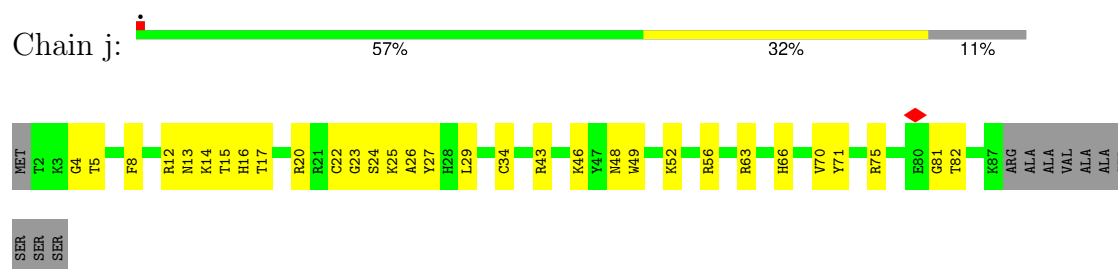




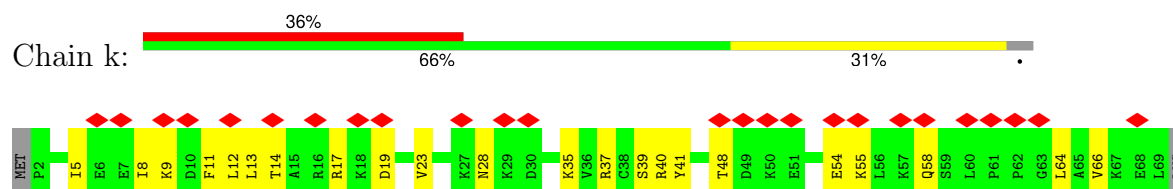
- Molecule 34: eL36



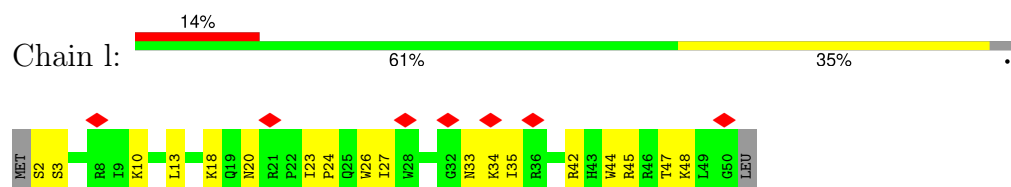
- Molecule 35: eL37



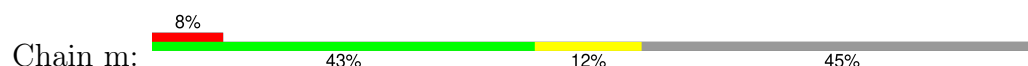
- Molecule 36: eL38

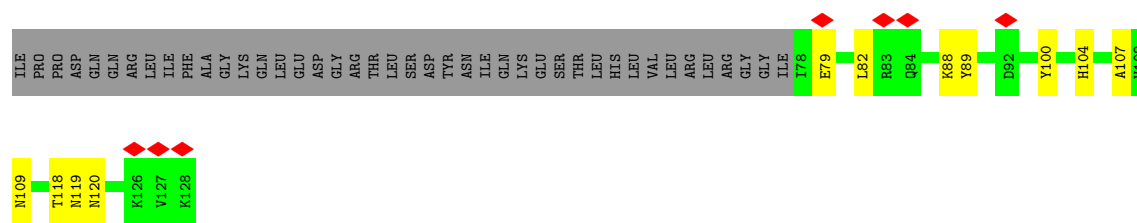


- Molecule 37: eL39

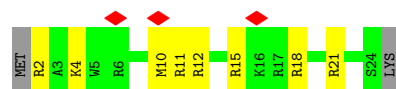


- Molecule 38: eL40

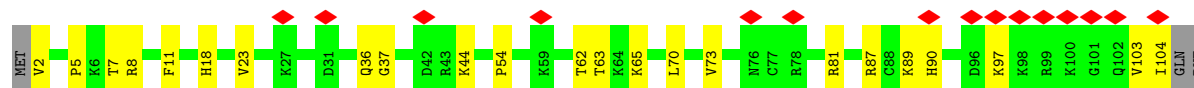
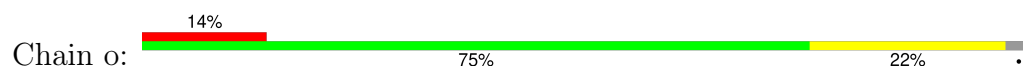




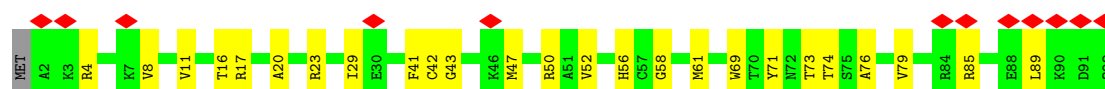
• Molecule 39: eL41



• Molecule 40: eL42



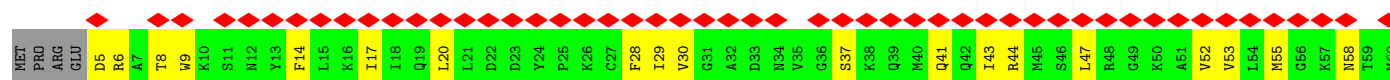
• Molecule 41: eL43

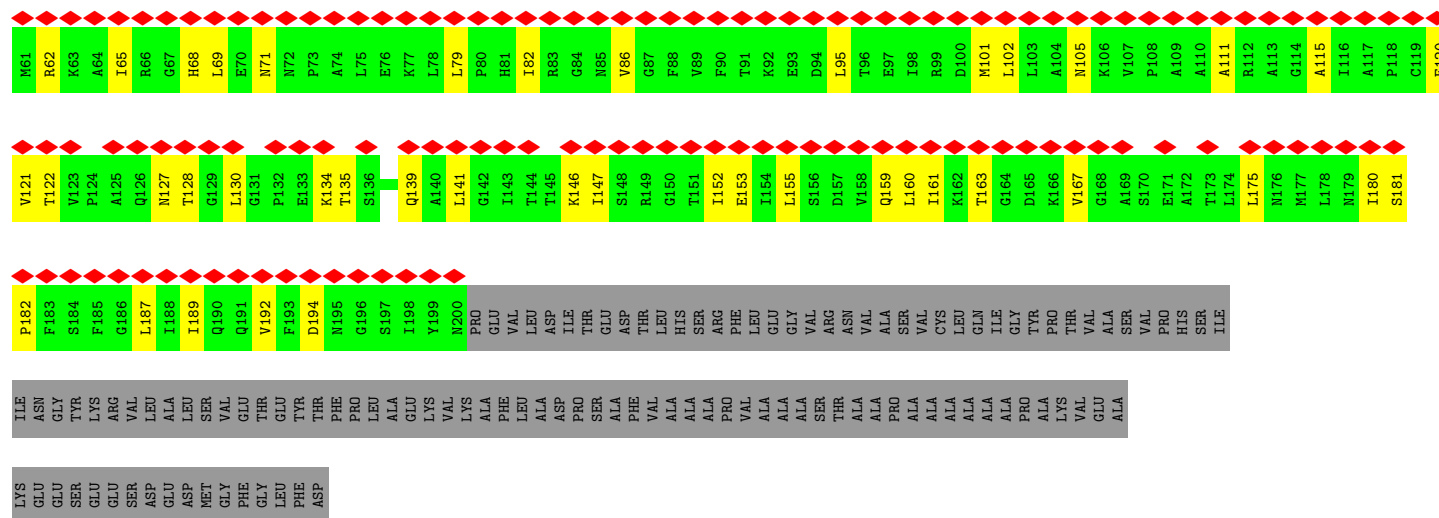


• Molecule 42: eL28

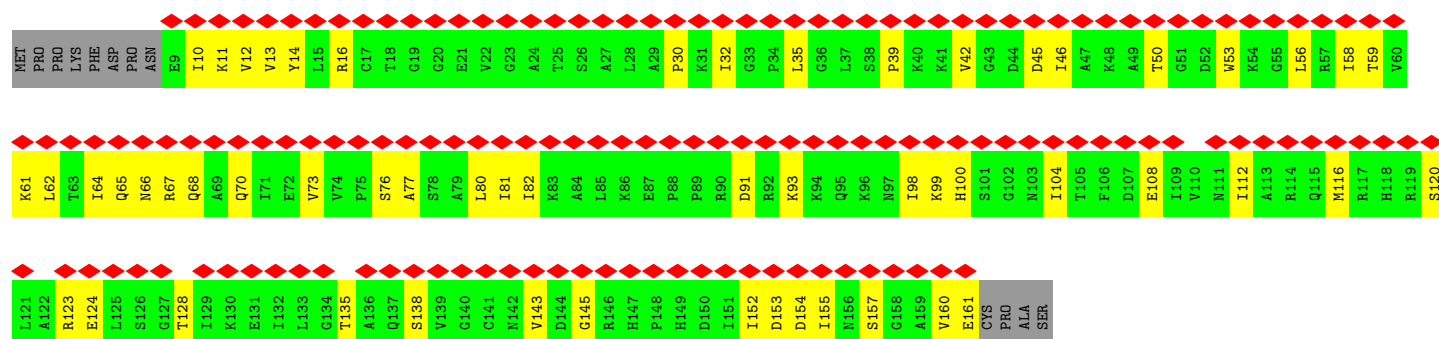
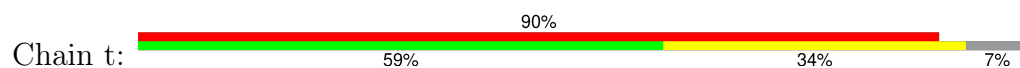


• Molecule 43: uL10

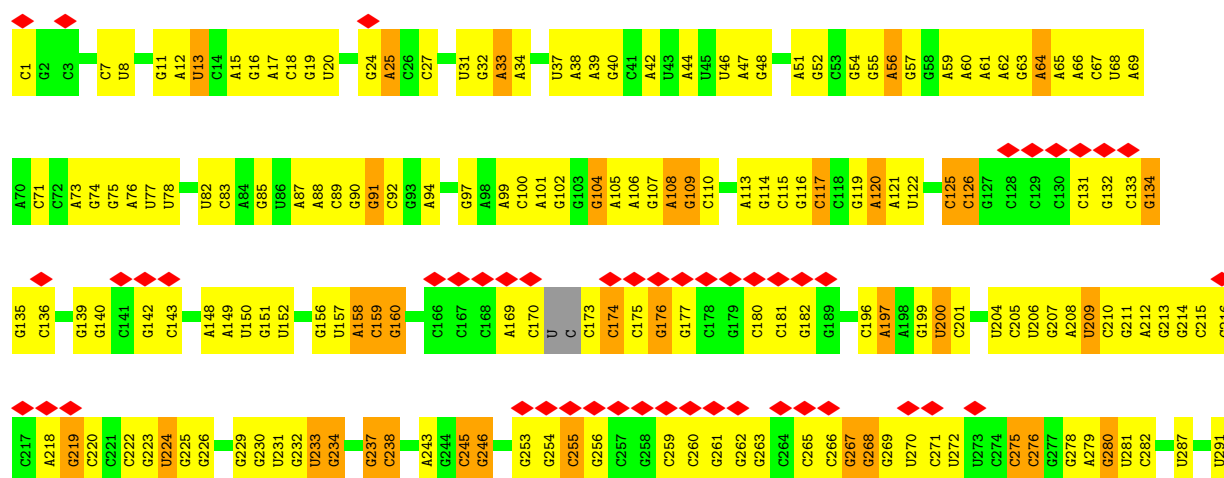
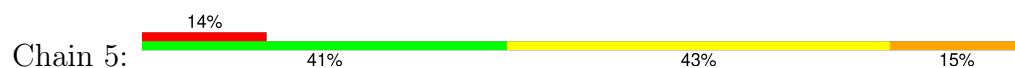




• Molecule 44: uL11



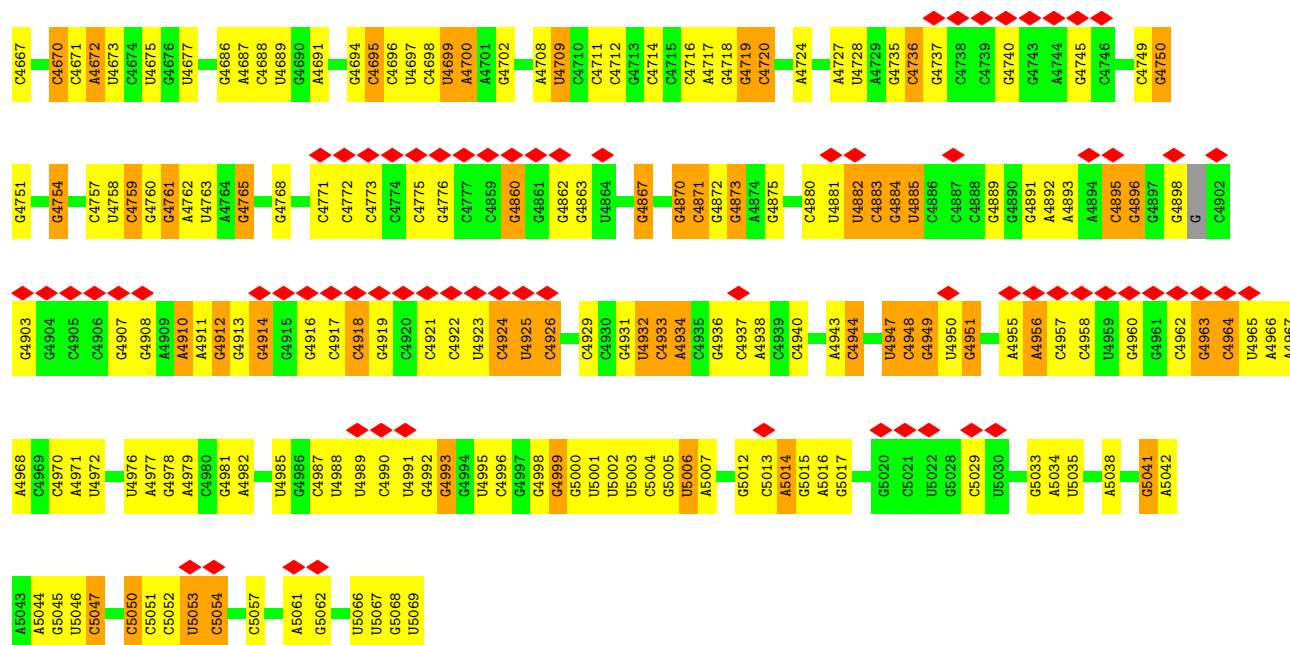
• Molecule 45: 28S rRNA



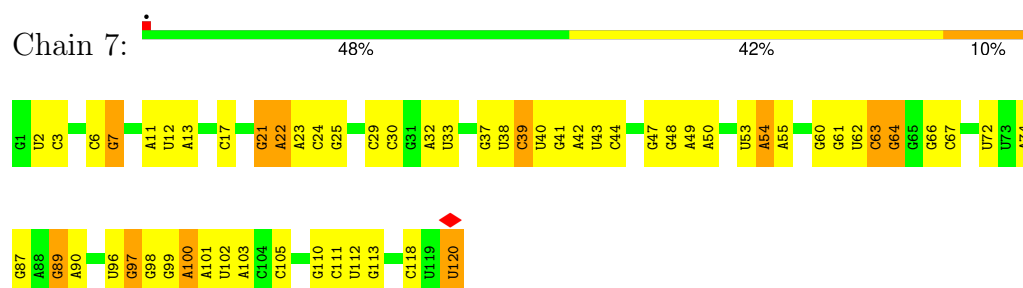




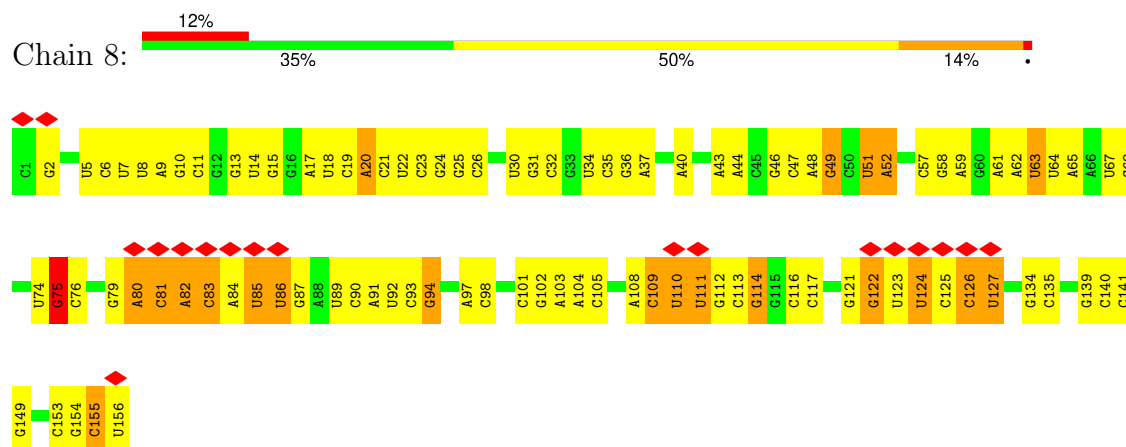




• Molecule 46: 5S rRNA



• Molecule 47: 5.8S rRNA



• Molecule 48: eEF2

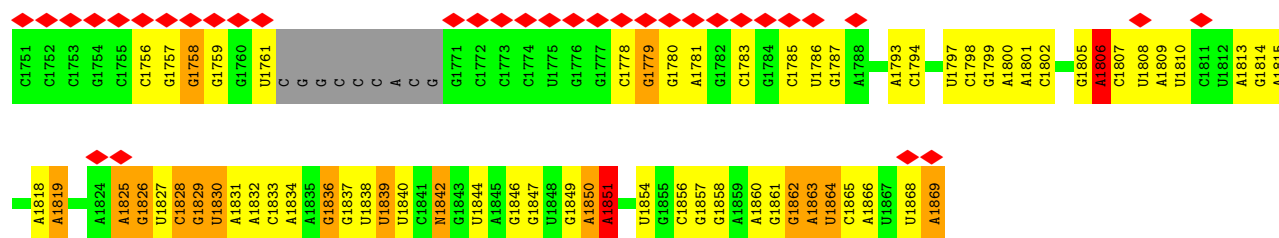


Q811	C812	F813	D815	H816	W817	Q818	I819	L820	P821	G822	D823	P824	F825	D826	N827	S828	S829	R830	P831	S832	Q833	V834	V835	A836	E837	T838	R839	K840	R841	F842	V843	L844	K845	E846	G847	I848	P849	A850	E792	L851	D852	N853	F854	L855	D856	K857	L858													
I749	Q750	C751	F752	E753	Q754	V755	V756	G757	G758	V759	Y760	L763	N764	R765	K766	R767	V770	F771	E772	E773	S774	T775	V776	A777	G778	T779	F780	M781	F782	V783	V784	K785	L786	V787	L788	P789	V790	N791	E792	L851	D852	N853	F854	L855	D856	K857	L858													
F683	Q684	W685	K688	E689	G690	A691	L692	C693	E694	F695	N696	R697	R698	R701	F702	D703	V704	H705	D706	V707	T708	L709	H710	A711	D712	A715	R716	G717	G718	I721	T722	L723	L724	R727	C728	L729	Y730	V733	L734	T735	A736	P738	R739	L740	M741	E742	F743	I744	T745	L746	V747	E748								
I617	D618	K619	G620	E621	R625	Q626	E627	L628	K629	Q630	R633	Y634	L635	A636	E637	K638	V639	E640	W641	D642	V643	A644	E645	T646	R647	E648	I649	W650	C651	D655	G656	P659	N660	I661	L662	T663	D664	L665	T666	K667	G668	V669	Q670	F671	L672	H673	E674	L675	K676	D677	S678	V679	W680	A681	O682					
T556	C557	L558	K559	D560	L561	E562	E563	D564	H565	A566	C567	I568	P569	I570	K571	K572	S573	D574	P575	V576	V577	S578	V579	R580	E581	T582	V583	S584	E585	S586	S587	N588	V589	L590	C591	L592	S595	P596	N597	K598	H599	N600	R601	L602	V603	M604	K605	A606	R607	F608	P609	P610	D611	L612	L613	A614	E615	D616		
V496	M497	K498	P499	S500	V501	S502	P503	V504	V505	R506	V507	A508	V509	E510	A511	R512	N513	P514	A515	D516	L517	P518	K519	L520	V521	E522	G523	L524	K525	R526	L527	A528	K529	S530	D531	P532	P536	M533	V534	Q535	C536	T537	L538	E539	E540	S541	G542	E543	H544	L545	T546	F547	G548	A549	G550	E551	L552	H553	L554	E555
P436	Q437	K438	K439	E440	D441	L442	Y443	L444	K445	P446	L447	Q448	R449	T450	L451	L452	M453	M454	G455	R456	Y457	V458	E459	P460	L461	E462	D463	V464	P465	C466	Q467	N468	L469	V470	G471	L472	V473	G474	V475	D476	F478	L479	V480	K481	T482	O483	T484	L485	T486	T487	F488	H490	A491	H492	N493	M494	R495			
P376	P377	D378	D379	E380	A381	A382	G383	G384	L385	K386	S387	C388	D389	P390	K391	G392	P393	L394	K395	K396	Y397	L398	S399	K400	M401	V402	P403	T404	D406	K407	R408	R409	F410	Y411	A412	F413	G414	R415	V416	F417	S418	G419	L420	V421	S422	T423	G424	L425	K426	V427	R428	L429	M430	G431	P432	N433	T435			
L315	T316	E317	K318	L319	D320	T321	K322	L323	D324	S325	E326	D327	K328	D329	K330	E331	G332	K333	P334	L335	L336	K337	A338	V339	M340	R341	R342	W343	A346	G347	D348	A349	L350	L351	Q352	K353	T354	T355	L356	H357	L358	P359	S360	P361	V362	T363	A364	Q365	K366	Y367	R368	C369	E370	L371	L372	E374	G375			
V253	E254	D255	M256	K257	K258	K259	L260	M261	G262	D263	R264	V265	F266	D267	F268	A269	N270	G271	K272	F273	S274	K275	S276	A277	T278	S279	P280	E281	G282	K283	K284	L285	T288	F289	C290	Q291	L292	T293	L294	D295	P296	L297	V300	F301	D302	A303	L304	M305	K306	F307	K308	K309	E310	E311	T312	A313	K314			
G124	A125	L126	V127	V128	V129	D130	C131	V132	S133	G134	V135	C136	V137	Q138	T139	E140	L143	R144	Q145	A146	T147	A148	E149	R150	V151	K152	P153	V154	L155	M156	M157	D161	R162	A163	L164	L165	Q168	L169	E170	P171	I172	E173	L174	Y175	Q176	T177	F178	Q179	R180	E183	N184	V187	I188	I189						
S190	T191	Y192	G193	E194	G195	E196	G198	G199	M200	M201	N202	I203	M204	T205	D206	P207	V208	L209	E210	T211	V212	G213	F214	G215	G220	W221	S222	F223	T224	L225	K226	Q227	F228	A229	E230	M231	T232	V233	A234	K235	F236	A237	A238	K239	G240	E241	G242	Q243	L244	G245	P246	E247	E248	R249	A250	K251	K252			
GLN	GLU	R66	C67	I68	T69	I70	K71	S72	T73	A74	I75	S76	L77	F78	Y79	E80	L81	S82	E83	N84	D85	L86	N87	F88	I89	K90	Q91	S92	K93	D94	G95	A96	G97	F98	L99	I100	N101	L102	I103	D104	S105	P106	G107	H108	V109	D110	F111	S112	S113	E114	V115	T116	A117	L118	L119	R120	V121	T122	D123	
MET	VAL	ASN	F4	T5	V6	D7	Q8	I9	S10	R10	A11	I12	M13	D14	K15	K16	A17	N18	I19	R20	N21	M22	S23	V24	I25	A26	H27	V28	D29	H30	G31	T36	D37	S38	L39	V40	C41	K42	A43	G44	I45	I46	ALA	SER	ALA	ALA	ALA	GLY	GLU	THR	ARG	PHE	THR	ASP	THR	ARG	LYS	ASP	GLU	

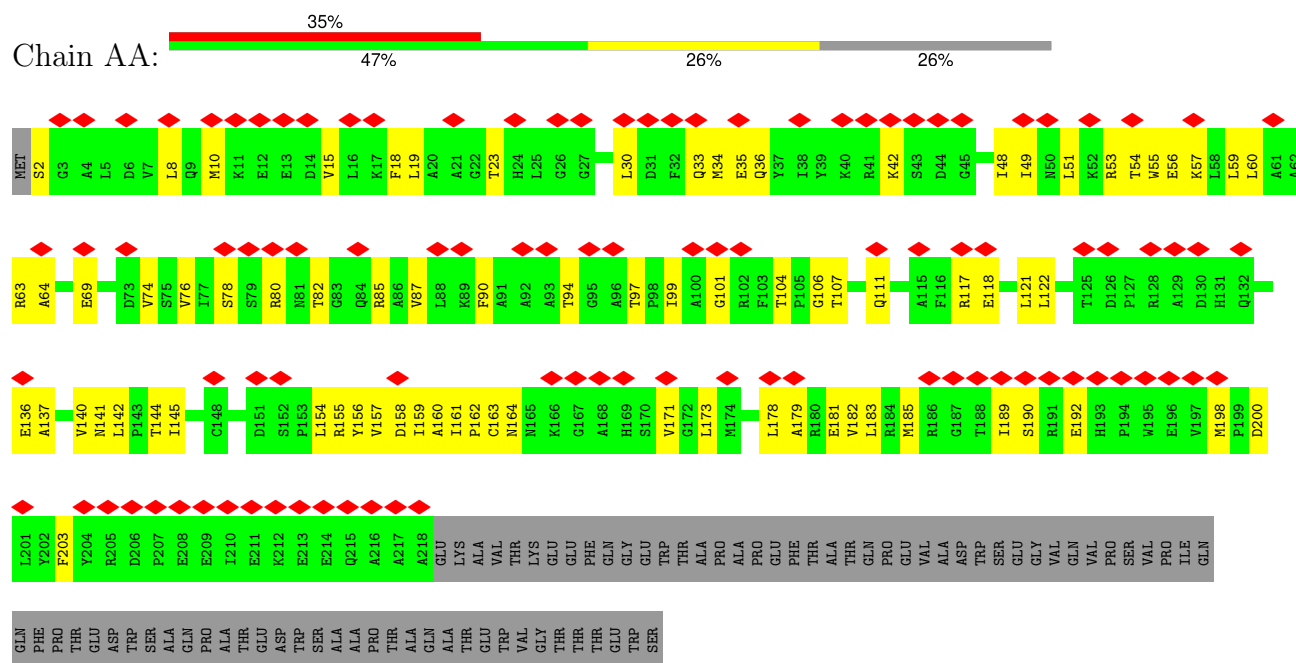
Chain 9:



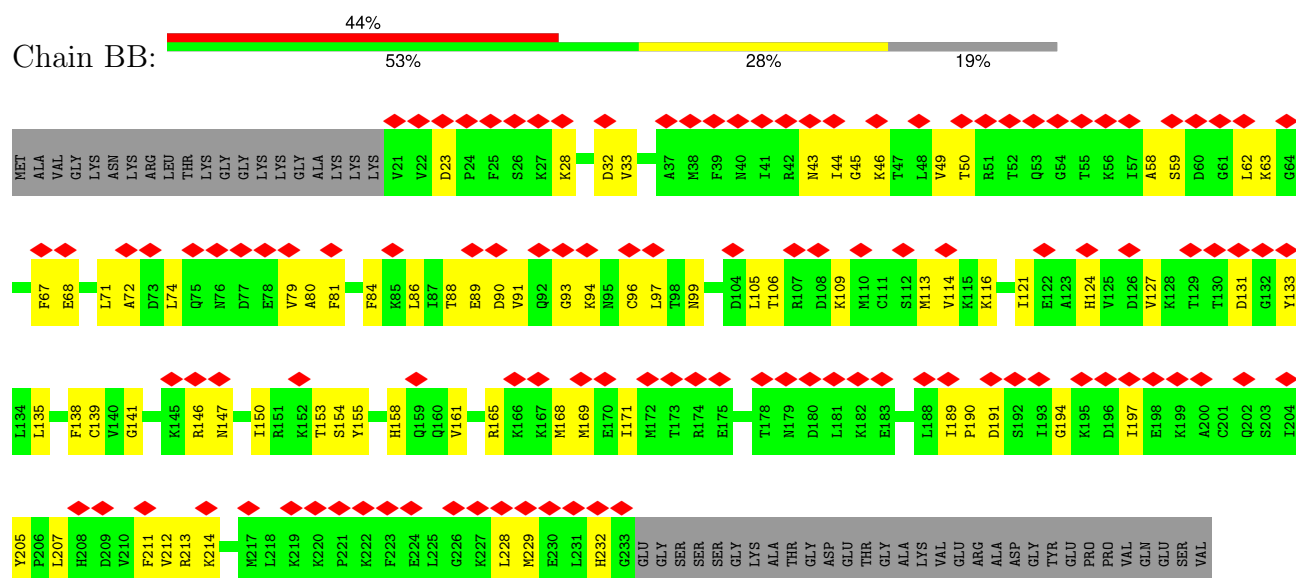




• Molecule 50: uS2



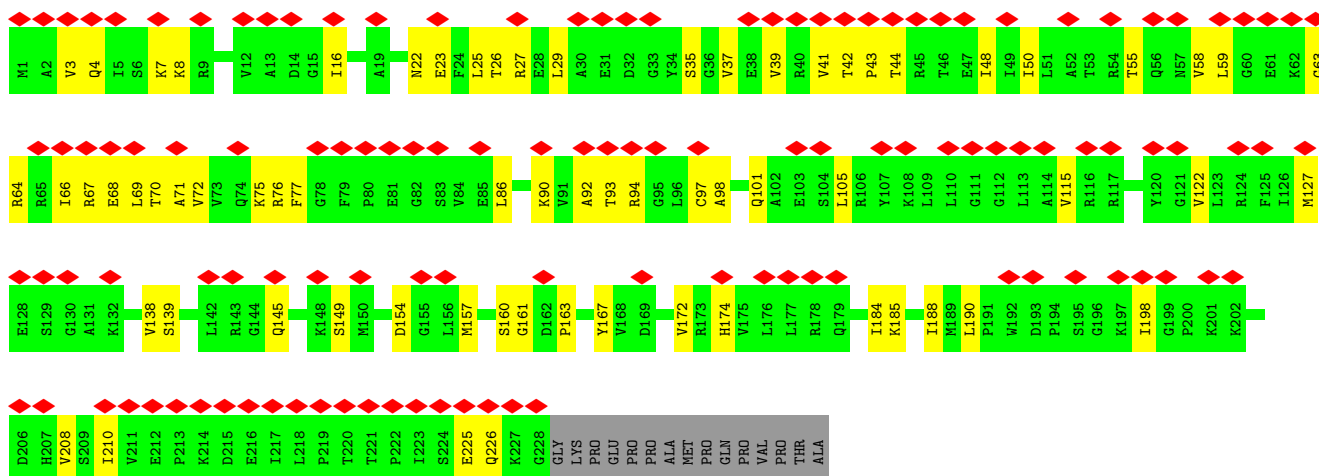
• Molecule 51: eS1



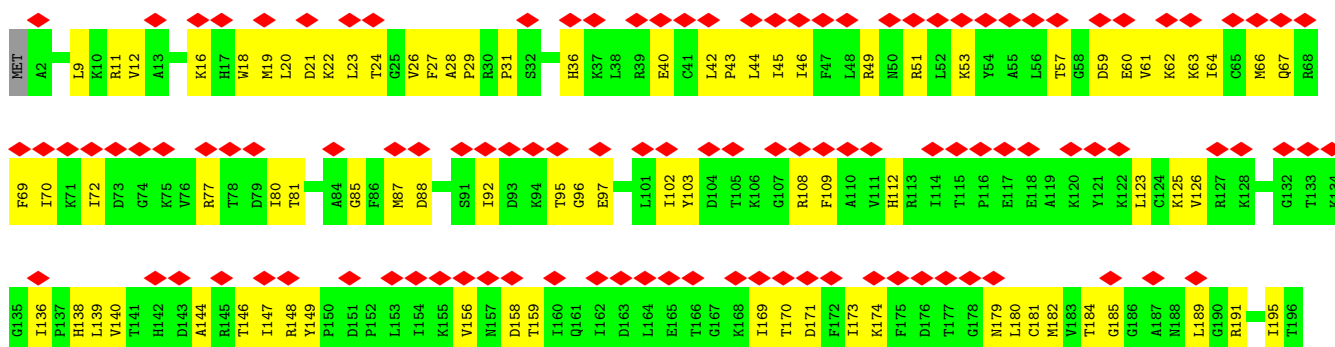
• Molecule 52: uS5



- Molecule 53: uS3

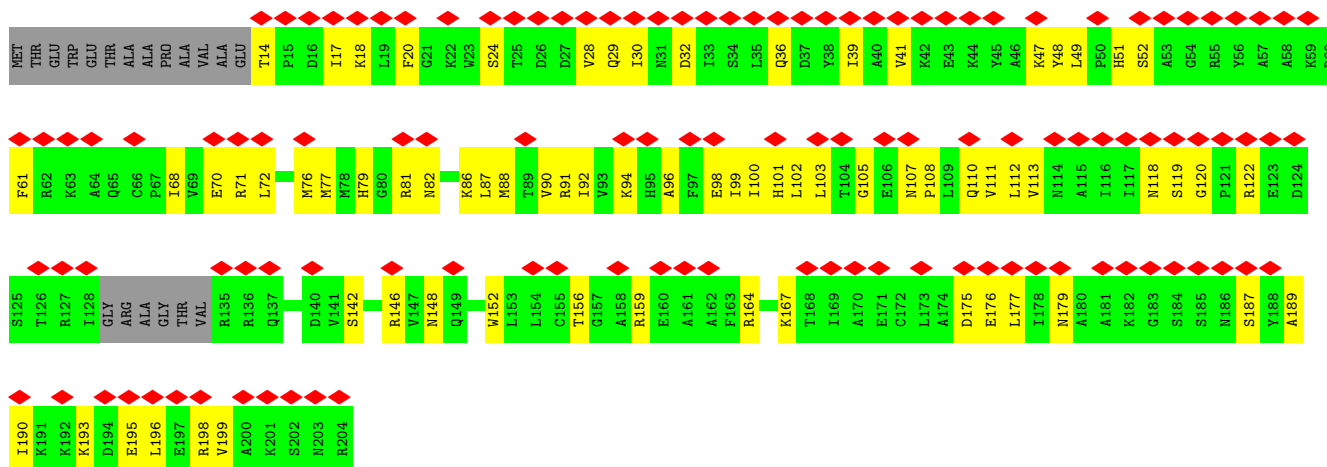


- Molecule 54: eS4

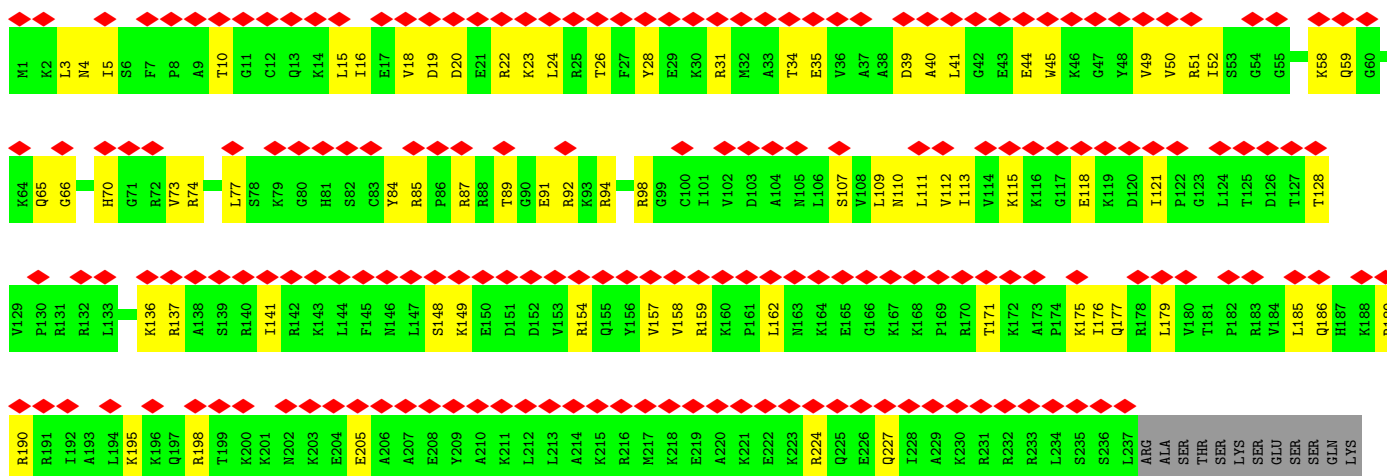
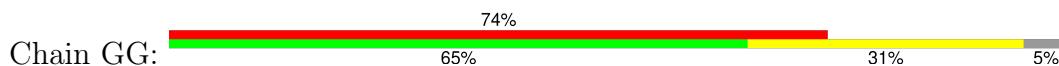




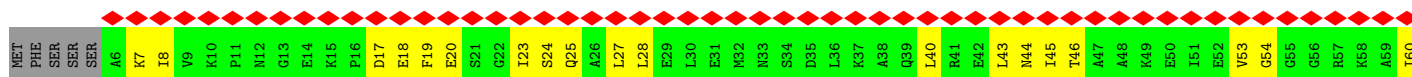
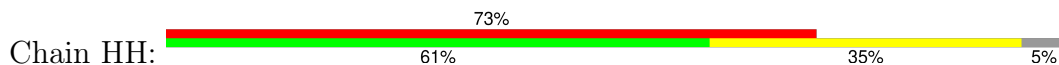
• Molecule 55: uS7



• Molecule 56: eS6

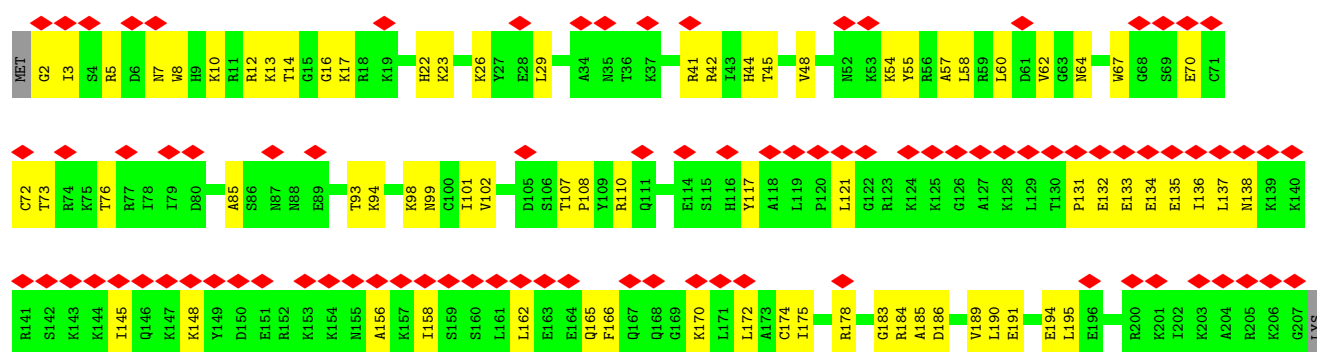
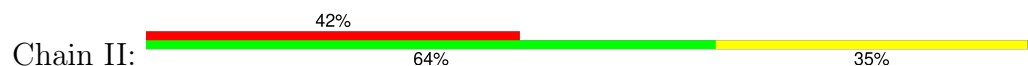


• Molecule 57: eS7

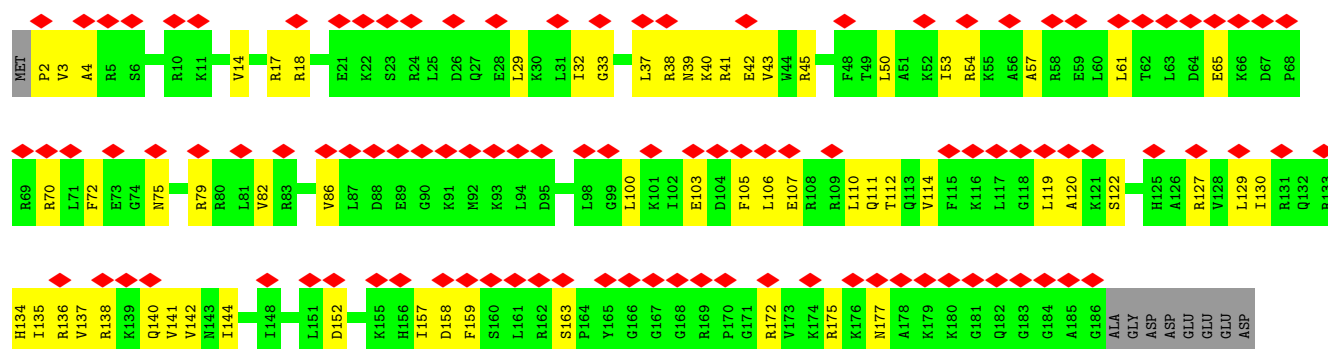




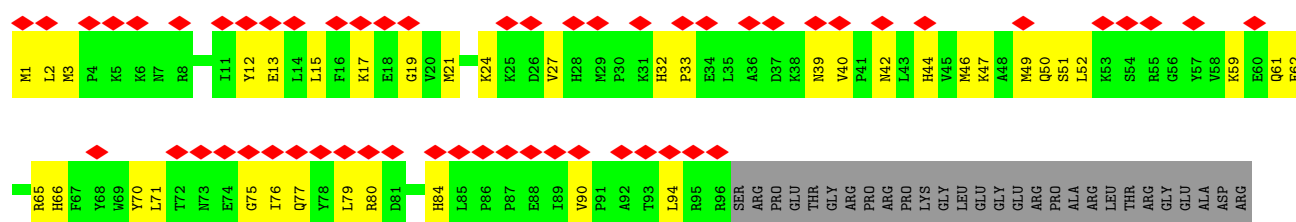
• Molecule 58: eS8



• Molecule 59: uS4



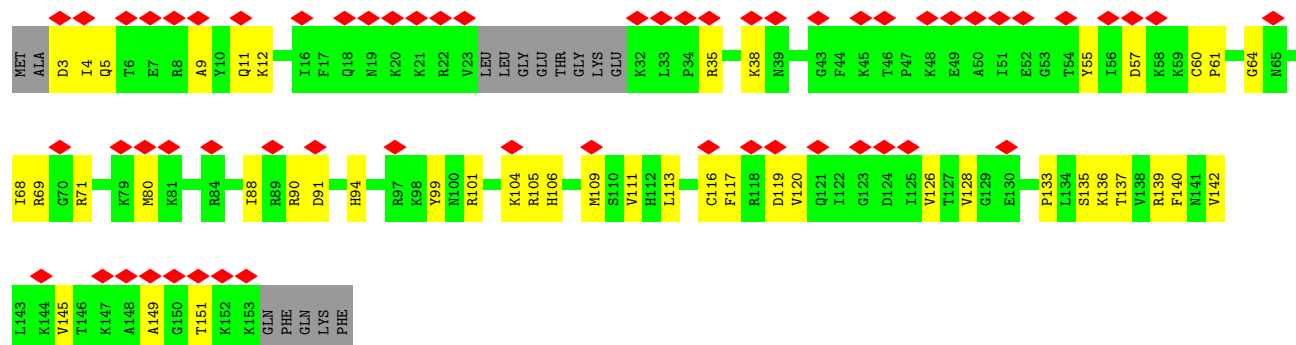
• Molecule 60: eS10



ASP
THR
TYR
ARG
ARG
SER
SER
ALA
VAL
PRO
PRO
GLY
GLY
ALA
ALA
GLY
GLY
ALA
SER
SER
ALA
THR
THR
PHE
PHE
GLN
GLY
PHE
GLY
GLY
ARG
ARG
GLY
GLY
GLN
GLN
PRO
PRO
GLN

• Molecule 61: uS17

Chain LL:



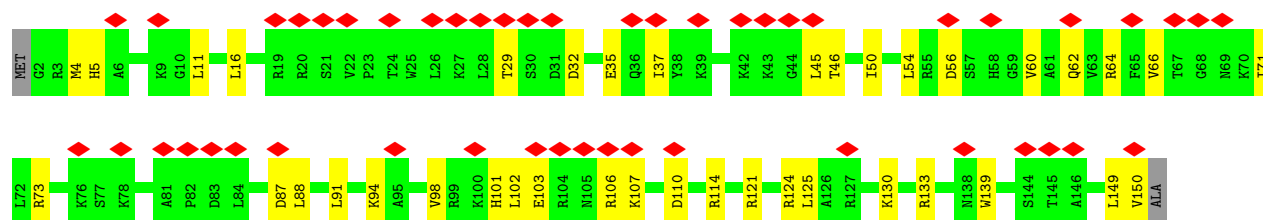
• Molecule 62: eS12

Chain MM:



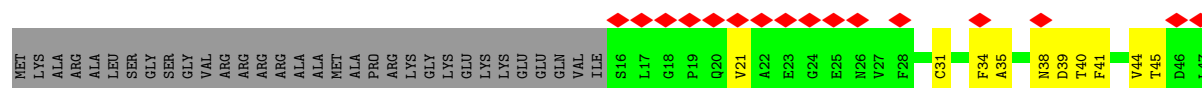
• Molecule 63: uS15

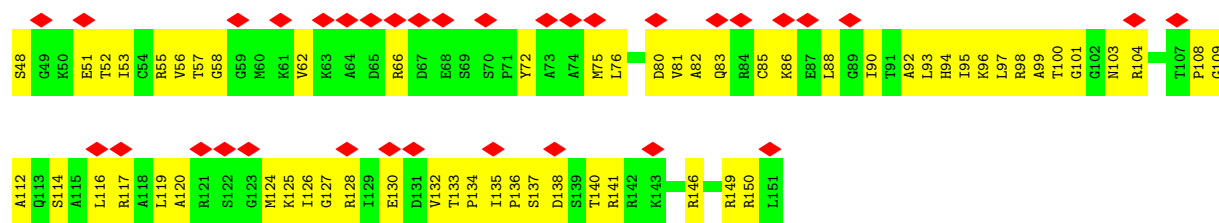
Chain NN:



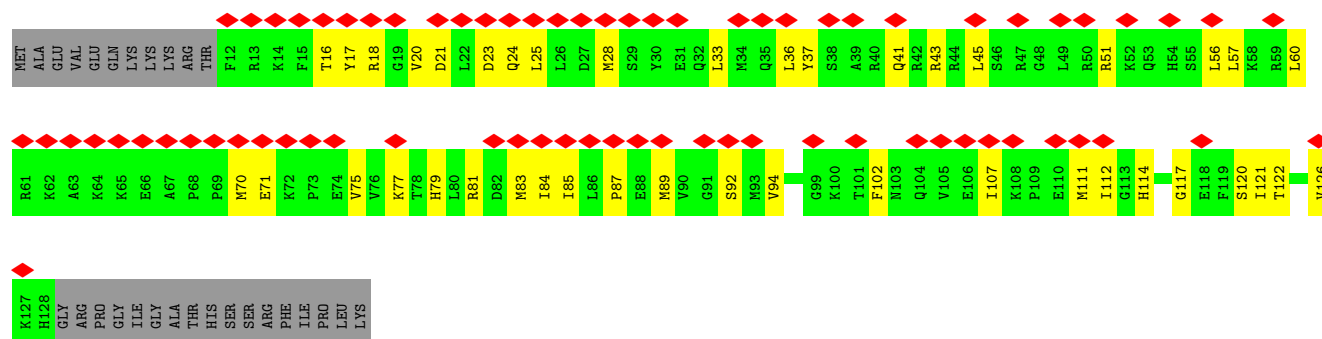
• Molecule 64: uS11

Chain OO:

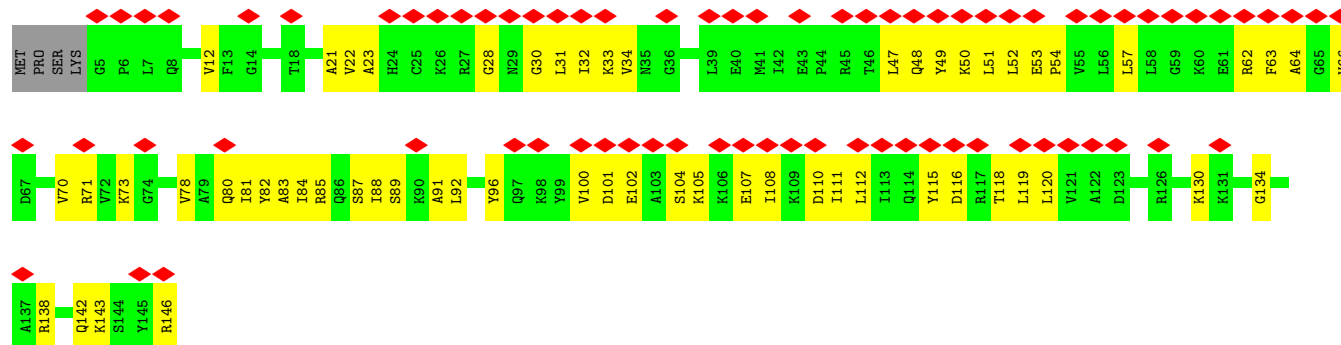




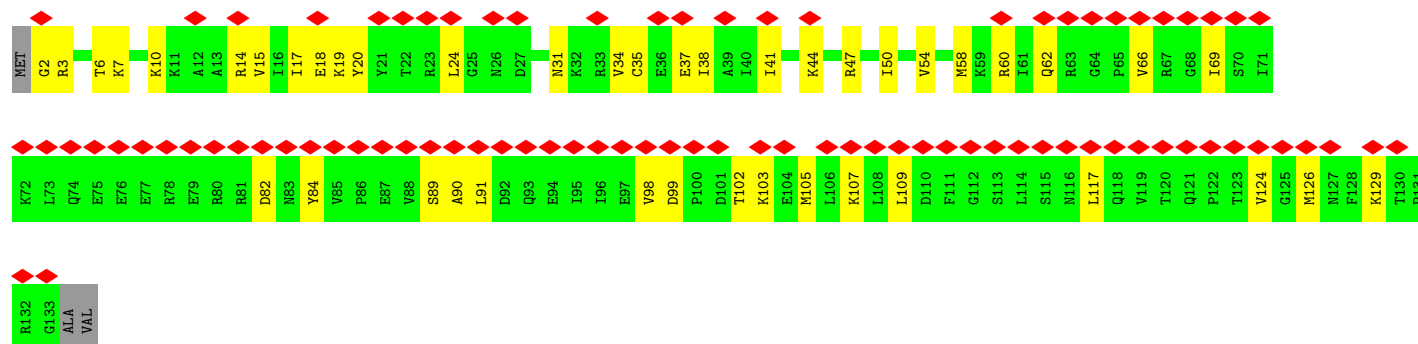
• Molecule 65: uS19



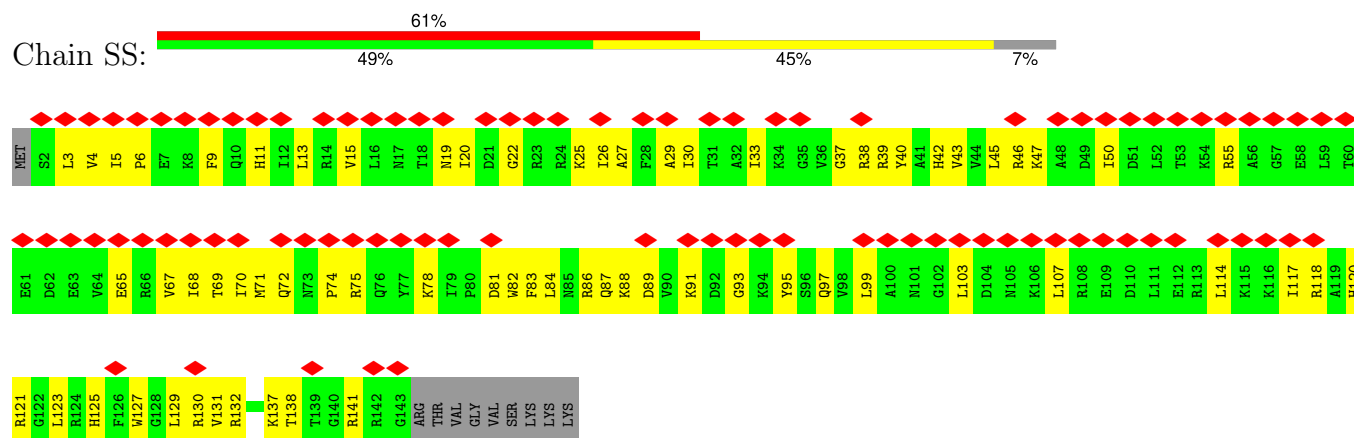
• Molecule 66: uS9



• Molecule 67: eS17



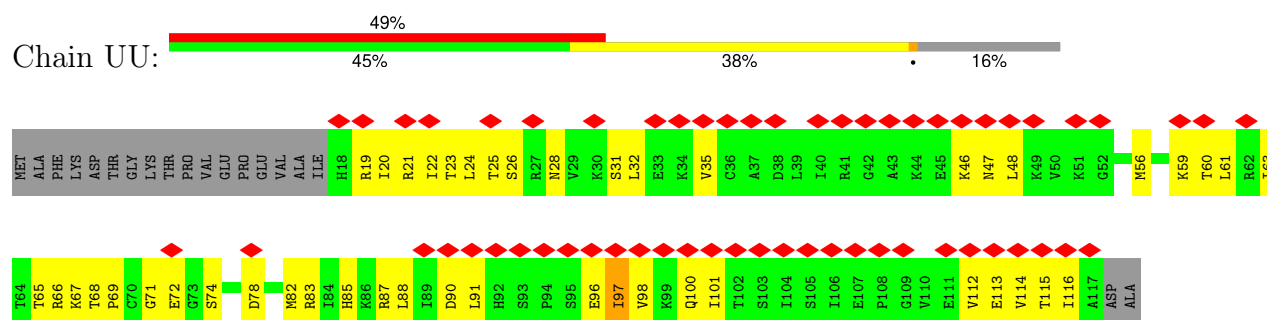
- Molecule 68: uS13



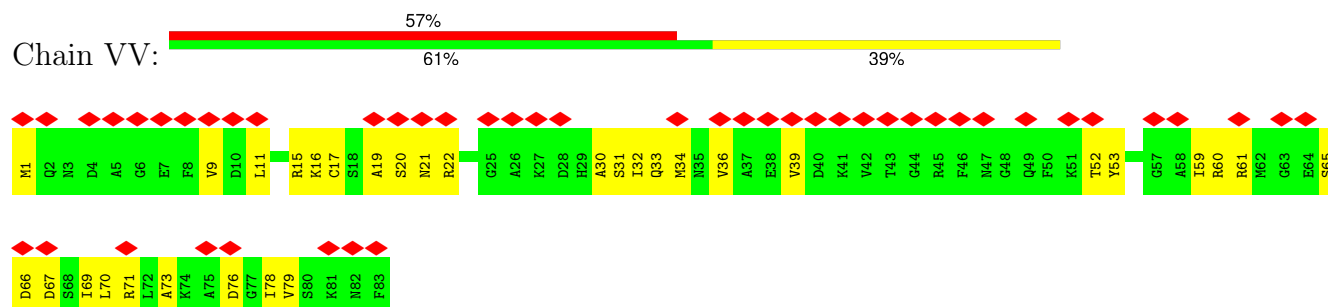
- Molecule 69: eS19



- Molecule 70: uS10

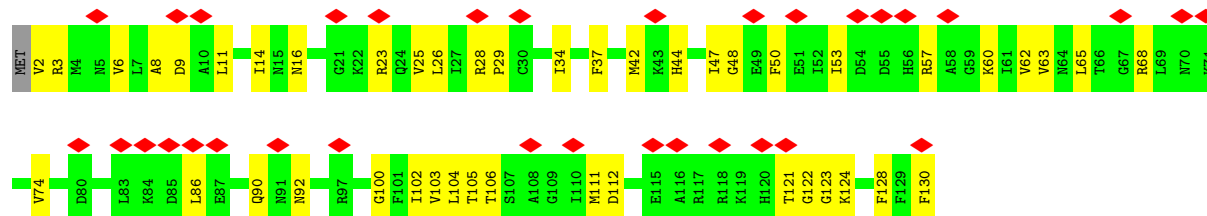


- Molecule 71: eS21



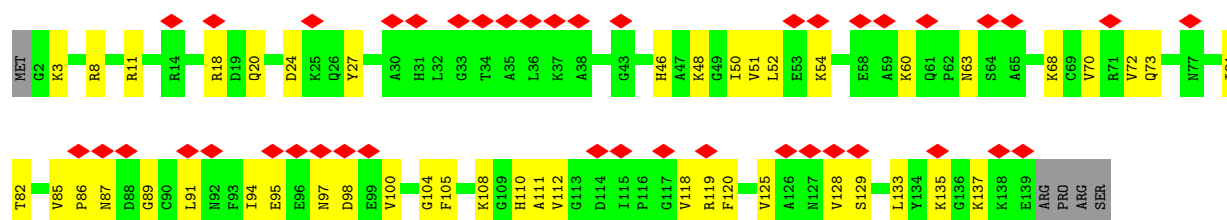
- Molecule 72: uS8

Chain WW:



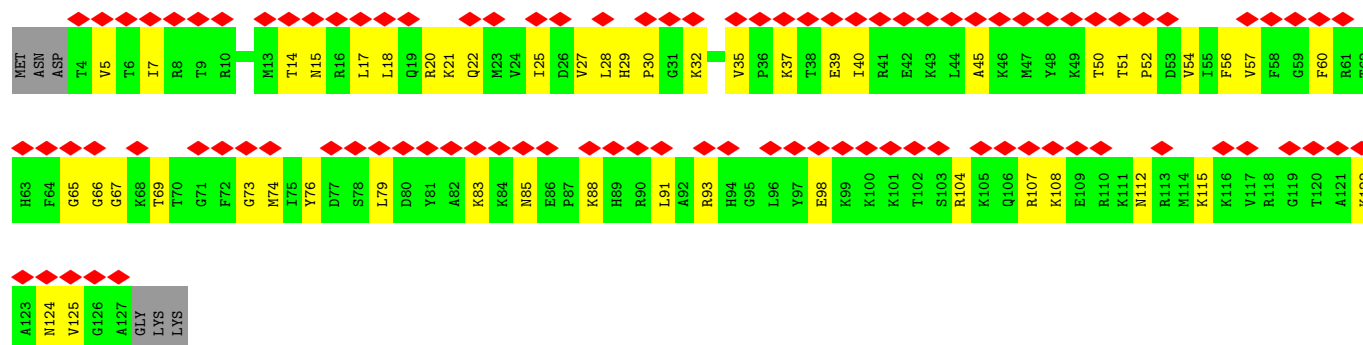
- Molecule 73: uS12

Chain XX:



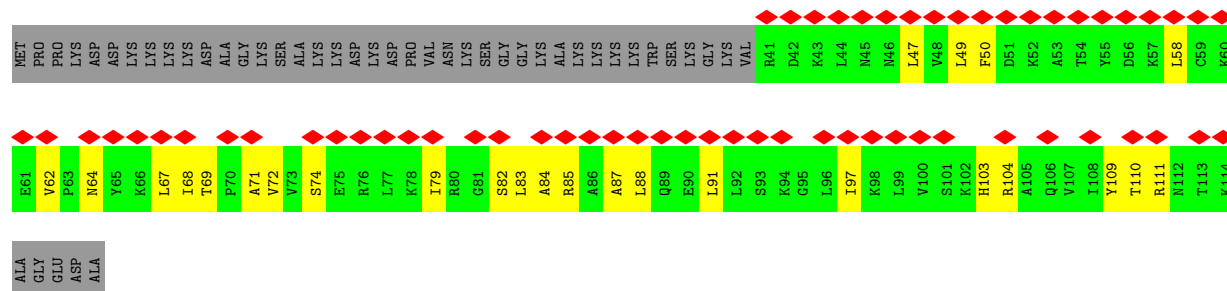
- Molecule 74: eS24

Chain YY:

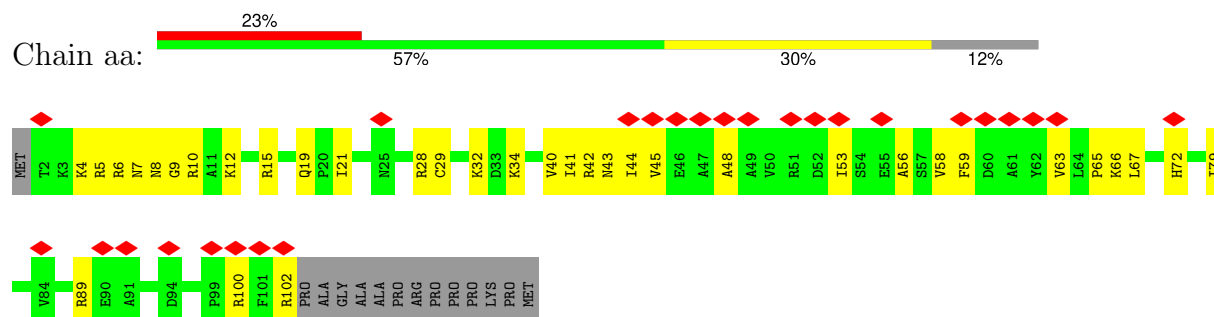


- Molecule 75: eS25

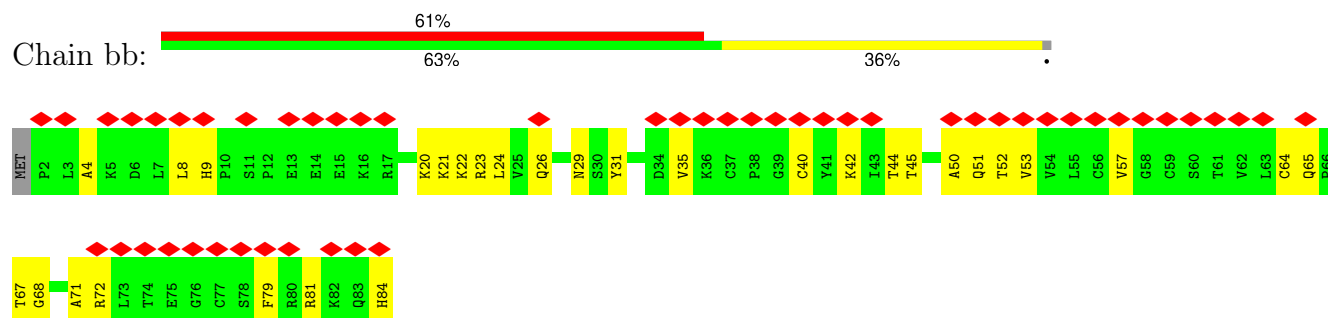
Chain ZZ:



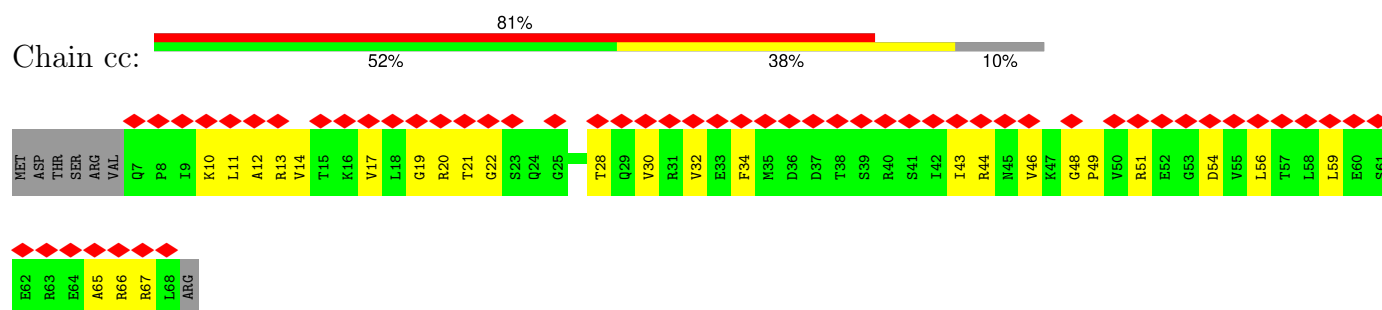
- Molecule 76: eS26



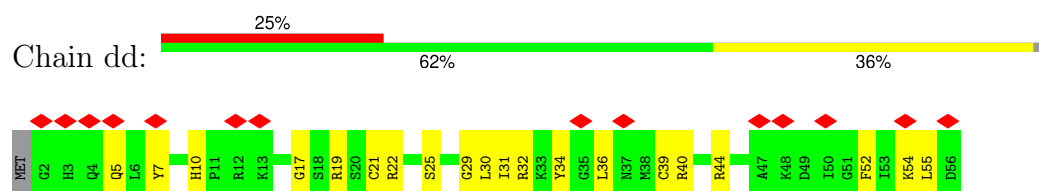
- Molecule 77: eS27



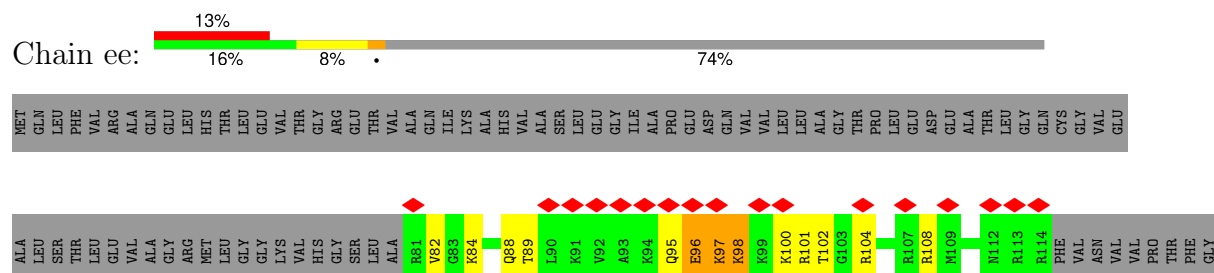
- Molecule 78: eS28



- Molecule 79: uS14

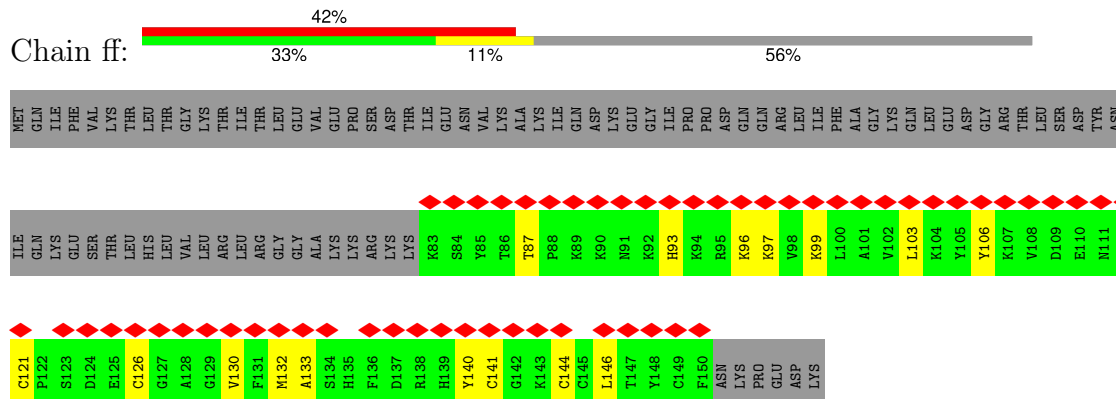


- Molecule 80: eS30

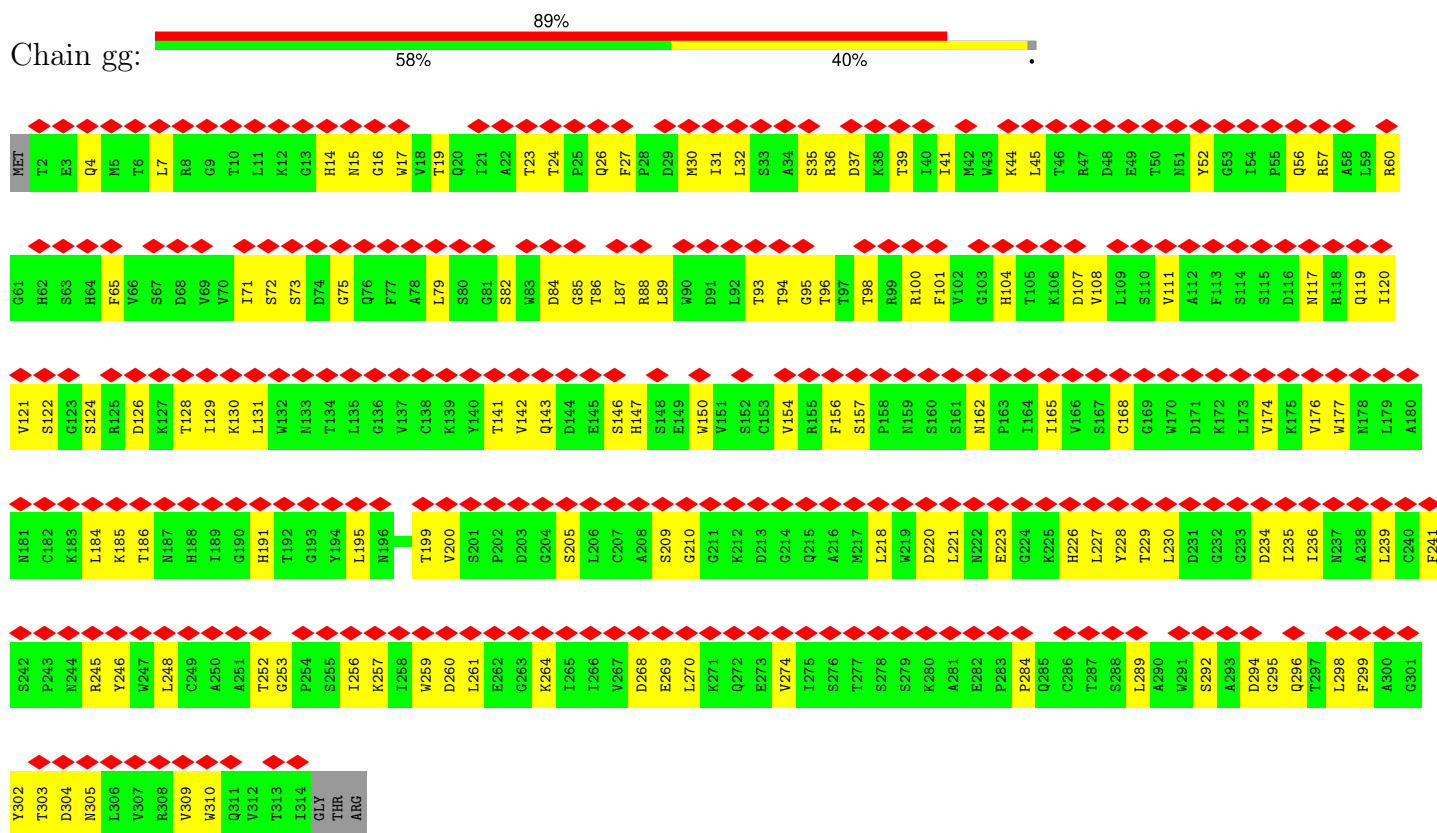


LYS
LYS
LYS
GLY
PRO
ASN
ALA
ASN
SER

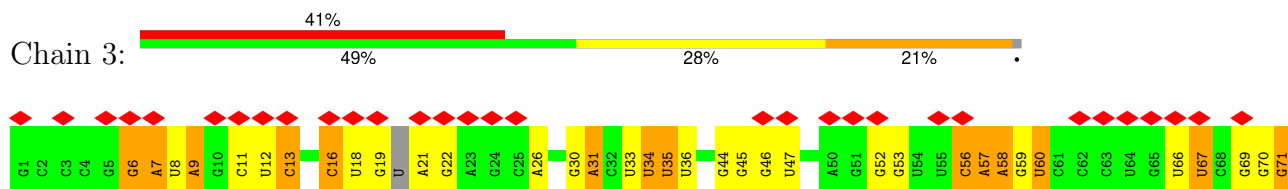
• Molecule 81: eS31



• Molecule 82: RACK1

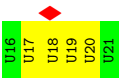


• Molecule 83: E-site tRNA

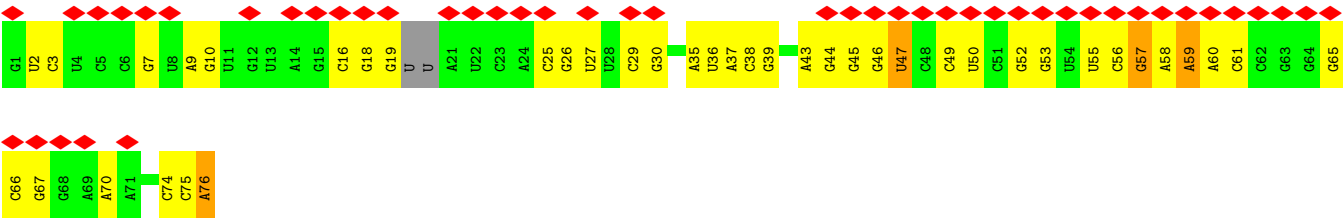




• Molecule 84: mRNA



• Molecule 85: P-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42975	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.943	Depositor
Minimum map value	-0.613	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, B8N, B9B, E3C, M7A, 4AC, PSU, 2MG, B8Q, 6MZ, 5MU, 5MC, MG, UY1, GDP, UR3, DDE, MA6, 34G, OMC, ZN, A2M, 1MA, OMU

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	0.37	0/1929	0.38	0/2586
2	B	0.36	0/3216	0.37	0/4311
3	C	0.38	0/2937	0.40	0/3946
4	D	0.29	0/2407	0.34	0/3224
5	E	0.29	0/1760	0.35	0/2362
6	F	0.39	0/1911	0.37	0/2549
7	G	0.30	0/1799	0.37	0/2424
8	H	0.33	0/1535	0.37	0/2063
9	I	0.33	0/1729	0.37	0/2308
10	J	0.29	0/1359	0.36	0/1817
11	L	0.31	0/1733	0.33	0/2316
12	M	0.32	0/1158	0.33	0/1547
13	N	0.40	0/1746	0.38	0/2338
14	O	0.36	0/1653	0.40	0/2210
15	P	0.39	0/1268	0.39	0/1700
16	Q	0.37	0/1539	0.39	0/2054
17	R	0.31	0/1518	0.36	0/2005
18	S	0.37	0/1501	0.40	0/2012
19	T	0.34	0/1326	0.34	0/1770
20	U	0.25	0/814	0.41	0/1092
21	V	0.34	0/987	0.38	0/1324
22	W	0.34	0/541	0.34	0/720
23	X	0.31	0/966	0.35	0/1301
24	Y	0.32	0/1132	0.40	0/1504
25	Z	0.29	0/1130	0.35	0/1507
26	a	0.40	0/1191	0.41	0/1590
27	b	0.32	0/619	0.38	0/818
28	c	0.32	0/742	0.34	0/995
29	d	0.32	0/846	0.35	0/1136
30	e	0.40	0/1071	0.39	0/1429
31	f	0.41	0/895	0.41	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	g	0.33	0/916	0.39	0/1220
33	h	0.30	0/1021	0.36	0/1348
34	i	0.27	0/841	0.35	0/1112
35	j	0.38	0/720	0.44	0/952
36	k	0.28	0/565	0.38	0/750
37	l	0.36	0/450	0.40	0/597
38	m	0.32	0/427	0.48	0/564
39	n	0.34	0/223	0.31	0/284
40	o	0.33	0/855	0.35	0/1128
41	p	0.33	0/718	0.33	0/953
42	r	0.34	0/1017	0.37	0/1364
43	s	0.16	0/1530	0.38	0/2064
44	t	0.16	0/1174	0.39	0/1582
45	5	0.39	1/82306 (0.0%)	0.36	0/128361
46	7	0.37	0/2858	0.31	0/4455
47	8	0.37	0/3675	0.34	0/5725
48	v	0.22	0/6623	0.40	0/8943
49	9	0.29	1/39726 (0.0%)	0.32	0/61882
50	AA	0.24	0/1747	0.34	0/2374
51	BB	0.23	0/1756	0.36	0/2350
52	CC	0.26	0/1753	0.38	0/2369
53	DD	0.23	0/1796	0.35	0/2417
54	EE	0.23	0/2118	0.36	0/2849
55	FF	0.23	0/1492	0.36	0/2005
56	GG	0.21	0/1946	0.35	0/2590
57	HH	0.20	0/1510	0.39	0/2022
58	II	0.24	0/1715	0.37	0/2287
59	JJ	0.22	0/1550	0.33	0/2069
60	KK	0.23	0/834	0.38	0/1125
61	LL	0.26	0/1195	0.34	0/1597
62	MM	0.16	0/918	0.39	0/1233
63	NN	0.24	0/1226	0.34	0/1649
64	OO	0.28	0/1029	0.41	0/1380
65	PP	0.22	0/994	0.39	0/1327
66	QQ	0.26	0/1146	0.41	0/1534
67	RR	0.21	0/1082	0.38	0/1452
68	SS	0.23	0/1190	0.41	0/1594
69	TT	0.23	0/1115	0.41	0/1493
70	UU	0.23	0/805	0.43	0/1081
71	VV	0.26	0/643	0.38	0/860
72	WW	0.27	0/1051	0.39	0/1406
73	XX	0.26	0/1086	0.39	0/1450
74	YY	0.20	0/1028	0.34	0/1366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	ZZ	0.21	0/604	0.37	0/810
76	aa	0.30	0/828	0.38	0/1109
77	bb	0.21	0/665	0.36	0/891
78	cc	0.16	0/490	0.38	0/656
79	dd	0.28	0/470	0.38	0/623
80	ee	0.24	0/289	0.61	0/374
81	ff	0.16	0/566	0.35	0/750
82	gg	0.19	0/2493	0.39	0/3394
83	3	0.23	0/1754	0.30	0/2725
84	w	0.24	0/131	0.32	0/200
85	2	0.21	0/1761	0.29	0/2739
All	All	0.33	2/233379 (0.0%)	0.36	0/341590

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
48	v	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	5	3785	A2M	O3'-P	5.30	1.61	1.56
49	9	668	A2M	O3'-P	5.08	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	v	701	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1891	0	1986	72	0
2	B	3148	0	3267	108	0
3	C	2883	0	3053	128	0
4	D	2361	0	2395	75	0
5	E	1726	0	1869	63	0
6	F	1875	0	1995	65	0
7	G	1768	0	1891	63	0
8	H	1516	0	1597	56	0
9	I	1691	0	1740	59	0
10	J	1336	0	1375	38	0
11	L	1702	0	1820	43	0
12	M	1137	0	1211	45	0
13	N	1701	0	1749	74	0
14	O	1621	0	1770	48	0
15	P	1242	0	1274	39	0
16	Q	1515	0	1634	56	0
17	R	1502	0	1659	37	0
18	S	1462	0	1508	56	0
19	T	1298	0	1366	48	0
20	U	800	0	825	32	0
21	V	973	0	1034	18	0
22	W	528	0	541	11	0
23	X	949	0	1016	31	0
24	Y	1115	0	1205	41	0
25	Z	1107	0	1182	33	0
26	a	1162	0	1209	61	0
27	b	609	0	650	19	0
28	c	732	0	767	21	0
29	d	833	0	891	23	0
30	e	1053	0	1147	39	0
31	f	876	0	912	43	0
32	g	906	0	999	36	0
33	h	1013	0	1147	35	0
34	i	830	0	916	24	0
35	j	705	0	737	36	0
36	k	559	0	624	18	0
37	l	438	0	469	19	0
38	m	421	0	454	11	0
39	n	222	0	264	10	0
40	o	842	0	912	22	0
41	p	708	0	756	19	0
42	r	1001	0	1060	46	0
43	s	1507	0	1564	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	t	1160	0	1218	46	0
45	5	75712	0	38336	1746	0
46	7	2558	0	1296	52	0
47	8	3315	0	1685	94	0
48	v	6516	0	6607	287	0
49	9	36291	0	18320	952	0
50	AA	1710	0	1708	84	0
51	BB	1729	0	1803	64	0
52	CC	1716	0	1806	74	0
53	DD	1768	0	1866	64	0
54	EE	2076	0	2177	88	0
55	FF	1471	0	1522	75	0
56	GG	1923	0	2089	68	0
57	HH	1488	0	1582	63	0
58	II	1686	0	1772	63	0
59	JJ	1525	0	1640	60	0
60	KK	810	0	836	29	0
61	LL	1175	0	1249	37	0
62	MM	908	0	939	53	0
63	NN	1202	0	1289	35	0
64	OO	1016	0	1039	84	0
65	PP	975	0	1022	43	0
66	QQ	1128	0	1195	67	0
67	RR	1068	0	1121	48	0
68	SS	1172	0	1229	75	0
69	TT	1097	0	1132	54	0
70	UU	795	0	862	42	0
71	VV	636	0	637	45	0
72	WW	1034	0	1080	49	0
73	XX	1069	0	1134	50	0
74	YY	1011	0	1083	44	0
75	ZZ	598	0	656	31	0
76	aa	814	0	864	36	0
77	bb	651	0	672	25	0
78	cc	488	0	514	30	0
79	dd	459	0	449	23	0
80	ee	289	0	332	19	0
81	ff	555	0	563	26	0
82	gg	2436	0	2393	112	0
83	3	1573	0	802	28	0
84	w	120	0	61	4	0
85	2	1577	0	804	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	2	1	0	0	0	0
86	5	198	0	0	0	0
86	7	5	0	0	0	0
86	8	1	0	0	0	0
86	9	56	0	0	0	0
86	A	2	0	0	0	0
86	I	2	0	0	0	0
86	P	1	0	0	0	0
86	QQ	1	0	0	0	0
86	TT	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	aa	1	0	0	0	0
86	e	1	0	0	0	0
86	f	1	0	0	0	0
86	g	1	0	0	0	0
86	o	1	0	0	0	0
86	w	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
88	v	28	0	12	0	0
89	9	35	0	40	0	0
All	All	220911	0	165876	5657	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 15.

The worst 5 of 5657 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)
45:5:2638:G:N2	45:5:2697:A:N1	2.03	1.04
45:5:3692:A:N6	45:5:3823:G:H21	1.56	1.04
45:5:1991:A:O2'	45:5:1992:U:O5'	1.78	1.01
3:C:92:PHE:O	3:C:100:ARG:NH1	1.95	0.99
42:r:98:ARG:NH2	45:5:2262:G:OP2	1.95	0.99

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	
1	A	245/257 (95%)	213 (87%)	32 (13%)	0	100	100
2	B	392/403 (97%)	356 (91%)	36 (9%)	0	100	100
3	C	360/425 (85%)	336 (93%)	24 (7%)	0	100	100
4	D	287/297 (97%)	274 (96%)	13 (4%)	0	100	100
5	E	209/291 (72%)	194 (93%)	15 (7%)	0	100	100
6	F	223/247 (90%)	207 (93%)	16 (7%)	0	100	100
7	G	214/319 (67%)	197 (92%)	17 (8%)	0	100	100
8	H	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
9	I	204/214 (95%)	189 (93%)	15 (7%)	0	100	100
10	J	165/178 (93%)	157 (95%)	8 (5%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	136/218 (62%)	128 (94%)	8 (6%)	0	100	100
13	N	201/204 (98%)	182 (90%)	19 (10%)	0	100	100
14	O	196/203 (97%)	187 (95%)	9 (5%)	0	100	100
15	P	151/184 (82%)	144 (95%)	7 (5%)	0	100	100
16	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
17	R	177/196 (90%)	168 (95%)	9 (5%)	0	100	100
18	S	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
19	T	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
20	U	96/128 (75%)	86 (90%)	10 (10%)	0	100	100
21	V	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
22	W	61/157 (39%)	57 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	X	114/156 (73%)	106 (93%)	8 (7%)	0	100	100
24	Y	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
25	Z	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
26	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
27	b	73/245 (30%)	66 (90%)	7 (10%)	0	100	100
28	c	92/115 (80%)	83 (90%)	9 (10%)	0	100	100
29	d	96/125 (77%)	93 (97%)	3 (3%)	0	100	100
30	e	126/135 (93%)	113 (90%)	13 (10%)	0	100	100
31	f	107/110 (97%)	97 (91%)	10 (9%)	0	100	100
32	g	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
33	h	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
34	i	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	j	84/97 (87%)	77 (92%)	7 (8%)	0	100	100
36	k	66/70 (94%)	63 (96%)	3 (4%)	0	100	100
37	l	47/51 (92%)	42 (89%)	5 (11%)	0	100	100
38	m	49/93 (53%)	46 (94%)	3 (6%)	0	100	100
39	n	21/25 (84%)	21 (100%)	0	0	100	100
40	o	101/106 (95%)	92 (91%)	9 (9%)	0	100	100
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	r	123/137 (90%)	110 (89%)	13 (11%)	0	100	100
43	s	194/318 (61%)	170 (88%)	24 (12%)	0	100	100
44	t	151/165 (92%)	120 (80%)	31 (20%)	0	100	100
48	v	830/858 (97%)	724 (87%)	106 (13%)	0	100	100
50	AA	215/295 (73%)	190 (88%)	25 (12%)	0	100	100
51	BB	211/264 (80%)	194 (92%)	17 (8%)	0	100	100
52	CC	219/293 (75%)	200 (91%)	19 (9%)	0	100	100
53	DD	226/243 (93%)	212 (94%)	14 (6%)	0	100	100
54	EE	260/263 (99%)	233 (90%)	27 (10%)	0	100	100
55	FF	181/204 (89%)	171 (94%)	10 (6%)	0	100	100
56	GG	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
57	HH	181/194 (93%)	166 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	II	204/208 (98%)	178 (87%)	26 (13%)	0	100	100
59	JJ	183/194 (94%)	170 (93%)	13 (7%)	0	100	100
60	KK	94/165 (57%)	83 (88%)	11 (12%)	0	100	100
61	LL	139/158 (88%)	121 (87%)	18 (13%)	0	100	100
62	MM	115/132 (87%)	103 (90%)	12 (10%)	0	100	100
63	NN	147/151 (97%)	134 (91%)	13 (9%)	0	100	100
64	OO	134/168 (80%)	108 (81%)	26 (19%)	0	100	100
65	PP	115/145 (79%)	103 (90%)	12 (10%)	0	100	100
66	QQ	140/146 (96%)	125 (89%)	15 (11%)	0	100	100
67	RR	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
68	SS	140/152 (92%)	126 (90%)	13 (9%)	1 (1%)	18	49
69	TT	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
70	UU	98/119 (82%)	88 (90%)	9 (9%)	1 (1%)	12	40
71	VV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
72	WW	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
73	XX	136/143 (95%)	125 (92%)	11 (8%)	0	100	100
74	YY	122/130 (94%)	112 (92%)	10 (8%)	0	100	100
75	ZZ	73/125 (58%)	67 (92%)	6 (8%)	0	100	100
76	aa	99/115 (86%)	88 (89%)	11 (11%)	0	100	100
77	bb	81/84 (96%)	69 (85%)	12 (15%)	0	100	100
78	cc	60/69 (87%)	54 (90%)	6 (10%)	0	100	100
79	dd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
80	ee	32/133 (24%)	22 (69%)	7 (22%)	3 (9%)	0	3
81	ff	65/156 (42%)	56 (86%)	9 (14%)	0	100	100
82	gg	311/317 (98%)	269 (86%)	42 (14%)	0	100	100
All	All	12208/14224 (86%)	11108 (91%)	1095 (9%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	ee	96	GLU
80	ee	98	LYS
70	UU	97	ILE

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Mol	Chain	Res	Type
80	ee	97	LYS
68	SS	74	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/199 (95%)	189 (100%)	0	100	100
2	B	336/348 (97%)	336 (100%)	0	100	100
3	C	302/347 (87%)	302 (100%)	0	100	100
4	D	245/250 (98%)	244 (100%)	1 (0%)	84	84
5	E	191/251 (76%)	191 (100%)	0	100	100
6	F	196/215 (91%)	196 (100%)	0	100	100
7	G	189/272 (70%)	189 (100%)	0	100	100
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	178/181 (98%)	178 (100%)	0	100	100
10	J	140/149 (94%)	140 (100%)	0	100	100
11	L	175/176 (99%)	175 (100%)	0	100	100
12	M	117/161 (73%)	117 (100%)	0	100	100
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	170/173 (98%)	170 (100%)	0	100	100
15	P	134/163 (82%)	134 (100%)	0	100	100
16	Q	164/165 (99%)	164 (100%)	0	100	100
17	R	158/175 (90%)	158 (100%)	0	100	100
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	88/114 (77%)	88 (100%)	0	100	100
21	V	100/107 (94%)	100 (100%)	0	100	100
22	W	55/126 (44%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	104/134 (78%)	104 (100%)	0	100	100
24	Y	124/135 (92%)	124 (100%)	0	100	100
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	119 (100%)	0	100	100
27	b	62/184 (34%)	62 (100%)	0	100	100
28	c	80/98 (82%)	80 (100%)	0	100	100
29	d	91/110 (83%)	91 (100%)	0	100	100
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/100 (98%)	98 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100
36	k	63/65 (97%)	63 (100%)	0	100	100
37	l	46/48 (96%)	46 (100%)	0	100	100
38	m	47/84 (56%)	47 (100%)	0	100	100
39	n	22/24 (92%)	22 (100%)	0	100	100
40	o	91/94 (97%)	91 (100%)	0	100	100
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	109/121 (90%)	109 (100%)	0	100	100
43	s	164/258 (64%)	164 (100%)	0	100	100
44	t	126/137 (92%)	126 (100%)	0	100	100
48	v	710/729 (97%)	709 (100%)	1 (0%)	88	90
50	AA	180/245 (74%)	180 (100%)	0	100	100
51	BB	194/231 (84%)	194 (100%)	0	100	100
52	CC	187/225 (83%)	187 (100%)	0	100	100
53	DD	190/202 (94%)	190 (100%)	0	100	100
54	EE	224/225 (100%)	224 (100%)	0	100	100
55	FF	158/170 (93%)	158 (100%)	0	100	100
56	GG	207/218 (95%)	207 (100%)	0	100	100
57	HH	165/174 (95%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	II	178/180 (99%)	178 (100%)	0	100	100
59	JJ	161/168 (96%)	161 (100%)	0	100	100
60	KK	87/136 (64%)	87 (100%)	0	100	100
61	LL	130/142 (92%)	130 (100%)	0	100	100
62	MM	99/108 (92%)	99 (100%)	0	100	100
63	NN	130/131 (99%)	130 (100%)	0	100	100
64	OO	106/130 (82%)	106 (100%)	0	100	100
65	PP	107/130 (82%)	107 (100%)	0	100	100
66	QQ	117/121 (97%)	117 (100%)	0	100	100
67	RR	119/121 (98%)	119 (100%)	0	100	100
68	SS	123/132 (93%)	123 (100%)	0	100	100
69	TT	111/115 (96%)	111 (100%)	0	100	100
70	UU	92/107 (86%)	92 (100%)	0	100	100
71	VV	67/67 (100%)	67 (100%)	0	100	100
72	WW	112/113 (99%)	112 (100%)	0	100	100
73	XX	110/115 (96%)	110 (100%)	0	100	100
74	YY	107/112 (96%)	107 (100%)	0	100	100
75	ZZ	66/103 (64%)	66 (100%)	0	100	100
76	aa	88/98 (90%)	88 (100%)	0	100	100
77	bb	75/76 (99%)	75 (100%)	0	100	100
78	cc	55/62 (89%)	55 (100%)	0	100	100
79	dd	48/49 (98%)	48 (100%)	0	100	100
80	ee	29/106 (27%)	29 (100%)	0	100	100
81	ff	61/140 (44%)	61 (100%)	0	100	100
82	gg	272/275 (99%)	272 (100%)	0	100	100
All	All	10635/12062 (88%)	10633 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	267	ASN
48	v	811	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
63	NN	123	HIS
65	PP	79	HIS
76	aa	25	ASN
17	R	86	ASN
17	R	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3506/3543 (98%)	744 (21%)	61 (1%)
46	7	119/120 (99%)	17 (14%)	1 (0%)
47	8	155/156 (99%)	35 (22%)	2 (1%)
49	9	1684/1869 (90%)	417 (24%)	24 (1%)
83	3	71/75 (94%)	20 (28%)	1 (1%)
84	w	5/6 (83%)	0	0
85	2	71/76 (93%)	10 (14%)	0
All	All	5611/5845 (95%)	1243 (22%)	89 (1%)

5 of 1243 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	13	U
45	5	15	A
45	5	25	A
45	5	33	A
45	5	39	A

5 of 89 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	5	4884	G
49	9	553	U
45	5	4932	U
49	9	140	U
49	9	870	A

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
45	OMG	5	1625	45	23,26,27	2.43	8 (34%)	32,38,41	1.99	9 (28%)
45	PSU	5	3715	45	17,20,22	2.15	9 (52%)	21,28,33	1.92	4 (19%)
45	5MC	5	4447	45	19,22,23	3.56	8 (42%)	26,32,35	1.25	3 (11%)
45	PSU	5	4457	45	17,20,22	2.20	9 (52%)	21,28,33	2.02	4 (19%)
45	OMU	5	2837	45	19,22,23	2.81	6 (31%)	25,31,34	1.93	5 (20%)
49	PSU	9	1081	49	18,21,22	2.19	10 (55%)	21,30,33	1.93	3 (14%)
45	OMC	5	2365	45	19,22,23	2.98	8 (42%)	25,31,34	0.84	0
45	OMG	5	3792	45	23,26,27	2.45	8 (34%)	32,38,41	1.99	9 (28%)
49	OMU	9	116	49	19,22,23	2.80	6 (31%)	25,31,34	1.74	6 (24%)
45	PSU	5	4293	45	17,20,22	2.36	9 (52%)	21,28,33	2.01	4 (19%)
45	PSU	5	4579	45	17,20,22	2.21	8 (47%)	21,28,33	1.85	4 (19%)
49	A2M	9	668	49,86	22,25,26	3.46	9 (40%)	30,36,39	2.66	14 (46%)
45	PSU	5	4500	45	17,20,22	2.10	8 (47%)	21,28,33	1.90	4 (19%)
45	OMG	5	3627	45	23,26,27	2.38	9 (39%)	32,38,41	2.13	9 (28%)
49	MA6	9	1850	49	23,26,27	1.42	4 (17%)	33,38,41	4.42	14 (42%)
45	A2M	5	400	45	22,25,26	3.57	9 (40%)	30,36,39	2.65	11 (36%)
45	OMU	5	3925	45	19,22,23	2.68	6 (31%)	25,31,34	1.90	5 (20%)
49	OMG	9	509	49,86	23,26,27	2.43	7 (30%)	32,38,41	1.92	9 (28%)
45	OMG	5	373	45	23,26,27	2.40	9 (39%)	32,38,41	2.07	10 (31%)
45	OMC	5	2804	45	19,22,23	2.91	8 (42%)	25,31,34	0.83	0
45	OMG	5	4499	45	23,26,27	2.48	9 (39%)	32,38,41	2.08	9 (28%)
45	UR3	5	4530	45	19,22,23	2.67	8 (42%)	26,32,35	1.64	4 (15%)
45	PSU	5	4361	45	17,20,22	2.25	8 (47%)	21,28,33	1.96	5 (23%)
45	PSU	5	4299	45	17,20,22	2.25	9 (52%)	21,28,33	1.98	5 (23%)
45	OMC	5	3841	45	19,22,23	2.75	8 (42%)	25,31,34	0.92	1 (4%)
45	PSU	5	4521	86,45	17,20,22	2.20	9 (52%)	21,28,33	1.94	4 (19%)
49	PSU	9	822	49	18,21,22	2.07	8 (44%)	21,30,33	1.95	4 (19%)
49	A2M	9	1678	49	22,25,26	3.56	9 (40%)	30,36,39	2.78	12 (40%)
49	A2M	9	159	49	22,25,26	3.53	9 (40%)	30,36,39	2.57	11 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	PSU	5	2632	45	17,20,22	2.17	8 (47%)	21,28,33	1.98	4 (19%)
45	OMG	5	4370	45	23,26,27	2.45	7 (30%)	32,38,41	1.99	9 (28%)
45	A2M	5	4523	86,45	22,25,26	3.59	10 (45%)	30,36,39	2.55	12 (40%)
45	OMU	5	4620	45	19,22,23	2.75	6 (31%)	25,31,34	1.98	5 (20%)
45	6MZ	5	4220	45	22,25,26	2.60	5 (22%)	29,36,39	2.22	10 (34%)
45	A2M	5	2363	86,45	22,25,26	3.64	9 (40%)	30,36,39	2.65	11 (36%)
45	PSU	5	4552	45	17,20,22	2.31	8 (47%)	21,28,33	2.00	4 (19%)
45	PSU	5	3853	45	17,20,22	2.24	10 (58%)	21,28,33	2.02	3 (14%)
45	PSU	5	1744	45	17,20,22	2.15	8 (47%)	21,28,33	2.07	4 (19%)
45	A2M	5	3760	49,45	22,25,26	3.46	8 (36%)	30,36,39	2.62	11 (36%)
49	PSU	9	823	49	18,21,22	2.09	9 (50%)	21,30,33	1.95	5 (23%)
49	6MZ	9	1832	49,86	22,25,26	2.69	4 (18%)	29,36,39	2.21	9 (31%)
45	A2M	5	2815	45	22,25,26	3.53	9 (40%)	30,36,39	2.64	10 (33%)
49	5MC	9	1374	49	19,22,23	3.73	8 (42%)	26,32,35	0.99	2 (7%)
49	4AC	9	1842	49	21,24,25	3.29	10 (47%)	28,34,37	1.04	4 (14%)
45	OMG	5	2424	45	23,26,27	2.45	9 (39%)	32,38,41	2.01	9 (28%)
45	PSU	5	4296	45	17,20,22	2.14	8 (47%)	21,28,33	2.06	4 (19%)
45	A2M	5	3830	45	22,25,26	3.52	10 (45%)	30,36,39	2.50	9 (30%)
45	OMG	5	3899	45	23,26,27	2.41	9 (39%)	32,38,41	2.03	9 (28%)
45	PSU	5	4442	45	17,20,22	2.18	10 (58%)	21,28,33	1.93	4 (19%)
45	PSU	5	1860	45	17,20,22	2.09	9 (52%)	21,28,33	1.84	4 (19%)
49	A2M	9	484	49	22,25,26	3.54	9 (40%)	30,36,39	2.66	12 (40%)
45	A2M	5	398	45	22,25,26	3.63	10 (45%)	30,36,39	2.58	12 (40%)
45	A2M	5	3724	45	22,25,26	3.55	9 (40%)	30,36,39	2.52	9 (30%)
45	A2M	5	1524	45	22,25,26	3.56	10 (45%)	30,36,39	2.81	12 (40%)
45	A2M	5	1326	45	22,25,26	3.64	10 (45%)	30,36,39	2.59	9 (30%)
45	OMG	5	1522	45	23,26,27	2.36	8 (34%)	32,38,41	2.04	10 (31%)
45	OMG	5	4623	45	23,26,27	2.37	8 (34%)	32,38,41	1.99	9 (28%)
45	PSU	5	3639	45	17,20,22	2.27	8 (47%)	21,28,33	1.93	4 (19%)
49	OMC	9	1703	49	19,22,23	3.01	8 (42%)	25,31,34	0.74	0
49	OMC	9	174	49	19,22,23	3.05	8 (42%)	25,31,34	0.84	0
45	A2M	5	2787	45	22,25,26	3.47	9 (40%)	30,36,39	2.57	10 (33%)
49	PSU	9	1243	49	18,21,22	2.10	8 (44%)	21,30,33	2.01	4 (19%)
45	PSU	5	4532	45	17,20,22	2.22	8 (47%)	21,28,33	1.95	4 (19%)
45	OMC	5	2824	45	19,22,23	2.85	8 (42%)	25,31,34	0.94	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	OMU	5	4227	45	19,22,23	2.78	6 (31%)	25,31,34	1.77	4 (16%)
45	OMU	5	4498	45	19,22,23	2.75	6 (31%)	25,31,34	1.88	5 (20%)
45	B9B	5	237	45	25,28,29	1.89	7 (28%)	35,40,43	2.48	16 (45%)
49	4AC	9	1337	49	21,24,25	3.31	10 (47%)	28,34,37	1.02	4 (14%)
45	PSU	5	3764	45	17,20,22	2.15	9 (52%)	21,28,33	1.80	4 (19%)
45	UY1	5	3818	86,45	19,22,23	4.33	9 (47%)	21,31,34	1.91	5 (23%)
49	UR3	9	1830	49	19,22,23	2.65	8 (42%)	26,32,35	1.56	4 (15%)
45	OMC	5	4536	45	19,22,23	2.81	8 (42%)	25,31,34	0.85	1 (4%)
45	2MG	5	1517	45	23,26,27	2.65	9 (39%)	33,38,41	2.26	13 (39%)
47	OMG	8	75	47	23,26,27	2.43	8 (34%)	32,38,41	1.95	8 (25%)
45	PSU	5	3920	45	17,20,22	2.25	8 (47%)	21,28,33	1.89	5 (23%)
45	OMG	5	4196	85,45	23,26,27	2.39	9 (39%)	32,38,41	1.99	9 (28%)
49	A2M	9	1031	49	22,25,26	3.53	9 (40%)	30,36,39	2.61	11 (36%)
45	PSU	5	3695	45	17,20,22	2.23	9 (52%)	21,28,33	1.86	3 (14%)
45	OMG	5	4392	45	23,26,27	2.37	8 (34%)	32,38,41	2.01	9 (28%)
49	OMC	9	1710	49	19,22,23	2.99	8 (42%)	25,31,34	0.80	0
45	A2M	5	3825	45	22,25,26	3.61	9 (40%)	30,36,39	2.57	11 (36%)
45	PSU	5	1683	45	17,20,22	2.25	9 (52%)	21,28,33	1.98	4 (19%)
49	OMG	9	683	49	23,26,27	2.45	9 (39%)	32,38,41	2.05	10 (31%)
49	OMC	9	517	49	19,22,23	3.03	8 (42%)	25,31,34	0.84	0
49	A2M	9	27	49	22,25,26	3.59	9 (40%)	30,36,39	2.55	9 (30%)
45	OMG	5	4228	45	23,26,27	2.36	9 (39%)	32,38,41	2.08	9 (28%)
49	OMG	9	644	49	23,26,27	2.44	9 (39%)	32,38,41	2.02	12 (37%)
49	M7A	9	1806	49	19,25,26	1.76	4 (21%)	25,37,40	4.20	8 (32%)
45	PSU	5	2508	45	17,20,22	2.15	9 (52%)	21,28,33	1.93	4 (19%)
49	OMU	9	121	49	19,22,23	2.90	6 (31%)	25,31,34	1.90	6 (24%)
45	OMG	5	4618	45	23,26,27	2.41	9 (39%)	32,38,41	2.05	10 (31%)
45	OMC	5	3869	45	19,22,23	2.76	7 (36%)	25,31,34	0.95	2 (8%)
45	OMG	5	4494	45	23,26,27	2.45	8 (34%)	32,38,41	1.92	9 (28%)
45	OMU	5	4306	45	19,22,23	2.73	6 (31%)	25,31,34	1.82	5 (20%)
45	1MA	5	1322	86,45	21,25,26	2.64	6 (28%)	30,37,40	2.73	7 (23%)
49	A2M	9	166	49	22,25,26	3.49	9 (40%)	30,36,39	2.59	10 (33%)
45	PSU	5	3762	45	17,20,22	2.12	8 (47%)	21,28,33	1.98	4 (19%)
45	A2M	5	1871	86,45	22,25,26	3.68	10 (45%)	30,36,39	2.54	10 (33%)
45	OMG	5	2876	45	23,26,27	2.47	7 (30%)	32,38,41	1.95	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	PSU	5	1782	45	17,20,22	2.13	9 (52%)	21,28,33	1.96	4 (19%)
49	B8N	9	1248	49	25,29,30	3.41	7 (28%)	28,42,45	2.11	7 (25%)
49	MA6	9	1851	49	23,26,27	1.49	5 (21%)	33,38,41	4.29	14 (42%)
48	DDE	v	715	48	18,20,21	0.91	1 (5%)	17,28,30	1.06	1 (5%)
45	A2M	5	3718	45	22,25,26	3.56	10 (45%)	30,36,39	2.51	11 (36%)
45	OMC	5	3887	45	19,22,23	2.89	8 (42%)	25,31,34	0.81	0
45	OMC	5	1340	45	19,22,23	2.86	7 (36%)	25,31,34	1.00	1 (4%)
45	A2M	5	3867	45	22,25,26	3.57	9 (40%)	30,36,39	2.70	11 (36%)
45	OMG	5	4637	45	23,26,27	2.47	8 (34%)	32,38,41	2.10	11 (34%)
45	PSU	5	3851	45	17,20,22	2.18	9 (52%)	21,28,33	1.95	5 (23%)
45	PSU	5	4423	45	17,20,22	2.10	9 (52%)	21,28,33	1.90	4 (19%)
49	PSU	9	612	49	18,21,22	2.12	9 (50%)	21,30,33	1.93	4 (19%)
45	PSU	5	4420	45	17,20,22	2.13	9 (52%)	21,28,33	1.86	4 (19%)
49	5MU	9	814	49	19,22,23	1.42	6 (31%)	27,32,35	2.30	8 (29%)
45	OMC	5	3808	45	19,22,23	2.90	8 (42%)	25,31,34	0.76	0
45	A2M	5	4571	45	22,25,26	3.57	9 (40%)	30,36,39	2.57	11 (36%)
45	PSU	5	4628	45	17,20,22	2.26	9 (52%)	21,28,33	2.00	4 (19%)
45	PSU	5	1781	45	17,20,22	2.16	10 (58%)	21,28,33	1.85	5 (23%)
45	OMC	5	3701	86,45	19,22,23	2.92	8 (42%)	25,31,34	0.93	0
49	B8Q	9	1219	49,86	18,22,23	2.76	4 (22%)	21,32,35	1.71	5 (23%)
45	OMC	5	2861	45	19,22,23	2.96	8 (42%)	25,31,34	0.78	0
49	E3C	9	568	49	19,23,24	3.30	6 (31%)	21,33,36	1.50	4 (19%)
45	A2M	5	1534	86,45	22,25,26	3.52	9 (40%)	30,36,39	2.77	12 (40%)
45	OMG	5	2364	45	23,26,27	2.41	8 (34%)	32,38,41	2.00	9 (28%)
45	PSU	5	3734	45	17,20,22	2.10	8 (47%)	21,28,33	1.87	4 (19%)
45	OMC	5	4456	45	19,22,23	2.89	8 (42%)	25,31,34	0.75	0
45	PSU	5	4353	45	17,20,22	2.16	9 (52%)	21,28,33	1.95	5 (23%)
45	PSU	5	4403	45	17,20,22	2.31	10 (58%)	21,28,33	1.89	5 (23%)
45	A2M	5	3785	45	22,25,26	3.50	9 (40%)	30,36,39	2.77	14 (46%)
45	PSU	5	1677	45	17,20,22	2.16	9 (52%)	21,28,33	1.90	4 (19%)
45	OMG	5	1316	45	23,26,27	2.44	8 (34%)	32,38,41	2.05	11 (34%)
45	PSU	5	1862	45	17,20,22	2.23	9 (52%)	21,28,33	2.03	4 (19%)
45	OMC	5	2422	86,45	19,22,23	2.94	8 (42%)	25,31,34	0.85	0
45	PSU	5	1792	45	17,20,22	2.22	10 (58%)	21,28,33	1.95	4 (19%)
49	PSU	9	119	49	18,21,22	2.04	9 (50%)	21,30,33	1.93	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
45	OMC	5	2351	45	19,22,23	2.82	8 (42%)	25,31,34	0.82	0
45	5MC	5	3782	86,45	19,22,23	3.61	8 (42%)	26,32,35	1.08	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	OMG	5	1625	45	-	2/9/27/28	0/3/3/3
45	PSU	5	3715	45	-	0/6/24/26	0/2/2/2
45	5MC	5	4447	45	-	4/7/25/26	0/2/2/2
45	PSU	5	4457	45	-	0/6/24/26	0/2/2/2
45	OMU	5	2837	45	-	0/9/27/28	0/2/2/2
49	PSU	9	1081	49	-	5/7/25/26	0/2/2/2
45	OMC	5	2365	45	-	2/9/27/28	0/2/2/2
45	OMG	5	3792	45	-	2/9/27/28	0/3/3/3
49	OMU	9	116	49	-	4/9/27/28	0/2/2/2
45	PSU	5	4293	45	-	0/6/24/26	0/2/2/2
45	PSU	5	4579	45	-	0/6/24/26	0/2/2/2
49	A2M	9	668	49,86	-	1/9/27/28	0/3/3/3
45	PSU	5	4500	45	-	2/6/24/26	0/2/2/2
45	OMG	5	3627	45	-	1/9/27/28	0/3/3/3
49	MA6	9	1850	49	-	4/11/29/30	0/3/3/3
45	A2M	5	400	45	-	0/9/27/28	0/3/3/3
45	OMU	5	3925	45	-	0/9/27/28	0/2/2/2
49	OMG	9	509	49,86	-	0/9/27/28	0/3/3/3
45	OMG	5	373	45	-	1/9/27/28	0/3/3/3
45	OMC	5	2804	45	-	2/9/27/28	0/2/2/2
45	OMG	5	4499	45	-	0/9/27/28	0/3/3/3
45	UR3	5	4530	45	-	0/7/25/26	0/2/2/2
45	PSU	5	4361	45	-	0/6/24/26	0/2/2/2
45	PSU	5	4299	45	-	0/6/24/26	0/2/2/2
45	OMC	5	3841	45	-	1/9/27/28	0/2/2/2
45	PSU	5	4521	86,45	-	0/6/24/26	0/2/2/2
49	PSU	9	822	49	-	2/7/25/26	0/2/2/2
49	A2M	9	1678	49	-	2/9/27/28	0/3/3/3
49	A2M	9	159	49	-	3/9/27/28	0/3/3/3
45	PSU	5	2632	45	-	0/6/24/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	OMG	5	4370	45	-	2/9/27/28	0/3/3/3
45	A2M	5	4523	86,45	-	0/9/27/28	0/3/3/3
45	OMU	5	4620	45	-	2/9/27/28	0/2/2/2
45	6MZ	5	4220	45	-	2/9/27/28	0/3/3/3
45	A2M	5	2363	86,45	-	2/9/27/28	0/3/3/3
45	PSU	5	4552	45	-	0/6/24/26	0/2/2/2
45	PSU	5	3853	45	-	0/6/24/26	0/2/2/2
45	PSU	5	1744	45	-	0/6/24/26	0/2/2/2
45	A2M	5	3760	49,45	-	3/9/27/28	0/3/3/3
49	PSU	9	823	49	-	0/7/25/26	0/2/2/2
49	6MZ	9	1832	49,86	-	0/9/27/28	0/3/3/3
45	A2M	5	2815	45	-	1/9/27/28	0/3/3/3
49	5MC	9	1374	49	-	0/7/25/26	0/2/2/2
49	4AC	9	1842	49	-	0/11/29/30	0/2/2/2
45	OMG	5	2424	45	-	2/9/27/28	0/3/3/3
45	PSU	5	4296	45	-	0/6/24/26	0/2/2/2
45	A2M	5	3830	45	-	0/9/27/28	0/3/3/3
45	OMG	5	3899	45	-	0/9/27/28	0/3/3/3
45	PSU	5	4442	45	-	0/6/24/26	0/2/2/2
45	PSU	5	1860	45	-	0/6/24/26	0/2/2/2
49	A2M	9	484	49	-	0/9/27/28	0/3/3/3
45	A2M	5	398	45	-	1/9/27/28	0/3/3/3
45	A2M	5	3724	45	-	0/9/27/28	0/3/3/3
45	A2M	5	1524	45	-	3/9/27/28	0/3/3/3
45	A2M	5	1326	45	-	2/9/27/28	0/3/3/3
45	OMG	5	1522	45	-	0/9/27/28	0/3/3/3
45	OMG	5	4623	45	-	1/9/27/28	0/3/3/3
45	PSU	5	3639	45	-	0/6/24/26	0/2/2/2
49	OMC	9	1703	49	-	2/9/27/28	0/2/2/2
49	OMC	9	174	49	-	3/9/27/28	0/2/2/2
45	A2M	5	2787	45	-	3/9/27/28	0/3/3/3
49	PSU	9	1243	49	-	2/7/25/26	0/2/2/2
45	PSU	5	4532	45	-	2/6/24/26	0/2/2/2
45	OMC	5	2824	45	-	1/9/27/28	0/2/2/2
45	OMU	5	4227	45	-	0/9/27/28	0/2/2/2
45	OMU	5	4498	45	-	0/9/27/28	0/2/2/2
45	B9B	5	237	45	-	2/11/29/30	0/3/3/3
49	4AC	9	1337	49	-	0/11/29/30	0/2/2/2
45	PSU	5	3764	45	-	0/6/24/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	UY1	5	3818	86,45	-	2/9/27/28	0/2/2/2
49	UR3	9	1830	49	-	2/7/25/26	0/2/2/2
45	OMC	5	4536	45	-	0/9/27/28	0/2/2/2
45	2MG	5	1517	45	-	0/9/27/28	0/3/3/3
47	OMG	8	75	47	-	2/9/27/28	0/3/3/3
45	PSU	5	3920	45	-	0/6/24/26	0/2/2/2
45	OMG	5	4196	85,45	-	0/9/27/28	0/3/3/3
49	A2M	9	1031	49	-	2/9/27/28	0/3/3/3
45	PSU	5	3695	45	-	3/6/24/26	0/2/2/2
45	OMG	5	4392	45	-	1/9/27/28	0/3/3/3
49	OMC	9	1710	49	-	0/9/27/28	0/2/2/2
45	A2M	5	3825	45	-	2/9/27/28	0/3/3/3
45	PSU	5	1683	45	-	0/6/24/26	0/2/2/2
49	OMG	9	683	49	-	0/9/27/28	0/3/3/3
49	OMC	9	517	49	-	3/9/27/28	0/2/2/2
49	A2M	9	27	49	-	0/9/27/28	0/3/3/3
45	OMG	5	4228	45	-	0/9/27/28	0/3/3/3
49	OMG	9	644	49	-	1/9/27/28	0/3/3/3
49	M7A	9	1806	49	-	3/7/37/38	0/3/3/3
45	PSU	5	2508	45	-	1/6/24/26	0/2/2/2
49	OMU	9	121	49	-	3/9/27/28	0/2/2/2
45	OMG	5	4618	45	-	1/9/27/28	0/3/3/3
45	OMC	5	3869	45	-	3/9/27/28	0/2/2/2
45	OMG	5	4494	45	-	0/9/27/28	0/3/3/3
45	OMU	5	4306	45	-	0/9/27/28	0/2/2/2
45	1MA	5	1322	86,45	-	1/7/25/26	0/3/3/3
49	A2M	9	166	49	-	2/9/27/28	0/3/3/3
45	PSU	5	3762	45	-	0/6/24/26	0/2/2/2
45	A2M	5	1871	86,45	-	0/9/27/28	0/3/3/3
45	OMG	5	2876	45	-	2/9/27/28	0/3/3/3
45	PSU	5	1782	45	-	0/6/24/26	0/2/2/2
49	B8N	9	1248	49	-	10/16/34/35	0/2/2/2
49	MA6	9	1851	49	-	5/11/29/30	0/3/3/3
48	DDE	v	715	48	-	6/20/21/23	0/1/1/1
45	A2M	5	3718	45	-	0/9/27/28	0/3/3/3
45	OMC	5	3887	45	-	1/9/27/28	0/2/2/2
45	OMC	5	1340	45	-	0/9/27/28	0/2/2/2
45	A2M	5	3867	45	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	OMG	5	4637	45	-	2/9/27/28	0/3/3/3
45	PSU	5	3851	45	-	0/6/24/26	0/2/2/2
45	PSU	5	4423	45	-	0/6/24/26	0/2/2/2
49	PSU	9	612	49	-	1/7/25/26	0/2/2/2
45	PSU	5	4420	45	-	2/6/24/26	0/2/2/2
49	5MU	9	814	49	-	0/7/25/26	0/2/2/2
45	OMC	5	3808	45	-	0/9/27/28	0/2/2/2
45	A2M	5	4571	45	-	0/9/27/28	0/3/3/3
45	PSU	5	4628	45	-	0/6/24/26	0/2/2/2
45	PSU	5	1781	45	-	2/6/24/26	0/2/2/2
45	OMC	5	3701	86,45	-	5/9/27/28	0/2/2/2
49	B8Q	9	1219	49,86	-	0/7/42/43	0/2/2/2
45	OMC	5	2861	45	-	0/9/27/28	0/2/2/2
49	E3C	9	568	49	-	4/9/44/45	0/2/2/2
45	A2M	5	1534	86,45	-	2/9/27/28	0/3/3/3
45	OMG	5	2364	45	-	3/9/27/28	0/3/3/3
45	PSU	5	3734	45	-	0/6/24/26	0/2/2/2
45	OMC	5	4456	45	-	0/9/27/28	0/2/2/2
45	PSU	5	4353	45	-	0/6/24/26	0/2/2/2
45	PSU	5	4403	45	-	0/6/24/26	0/2/2/2
45	A2M	5	3785	45	-	2/9/27/28	0/3/3/3
45	PSU	5	1677	45	-	4/6/24/26	0/2/2/2
45	OMG	5	1316	45	-	2/9/27/28	0/3/3/3
45	PSU	5	1862	45	-	1/6/24/26	0/2/2/2
45	OMC	5	2422	86,45	-	1/9/27/28	0/2/2/2
45	PSU	5	1792	45	-	0/6/24/26	0/2/2/2
49	PSU	9	119	49	-	1/7/25/26	0/2/2/2
45	OMC	5	2351	45	-	1/9/27/28	0/2/2/2
45	5MC	5	3782	86,45	-	0/7/25/26	0/2/2/2

The worst 5 of 1110 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	9	1832	6MZ	C6-N6	11.26	1.47	1.34
45	5	3818	UY1	C6-C5	10.93	1.47	1.35
45	5	4220	6MZ	C6-N6	10.49	1.46	1.34
45	5	3818	UY1	C2-N1	9.94	1.49	1.36
45	5	398	A2M	C2'-C1'	-9.69	1.29	1.53

The worst 5 of 852 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	9	1850	MA6	N1-C6-N6	-16.39	96.89	116.86
49	9	1851	MA6	N1-C6-N6	-15.81	97.60	116.86
49	9	1806	M7A	C5-C6-N6	13.89	147.35	123.75
49	9	1806	M7A	N6-C6-N1	-11.38	93.02	118.38
49	9	1850	MA6	C5-C6-N6	11.32	143.25	125.33

There are no chirality outliers.

5 of 163 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	v	715	DDE	CBI-CBW-NCB-CAB
48	v	715	DDE	CBI-CBW-NCB-CAC
48	v	715	DDE	CBI-CBW-NCB-CAA
48	v	715	DDE	CAU-CBW-NCB-CAB
48	v	715	DDE	CAU-CBW-NCB-CAC

There are no ring outliers.

88 monomers are involved in 149 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	5	1625	OMG	2	0
45	5	3715	PSU	1	0
45	5	4447	5MC	2	0
45	5	4457	PSU	1	0
49	9	1081	PSU	1	0
45	5	2365	OMC	3	0
45	5	3792	OMG	1	0
49	9	116	OMU	2	0
49	9	668	A2M	1	0
45	5	4500	PSU	2	0
45	5	3627	OMG	1	0
49	9	1850	MA6	2	0
45	5	400	A2M	2	0
49	9	509	OMG	3	0
45	5	373	OMG	1	0
45	5	4499	OMG	1	0
45	5	4530	UR3	1	0
45	5	4361	PSU	1	0
45	5	4521	PSU	1	0
49	9	159	A2M	2	0
45	5	2632	PSU	1	0
45	5	4370	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	5	4620	OMU	3	0
45	5	4220	6MZ	2	0
45	5	2363	A2M	2	0
45	5	3853	PSU	2	0
49	9	1374	5MC	1	0
49	9	1842	4AC	5	0
45	5	2424	OMG	2	0
45	5	4296	PSU	1	0
45	5	4442	PSU	1	0
49	9	484	A2M	2	0
45	5	3724	A2M	1	0
45	5	1524	A2M	2	0
45	5	1326	A2M	1	0
45	5	4623	OMG	3	0
45	5	3639	PSU	1	0
49	9	1243	PSU	1	0
45	5	4532	PSU	2	0
45	5	2824	OMC	1	0
45	5	237	B9B	2	0
49	9	1337	4AC	4	0
45	5	3818	UY1	2	0
49	9	1830	UR3	1	0
45	5	4536	OMC	1	0
45	5	1517	2MG	1	0
47	8	75	OMG	2	0
45	5	3920	PSU	1	0
45	5	4196	OMG	1	0
49	9	1031	A2M	1	0
45	5	3695	PSU	1	0
45	5	4392	OMG	1	0
49	9	683	OMG	1	0
49	9	517	OMC	2	0
49	9	27	A2M	4	0
49	9	644	OMG	1	0
49	9	1806	M7A	1	0
49	9	121	OMU	2	0
45	5	3869	OMC	2	0
45	5	1322	1MA	4	0
49	9	166	A2M	3	0
45	5	3762	PSU	1	0
45	5	1871	A2M	1	0
45	5	2876	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	9	1851	MA6	1	0
48	v	715	DDE	4	0
45	5	3718	A2M	2	0
45	5	1340	OMC	1	0
45	5	3867	A2M	4	0
45	5	4637	OMG	3	0
49	9	612	PSU	2	0
45	5	4420	PSU	1	0
49	9	814	5MU	2	0
45	5	3808	OMC	1	0
45	5	4628	PSU	1	0
45	5	2861	OMC	1	0
45	5	1534	A2M	3	0
45	5	2364	OMG	2	0
45	5	3734	PSU	1	0
45	5	4456	OMC	1	0
45	5	4403	PSU	1	0
45	5	3785	A2M	3	0
45	5	1316	OMG	2	0
45	5	1862	PSU	1	0
45	5	2422	OMC	2	0
49	9	119	PSU	4	0
45	5	2351	OMC	2	0
45	5	3782	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 284 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	GDP	v	900	-	29,30,30	1.17	4 (13%)	45,47,47	1.74	7 (15%)
89	34G	9	1957	-	39,39,39	1.79	9 (23%)	51,56,56	2.39	22 (43%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	GDP	v	900	-	-	5/16/32/32	0/3/3/3
89	34G	9	1957	-	-	8/14/49/49	0/5/5/5

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	9	1957	34G	CBC-CBG	5.90	1.57	1.52
89	9	1957	34G	CBD-CBH	3.78	1.57	1.52
89	9	1957	34G	CAO-CBG	3.55	1.57	1.53
88	v	900	GDP	C6-N1	-2.80	1.33	1.38
89	9	1957	34G	CAQ-NBI	2.80	1.51	1.47

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	9	1957	34G	CAN-NBI-CAQ	6.23	122.29	110.32
89	9	1957	34G	CAX-CBD-CBH	-5.74	114.17	121.58
88	v	900	GDP	C5-C4-N3	-5.65	119.40	128.39
88	v	900	GDP	C2-N3-C4	4.78	120.53	112.30
89	9	1957	34G	CAW-CBC-CBG	-4.70	115.74	121.38

There are no chirality outliers.

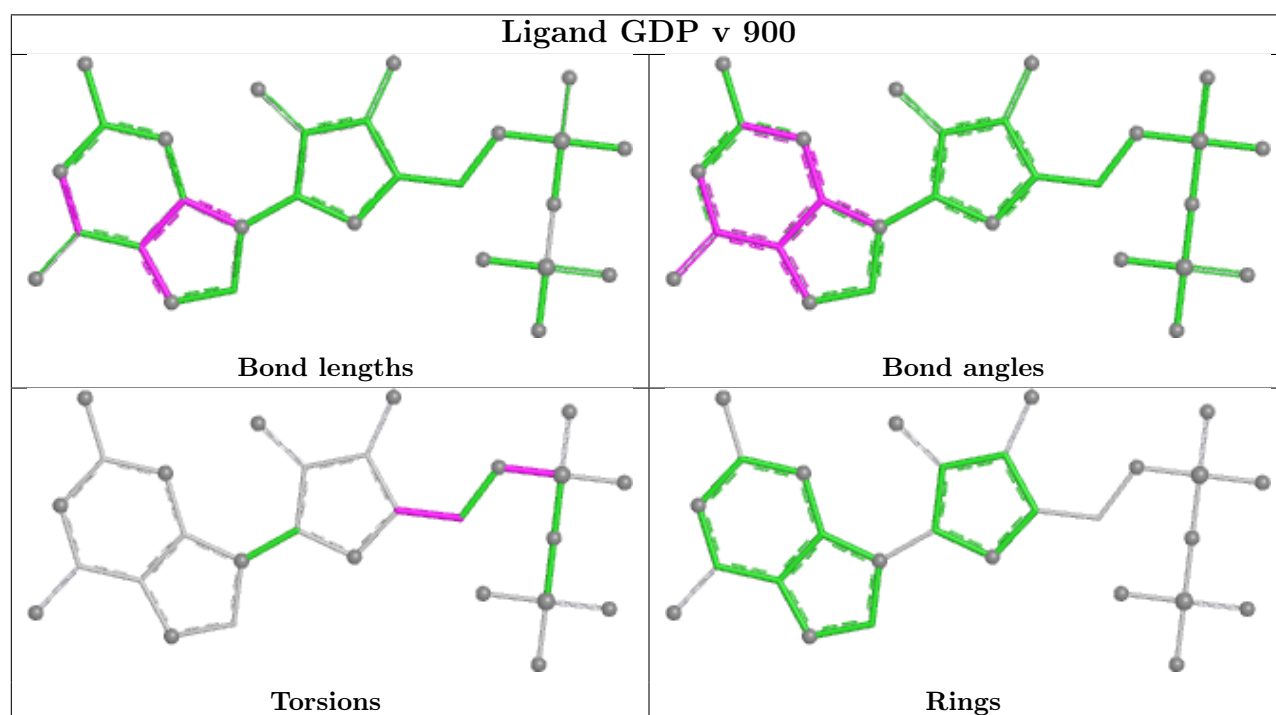
5 of 13 torsion outliers are listed below:

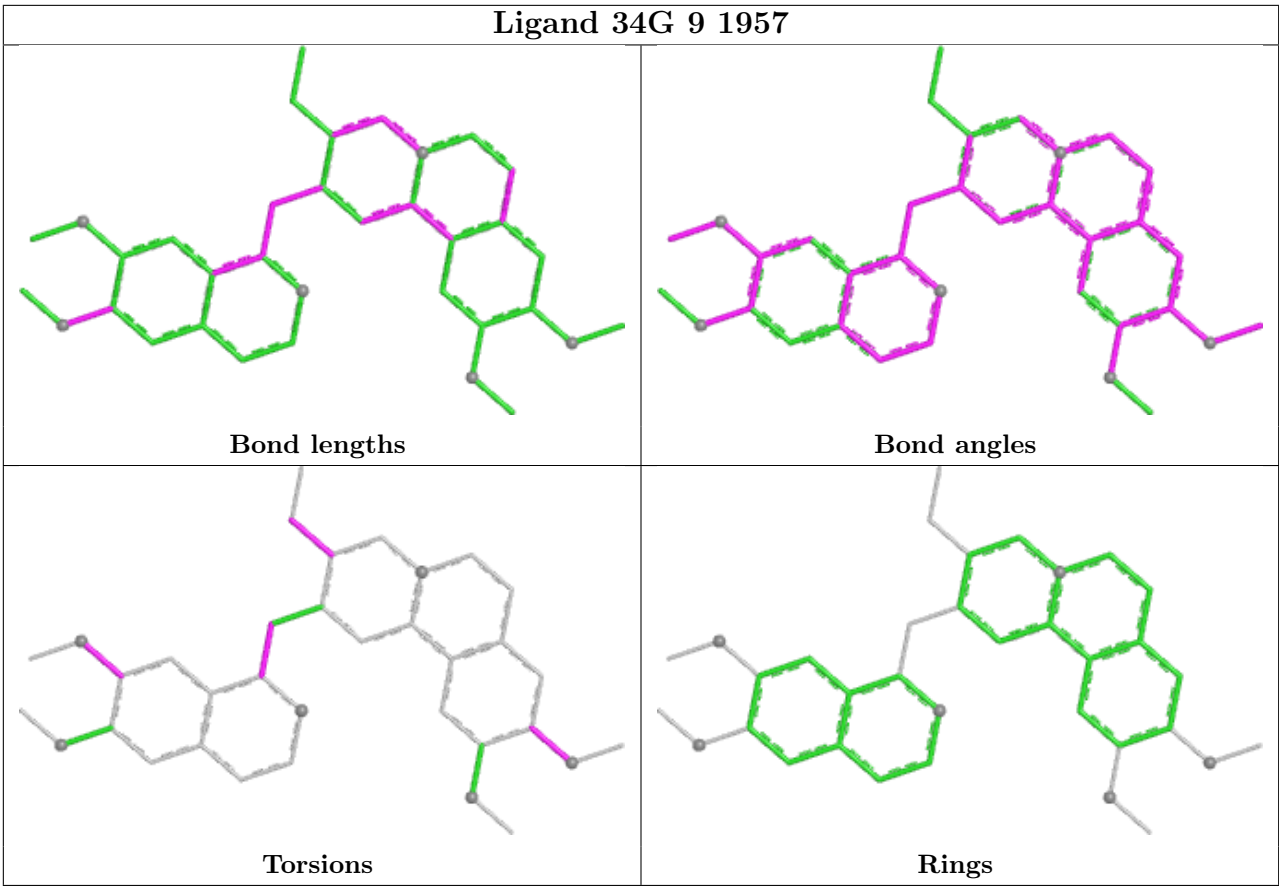
Mol	Chain	Res	Type	Atoms
88	v	900	GDP	C5'-O5'-PA-O3A
88	v	900	GDP	C5'-O5'-PA-O2A
89	9	1957	34G	CAA-CAJ-CBE-CAQ
89	9	1957	34G	CBF-CAO-CBG-NAR
89	9	1957	34G	CBF-CAO-CBG-CBC

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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
45	5	21
49	9	4
83	3	2
85	2	1
81	ff	1

The worst 5 of 29 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	42.68
1	5	1219:G	O3'	1233:G	P	19.25

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	523:C	O3'	638:G	P	17.08
1	5	1406(C):G	O3'	1411:C	P	16.39
1	5	4138:C	O3'	4146:G	P	15.58

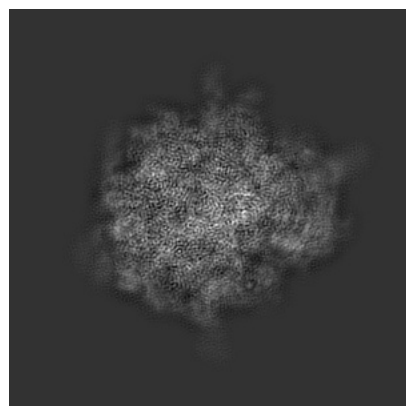
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43189. These allow visual inspection of the internal detail of the map and identification of artifacts.

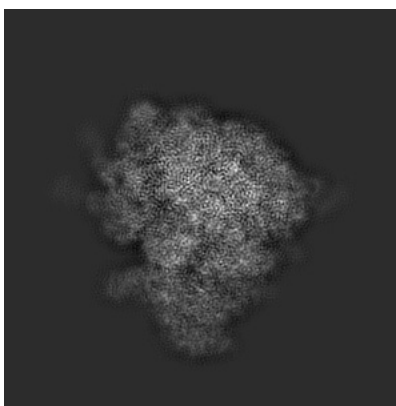
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

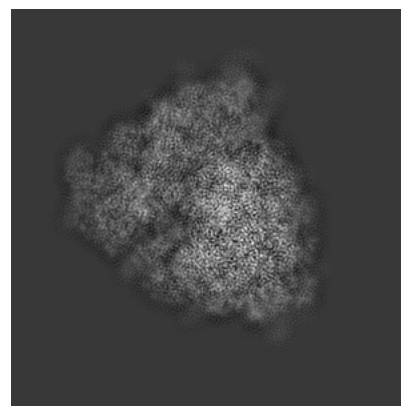
6.1.1 Primary map



X

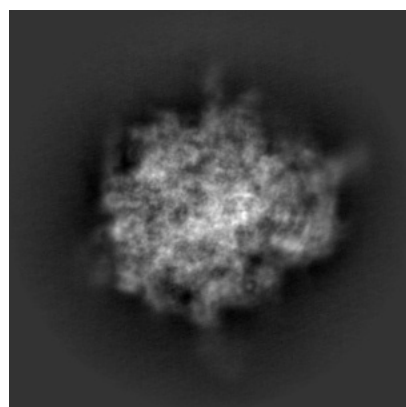


Y

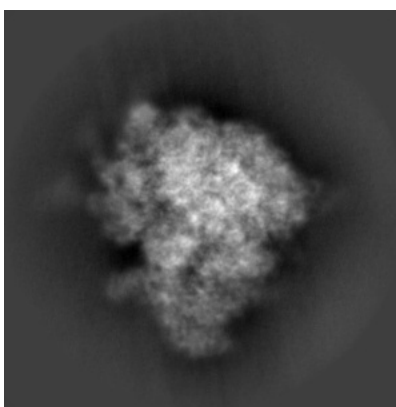


Z

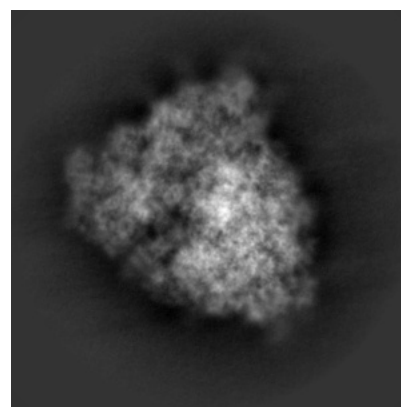
6.1.2 Raw map



X



Y

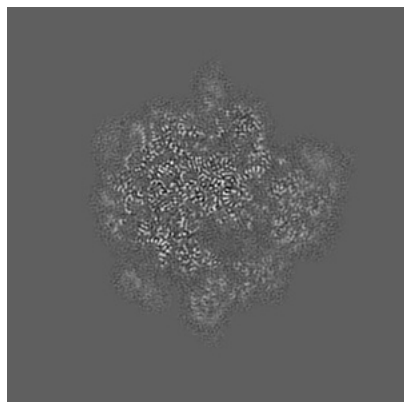


Z

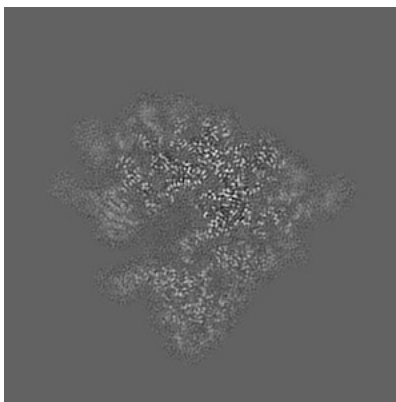
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

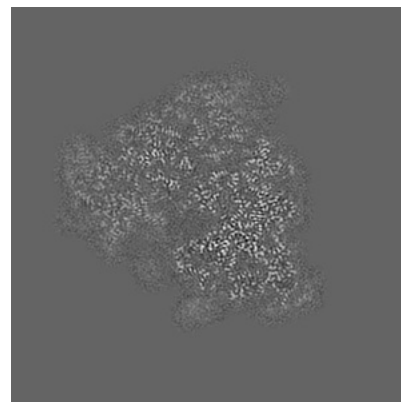
6.2.1 Primary map



X Index: 160

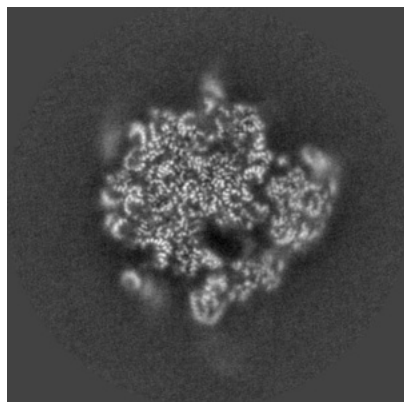


Y Index: 160

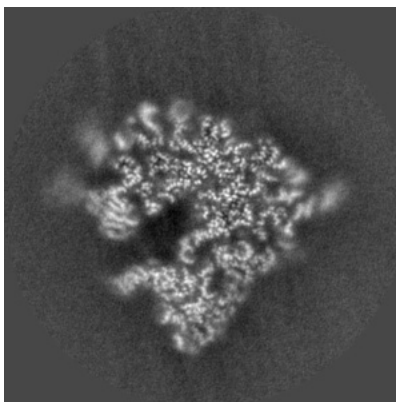


Z Index: 160

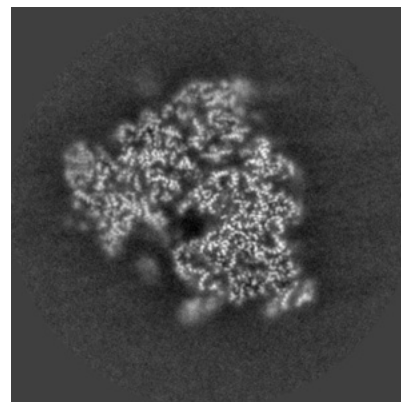
6.2.2 Raw map



X Index: 160



Y Index: 160

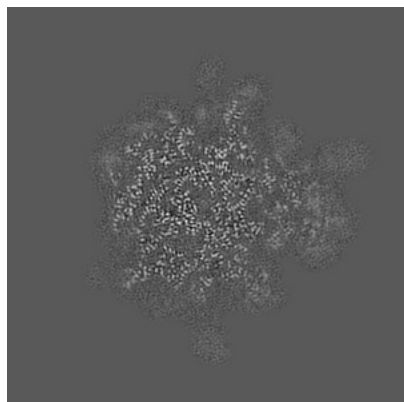


Z Index: 160

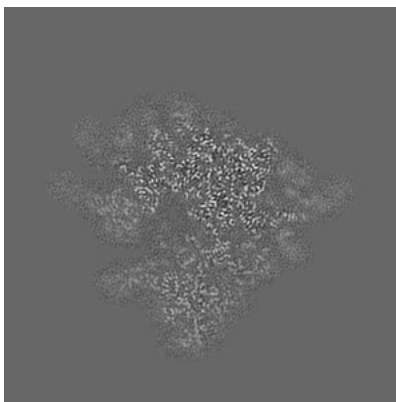
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

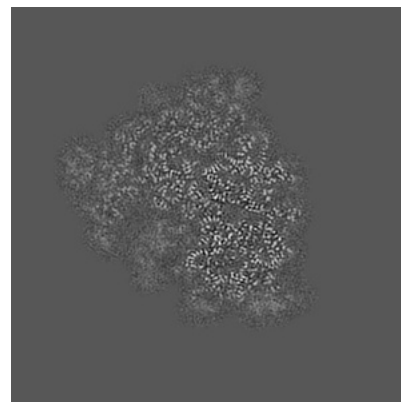
6.3.1 Primary map



X Index: 177

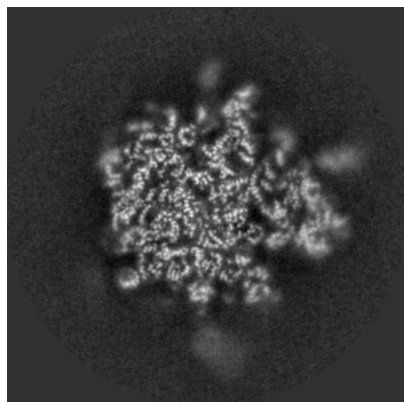


Y Index: 165

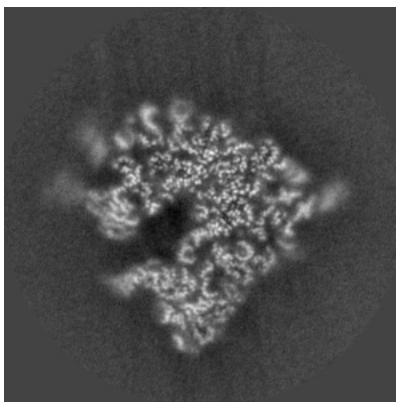


Z Index: 171

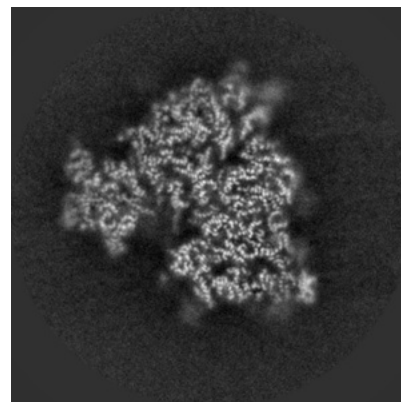
6.3.2 Raw map



X Index: 175



Y Index: 161

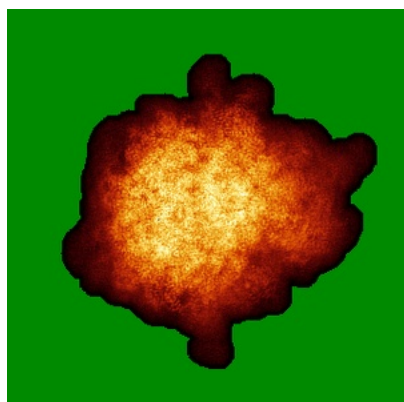


Z Index: 153

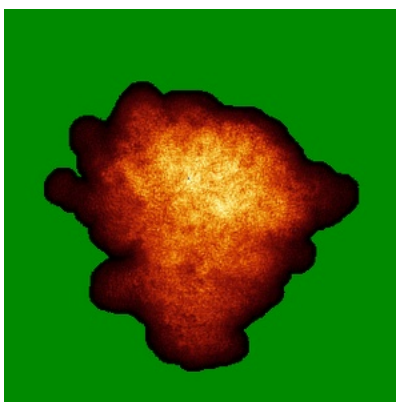
The images above show the largest variance slices of the map in three orthogonal directions.

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

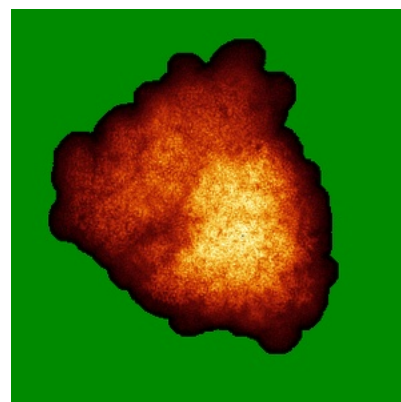
6.4.1 Primary map



X

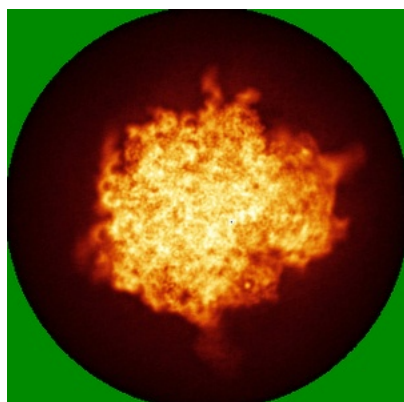


Y

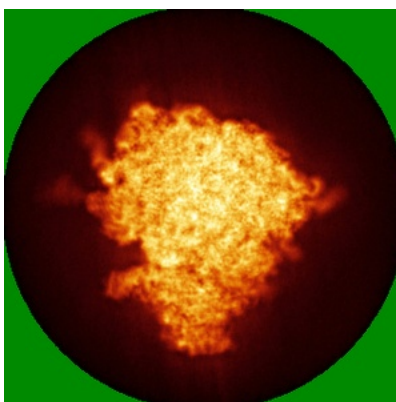


Z

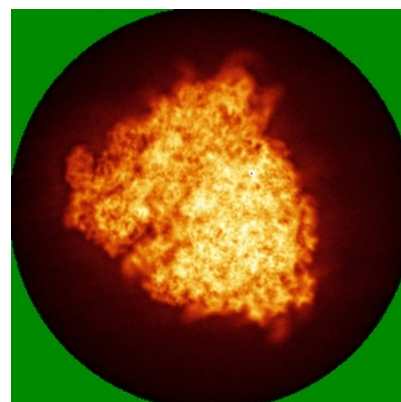
6.4.2 Raw map



X



Y

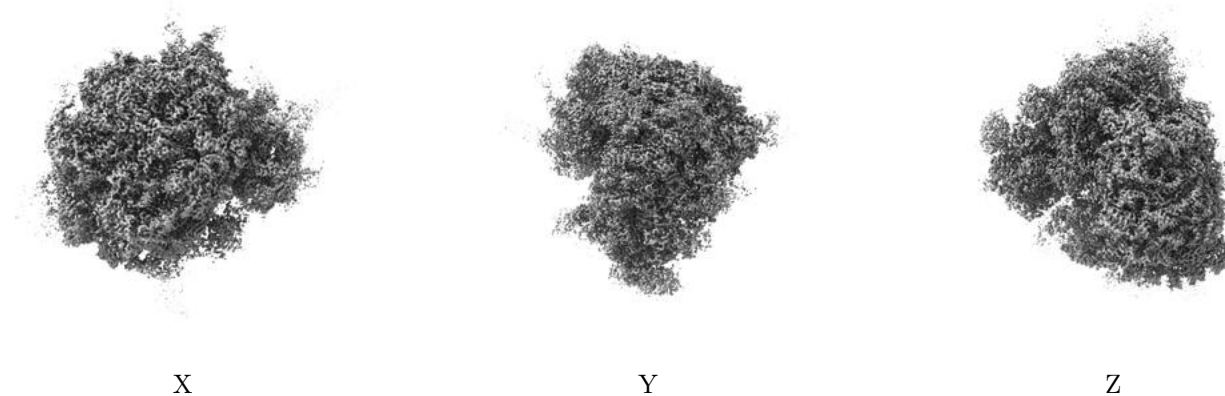


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

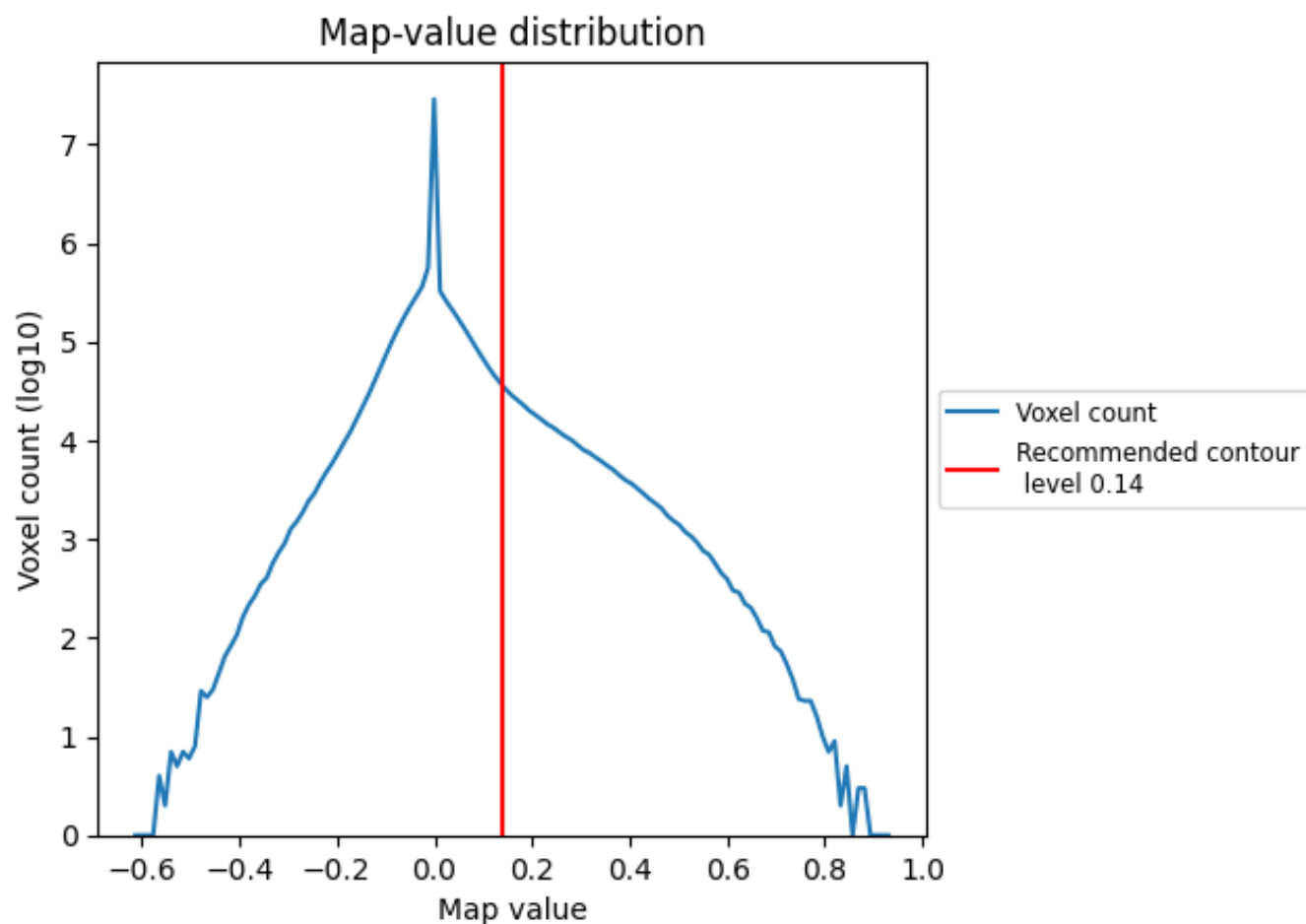
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

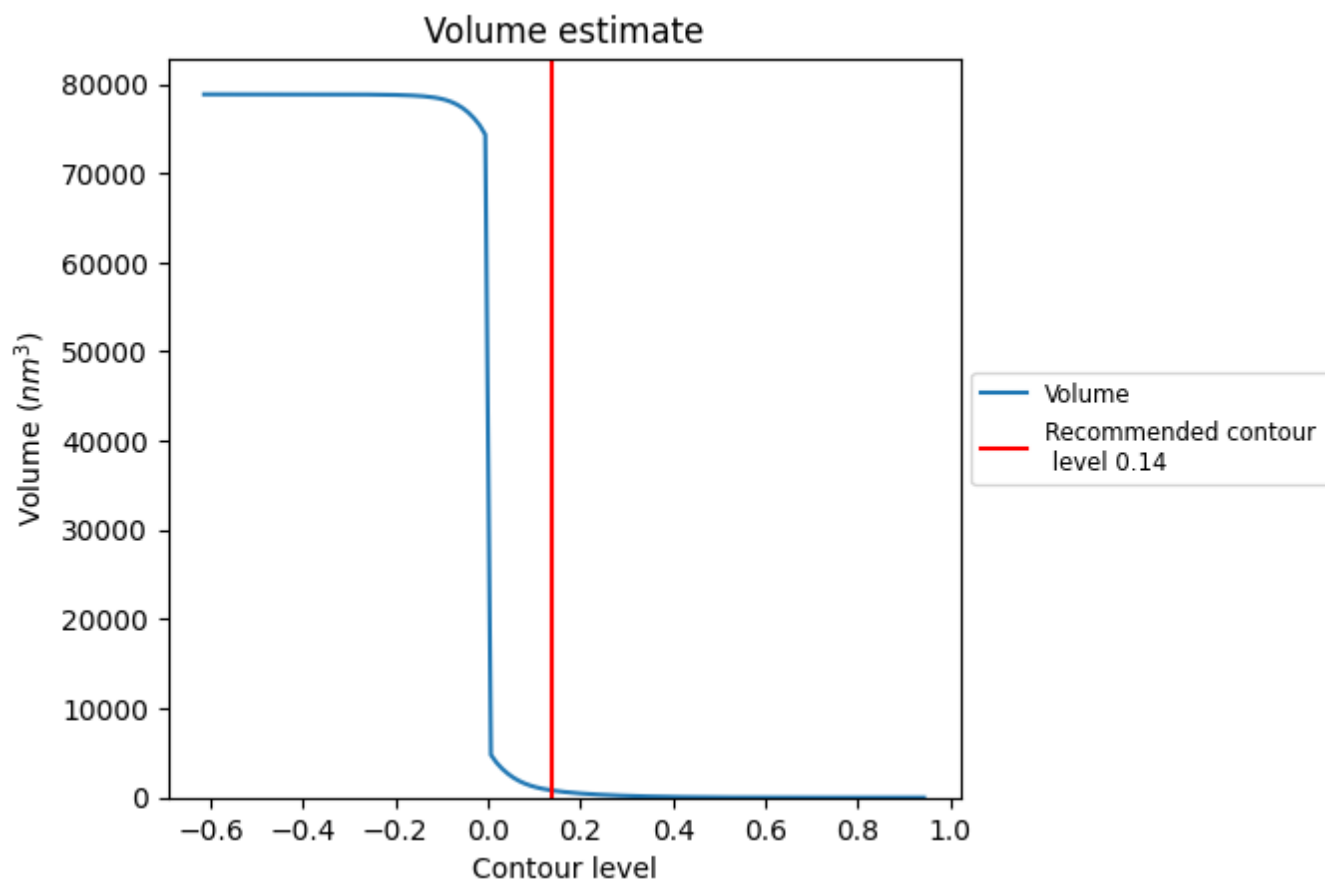
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

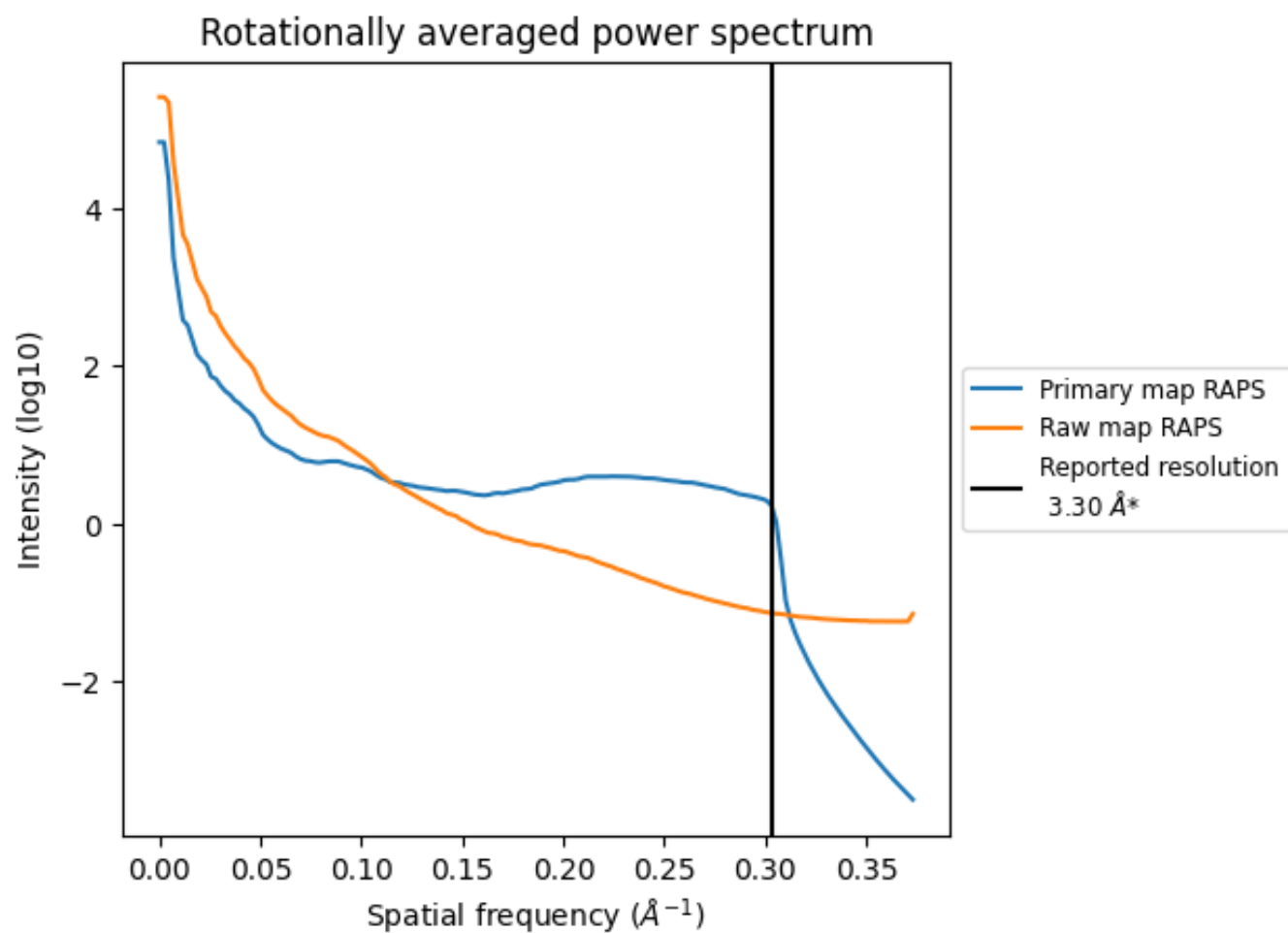
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 793 nm³; this corresponds to an approximate mass of 717 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

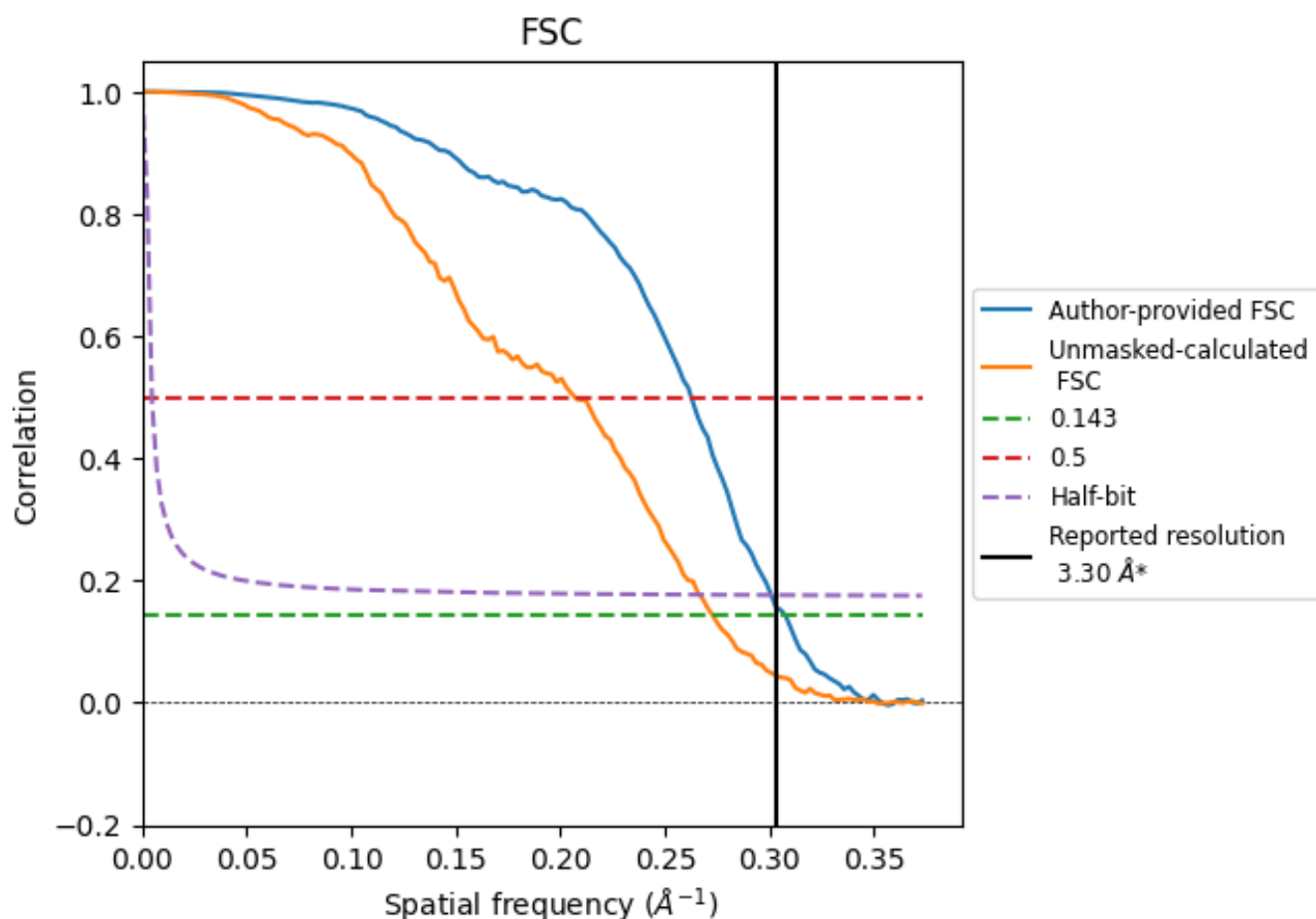


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

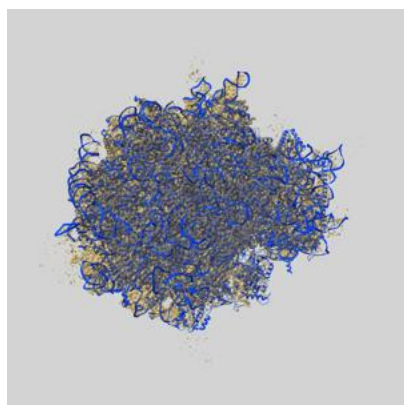
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.25	3.81	3.32
Unmasked-calculated*	3.67	4.83	3.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.67 differs from the reported value 3.3 by more than 10 %

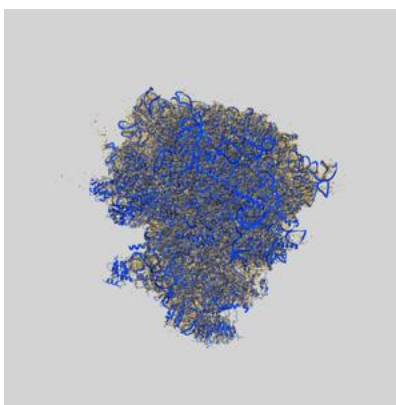
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43189 and PDB model 8VFT. Per-residue inclusion information can be found in section [3](#) on page [26](#).

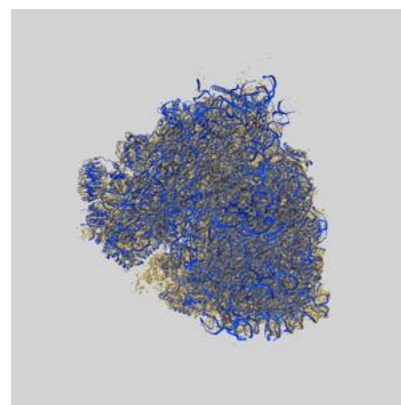
9.1 Map-model overlay [i](#)



X



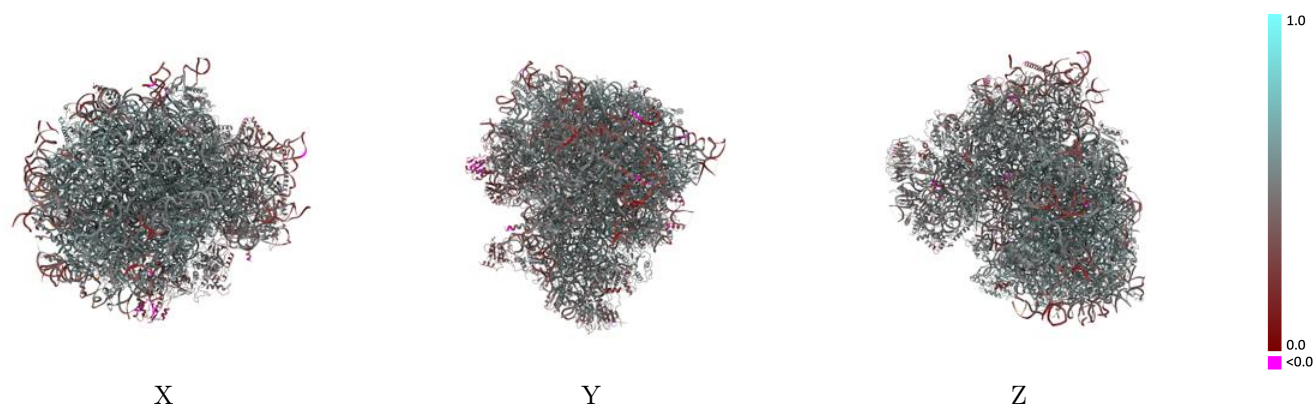
Y



Z

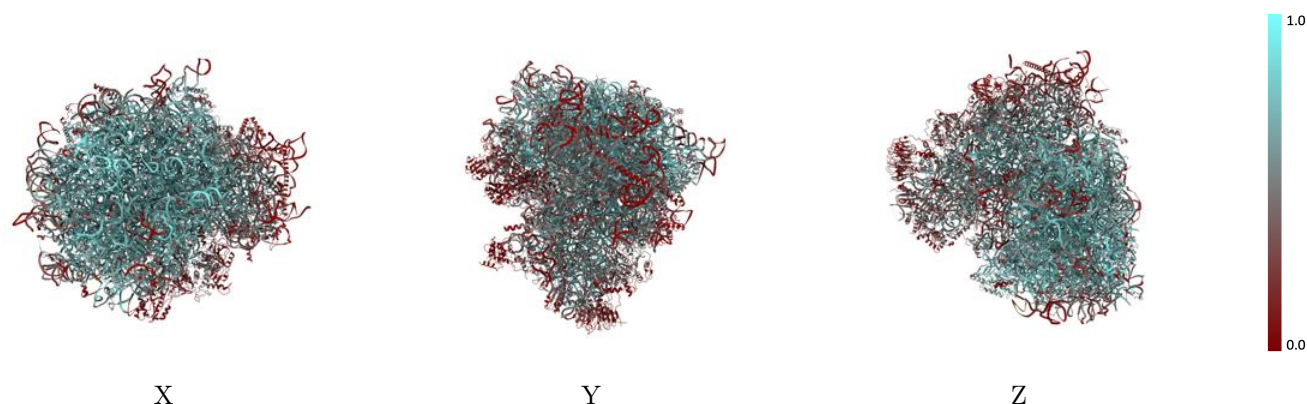
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



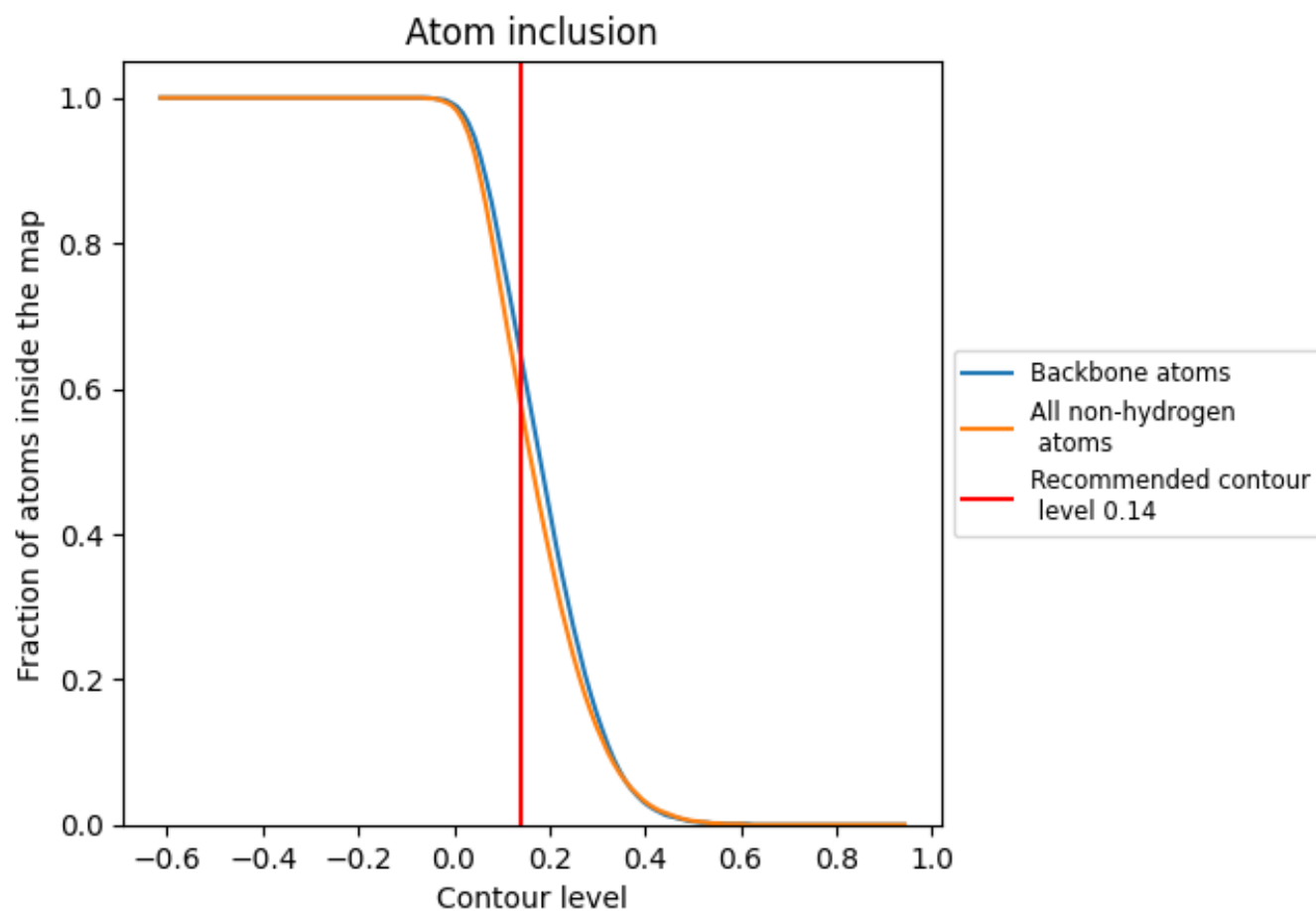
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 58% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5780	 0.4930
2	 0.3500	 0.4200
3	 0.4350	 0.4340
5	 0.6930	 0.4940
7	 0.7890	 0.5260
8	 0.7080	 0.4960
9	 0.5590	 0.4610
A	 0.7070	 0.5670
AA	 0.4150	 0.4890
B	 0.6700	 0.5550
BB	 0.4020	 0.5080
C	 0.6780	 0.5510
CC	 0.4620	 0.5120
D	 0.6170	 0.5350
DD	 0.3760	 0.4750
E	 0.5970	 0.5400
EE	 0.3650	 0.4970
F	 0.6790	 0.5540
FF	 0.3350	 0.4700
G	 0.5580	 0.5160
GG	 0.2490	 0.4410
H	 0.6000	 0.5320
HH	 0.2380	 0.4450
I	 0.6260	 0.5460
II	 0.4180	 0.4990
J	 0.5640	 0.5180
JJ	 0.3930	 0.4810
KK	 0.3720	 0.4840
L	 0.5950	 0.5300
LL	 0.4630	 0.5200
M	 0.6370	 0.5390
MM	 0.0390	 0.3330
N	 0.7410	 0.5720
NN	 0.4830	 0.5180
O	 0.6940	 0.5570



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Chain	Atom inclusion	Q-score
OO	 0.4600	 0.5040
P	 0.6860	 0.5550
PP	 0.3560	 0.4800
Q	 0.6790	 0.5640
QQ	 0.3790	 0.4830
R	 0.5880	 0.5230
RR	 0.3050	 0.4410
S	 0.6760	 0.5550
SS	 0.3380	 0.4590
T	 0.6100	 0.5370
TT	 0.3900	 0.4780
U	 0.4460	 0.4910
UU	 0.3400	 0.4720
V	 0.6350	 0.5550
VV	 0.3760	 0.4920
W	 0.6310	 0.5520
WW	 0.5080	 0.5230
X	 0.6310	 0.5450
XX	 0.5160	 0.5350
Y	 0.6280	 0.5450
YY	 0.2940	 0.4790
Z	 0.5880	 0.5300
ZZ	 0.2370	 0.4460
a	 0.7110	 0.5580
aa	 0.5270	 0.5200
b	 0.5230	 0.5030
bb	 0.3300	 0.4900
c	 0.6130	 0.5250
cc	 0.1260	 0.2290
d	 0.6470	 0.5440
dd	 0.5790	 0.5260
e	 0.6900	 0.5590
ee	 0.3970	 0.4730
f	 0.7300	 0.5720
ff	 0.0940	 0.3870
g	 0.6170	 0.5320
gg	 0.2000	 0.4340
h	 0.5960	 0.5370
i	 0.5650	 0.5080
j	 0.7430	 0.5650
k	 0.4970	 0.5040
l	 0.6720	 0.5390

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Chain	Atom inclusion	Q-score
m	 0.6490	 0.5560
n	 0.6520	 0.5460
o	 0.6280	 0.5600
p	 0.6210	 0.5410
r	 0.6690	 0.5510
s	 0.1230	 0.2650
t	 0.0660	 0.3450
v	 0.2620	 0.4440
w	 0.6280	 0.5140