wwPDB EM Validation Summary Report

Mar 8, 2026 – 08:25 PM UTC

PDB ID	:	7SYP / pdb_00007syp
EMDB ID	:	EMD-25536
Title	:	Structure of the wt IRES and 40S ribosome binary complex, open conformation. Structure 10(wt)
Authors	:	Brown, Z.P.; Abaeva, I.S.; De, S.; Hellen, C.U.T.; Pestova, T.V.; Frank, J.
Deposited on	:	2021-11-25
Resolution	:	4.00 Å(reported)
Based on initial models	:	5FLX, 6D9J

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 (i) 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 (i)) were used in the production of this report:

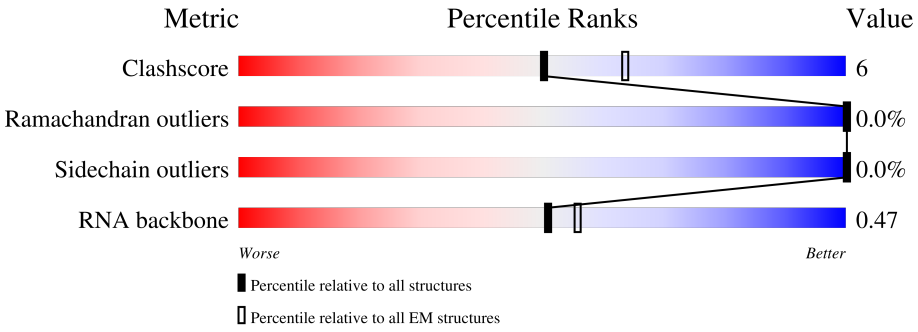
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

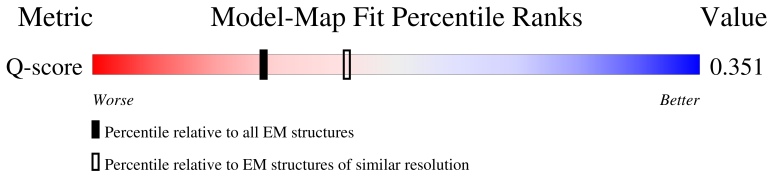
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	2	1870	6% 55% 30% • 10%
2	B	295	10% 62% 11% 26%
3	C	264	9% 69% 11% 19%

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Mol	Chain	Length	Quality of chain
4	D	221	12% 83% 17%
5	E	281	31% 72% 9% 19%
6	F	263	5% 79% 20%
7	G	204	10% 74% 20% 6%
8	H	249	16% 79% 16% 5%
9	I	432	18% 37% 6% 57%
10	J	208	15% 84% 15%
11	K	194	11% 78% 18% 5%
12	L	149	33% 54% 10% 36%
13	M	158	19% 78% 17%
14	N	132	88% 73% 16% 11%
15	O	151	10% 77% 21%
16	P	168	5% 68% 12% 19%
17	Q	145	48% 61% 22% 17%
18	R	172	13% 69% 14% 17%
19	S	135	52% 82% 16%
20	T	152	43% 74% 20% 5%
21	U	145	11% 82% 15%
22	V	119	45% 75% 9% 16%
23	W	83	10% 87% 13%
24	X	130	78% 22%
25	Y	143	8% 82% 17%
26	Z	131	73% 21% 5%
27	a	124	23% 48% 15% 38%
28	b	101	15% 75% 25%

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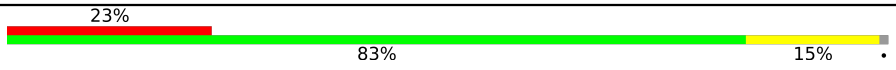
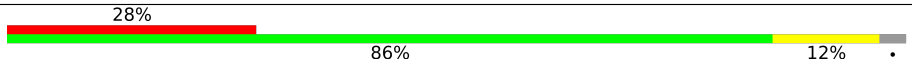
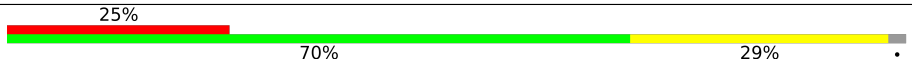
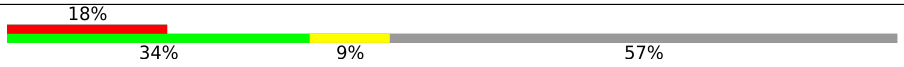
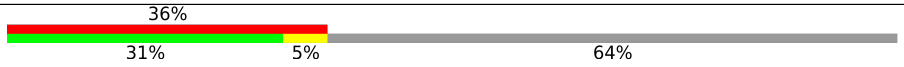
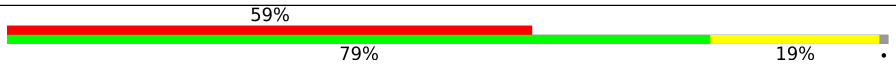
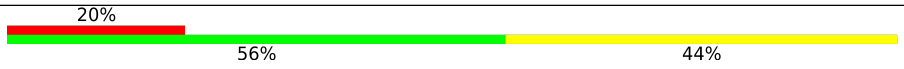
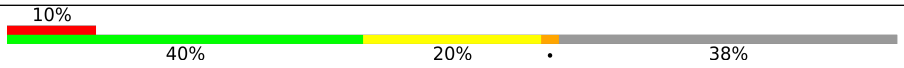
Mol	Chain	Length	Quality of chain
29	c	84	
30	d	69	
31	e	56	
32	f	133	
33	g	188	
34	h	317	
35	n	25	
36	7	12	
37	z	400	

2 Entry composition (i)

There are 38 unique types of molecules in this entry. The entry contains 80436 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1680	35864	16009	6439	11737	1679	0	0

- Molecule 2 is a protein called uS2 (SA).

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a protein called eS1.

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

- Molecule 4 is a protein called uS5.

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

- Molecule 5 is a protein called uS3.

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

- Molecule 6 is a protein called eS4 (S4 X isoform).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	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
F	25	GLY	SER	conflict	UNP G1TK17
F	51	ARG	LYS	conflict	UNP G1TK17
F	78	THR	ALA	conflict	UNP G1TK17
F	156	VAL	MET	conflict	UNP G1TK17

- Molecule 7 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 8 is a protein called eS6.

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

- Molecule 9 is a protein called eS7.

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

- Molecule 10 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	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
J	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 11 is a protein called uS4.

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

- Molecule 12 is a protein called eS10.

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

- Molecule 13 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	151	Total	C	N	O	S	0	0
			1233	785	231	211	6		

- Molecule 14 is a protein called eS12.

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

- Molecule 15 is a protein called uS15.

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

- Molecule 16 is a protein called uS11.

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

- Molecule 17 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 18 is a protein called uS9.

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

- Molecule 19 is a protein called eS17.

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

- Molecule 20 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 21 is a protein called eS19.

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

- Molecule 22 is a protein called uS10.

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

- Molecule 23 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	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
W	3	ASN	SER	conflict	UNP G1TM82
W	4	ASP	ASN	conflict	UNP G1TM82
W	33	GLN	PRO	conflict	UNP G1TM82
W	50	PHE	SER	conflict	UNP G1TM82
W	75	ALA	SER	conflict	UNP G1TM82
W	76	ASP	HIS	conflict	UNP G1TM82

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Chain	Residue	Modelled	Actual	Comment	Reference
W	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 24 is a protein called uS8.

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

- Molecule 25 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 26 is a protein called eS24.

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

- Molecule 27 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	77	Total	C	N	O	S	0	0
			614	393	114	106	1		

- Molecule 28 is a protein called eS26.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	28	ARG	CYS	conflict	UNP G1TFE8
b	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 29 is a protein called eS27.

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

- Molecule 30 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	67	Total	C	N	O	S	0	0
			530	321	108	99	2		

- Molecule 31 is a protein called uS14.

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

- Molecule 32 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 33 is a protein called eS31.

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

- Molecule 34 is a protein called Receptor for Activated C Kinase 1 (RACK1).

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

- Molecule 35 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 36 is a RNA chain called HCV IRES partially loaded mRNA portion.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	7	12	Total	C	O	P	0	0
			144	60	72	12		

- Molecule 37 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	z	249	Total	C	N	O	P	0	0
			5318	2369	951	1749	249		

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

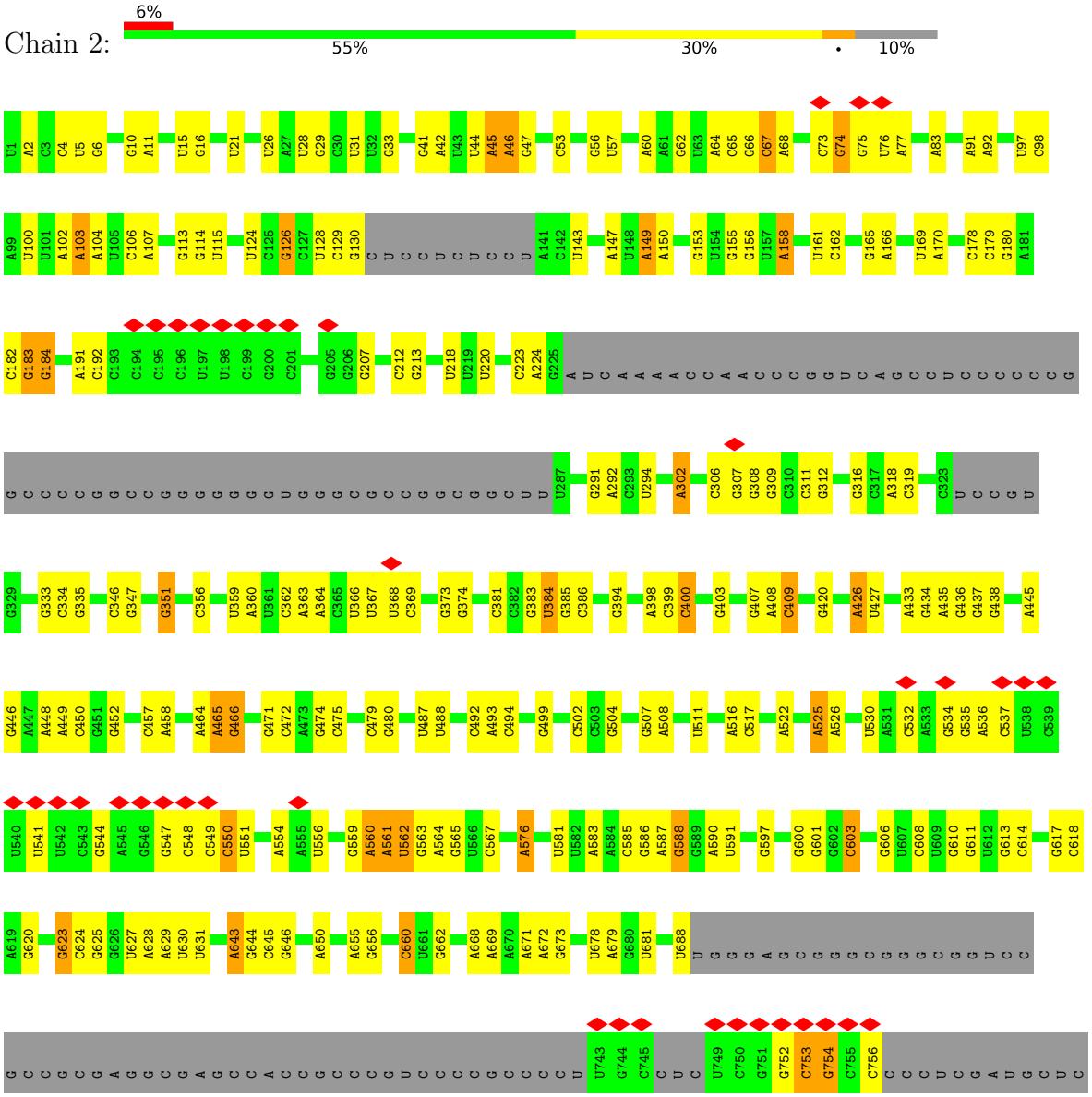
Mol	Chain	Residues	Atoms		AltConf
38	b	1	Total	Zn	0
			1	1	
38	g	1	Total	Zn	0
			1	1	

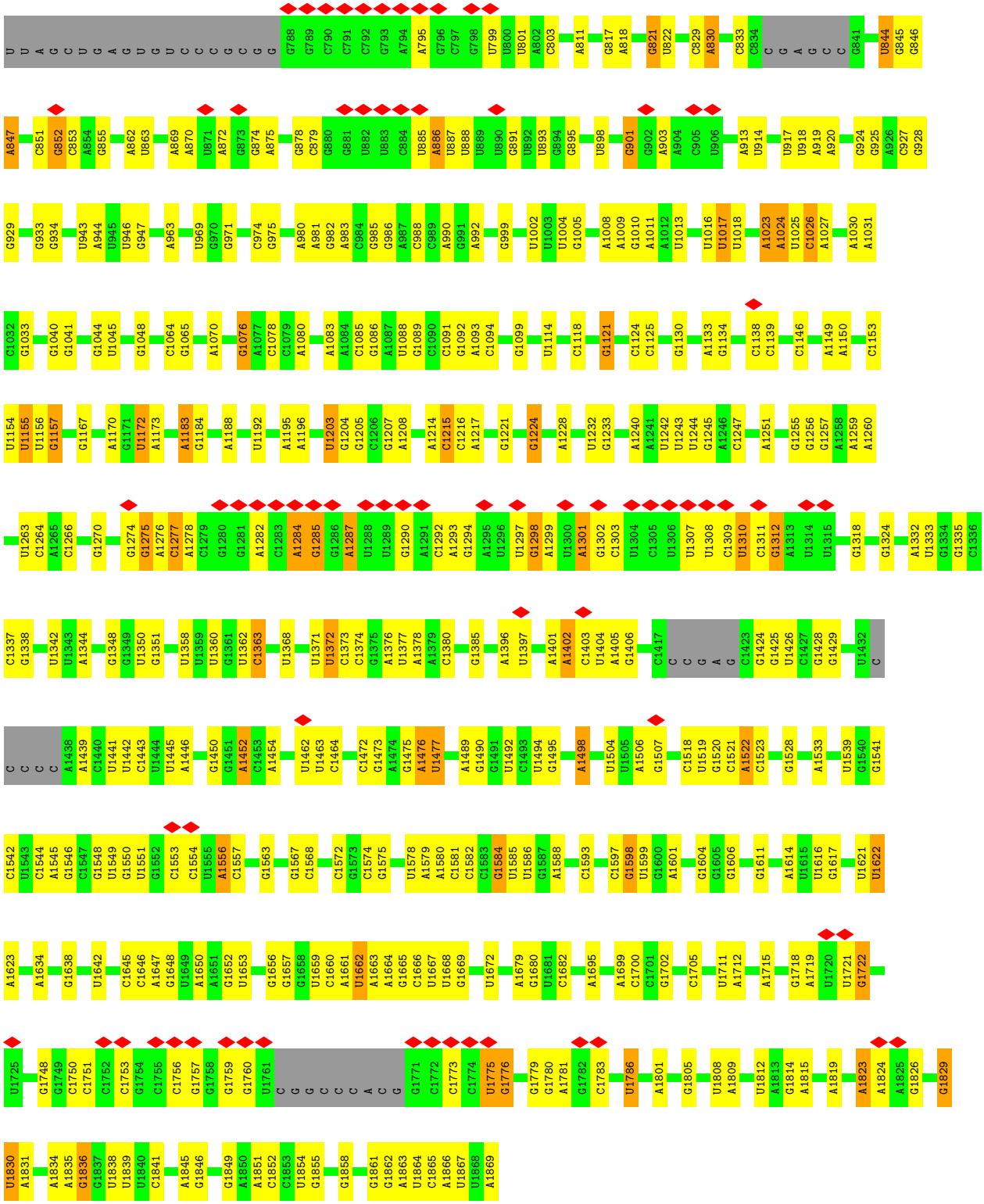
3 Residue-property plots (i)

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

- Molecule 1: 18S rRNA

Chain 2:

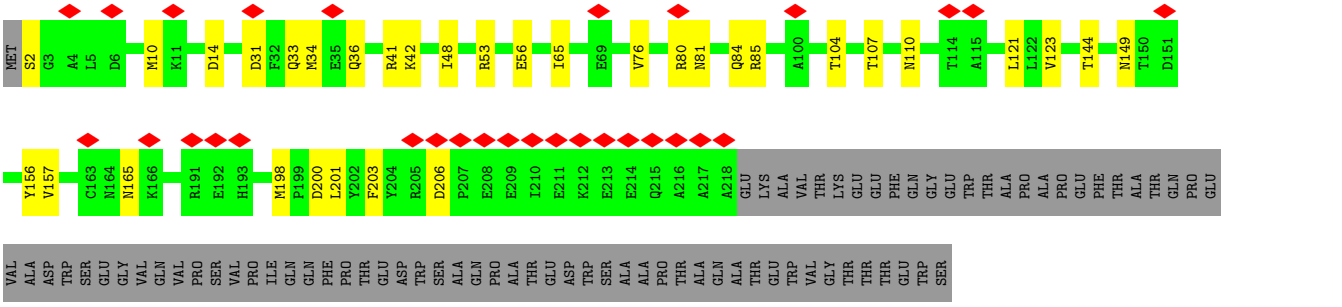




• Molecule 2: uS2 (SA)

Chain B:

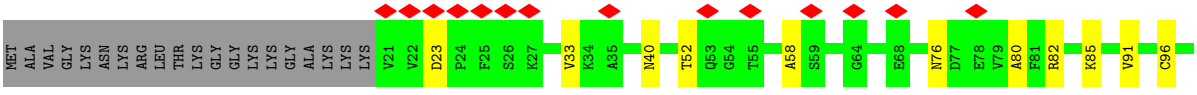


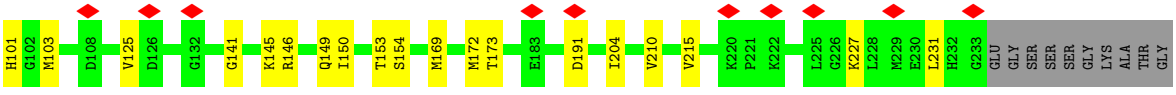


• Molecule 3: eS1

Chain C:





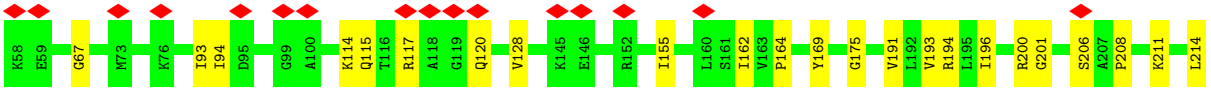


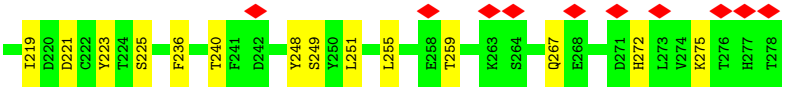


• Molecule 4: uS5

Chain D:



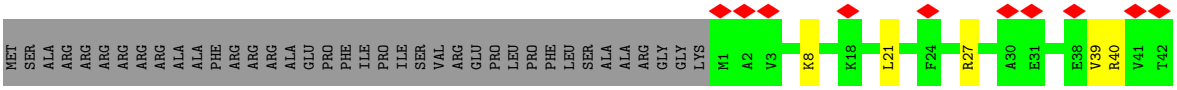


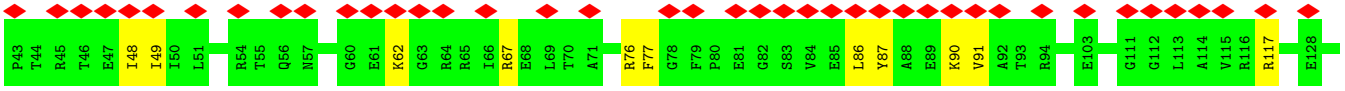


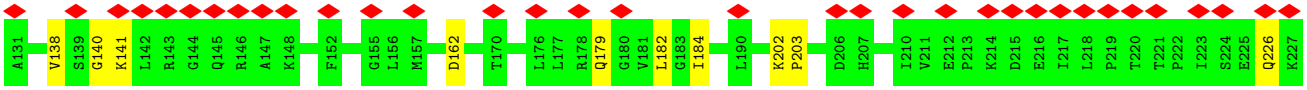
• Molecule 5: uS3

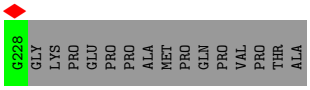
Chain E:



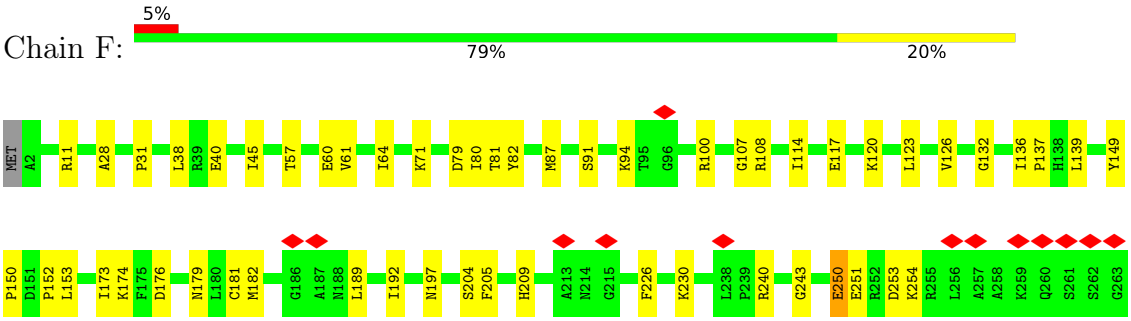




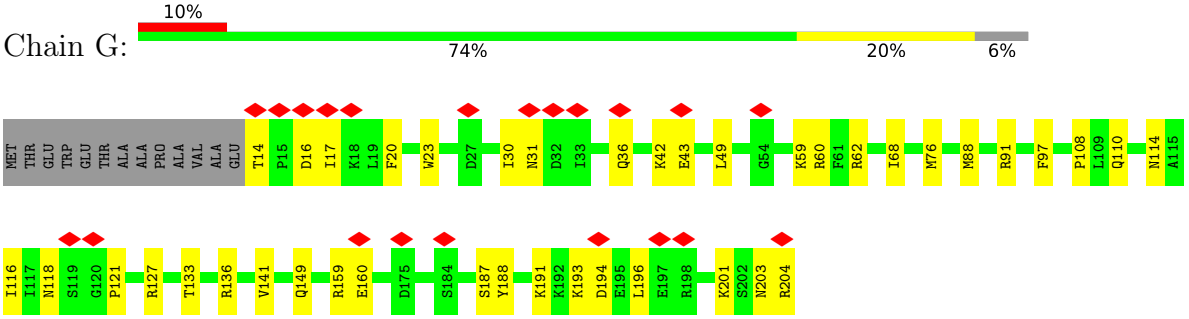




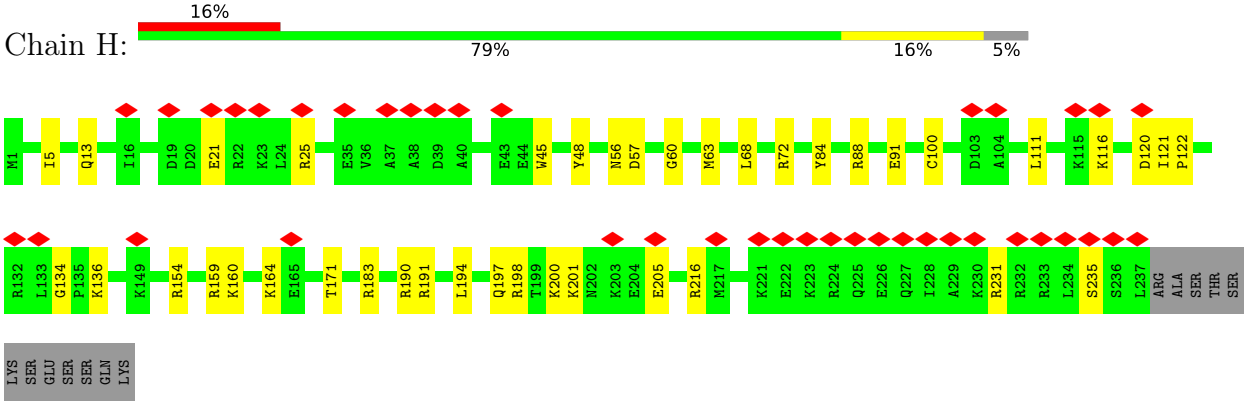
- Molecule 6: eS4 (S4 X isoform)



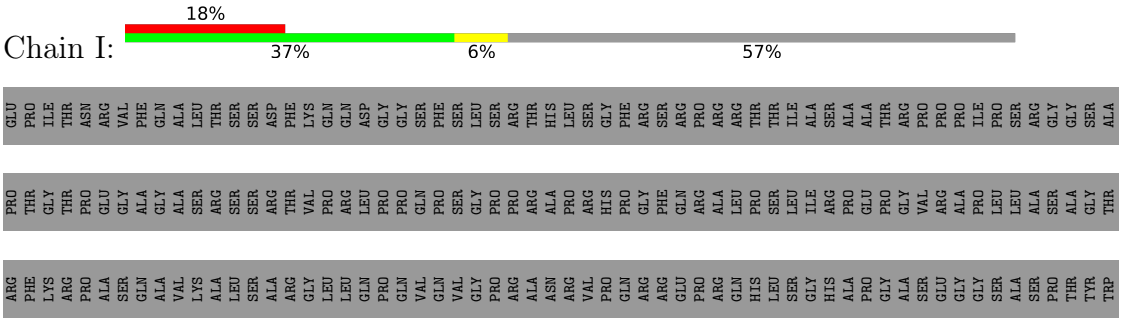
- Molecule 7: uS7

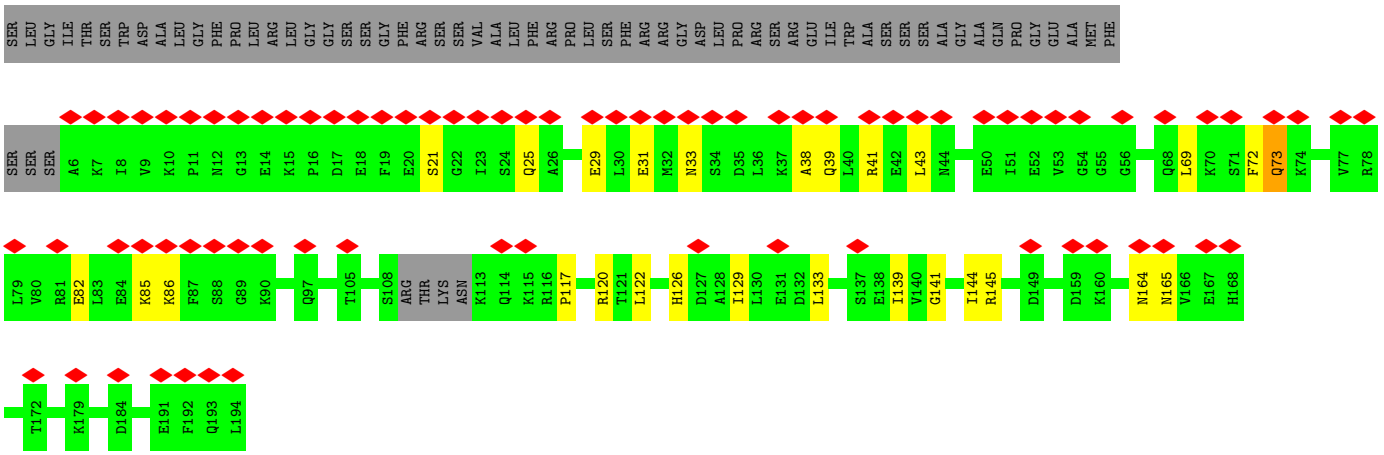


- Molecule 8: eS6



- Molecule 9: eS7

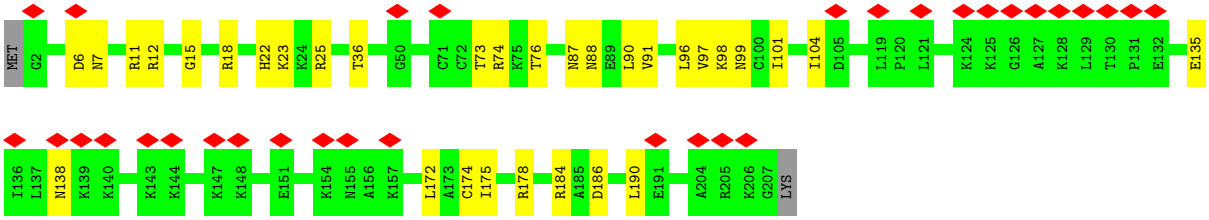




• Molecule 10: eS8

Chain J:

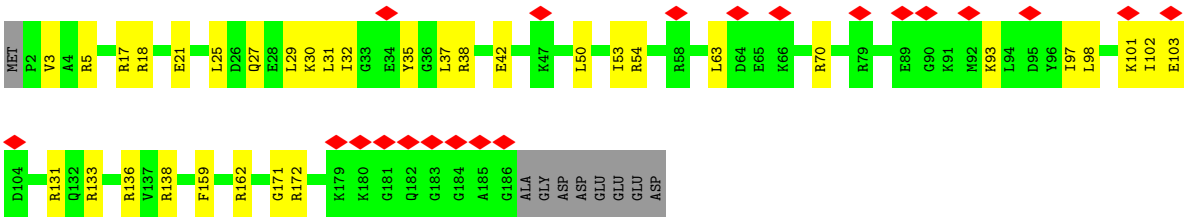




• Molecule 11: uS4

Chain K:

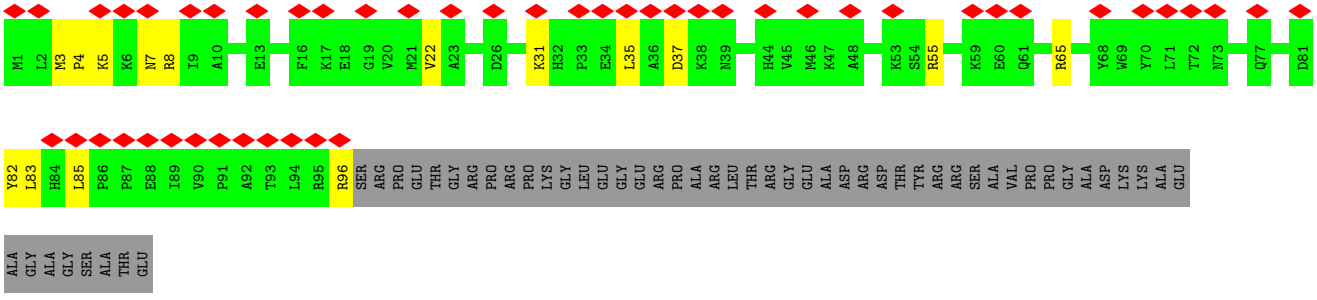




• Molecule 12: eS10

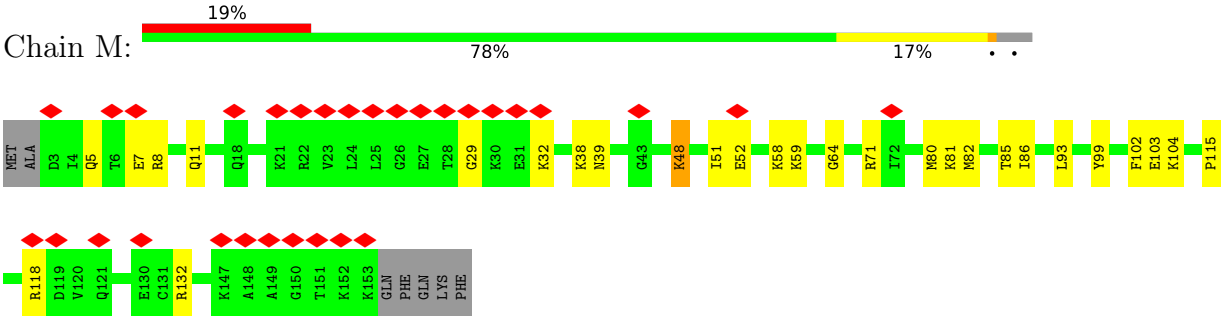
Chain L:





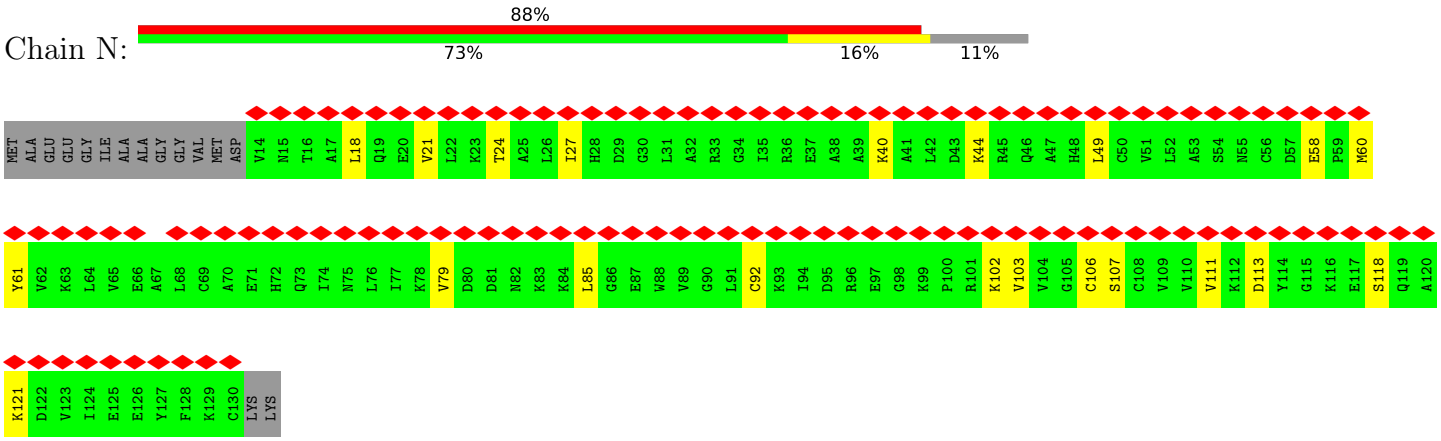
• Molecule 13: uS17

Chain M:



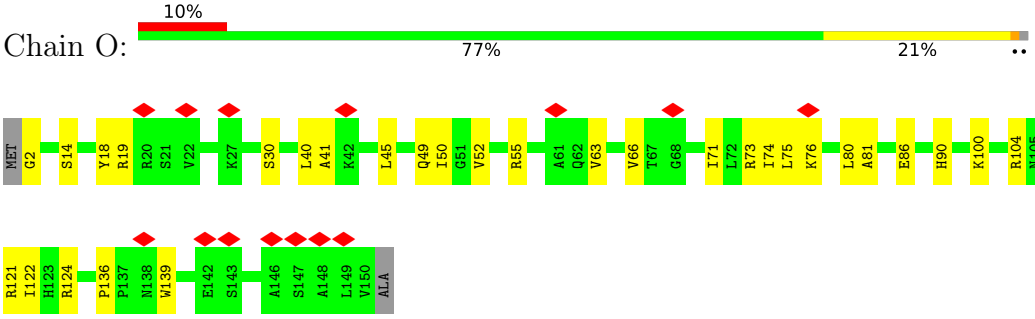
• Molecule 14: eS12

Chain N:



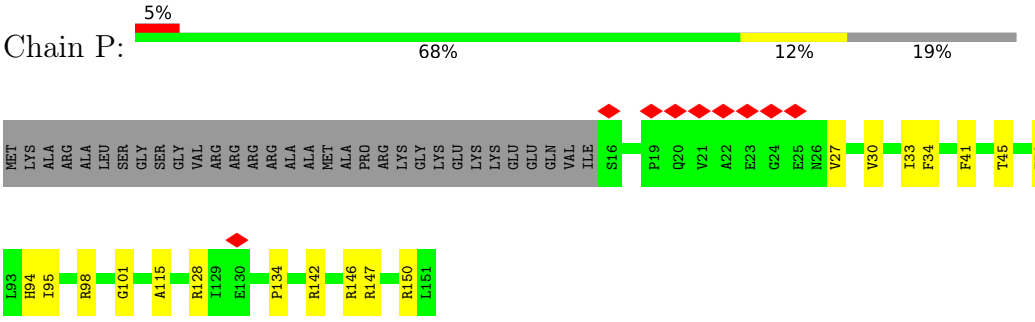
• Molecule 15: uS15

Chain O:



• Molecule 16: uS11

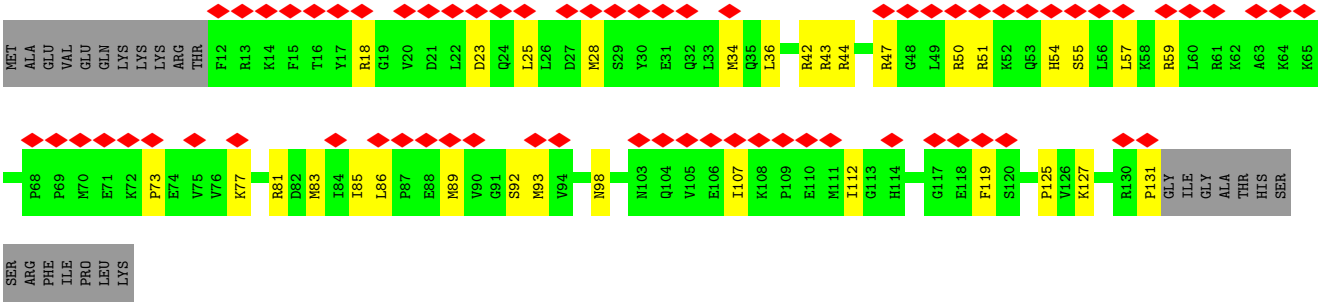
Chain P:



• Molecule 17: uS19

Chain Q:

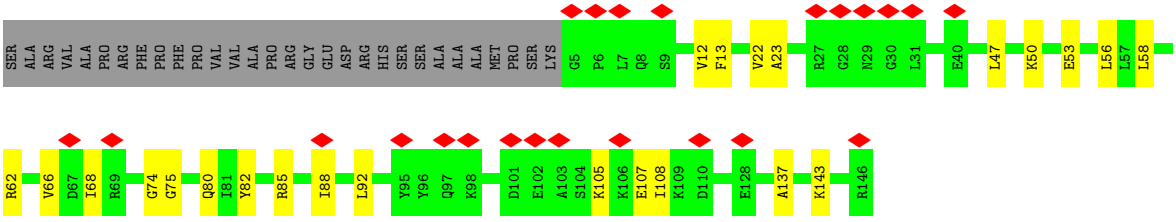




• Molecule 18: uS9

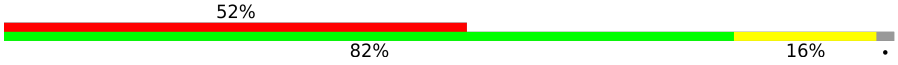
Chain R:

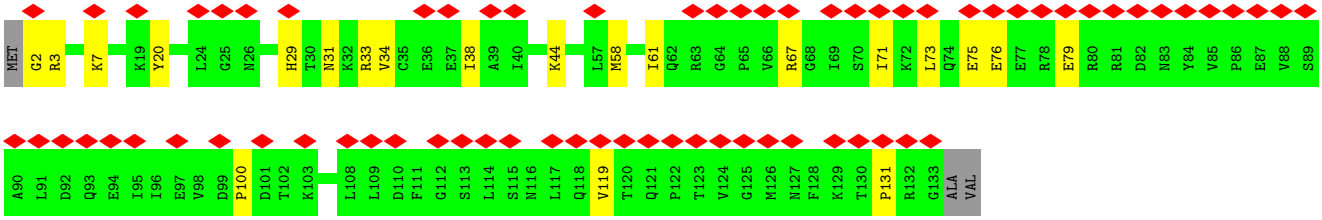




• Molecule 19: eS17

Chain S:

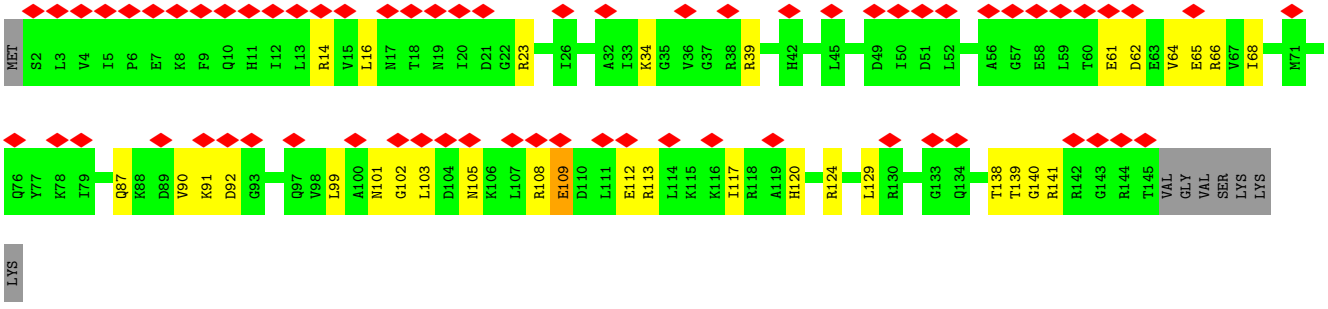




• Molecule 20: uS13

Chain T:

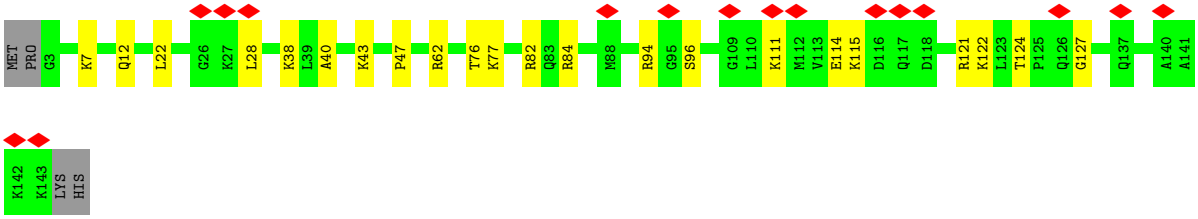




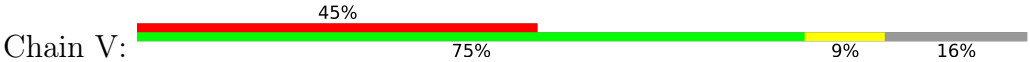
• Molecule 21: eS19

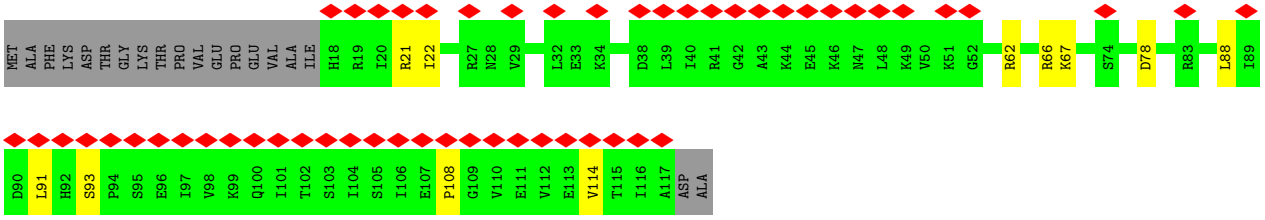
Chain U:



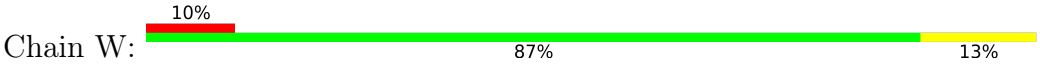


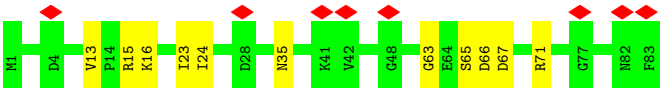
• Molecule 22: uS10



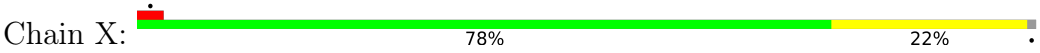


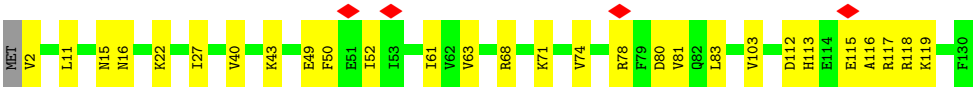
• Molecule 23: eS21



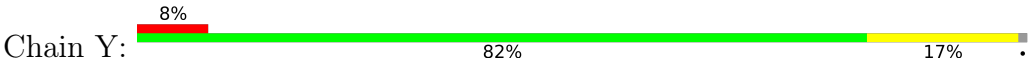


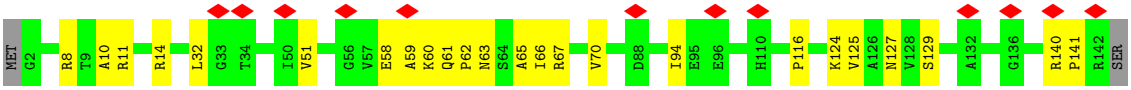
• Molecule 24: uS8





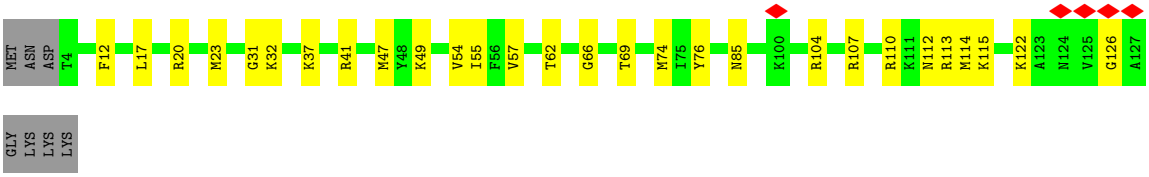
• Molecule 25: uS12





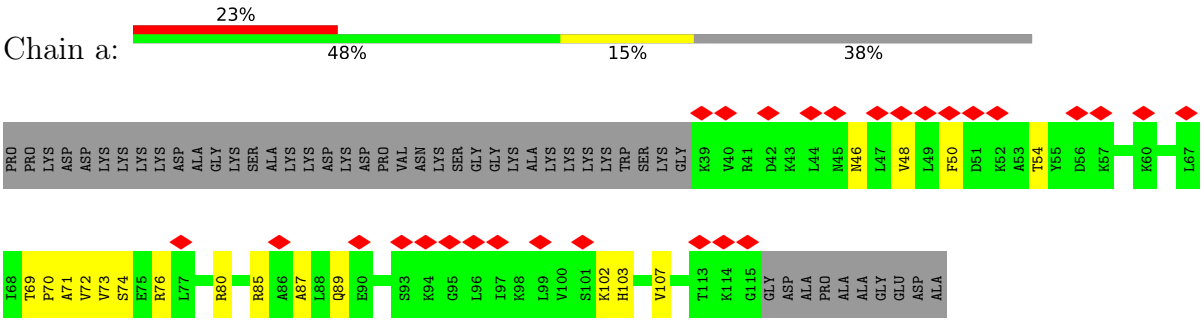
• Molecule 26: eS24





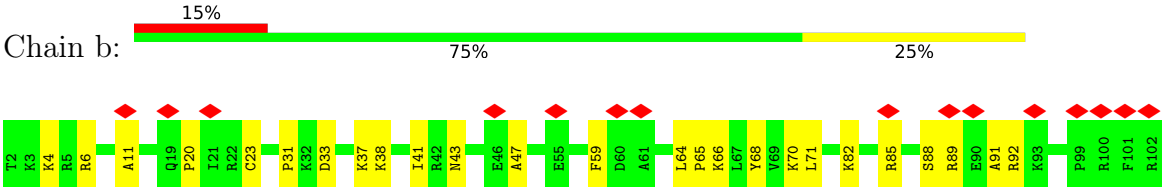
• Molecule 27: eS25

Chain a:



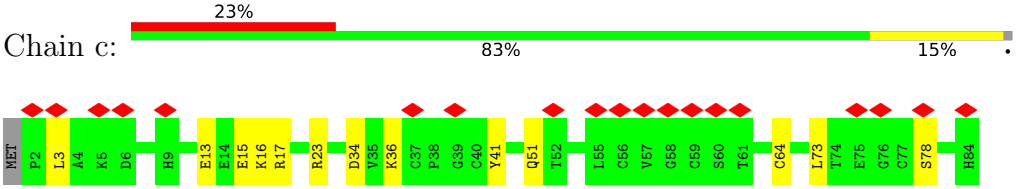
• Molecule 28: eS26

Chain b:



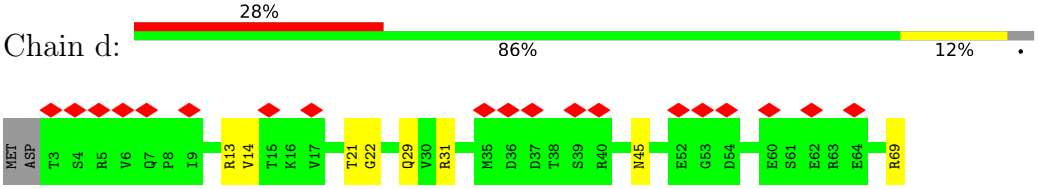
• Molecule 29: eS27

Chain c:



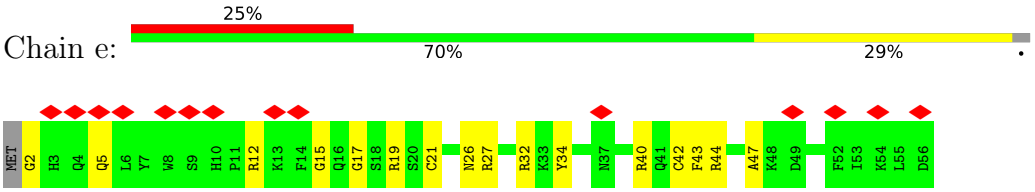
• Molecule 30: eS28

Chain d:



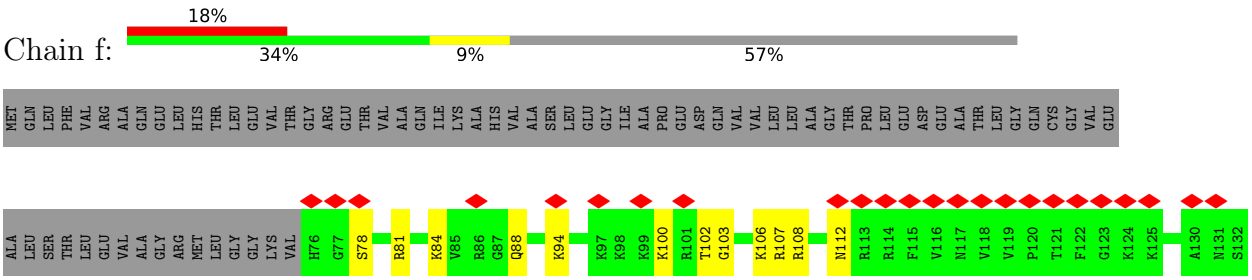
• Molecule 31: uS14

Chain e:



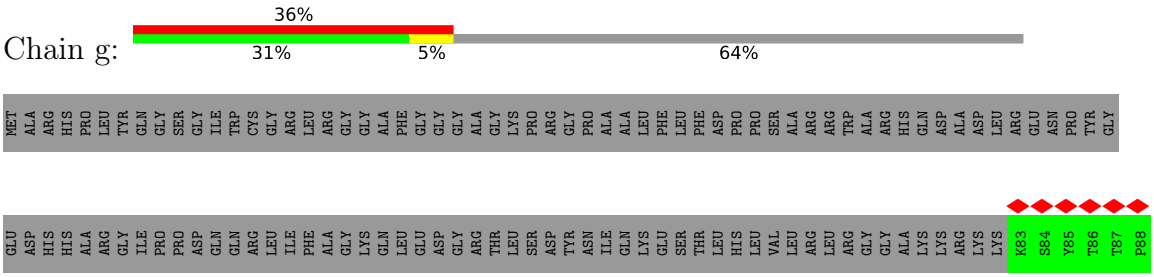
• Molecule 32: eS30

Chain f:



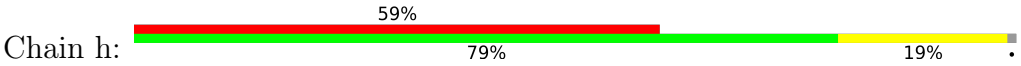
• Molecule 33: eS31

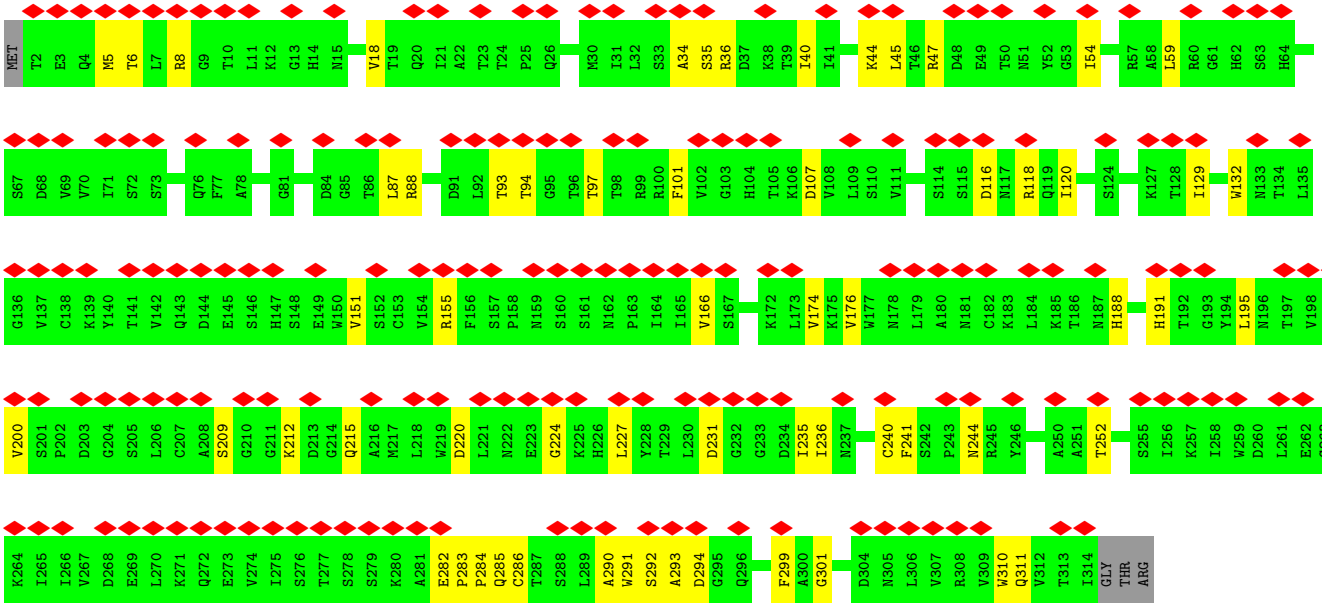
Chain g:



• Molecule 34: Receptor for Activated C Kinase 1 (RACK1)

Chain h:





• Molecule 35: eL41

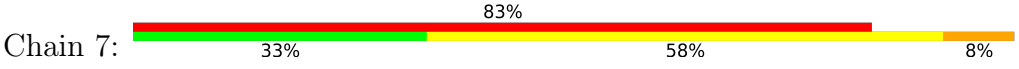
Chain n:





• Molecule 36: HCV IRES partially loaded mRNA portion

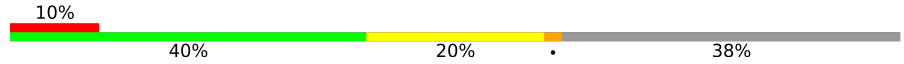
Chain 7:

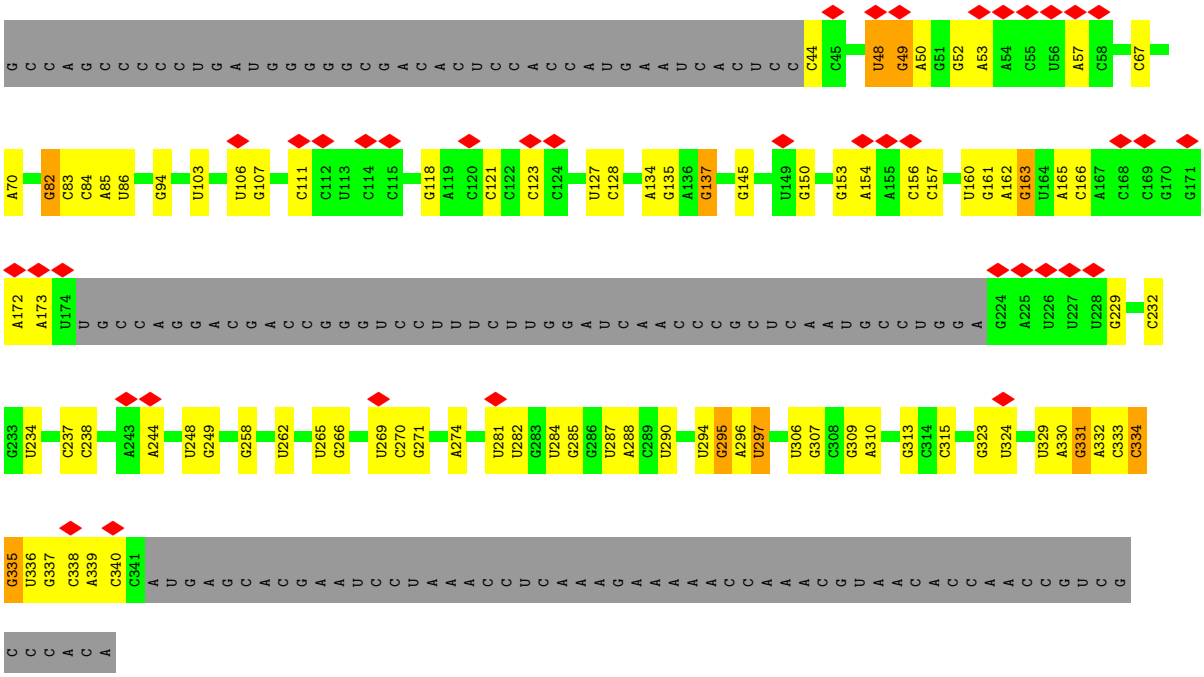




• Molecule 37: HCV IRES

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	97108	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	70.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	56000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	380.0, 380.0, 380.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	2	0.14	0/40102	0.32	0/62495
2	B	0.20	0/1747	0.53	0/2374
3	C	0.19	0/1756	0.52	0/2350
4	D	0.20	0/1753	0.55	0/2369
5	E	0.25	1/1796 (0.1%)	0.51	0/2417
6	F	0.24	1/2118 (0.0%)	0.49	0/2849
7	G	0.24	0/1531	0.62	1/2059 (0.0%)
8	H	0.16	0/1946	0.42	0/2590
9	I	0.25	0/1510	0.68	3/2022 (0.1%)
10	J	0.17	0/1715	0.46	0/2287
11	K	0.23	0/1550	0.58	0/2069
12	L	0.18	0/834	0.54	0/1125
13	M	0.23	0/1254	0.58	1/1677 (0.1%)
14	N	0.18	0/918	0.50	2/1233 (0.2%)
15	O	0.28	0/1226	0.65	2/1649 (0.1%)
16	P	0.17	0/1029	0.44	0/1380
17	Q	0.20	0/1017	0.53	0/1358
18	R	0.22	0/1146	0.58	1/1534 (0.1%)
19	S	0.24	0/1082	0.69	2/1452 (0.1%)
20	T	0.27	0/1208	0.71	5/1618 (0.3%)
21	U	0.17	0/1115	0.44	0/1493
22	V	0.22	0/805	0.54	0/1081
23	W	0.21	0/643	0.55	0/860
24	X	0.25	0/1051	0.59	0/1406
25	Y	0.19	0/1116	0.53	0/1490
26	Z	0.18	0/1028	0.49	0/1366
27	a	0.34	0/620	0.83	0/831
28	b	0.18	0/828	0.47	0/1109
29	c	0.21	0/665	0.61	0/891
30	d	0.28	0/532	0.64	0/712
31	e	0.19	0/470	0.54	0/623
32	f	0.22	0/462	0.57	1/607 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	g	0.16	0/567	0.43	0/753
34	h	0.16	0/2493	0.43	0/3394
35	n	0.21	0/240	0.65	0/305
36	7	0.03	0/155	0.06	0/236
37	z	0.13	0/5942	0.27	0/9262
All	All	0.18	2/85970 (0.0%)	0.43	18/125326 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	0	1
25	Y	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	40	GLU	CA-CB	7.66	1.64	1.53
5	E	162	ASP	C-N	6.51	1.41	1.34

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	I	38	ALA	CA-C-N	-6.86	111.58	122.08
9	I	38	ALA	C-N-CA	-6.86	111.58	122.08
15	O	119	GLU	N-CA-CB	6.70	120.62	110.30
20	T	109	GLU	CA-CB-CG	6.52	127.14	114.10
20	T	109	GLU	N-CA-CB	6.45	120.91	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	250	GLU	Peptide
25	Y	61	GLN	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35864	0	18113	278	0
2	B	1710	0	1708	21	0
3	C	1729	0	1803	20	0
4	D	1716	0	1806	25	0
5	E	1768	0	1866	17	0
6	F	2076	0	2177	33	0
7	G	1509	0	1563	25	0
8	H	1923	0	2089	30	0
9	I	1488	0	1582	17	0
10	J	1686	0	1772	21	0
11	K	1525	0	1640	25	0
12	L	810	0	836	12	0
13	M	1233	0	1310	19	0
14	N	908	0	939	11	0
15	O	1202	0	1289	22	0
16	P	1016	0	1039	15	0
17	Q	997	0	1045	21	0
18	R	1128	0	1195	14	0
19	S	1068	0	1121	14	0
20	T	1190	0	1249	22	0
21	U	1097	0	1130	16	0
22	V	795	0	862	9	0
23	W	636	0	637	10	0
24	X	1034	0	1080	21	0
25	Y	1098	0	1167	17	0
26	Z	1011	0	1083	21	0
27	a	614	0	678	14	0
28	b	814	0	863	16	0
29	c	651	0	672	9	0
30	d	530	0	561	6	0
31	e	459	0	452	16	0
32	f	457	0	502	6	0
33	g	555	0	563	6	0
34	h	2436	0	2393	38	0
35	n	239	0	289	8	0
36	7	144	0	73	1	0
37	z	5318	0	2689	23	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	1	0	0	0	0
38	g	1	0	0	0	0
All	All	80436	0	61836	733	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 6.

The worst 5 of 733 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)
1:2:1472:C:H42	1:2:1476:A:H62	1.07	0.97
1:2:934:G:H1	1:2:1008:A:H2	1.15	0.90
37:z:145:G:H1	37:z:248:U:H3	1.20	0.89
1:2:1748:G:H1	1:2:1786:U:H3	1.22	0.88
1:2:1656:G:H1	1:2:1668:U:H3	0.89	0.85

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	215/295 (73%)	199 (93%)	16 (7%)	0	100	100
3	C	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
4	D	219/221 (99%)	207 (94%)	12 (6%)	0	100	100
5	E	226/281 (80%)	221 (98%)	5 (2%)	0	100	100
6	F	260/263 (99%)	253 (97%)	7 (3%)	0	100	100
7	G	189/204 (93%)	178 (94%)	11 (6%)	0	100	100
8	H	235/249 (94%)	228 (97%)	7 (3%)	0	100	100
9	I	181/432 (42%)	170 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	204/208 (98%)	198 (97%)	6 (3%)	0	100	100
11	K	183/194 (94%)	179 (98%)	4 (2%)	0	100	100
12	L	94/149 (63%)	90 (96%)	4 (4%)	0	100	100
13	M	149/158 (94%)	140 (94%)	9 (6%)	0	100	100
14	N	115/132 (87%)	106 (92%)	9 (8%)	0	100	100
15	O	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
16	P	134/168 (80%)	125 (93%)	9 (7%)	0	100	100
17	Q	118/145 (81%)	110 (93%)	8 (7%)	0	100	100
18	R	140/172 (81%)	134 (96%)	6 (4%)	0	100	100
19	S	130/135 (96%)	118 (91%)	12 (9%)	0	100	100
20	T	142/152 (93%)	132 (93%)	10 (7%)	0	100	100
21	U	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
22	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
23	W	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
24	X	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
25	Y	139/143 (97%)	128 (92%)	10 (7%)	1 (1%)	18	54
26	Z	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
27	a	75/124 (60%)	70 (93%)	5 (7%)	0	100	100
28	b	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
29	c	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
30	d	65/69 (94%)	62 (95%)	3 (5%)	0	100	100
31	e	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
32	f	55/133 (41%)	50 (91%)	5 (9%)	0	100	100
33	g	66/188 (35%)	62 (94%)	4 (6%)	0	100	100
34	h	311/317 (98%)	292 (94%)	19 (6%)	0	100	100
35	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4826/5821 (83%)	4597 (95%)	228 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	Y	62	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/245 (74%)	180 (100%)	0	100	100
3	C	194/231 (84%)	194 (100%)	0	100	100
4	D	187/187 (100%)	187 (100%)	0	100	100
5	E	190/232 (82%)	190 (100%)	0	100	100
6	F	224/225 (100%)	224 (100%)	0	100	100
7	G	161/170 (95%)	161 (100%)	0	100	100
8	H	207/218 (95%)	207 (100%)	0	100	100
9	I	165/360 (46%)	164 (99%)	1 (1%)	78	81
10	J	178/180 (99%)	178 (100%)	0	100	100
11	K	161/168 (96%)	161 (100%)	0	100	100
12	L	87/125 (70%)	87 (100%)	0	100	100
13	M	136/142 (96%)	136 (100%)	0	100	100
14	N	99/108 (92%)	99 (100%)	0	100	100
15	O	130/131 (99%)	130 (100%)	0	100	100
16	P	106/130 (82%)	106 (100%)	0	100	100
17	Q	109/130 (84%)	109 (100%)	0	100	100
18	R	117/140 (84%)	117 (100%)	0	100	100
19	S	119/121 (98%)	119 (100%)	0	100	100
20	T	125/132 (95%)	125 (100%)	0	100	100
21	U	111/116 (96%)	111 (100%)	0	100	100
22	V	92/107 (86%)	92 (100%)	0	100	100
23	W	67/67 (100%)	67 (100%)	0	100	100
24	X	112/113 (99%)	112 (100%)	0	100	100
25	Y	113/115 (98%)	113 (100%)	0	100	100
26	Z	107/113 (95%)	107 (100%)	0	100	100
27	a	68/102 (67%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	b	88/88 (100%)	88 (100%)	0	100	100
29	c	75/76 (99%)	75 (100%)	0	100	100
30	d	60/62 (97%)	60 (100%)	0	100	100
31	e	48/49 (98%)	48 (100%)	0	100	100
32	f	47/106 (44%)	46 (98%)	1 (2%)	47	65
33	g	61/154 (40%)	61 (100%)	0	100	100
34	h	272/275 (99%)	272 (100%)	0	100	100
35	n	24/24 (100%)	24 (100%)	0	100	100
All	All	4220/4942 (85%)	4218 (100%)	2 (0%)	100	100

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

Mol	Chain	Res	Type
9	I	39	GLN
32	f	88	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
22	V	47	ASN
26	Z	15	ASN
34	h	311	GLN
23	W	2	GLN
24	X	92	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1669/1870 (89%)	373 (22%)	8 (0%)
36	7	11/12 (91%)	8 (72%)	0
37	z	247/400 (61%)	66 (26%)	0
All	All	1927/2282 (84%)	447 (23%)	8 (0%)

5 of 447 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A

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Mol	Chain	Res	Type
1	2	4	C
1	2	11	A
1	2	26	U
1	2	33	G

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1759	G
1	2	1308	U
1	2	874	G
1	2	627	U
1	2	886	A

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

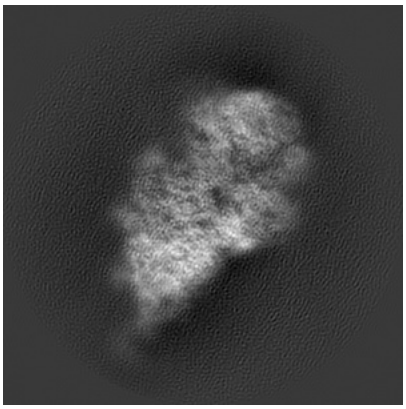
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-25536. These allow visual inspection of the internal detail of the map and identification of artifacts.

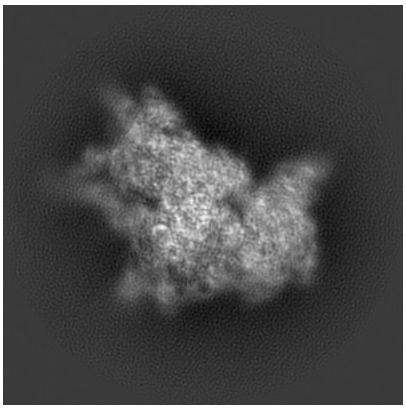
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

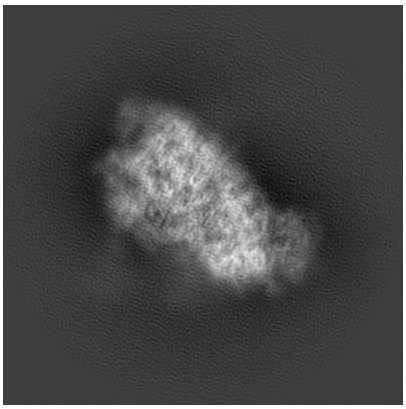
6.1.1 Primary map



X

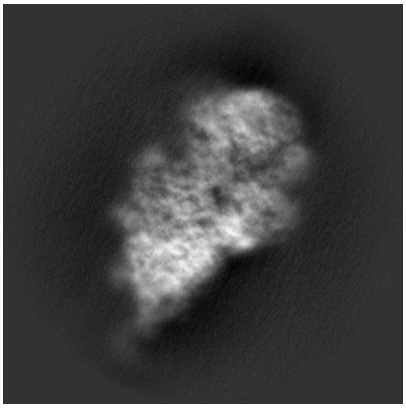


Y

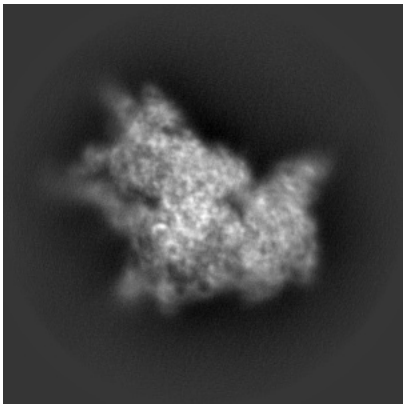


Z

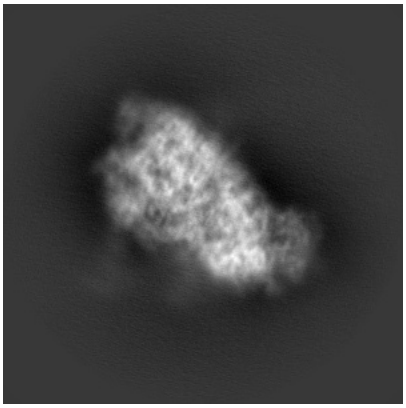
6.1.2 Raw map



X



Y

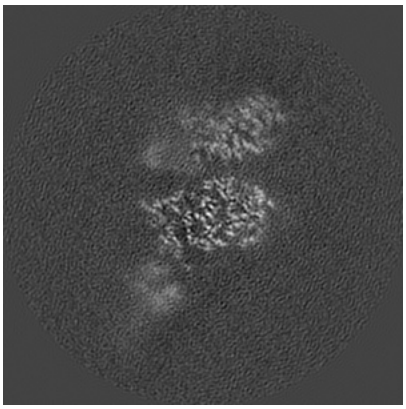


Z

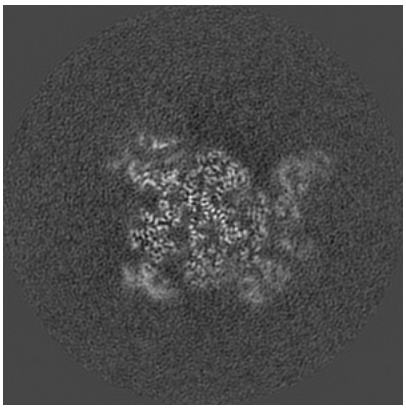
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

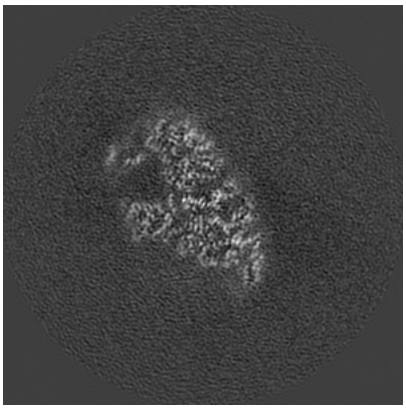
6.2.1 Primary map



X Index: 200

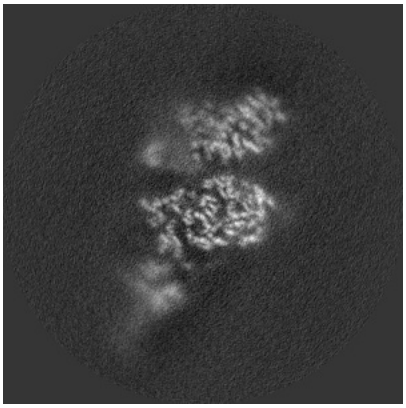


Y Index: 200

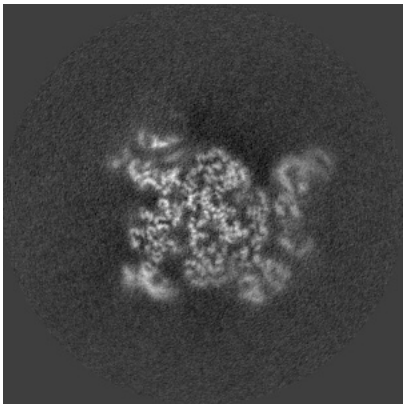


Z Index: 200

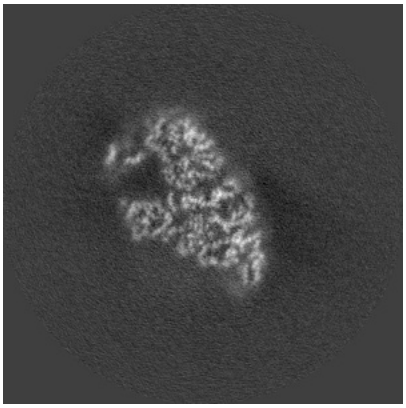
6.2.2 Raw map



X Index: 200



Y Index: 200

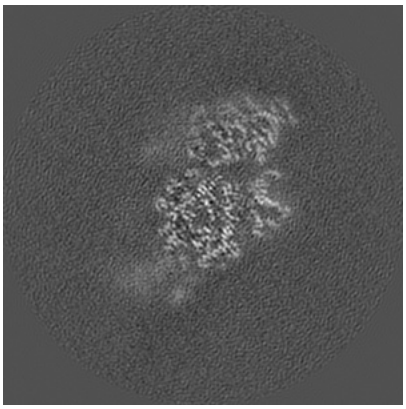


Z Index: 200

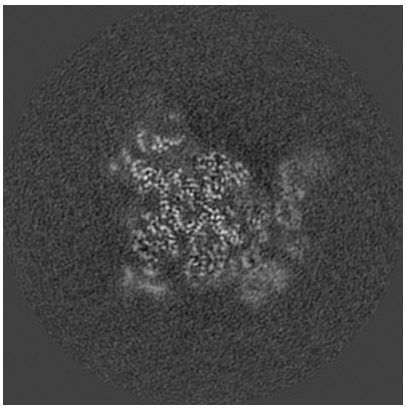
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

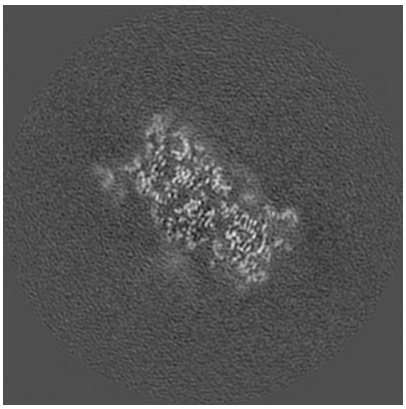
6.3.1 Primary map



X Index: 188

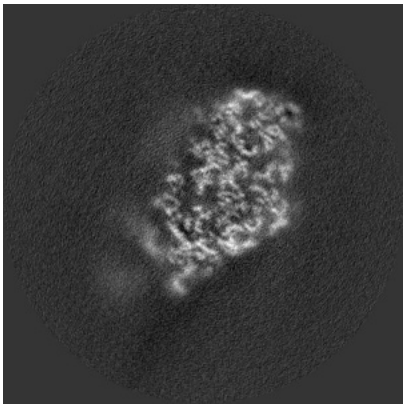


Y Index: 196

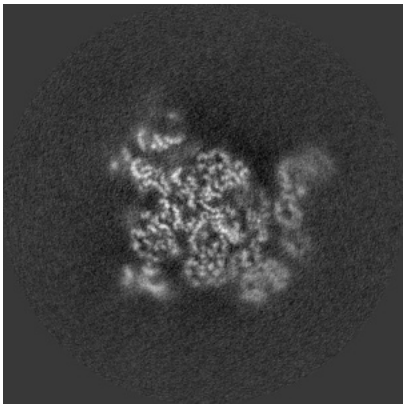


Z Index: 175

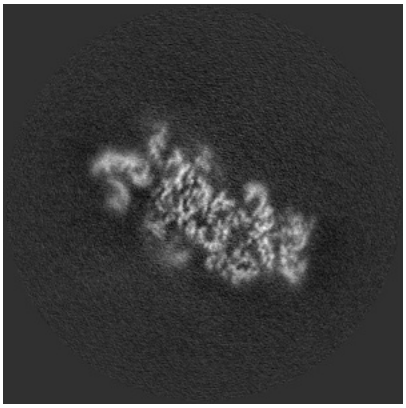
6.3.2 Raw map



X Index: 176



Y Index: 197

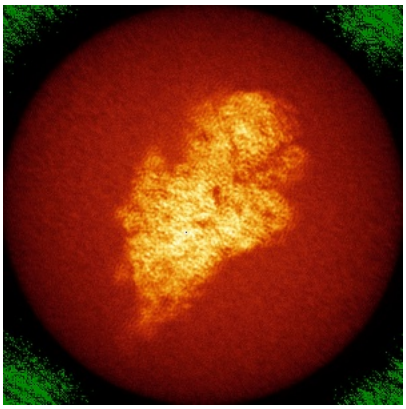


Z Index: 161

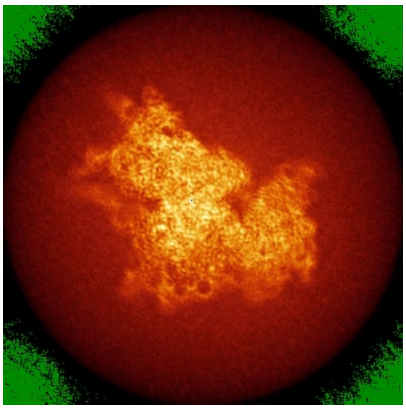
The images above show the largest variance slices of the map in three orthogonal directions.

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

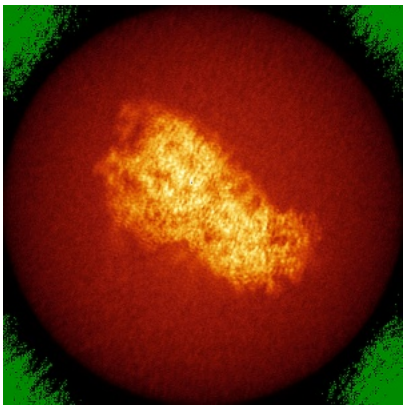
6.4.1 Primary map



X

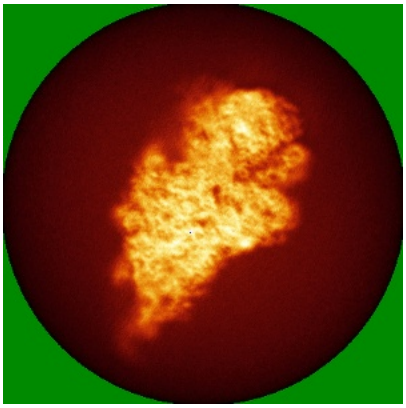


Y

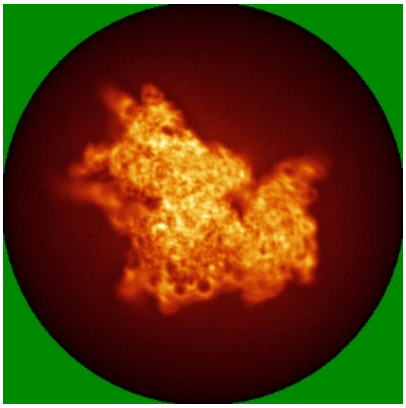


Z

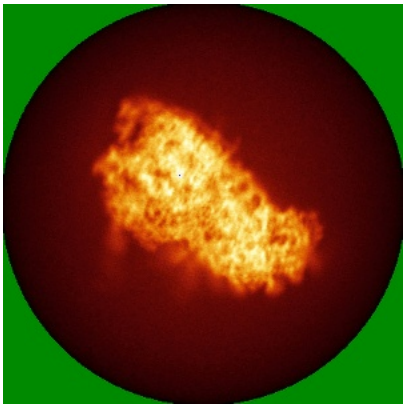
6.4.2 Raw map



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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.017. 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



X Y Z

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.

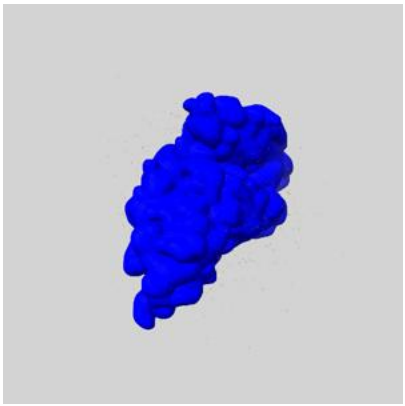
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

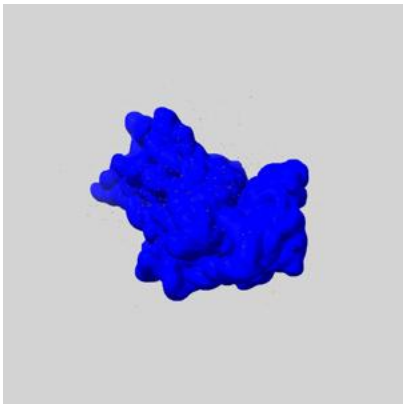
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

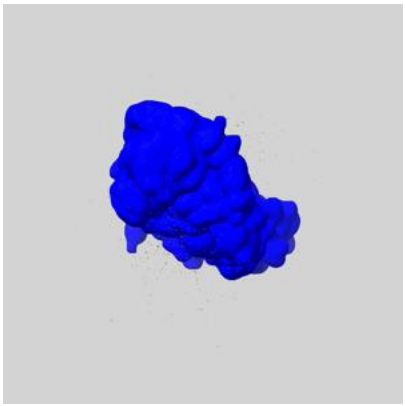
6.6.1 emd_25536_msk_1.map



X



Y

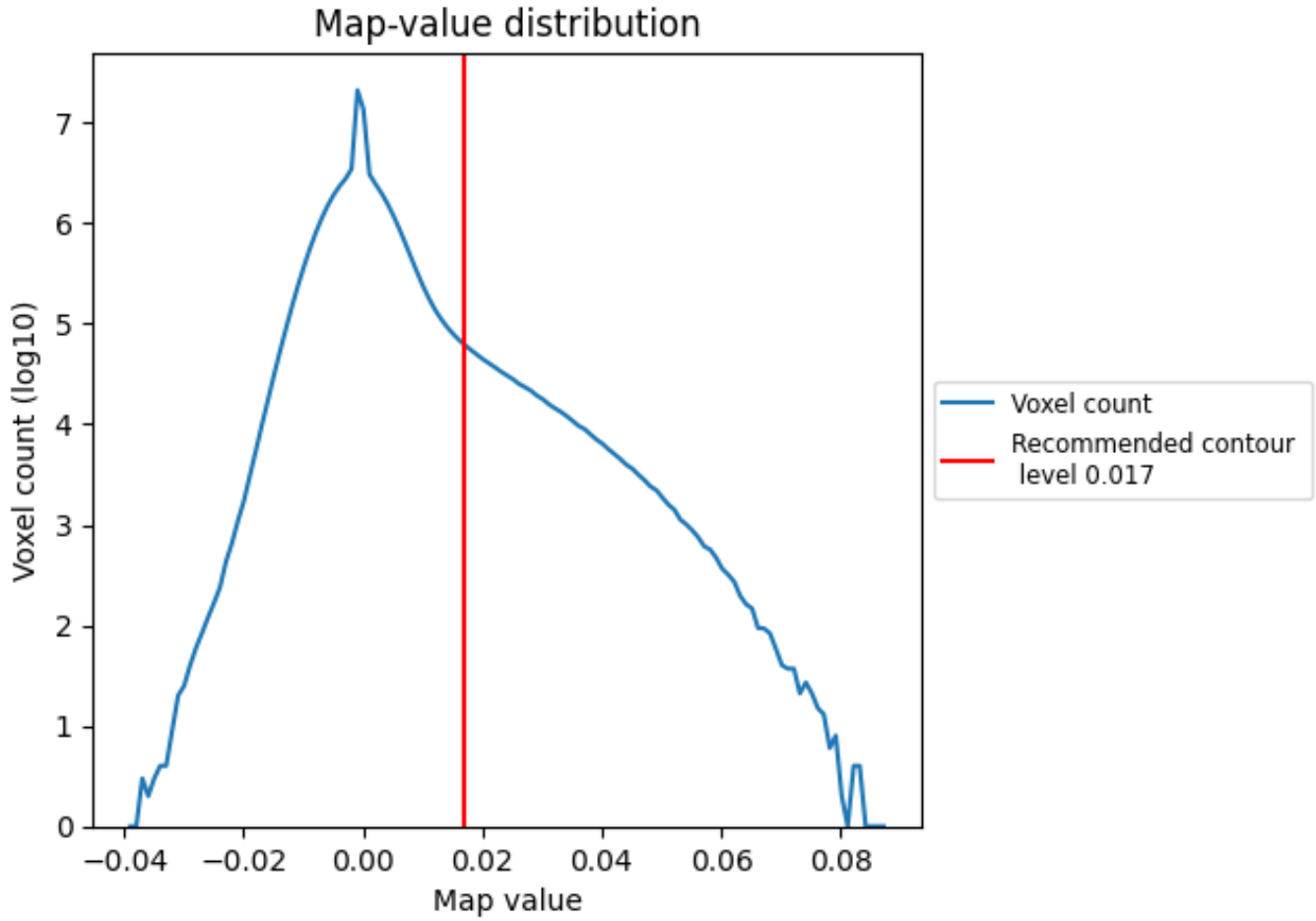


Z

7 Map analysis

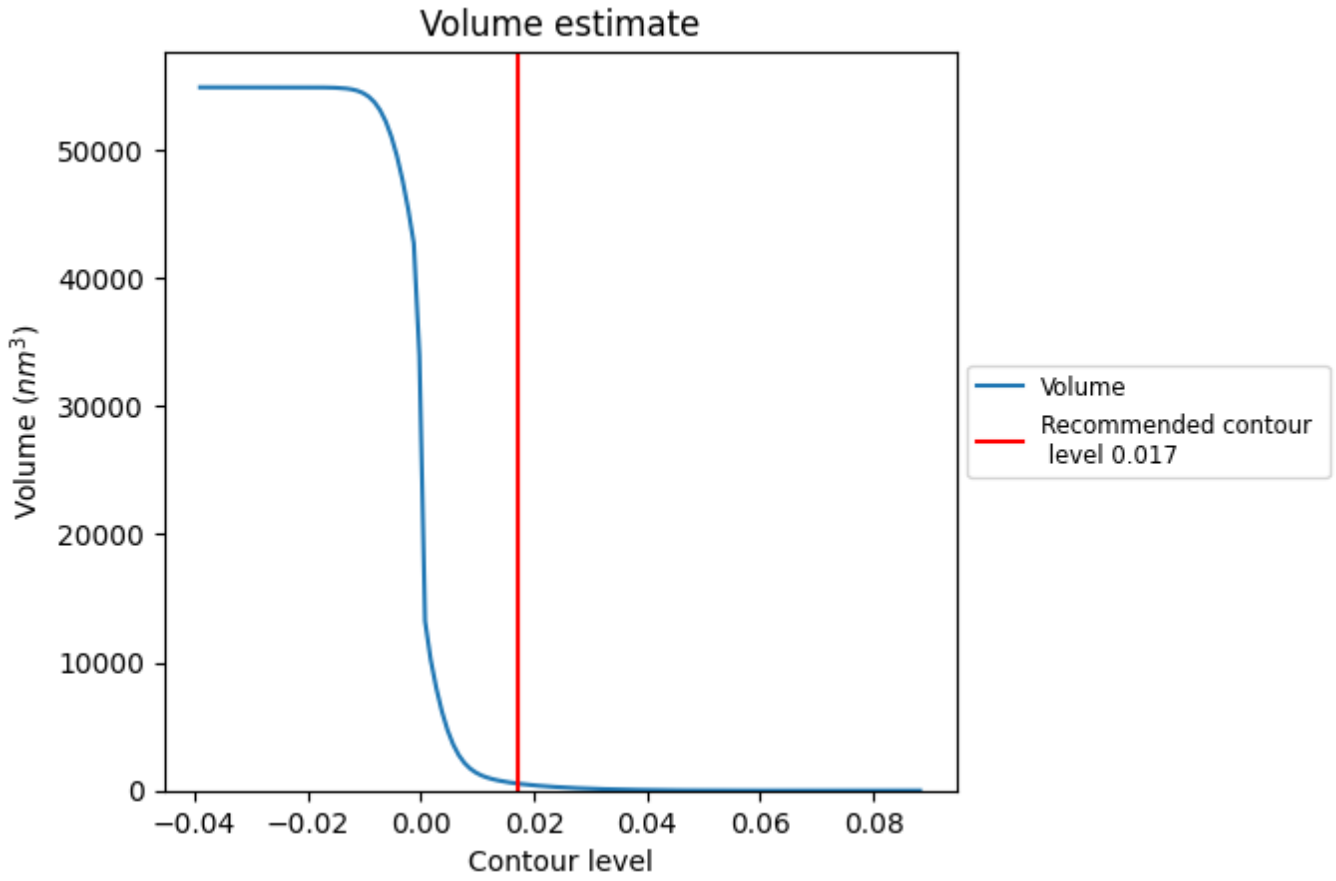
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

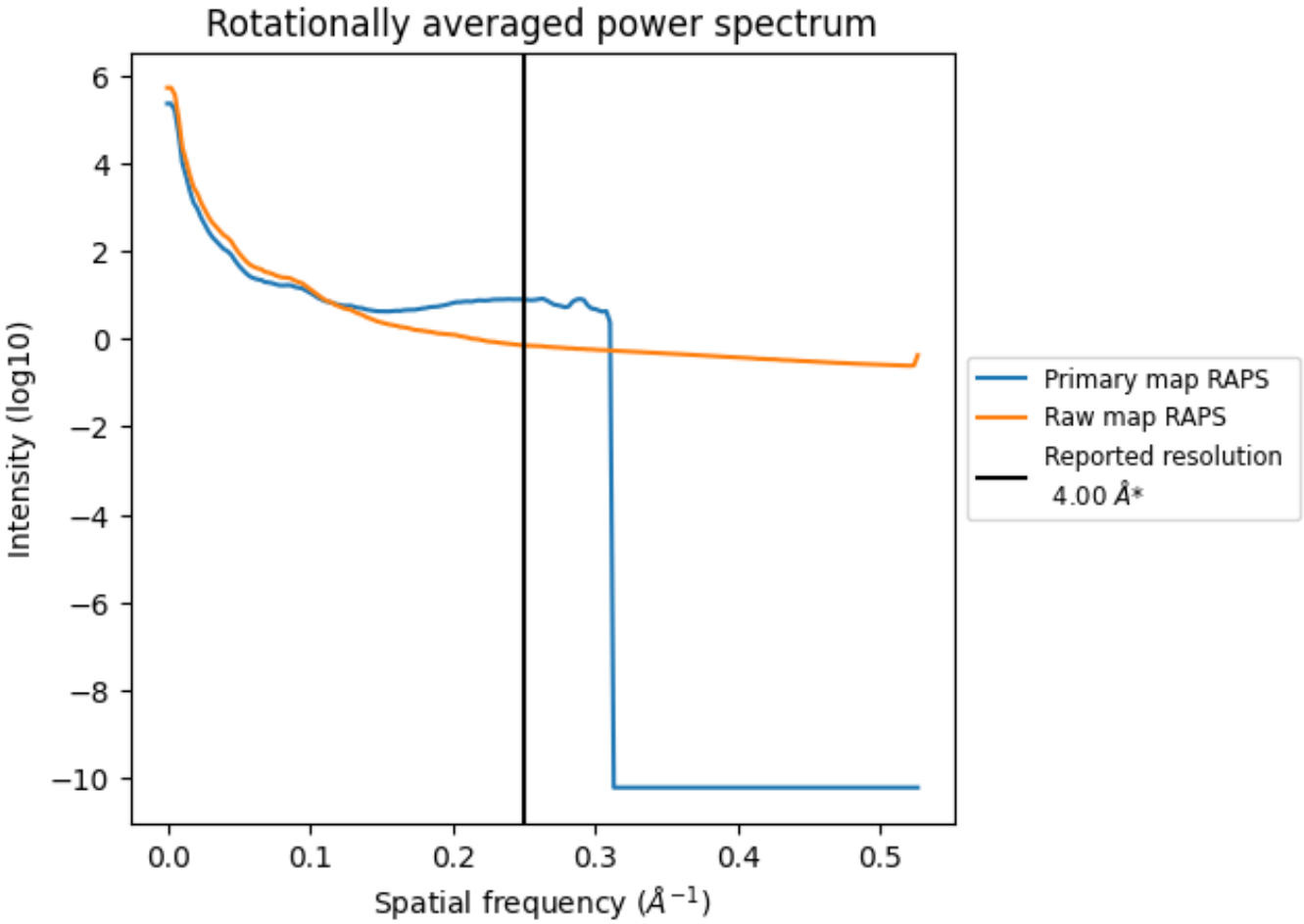
7.2 Volume estimate (i)



The volume at the recommended contour level is 553 nm^3; this corresponds to an approximate mass of 499 kDa.

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

7.3 Rotationally averaged power spectrum (i)

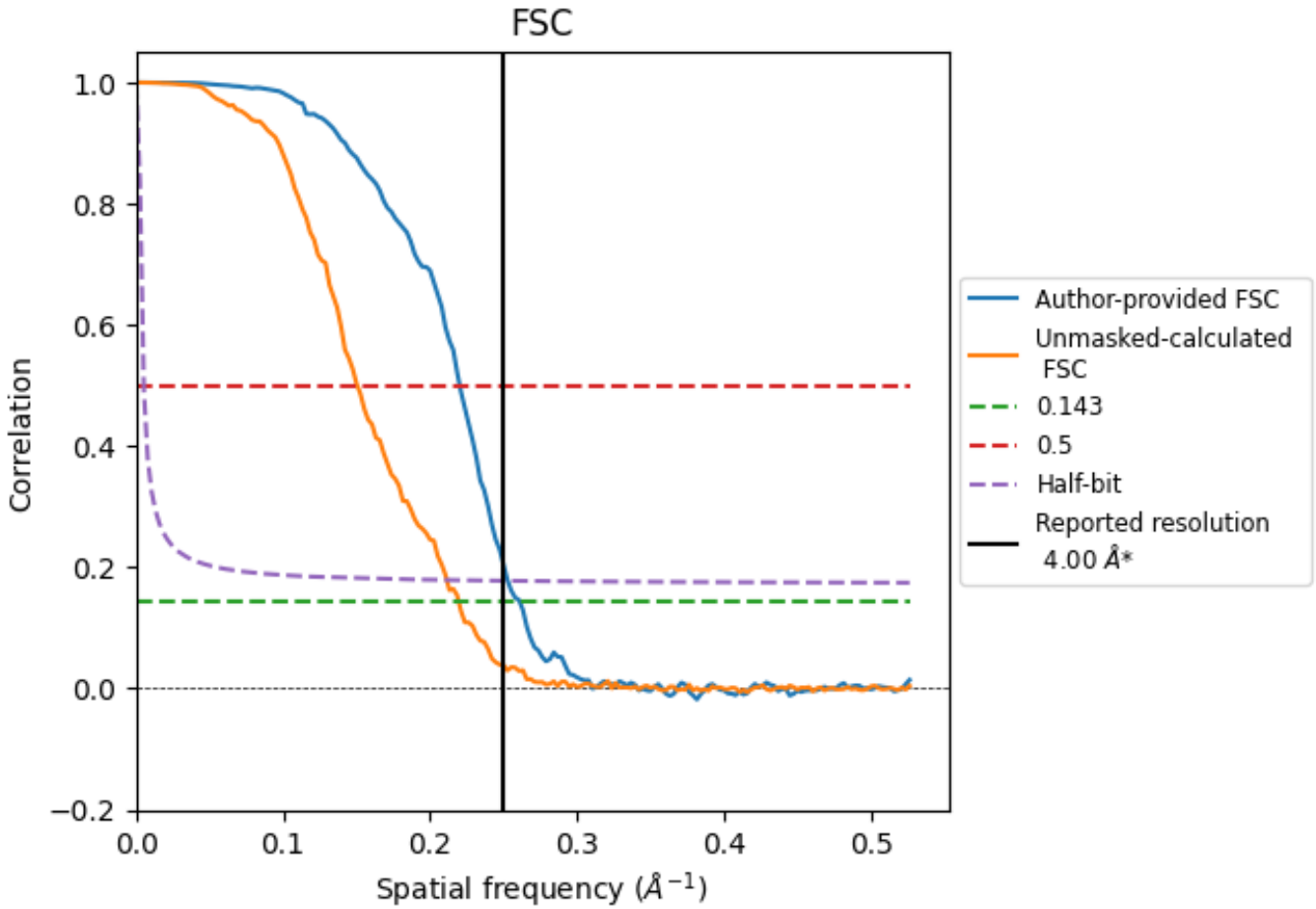


*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

8.2 Resolution estimates (i)

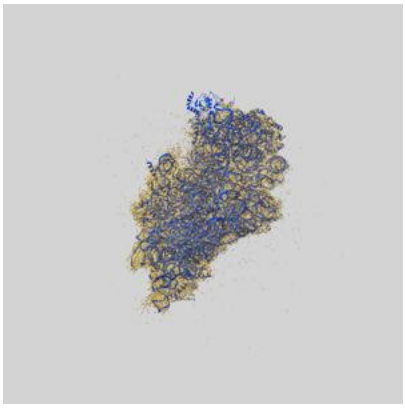
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.83	4.54	3.95
Unmasked-calculated*	4.56	6.64	4.73

*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 4.56 differs from the reported value 4.0 by more than 10 %

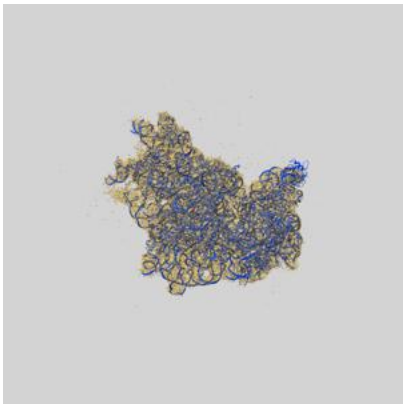
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-25536 and PDB model 7SYP. Per-residue inclusion information can be found in section 3 on page 12.

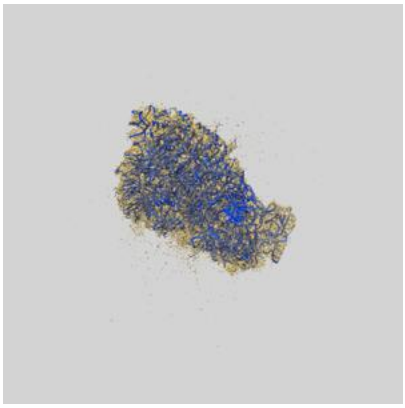
9.1 Map-model overlay



X



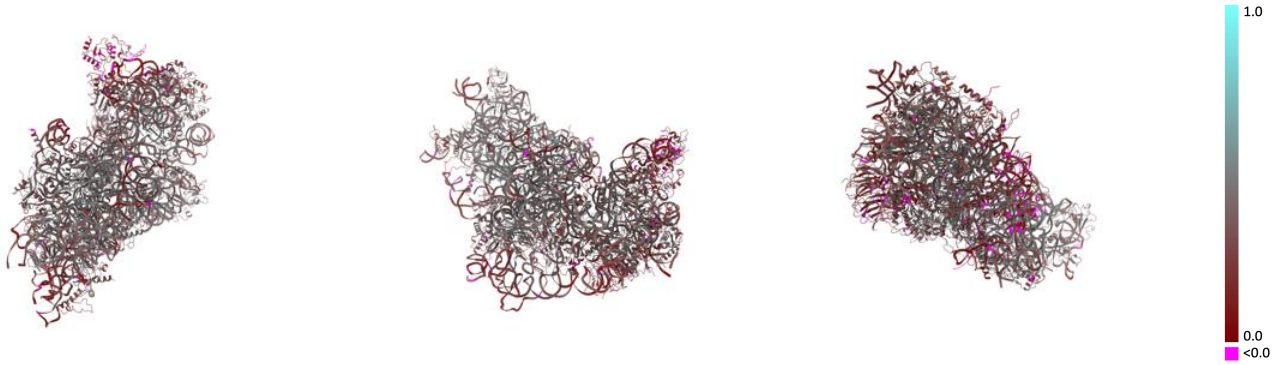
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.017 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.

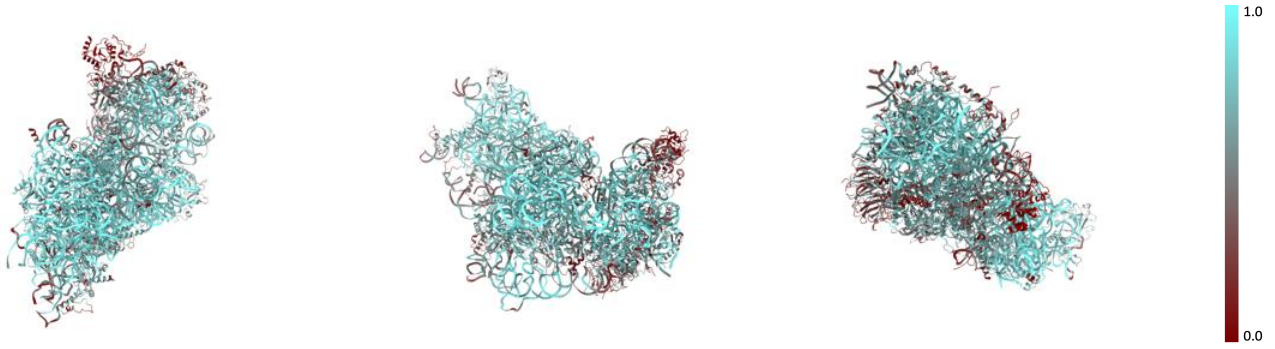
9.2 Q-score mapped to coordinate model



X Y Z

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

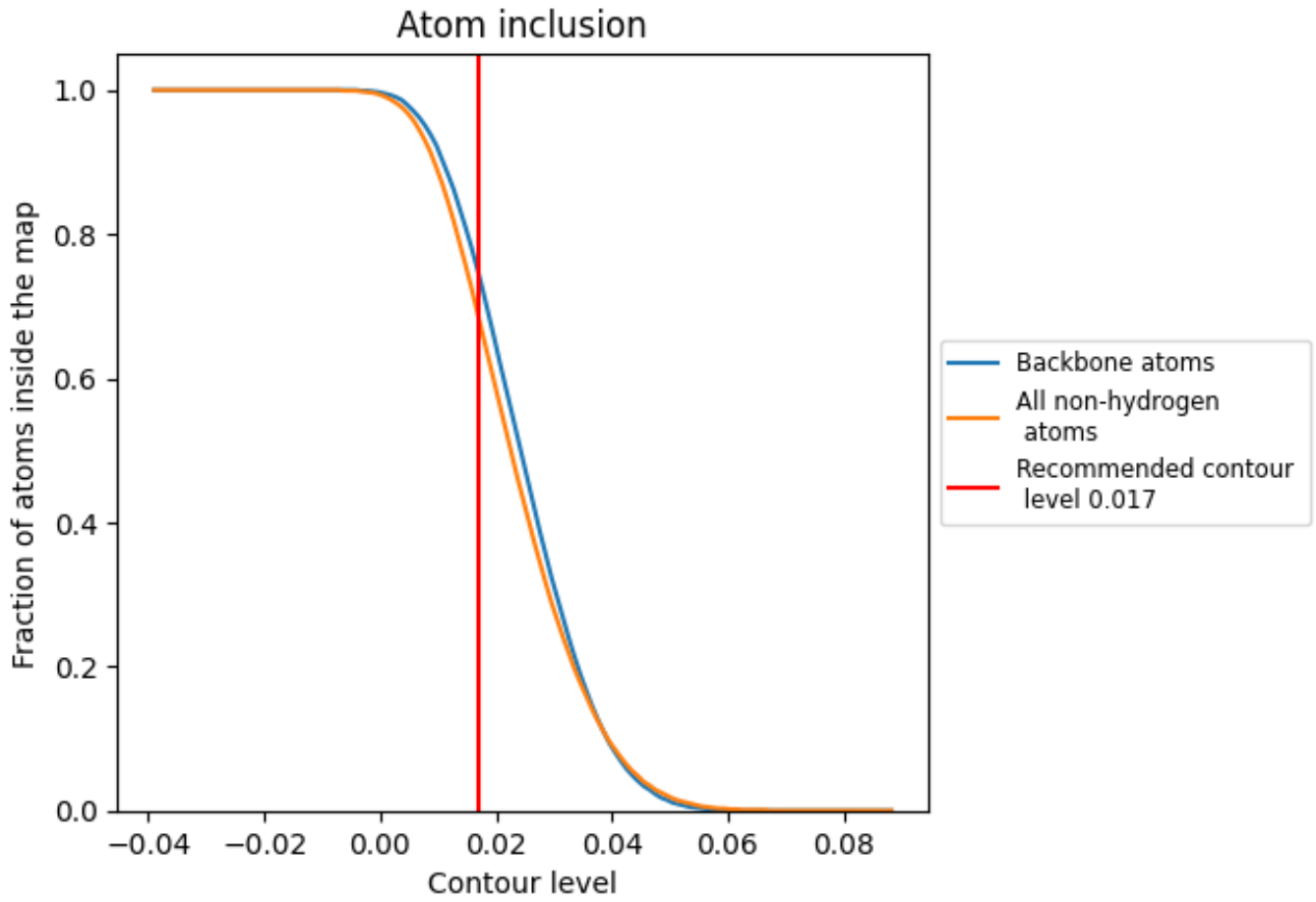
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.017).

9.4 Atom inclusion (i)



At the recommended contour level, 74% of all backbone atoms, 68% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6840	0.3510
2	0.8110	0.3730
7	0.2220	0.2170
B	0.6370	0.3560
C	0.6830	0.3960
D	0.6480	0.3910
E	0.4790	0.3320
F	0.7440	0.4190
G	0.6600	0.3800
H	0.6380	0.3520
I	0.4340	0.3280
J	0.6490	0.3860
K	0.7030	0.3990
L	0.4040	0.2380
M	0.6390	0.3950
N	0.0250	0.1600
O	0.6870	0.3780
P	0.7220	0.3950
Q	0.3670	0.2310
R	0.6380	0.3630
S	0.4180	0.2720
T	0.4510	0.3120
U	0.6890	0.3690
V	0.3550	0.2630
W	0.6540	0.3740
X	0.6740	0.4030
Y	0.6800	0.4060
Z	0.7430	0.3910
a	0.4940	0.3170
b	0.6730	0.3980
c	0.5990	0.3650
d	0.5280	0.3580
e	0.5760	0.3390
f	0.4500	0.2010
g	0.0440	0.1430



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Chain	Atom inclusion	Q-score
h	0.3630	0.2360
n	0.5780	0.3250
z	0.6650	0.2660