



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:53 PM UTC

PDB ID : 9OGY / pdb_00009ogy
EMDB ID : EMD-70479
Title : Megrivirus E 3' internal ribosome entry site (IRES) RNA core region bound to rabbit ribosome
Authors : Sherlock, M.E.; Kieft, J.S.
Deposited on : 2025-05-02
Resolution : 3.28 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

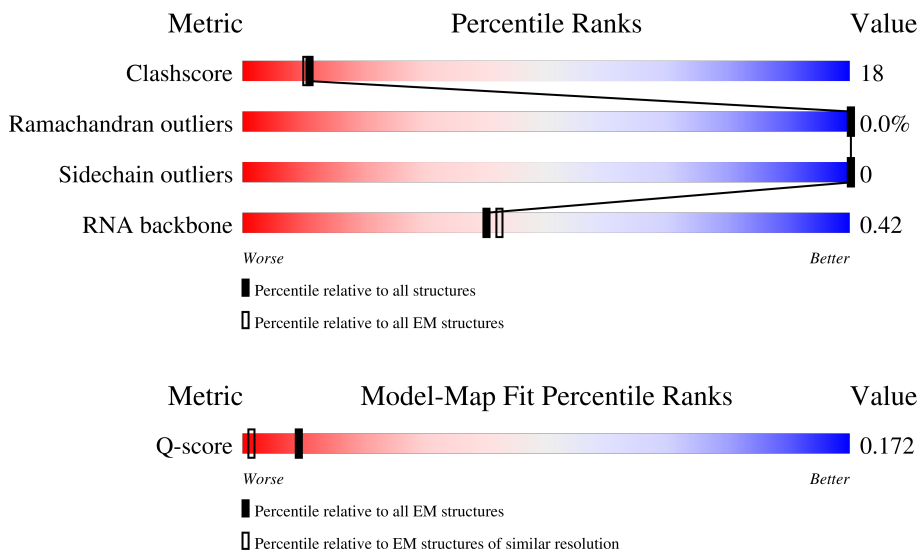
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.28 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	14492 (2.78 - 3.78)

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	2	1870	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">16%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">31%</div> <div style="text-align: center;">46%</div> <div style="text-align: center;">13%</div> <div style="text-align: center;">10%</div> </div>
2	A	270	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">28%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">10%</div> <div style="text-align: center;">19%</div> <div style="text-align: center;">10%</div> <div style="text-align: center;">60%</div> </div>
3	B	295	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">9%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">36%</div> <div style="text-align: center;">37%</div> <div style="text-align: center;">26%</div> </div>

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Mol	Chain	Length	Quality of chain
4	C	264	5% 42% 38% 19%
5	D	221	15% 65% 35%
6	E	281	64% 52% 30% 19%
7	F	263	6% 55% 45%
8	G	204	42% 52% 42% 6%
9	H	249	43% 58% 37% 5%
10	I	432	24% 18% 57%
11	J	208	33% 60% 39%
12	K	194	12% 57% 39% 5%
13	L	149	61% 38% 26% 36%
14	M	158	15% 55% 41%
15	N	132	89% 73% 16% 11%
16	O	151	5% 56% 43%
17	P	168	21% 55% 26% 19%
18	Q	145	46% 48% 34% 17%
19	R	172	53% 43% 40% 17%
20	S	135	67% 50% 47%
21	T	152	39% 61% 34% 5%
22	U	145	41% 63% 34%
23	V	119	65% 45% 39% 16%
24	W	83	10% 71% 29%
25	X	130	64% 35%
26	Y	143	31% 62% 36%
27	Z	131	13% 58% 37% 5%
28	a	124	34% 44% 19% 38%

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Mol	Chain	Length	Quality of chain
29	b	101	
30	c	84	
31	d	69	
32	e	56	
33	f	133	
34	g	188	
35	h	317	
36	n	25	

2 Entry composition i

There are 37 unique types of molecules in this entry. The entry contains 77254 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 ribosomal RNA.

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 RNA chain called Megrivirus E 3' IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A	107	2280	1018	404	752	106	0	0

- Molecule 3 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	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 4 is a protein called 40S ribosomal protein S3a.

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

- Molecule 5 is a protein called 40S ribosomal protein S2.

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

- Molecule 6 is a protein called Ribosomal protein S3.

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

- Molecule 7 is a protein called 40S ribosomal protein S4.

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

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 8 is a protein called Ribosomal protein S5.

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

- Molecule 9 is a protein called 40S ribosomal protein S6.

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

- Molecule 10 is a protein called eS7.

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

- Molecule 11 is a protein called 40S ribosomal protein S8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 12 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 13 is a protein called S10_ plectin domain-containing protein.

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

- Molecule 14 is a protein called Ribosomal protein S11.

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

- Molecule 15 is a protein called 40S ribosomal protein S12.

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

- Molecule 16 is a protein called Ribosomal protein S13.

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

- Molecule 17 is a protein called Ribosomal protein S14.

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

- Molecule 18 is a protein called uS19.

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

- Molecule 19 is a protein called Ribosomal protein S16.

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

- Molecule 20 is a protein called eS17.

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

- Molecule 21 is a protein called uS13.

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

- Molecule 22 is a protein called eS19.

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

- Molecule 23 is a protein called uS10.

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

- Molecule 24 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	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
W	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 25 is a protein called Ribosomal protein S15a.

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

- Molecule 26 is a protein called uS12.

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

- Molecule 27 is a protein called eS24.

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

- Molecule 28 is a protein called eS25.

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

- Molecule 29 is a protein called eS26.

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

- Molecule 30 is a protein called 40S ribosomal protein S27.

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

- Molecule 31 is a protein called Ribosomal protein S28.

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

- Molecule 32 is a protein called eS29.

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

- Molecule 33 is a protein called 40S ribosomal protein S30.

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

- Molecule 34 is a protein called eS31.

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

- Molecule 35 is a protein called RACK1.

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

- Molecule 36 is a protein called eL41.

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

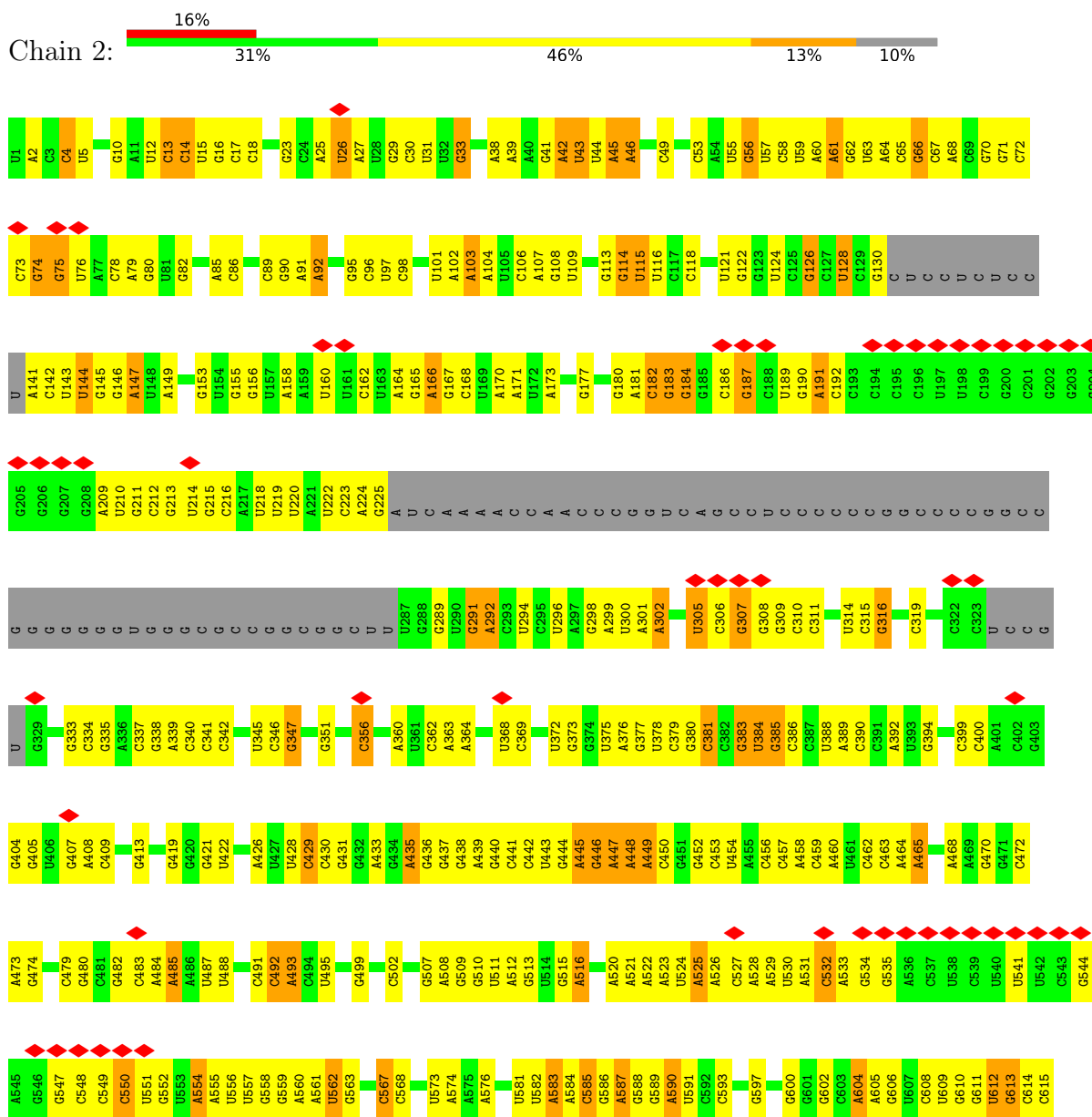
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

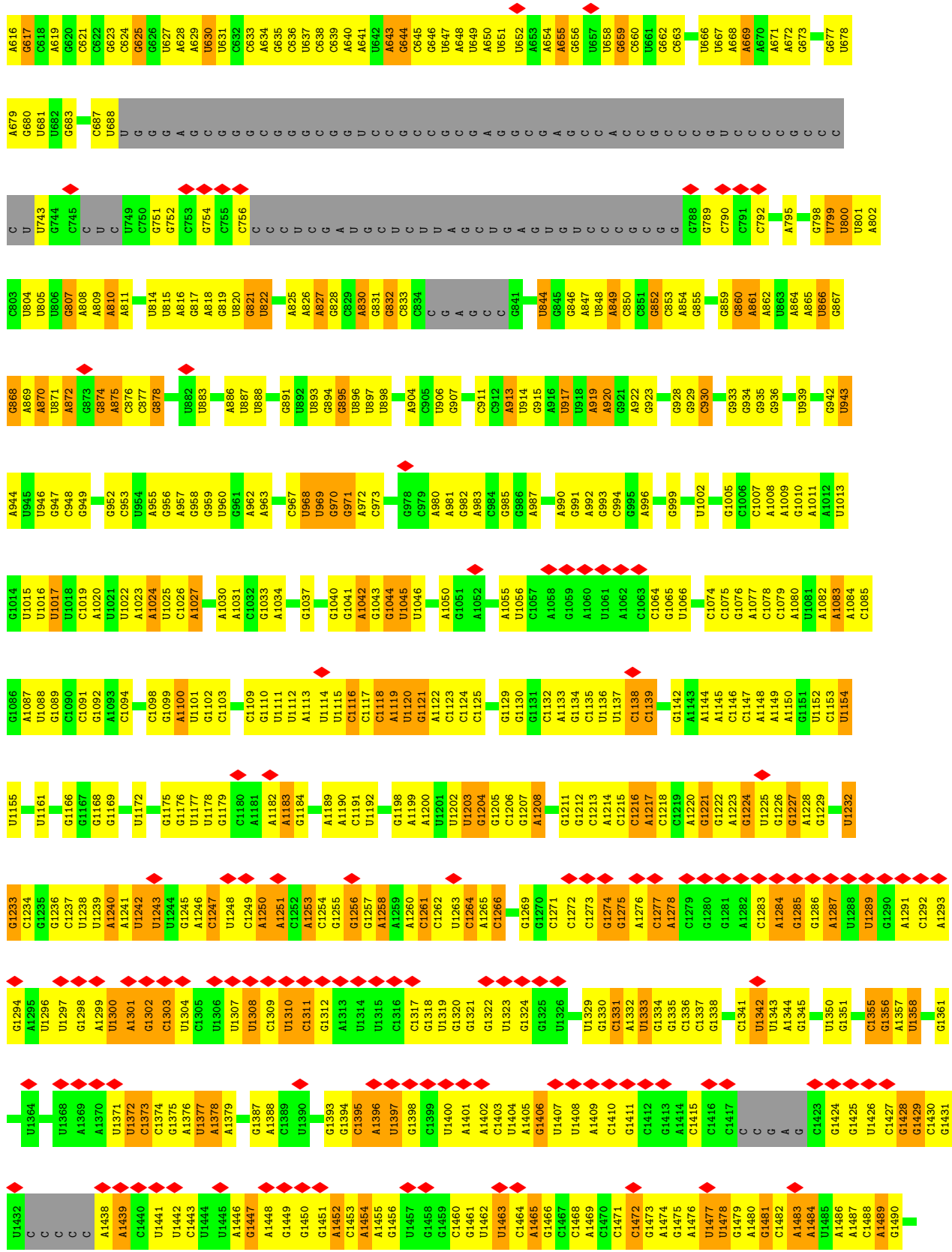
Mol	Chain	Residues	Atoms		AltConf
37	b	1	Total	Zn	0
			1	1	
37	g	1	Total	Zn	0
			1	1	

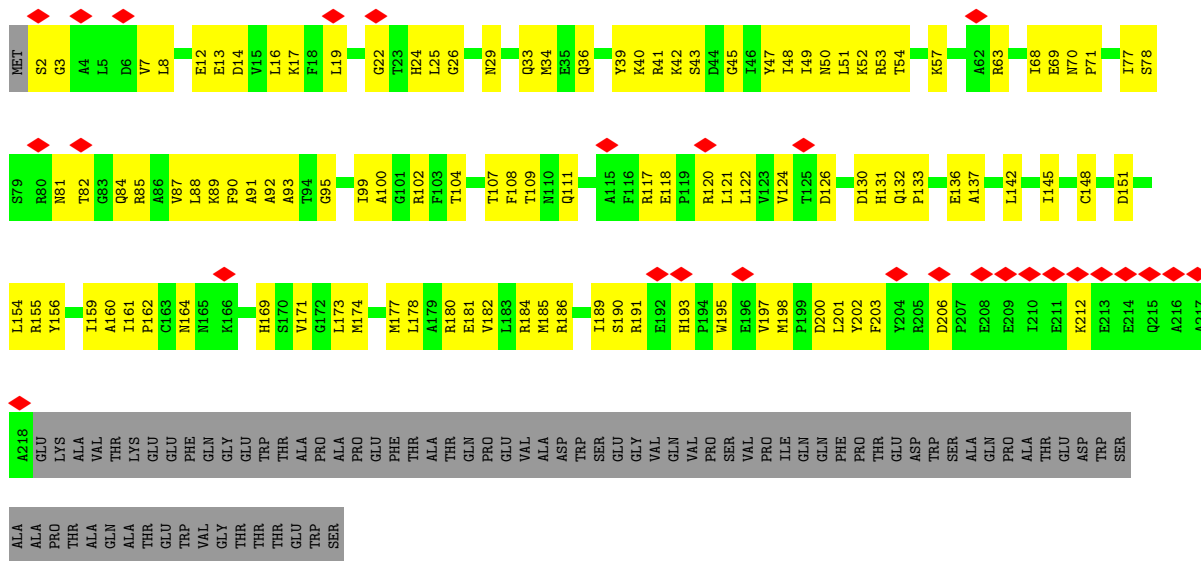
3 Residue-property plots

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

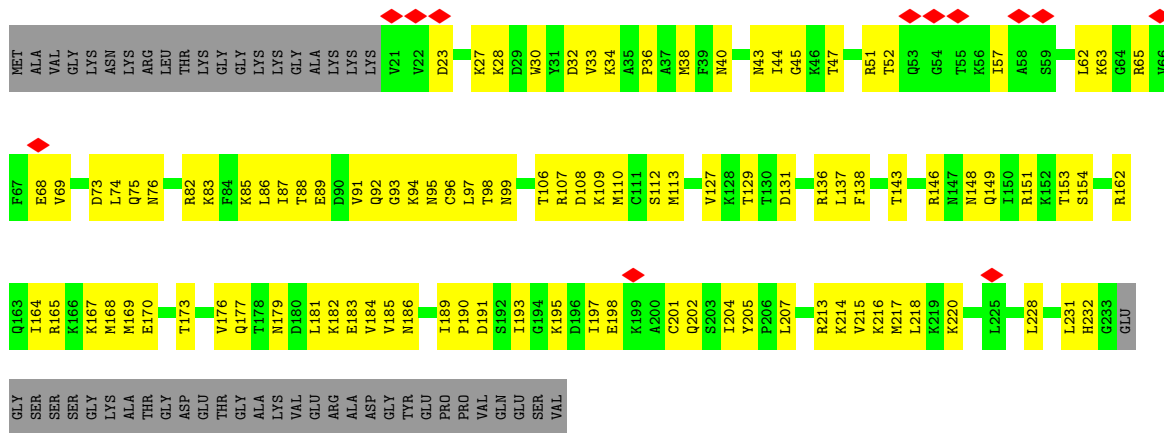
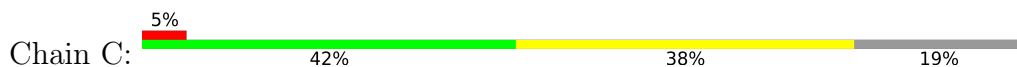
• Molecule 1: 18S ribosomal RNA



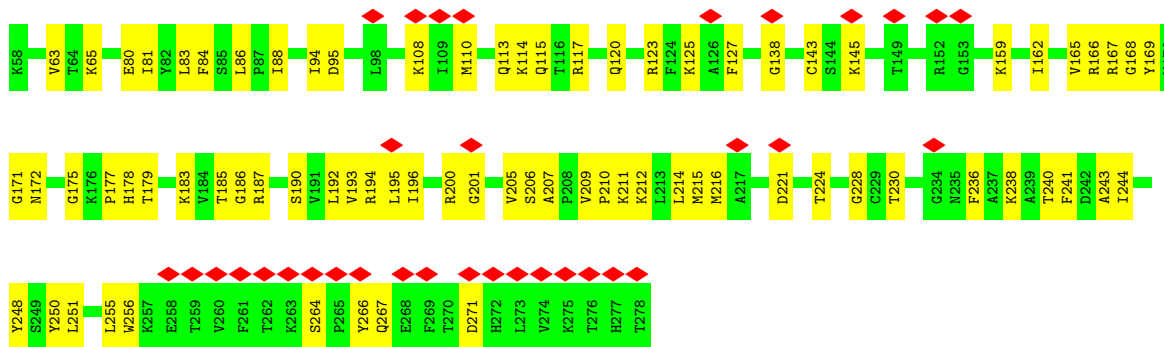




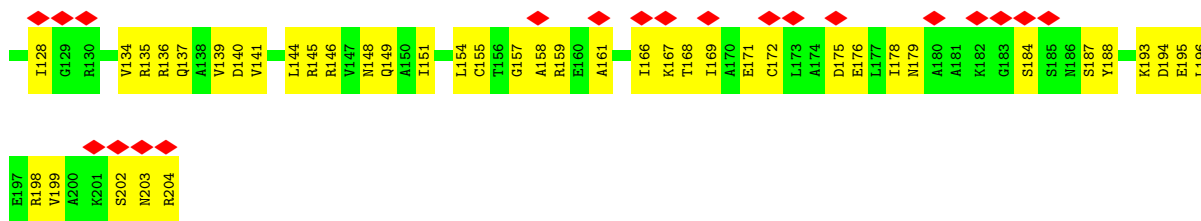
• Molecule 4: 40S ribosomal protein S3a



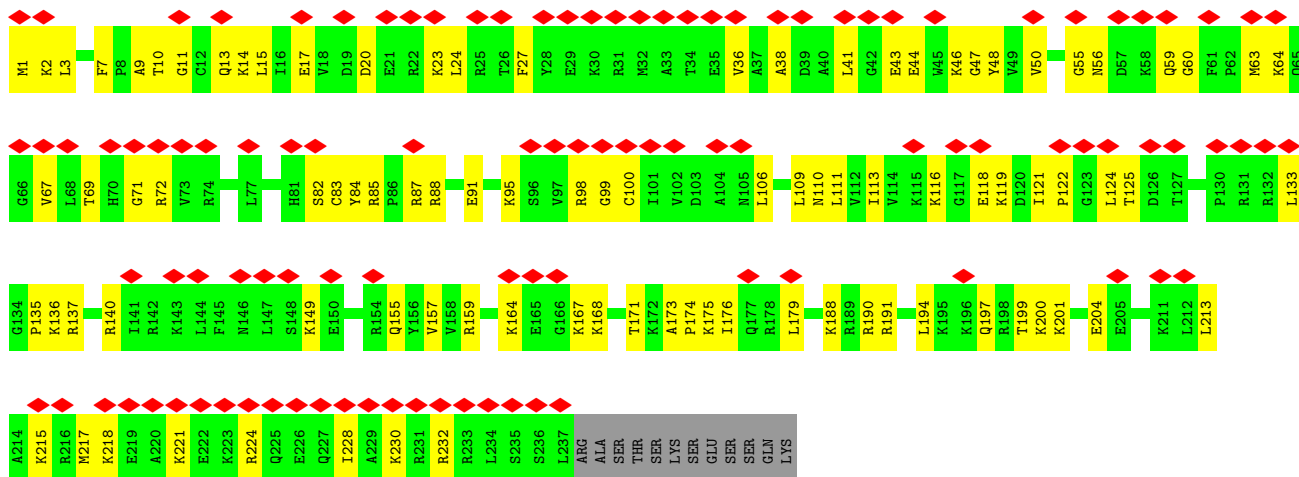
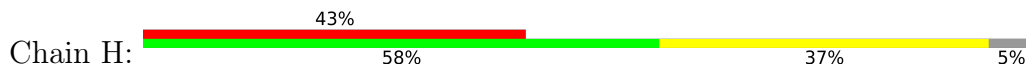
• Molecule 5: 40S ribosomal protein S2

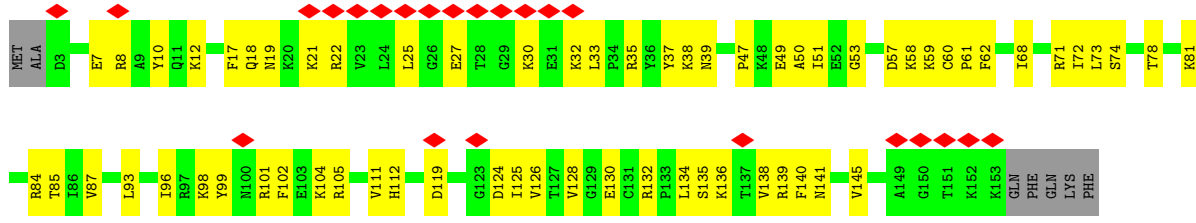


• Molecule 6: Ribosomal protein S3

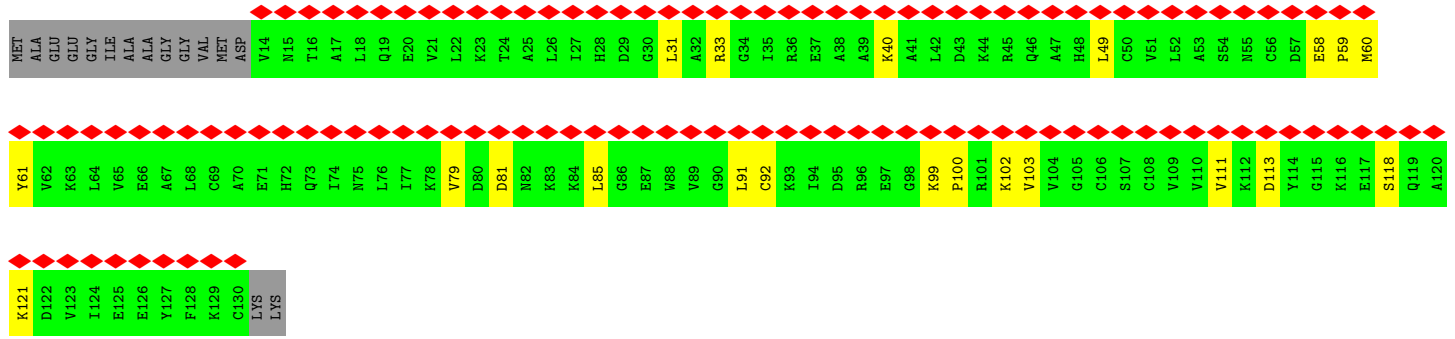
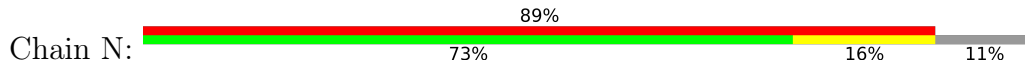


• Molecule 9: 40S ribosomal protein S6

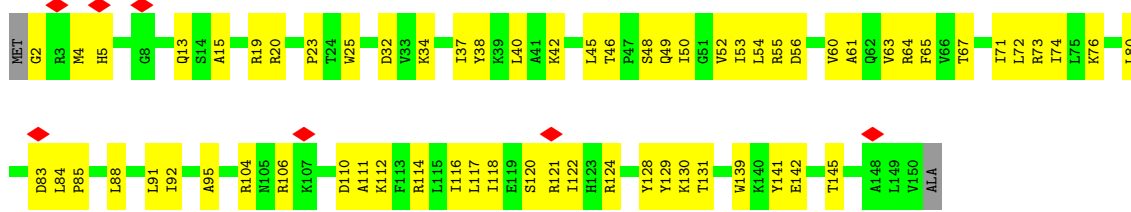




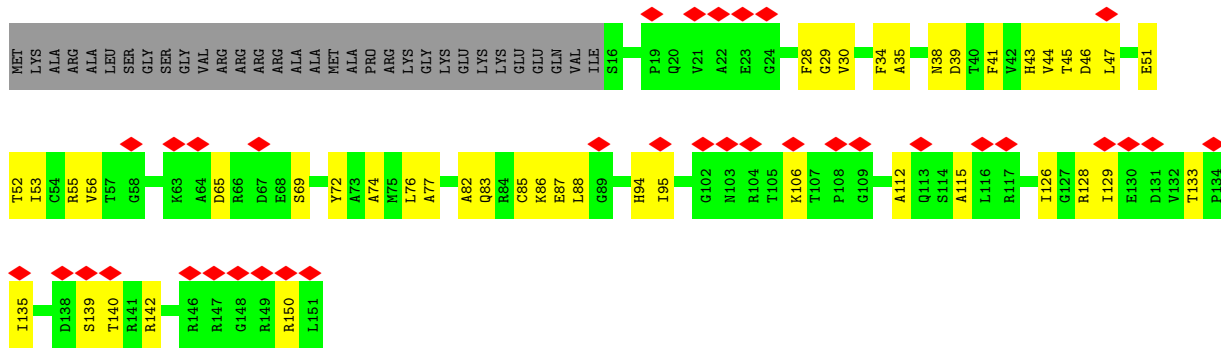
• Molecule 15: 40S ribosomal protein S12



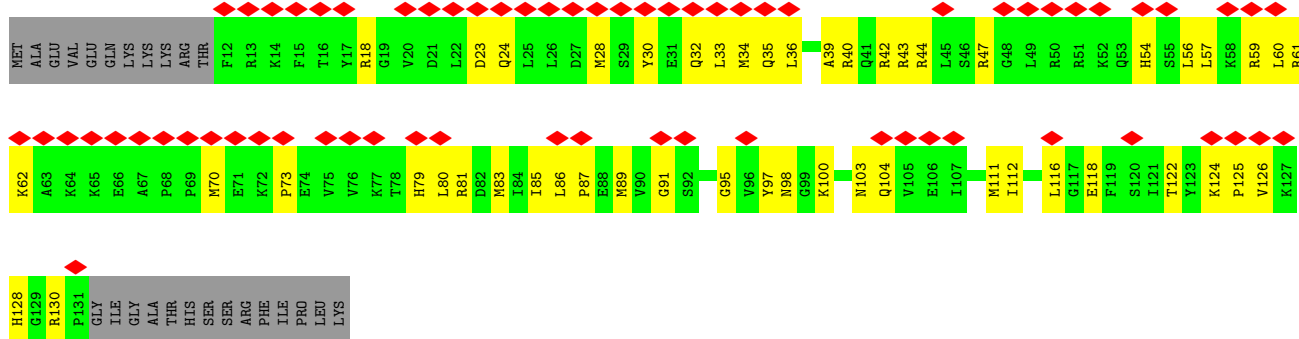
• Molecule 16: Ribosomal protein S13



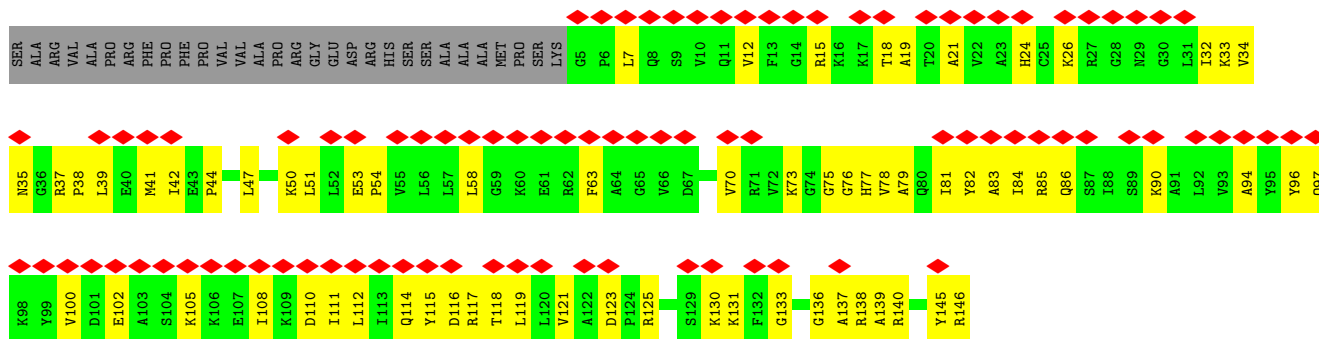
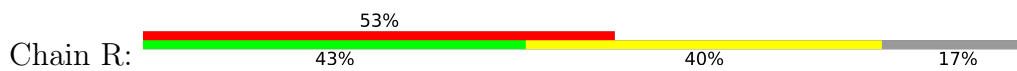
• Molecule 17: Ribosomal protein S14



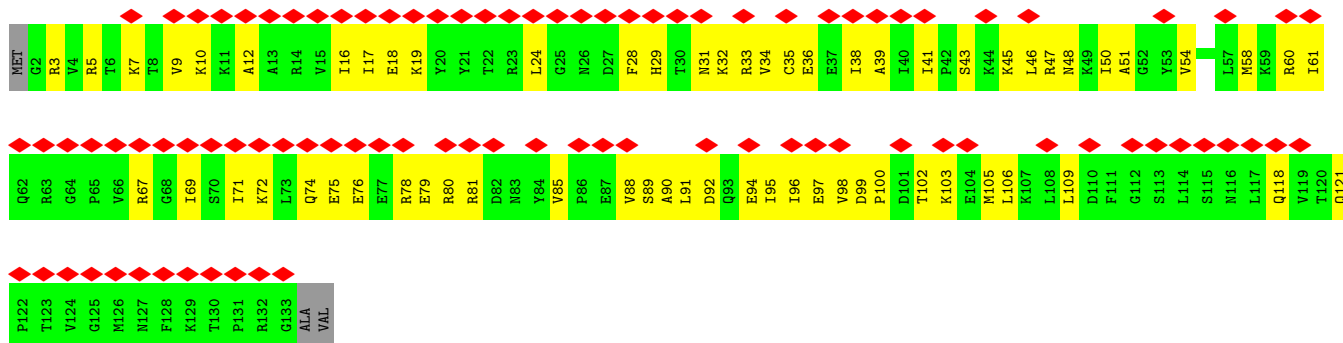
• Molecule 18: uS19



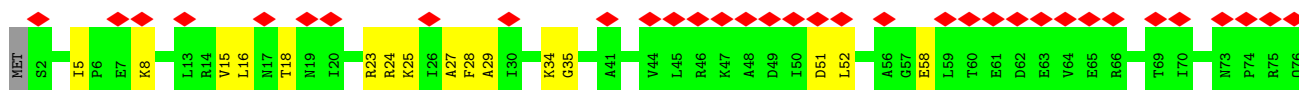
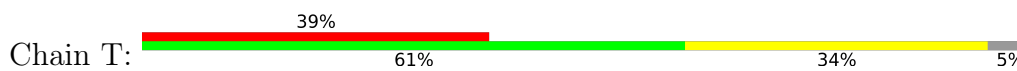
• Molecule 19: Ribosomal protein S16

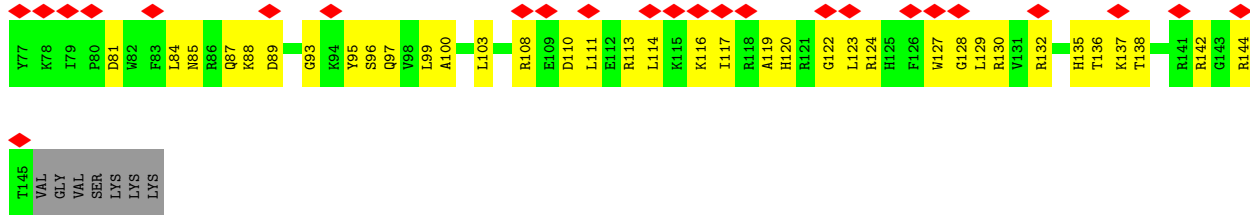


• Molecule 20: eS17

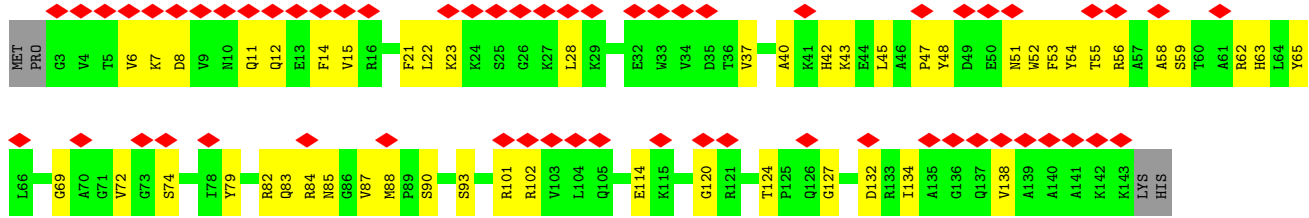


• Molecule 21: uS13

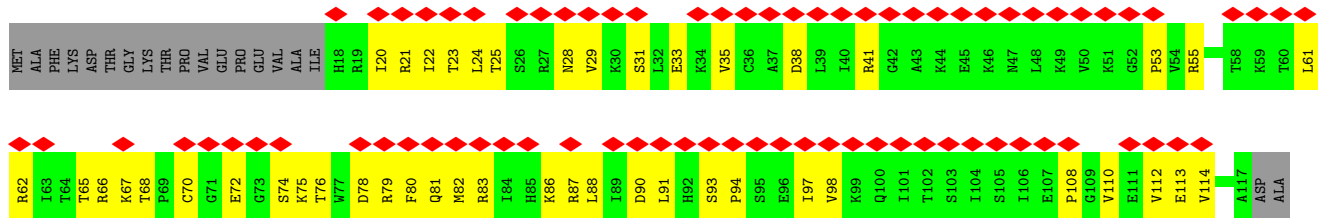
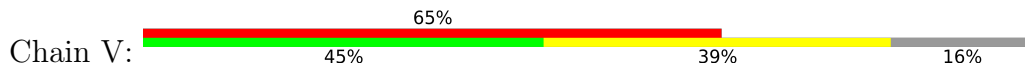




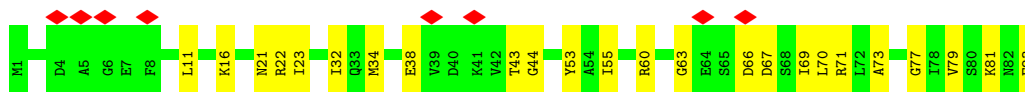
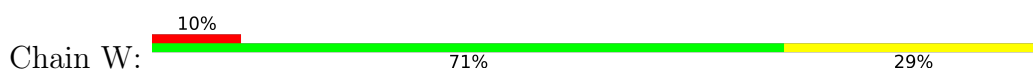
• Molecule 22: eS19



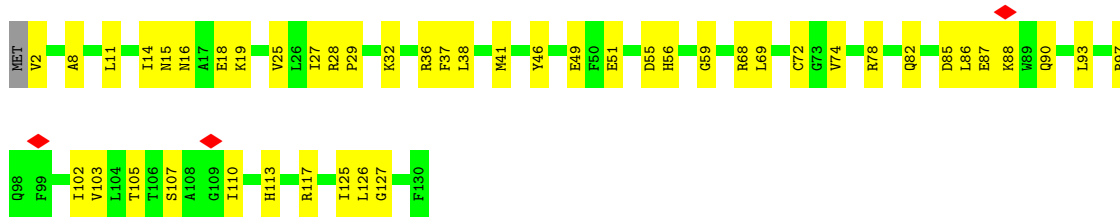
• Molecule 23: uS10



• Molecule 24: 40S ribosomal protein S21

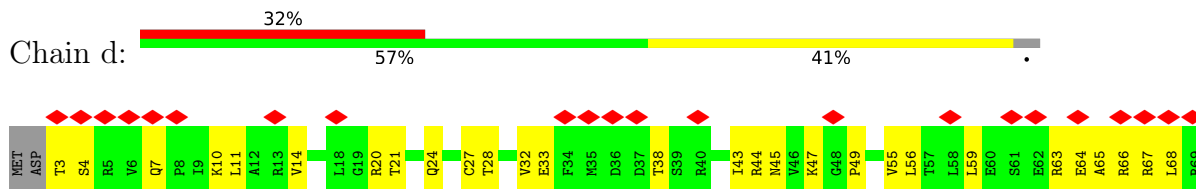


• Molecule 25: Ribosomal protein S15a

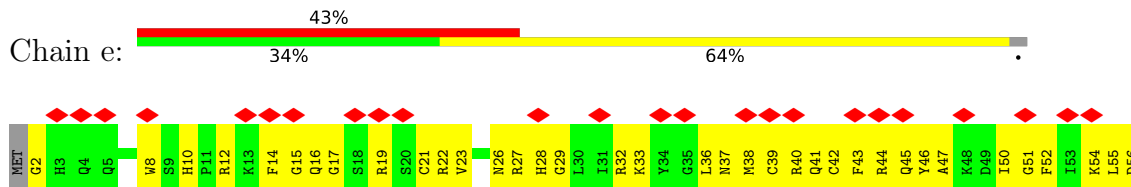


• Molecule 26: uS12

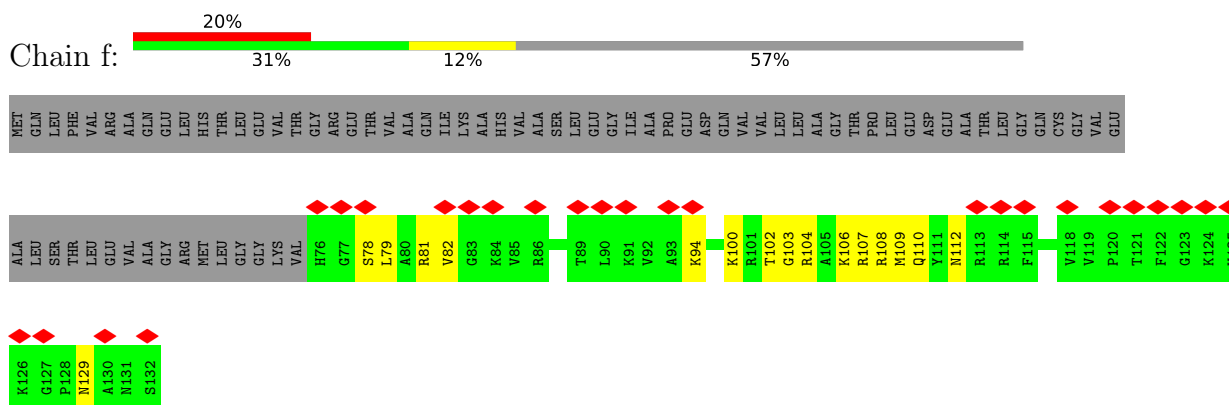
• Molecule 31: Ribosomal protein S28



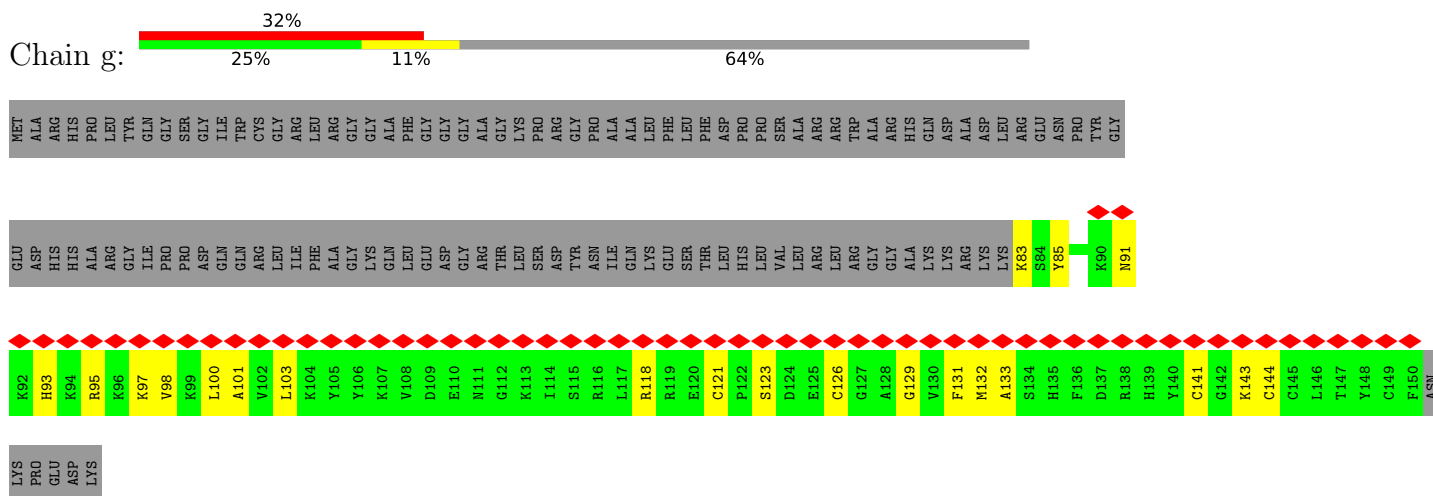
• Molecule 32: eS29



• Molecule 33: 40S ribosomal protein S30



• Molecule 34: eS31

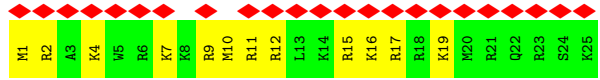
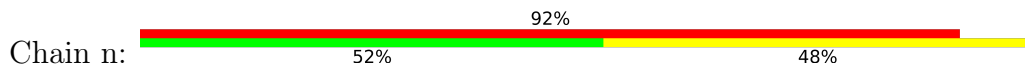


• Molecule 35: RACK1





• Molecule 36: eL41



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64736	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.249	Depositor
Minimum map value	-1.355	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	422.656, 422.656, 422.656	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8255, 0.8255, 0.8255	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
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	0.18	0/40102	0.30	0/62495
2	A	0.13	0/2547	0.31	0/3967
3	B	0.20	0/1747	0.39	0/2374
4	C	0.29	0/1756	0.40	0/2350
5	D	0.23	0/1753	0.44	0/2369
6	E	0.13	0/1796	0.36	0/2417
7	F	0.14	0/2118	0.36	0/2849
8	G	0.16	0/1531	0.44	0/2059
9	H	0.11	0/1946	0.30	0/2590
10	I	0.26	0/1510	0.58	4/2022 (0.2%)
11	J	0.12	0/1715	0.34	0/2287
12	K	0.14	0/1550	0.35	0/2069
13	L	0.11	0/834	0.31	0/1125
14	M	0.16	0/1254	0.37	0/1677
15	N	0.09	0/918	0.25	0/1233
16	O	0.27	0/1226	0.44	0/1649
17	P	0.23	0/1029	0.42	0/1380
18	Q	0.13	0/1017	0.35	0/1358
19	R	0.18	0/1146	0.41	0/1534
20	S	0.14	0/1082	0.36	0/1452
21	T	0.16	0/1208	0.40	0/1618
22	U	0.17	0/1115	0.39	0/1493
23	V	0.13	0/805	0.35	0/1081
24	W	0.21	0/643	0.48	0/860
25	X	0.31	0/1051	0.46	0/1406
26	Y	0.17	0/1116	0.41	0/1490
27	Z	0.13	0/1028	0.36	0/1366
28	a	0.13	0/620	0.38	0/831
29	b	0.23	0/828	0.42	0/1109
30	c	0.27	0/665	0.44	0/891
31	d	0.17	0/532	0.42	0/712
32	e	0.15	0/470	0.38	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.10	0/462	0.28	0/607
34	g	0.08	0/567	0.26	0/753
35	h	0.10	0/2493	0.32	0/3394
36	n	0.16	0/240	0.47	0/305
All	All	0.18	0/82420	0.34	4/119795 (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
26	Y	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	190	PRO	CA-N-CD	-9.71	98.40	112.00
10	I	190	PRO	N-CD-CG	-5.90	94.34	103.20
10	I	65	PRO	CA-C-N	5.42	124.67	120.33
10	I	65	PRO	C-N-CA	5.42	124.67	120.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	Y	61	GLN	Peptide

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	2	35864	0	18113	1053	0
2	A	2280	0	1153	64	0
3	B	1710	0	1708	103	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	1729	0	1803	73	0
5	D	1716	0	1806	71	0
6	E	1768	0	1866	76	0
7	F	2076	0	2177	99	0
8	G	1509	0	1563	84	0
9	H	1923	0	2089	81	0
10	I	1488	0	1582	63	0
11	J	1686	0	1772	72	0
12	K	1525	0	1640	64	0
13	L	810	0	836	30	0
14	M	1233	0	1310	64	0
15	N	908	0	939	14	0
16	O	1202	0	1289	60	0
17	P	1016	0	1039	36	0
18	Q	997	0	1045	50	0
19	R	1128	0	1195	58	0
20	S	1068	0	1121	60	0
21	T	1190	0	1249	55	0
22	U	1097	0	1130	50	0
23	V	795	0	862	40	0
24	W	636	0	637	25	0
25	X	1034	0	1080	43	0
26	Y	1098	0	1167	53	0
27	Z	1011	0	1083	39	0
28	a	614	0	678	23	0
29	b	814	0	863	32	0
30	c	651	0	672	14	0
31	d	530	0	561	30	0
32	e	459	0	452	38	0
33	f	457	0	502	23	0
34	g	555	0	563	16	0
35	h	2436	0	2393	97	0
36	n	239	0	289	13	0
37	b	1	0	0	0	0
37	g	1	0	0	0	0
All	All	77254	0	60227	2459	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 18.

The worst 5 of 2459 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:N4	1:2:1476:A:H62	1.37	1.20
1:2:1472:C:H42	1:2:1476:A:N6	1.41	1.18
1:2:1276:A:H62	1:2:1321:G:H21	1.05	0.98
22:U:85:ASN:HB3	22:U:88:MET:HB2	1.46	0.98
1:2:1452:A:H61	1:2:1473:G:H21	1.10	0.97

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	
3	B	215/295 (73%)	191 (89%)	24 (11%)	0	100	100
4	C	211/264 (80%)	191 (90%)	20 (10%)	0	100	100
5	D	219/221 (99%)	203 (93%)	16 (7%)	0	100	100
6	E	226/281 (80%)	212 (94%)	14 (6%)	0	100	100
7	F	260/263 (99%)	244 (94%)	16 (6%)	0	100	100
8	G	189/204 (93%)	176 (93%)	13 (7%)	0	100	100
9	H	235/249 (94%)	227 (97%)	8 (3%)	0	100	100
10	I	181/432 (42%)	172 (95%)	9 (5%)	0	100	100
11	J	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
12	K	183/194 (94%)	178 (97%)	5 (3%)	0	100	100
13	L	94/149 (63%)	89 (95%)	5 (5%)	0	100	100
14	M	149/158 (94%)	138 (93%)	11 (7%)	0	100	100
15	N	115/132 (87%)	105 (91%)	10 (9%)	0	100	100
16	O	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
17	P	134/168 (80%)	124 (92%)	10 (8%)	0	100	100
18	Q	118/145 (81%)	109 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	R	140/172 (81%)	130 (93%)	10 (7%)	0	100	100
20	S	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
21	T	142/152 (93%)	125 (88%)	17 (12%)	0	100	100
22	U	139/145 (96%)	128 (92%)	11 (8%)	0	100	100
23	V	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
24	W	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
25	X	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
26	Y	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	18	48
27	Z	122/131 (93%)	116 (95%)	6 (5%)	0	100	100
28	a	75/124 (60%)	72 (96%)	3 (4%)	0	100	100
29	b	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
30	c	81/84 (96%)	76 (94%)	5 (6%)	0	100	100
31	d	65/69 (94%)	59 (91%)	6 (9%)	0	100	100
32	e	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
33	f	55/133 (41%)	52 (94%)	3 (6%)	0	100	100
34	g	66/188 (35%)	63 (96%)	3 (4%)	0	100	100
35	h	311/317 (98%)	289 (93%)	22 (7%)	0	100	100
36	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4826/5821 (83%)	4492 (93%)	333 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	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	
3	B	180/245 (74%)	180 (100%)	0	100	100
4	C	194/231 (84%)	194 (100%)	0	100	100
5	D	187/187 (100%)	187 (100%)	0	100	100
6	E	190/232 (82%)	190 (100%)	0	100	100
7	F	224/225 (100%)	224 (100%)	0	100	100
8	G	161/170 (95%)	161 (100%)	0	100	100
9	H	207/218 (95%)	207 (100%)	0	100	100
10	I	165/360 (46%)	165 (100%)	0	100	100
11	J	178/180 (99%)	178 (100%)	0	100	100
12	K	161/168 (96%)	161 (100%)	0	100	100
13	L	87/125 (70%)	87 (100%)	0	100	100
14	M	136/142 (96%)	136 (100%)	0	100	100
15	N	99/108 (92%)	99 (100%)	0	100	100
16	O	130/131 (99%)	130 (100%)	0	100	100
17	P	106/130 (82%)	106 (100%)	0	100	100
18	Q	109/130 (84%)	109 (100%)	0	100	100
19	R	117/140 (84%)	117 (100%)	0	100	100
20	S	119/121 (98%)	119 (100%)	0	100	100
21	T	125/132 (95%)	125 (100%)	0	100	100
22	U	111/116 (96%)	111 (100%)	0	100	100
23	V	92/107 (86%)	92 (100%)	0	100	100
24	W	67/67 (100%)	67 (100%)	0	100	100
25	X	112/113 (99%)	112 (100%)	0	100	100
26	Y	113/115 (98%)	113 (100%)	0	100	100
27	Z	107/113 (95%)	107 (100%)	0	100	100
28	a	68/102 (67%)	68 (100%)	0	100	100
29	b	88/88 (100%)	88 (100%)	0	100	100
30	c	75/76 (99%)	75 (100%)	0	100	100
31	d	60/62 (97%)	60 (100%)	0	100	100
32	e	48/49 (98%)	48 (100%)	0	100	100
33	f	47/106 (44%)	47 (100%)	0	100	100
34	g	61/154 (40%)	61 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	h	272/275 (99%)	272 (100%)	0	100	100
36	n	24/24 (100%)	24 (100%)	0	100	100
All	All	4220/4942 (85%)	4220 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
20	S	83	ASN
29	b	25	ASN
21	T	10	GLN
25	X	120	HIS
30	c	9	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1669/1870 (89%)	414 (24%)	13 (0%)
2	A	105/270 (38%)	38 (36%)	7 (6%)
All	All	1774/2140 (82%)	452 (25%)	20 (1%)

5 of 452 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	13	C
1	2	14	C
1	2	26	U

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	9282	C
2	A	9298	C
2	A	9304	G
2	A	9303	C
1	2	860	G

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.

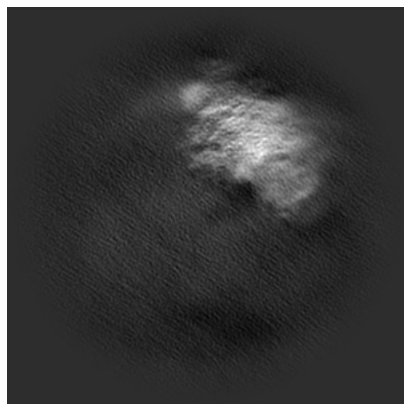
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70479. These allow visual inspection of the internal detail of the map and identification of artifacts.

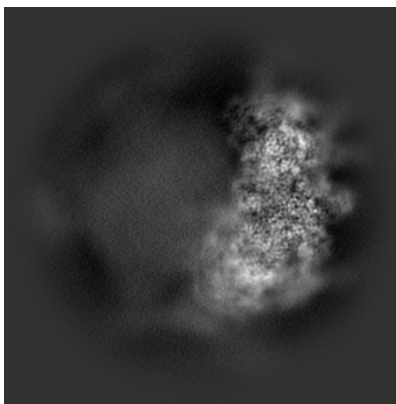
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

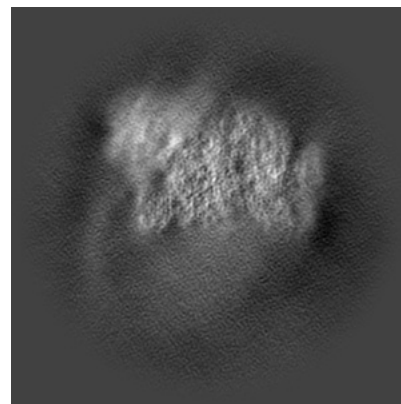
6.1.1 Primary map



X

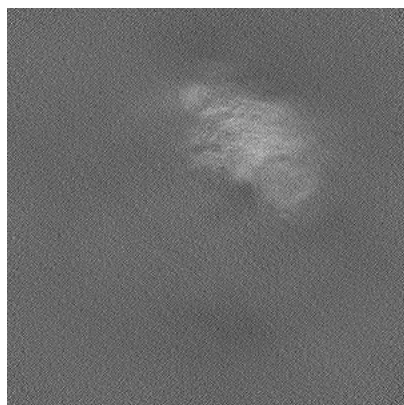


Y

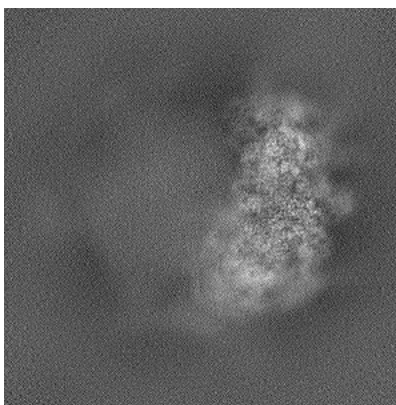


Z

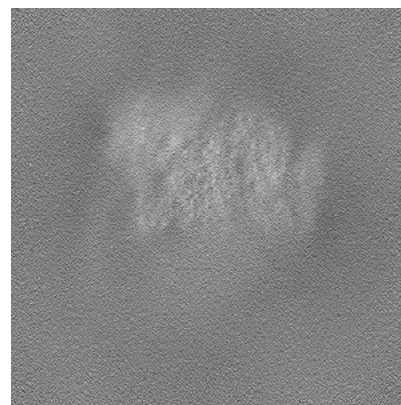
6.1.2 Raw map



X



Y

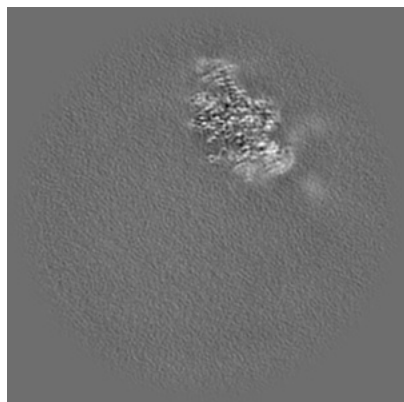


Z

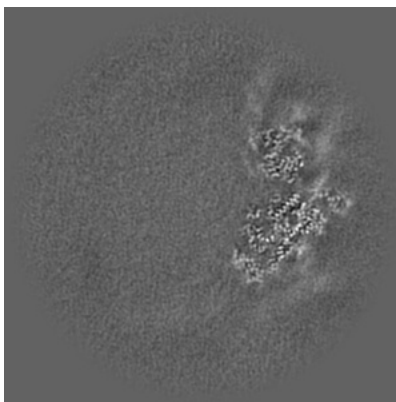
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

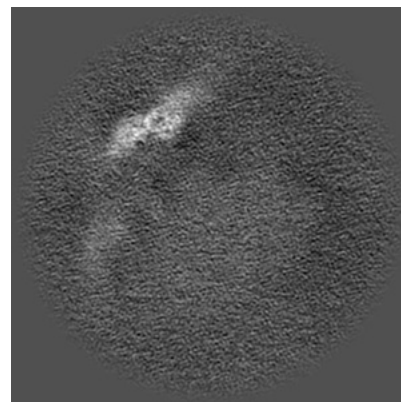
6.2.1 Primary map



X Index: 256

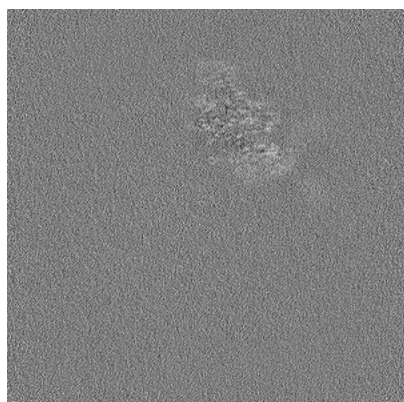


Y Index: 256

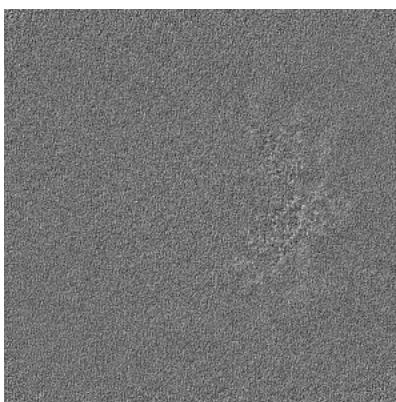


Z Index: 256

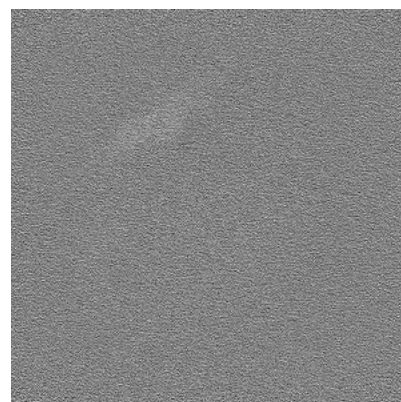
6.2.2 Raw map



X Index: 256



Y Index: 256

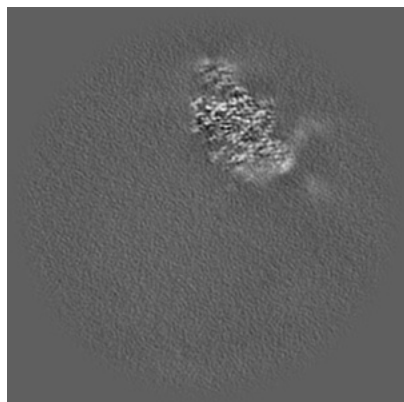


Z Index: 256

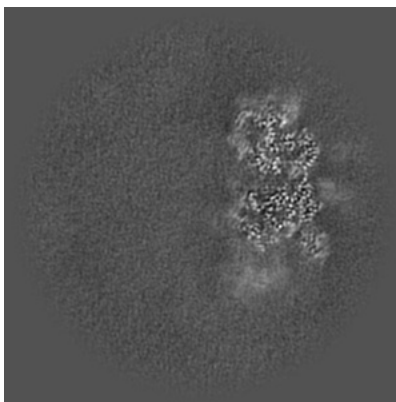
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

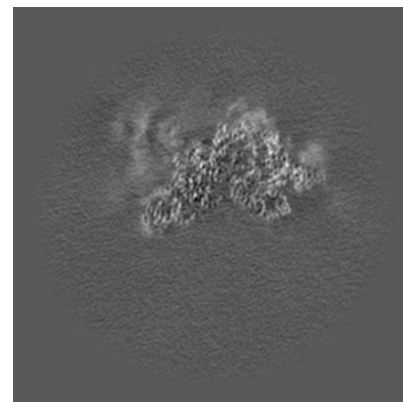
6.3.1 Primary map



X Index: 259

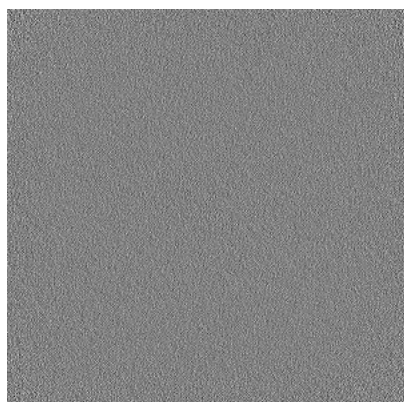


Y Index: 302

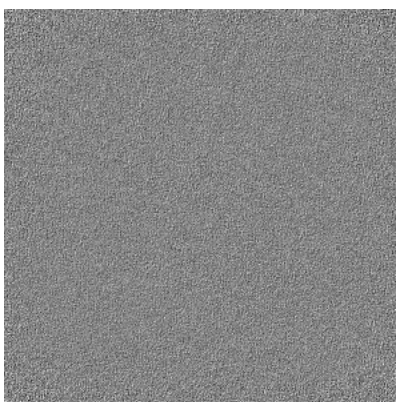


Z Index: 338

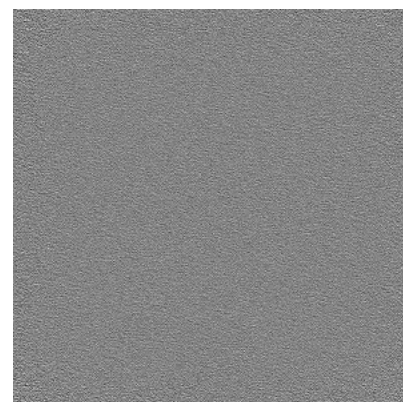
6.3.2 Raw map



X Index: 0



Y Index: 0

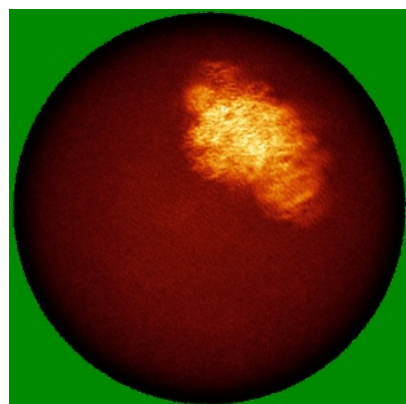


Z Index: 0

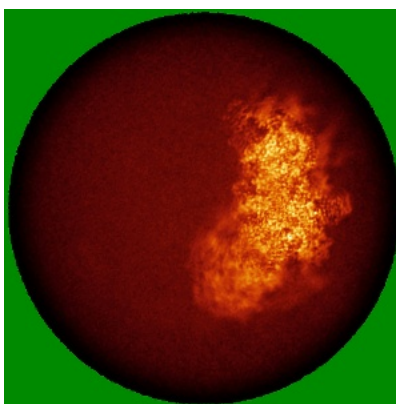
The images above show the largest variance slices of the map in three orthogonal directions.

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

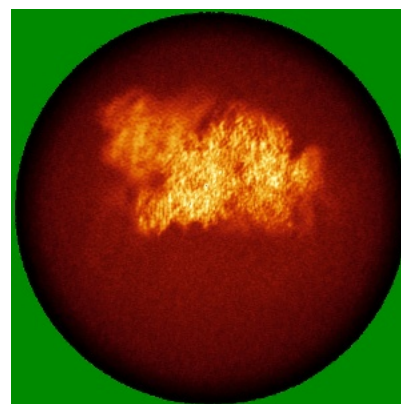
6.4.1 Primary map



X

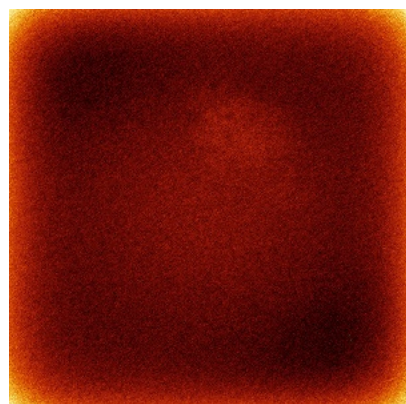


Y

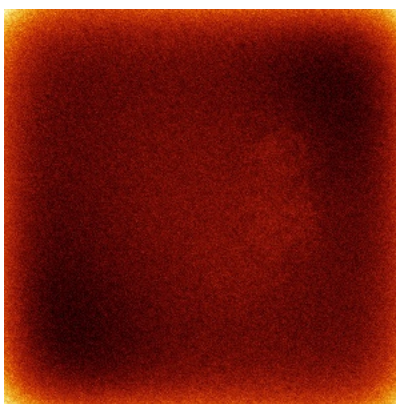


Z

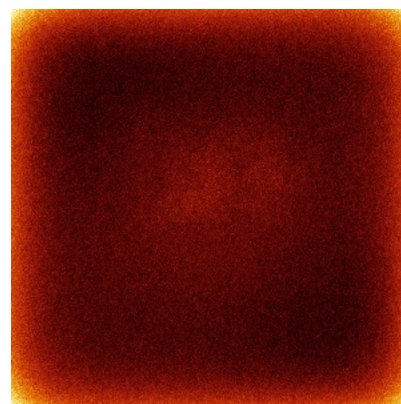
6.4.2 Raw map



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 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

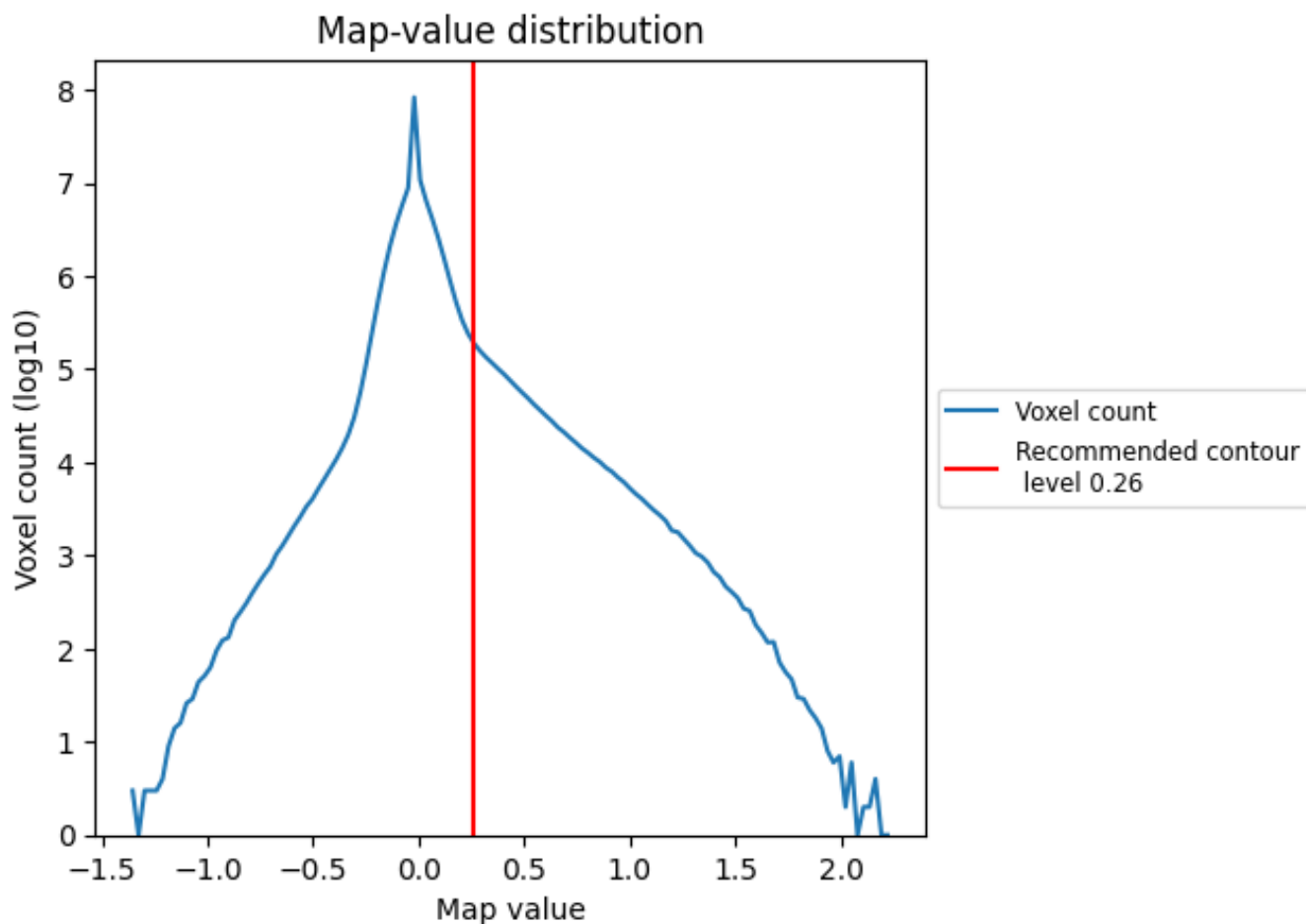
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

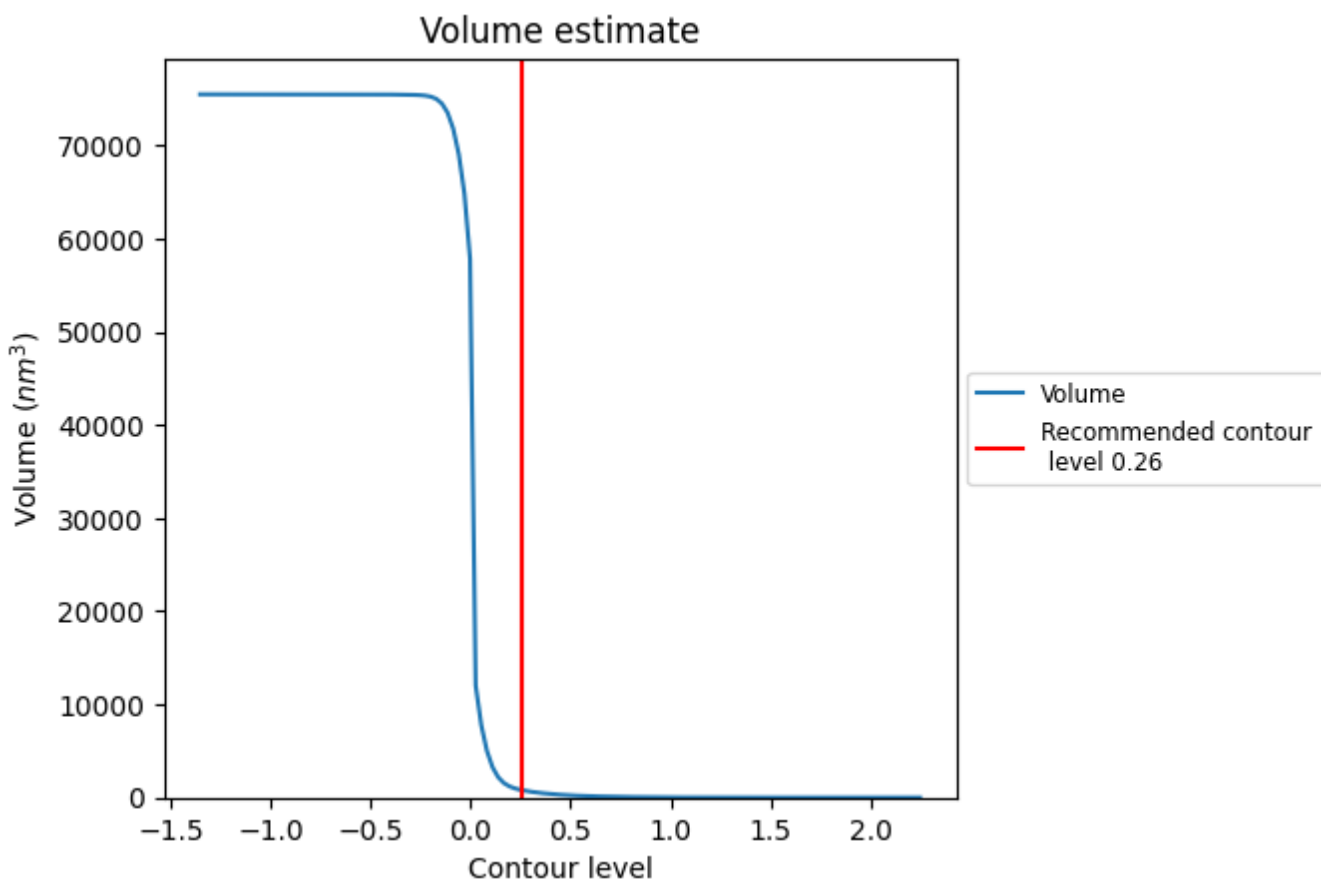
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

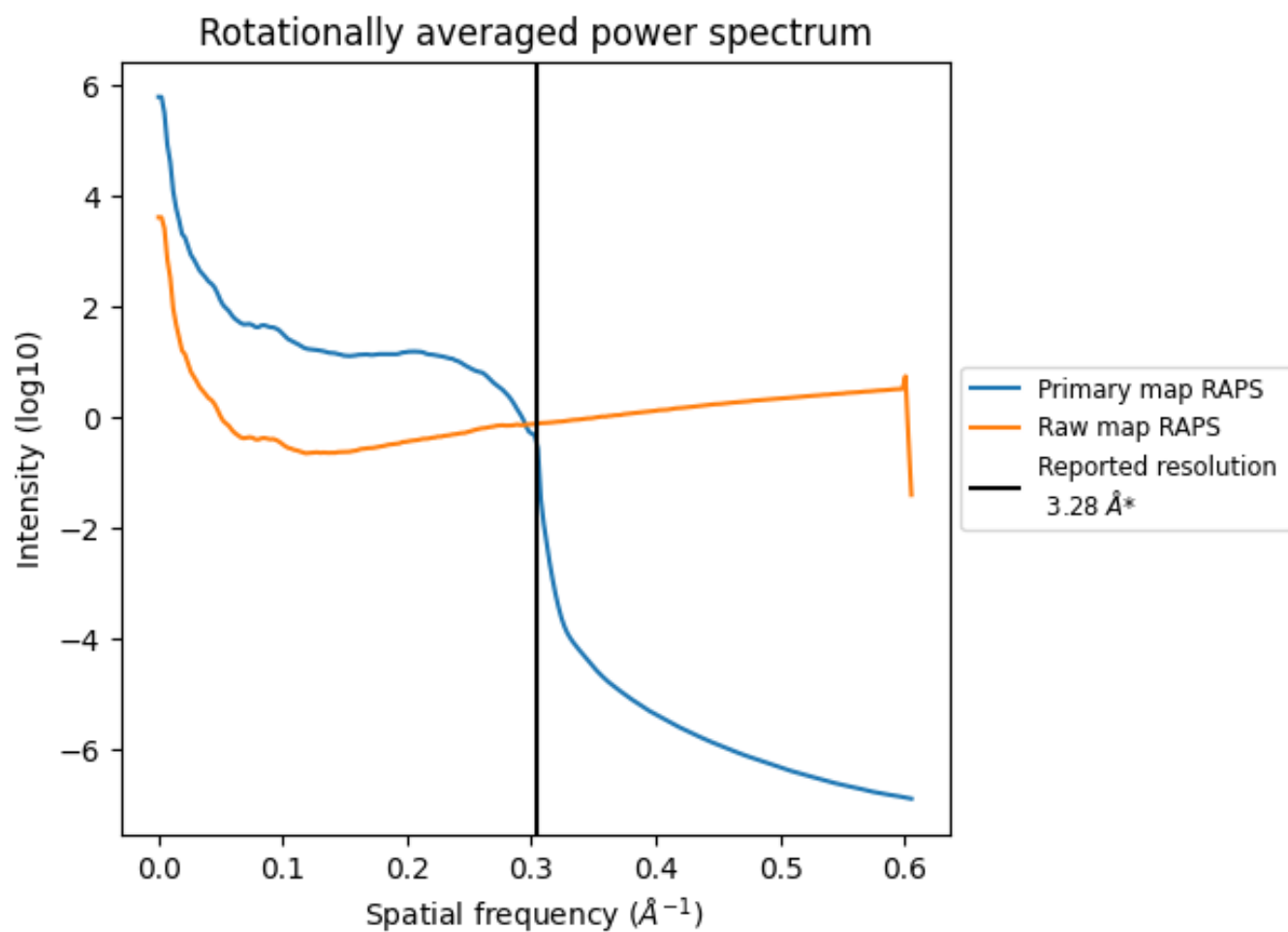
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 782 nm³; this corresponds to an approximate mass of 706 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

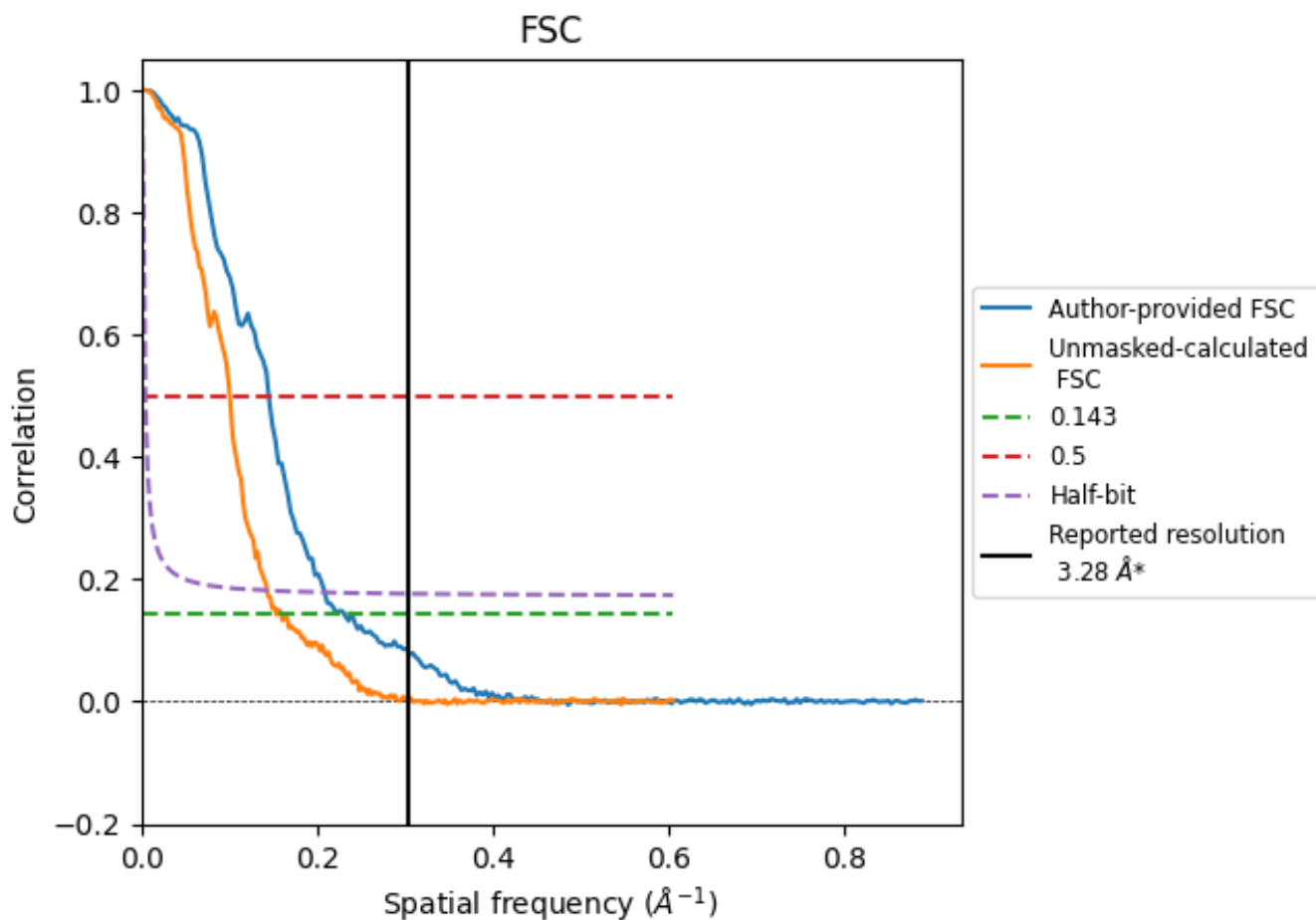


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

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 0.305 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	4.33	6.89	4.80
Unmasked-calculated*	6.51	9.94	6.98

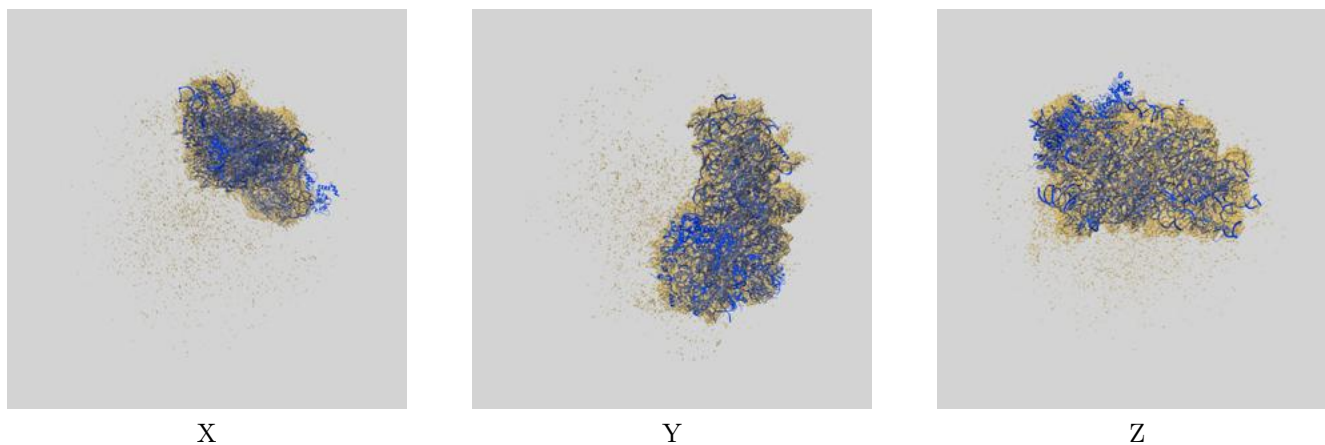
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.33 differs from the reported value 3.28 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.51 differs from the reported value 3.28 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70479 and PDB model 9OGY. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



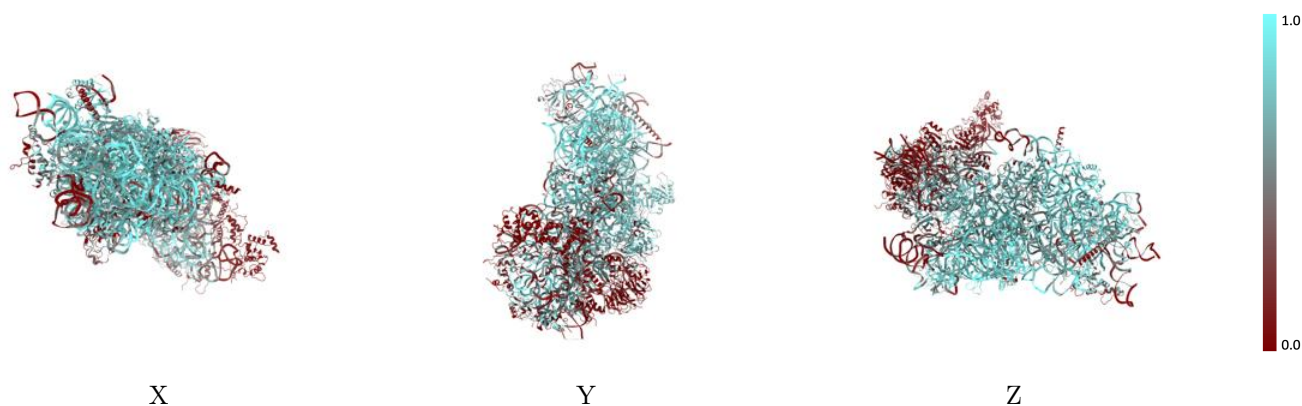
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



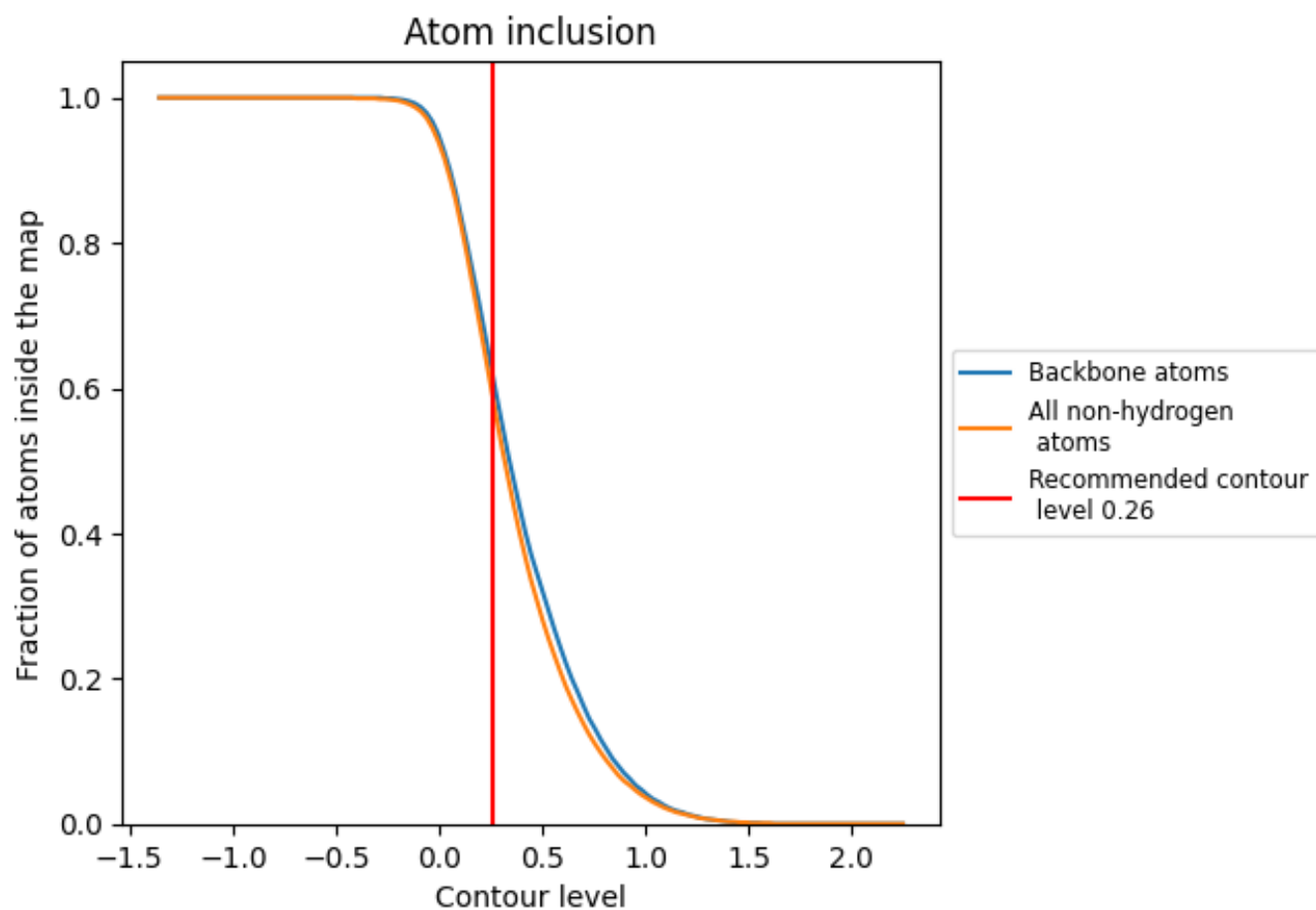
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.26).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 59% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5880	 0.1720
2	 0.6910	 0.1890
A	 0.2820	 0.0350
B	 0.6930	 0.2280
C	 0.8050	 0.3600
D	 0.6640	 0.2150
E	 0.1930	 0.0330
F	 0.7640	 0.3090
G	 0.5050	 -0.0120
H	 0.4510	 0.1990
I	 0.7410	 0.3000
J	 0.5210	 0.2680
K	 0.6650	 0.1950
L	 0.0630	 0.0050
M	 0.6570	 0.3280
N	 0.0020	 -0.0210
O	 0.7880	 0.4040
P	 0.6270	 0.2160
Q	 0.3910	 0.0350
R	 0.2960	 0.0030
S	 0.2810	 0.0790
T	 0.4880	 -0.0160
U	 0.5150	 0.0410
V	 0.1960	 0.0180
W	 0.7300	 0.2940
X	 0.8190	 0.3750
Y	 0.5450	 0.1980
Z	 0.7260	 0.2220
a	 0.3520	 0.0270
b	 0.6870	 0.2620
c	 0.8560	 0.3850
d	 0.5510	 0.0080
e	 0.4080	 0.0230
f	 0.4410	 0.0810
g	 0.1180	 0.0050



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Chain	Atom inclusion	Q-score
h	 0.0540	 -0.0070
n	 0.0870	 0.1400