



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 09:26 AM UTC

PDB ID : 6G5I / pdb_00006g5i
EMDB ID : EMD-4353
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State R
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-29
Resolution : 3.50 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

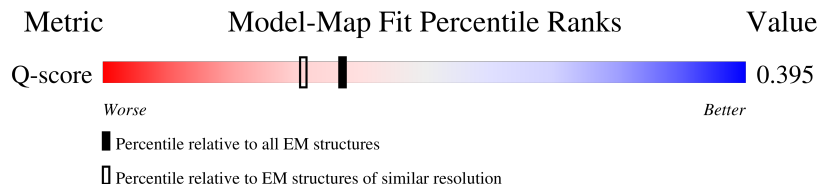
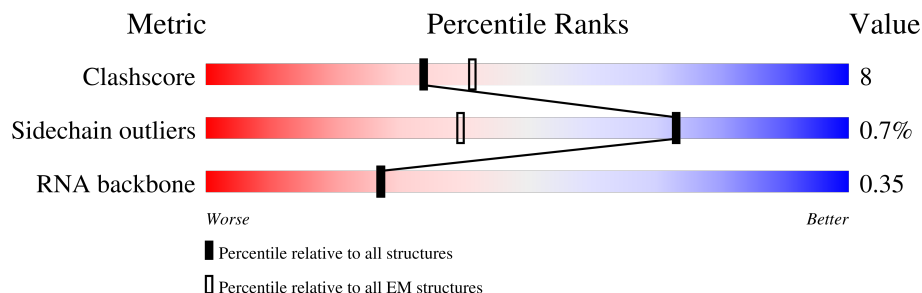
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	1882	
2	A	295	
3	B	264	
4	C	293	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	133	
27	Z	125	
28	b	84	
29	c	69	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	d	56	
31	e	59	
32	f	156	
33	g	317	
34	x	252	
35	y	412	
36	z	568	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 77185 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
1	2	1657	Total	C	N	O	P	0	0
			35380	15792	6352	11579	1657		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	216	Total	C	N	O	S	0	0
			1705	1083	299	315	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

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

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 7 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1009	618	198	187	6		

- Molecule 17 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	122	Total	C	N	O	S	0	0
			990	621	184	182	3		

- Molecule 20 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called 40S ribosomal protein S15a.

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

- Molecule 25 is a protein called 40S ribosomal protein S23.

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

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 29 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 30 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	55	Total	C	N	O	S	0	0
			458	286	94	73	5		

- Molecule 31 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 32 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	63	Total	C	N	O	S	0	0
			510	320	97	86	7		

- Molecule 33 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 34 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	175	Total	C	N	O	S	0	0
			1365	878	249	234	4		

- Molecule 35 is a protein called RNA-binding protein NOB1.

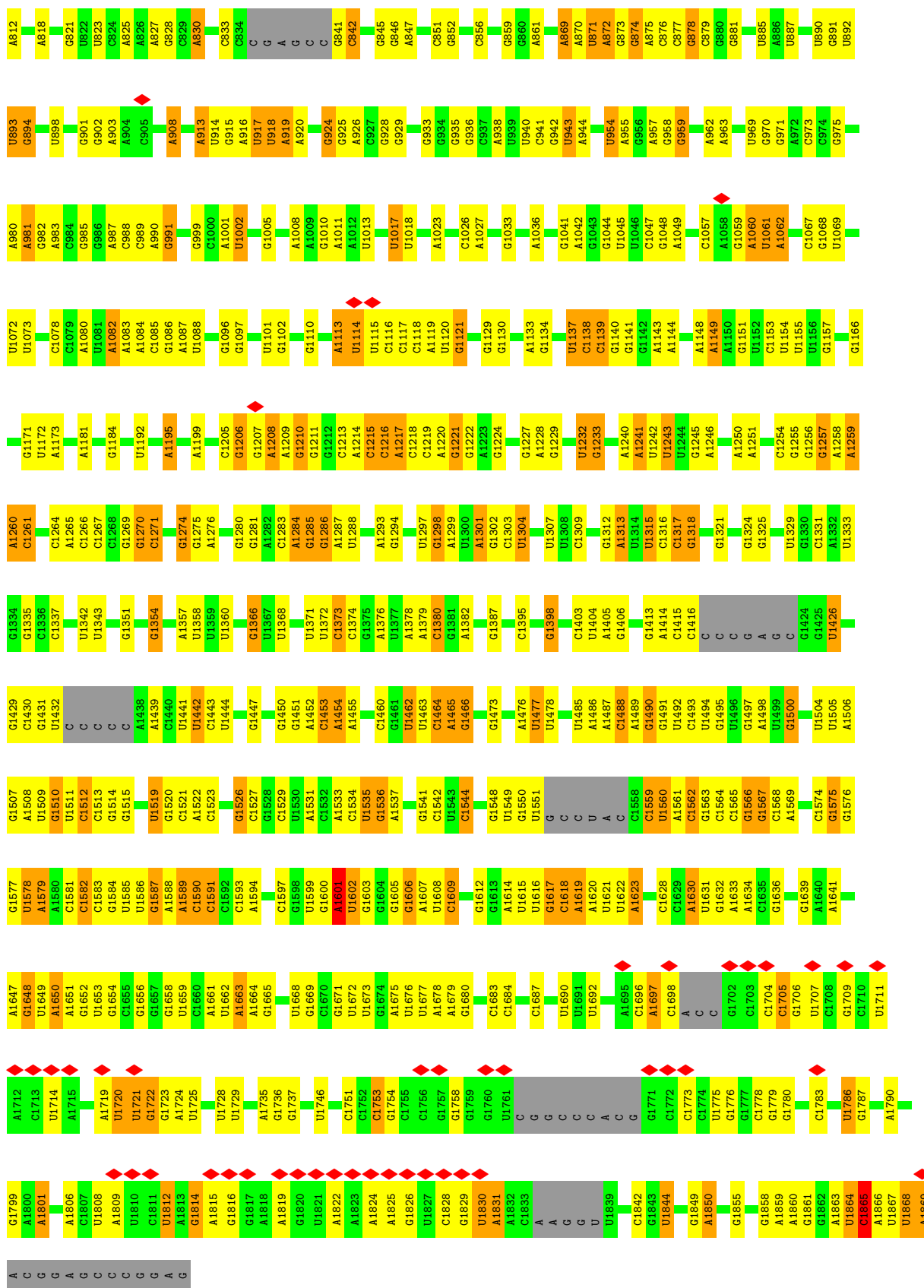
Mol	Chain	Residues	Atoms					AltConf	Trace
35	y	317	Total	C	N	O	S	0	0
			2490	1576	456	448	10		

- Molecule 36 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	z	29	Total	C	N	O	S	0	0
			257	160	57	39	1		

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

Mol	Chain	Residues	Atoms		AltConf
37	d	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	
37	y	1	Total	Zn	0
			1	1	



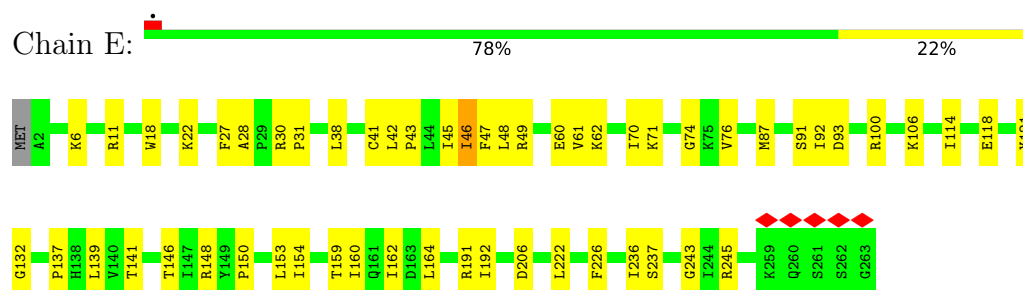
- Molecule 2: 40S ribosomal protein SA

[illegible]

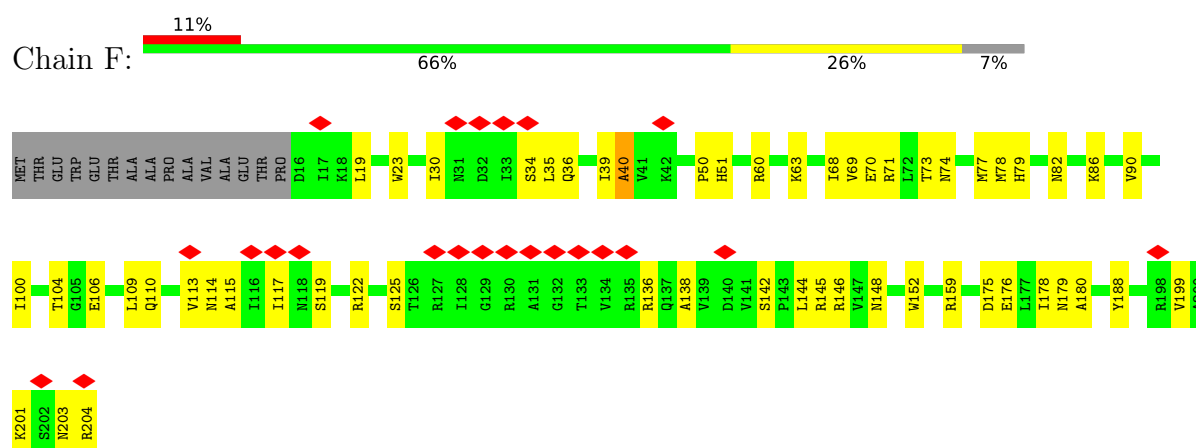
Protein	Residue	Score	Rank	Category
Protein 1	GLU	1.18	118	High
	THR	1.19	119	High
	GLY	1.20	120	High
	ALA	1.36	136	High
	LYS	1.37	137	High
	VAL	1.40	140	High
	GLU	1.46	146	High
	ASP	1.49	149	High
	GLY	1.53	153	High
	TYR	1.57	157	High
Protein 2	GLU	1.61	161	High
	PRO	1.62	162	High
	VAL	1.76	176	High
	GLN	1.80	180	High
	GLU	1.81	181	High
	ASP	1.82	182	High
	GLY	1.84	184	High
	LYS	1.85	185	High
	THR	1.86	186	High
	GLU	1.88	188	High
Protein 3	SER	1.89	189	High
	VAL	1.97	197	High
	GLY	2.10	210	High
	GLU	2.13	213	High
	LYS	2.14	214	High
	THR	2.17	217	High
	GLY	2.19	219	High
	ASP	2.20	220	High
	GLY	2.29	229	High
	GLU	2.33	233	High
Protein 4	GLY	2.33	233	High
	SER	2.33	233	High
	SER	2.33	233	High
	SER	2.33	233	High
	GLY	2.33	233	High
	LYS	2.33	233	High
	ALA	2.33	233	High
	THR	2.33	233	High
	GLY	2.33	233	High
	ASP	2.33	233	High

C182	L66	MET
S190	V70	ALA
V193	L78	ASP
I196	I81	ALA
R200	I93	GLY
P210	I94	ALA
L213	D95	GLY
L214	F96	PRO
M215	F97	GLY
M216	L98	PRO
A217	G99	GLY
G218	L102	PRO
D221	K103	GLY
C222	D104	MET
Y223	E105	GLY
R227	M110	ASN
T240	R117	ARG
I244	A118	GLY
T247	G119	GLY
D254	Q120	GLY
T259	R121	PHE
K275	F127	GLY
T276	V128	SER
HIS	A129	GLY
THR	I130	ILE
THR	G131	ARG
ARG	D132	GLY
VAL	Y133	GLY
SER	M134	ARG
VAL	V137	ARG
VAL	G138	ARG
GLN	L139	GLY
ARG	C140	GLY
THR	V141	GLY
GLN	E146	ARG
ALA	A150	ARG
PRO	R166	ALA
ALA	R167	ARG
VAL	G168	GLY
ALA	Y169	GLY
THR	W170	LYS
THR	G171	ALA
	M172	GLU
	K173	ASP
	I174	LYS
	G175	ASP
	T176	E59

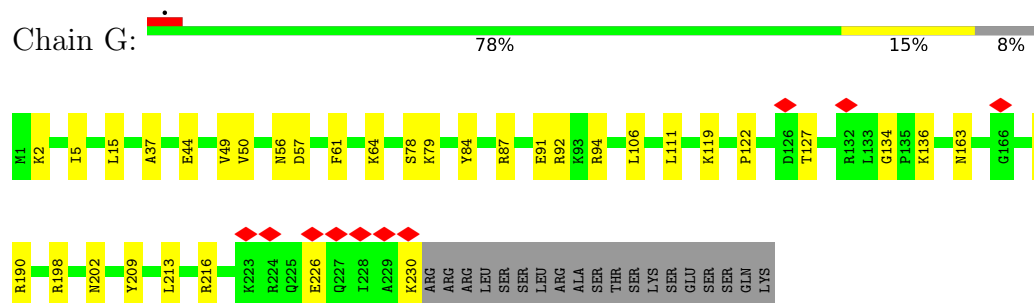
- Molecule 6: 40S ribosomal protein S4, X isoform



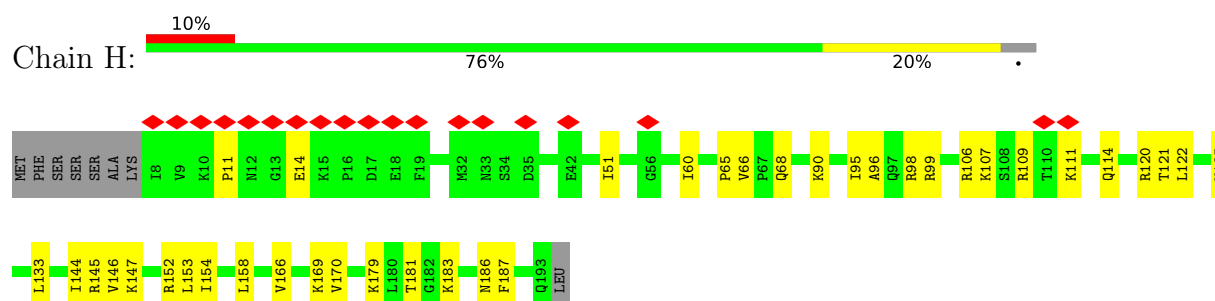
- Molecule 7: 40S ribosomal protein S5



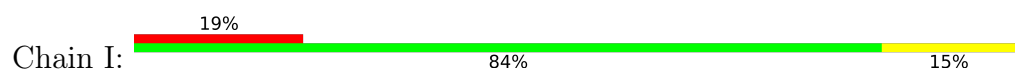
- Molecule 8: 40S ribosomal protein S6

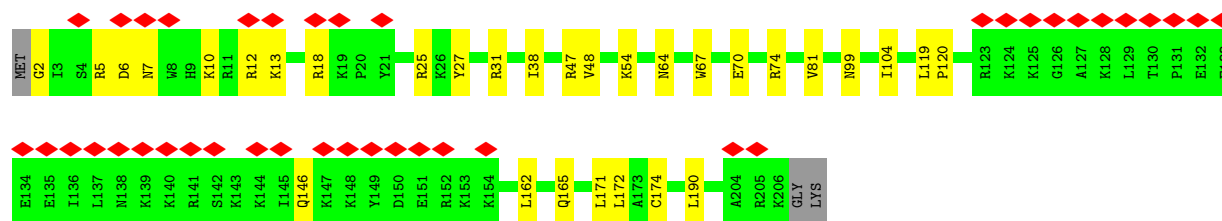


- Molecule 9: 40S ribosomal protein S7



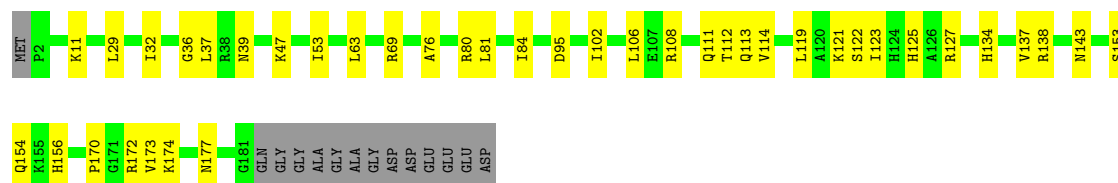
- Molecule 10: 40S ribosomal protein S8





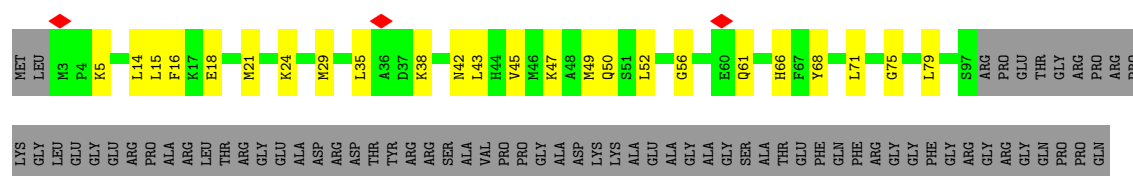
- Molecule 11: 40S ribosomal protein S9

Chain J: 72% 21% 7%



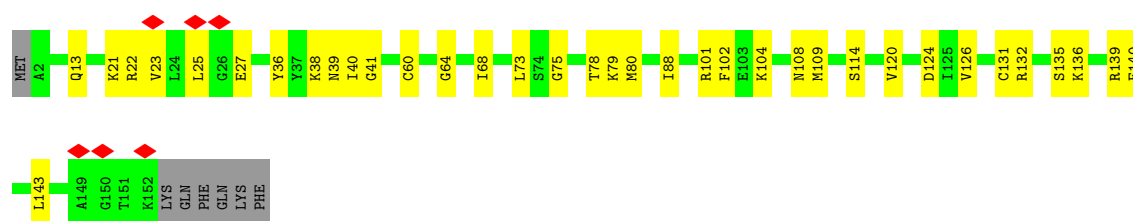
- Molecule 12: 40S ribosomal protein S10

Chain K: 43% 15% 42%



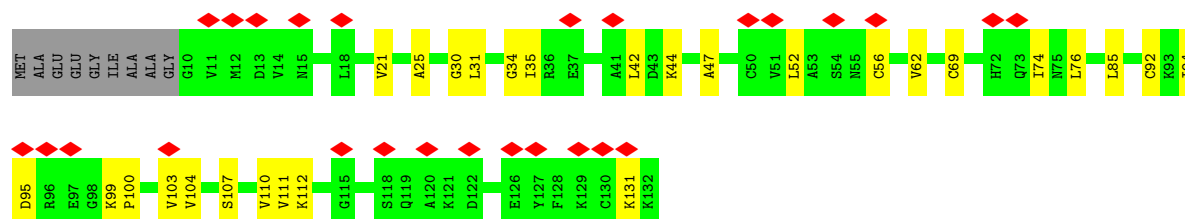
- Molecule 13: 40S ribosomal protein S11

Chain L: 73% 23% 4%



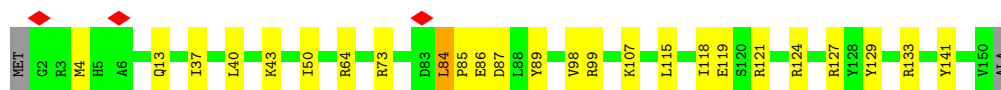
- Molecule 14: 40S ribosomal protein S12

Chain M: 20% 72% 21% 7%



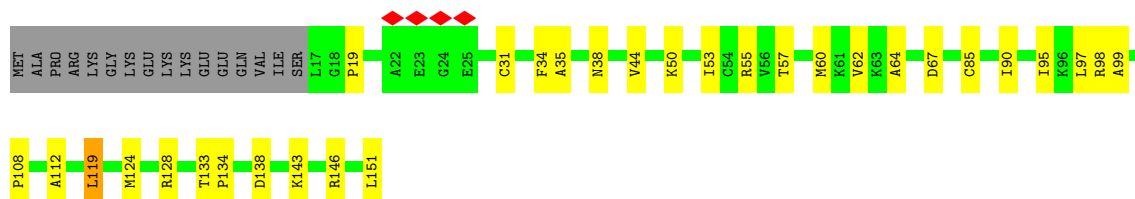
- Molecule 15: 40S ribosomal protein S13

Chain N:  82% 16% ..



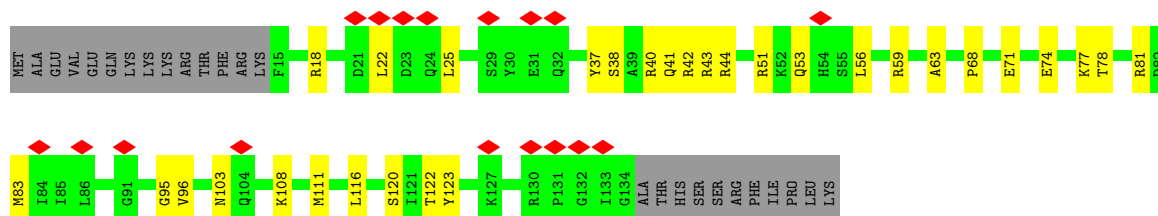
- Molecule 16: 40S ribosomal protein S14

Chain O:  69% 20% 11%



- Molecule 17: 40S ribosomal protein S15

Chain P:  12% 61% 21% 17%



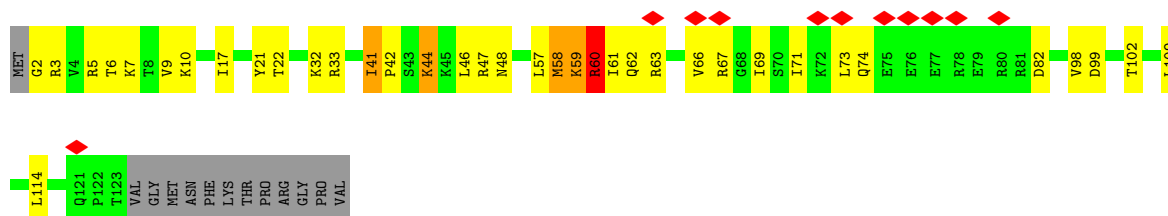
- Molecule 18: 40S ribosomal protein S16

Chain Q:  77% 18% 5%

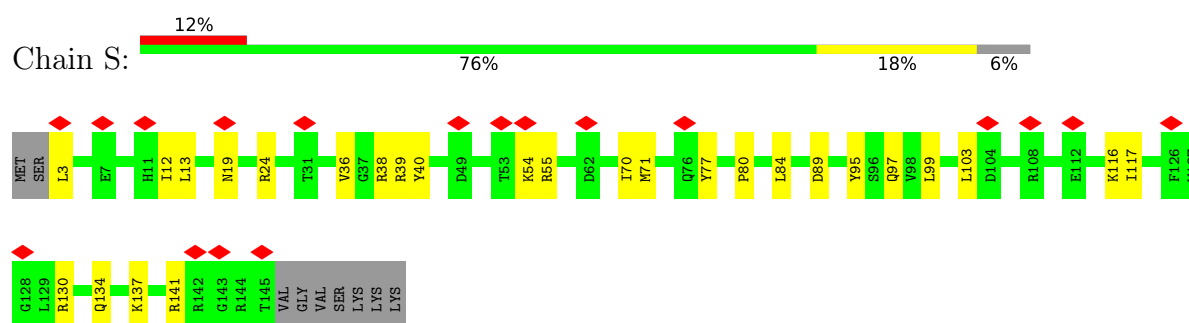


- Molecule 19: 40S ribosomal protein S17

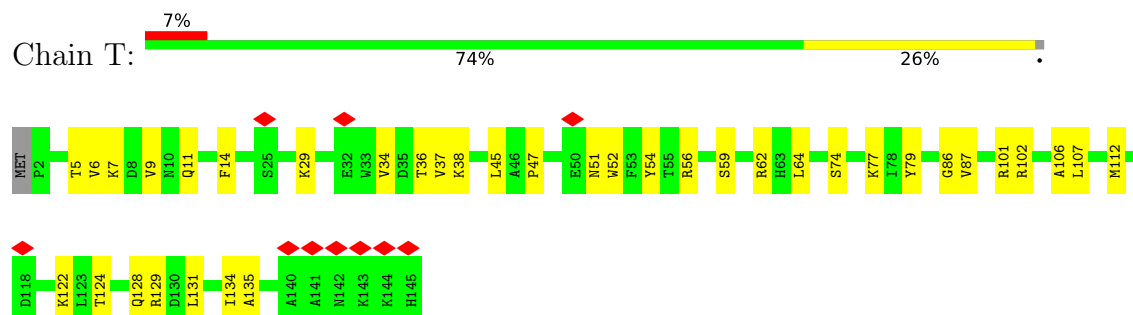
Chain R:  8% 63% 24% 10%



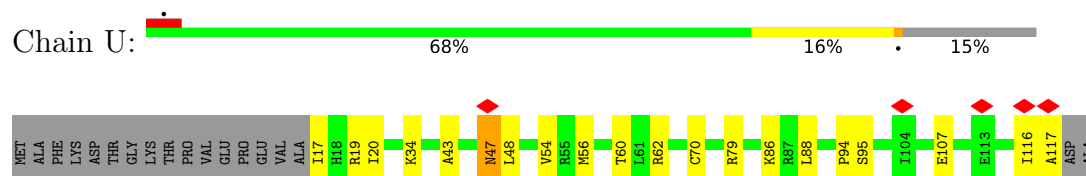
- Molecule 20: 40S ribosomal protein S18



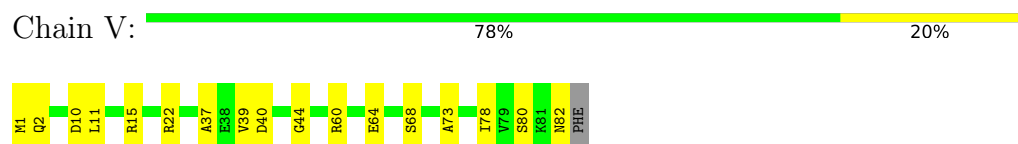
- Molecule 21: 40S ribosomal protein S19



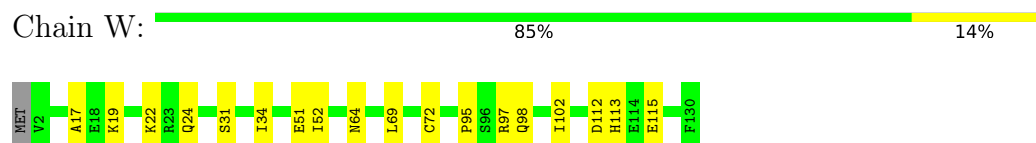
- Molecule 22: 40S ribosomal protein S20



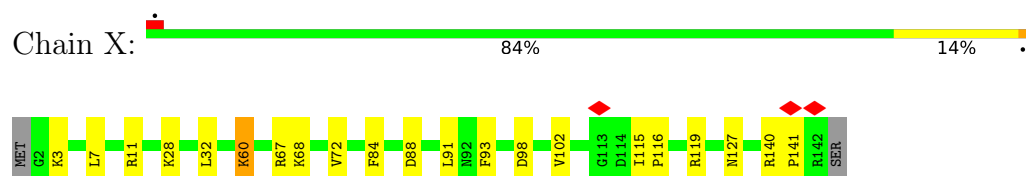
- Molecule 23: 40S ribosomal protein S21



- Molecule 24: 40S ribosomal protein S15a



- Molecule 25: 40S ribosomal protein S23



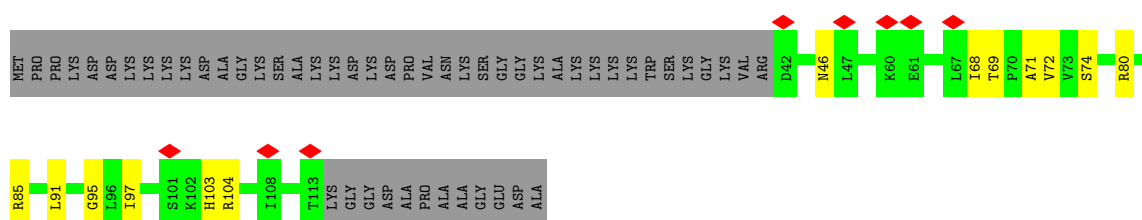
- Molecule 26: 40S ribosomal protein S24

Chain Y:  77% 14% 7%



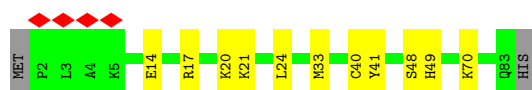
- Molecule 27: 40S ribosomal protein S25

Chain Z:  6% 47% 10% 42%



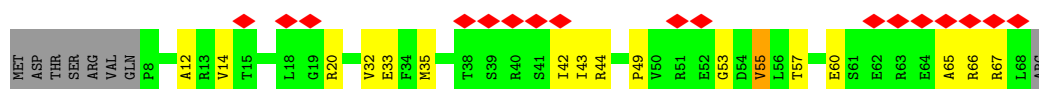
- Molecule 28: 40S ribosomal protein S27

Chain b:  5% 85% 13%



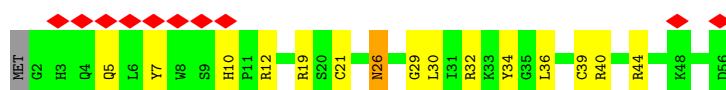
- Molecule 29: 40S ribosomal protein S28

Chain c:  25% 64% 23% 12%



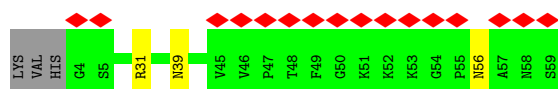
- Molecule 30: 40S ribosomal protein S29

Chain d:  18% 71% 25%

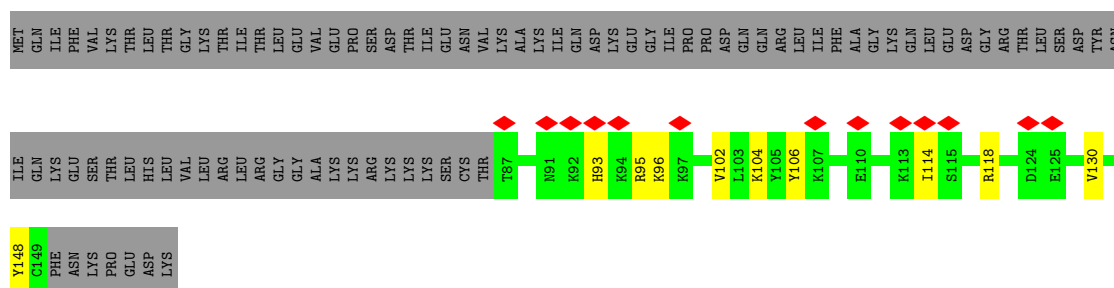


- Molecule 31: 40S ribosomal protein S30

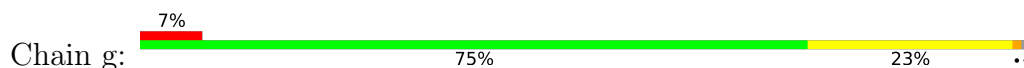
Chain e:  27% 90% 5% 5%



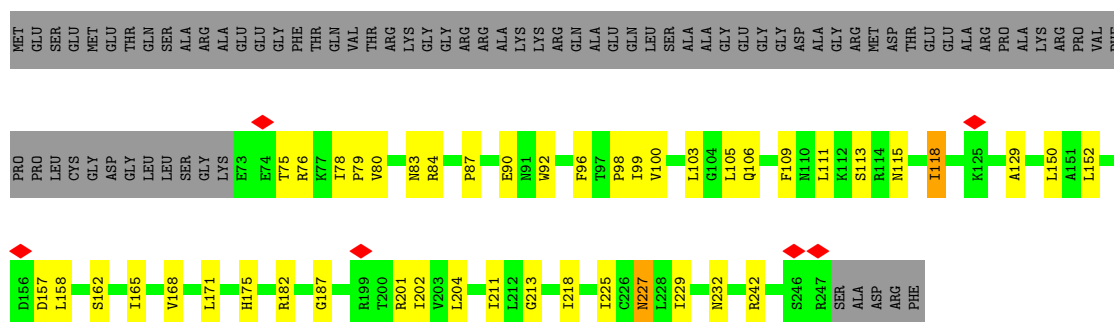
- Molecule 32: Ribosomal protein S27a



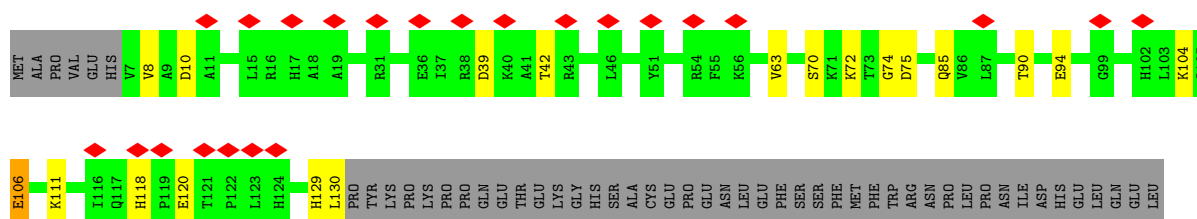
• Molecule 33: Receptor of activated protein C kinase 1

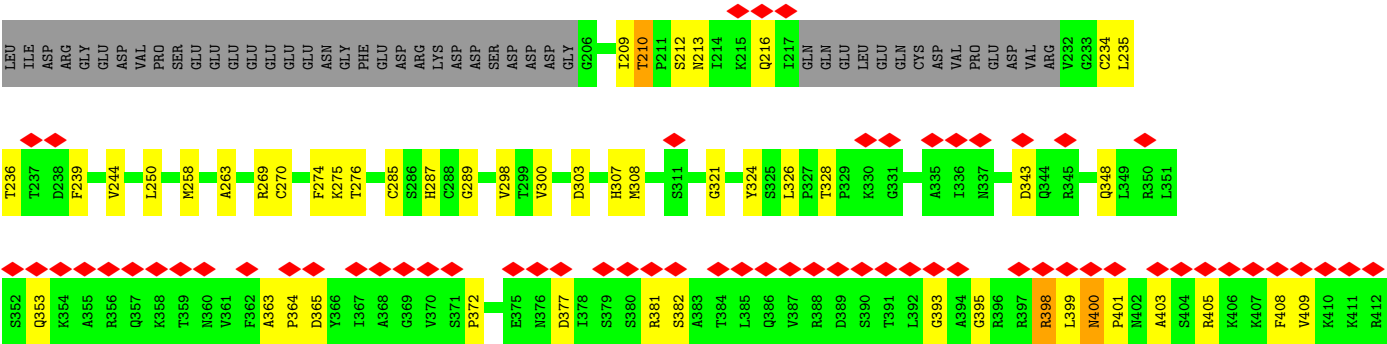


• Molecule 34: RNA-binding protein PNO1

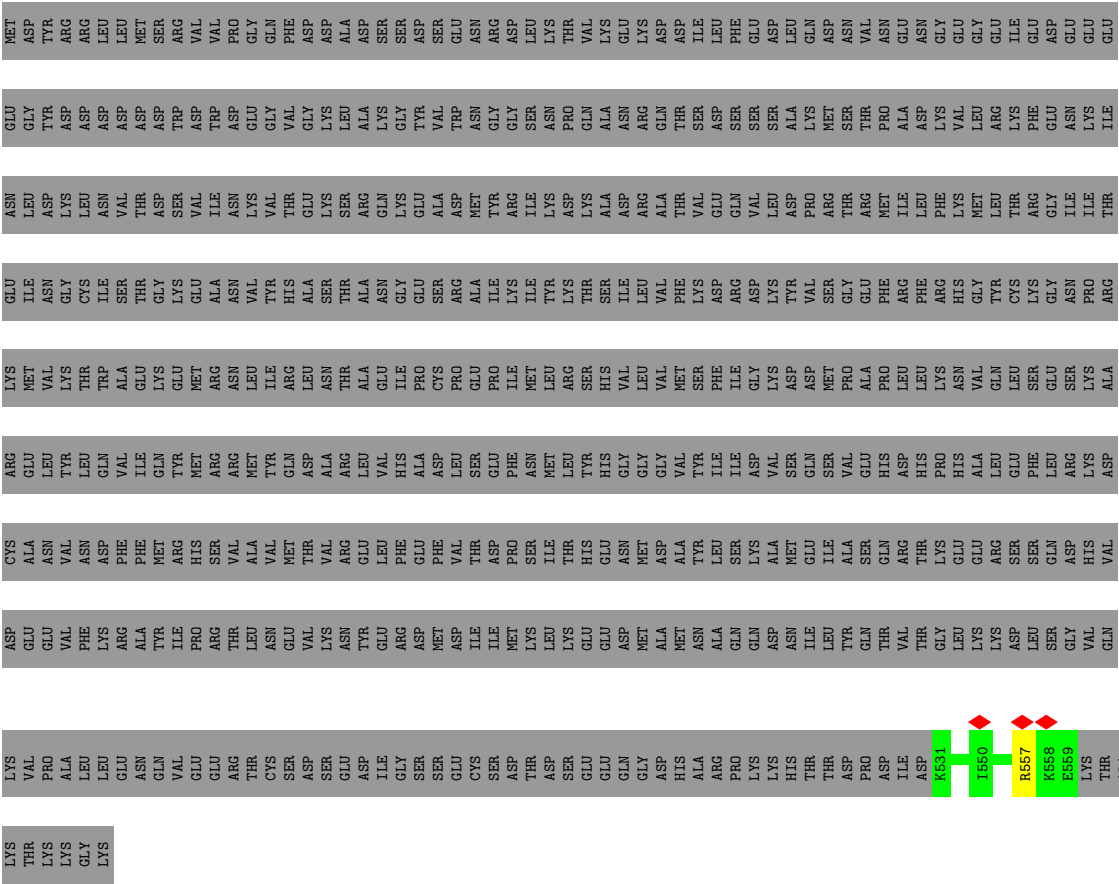


• Molecule 35: RNA-binding protein NOB1





• Molecule 36: Serine/threonine-protein kinase RIO1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83883	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.194	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	0.45	0/39560	0.56	4/61645 (0.0%)
2	A	0.54	0/1742	0.83	2/2367 (0.1%)
3	B	0.44	0/1756	0.79	0/2350
4	C	0.53	0/1726	0.82	1/2332 (0.0%)
5	D	0.37	0/1780	0.82	0/2397
6	E	0.54	0/2118	0.81	0/2849
7	F	0.35	0/1516	0.86	1/2037 (0.0%)
8	G	0.39	0/1885	0.75	0/2510
9	H	0.36	0/1524	0.78	0/2042
10	I	0.41	0/1711	0.73	0/2282
11	J	0.54	0/1524	0.85	2/2035 (0.1%)
12	K	0.33	0/824	0.76	0/1112
13	L	0.54	0/1250	0.73	0/1673
14	M	0.32	0/963	0.78	2/1291 (0.2%)
15	N	0.47	0/1226	0.84	0/1649
16	O	0.41	0/1022	0.76	0/1372
17	P	0.32	0/1003	0.67	0/1341
18	Q	0.40	0/1126	0.85	0/1506
19	R	0.40	0/1002	0.89	3/1345 (0.2%)
20	S	0.30	0/1202	0.69	0/1610
21	T	0.33	0/1142	0.79	0/1530
22	U	0.39	0/813	0.83	0/1092
23	V	0.46	0/631	0.68	0/844
24	W	0.63	0/1051	0.85	0/1406
25	X	0.50	0/1116	0.83	0/1490
26	Y	0.47	0/1031	0.82	1/1370 (0.1%)
27	Z	0.32	0/580	0.76	0/780
28	b	0.40	0/653	0.78	0/876
29	c	0.33	0/481	0.79	0/643
30	d	0.38	0/469	0.69	0/623
31	e	0.38	0/447	0.72	0/587
32	f	0.29	0/520	0.67	0/690

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.32	0/2497	0.72	2/3399 (0.1%)
34	x	0.41	0/1387	0.85	0/1871
35	y	0.36	0/2539	0.74	0/3430
36	z	0.34	0/258	0.81	0/331
All	All	0.44	0/82075	0.68	18/118707 (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
2	A	0	1
5	D	0	1
7	F	0	2
13	L	0	1
20	S	0	1
25	X	0	2
26	Y	0	1
29	c	0	1
33	g	0	2
34	x	0	2
35	y	0	3
All	All	0	17

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	44	LYS	N-CA-C	11.07	124.72	111.33
26	Y	119	GLY	N-CA-C	8.18	122.54	112.73
19	R	60	ARG	CA-C-N	8.00	131.42	120.46
19	R	60	ARG	C-N-CA	8.00	131.42	120.46
11	J	137	VAL	CA-C-N	6.66	134.26	121.54

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	189	ILE	Peptide
5	D	194	PRO	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
7	F	138	ALA	Peptide
7	F	40	ALA	Peptide
13	L	41	GLY	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	35380	0	17863	426	0
2	A	1705	0	1706	43	0
3	B	1729	0	1803	32	0
4	C	1690	0	1777	63	0
5	D	1752	0	1848	30	0
6	E	2076	0	2177	39	0
7	F	1495	0	1549	42	0
8	G	1862	0	2018	28	0
9	H	1501	0	1593	24	0
10	I	1682	0	1769	25	0
11	J	1499	0	1618	27	0
12	K	800	0	818	20	0
13	L	1229	0	1302	24	0
14	M	953	0	990	19	0
15	N	1202	0	1289	20	0
16	O	1009	0	1034	26	0
17	P	984	0	1028	28	0
18	Q	1109	0	1174	19	0
19	R	990	0	1037	80	0
20	S	1184	0	1244	22	0
21	T	1122	0	1153	29	0
22	U	803	0	873	13	0
23	V	625	0	628	14	0
24	W	1034	0	1080	13	0
25	X	1098	0	1167	16	0
26	Y	1014	0	1082	14	0
27	Z	574	0	627	12	0
28	b	640	0	665	7	0
29	c	479	0	507	16	0
30	d	458	0	448	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	e	442	0	487	3	0
32	f	510	0	521	9	0
33	g	2440	0	2396	46	0
34	x	1365	0	1447	43	0
35	y	2490	0	2543	66	0
36	z	257	0	302	1	0
37	d	1	0	0	0	0
37	f	1	0	0	0	0
37	y	1	0	0	0	0
All	All	77185	0	61563	1095	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 8.

The worst 5 of 1095 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)
19:R:66:VAL:CG1	19:R:69:ILE:HG12	1.23	1.65
19:R:66:VAL:HG12	19:R:69:ILE:CG1	1.32	1.53
19:R:66:VAL:HG12	19:R:69:ILE:CD1	1.41	1.50
19:R:66:VAL:CG1	19:R:69:ILE:CG1	1.86	1.43
4:C:103:LYS:HD2	4:C:133:TYR:CE2	1.60	1.36

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	A	180/243 (74%)	178 (99%)	2 (1%)	65	74
3	B	194/231 (84%)	193 (100%)	1 (0%)	81	80
4	C	184/225 (82%)	180 (98%)	4 (2%)	45	65
5	D	189/202 (94%)	188 (100%)	1 (0%)	81	80
6	E	224/225 (100%)	221 (99%)	3 (1%)	61	72
7	F	159/170 (94%)	159 (100%)	0	100	100
8	G	200/218 (92%)	200 (100%)	0	100	100
9	H	167/174 (96%)	166 (99%)	1 (1%)	78	79
10	I	178/180 (99%)	178 (100%)	0	100	100
11	J	160/168 (95%)	159 (99%)	1 (1%)	78	79
12	K	86/136 (63%)	86 (100%)	0	100	100
13	L	135/142 (95%)	134 (99%)	1 (1%)	76	78
14	M	104/108 (96%)	104 (100%)	0	100	100
15	N	130/131 (99%)	129 (99%)	1 (1%)	73	77
16	O	105/119 (88%)	104 (99%)	1 (1%)	68	75
17	P	107/130 (82%)	107 (100%)	0	100	100
18	Q	115/121 (95%)	115 (100%)	0	100	100
19	R	110/122 (90%)	106 (96%)	4 (4%)	31	57
20	S	124/132 (94%)	124 (100%)	0	100	100
21	T	114/115 (99%)	113 (99%)	1 (1%)	70	76
22	U	93/107 (87%)	92 (99%)	1 (1%)	65	74
23	V	66/67 (98%)	66 (100%)	0	100	100
24	W	112/113 (99%)	112 (100%)	0	100	100
25	X	113/115 (98%)	113 (100%)	0	100	100
26	Y	108/115 (94%)	106 (98%)	2 (2%)	50	68
27	Z	64/103 (62%)	64 (100%)	0	100	100
28	b	74/76 (97%)	74 (100%)	0	100	100
29	c	54/62 (87%)	53 (98%)	1 (2%)	50	68
30	d	48/49 (98%)	47 (98%)	1 (2%)	47	66
31	e	45/48 (94%)	45 (100%)	0	100	100
32	f	56/140 (40%)	56 (100%)	0	100	100
33	g	272/275 (99%)	272 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	x	146/208 (70%)	143 (98%)	3 (2%)	47	66
35	y	275/367 (75%)	273 (99%)	2 (1%)	76	78
36	z	28/512 (6%)	28 (100%)	0	100	100
All	All	4519/5649 (80%)	4488 (99%)	31 (1%)	73	78

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	N	84	LEU
34	x	225	ILE
19	R	58	MET
35	y	398	ARG
29	c	55	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
15	N	13	GLN
34	x	227	ASN
18	Q	29	ASN
34	x	106	GLN
35	y	307	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1644/1882 (87%)	534 (32%)	0

5 of 534 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	3	C
1	2	4	C
1	2	5	U
1	2	14	C
1	2	17	C

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

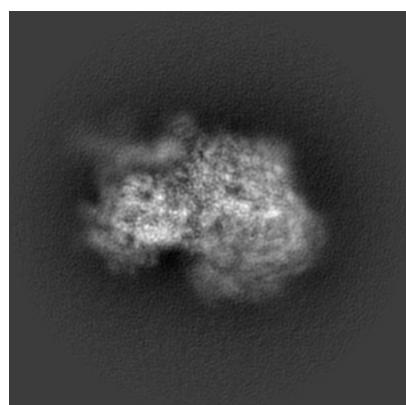
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4353. These allow visual inspection of the internal detail of the map and identification of artifacts.

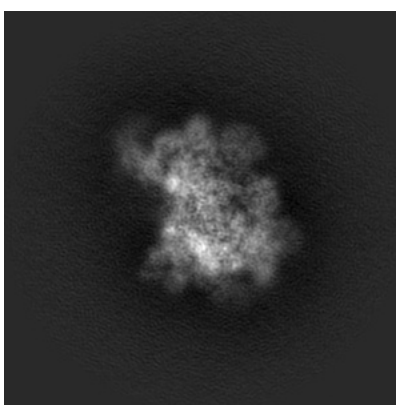
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

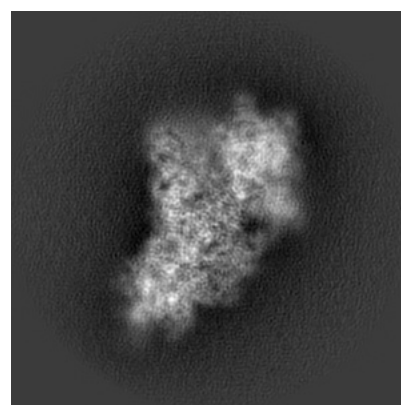
6.1.1 Primary map



X



Y

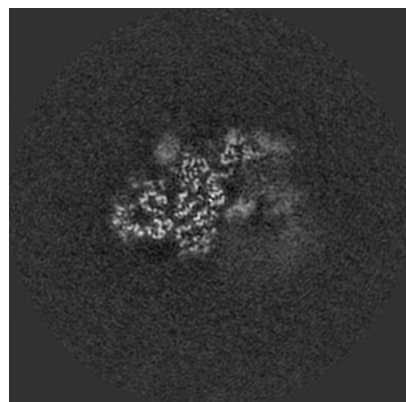


Z

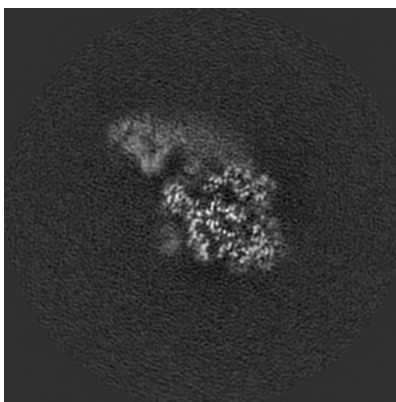
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

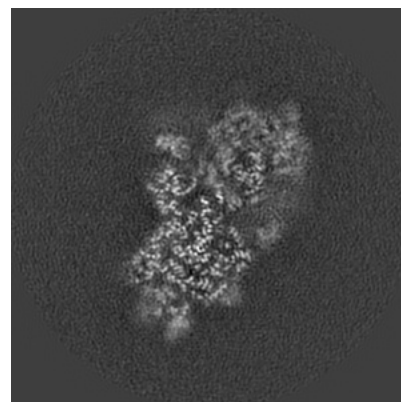
6.2.1 Primary map



X Index: 180



Y Index: 180

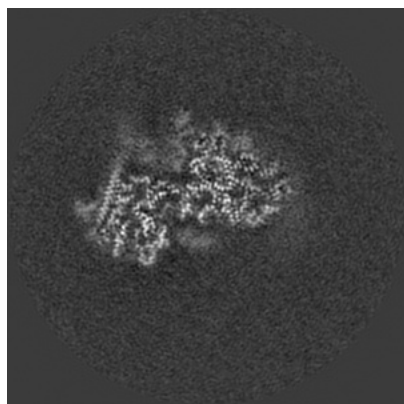


Z Index: 180

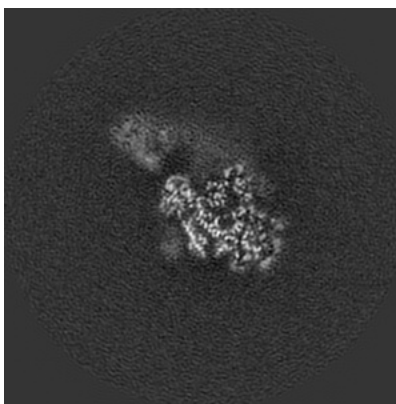
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

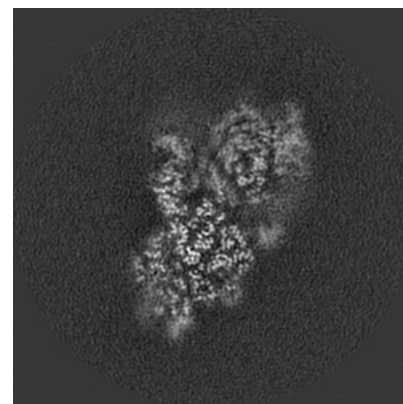
6.3.1 Primary map



X Index: 145



Y Index: 175

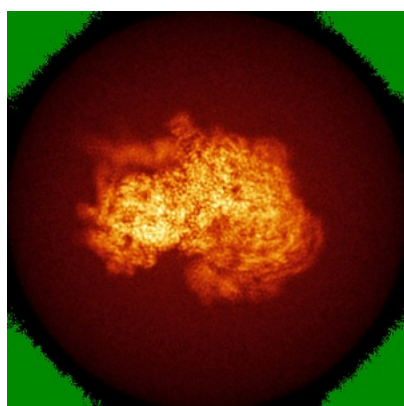


Z Index: 178

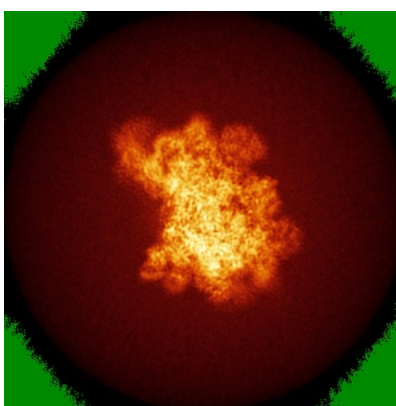
The images above show the largest variance slices of the map in three orthogonal directions.

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

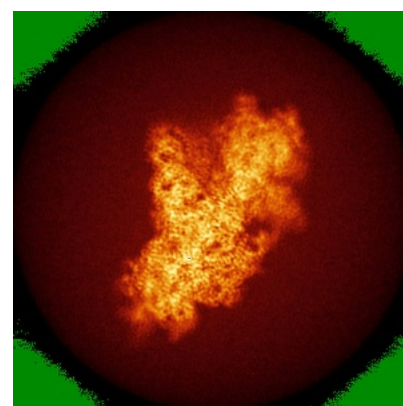
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

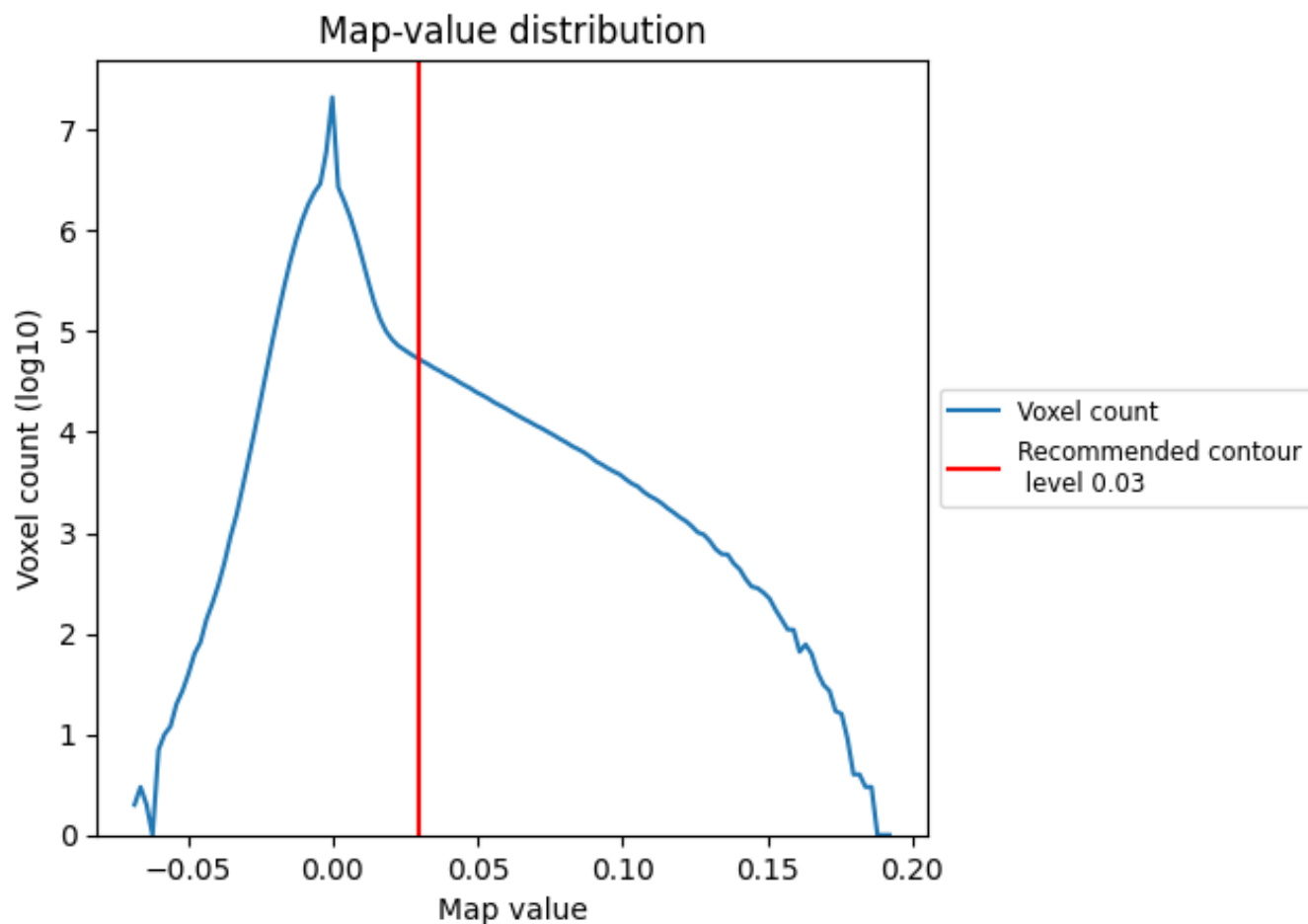
6.6 Mask visualisation

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

7 Map analysis [i](#)

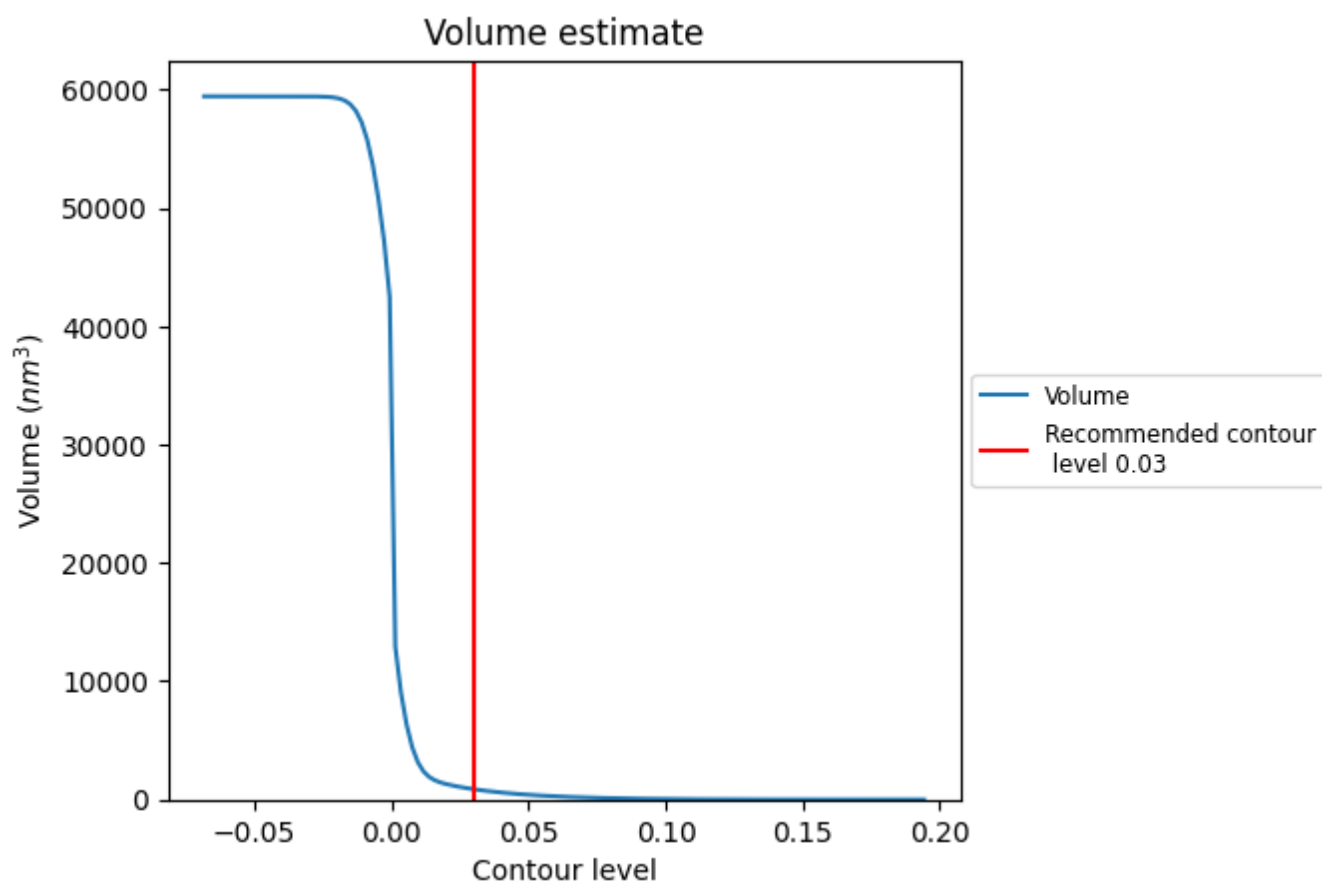
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

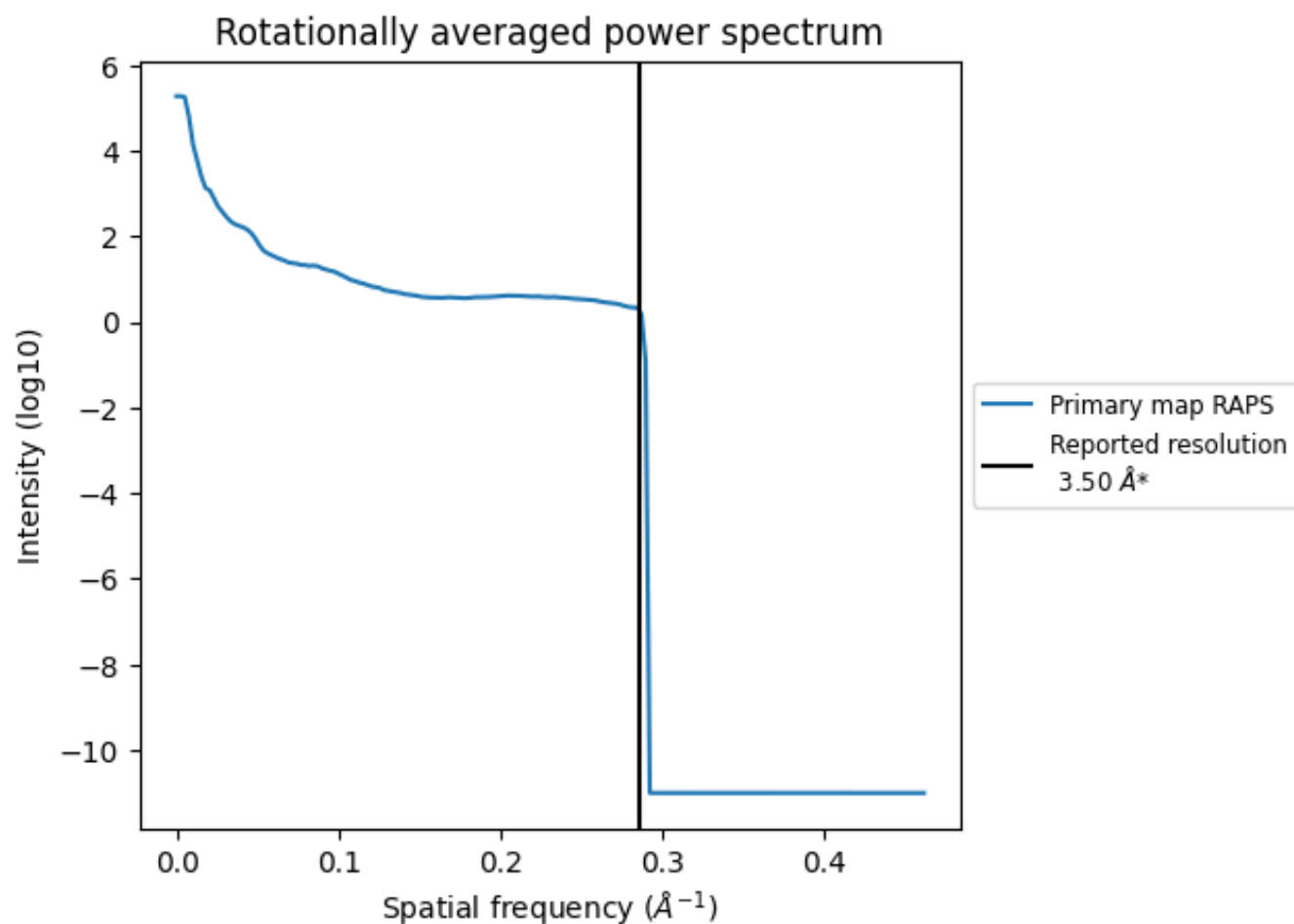
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 873 nm³; this corresponds to an approximate mass of 789 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

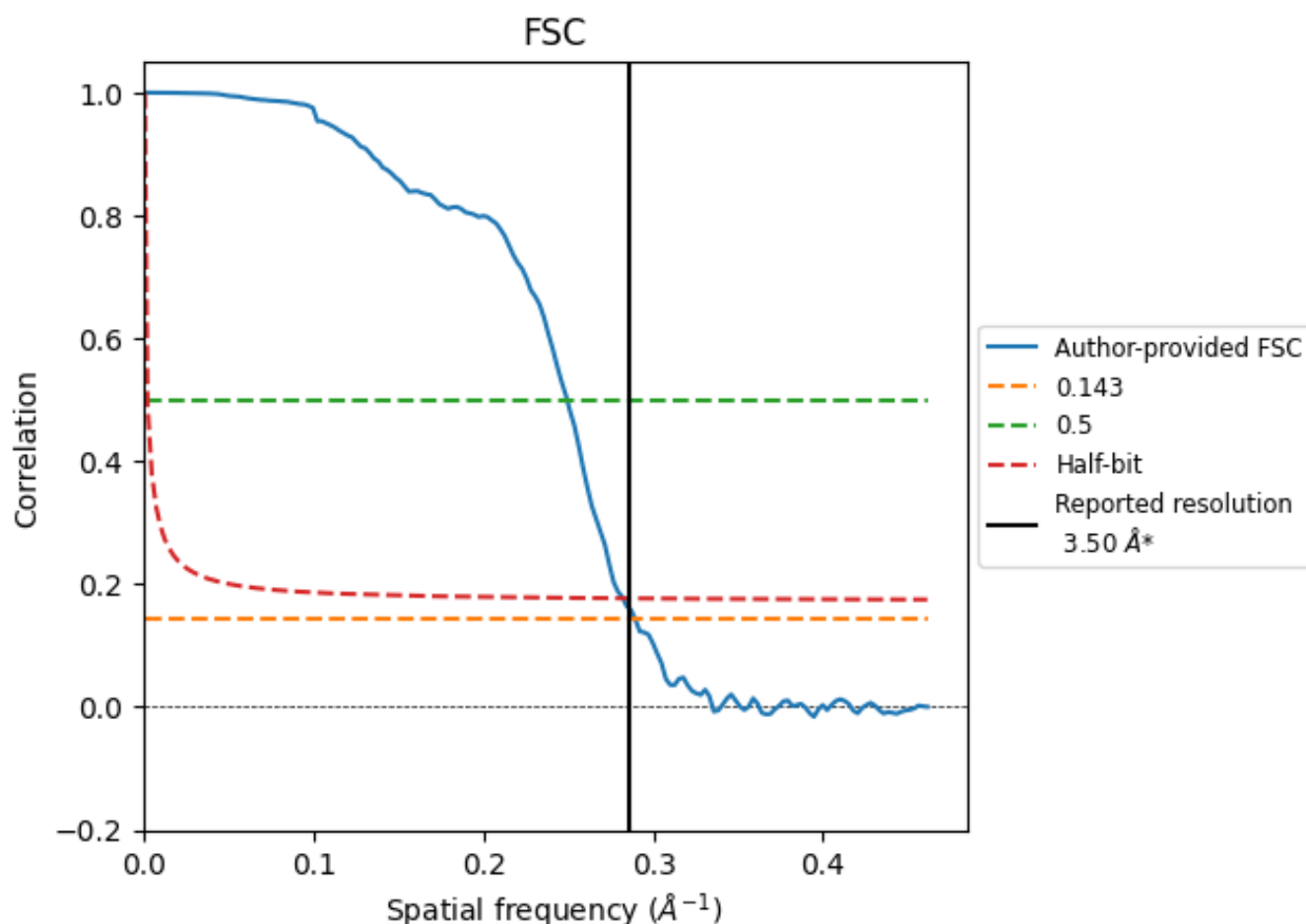


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.46	4.01	3.54
Unmasked-calculated*	-	-	-

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

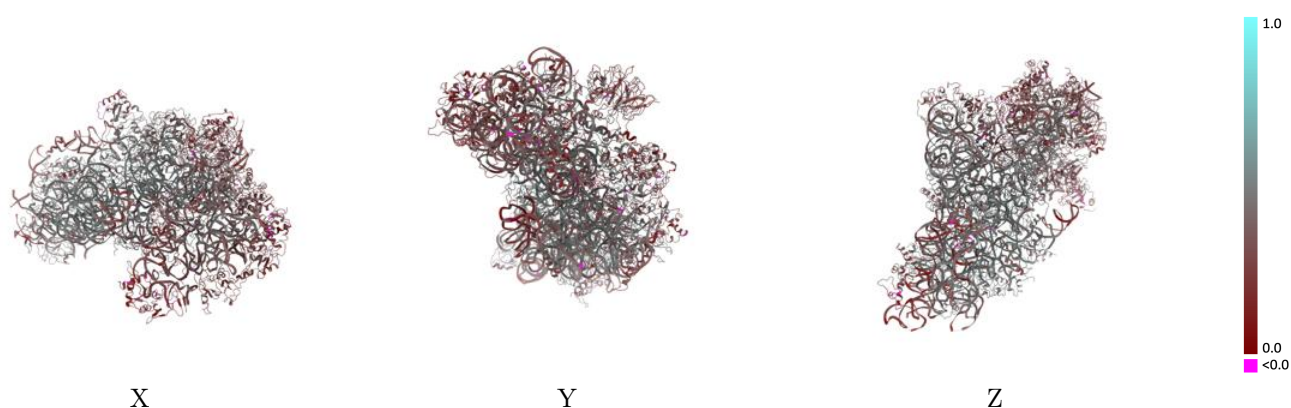
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4353 and PDB model 6G5I. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

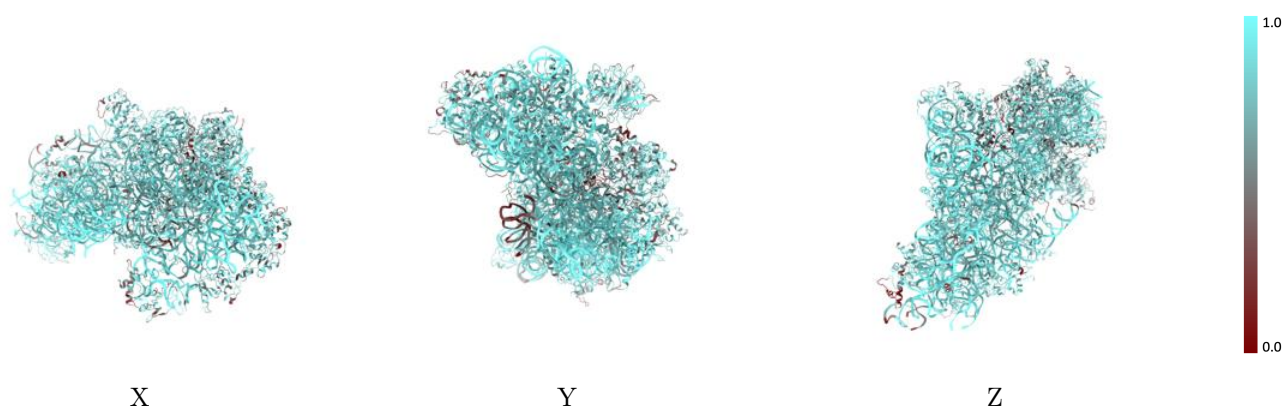
This section was not generated.

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



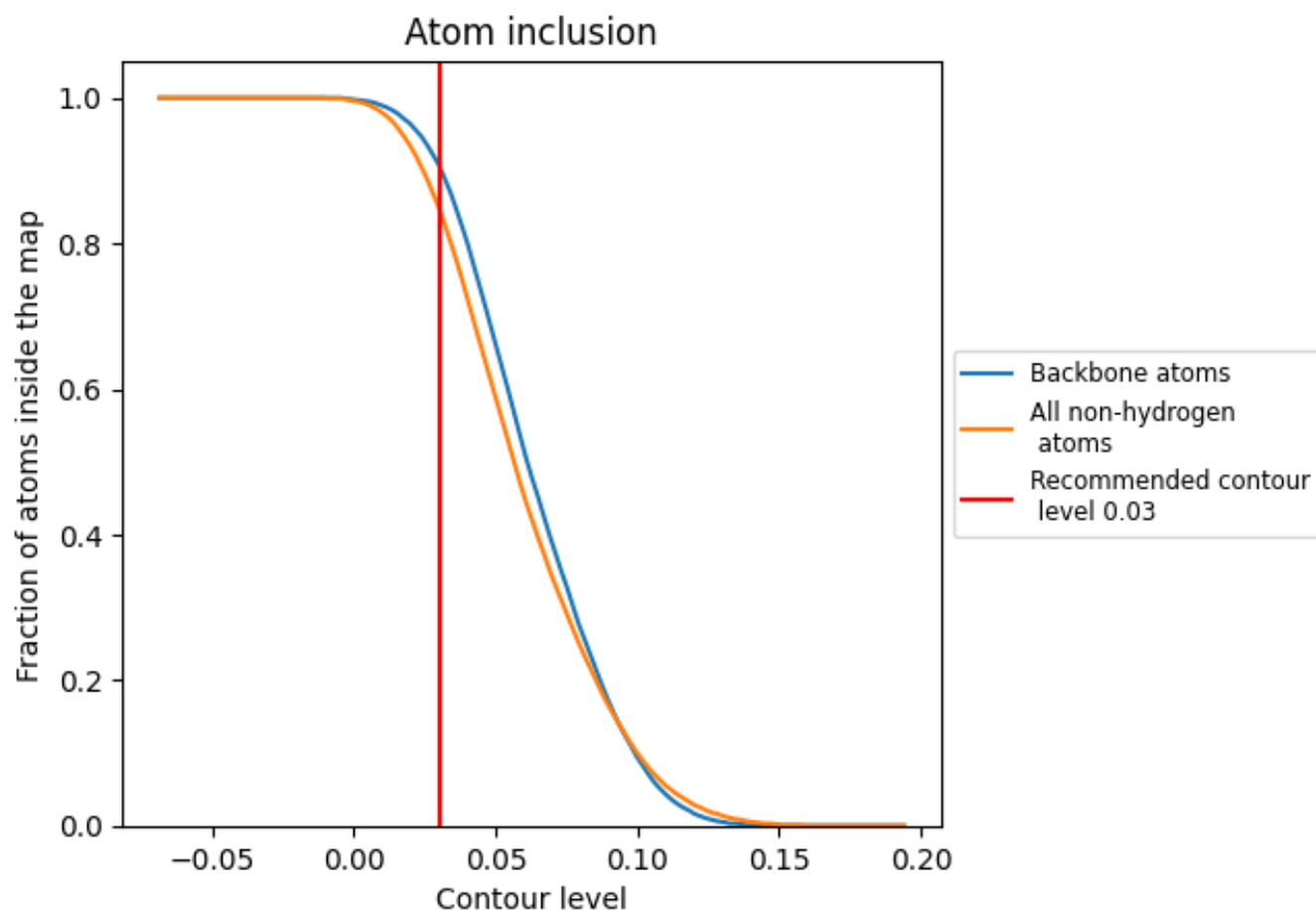
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8500	 0.3950
2	 0.9340	 0.4140
A	 0.8590	 0.4370
B	 0.8390	 0.4150
C	 0.8310	 0.4650
D	 0.7070	 0.3450
E	 0.8600	 0.4720
F	 0.7180	 0.2950
G	 0.8520	 0.4030
H	 0.7490	 0.3450
I	 0.7140	 0.3860
J	 0.8750	 0.4650
K	 0.8260	 0.3120
L	 0.8550	 0.4700
M	 0.6440	 0.2260
N	 0.8550	 0.4440
O	 0.8220	 0.4020
P	 0.7280	 0.3040
Q	 0.8130	 0.3760
R	 0.7280	 0.3800
S	 0.7230	 0.2690
T	 0.7780	 0.3090
U	 0.7770	 0.3640
V	 0.8300	 0.4530
W	 0.8490	 0.4890
X	 0.8420	 0.4800
Y	 0.9030	 0.4560
Z	 0.7090	 0.2580
b	 0.8090	 0.4300
c	 0.5710	 0.2700
d	 0.7300	 0.3990
e	 0.6580	 0.3720
f	 0.6400	 0.2300
g	 0.7890	 0.3220
x	 0.7490	 0.4010



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
y	 0.5770	 0.2950
z	 0.6100	 0.3640