



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 02:26 PM UTC

PDB ID : 8EUY / pdb_00008euy
EMDB ID : EMD-24420
Title : Ytm1 associated nascent 60S ribosome (-fkbp39) State 1A
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-19
Resolution : 3.00 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:

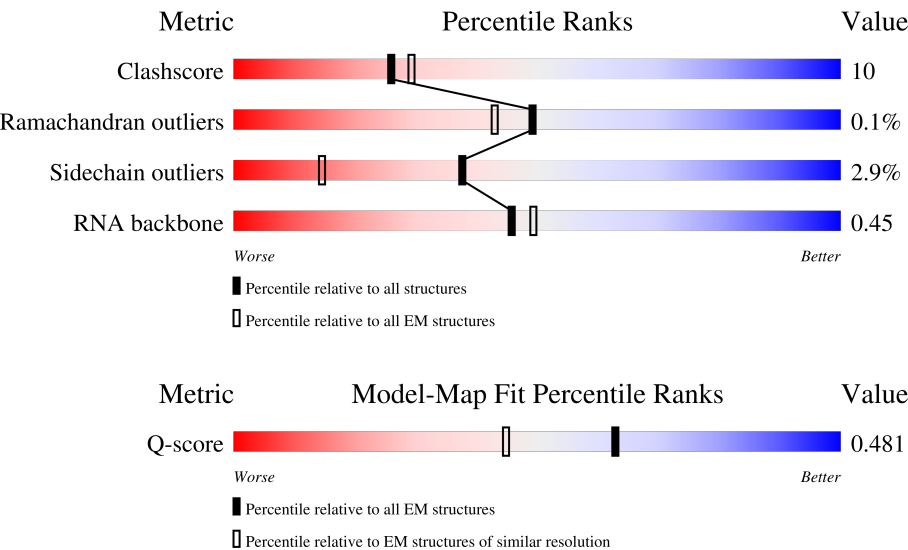
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.00 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.



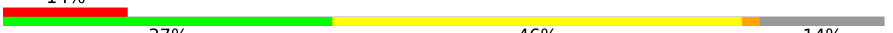
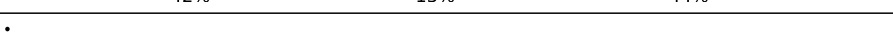
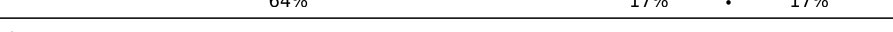
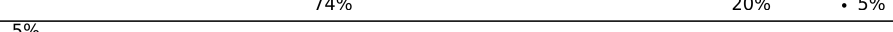
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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 $\leq 5\%$. 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	1	3497	23%14%59%
2	2	165	53%21%5%21%
3	3	302	52%11%36%

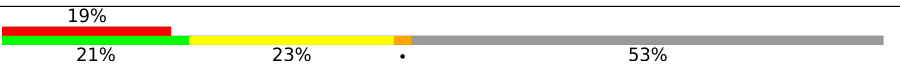
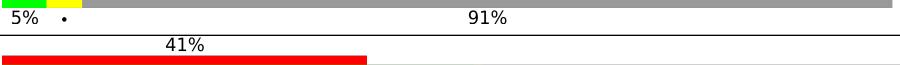
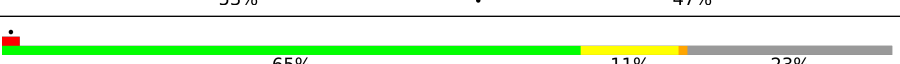
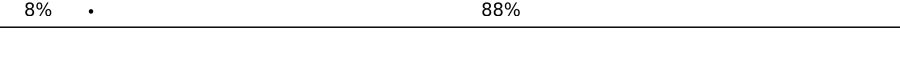
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Mol	Chain	Length	Quality of chain
4	4	217	
5	5	387	
6	6	300	
7	A	295	
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	

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Mol	Chain	Length	Quality of chain
29	h	122	
30	i	99	
31	j	91	
32	m	740	
33	o	276	
34	r	260	
35	t	249	
36	u	192	
37	v	209	
38	x	306	
39	y	244	
40	T	160	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 80249 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 RNA (1095-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1433	Total	C	N	O	P	0	0
			30681	13703	5554	9991	1433		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (148-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	130	Total	C	N	O	P	0	0
			2762	1236	487	909	130		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	192	Total	C	N	O	S	0	0
			1596	1010	304	276	6		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	210	Total	C	N	O	S	0	0
			1770	1153	302	307	8		

- Molecule 5 is a protein called Ribosome biogenesis protein nsal.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	340	Total	C	N	O	S	0	0
			2686	1716	468	491	11		

- Molecule 6 is a RNA chain called RNA (93-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	56	Total	C	N	O	P	0	0
			1160	522	171	411	56		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	254	Total	C	N	O	S	0	0
			2057	1303	374	372	8		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	332	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	329	Total	C	N	O	S	0	0
			2572	1631	487	451	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	406	Total	C	N	O	S	0	0
			3001	1931	519	542	9		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	240	Total	C	N	O	S	0	0
			1944	1250	356	335	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	164	Total	C	N	O	S	1	0
			1273	816	223	232	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	155	Total	C	N	O		0	0
			764	454	155	155			

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	89	Total	C	N	O		0	0
			444	266	89	89			

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	243	Total	C	N	O		0	0
			1205	719	243	243			

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	187	Total	C	N	O	S	0	0
			1487	958	281	245	3		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	145	Total	C	N	O	S	0	0
			1139	725	207	204	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	168	Total	C	N	O	S	0	0
			1402	906	260	231	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	113	Total	C	N	O	0	0
			554	327	113	114		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	b	120	Total	C	N	O	0	0
			594	354	120	120		

- Molecule 27 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	124	Total	C	N	O	S	0	0
			995	621	202	167	5		

- Molecule 28 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 29 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	121	Total	C	N	O	S	0	0
			999	629	194	176			

- Molecule 30 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	98	Total	C	N	O	S	0	0
			768	478	159	130	1		

- Molecule 31 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 32 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	m	92	Total	C	N	O	S	0	0
			725	447	128	150			

- Molecule 33 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	129	Total	C	N	O	S	0	0
			992	636	180	170	6		

- Molecule 34 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	r	50	Total	C	N	O	0	0
			249	149	50	50		

- Molecule 35 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	t	23	Total	C	N	O	0	0
			216	132	49	35		

- Molecule 36 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	u	102	Total	C	N	O	0	0
			506	302	102	102		

- Molecule 37 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 38 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	x	305	Total	C	N	O	S	0	0
			2516	1578	463	467	8		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	y	198	Total	C	N	O	0	0
			974	578	198	198		

- Molecule 40 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	T	19	Total	C	N	O	0	0
			147	93	26	28		

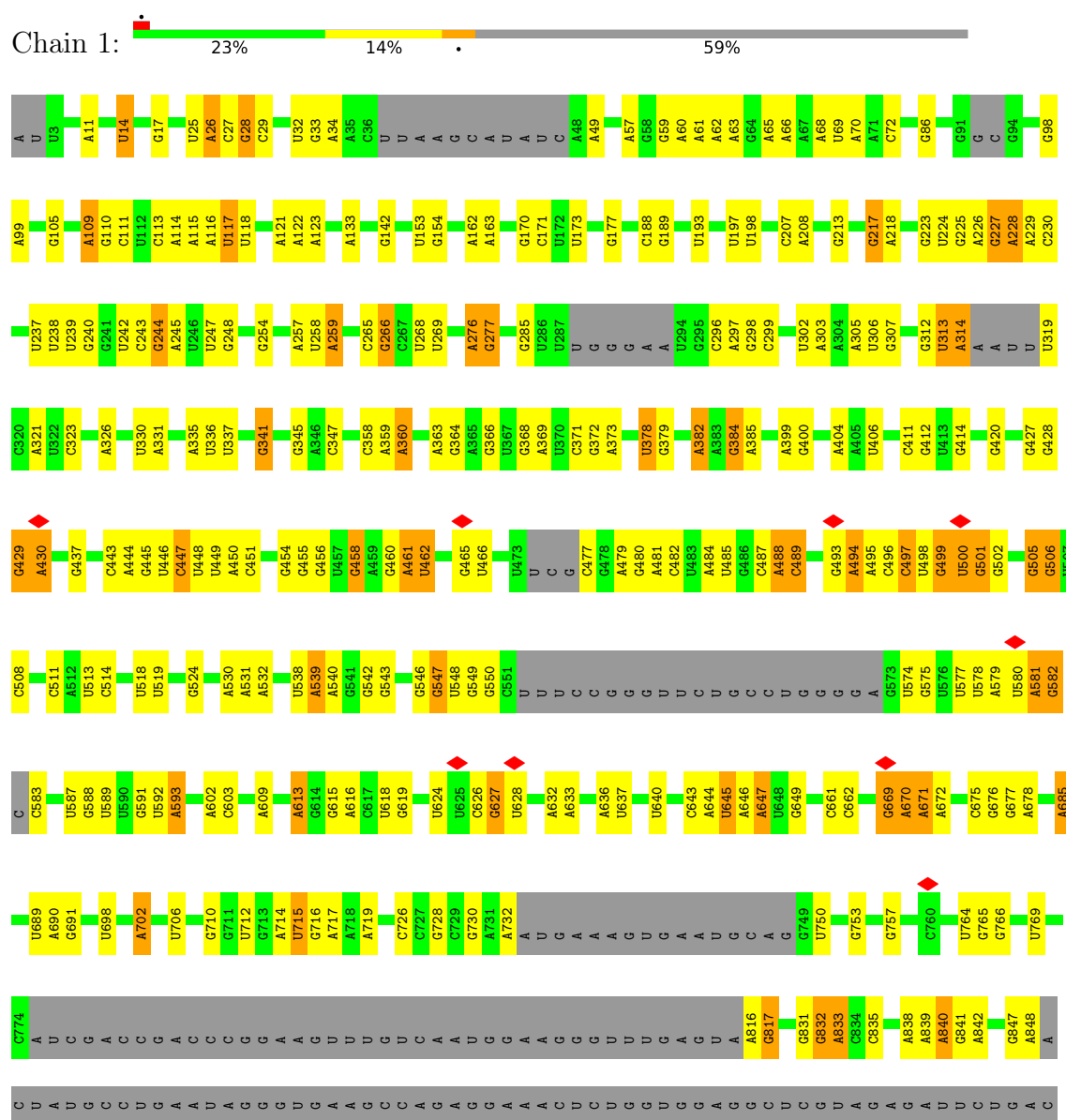
- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

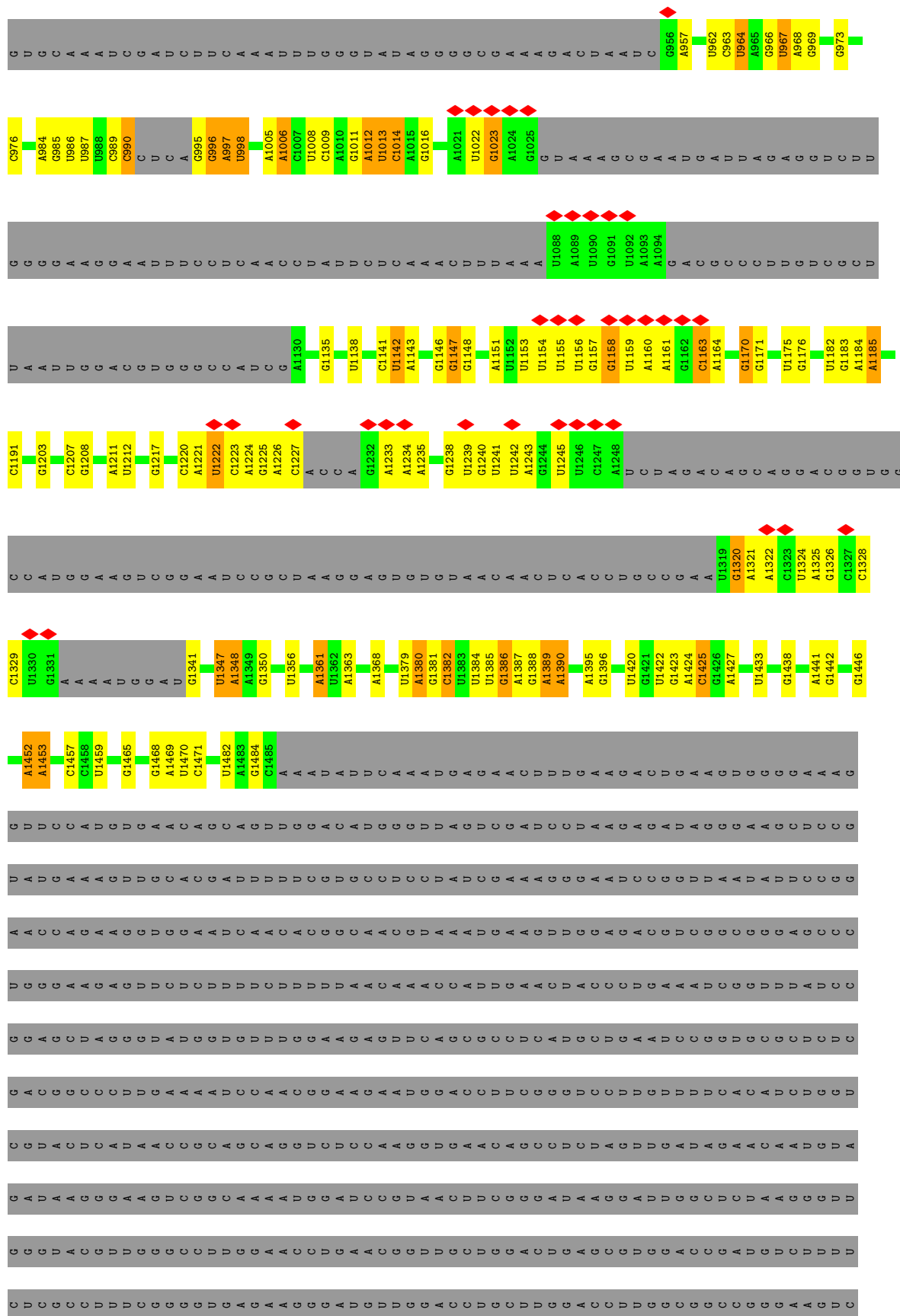
Mol	Chain	Residues	Atoms		AltConf
41	j	1	Total	Zn	0
			1	1	

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.

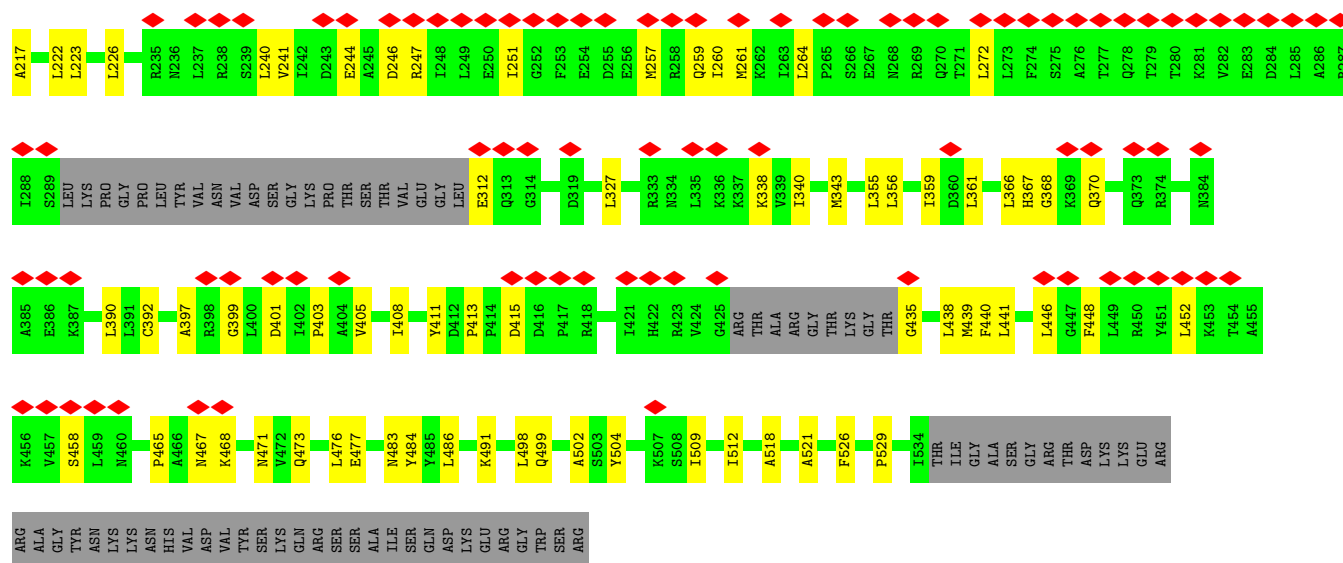
• Molecule 1: RNA (1095-MER)





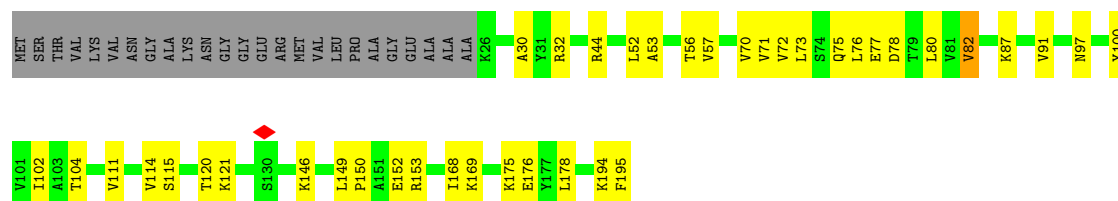






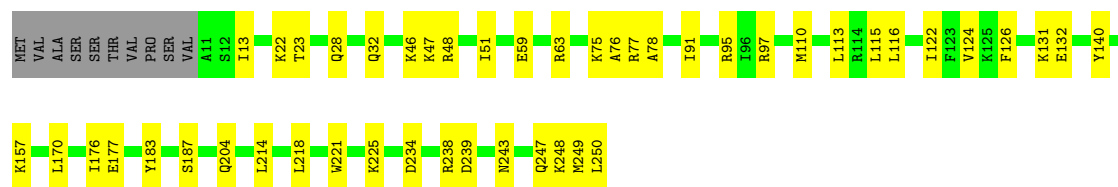
• Molecule 11: 60S ribosomal protein L6

Chain E: 67% 20% 13%



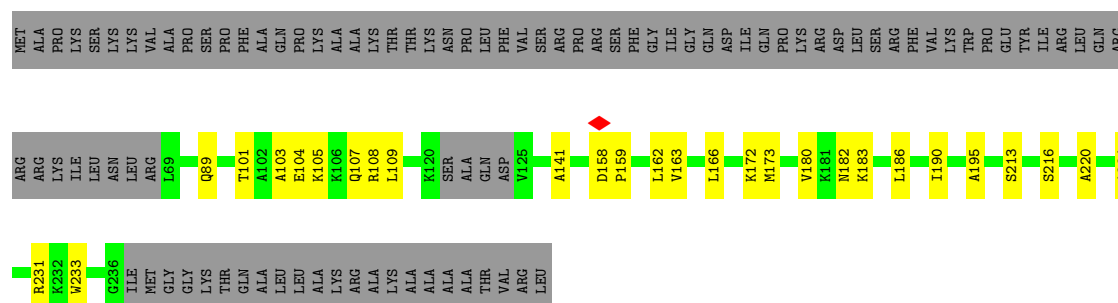
• Molecule 12: 60S ribosomal protein L7-B

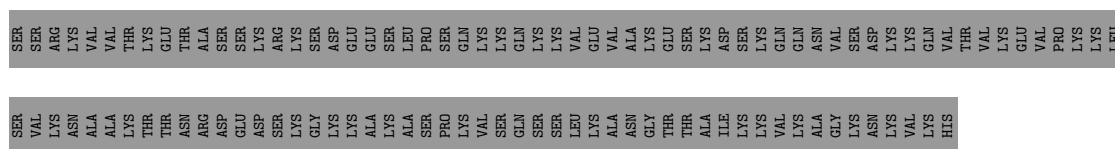
Chain F: 77% 19%



• Molecule 13: 60S ribosomal protein L8

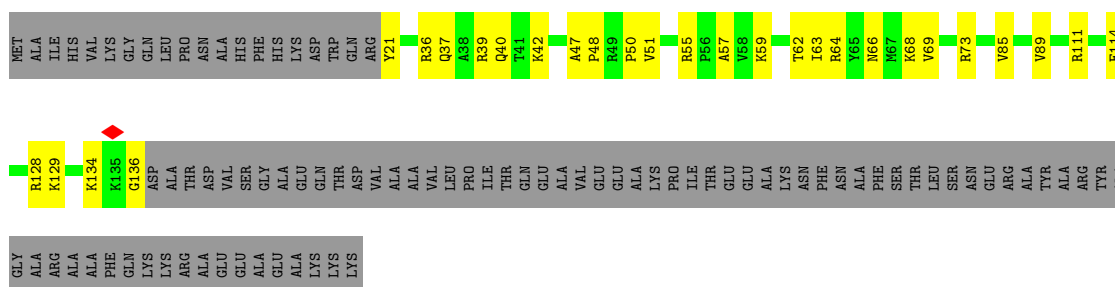
Chain G: 53% 11% 37%





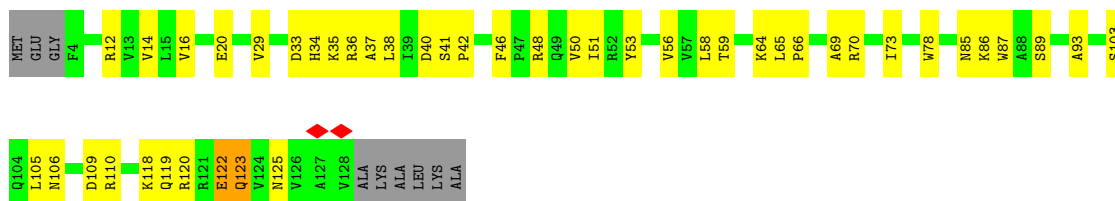
• Molecule 17: 60S ribosomal protein L13

Chain L: 42% 13% 44%



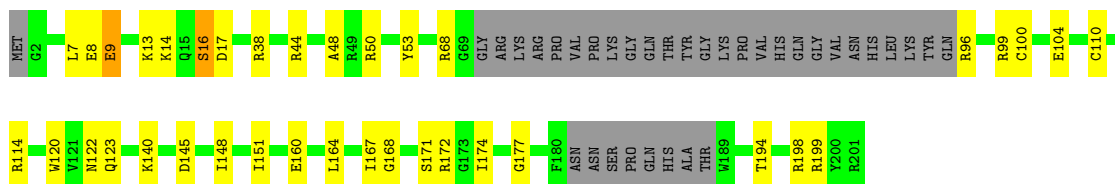
• Molecule 18: 60S ribosomal protein L14

Chain M: 60% 32% 7%



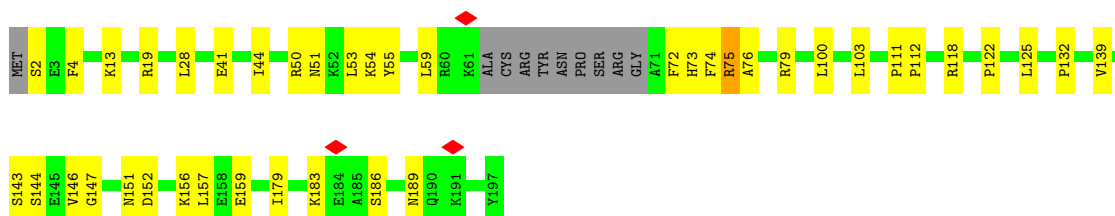
• Molecule 19: 60S ribosomal protein L15-A

Chain N: 64% 17% 17%

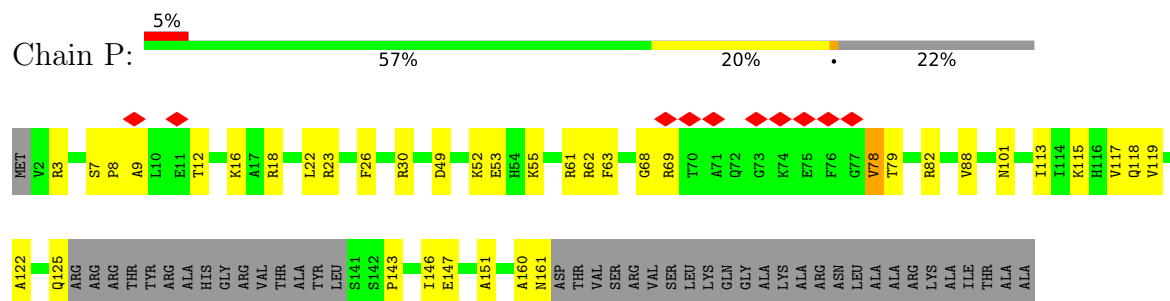


• Molecule 20: 60S ribosomal protein L16-B

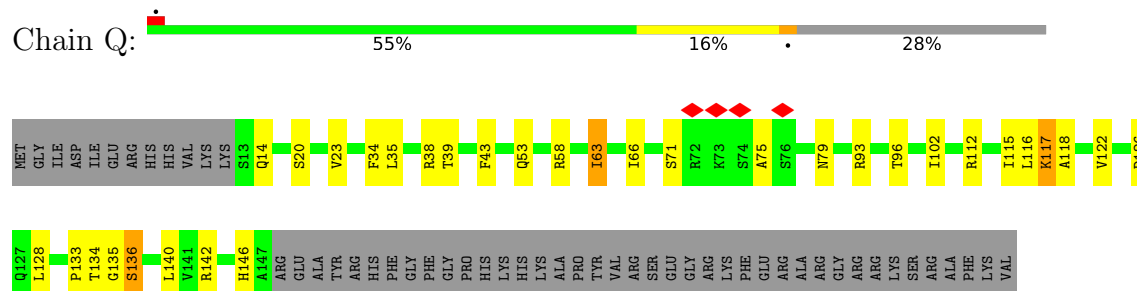
Chain O: 74% 20% 5%



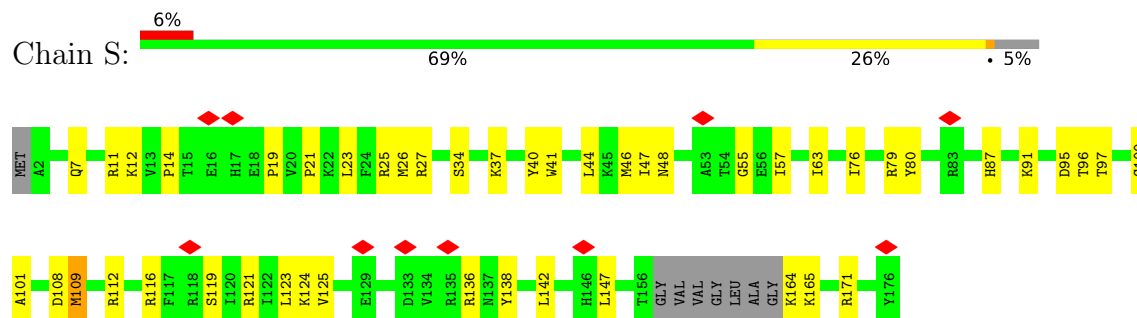
- Molecule 21: 60S ribosomal protein L17-A



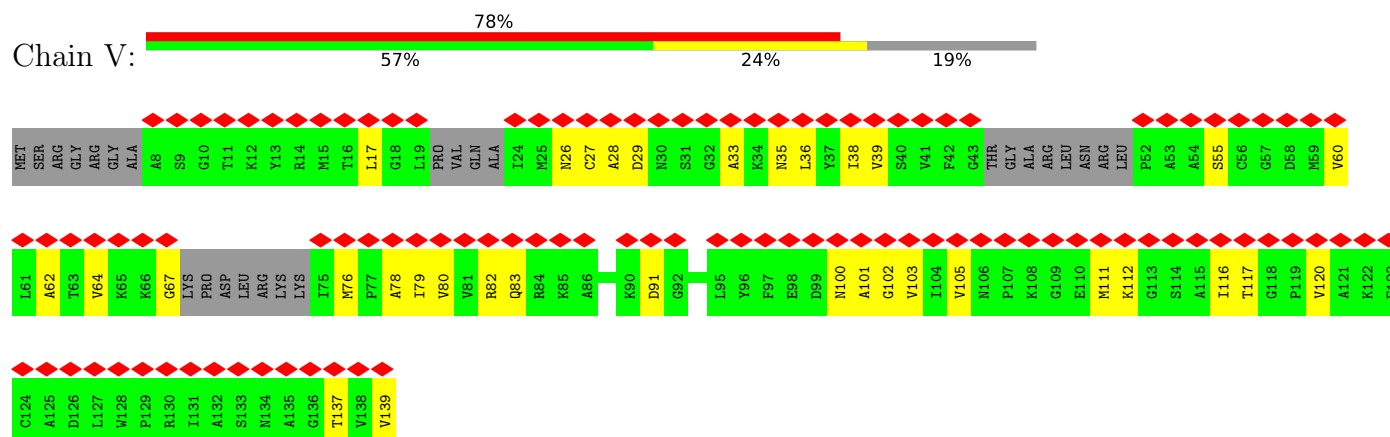
- Molecule 22: 60S ribosomal protein L18-A



- Molecule 23: 60S ribosomal protein L20-A



- Molecule 24: 60S ribosomal protein L23-A

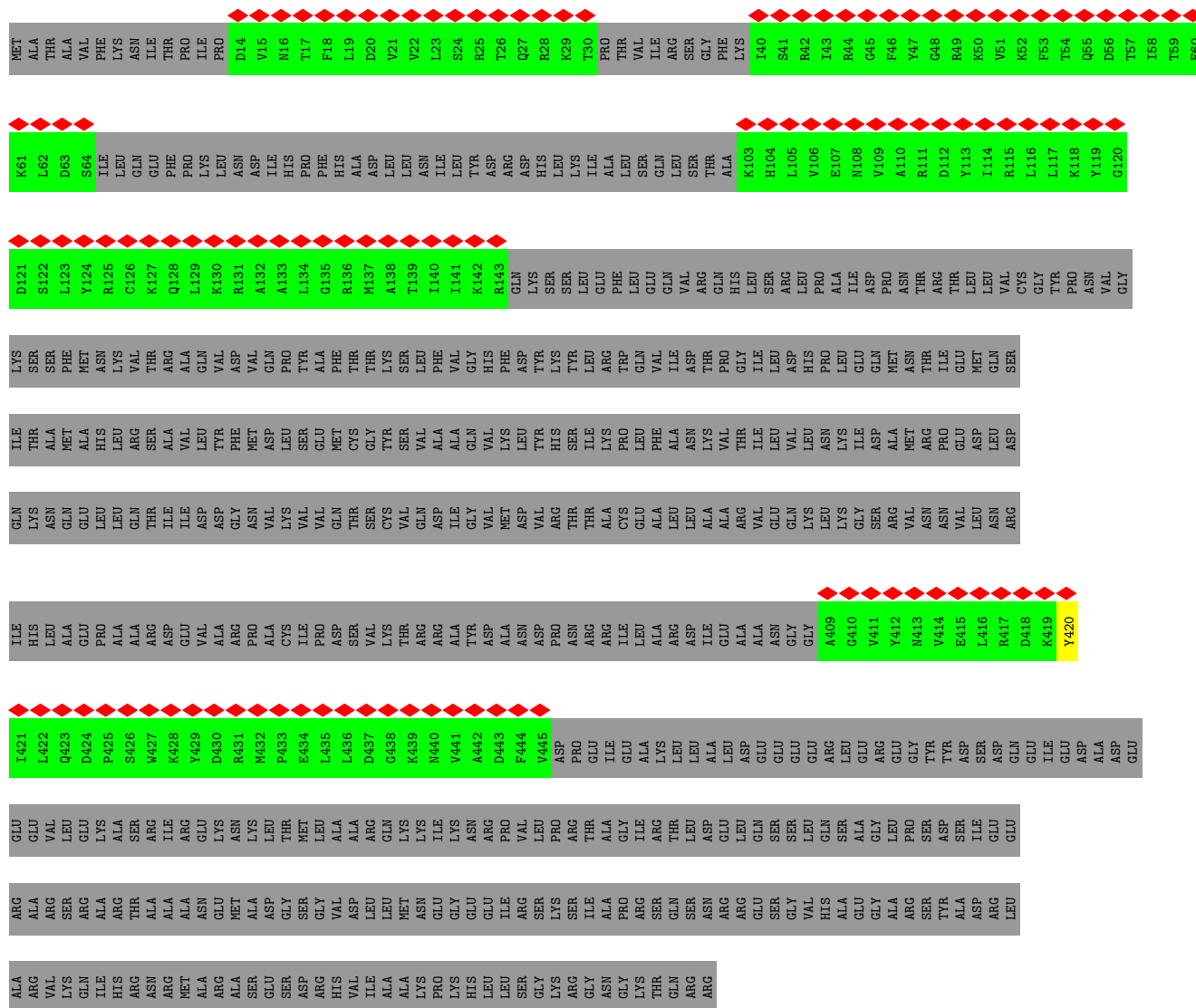


- Molecule 25: 60S ribosomal protein L26

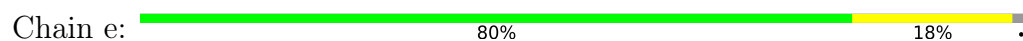




- Molecule 26: Probable nucleolar GTP-binding protein 1



- Molecule 27: 60S ribosomal protein L32-A



- Molecule 28: 60S ribosomal protein L33-B



ILE	LEU	ALA	GLY	GLY	GLY	PRO	ALA	LEU
VAL	CYS	VAL	THR	ILE	VAL	ASP	ASP	ASP
PRO	THR	THR	THR	THR	THR	THR	THR	THR
LEU	PHE	PHE	HIS	HIS	VAL	ASP	GLY	GLY
LYS	ASP	HIS	THR	VAL	ALA	ASP	ASP	ALA
ILE	LEU	PRO	THR	ALA	THR	PRO	ASP	PRO
LEU	ASP	THR	THR	THR	VAL	VAL	GLY	ARG
ARG	PHE	MET	VAL	VAL	THR	VAL	GLY	ARG
LEU	ASN	THR	THR	THR	THR	ALA	VAL	VAL
ASN	SER	PRO	TYR	SER	PRO	VAL	VAL	ARG
HIS	SER	LYS	LEU	GLY	LYS	VAL	ILE	THR
VAL	PRO	LEU	LEU	SER	THR	ALA	ILE	ARG
VAL	TYR	VAL	VAL	SER	SER	VAL	TRP	LYS
ASP	VAL	ALA	ILE	ILE	ILE	ASP	TRP	LEU
ASN	ASN	THR	GLN	THR	GLN	GLY	GLY	ASN
VAL	LEU	ARG	THR	THR	THR	THR	GLY	THR
GLY	ARG	VAL	THR	SER	SER	THR	GLY	PRO
VAL	HIS	VAL	VAL	THR	THR	THR	ARG	GLY
LEU	SER	ARG	VAL	HIS	THR	THR	ARG	SER
SER	SER	ILE	ARG	ARG	THR	THR	THR	THR
THR	ALA	THR	THR	THR	THR	THR	THR	THR
CYS	ALA	TYR	THR	ARG	THR	PRO	THR	PRO
TRP	LEU	ASN	GLY	GLY	GLY	LYS	LYS	PRO
HIS	ARG	LEU	ASP	ASP	THR	ILE	ILE	LYS
PRO	ASP	VAL	THR	THR	THR	ASP	THR	LEU
LYS	VAL	GLN	LEU	ALA	THR	ASP	THR	PRO
ALA	SER	LEU	SER	SER	THR	GLY	GLY	GLY
ALA	PRO	LEU	SER	SER	THR	ILE	ILE	ASN
GLY	LEU	THR	LEU	SER	THR	GLY	THR	PRO
GLY	CYS	VAL	GLY	GLN	GLN	LEU	ASP	THR
GLY	GLY	SER	VAL	ALA	ALA	PHE	SER	ARG
GLU	GLY	LYS	LYS	VAL	VAL	THR	THR	CYS
ILE	SER	TRP	TRP	LEU	THR	SER	GLU	THR
ARG	ASP	VAL	ILE	THR	THR	ALA	ASP	ASN
MET	ASP	SER	HIS	THR	SER	PRO	ALA	VAL
TRP	GLY	SER	SER	GLN	GLN	TYR	VAL	PHE
THR	ASP	LEU	SER	SER	THR	GLN	ASN	ILE
		SER	GLY	GLY	GLY	GLY	ASN	GLY
		VAL	SER	SER	SER	THR	THR	THR
		GLN	VAL	ARG	SER	THR	LYS	CYS
		VAL	HIS	THR	LEU	GLY	SER	LEU
		PHE	SER	ALA	ALA	THR	SER	GLY
		HIS	SER	SER	SER	ILE	HIS	VAL
		GLY	GLY	GLN	THR	LYS	THR	VAL
		ARG	ASP	THR	ARG	GLN	THR	ARG
		VAL	HIS	PRO	ARG	THR	THR	VAL
		TYR	VAL	PHE	GLY	GLY	SER	SER
		SER	ILE	SER	THR	LYS	ILE	VAL
		ASP	ILE	LYS	LYS	THR	ILE	VAL
		LEU	GLY	SER	SER	GLN	GLN	HIS
		LEU	THR	LYS	THR	THR	THR	VAL
		ALA	TYR	GLY	THR	LEU	LEU	SER
		ASN	ASP	SER	SER	GLN	GLY	GLY
		LEU	VAL	VAL	VAL	THR	THR	ASN
		THR	GLN	THR	THR	THR	THR	THR

- Molecule 33: Uncharacterized RNA-binding protein C1827.05c



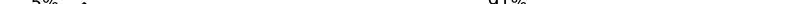
HIS PRO LYS ALA ALA SER PRO PRO VAL SER SER LYS SER SER LYS LYS LYS LYS HIS HIS LYS	F191	M121	◆	G129	P130	V131	L132	◆	R133	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210	H211	◆	GLU	L151	E152	F153	E154	S155	L156	D157	V158	A159	◆	V162	A163	E164	T165	M166	H167	◆	L170	L171	◆	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189	M190
	K192	M123			G129	P130	V131			L132	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210		H211	GLU	L151	E152	F153	E154	S155	L156	D157	V158		A159	V162	A163	E164	T165	M166		H167	L170		L171	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189
	ALA	D195	◆	G129	P130	V131	L132	◆	R133	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210	H211	◆	GLU	L151	E152	F153	E154	S155	L156	D157	V158	A159	◆	V162	A163	E164	T165	M166	H167	◆	L170	L171	◆	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189	M190
	ALA	D195			G129	P130	V131			L132	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210		H211	GLU	L151	E152	F153	E154	S155	L156	D157	V158		A159	V162	A163	E164	T165	M166		H167	L170		L171	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189
	VAL	P197	◆	G129	P130	V131	L132	◆	R133	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210	H211	◆	GLU	L151	E152	F153	E154	S155	L156	D157	V158	A159	◆	V162	A163	E164	T165	M166	H167	◆	L170	L171	◆	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189	M190
	VAL	P197			G129	P130	V131			L132	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210		H211	GLU	L151	E152	F153	E154	S155	L156	D157	V158		A159	V162	A163	E164	T165	M166		H167	L170		L171	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189
	LYS	F198	◆	G129	P130	V131	L132	◆	R133	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210	H211	◆	GLU	L151	E152	F153	E154	S155	L156	D157	V158	A159	◆	V162	A163	E164	T165	M166	H167	◆	L170	L171	◆	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189	M190
	LYS	F198			G129	P130	V131			L132	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210		H211	GLU	L151	E152	F153	E154	S155	L156	D157	V158		A159	V162	A163	E164	T165	M166		H167	L170		L171	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189
	LYS	R200	◆	G129	P130	V131	L132	◆	R133	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210	H211	◆	GLU	L151	E152	F153	E154	S155	L156	D157	V158	A159	◆	V162	A163	E164	T165	M166	H167	◆	L170	L171	◆	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189	M190
	LYS	R200			G129	P130	V131			L132	R200	I201	P202	H203	A204	T205	T206	A207	R208	L209	Q210		H211	GLU	L151	E152	F153	E154	S155	L156	D157	V158		A159	V162	A163	E164	T165	M166		H167	L170		L171	L175	G178	K179	V180	I181	P182	E183	D184	Q185	V186	H187	E188	N189

SER SER ALA GLU GLU PRO PRO SER SER LYS SER SER LYS VAL ASN GLN PRO LYS LYS LYS LYS VAL LEU ARG GLU GLU ASP LYS LYS VAL VAL LYS LYS ASP LYS ALA GLU GLU THR LYS GLU PHE PHE PRO GLY PHE GLY SER	SER	ASP	ASP	ASP	GLU	GLU	ASP	SER	PRO	LYS	ASN	ALA	LEU	VAL	ASN	THR	SER	ARG	GLN	LYS	ILE	LYS	NET	SER	VAL	ASP	LEU	GLY	ARG	GLU	GLU	ASP	LYS	LYS	LYS	VAL	SER	GLU	GLU	ILE	SER	ASN	LYS	ASN	GLN	GLY	LEU	GLN	HIS	VAL	ASP	ASN	GLY	GLY	GLY	ASP	LYS	GLU	PHE	PHE	PRO	GLY	PHE	GLY	GLY	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
	K102	K103	K104	G105	V106	L107	Y108	Y109	G110	L111	L112	P113	H114	G115	F116	Y117	E118	K119	Q120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					

- Molecule 34: Ribosome biogenesis protein nsa2

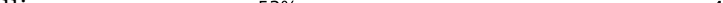
[illegible]

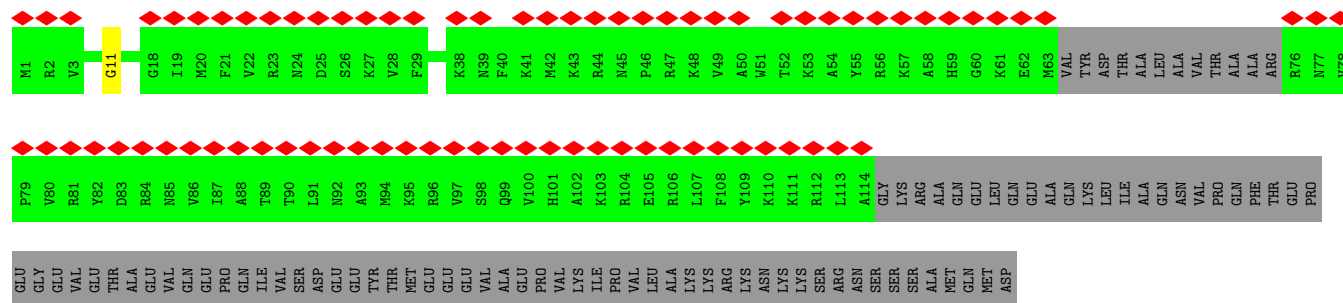
- Molecule 35: 60S ribosomal protein L7-A

Chain t:  5% 91%

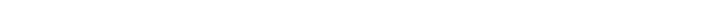


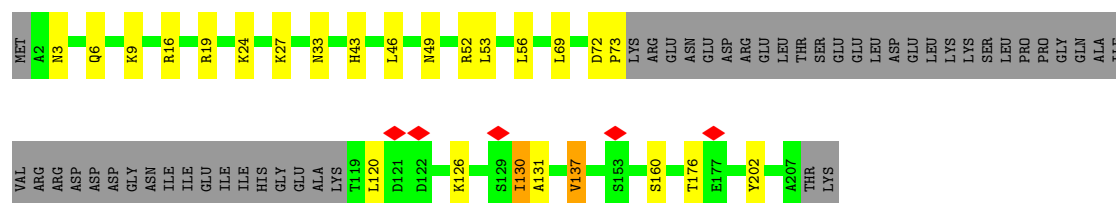
- Molecule 36: Ribosome biogenesis protein rlp24

Chain u:  41% 53% 47%



- Molecule 37: Nucleolar protein 16

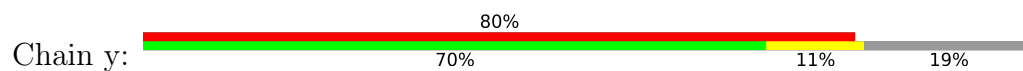
Chain v:  65% 11% 23%



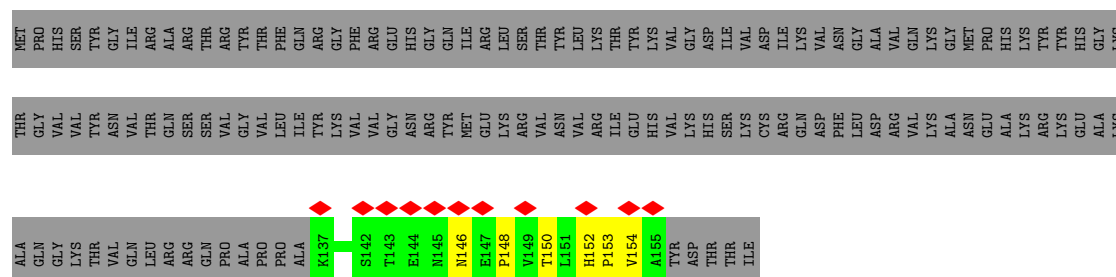
- Molecule 38: Brix domain-containing protein C4F8.04

Chain x: 81% 18%

- Molecule 39: Eukaryotic translation initiation factor 6



- Molecule 40: 60S ribosomal protein L21-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220000	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.774	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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	1	0.17	0/34328	0.24	0/53470
2	2	0.16	0/3084	0.21	0/4794
3	3	0.23	0/1627	0.28	0/2188
4	4	0.16	0/1817	0.27	0/2454
5	5	0.14	0/2739	0.31	0/3702
6	6	0.35	0/1287	0.64	0/1990
7	A	0.12	0/2096	0.29	0/2826
8	B	0.21	0/2694	0.49	0/3619
9	C	0.20	0/2618	0.31	0/3531
10	D	0.10	0/3052	0.26	0/4138
11	E	0.15	0/1356	0.30	0/1829
12	F	0.15	0/1982	0.24	0/2658
13	G	0.17	0/1291	0.29	0/1742
14	H	0.09	0/761	0.23	0/1054
15	J	0.05	0/443	0.17	0/618
16	K	0.07	0/1203	0.22	0/1675
17	L	0.22	0/960	0.30	0/1288
18	M	0.15	0/1024	0.32	0/1375
19	N	0.19	0/1436	0.26	0/1920
20	O	0.15	0/1515	0.30	0/2028
21	P	0.13	0/1161	0.26	0/1559
22	Q	0.18	0/1058	0.28	0/1421
23	S	0.13	0/1438	0.30	1/1932 (0.1%)
24	V	0.07	0/550	0.22	0/755
25	Y	0.18	0/1008	0.35	0/1341
26	b	0.05	0/590	0.16	0/816
27	e	0.20	0/1009	0.26	0/1345
28	f	0.18	0/859	0.29	0/1152
29	h	0.17	0/1008	0.33	0/1340
30	i	0.15	0/775	0.27	0/1030
31	j	0.12	0/575	0.22	0/761
32	m	0.12	0/738	0.23	0/997

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	o	0.24	0/1014	0.56	0/1366
34	r	0.05	0/247	0.16	0/342
35	t	0.22	0/218	0.33	0/287
36	u	0.05	0/504	0.17	0/700
37	v	0.13	0/1319	0.25	0/1769
38	x	0.15	0/2562	0.27	0/3432
39	y	0.08	0/971	0.22	0/1345
40	T	0.08	0/151	0.20	0/207
All	All	0.17	0/85068	0.28	1/122796 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	S	19	PRO	CA-N-CD	-5.27	104.62	112.00

There are no chirality outliers.

There are no planarity outliers.

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	1	30681	0	15431	362	0
2	2	2762	0	1399	25	0
3	3	1596	0	1645	28	0
4	4	1770	0	1788	39	0
5	5	2686	0	2745	56	0
6	6	1160	0	586	118	0
7	A	2057	0	2088	61	0
8	B	2641	0	2727	202	0
9	C	2572	0	2705	50	0
10	D	3001	0	2897	56	0
11	E	1328	0	1408	27	0
12	F	1944	0	2035	30	0
13	G	1273	0	1348	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	H	764	0	330	19	0
15	J	444	0	202	6	0
16	K	1205	0	528	10	0
17	L	942	0	1012	23	0
18	M	1007	0	1072	30	0
19	N	1406	0	1441	27	0
20	O	1487	0	1585	34	0
21	P	1139	0	1158	28	0
22	Q	1047	0	1142	22	0
23	S	1402	0	1451	38	0
24	V	554	0	272	21	0
25	Y	998	0	1090	18	0
26	b	594	0	258	1	0
27	e	995	0	1059	20	0
28	f	839	0	866	16	0
29	h	999	0	1092	22	0
30	i	768	0	835	25	0
31	j	563	0	578	13	0
32	m	725	0	660	16	0
33	o	992	0	939	78	0
34	r	249	0	117	0	0
35	t	216	0	219	19	0
36	u	506	0	226	2	0
37	v	1299	0	1347	19	0
38	x	2516	0	2524	38	0
39	y	974	0	448	17	0
40	T	147	0	140	9	0
41	j	1	0	0	0	0
All	All	80249	0	61393	1383	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 10.

The worst 5 of 1383 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)
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.30	0.95
8:B:58:ARG:HB2	8:B:356:LEU:HD22	1.49	0.93
1:1:543:G:H1	1:1:582:G:H22	1.15	0.92
8:B:211:GLN:HB2	8:B:285:ILE:HG13	1.50	0.92
6:6:59:A:H3'	6:6:60:A:H8	1.32	0.92

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	3	190/302 (63%)	183 (96%)	7 (4%)	0	100	100
4	4	208/217 (96%)	203 (98%)	5 (2%)	0	100	100
5	5	336/387 (87%)	314 (94%)	22 (6%)	0	100	100
7	A	250/295 (85%)	238 (95%)	10 (4%)	2 (1%)	16	50
8	B	328/388 (84%)	311 (95%)	16 (5%)	1 (0%)	36	70
9	C	325/363 (90%)	308 (95%)	17 (5%)	0	100	100
10	D	400/578 (69%)	391 (98%)	9 (2%)	0	100	100
11	E	168/195 (86%)	155 (92%)	13 (8%)	0	100	100
12	F	238/250 (95%)	231 (97%)	7 (3%)	0	100	100
13	G	161/259 (62%)	156 (97%)	5 (3%)	0	100	100
14	H	149/190 (78%)	141 (95%)	8 (5%)	0	100	100
15	J	87/333 (26%)	87 (100%)	0	0	100	100
16	K	239/373 (64%)	229 (96%)	9 (4%)	1 (0%)	30	65
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	120 (98%)	3 (2%)	0	100	100
19	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
20	O	183/197 (93%)	180 (98%)	3 (2%)	0	100	100
21	P	141/187 (75%)	135 (96%)	6 (4%)	0	100	100
22	Q	133/187 (71%)	127 (96%)	6 (4%)	0	100	100
23	S	164/176 (93%)	154 (94%)	10 (6%)	0	100	100
24	V	105/139 (76%)	99 (94%)	6 (6%)	0	100	100
25	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	b	112/642 (17%)	112 (100%)	0	0	100	100
27	e	122/127 (96%)	120 (98%)	2 (2%)	0	100	100
28	f	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
29	h	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
30	i	96/99 (97%)	92 (96%)	3 (3%)	1 (1%)	12	45
31	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
32	m	86/740 (12%)	80 (93%)	6 (7%)	0	100	100
33	o	125/276 (45%)	116 (93%)	7 (6%)	2 (2%)	7	34
34	r	46/260 (18%)	46 (100%)	0	0	100	100
35	t	21/249 (8%)	21 (100%)	0	0	100	100
36	u	98/192 (51%)	96 (98%)	2 (2%)	0	100	100
37	v	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	21	56
38	x	303/306 (99%)	300 (99%)	3 (1%)	0	100	100
39	y	192/244 (79%)	180 (94%)	12 (6%)	0	100	100
40	T	17/160 (11%)	17 (100%)	0	0	100	100
All	All	5992/9510 (63%)	5765 (96%)	219 (4%)	8 (0%)	49	80

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	K	153	ILE
7	A	118	ASN
7	A	248	PHE
33	o	197	PRO
37	v	130	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	169/271 (62%)	164 (97%)	5 (3%)	36	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	191/197 (97%)	184 (96%)	7 (4%)	30	64
5	5	301/345 (87%)	294 (98%)	7 (2%)	44	74
7	A	228/266 (86%)	225 (99%)	3 (1%)	61	81
8	B	282/326 (86%)	271 (96%)	11 (4%)	28	62
9	C	275/297 (93%)	271 (98%)	4 (2%)	57	80
10	D	288/505 (57%)	284 (99%)	4 (1%)	59	80
11	E	139/155 (90%)	134 (96%)	5 (4%)	31	65
12	F	201/210 (96%)	197 (98%)	4 (2%)	48	76
13	G	135/212 (64%)	132 (98%)	3 (2%)	45	74
17	L	97/167 (58%)	93 (96%)	4 (4%)	27	61
18	M	108/113 (96%)	103 (95%)	5 (5%)	24	58
19	N	146/176 (83%)	142 (97%)	4 (3%)	39	71
20	O	154/162 (95%)	152 (99%)	2 (1%)	61	81
21	P	118/149 (79%)	115 (98%)	3 (2%)	42	72
22	Q	116/159 (73%)	108 (93%)	8 (7%)	14	45
23	S	149/154 (97%)	147 (99%)	2 (1%)	61	81
25	Y	110/111 (99%)	104 (94%)	6 (6%)	19	53
27	e	106/107 (99%)	105 (99%)	1 (1%)	70	85
28	f	89/91 (98%)	87 (98%)	2 (2%)	45	74
29	h	106/107 (99%)	104 (98%)	2 (2%)	50	76
30	i	79/84 (94%)	69 (87%)	10 (13%)	4	20
31	j	58/71 (82%)	55 (95%)	3 (5%)	21	55
32	m	76/659 (12%)	76 (100%)	0	100	100
33	o	95/246 (39%)	89 (94%)	6 (6%)	16	48
35	t	22/223 (10%)	22 (100%)	0	100	100
37	v	138/181 (76%)	135 (98%)	3 (2%)	45	74
38	x	272/273 (100%)	264 (97%)	8 (3%)	37	70
40	T	17/139 (12%)	17 (100%)	0	100	100
All	All	4265/6156 (69%)	4143 (97%)	122 (3%)	38	70

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	M	14	VAL
33	o	208	ARG
22	Q	23	VAL
33	o	203	HIS
38	x	175	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
33	o	189	ASN
37	v	21	ASN
9	C	223	ASN
9	C	201	HIS
38	x	13	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1408/3497 (40%)	354 (25%)	23 (1%)
2	2	126/165 (76%)	25 (19%)	0
6	6	54/300 (18%)	36 (66%)	3 (5%)
All	All	1588/3962 (40%)	415 (26%)	26 (1%)

5 of 415 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	11	A
1	1	14	U
1	1	26	A
1	1	28	G
1	1	32	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1159	U
1	1	3189	C
6	6	71	U
1	1	1389	A
1	1	3217	U

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 1 ligands modelled in this entry, 1 is 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-24420. 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](#)

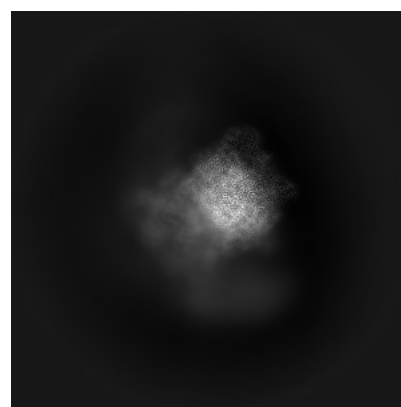
6.1.1 Primary map



X



Y

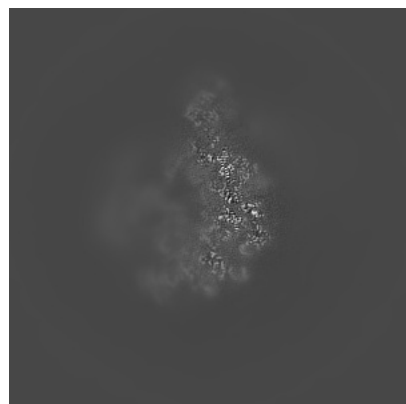


Z

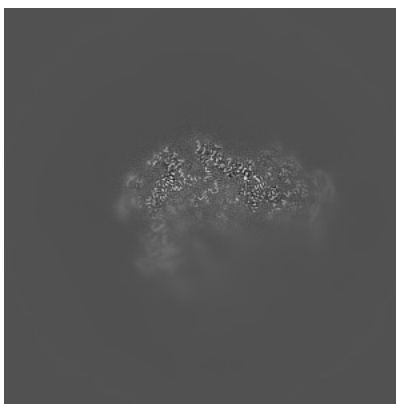
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

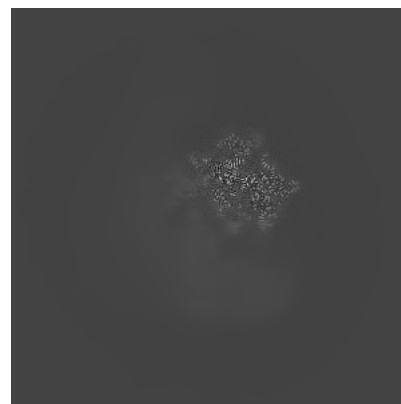
6.2.1 Primary map



X Index: 256



Y Index: 256

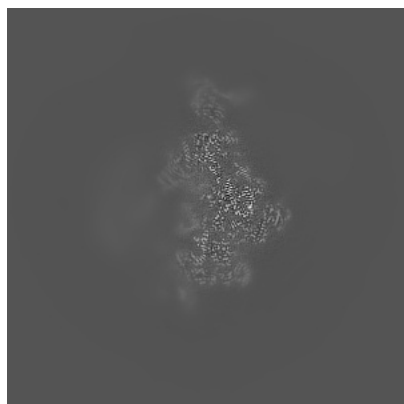


Z Index: 256

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

6.3 Largest variance slices [i](#)

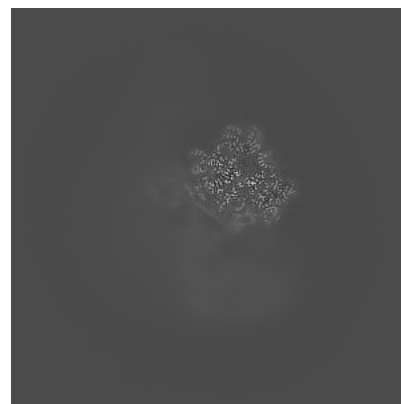
6.3.1 Primary map



X Index: 282



Y Index: 274

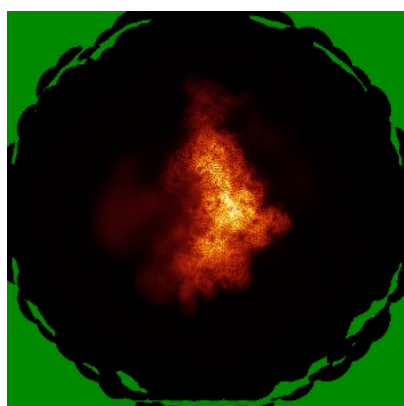


Z Index: 249

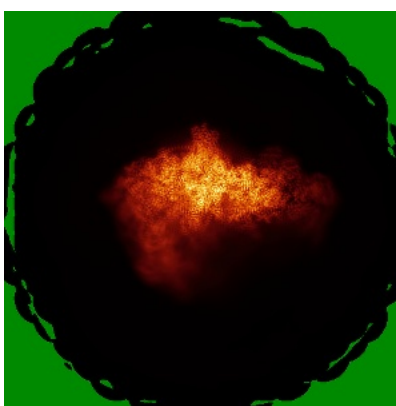
The images above show the largest variance slices of the map in three orthogonal directions.

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

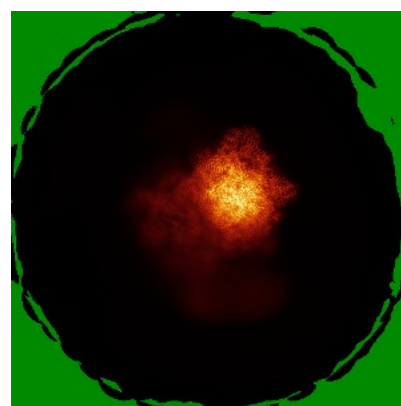
6.4.1 Primary map



X



Y

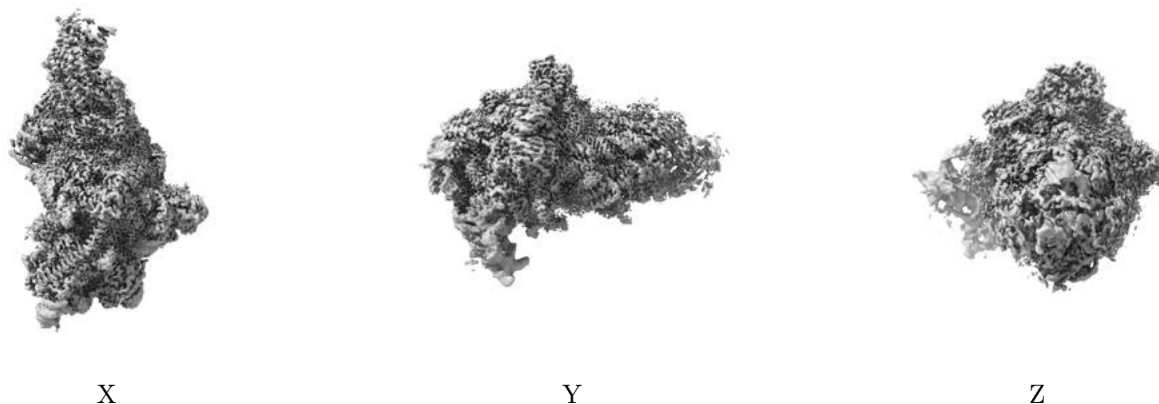


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

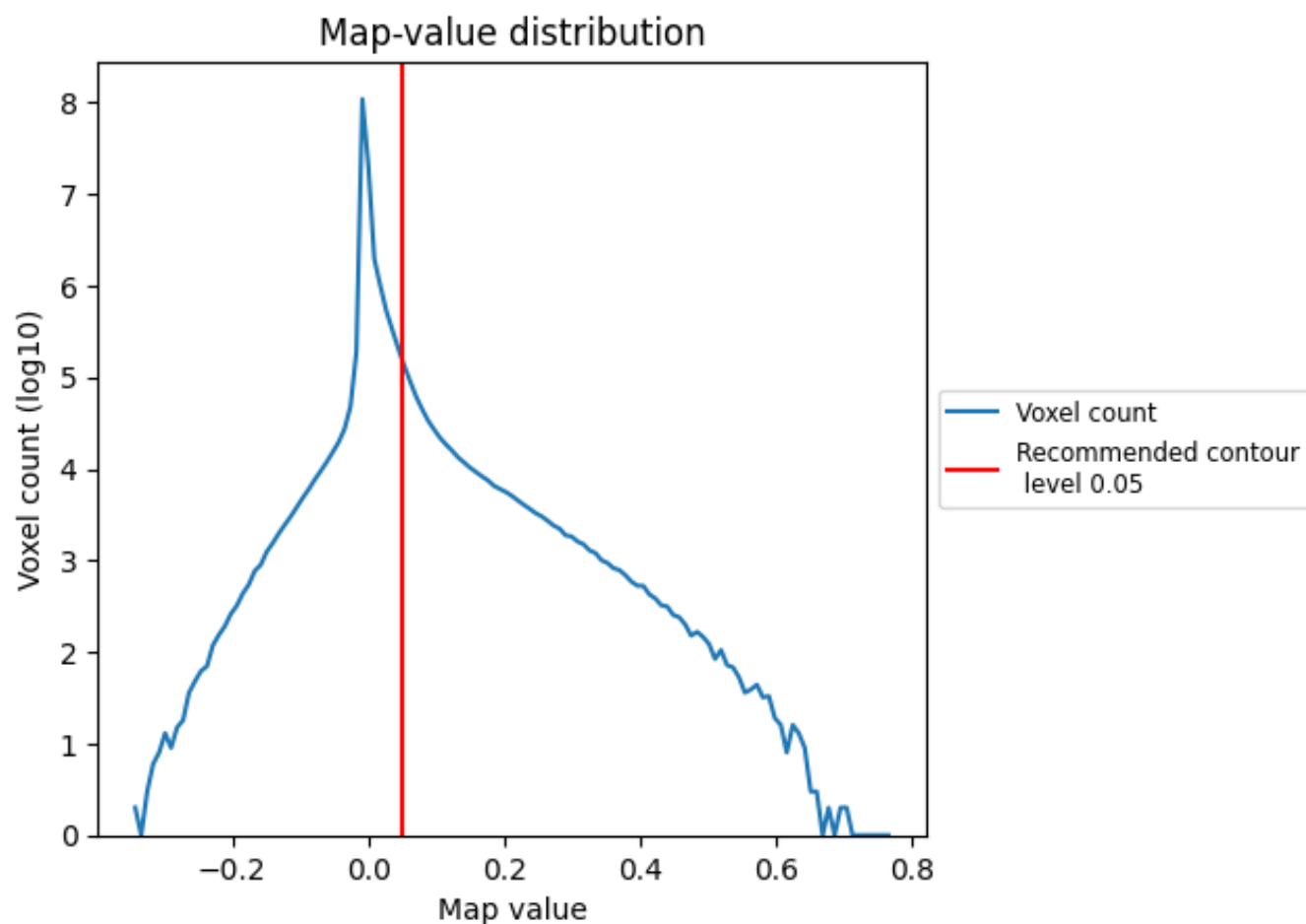
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

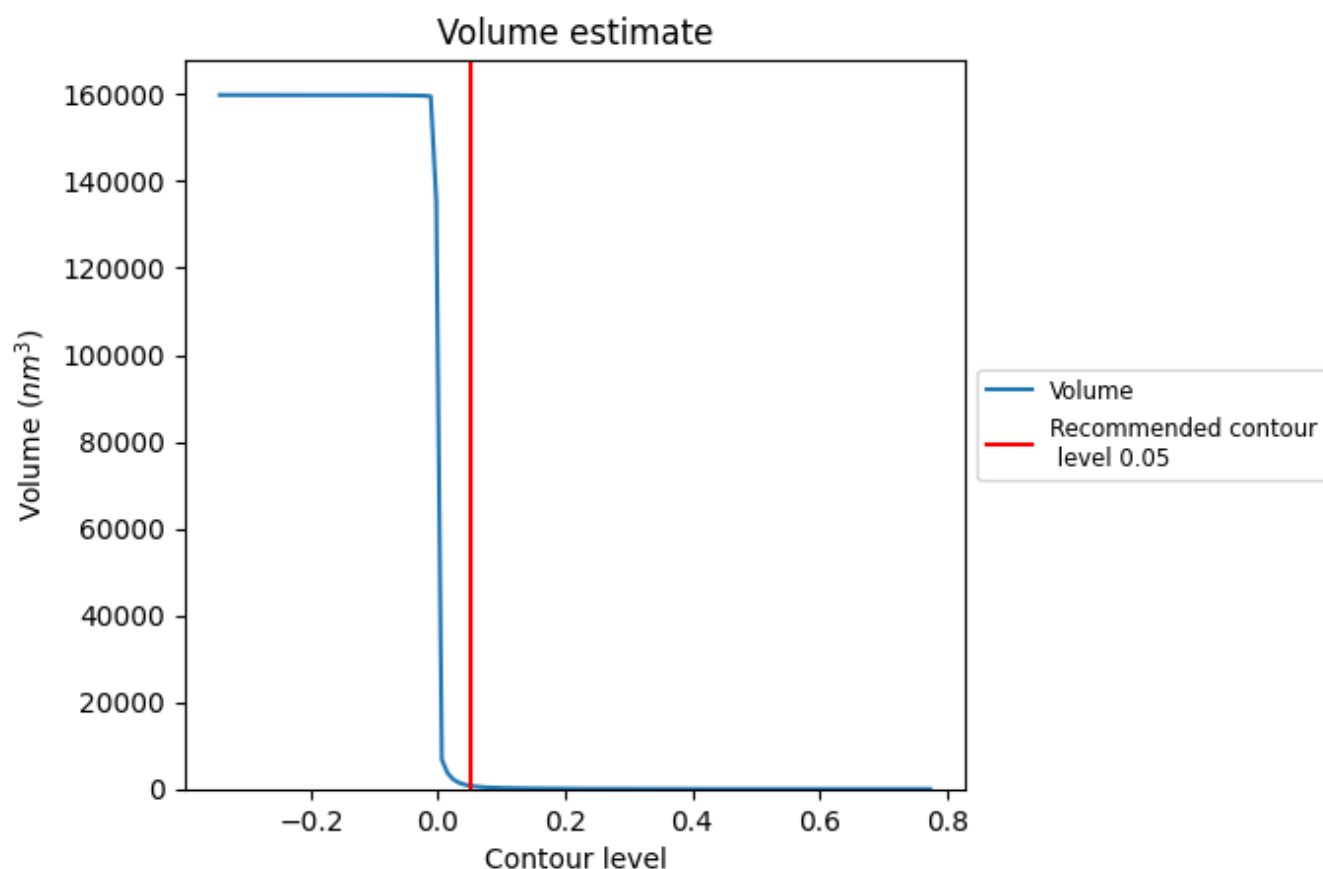
This section contains the results of statistical analysis of the map.

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.

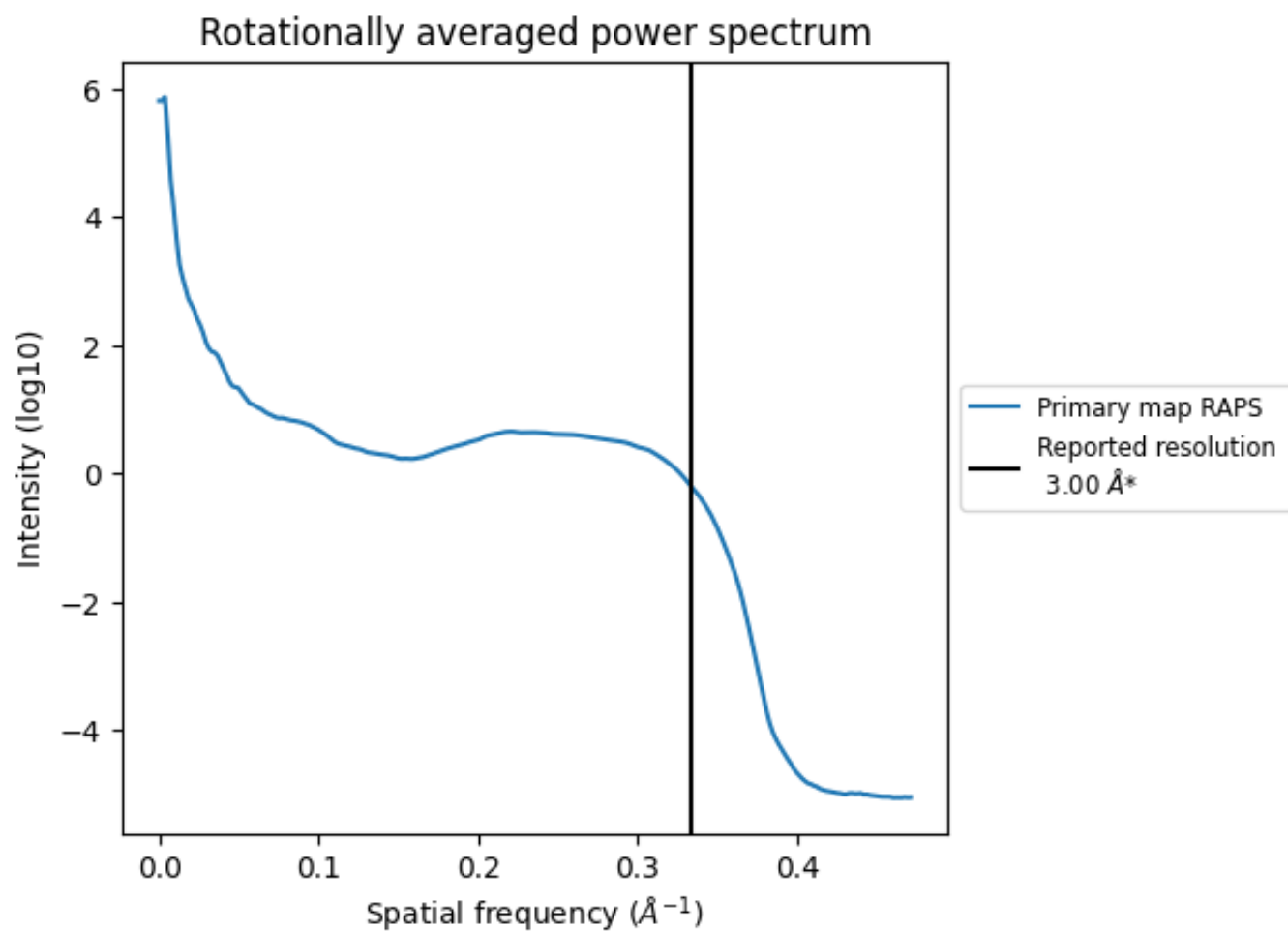
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 754 nm³; this corresponds to an approximate mass of 681 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 0.333 Å⁻¹

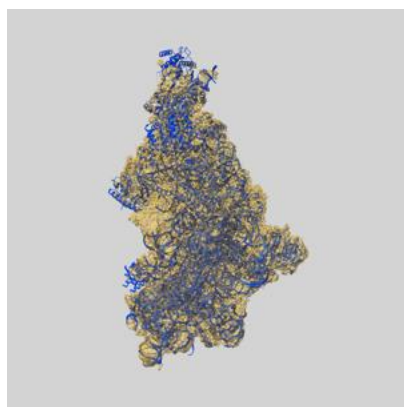
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

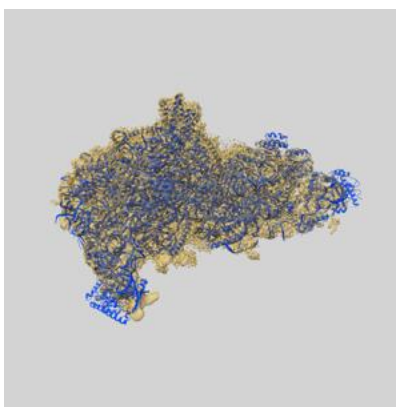
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24420 and PDB model 8EUY. Per-residue inclusion information can be found in section [3](#) on page [12](#).

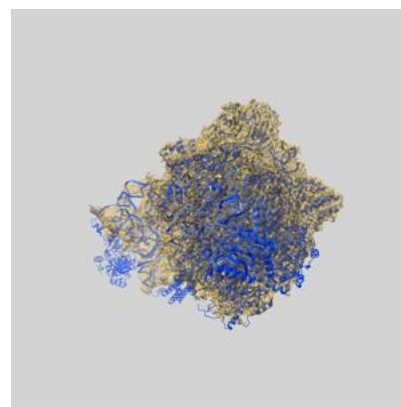
9.1 Map-model overlay [i](#)



X



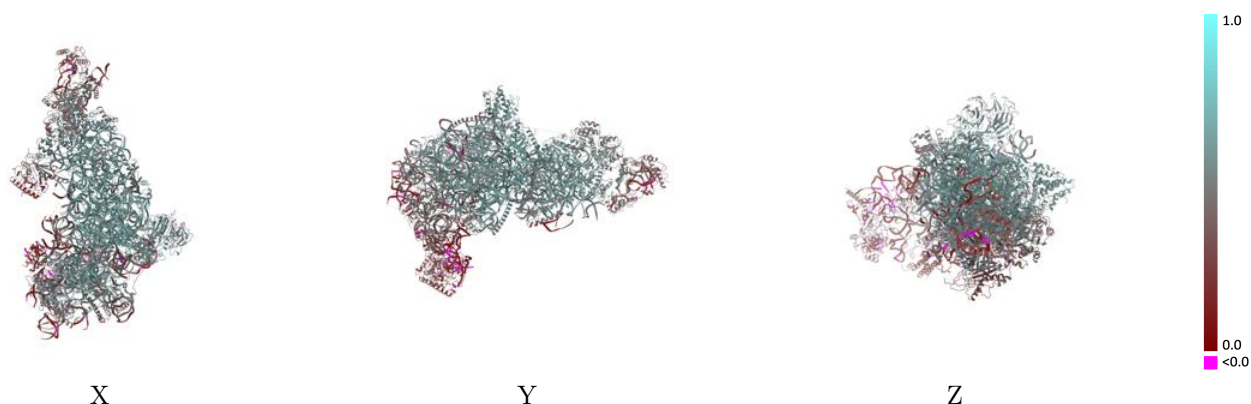
Y



Z

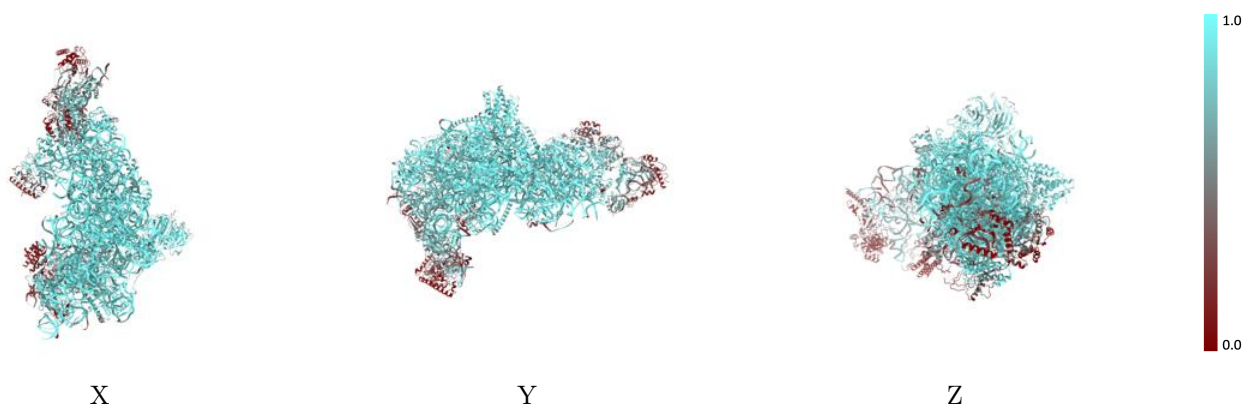
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



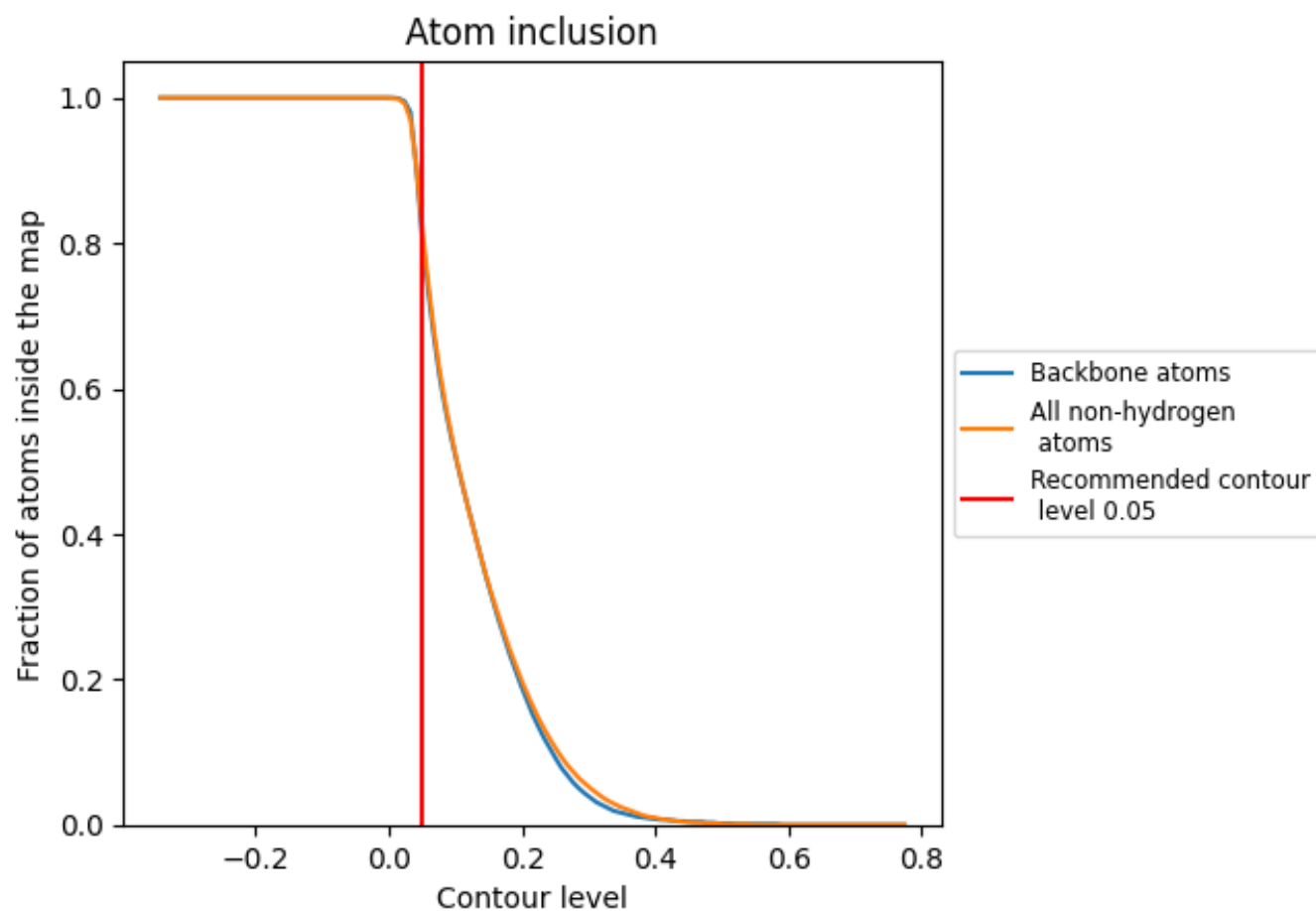
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 82% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8220	 0.4810
1	 0.8910	 0.4590
2	 0.9300	 0.5240
3	 0.9480	 0.6070
4	 0.9350	 0.5900
5	 0.8960	 0.5460
6	 0.4690	 0.1990
A	 0.7330	 0.3900
B	 0.6590	 0.2860
C	 0.9790	 0.6230
D	 0.5450	 0.4790
E	 0.9140	 0.5420
F	 0.9440	 0.5790
G	 0.9390	 0.5790
H	 0.2280	 0.3100
J	 0.3740	 0.2880
K	 0.4270	 0.3990
L	 0.9760	 0.6280
M	 0.9220	 0.5050
N	 0.9870	 0.6140
O	 0.9010	 0.4930
P	 0.8760	 0.5360
Q	 0.9590	 0.5920
S	 0.8350	 0.4790
T	 0.3740	 0.3860
V	 0.0670	 0.1860
Y	 0.9750	 0.6070
b	 0.0100	 0.2360
e	 0.9840	 0.6280
f	 0.9840	 0.6140
h	 0.8530	 0.5270
i	 0.9410	 0.5740
j	 0.9520	 0.5980
m	 0.7230	 0.4810
o	 0.4580	 0.3660



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Chain	Atom inclusion	Q-score
r	 0.0600	 0.2490
t	 0.5120	 0.4230
u	 0.2330	 0.2230
v	 0.8930	 0.5610
x	 0.9300	 0.5810
y	 0.0180	 0.2290