



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:31 AM UTC

PDB ID : 8FKQ / pdb_00008fkq
EMDB ID : EMD-29253
Title : Human nucleolar pre-60S ribosomal subunit (State A2)
Authors : Vanden Broeck, A.; Klinge, S.
Deposited on : 2022-12-21
Resolution : 2.76 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

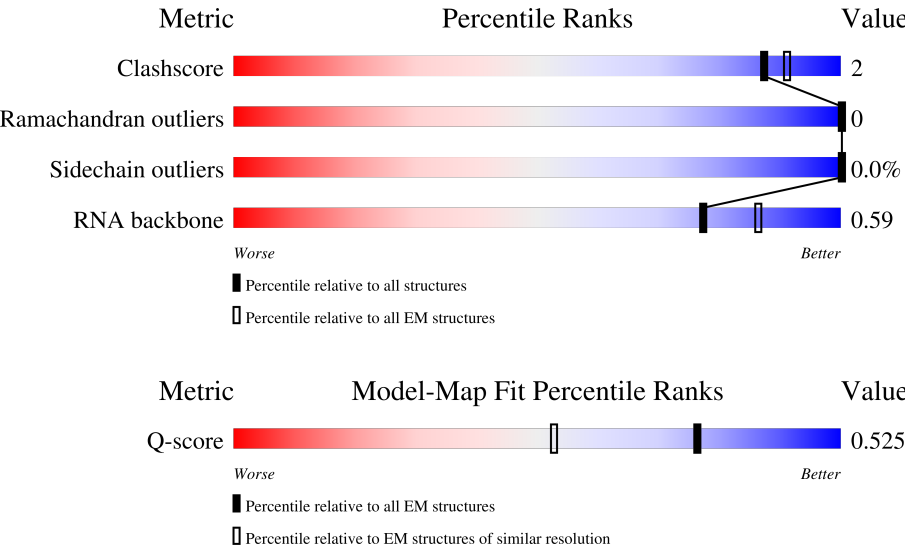
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.76 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.



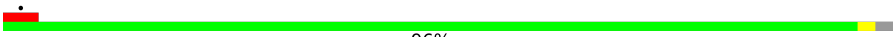
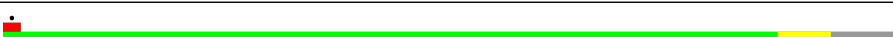
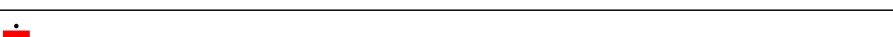
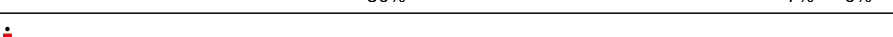
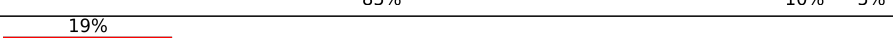
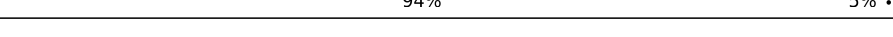
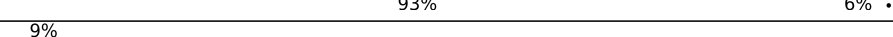
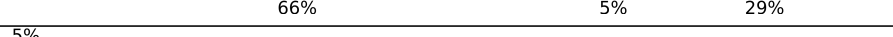
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10642 (2.26 - 3.26)

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	L1	157	
2	L2	1167	
3	L3	5070	

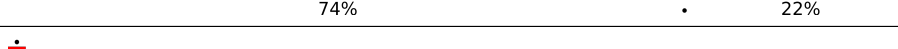
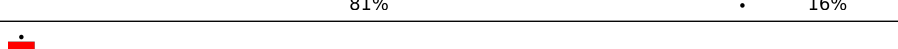
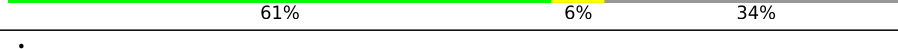
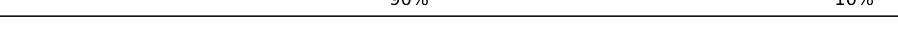
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Mol	Chain	Length	Quality of chain
4	L6	211	
5	L7	203	
6	L8	215	
7	L9	204	
8	LA	184	
9	LB	188	
10	LC	176	
11	LE	160	
12	LG	140	
13	LH	156	
14	LI	145	
15	LK	148	
16	LL	137	
17	LN	403	
18	LQ	135	
19	LS	123	
20	LT	110	
21	LU	105	
22	LW	97	
23	NE	361	
24	NG	282	
25	NN	473	
26	SA	427	
27	SC	288	
28	SD	248	

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Mol	Chain	Length	Quality of chain
29	SE	266	
30	SH	293	
31	SI	255	
32	SJ	847	
33	SK	245	
34	SL	490	
35	SM	588	
36	SN	306	
37	SO	353	
38	SR	634	
39	SS	746	
40	ST	365	
41	SV	163	
42	SW	670	
43	SZ	178	

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 93805 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 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L1	150	Total	C	N	O	P	0	0
			3189	1423	561	1055	150		

- Molecule 2 is a RNA chain called ITS2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L2	69	Total	C	N	O	P	0	0
			1468	653	263	483	69		

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L3	1565	Total	C	N	O	P	0	0
			33557	14935	6157	10900	1565		

- Molecule 4 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L6	114	Total	C	N	O	S	0	0
			936	583	206	146	1		

- Molecule 5 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L7	184	Total	C	N	O	S	0	0
			1507	976	290	237	4		

- Molecule 6 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L8	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 7 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L9	183	Total	C	N	O	S	1	0
			1553	979	327	243	4		

- Molecule 8 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	121	Total	C	N	O	S	0	0
			981	616	182	176	7		

- Molecule 9 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	151	Total	C	N	O	S	0	0
			1223	768	247	203	5		

- Molecule 10 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	173	Total	C	N	O	S	0	0
			1431	908	281	231	11		

- Molecule 11 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	108	Total	C	N	O		0	0
			702	430	138	134			

- Molecule 12 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LG	114	Total	C	N	O	S	0	0
			844	532	155	152	5		

- Molecule 13 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LH	20	Total	C	N	O		0	0
			146	95	29	22			

- Molecule 14 is a protein called 60S ribosomal protein L26.

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

- Molecule 15 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LK	108	Total	C	N	O	S	0	0
			642	388	137	115	2		

- Molecule 16 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LL	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 17 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LN	377	Total	C	N	O	S	0	0
			3044	1937	566	527	14		

- Molecule 18 is a protein called 60S ribosomal protein L32.

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

- Molecule 19 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 20 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 21 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	102	Total	C	N	O	S	1	0
			840	526	180	129	5		

- Molecule 22 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LW	69	Total	C	N	O	S	0	0
			563	346	126	86	5		

- Molecule 23 is a protein called Surfeit locus protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	NE	156	Total	C	N	O	S	0	0
			1331	810	293	226	2		

- Molecule 24 is a protein called RRP15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	NG	89	Total	C	N	O	S	0	0
			738	456	145	133	4		

- Molecule 25 is a protein called Suppressor of SWI4 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	NN	244	Total	C	N	O	S	0	0
			1950	1230	371	338	11		

- Molecule 26 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SA	329	Total	C	N	O	S	0	0
			2645	1675	522	435	13		

- Molecule 27 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SC	211	Total	C	N	O	S	0	0
			1692	1090	320	278	4		

- Molecule 28 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SD	212	Total	C	N	O	S	0	0
			1755	1127	334	285	9		

- Molecule 29 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SE	186	Total	C	N	O	S	0	0
			1498	951	290	253	4		

- Molecule 30 is a protein called MKI67 FHA domain-interacting nucleolar phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SH	150	Total	C	N	O	S	0	0
			1267	819	224	220	4		

- Molecule 31 is a protein called 60S ribosomal protein L7-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SI	199	Total	C	N	O	S	1	0
			1661	1076	311	270	4		

- Molecule 32 is a protein called pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SJ	72	Total	C	N	O		0	0
			609	385	114	110			

- Molecule 33 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SK	226	Total	C	N	O	S	0	0
			1721	1070	296	343	12		

- Molecule 34 is a protein called Ribosomal L1 domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SL	243	Total	C	N	O	S	0	0
			1960	1254	344	356	6		

- Molecule 35 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SM	437	Total	C	N	O	S	0	0
			3452	2229	603	609	11		

- Molecule 36 is a protein called Probable rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SN	168	Total	C	N	O	S	0	0
			1308	821	247	235	5		

- Molecule 37 is a protein called Ribosome biogenesis protein BRX1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SO	296	Total	C	N	O	S	0	0
			2460	1583	446	416	15		

- Molecule 38 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SR	77	Total	C	N	O	S	0	0
			642	411	107	122	2		

- Molecule 39 is a protein called Ribosome biogenesis protein BOP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	SS	235	Total	C	N	O	P	S	0	0
			1955	1238	348	360	2	7		

- Molecule 40 is a protein called Ribosome biogenesis regulatory protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ST	36	Total	C	N	O	S	0	0
			263	160	51	51	1		

- Molecule 41 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SV	137	Total	C	N	O	S	0	0
			1171	745	227	189	10		

- Molecule 42 is a protein called ATP-dependent RNA helicase DDX18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SW	445	Total	C	N	O	S	0	0
			3560	2288	609	646	17		

- Molecule 43 is a protein called Nucleolar protein 16.

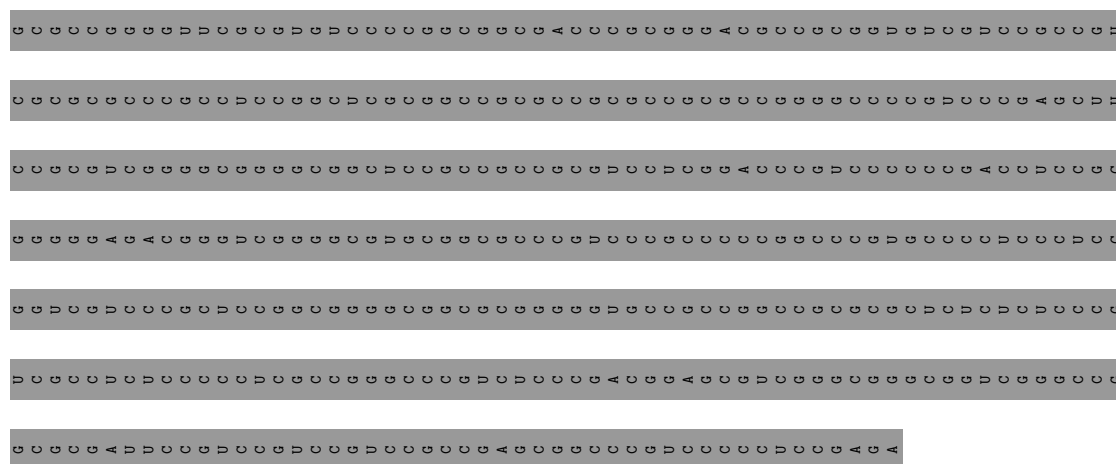
Mol	Chain	Residues	Atoms					AltConf	Trace
43	SZ	160	Total	C	N	O	S	0	0
			1338	835	260	238	5		

- Molecule 44 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

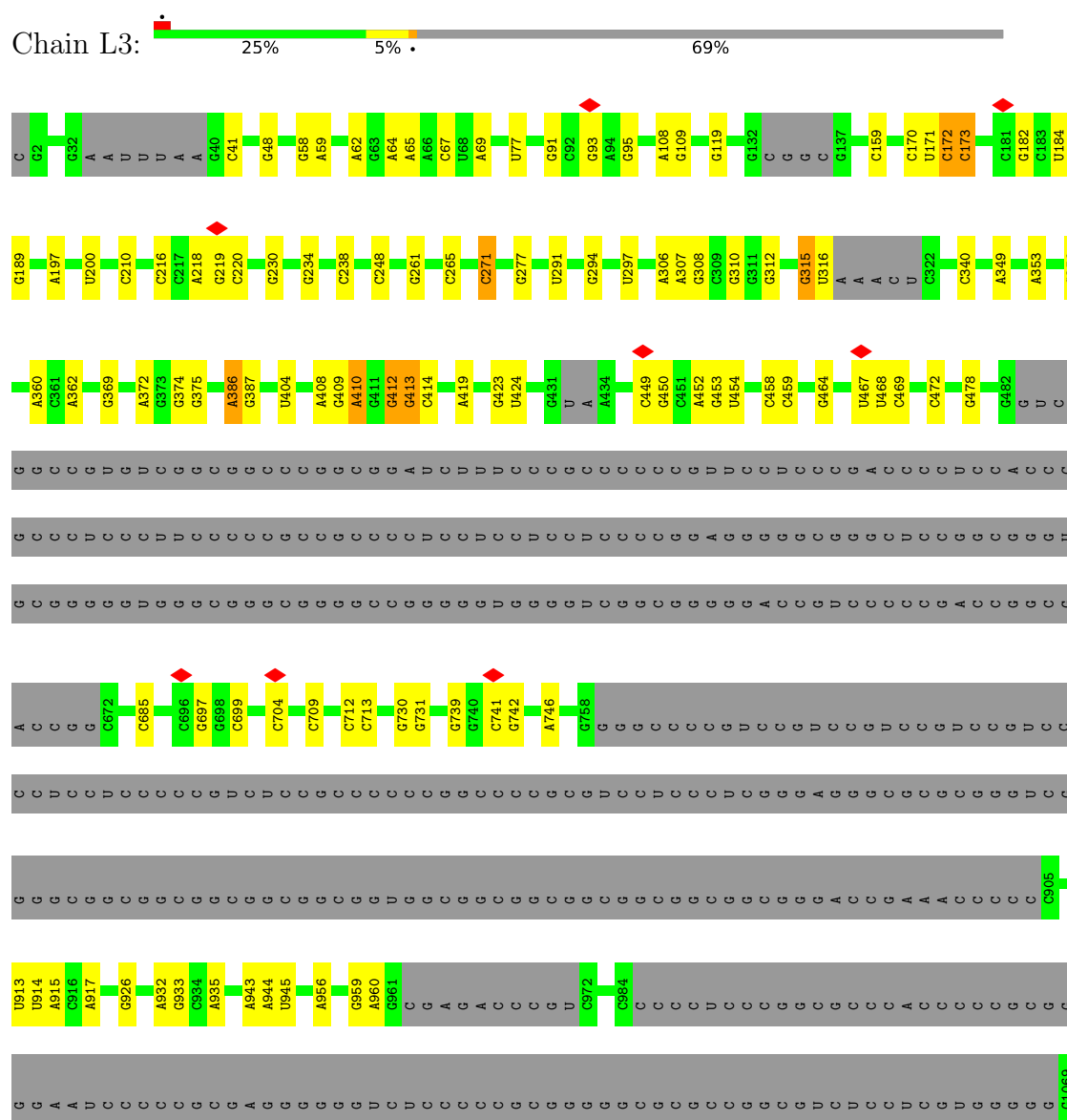
Mol	Chain	Residues	Atoms		AltConf
44	L1	4	Total	Mg	0
			4	4	
44	L2	1	Total	Mg	0
			1	1	
44	L3	42	Total	Mg	0
			42	42	
44	L9	1	Total	Mg	0
			1	1	
44	LQ	1	Total	Mg	0
			1	1	
44	LT	1	Total	Mg	0
			1	1	
44	SA	1	Total	Mg	0
			1	1	

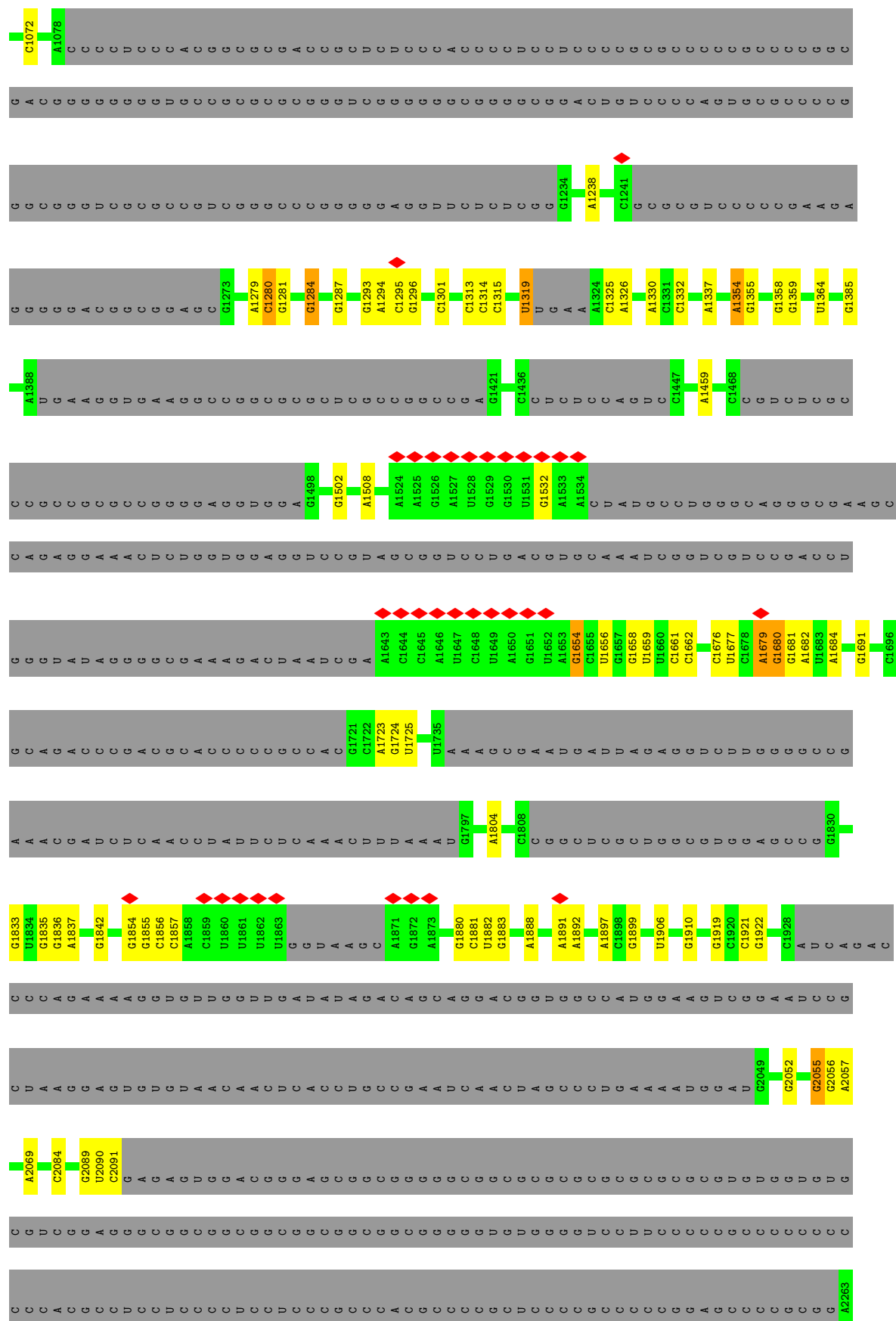
- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
45	LW	1	Total	Zn	0
			1	1	
45	SV	1	Total	Zn	0
			1	1	



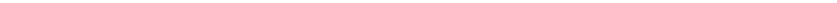
• Molecule 3: 28S rRNA

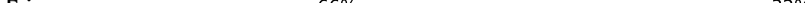






MET
G2
F54
N40
R65
R108
T122
F123
D124
K132
F152
GLY
LYS
ALA
PRO
GLY
THR
PRO
HIS
SER
HIS
THR
LYS
PRO
TYR
VAL
ARG
SER
LYS
GLY
ARG
PHE
GLU
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ARG
GLY
TYR
LYS
ASN

- Chain LC:  96%

- Chain LE: 

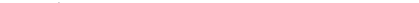
Sequence logo for the 1000bp upstream region of the human POU3F1 gene. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows amino acid positions from -1000 to +1000. The logo is divided into two main sections: a grey section for positions -1000 to -133 and a green section for positions -133 to +1000. The green section contains several red diamond markers indicating specific positions: K87, R92, I93, K115, A119, K120, E121, V126, I154, P155, K43, K55, Q69, H70, A71, K78, Q79, V80, K81, Q82, K83, and K93. The sequence of amino acids is shown below the logo, with the green section containing a large number of amino acids, many of which are repeated.

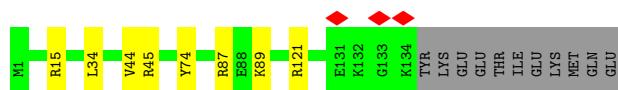
- Chain LG:  7% 79% 19%

MET	SER	LYS	ARG	GLY	ARG	GLY	GLY	SER	SER	GLY	ALA	LYS	PHE	ARG	ILE	SER	LEU	G19	G44	ILE	LYS	GLY	ARG	LEU	ASN	ARG	P53	K67	G68	K69	P70	E71	L72	R73	K74	K75	R85	V94	P95	L96	E99	L100
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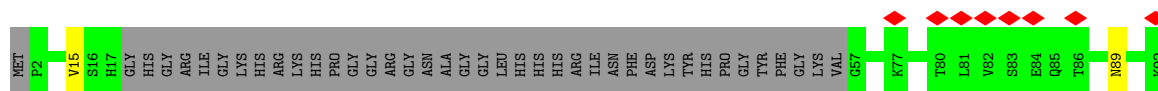
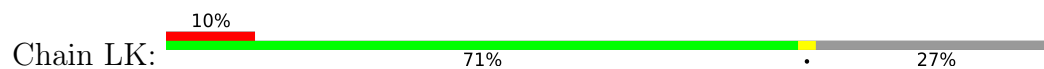
- Chain LH: 13% 87%

ASP	GLY	GLU	LYS	LYS	ALA	TYR	VAL	ARG	LEU	LEU	ALA	PRO	ASP	THR	GLU	SER	ASP	ALA	LEU	ASP	VAL	ALA	ASN	LYS	ILE	ILE	ILE	ILE																																		
LEU	ASP	HIS	TYR	ALA	ILE	ILE	PHE	PRO	LEU	THR	THR	THR	THR	THR	GLU	SER	SER	MET	LYS	LYS	ILE	GLU	ASP	ASN	ASN	THR	LEU	VAL	PHE	ILE	VAL	ASP	VAL	LYS	ALA	ASN	LYS	HIS	GLN	ILE	LYS	GLN	ASP	ILE	ILE	VAL	ALA	LYS	LEU	TYR	LEU	LYS	VAL	VAL	ASN	VAL	THR	THR	THR	ARG	ILE	PRO
MET	ALA	PRO	LYS	ALA	LYS	GLU	ALA	PRO	ALA	PRO	PRO	PRO	PRO	PRO	K14	K15	E16	K23	K30	G31	V32	H33	SER	HIS	LYS	LYS	LYS	LYS	ILE	ARG	THR	SER	PRO	THR	PHE	ARG	ARG	PRO	LYS	THR	LEU	ARG	LEU	ARG	ARG	GLN	PRO	LYS	TYR	PRO	ARG	LYS	SER	ALA	PRO	ARG	ARG	ASN	TYR			

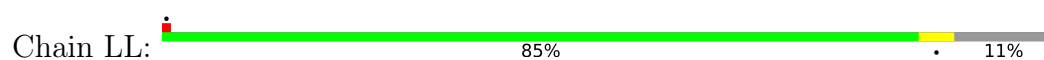
- Chain LI:  87% 6% 8%



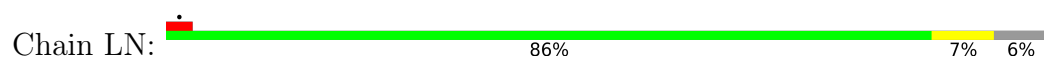
- Molecule 15: 60S ribosomal protein L27a



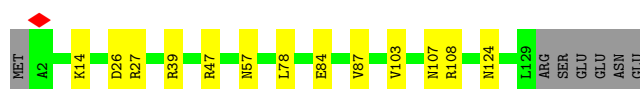
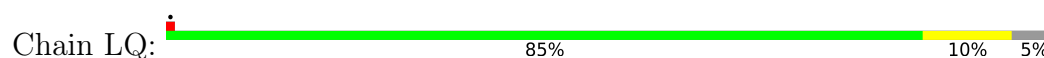
- Molecule 16: 60S ribosomal protein L28



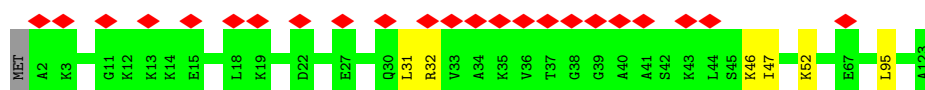
- Molecule 17: 60S ribosomal protein L3



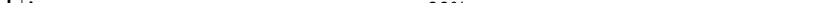
- Molecule 18: 60S ribosomal protein L32



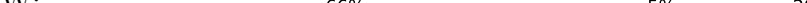
- Molecule 19: 60S ribosomal protein L35



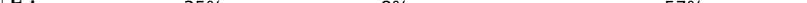
- Molecule 20: 60S ribosomal protein L35a

- Chain LU:  9% 90% 8%

Bar chart showing the number of mutations for various amino acids. The y-axis is labeled 'MET' and ranges from 0 to 10. The x-axis lists amino acids: A2, L3, R4, M7, G10, L11, N12, K13, E46, V47, C48, G49, F50, Y53, V77, R82, V93, M97, K103, LYS, and ASP. The bars are colored green for A2, L3, R4, M7, G10, L11, N12, K13, E46, V47, C48, G49, F50, Y53, V77, R82, V93, M97, and K103. The bars for LYS and ASP are grey. Red diamonds are placed above the bars for A2, L3, R4, M7, G10, L11, N12, K13, E46, V47, C48, G49, F50, Y53, V77, R82, V93, M97, and K103.

- Chain LW: 

[illegible]

- Chain NE: 

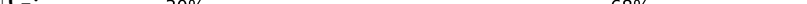
MET	ALA	SER	LEU	LEU	ALA	ASP	LYS	TYR	GLN	SER	LEU	ALA	ALA	LYS	LYS	ILE	CYS	HIS	SER	PRO	GLU	GLN	GLN	ALA	ARG	THR	ALA	GLY	LYS	THR	GLN	GLY	PRO	PRO	LYS	LYS	LYS	ARG	LYS	THR	GLN	LYS	LYS	PHE	ARG	LYS	ARG	ARG	GLU	GLU
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LYS	ALA	ALA	GLU	HIS	LYS	ALA	LYS	SER	LEU	GLY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

VAL	GLU	ALA	THR	PRO	GLY	GLU	ALA	CYS	THR	GLU	PRO	ARG	GLY	GLU	PRO	P196	K202	V205	SER	GLU	ASP	GLU	PRO	ALA	S212	R216	R221	V224	R227	L228	T232	G233	L250	L253	D257	L264	E265	A266	K267	K268	W270	T271	N272	L273	L274	Y275	K276
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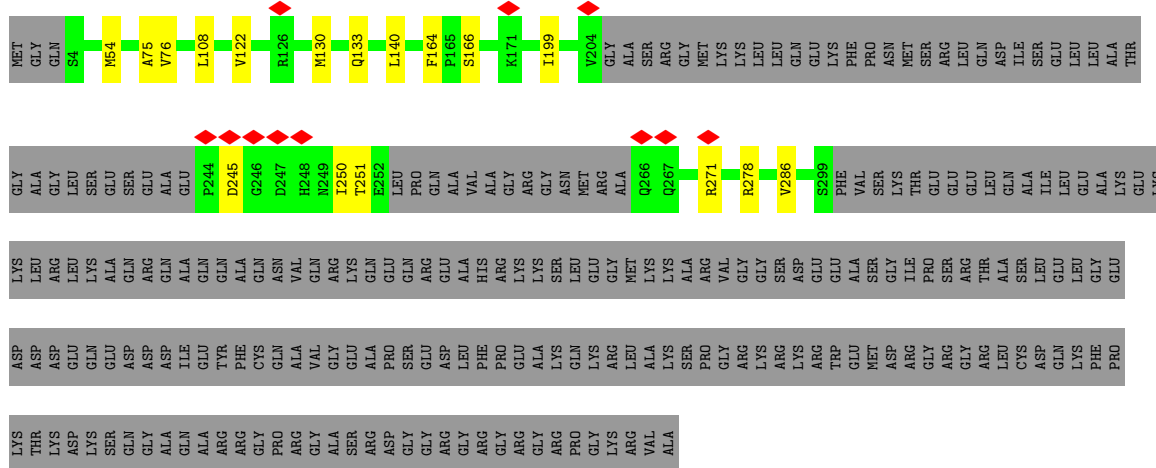
V280	K281	1282	R283	R310	R321	R332	R336	R337	E338	R339	R340	R343	A344	R345	K346	K347	C348	R349	I350	L351	P352	Q353	D354	L355	E356	R357	ALA	GLY	LEU	VAL
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----

- Chain NG:  13% 30% 68%

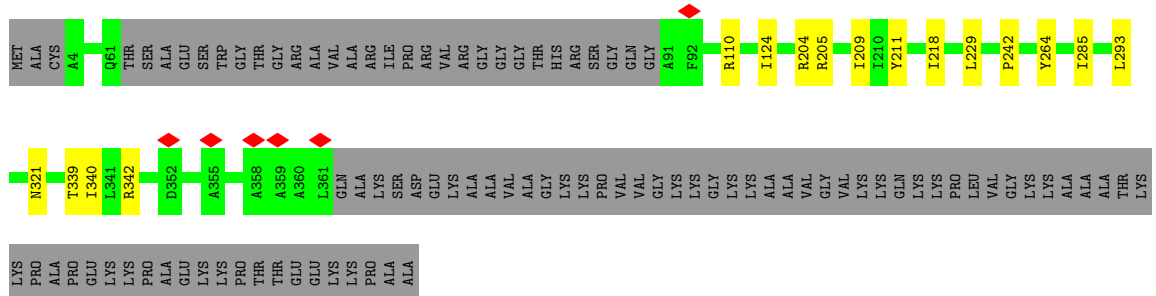
[illegible]

ASP	ALA	ALA	ILE	GLU	ALA	ASP	SER	GLU	GLY	ASP	ALA	GLU	PRO	CYS	ASP	LYS	ASN	GLU	GLU	ASN	VAL	SER	GLY	THR	ASN	MET	GLY	TRP	ASP	ALA	ALA	MET	LYS	VAL	LEU	LYS	LYS	THR	PRO	GLU	SER	LYS	PRO	THR	ILE	LEU	VAL	LYS	ASN	LYS	GLY
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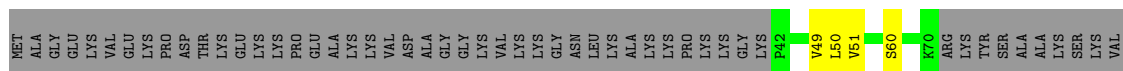
- Molecule 25: Suppressor of SWI4 1 homolog

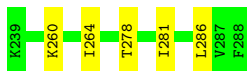


- Molecule 26: 60S ribosomal protein L4



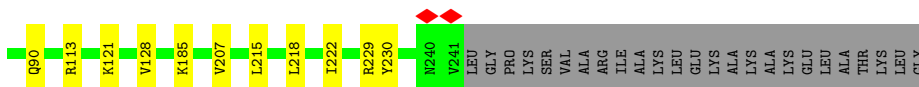
- Molecule 27: 60S ribosomal protein L6



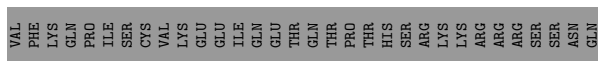
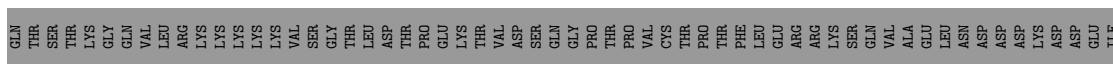


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|------|------|------|------|------|------|------|------|------|------|
| MET | GLU | GLY | VAL | GLU | GLU | LYS | LYS | LYS | GLU | VAL | PRO | ALA | ALA | VAL | PRO | THR | LEU | LYS | LYS | LYS | ARG | ARG | ASN | PHE | ALA | GLU | LEU | LYS | ILE | LYS | ARG | ARG | LEU | LYS | LYS | F37 | K107 | V108 | D171 | M172 | A176 | G180 | D232 | R236 | R237 | R238 |
|------|------|------|------|------|------|------|------|------|------|

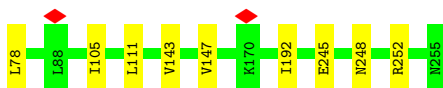
- | |
|-----|
| MET | PRO | LYS | GLY | LYS | LYS | ALA | LYS | LYS | VAL | VAL | ALA | PRO | ALA | ALA | PRO | ALA | ALA | VAL | VAL | LYS | LYS | GLN | GLU | ALA | ALA | LYS | LYS | LYS | VAL | VAL | ASN | PRO | PRO | LEU | PHE | PHE | GLY | ILE | ILE | GLY | GLN | ASP | ILE | GLN | GLN | PRO | LYS | ARG | ASP | LEU | THR | ARG | PHE | VAL | K56 | P57 | W58 | Y59 | T60 |
|-----|



- | | | | | | | | | | | | | |
|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|----|
| NET | ALA | THR | PHE | SER | GLY | PRO | ALA | GLY | ILE | SER | LEU | PRO | ASN | GLN | GLU | ASP | VAL | GLU | PHE | GLN | LYS | GLN | GLU | VAL | ALA | GLN | VAL | ARG | LYS | ARG | LYS | GLN | GLN | GLU | GLN | L42 | D133 | I136 | K168 | G191 | THR | THR | SER | SER | LYS | THR | THR | ASN | PC |
|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|----|

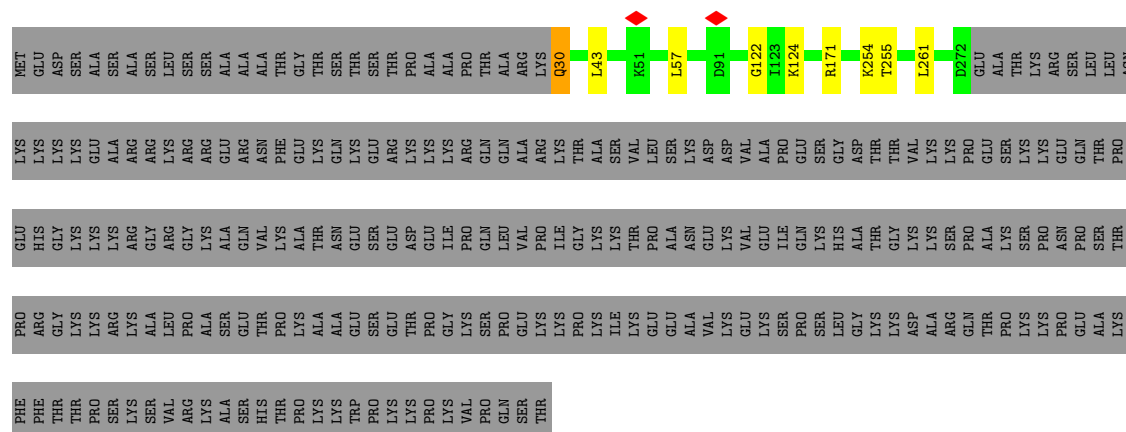


- [illegible]

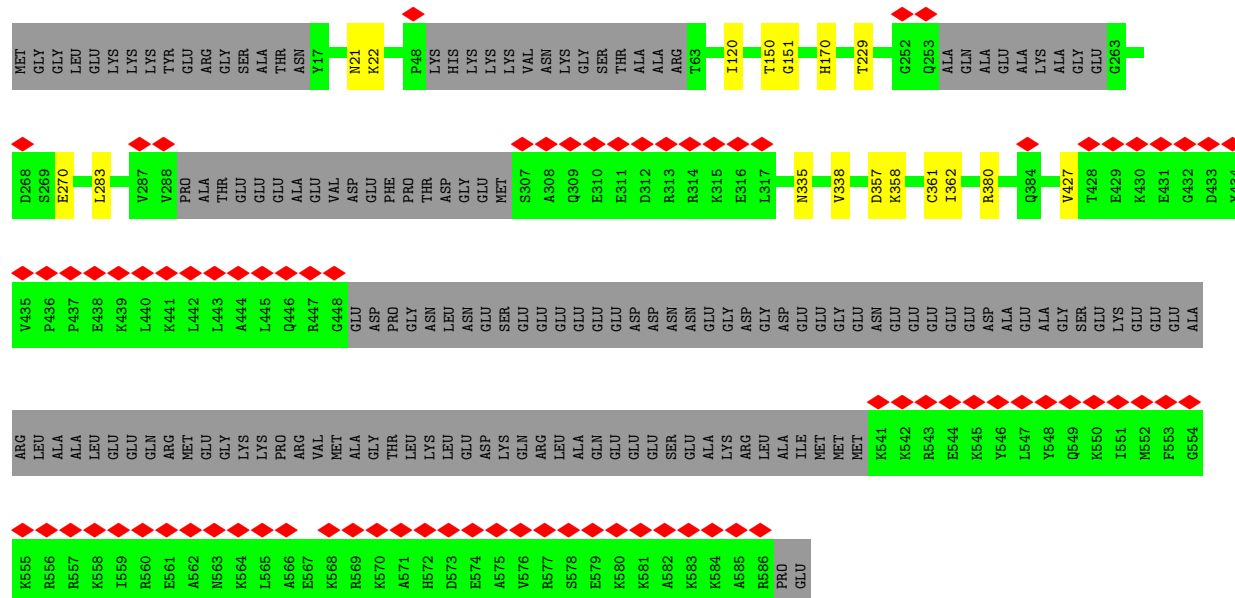
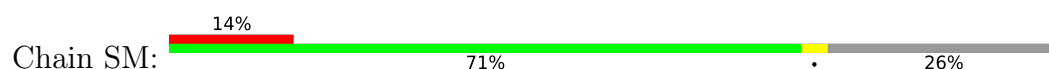


- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

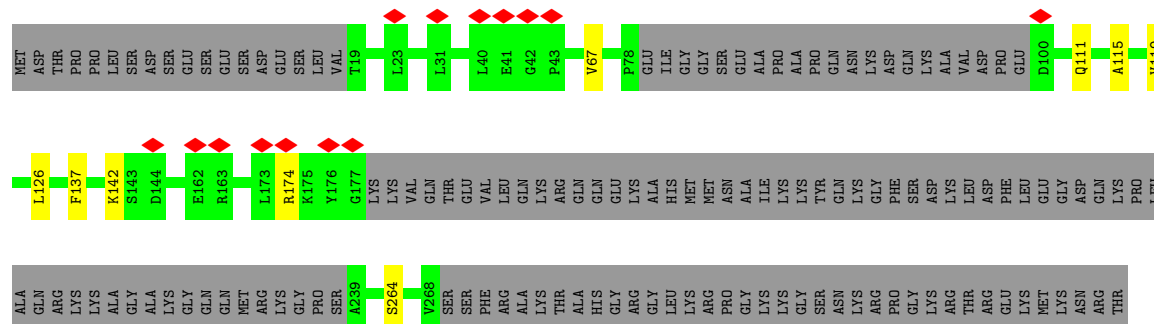




• Molecule 35: Pescadillo homolog

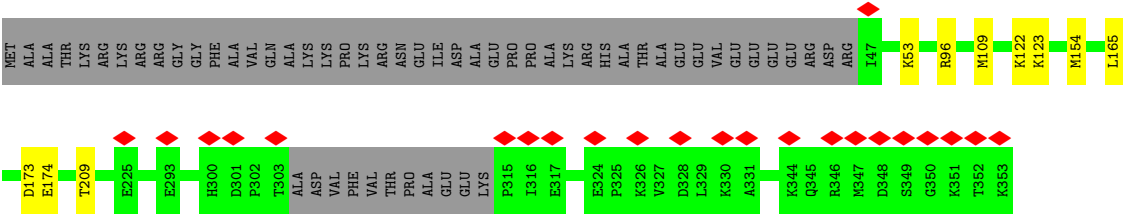
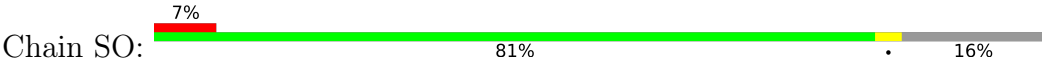


• Molecule 36: Probable rRNA-processing protein EBP2

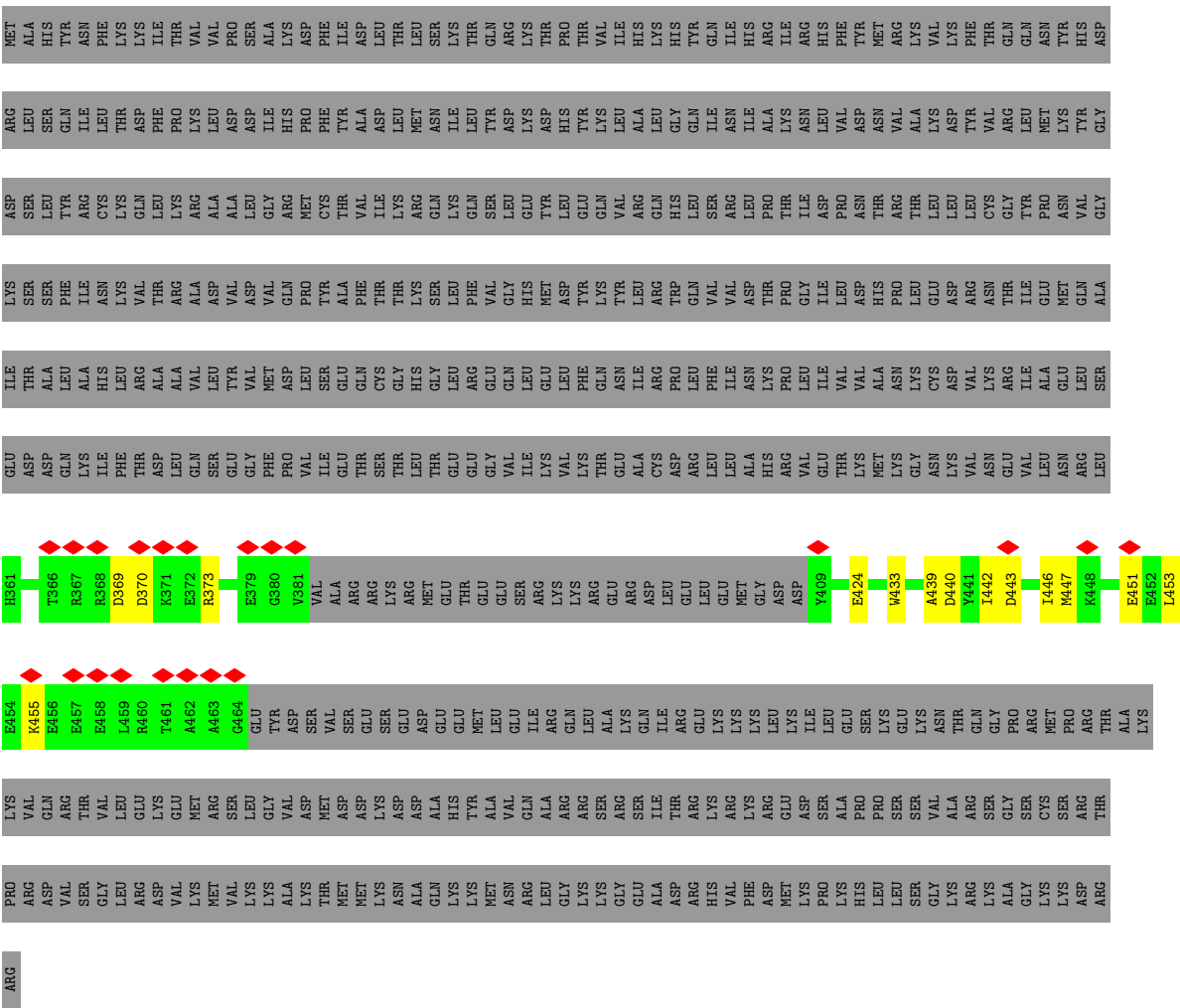


HIS

- Molecule 37: Ribosome biogenesis protein BRX1 homolog

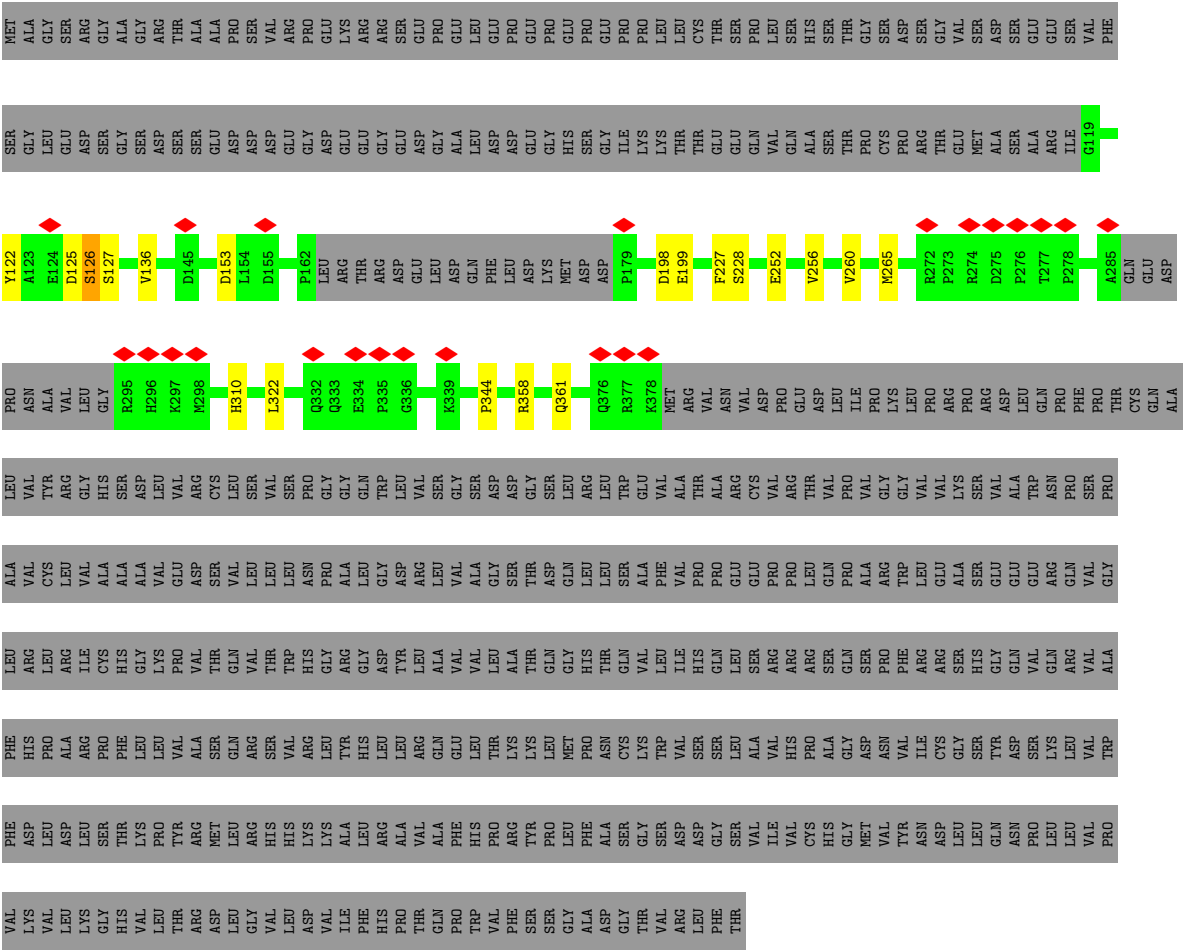


- Molecule 38: GTP-binding protein 4

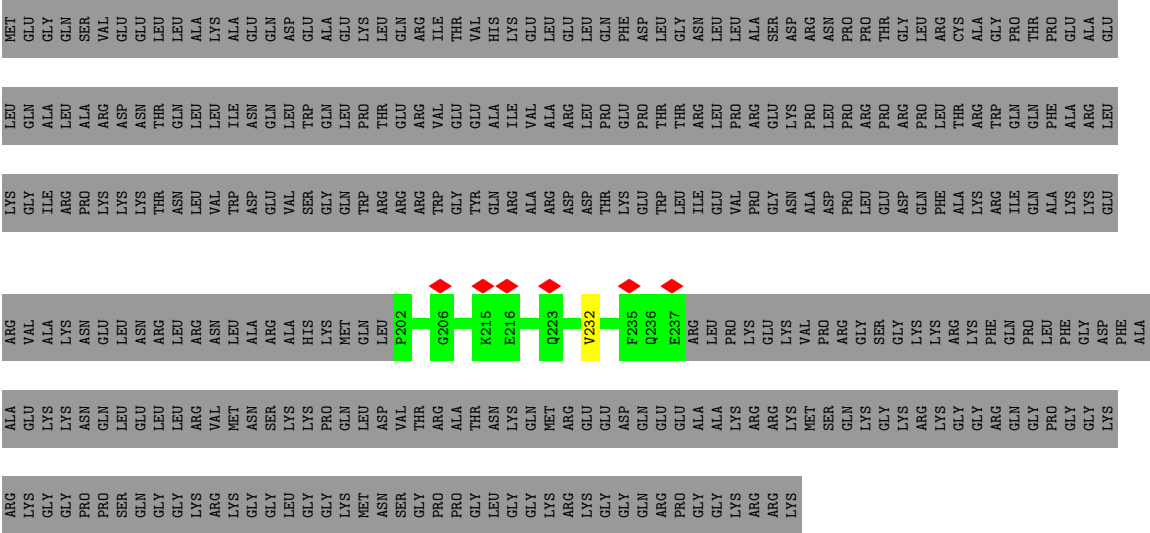


- Molecule 39: Ribosome biogenesis protein BOP1

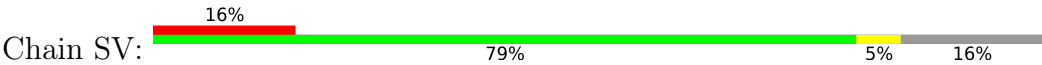


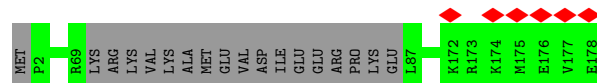


● Molecule 40: Ribosome biogenesis regulatory protein homolog



● Molecule 41: Probable ribosome biogenesis protein RLP24





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68600	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.040	Depositor
Minimum map value	-0.046	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.141	Depositor
Recommended contour level	0.75	Depositor
Map size (Å)	514.56, 514.56, 514.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	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, SEP, HIC, MG

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	L1	0.12	0/3559	0.24	0/5539
2	L2	0.15	0/1634	0.27	0/2538
3	L3	0.13	0/37504	0.26	0/58442
4	L6	0.15	0/953	0.33	0/1276
5	L7	0.16	0/1534	0.37	0/2049
6	L8	0.12	0/1133	0.28	0/1516
7	L9	0.15	0/1595	0.33	0/2132
8	LA	0.13	0/997	0.30	0/1334
9	LB	0.15	0/1239	0.31	0/1658
10	LC	0.16	0/1469	0.31	0/1971
11	LE	0.16	0/708	0.41	0/958
12	LG	0.14	0/856	0.35	0/1149
13	LH	0.14	0/146	0.26	0/190
14	LI	0.15	0/1132	0.33	0/1504
15	LK	0.18	0/648	0.40	0/880
16	LL	0.16	0/995	0.35	0/1334
17	LN	0.15	0/3092	0.33	0/4133
18	LQ	0.13	0/1071	0.30	0/1429
19	LS	0.12	0/1023	0.30	0/1351
20	LT	0.14	0/895	0.30	0/1198
21	LU	0.15	0/854	0.34	0/1129
22	LW	0.11	0/573	0.33	0/755
23	NE	0.12	0/1339	0.27	0/1767
24	NG	0.12	0/743	0.27	0/986
25	NN	0.16	0/1988	0.36	0/2678
26	SA	0.14	0/2694	0.29	0/3617
27	SC	0.13	0/1725	0.32	0/2316
28	SD	0.13	0/1789	0.29	0/2388
29	SE	0.15	0/1524	0.33	0/2056
30	SH	0.15	0/1298	0.30	0/1742
31	SI	0.14	0/1702	0.31	0/2289
32	SJ	0.13	0/623	0.37	0/836

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	SK	0.15	0/1745	0.36	0/2374
34	SL	0.14	0/1994	0.31	0/2684
35	SM	0.11	0/3530	0.25	0/4779
36	SN	0.12	0/1327	0.30	0/1774
37	SO	0.13	0/2521	0.31	0/3384
38	SR	0.20	0/657	0.45	0/887
39	SS	0.14	0/1994	0.32	0/2703
40	ST	0.10	0/267	0.25	0/357
41	SV	0.16	0/1194	0.33	0/1582
42	SW	0.12	0/3631	0.28	0/4900
43	SZ	0.12	0/1364	0.27	0/1826
All	All	0.14	0/99259	0.29	0/142390

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	L1	3189	0	1618	7	0
2	L2	1468	0	755	3	0
3	L3	33557	0	17010	107	0
4	L6	936	0	1017	4	0
5	L7	1507	0	1649	13	0
6	L8	1111	0	1174	8	0
7	L9	1553	0	1592	8	0
8	LA	981	0	1013	2	0
9	LB	1223	0	1330	6	0
10	LC	1431	0	1477	5	0
11	LE	702	0	561	3	0
12	LG	844	0	883	3	0
13	LH	146	0	176	0	0
14	LI	1115	0	1205	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	LK	642	0	455	2	0
16	LL	980	0	1041	5	0
17	LN	3044	0	3178	24	0
18	LQ	1053	0	1147	10	0
19	LS	1015	0	1148	5	0
20	LT	876	0	912	5	0
21	LU	840	0	930	8	0
22	LW	563	0	596	5	0
23	NE	1331	0	1430	25	0
24	NG	738	0	786	8	0
25	NN	1950	0	2005	16	0
26	SA	2645	0	2823	11	0
27	SC	1692	0	1839	18	0
28	SD	1755	0	1859	5	0
29	SE	1498	0	1601	9	0
30	SH	1267	0	1291	2	0
31	SI	1661	0	1752	7	0
32	SJ	609	0	600	1	0
33	SK	1721	0	1695	15	0
34	SL	1960	0	2052	7	0
35	SM	3452	0	3376	11	0
36	SN	1308	0	1286	8	0
37	SO	2460	0	2551	9	0
38	SR	642	0	630	11	0
39	SS	1955	0	1871	14	0
40	ST	263	0	260	1	0
41	SV	1171	0	1232	10	0
42	SW	3560	0	3641	24	0
43	SZ	1338	0	1352	0	0
44	L1	4	0	0	0	0
44	L2	1	0	0	0	0
44	L3	42	0	0	0	0
44	L9	1	0	0	0	0
44	LQ	1	0	0	0	0
44	LT	1	0	0	0	0
44	SA	1	0	0	0	0
45	LW	1	0	0	0	0
45	SV	1	0	0	0	0
All	All	93805	0	76799	328	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 2.

The worst 5 of 328 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)
34:SL:30:GLN:HE21	34:SL:30:GLN:N	1.69	0.90
3:L3:404:U:O2'	14:LI:87:ARG:NH2	2.13	0.81
23:NE:228:LEU:HD21	23:NE:271:THR:HG21	1.64	0.80
3:L3:2055:G:OP2	5:L7:133:ARG:NH1	2.17	0.78
12:LG:85:ARG:NH1	12:LG:99:GLU:O	2.17	0.77

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	
4	L6	112/211 (53%)	110 (98%)	2 (2%)	0	100	100
5	L7	180/203 (89%)	179 (99%)	1 (1%)	0	100	100
6	L8	133/215 (62%)	131 (98%)	2 (2%)	0	100	100
7	L9	180/204 (88%)	179 (99%)	1 (1%)	0	100	100
8	LA	115/184 (62%)	113 (98%)	2 (2%)	0	100	100
9	LB	149/188 (79%)	149 (100%)	0	0	100	100
10	LC	171/176 (97%)	171 (100%)	0	0	100	100
11	LE	102/160 (64%)	101 (99%)	1 (1%)	0	100	100
12	LG	110/140 (79%)	110 (100%)	0	0	100	100
13	LH	18/156 (12%)	18 (100%)	0	0	100	100
14	LI	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
15	LK	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
16	LL	120/137 (88%)	118 (98%)	2 (2%)	0	100	100
17	LN	372/403 (92%)	367 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LQ	126/135 (93%)	126 (100%)	0	0	100	100
19	LS	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
20	LT	107/110 (97%)	107 (100%)	0	0	100	100
21	LU	101/105 (96%)	100 (99%)	1 (1%)	0	100	100
22	LW	65/97 (67%)	65 (100%)	0	0	100	100
23	NE	152/361 (42%)	150 (99%)	2 (1%)	0	100	100
24	NG	87/282 (31%)	87 (100%)	0	0	100	100
25	NN	238/473 (50%)	234 (98%)	4 (2%)	0	100	100
26	SA	325/427 (76%)	321 (99%)	4 (1%)	0	100	100
27	SC	205/288 (71%)	203 (99%)	2 (1%)	0	100	100
28	SD	210/248 (85%)	205 (98%)	5 (2%)	0	100	100
29	SE	184/266 (69%)	183 (100%)	1 (0%)	0	100	100
30	SH	148/293 (50%)	145 (98%)	3 (2%)	0	100	100
31	SI	198/255 (78%)	196 (99%)	2 (1%)	0	100	100
32	SJ	70/847 (8%)	70 (100%)	0	0	100	100
33	SK	224/245 (91%)	219 (98%)	5 (2%)	0	100	100
34	SL	241/490 (49%)	236 (98%)	5 (2%)	0	100	100
35	SM	427/588 (73%)	425 (100%)	2 (0%)	0	100	100
36	SN	162/306 (53%)	161 (99%)	1 (1%)	0	100	100
37	SO	292/353 (83%)	288 (99%)	4 (1%)	0	100	100
38	SR	73/634 (12%)	71 (97%)	2 (3%)	0	100	100
39	SS	227/746 (30%)	225 (99%)	2 (1%)	0	100	100
40	ST	34/365 (9%)	33 (97%)	1 (3%)	0	100	100
41	SV	135/163 (83%)	133 (98%)	2 (2%)	0	100	100
42	SW	441/670 (66%)	433 (98%)	8 (2%)	0	100	100
43	SZ	156/178 (88%)	155 (99%)	1 (1%)	0	100	100
All	All	6746/11718 (58%)	6669 (99%)	77 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	
4	L6	98/177 (55%)	98 (100%)	0	100	100
5	L7	157/174 (90%)	157 (100%)	0	100	100
6	L8	115/161 (71%)	115 (100%)	0	100	100
7	L9	156/172 (91%)	156 (100%)	0	100	100
8	LA	111/163 (68%)	111 (100%)	0	100	100
9	LB	136/165 (82%)	136 (100%)	0	100	100
10	LC	154/157 (98%)	154 (100%)	0	100	100
11	LE	47/140 (34%)	47 (100%)	0	100	100
12	LG	87/107 (81%)	87 (100%)	0	100	100
13	LH	13/133 (10%)	13 (100%)	0	100	100
14	LI	124/135 (92%)	124 (100%)	0	100	100
15	LK	29/121 (24%)	29 (100%)	0	100	100
16	LL	106/121 (88%)	106 (100%)	0	100	100
17	LN	328/348 (94%)	328 (100%)	0	100	100
18	LQ	114/121 (94%)	114 (100%)	0	100	100
19	LS	109/110 (99%)	109 (100%)	0	100	100
20	LT	88/89 (99%)	88 (100%)	0	100	100
21	LU	87/89 (98%)	87 (100%)	0	100	100
22	LW	58/80 (72%)	58 (100%)	0	100	100
23	NE	136/294 (46%)	136 (100%)	0	100	100
24	NG	83/246 (34%)	83 (100%)	0	100	100
25	NN	218/398 (55%)	218 (100%)	0	100	100
26	SA	279/348 (80%)	279 (100%)	0	100	100
27	SC	187/252 (74%)	187 (100%)	0	100	100
28	SD	182/215 (85%)	182 (100%)	0	100	100
29	SE	159/223 (71%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	SH	140/274 (51%)	140 (100%)	0	100	100
31	SI	182/228 (80%)	182 (100%)	0	100	100
32	SJ	64/733 (9%)	64 (100%)	0	100	100
33	SK	196/213 (92%)	196 (100%)	0	100	100
34	SL	226/437 (52%)	225 (100%)	1 (0%)	84	91
35	SM	350/509 (69%)	350 (100%)	0	100	100
36	SN	126/260 (48%)	126 (100%)	0	100	100
37	SO	274/319 (86%)	274 (100%)	0	100	100
38	SR	69/574 (12%)	69 (100%)	0	100	100
39	SS	208/648 (32%)	208 (100%)	0	100	100
40	ST	27/300 (9%)	27 (100%)	0	100	100
41	SV	127/149 (85%)	127 (100%)	0	100	100
42	SW	394/591 (67%)	394 (100%)	0	100	100
43	SZ	141/158 (89%)	141 (100%)	0	100	100
All	All	5885/10132 (58%)	5884 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	SL	30	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
33	SK	162	HIS
41	SV	17	HIS
34	SL	218	HIS
38	SR	436	HIS
41	SV	132	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L1	147/157 (93%)	14 (9%)	1 (0%)
2	L2	65/1167 (5%)	9 (13%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L3	1532/5070 (30%)	204 (13%)	5 (0%)
All	All	1744/6394 (27%)	227 (13%)	6 (0%)

5 of 227 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L1	34	U
1	L1	59	A
1	L1	62	A
1	L1	63	U
1	L1	82	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L3	1880	G
3	L3	2267	U
3	L3	4679	G
3	L3	172	C
1	L1	156	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
39	SEP	SS	126	39	8,9,10	1.58	1 (12%)	7,12,14	1.20	1 (14%)
39	SEP	SS	127	39	8,9,10	1.58	1 (12%)	7,12,14	1.31	1 (14%)
17	HIC	LN	245	17	10,11,12	1.51	1 (10%)	9,14,16	1.20	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	SEP	SS	126	39	-	0/6/8/10	-
39	SEP	SS	127	39	-	3/6/8/10	-
17	HIC	LN	245	17	-	0/5/6/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	SS	126	SEP	P-O1P	3.46	1.61	1.50
39	SS	127	SEP	P-O1P	3.44	1.61	1.50
17	LN	245	HIC	CD2-CG	3.00	1.41	1.36

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	LN	245	HIC	NE2-CE1-ND1	-2.90	111.56	112.66
39	SS	127	SEP	OG-CB-CA	2.83	110.90	108.14
39	SS	126	SEP	OG-CB-CA	2.50	110.58	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	SS	127	SEP	CA-CB-OG-P
39	SS	127	SEP	N-CA-CB-OG
39	SS	127	SEP	C-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	SS	126	SEP	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 53 ligands modelled in this entry, 53 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

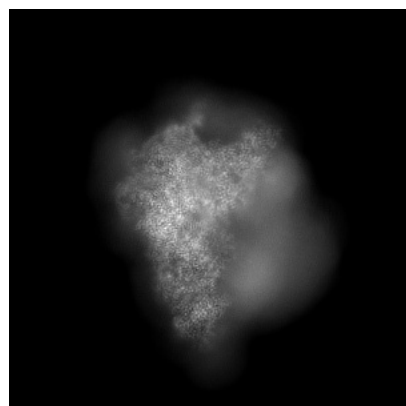
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29253. These allow visual inspection of the internal detail of the map and identification of artifacts.

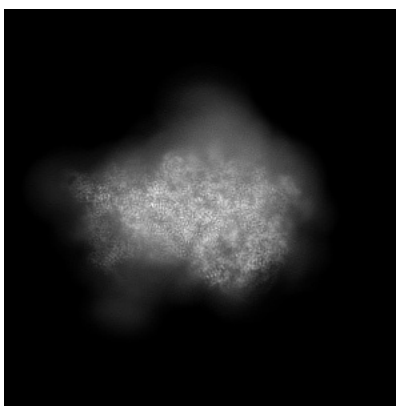
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

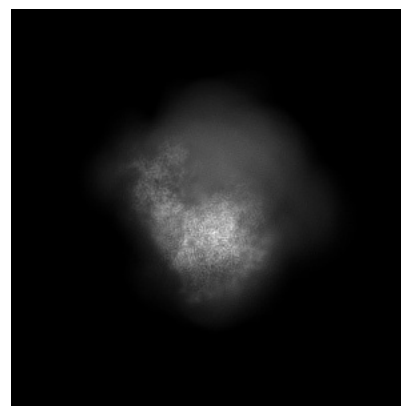
6.1.1 Primary map



X

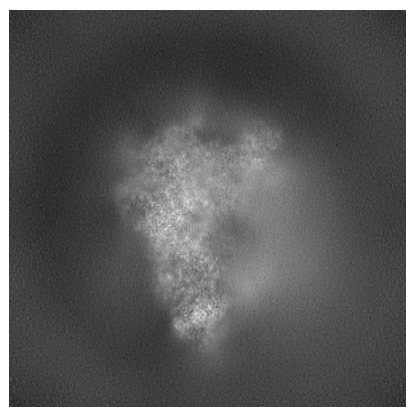


Y

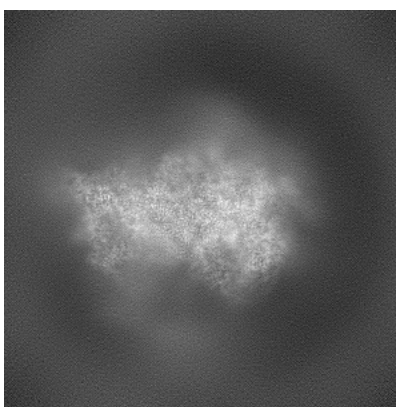


Z

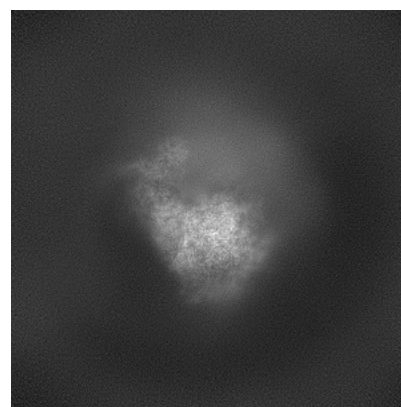
6.1.2 Raw map



X



Y

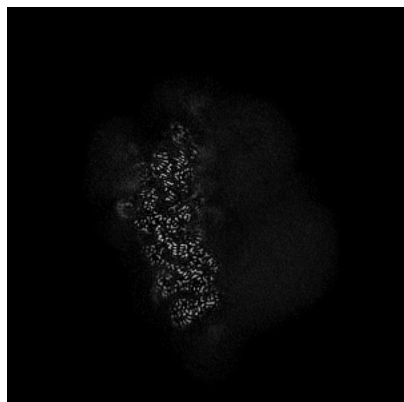


Z

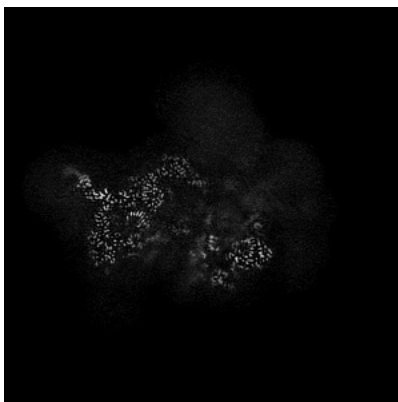
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

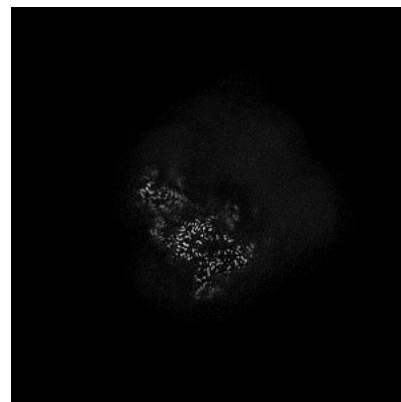
6.2.1 Primary map



X Index: 240

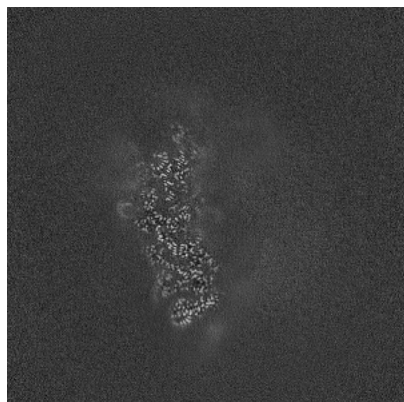


Y Index: 240

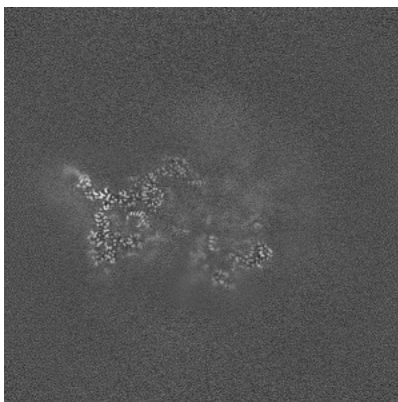


Z Index: 240

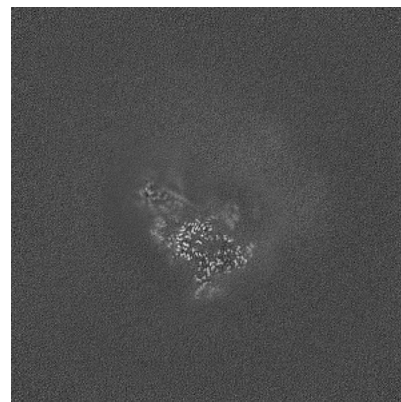
6.2.2 Raw map



X Index: 240



Y Index: 240

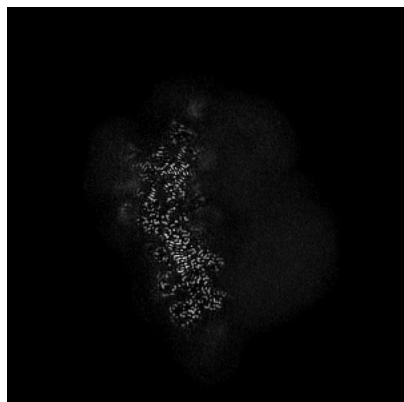


Z Index: 240

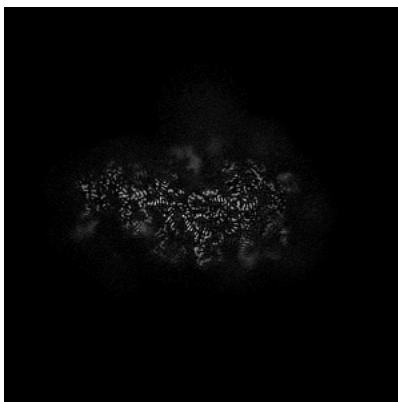
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

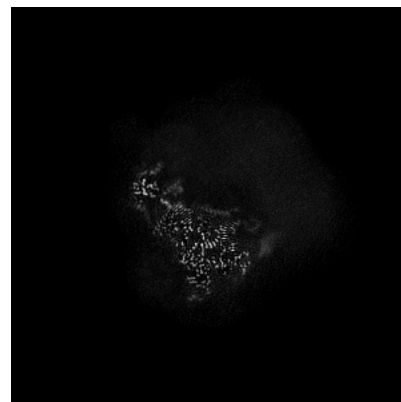
6.3.1 Primary map



X Index: 244

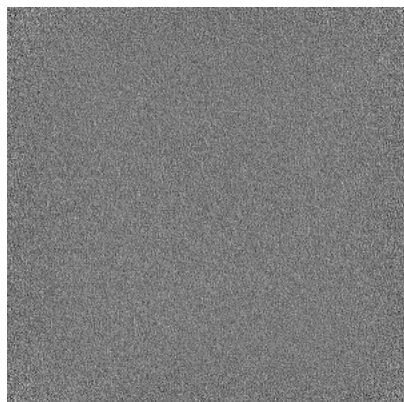


Y Index: 205

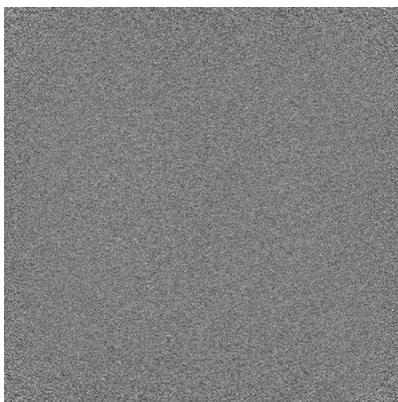


Z Index: 249

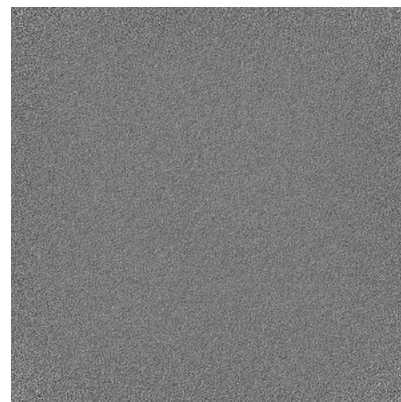
6.3.2 Raw map



X Index: 0



Y Index: 0

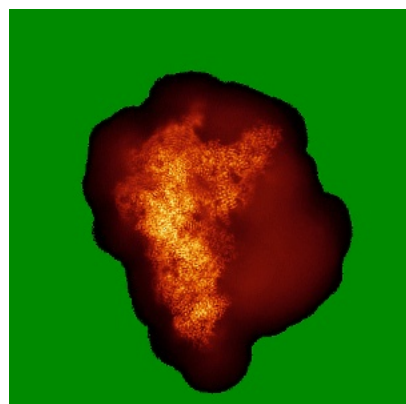


Z Index: 0

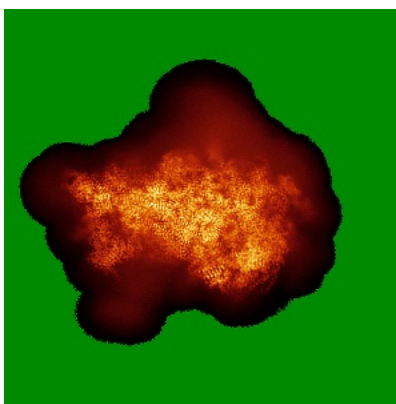
The images above show the largest variance slices of the map in three orthogonal directions.

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

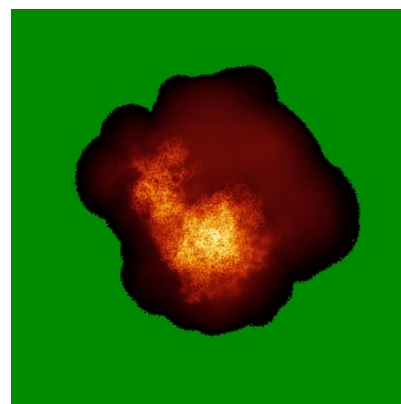
6.4.1 Primary map



X

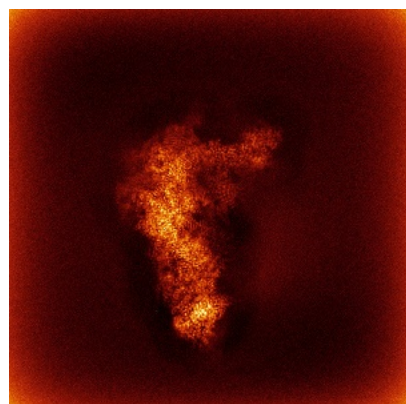


Y

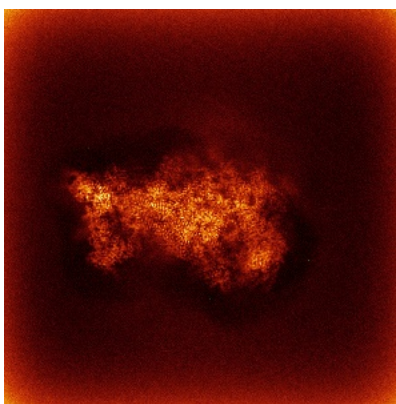


Z

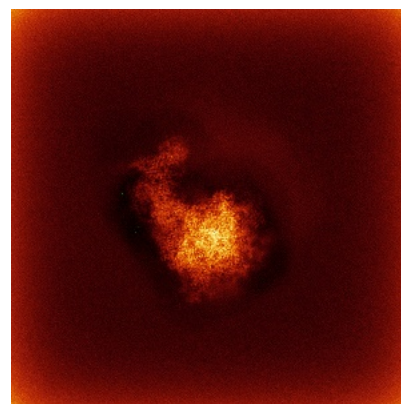
6.4.2 Raw map



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](#)

This section was not generated.

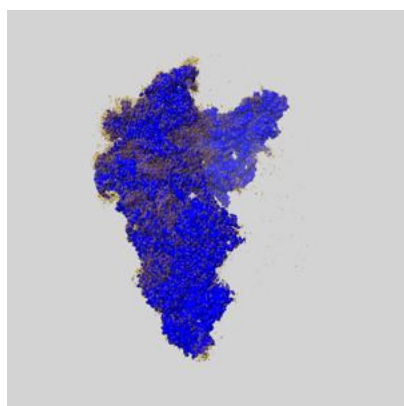
6.6 Mask visualisation [i](#)

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

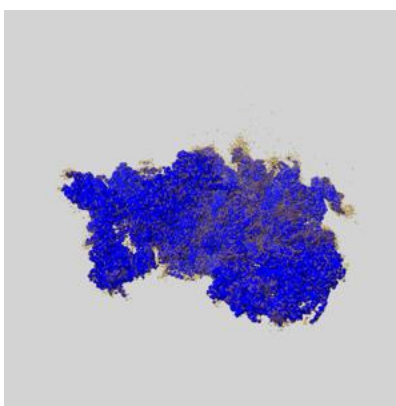
A mask typically either:

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

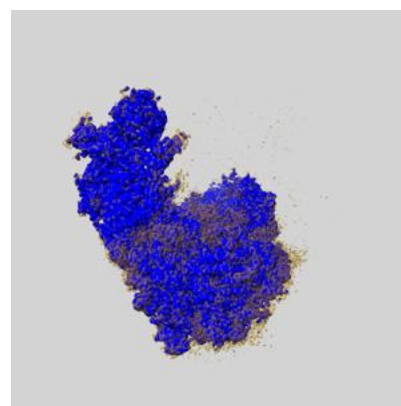
6.6.1 emd_29253_msk_1.map [i](#)



X



Y

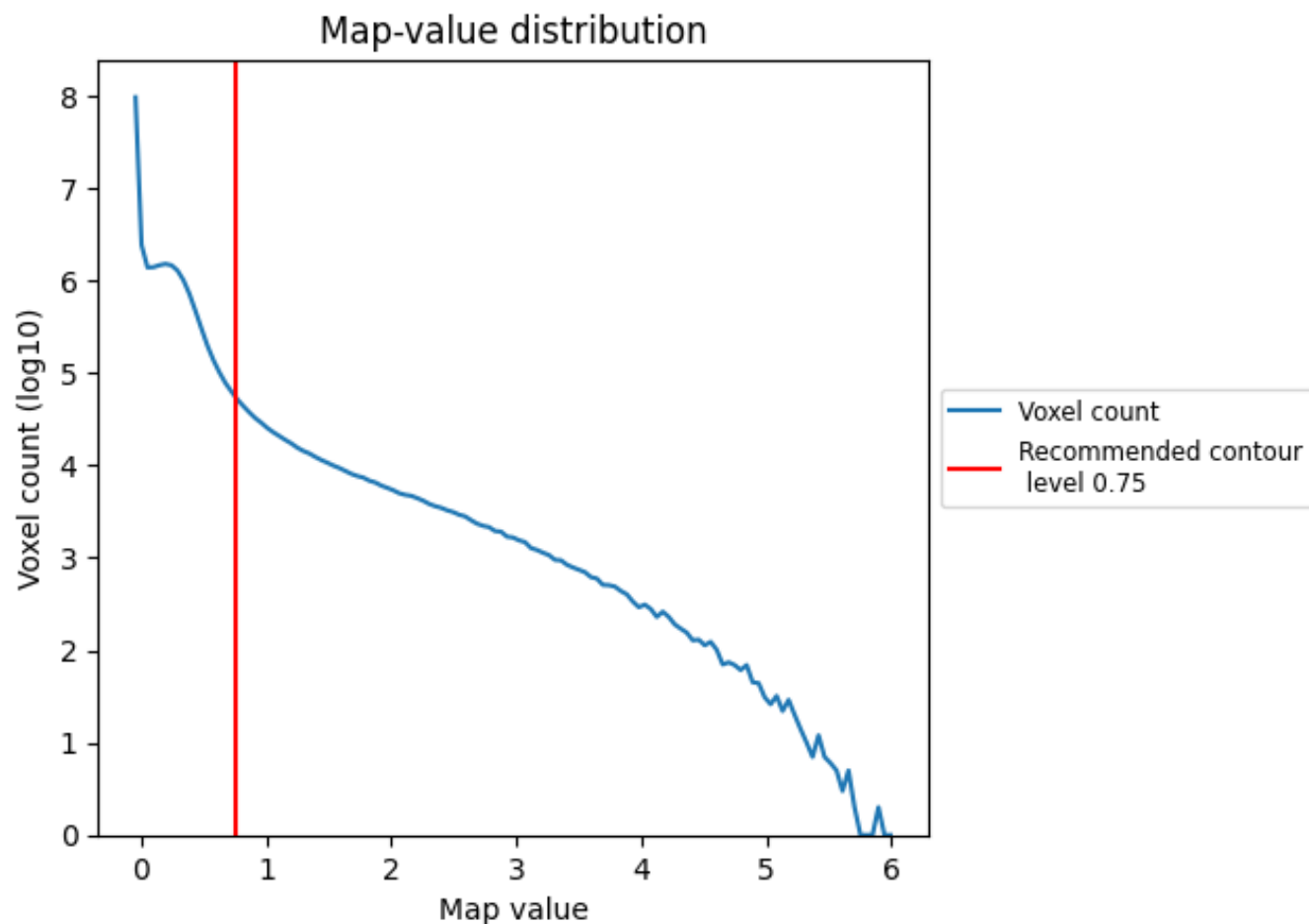


Z

7 Map analysis [i](#)

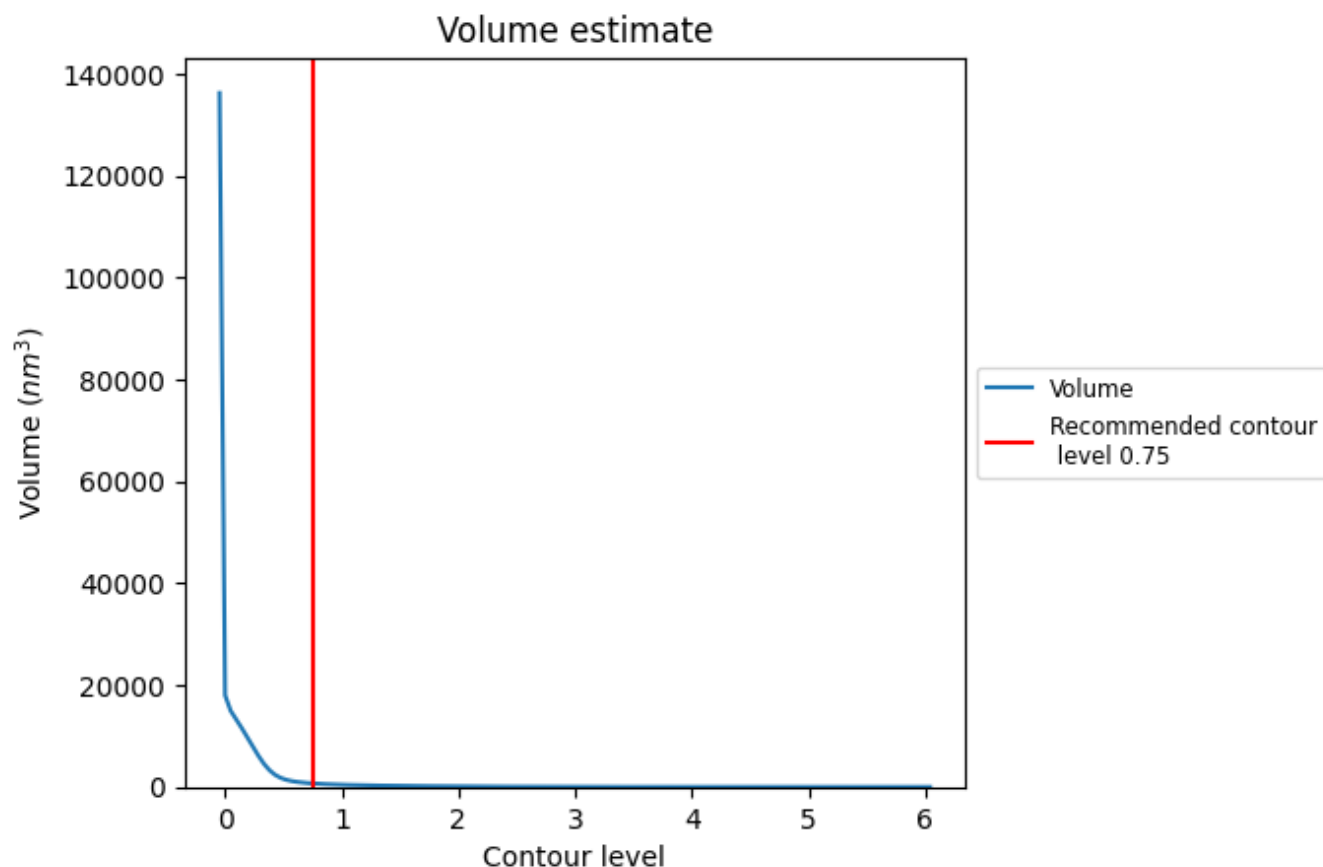
This section contains the results of statistical analysis of the map.

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.

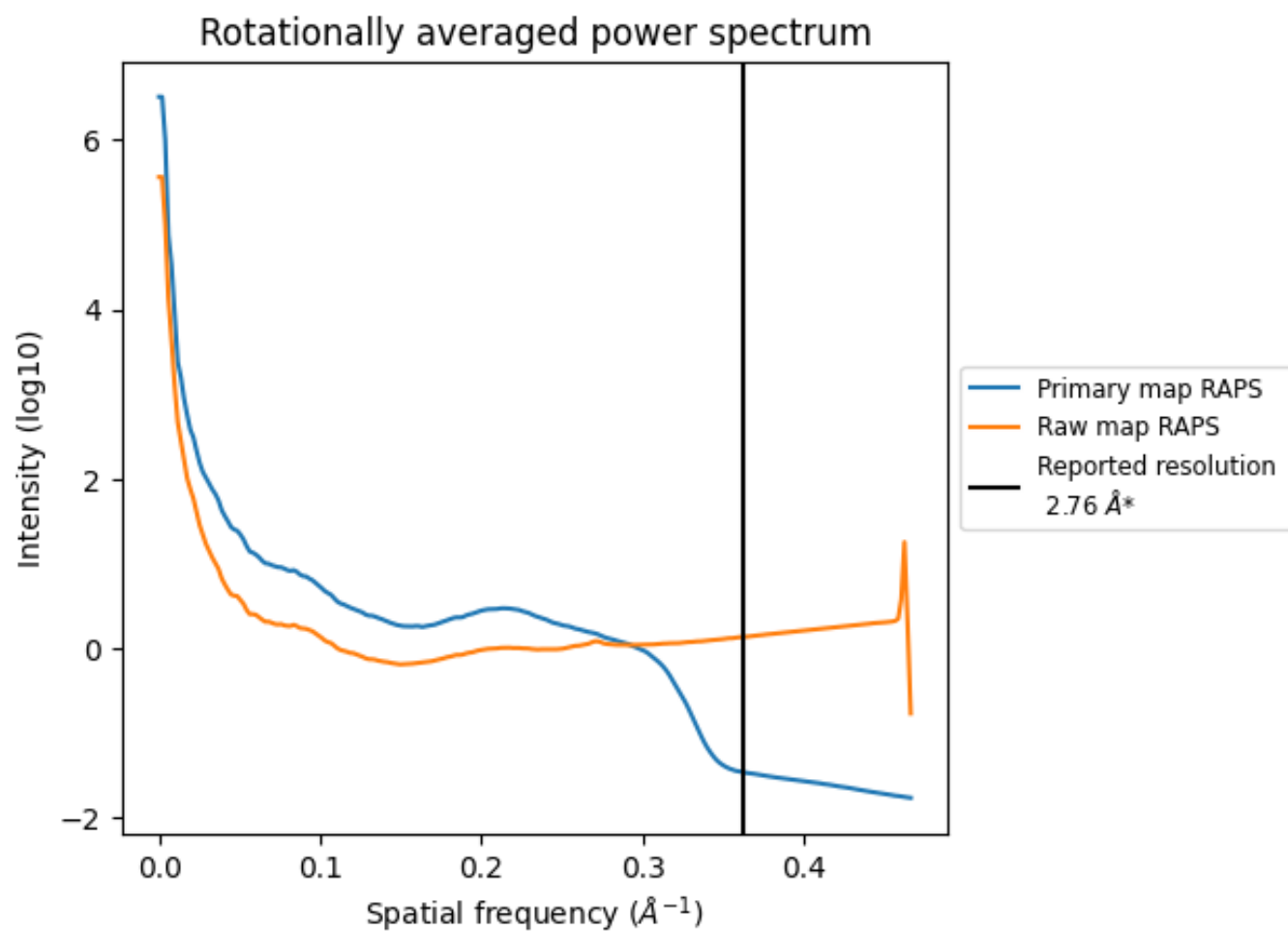
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 696 nm^3 ; this corresponds to an approximate mass of 629 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 ⓘ

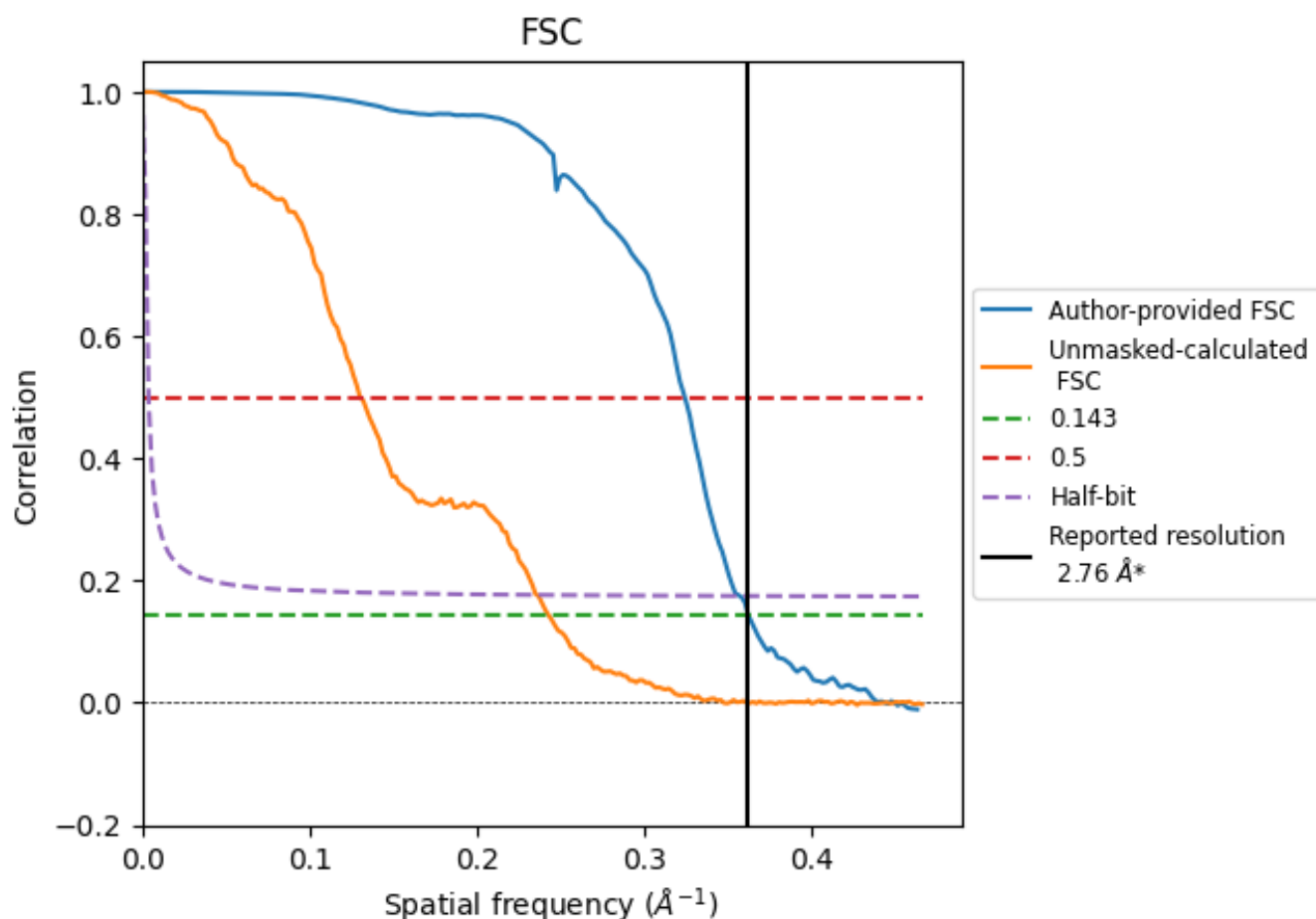


*Reported resolution corresponds to spatial frequency of 0.362 Å⁻¹

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 0.362 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

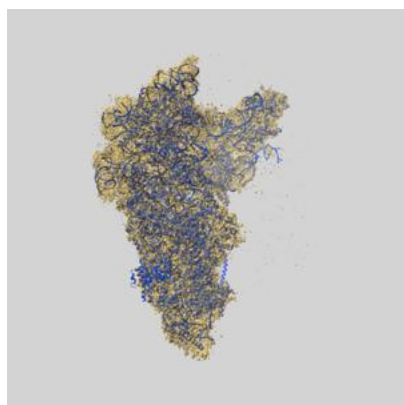
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.76	3.08	2.80
Unmasked-calculated*	4.11	7.67	4.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.11 differs from the reported value 2.76 by more than 10 %

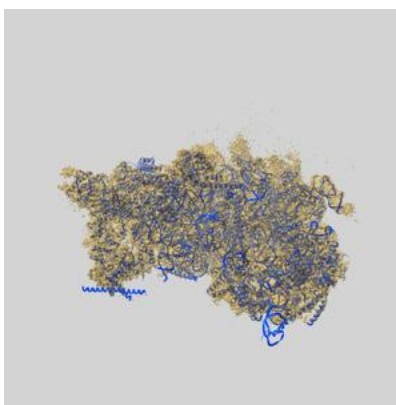
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29253 and PDB model 8FKQ. Per-residue inclusion information can be found in section 3 on page 12.

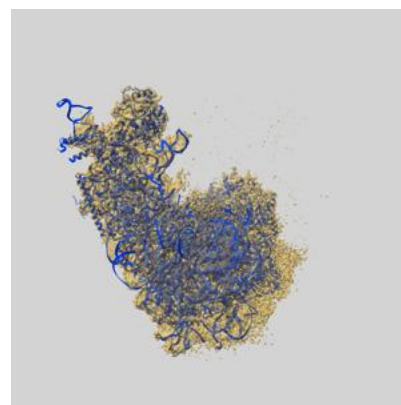
9.1 Map-model overlay [i](#)



X



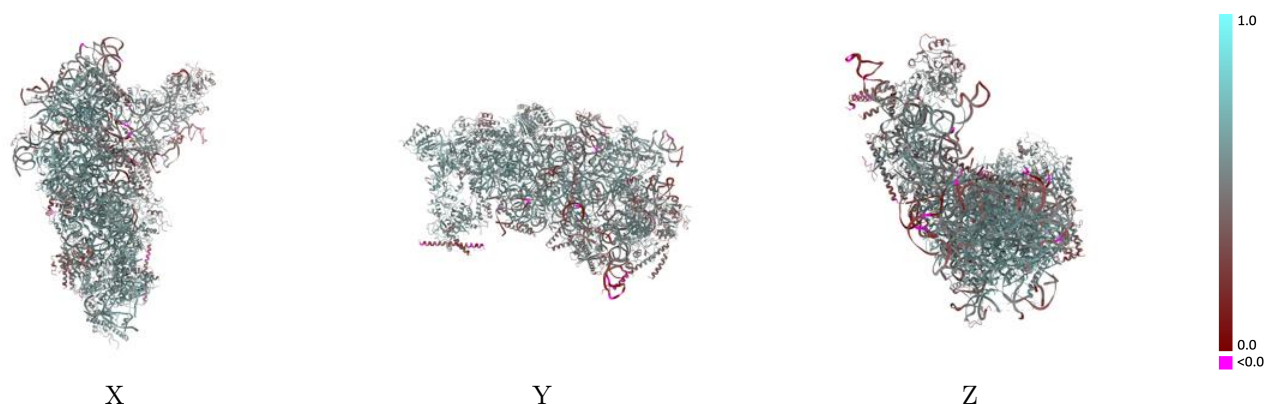
Y



Z

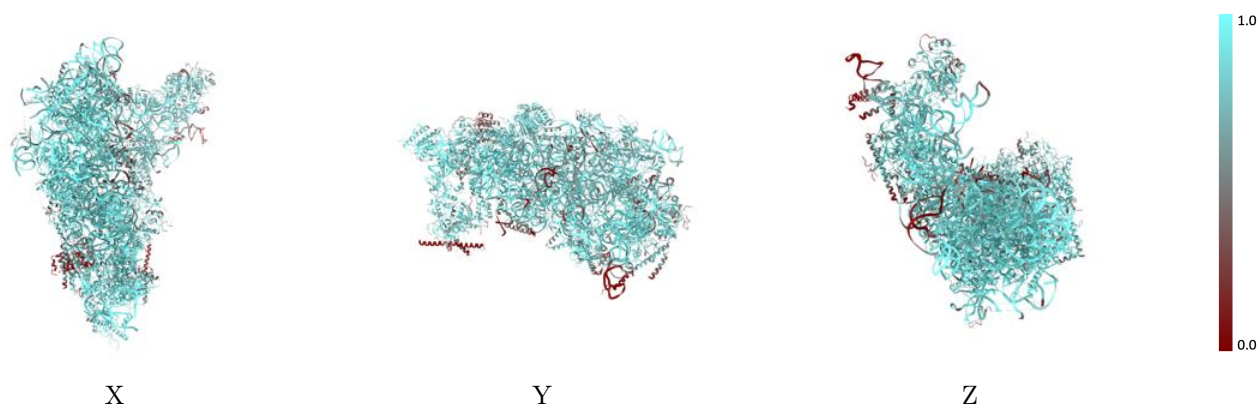
The images above show the 3D surface view of the map at the recommended contour level 0.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



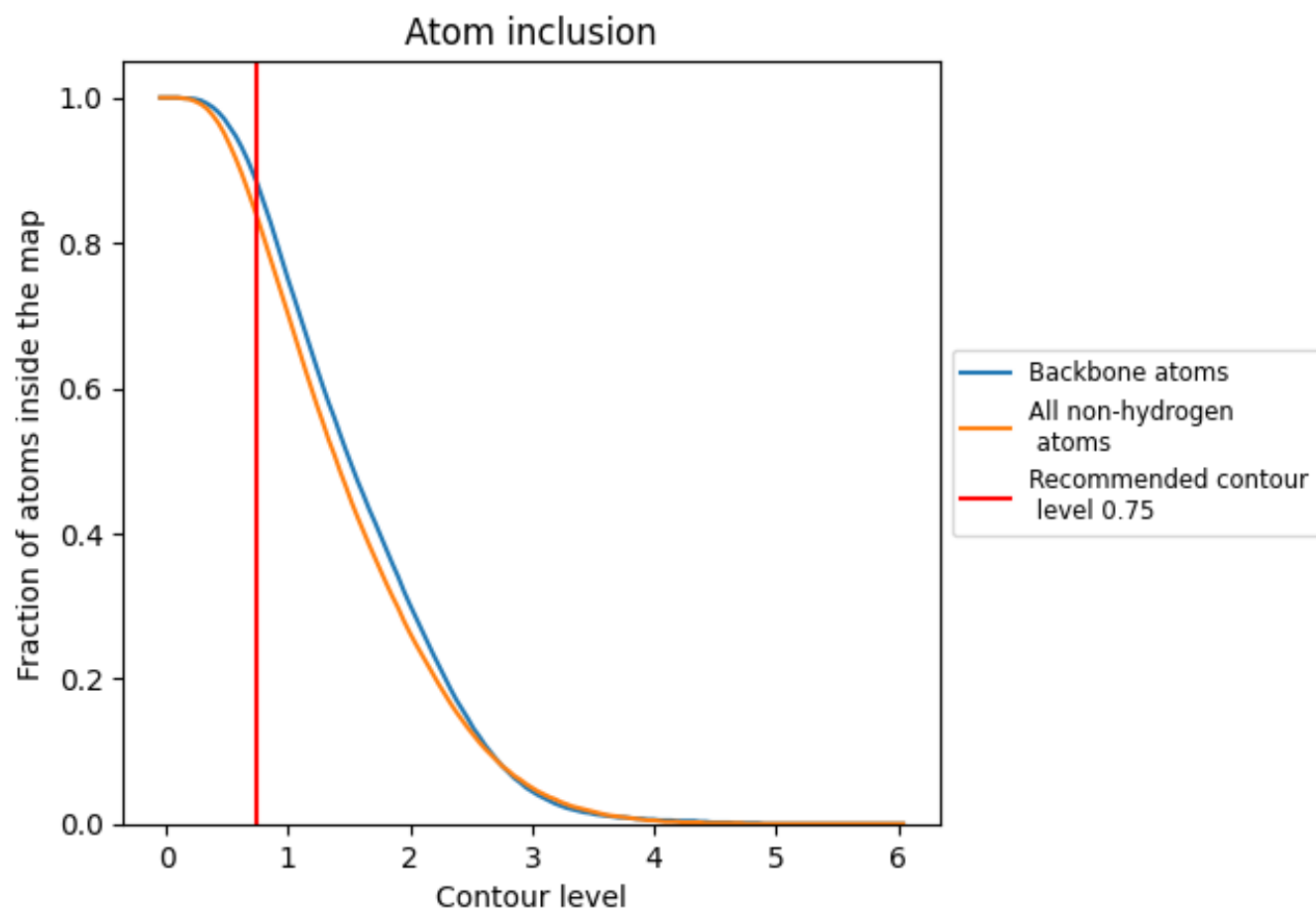
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.75).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (0.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8340	 0.5250
L1	 0.8310	 0.5210
L2	 0.9460	 0.5650
L3	 0.8780	 0.5130
L6	 0.9520	 0.6070
L7	 0.7960	 0.5040
L8	 0.8190	 0.5300
L9	 0.9660	 0.6190
LA	 0.8040	 0.5230
LB	 0.9550	 0.6180
LC	 0.8010	 0.5400
LE	 0.7100	 0.4250
LG	 0.7420	 0.4720
LH	 0.5200	 0.4810
LI	 0.8860	 0.5890
LK	 0.7910	 0.4190
LL	 0.9590	 0.6170
LN	 0.8520	 0.5470
LQ	 0.9550	 0.6230
LS	 0.6940	 0.5150
LT	 0.9640	 0.6220
LU	 0.8400	 0.5670
LW	 0.7300	 0.5510
NE	 0.6820	 0.3950
NG	 0.4440	 0.3450
NN	 0.8260	 0.5010
SA	 0.9490	 0.6140
SC	 0.8180	 0.5320
SD	 0.9520	 0.6100
SE	 0.9400	 0.5970
SH	 0.8810	 0.5730
SI	 0.8440	 0.5770
SJ	 0.6870	 0.5180
SK	 0.7200	 0.4520
SL	 0.8550	 0.5650



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Chain	Atom inclusion	Q-score
SM	 0.7280	 0.5010
SN	 0.7390	 0.4810
SO	 0.7930	 0.5360
SR	 0.5470	 0.3920
SS	 0.7510	 0.5090
ST	 0.6060	 0.4910
SV	 0.6420	 0.4330
SW	 0.6170	 0.4790
SZ	 0.8540	 0.5540