



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:16 PM UTC

PDB ID : 8IA0 / pdb_00008ia0
EMDB ID : EMD-35290
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Puf6
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.70 Å(reported)
Based on initial model : .

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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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

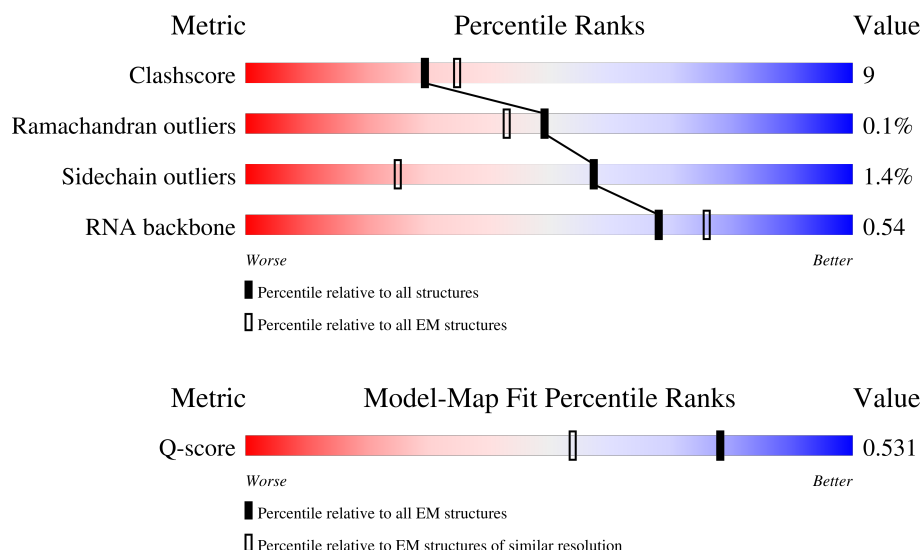
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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	C1	3341	
2	C2	319	
3	CA	316	

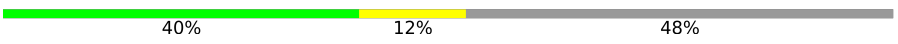
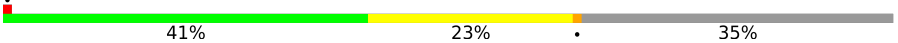
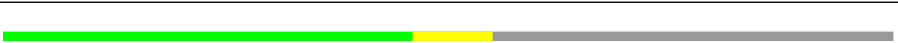
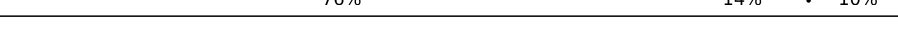
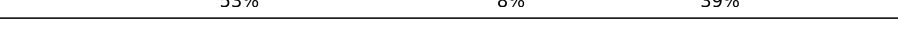
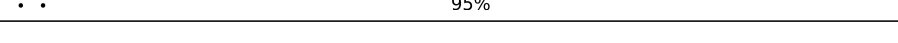
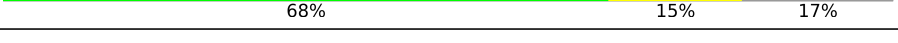
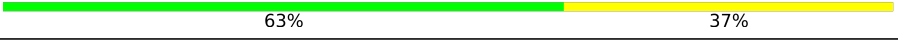
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	CB	391	
5	CC	801	
6	CD	495	
7	CE	598	
8	CF	270	
9	CG	184	
10	CH	661	
11	CI	414	
12	CJ	679	
13	CK	261	
14	CL	558	
15	CM	249	
15	LF	249	
16	CN	246	
17	CO	120	
18	CP	751	
19	CQ	225	
20	CR	237	
21	CS	834	
22	CT	688	
23	CU	451	
24	CV	147	
25	CW	679	
26	CX	203	
27	CY	788	

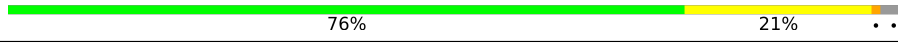
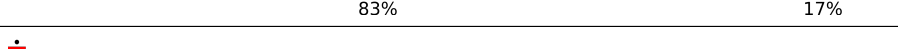
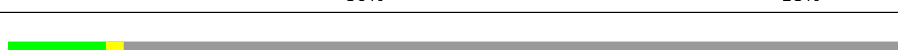
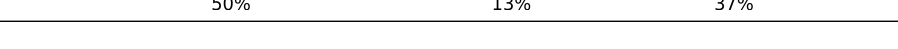
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	CZ	697	
29	Ca	227	
30	Cz	123	
31	LA	254	
32	LB	392	
33	LC	365	
34	LE	200	
35	LG	262	
36	LH	192	
37	LK	165	
38	LL	213	
39	LM	142	
40	LN	203	
41	LO	204	
42	LP	187	
43	LQ	213	
44	LR	2898	
45	LS	174	
46	LT	160	
47	LU	127	
48	LV	139	
49	LX	156	
50	LY	138	
51	LZ	135	
52	Lc	108	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	Ld	120	
54	Le	131	
55	Lf	109	
56	Lg	119	
57	Lh	935	
58	Li	110	
59	Lj	95	
60	Lk	81	
61	Lp	92	
62	Ll	51	
63	Lq	217	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 177631 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 (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	2928	Total	C	N	O	P	0	0
			62650	27959	11356	20407	2928		

- Molecule 2 is a RNA chain called RNA (319-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	256	Total	C	N	O	P	0	0
			5456	2435	974	1791	256		

- Molecule 3 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CA	251	Total	C	N	O	S	0	0
			2069	1324	381	357	7		

- Molecule 4 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CB	260	Total	C	N	O	S	0	0
			2063	1322	367	371	3		

- Molecule 5 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	CC	658	Total	C	N	O	P	S	0	0
			5297	3368	931	983	2	13		

- Molecule 6 is a protein called Ribosome biogenesis protein YTM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CD	460	Total	C	N	O	S	0	0
			3468	2173	610	679	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CD	88	ASP	GLU	conflict	UNP G0SFB5

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CE	463	Total	C	N	O	S	0	0
			3673	2352	643	667	11		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CF	245	Total	C	N	O	S	0	0
			1945	1222	352	362	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CG	177	Total	C	N	O	S	0	0
			1396	884	247	253	12		

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CH	542	Total	C	N	O	S	0	0
			4388	2784	770	818	16		

- Molecule 11 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 12 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CJ	494	Total	C	N	O	S	0	0
			4040	2575	719	734	12		

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CK	229	Total	C	N	O	S	0	0
			1835	1149	362	320	4		

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CL	397	Total	C	N	O		0	0
			2239	1350	459	430			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 15 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CM	223	Total	C	N	O	S	0	0
			1820	1169	340	308	3		
15	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CN	246	Total	C	N	O	S	0	0
			1856	1158	322	369	7		

- Molecule 17 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CP	356	Total	C	N	O	S	0	0
			2798	1777	495	510	16		

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	179	Total	C	N	O	S	0	0
			1485	926	304	245	10		

- Molecule 20 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	629	Total	C	N	O	S	0	0
			5082	3220	925	918	19		

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CT	488	Total	C	N	O	S	0	0
			3911	2486	690	719	16		

- Molecule 23 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CU	178	Total	C	N	O	S	0	0
			1415	876	265	271	3		

- Molecule 24 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	CV	139	Total	C	N	O	0	0
			1073	672	213	188		

- Molecule 25 is a protein called ATP-dependent RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CW	540	Total	C	N	O	S	0	0
			4310	2748	765	783	14		

- Molecule 26 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CX	88	Total	C	N	O	S	0	0
			701	435	128	135	3		

- Molecule 27 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CY	420	Total	C	N	O	S	0	0
			3413	2191	619	591	12		

- Molecule 28 is a protein called PUM-HD domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CZ	576	Total	C	N	O	S	0	0
			3975	2502	708	753	12		

- Molecule 29 is a protein called Nucleolar protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ca	117	Total	C	N	O	S	0	0
			982	609	199	173	1		

- Molecule 30 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cz	70	Total	C	N	O	S	0	0
			592	368	120	101	3		

- Molecule 31 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LA	166	Total	C	N	O	S	0	0
			1259	798	233	226	2		

- Molecule 32 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LB	356	Total	C	N	O	S	0	0
			2829	1798	518	501	12		

- Molecule 33 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LC	362	Total	C	N	O	S	0	0
			2752	1738	526	479	9		

- Molecule 34 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LE	179	Total	C	N	O	S	0	0
			1403	898	255	247	3		

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LG	205	Total	C	N	O	S	0	0
			1651	1065	298	283	5		

- Molecule 36 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LH	190	Total	C	N	O	S	0	0
			1496	950	268	272	6		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 37 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LK	146	Total	C	N	O	S	0	0
			1112	701	203	206	2		

- Molecule 38 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LL	117	Total	C	N	O	S	0	0
			964	608	206	148	2		

- Molecule 39 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LM	137	Total	C	N	O	S	0	0
			1101	699	211	190	1		

- Molecule 40 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LN	183	Total	C	N	O	S	0	0
			1563	974	332	253	4		

- Molecule 41 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LO	204	Total	C	N	O	S	0	0
			1618	1039	306	267	6		

- Molecule 42 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LP	169	Total	C	N	O	S	0	0
			1345	835	273	234	3		

- Molecule 43 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LQ	129	Total	C	N	O	S	0	0
			1021	646	200	173	2		

- Molecule 44 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LR	148	Total	C	N	O	S	0	0
			1219	756	253	205	5		

- Molecule 45 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LS	174	Total	C	N	O	S	0	0
			1433	922	267	239	5		

- Molecule 46 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LT	126	Total	C	N	O	S	0	0
			1014	643	196	173	2		

- Molecule 47 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LU	105	Total	C	N	O	S	0	0
			850	551	147	151	1		

- Molecule 48 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LV	135	Total	C	N	O	S	0	0
			995	633	185	170	7		

- Molecule 49 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	LX	137	Total	C	N	O	0	0
			1062	678	194	190		

- Molecule 50 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 51 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

- Molecule 52 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lc	98	Total	C	N	O	S	0	0
			731	463	126	137	5		

- Molecule 53 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ld	109	Total	C	N	O	S	0	0
			890	563	171	155	1		

- Molecule 54 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Le	127	Total	C	N	O	S	0	0
			1025	645	209	164	7		

- Molecule 55 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 56 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lg	117	Total	C	N	O	S	0	0
			930	578	189	159	4		

- Molecule 57 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Lh	121	Total	C	N	O	0	0
			995	633	196	166		

- Molecule 58 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Li	88	Total	C	N	O	S	0	0
			731	449	162	119	1		

- Molecule 59 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lj	74	Total	C	N	O	S	0	0
			595	365	132	93	5		

- Molecule 60 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lk	75	Total	C	N	O	S	0	0
			620	394	117	107	2		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	SER	deletion	UNP G0SG89
Lk	?	-	LYS	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	ALA	deletion	UNP G0SG89
Lk	?	-	PHE	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89

- Molecule 61 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lp	58	Total	C	N	O	S	0	0
			436	266	85	79	6		

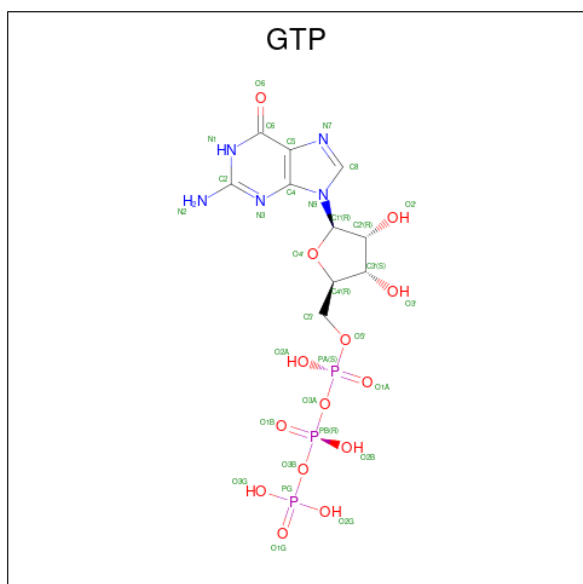
- Molecule 62 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	Ll	38	Total	C	N	O	0	0
			322	204	68	50		

- Molecule 63 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lq	207	Total	C	N	O	S	0	0
			1600	1016	285	291	8		

- Molecule 64 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

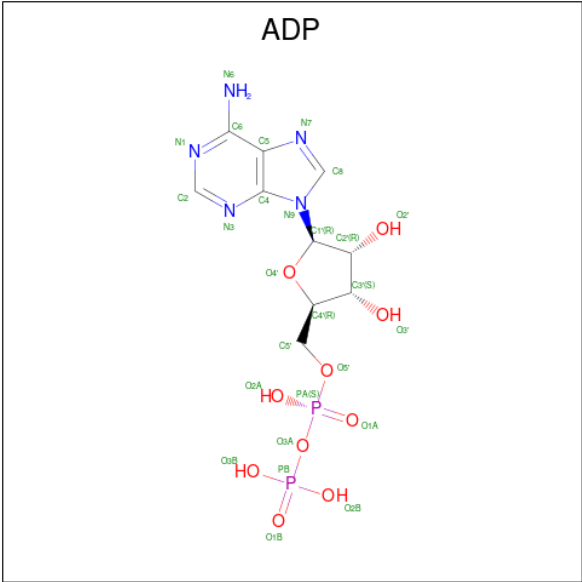


Mol	Chain	Residues	Atoms					AltConf
64	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	CQ	1	Total	Zn	0
			1	1	
65	Lj	1	Total	Zn	0
			1	1	
65	Lp	1	Total	Zn	0
			1	1	

- Molecule 66 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
66	CW	1	Total	C	N	O	P	0
			27	10	5	10	2	

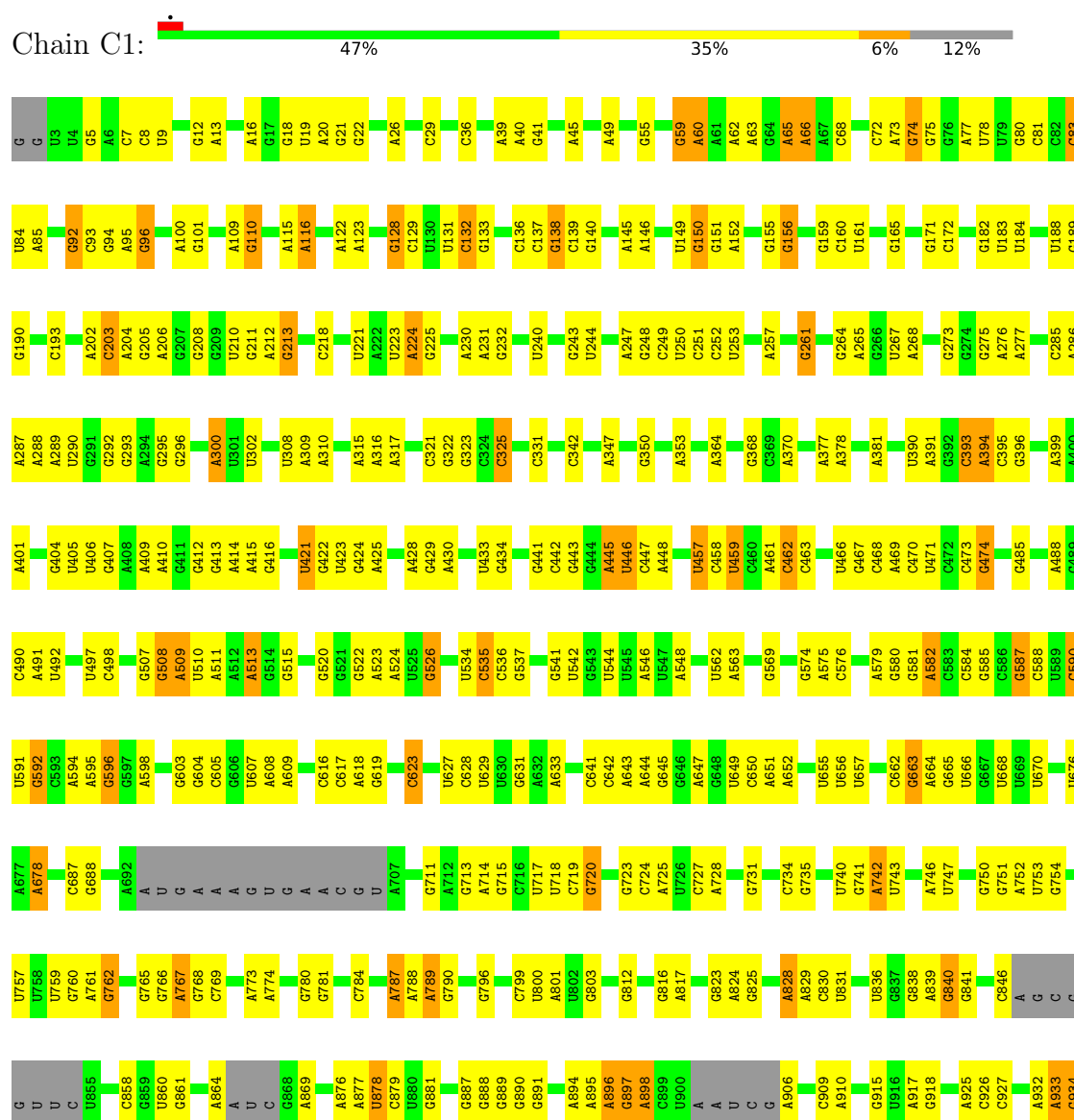
- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	CW	1	Total	Mg	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 (3341-MER)

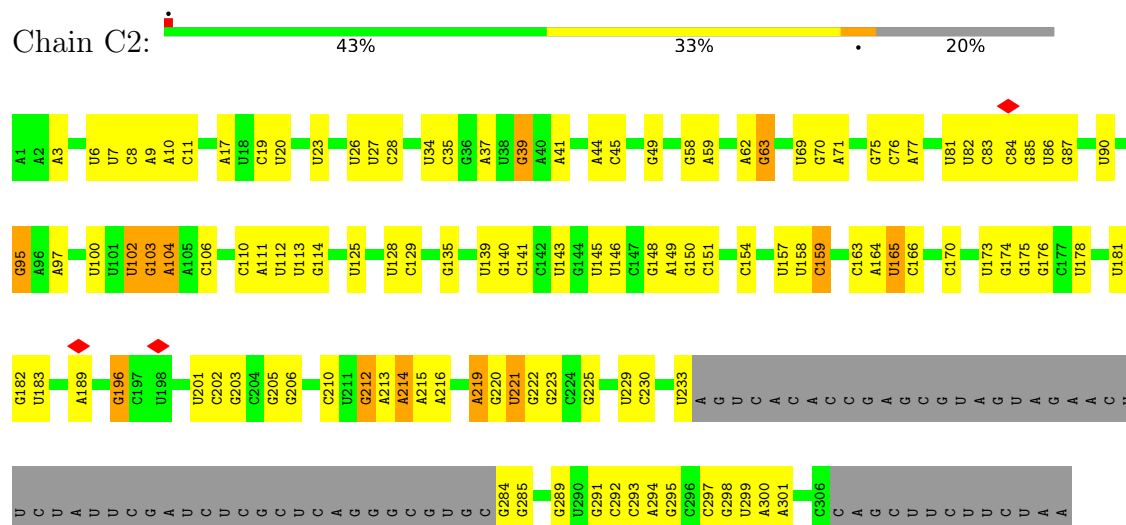


WORLDWIDE
PDB
PROTEIN DATA BANK

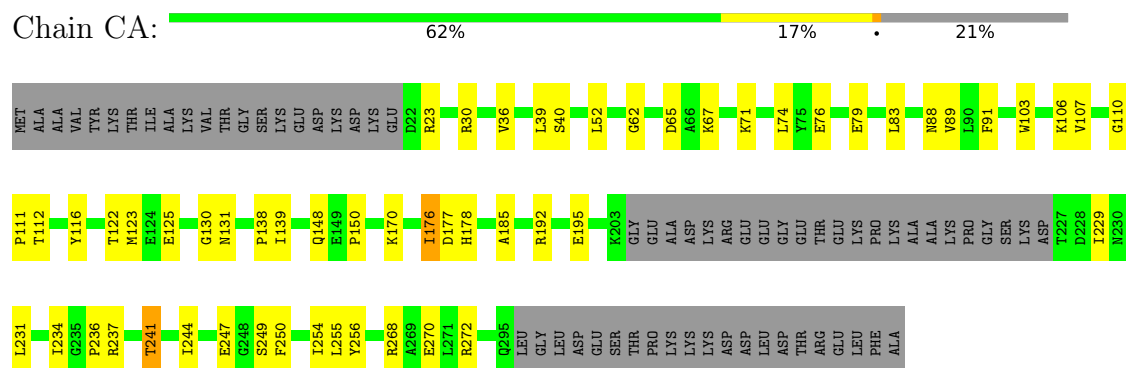




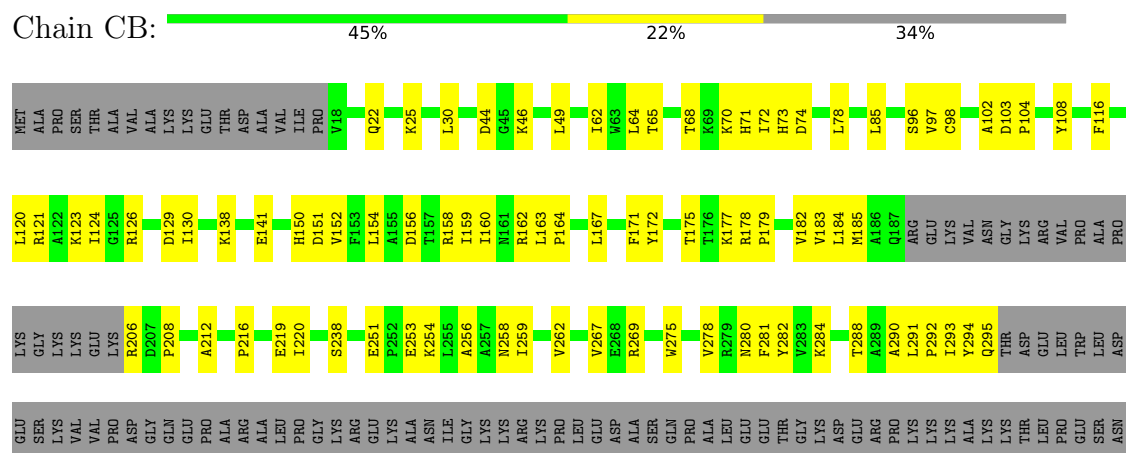
• Molecule 2: RNA (319-MER)



• Molecule 3: Brix domain-containing protein

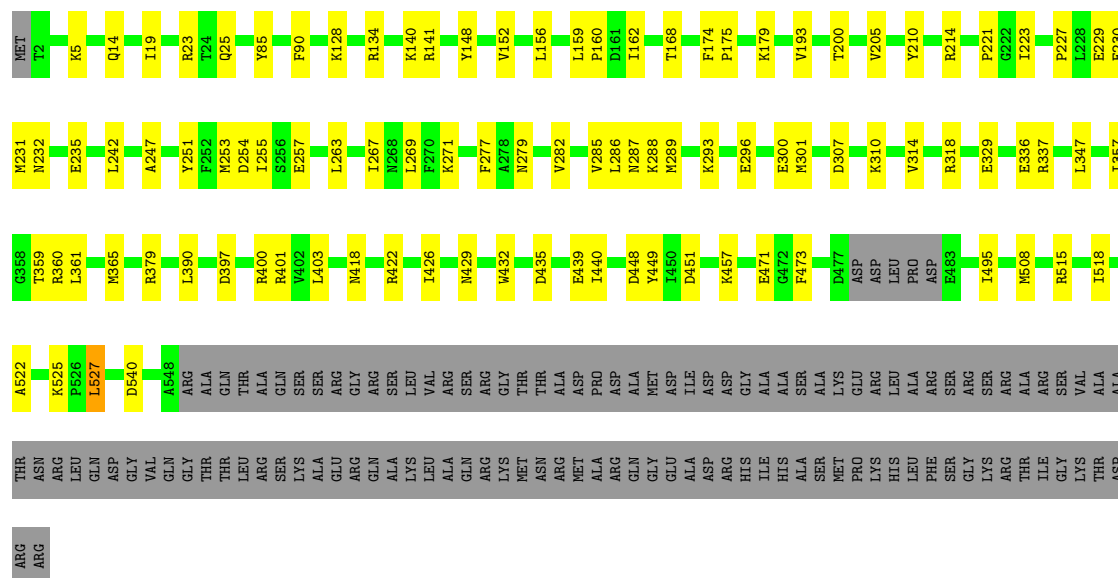


• Molecule 4: Ribosome biogenesis protein C8F11.04



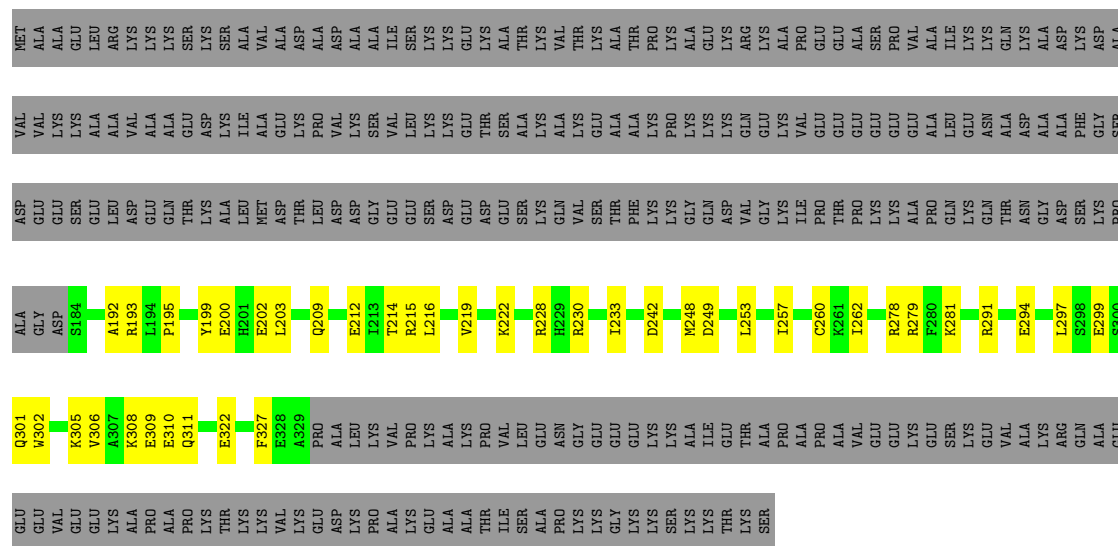






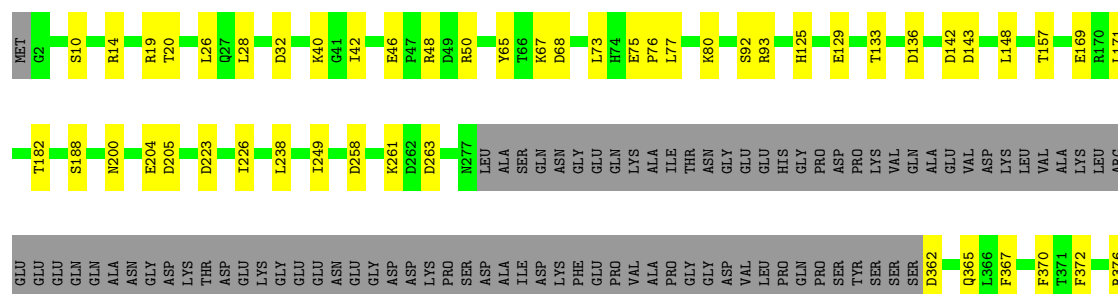
• Molecule 11: Putative RNA-binding protein

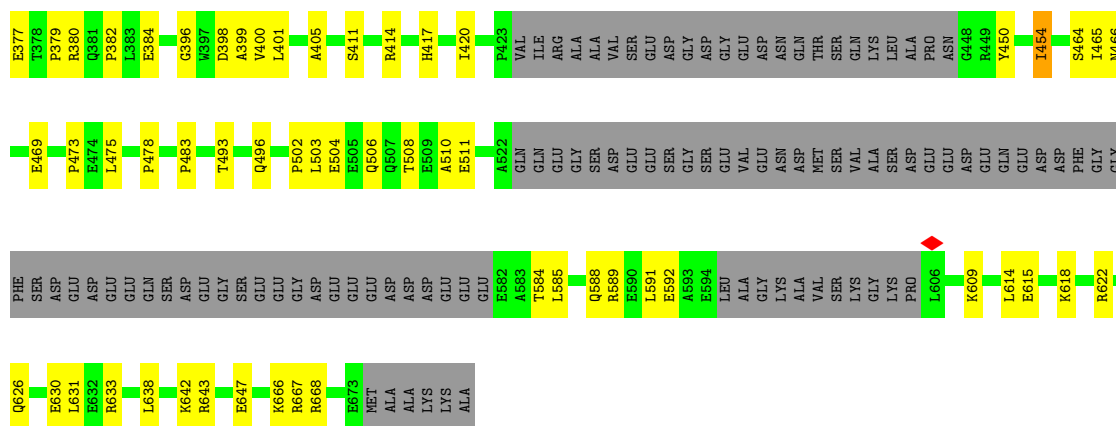
Chain CI: 25% 10% 65%



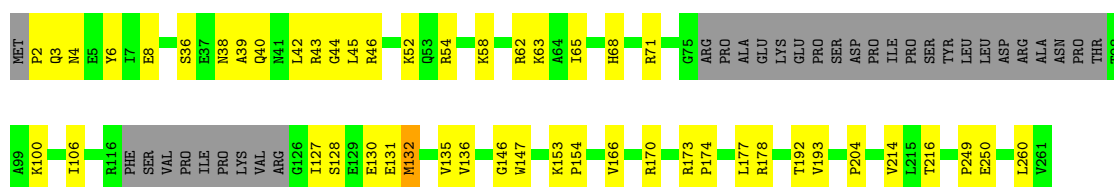
• Molecule 12: Pescadillo homolog

Chain CJ: 57% 15% 27%

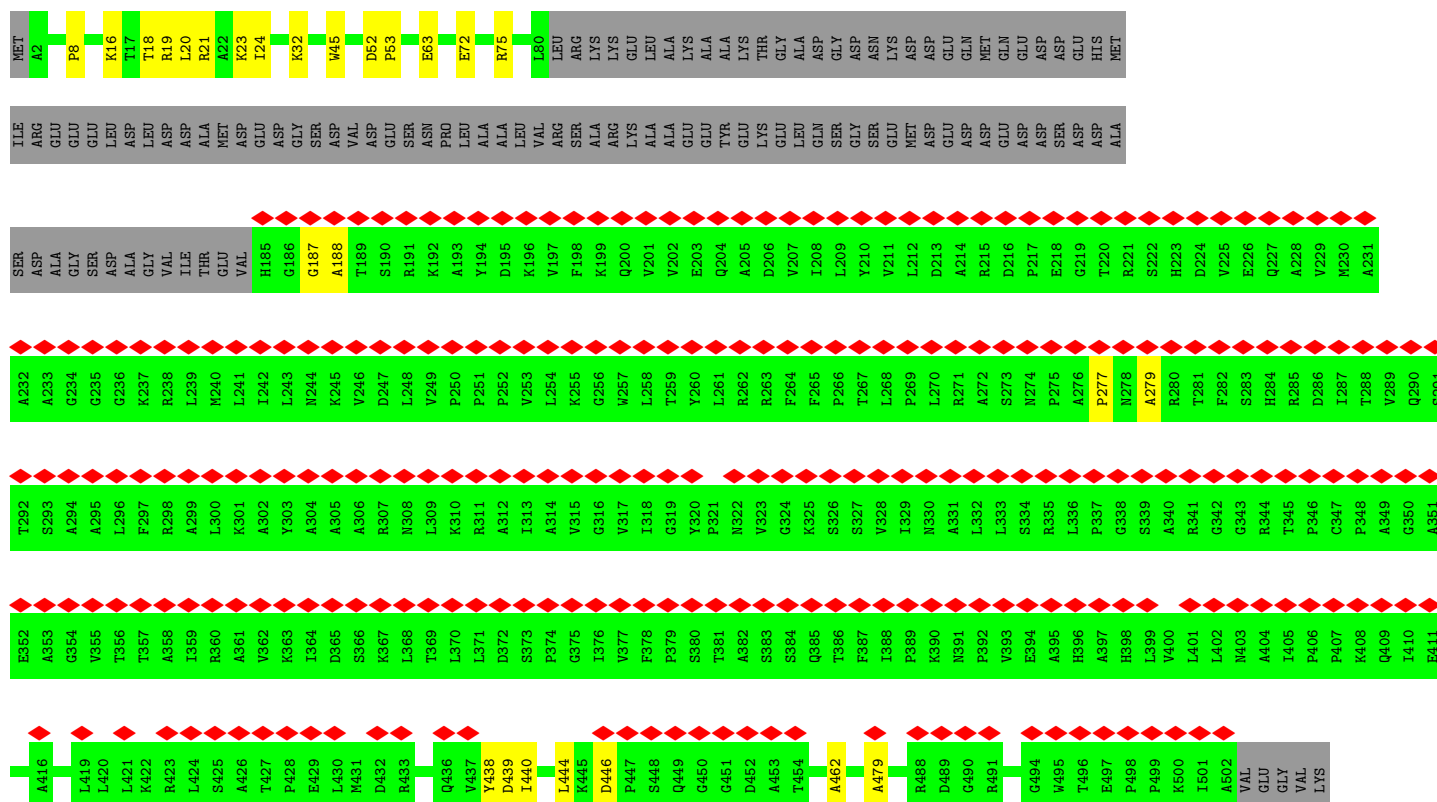




• Molecule 13: Ribosome biogenesis protein NSA2 homolog



• Molecule 14: Putative GTP binding protein



GLY GLY ASN THR GLY LYS VAL ARG LYS ILE ASP ALA ASP GLN GLU VAL K20 PRO ASP GLN LYS ILE VAL THR GLU TRP ALA LYS PHE LYS LEU GLY LEU TRP GLY ASP GLU GLN THR GLU GLY ASP LYS MET GLU ALA

- Molecule 15: 60S ribosomal protein 17-like protein

Chain CM: 72% 18% 10%

MET SER THR THR VAL PRO THR GLN ASP I12 T17 L18 L19 K20 R29 A30 E31 K52 E55 K56 Y57 Q64 K68 I69 R73 S80 F81 H82 I83 P84 V90 F91 K100 I101 P102 P105 T108 V123 K124 T129 M132 I133 K134

P145 N146 R151 E152 L153 R166 T170 D171 E176 I184 I185 C186 I187 E188 D189 E193 V197 W209 L213 S214 G219 PHE ARG PRO ARG LYS PHE LYS HIS PHE ILE GLU GLY ASP LEU G235 T241 L244 M248 H249

- Molecule 15: 60S ribosomal protein 17-like protein

Chain LF: 87% 12%

MET SER S3 L18 E31 V49 R62 R66 R73 K76 Q77 I85 N99 K104 P105 L114 V121 T126 K127 A128 T129 A130 P138 I154 N178 Y182 I187 Q203 L213 N217 R221 K224 G232 D233 L234

R237 R240 R249

- Molecule 16: Eukaryotic translation initiation factor 6

Chain CN: 80% 20%

M1 N11 E12 S22 E32 E39 D44 R50 I53 T56 R67 L70 D78 Q79 R85 P89 D90 D91 I94 E98 E99 R100 L101 V107 I108 V109 D112 H113 L116 I117 L121 E122 G149 M152 M156 S166 I167

Q168 D169 Q170 E172 L177 V182 A183 M197 D201 G207 L208 D209 V221 T233 S236 M237 Y246

- Molecule 17: DUF2423 domain-containing protein

Chain CO: 44% 8% 48%

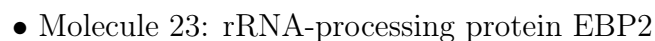
MET A2 R9 L30 L37 M38 A43 PRO LYS PRO ASP ILE GLU MET LYS GLU GLU GLU SER GLU ALA THR ALA LYS GLN PRO LYS LEU GLU THR THR LYS ASP ASP THR ALA MET ASP VAL ASP GLY LYS ALA PRO THR LEU S83 G92 D95 SER ARG LYS ARG

GLY LYS S104 S105 I106 V107 M110 LYS PRO PRO ARG ASN ASN LEU LYS LYS

- Molecule 18: RNA methyltransferase nop2-like protein

Chain CP: 35% 12% 53%

MET GLY THR LYS ARG ARG LYS HIS GLN PRO PRO GLU PRO PRO LEU PRO GLU GLU HIS PHE LEU LYS LYS THR ARG LYS GLY LEU VAL GLU ASP THR THR PRO PRO ALA GLU PRO PRO ASP MET ASP ALA LYS LYS ARG ARG THR THR LYS THR LYS GLU GLU THR LYS PRO HIS LYS ARG ALA



Device Type	Percentage
Smartphone	61%
Tablet	33%
Feature phone	6%

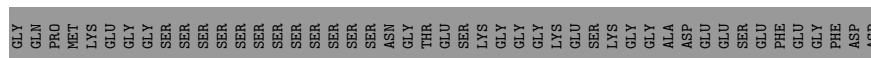


84% 10% 5%

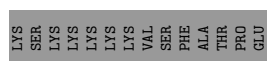
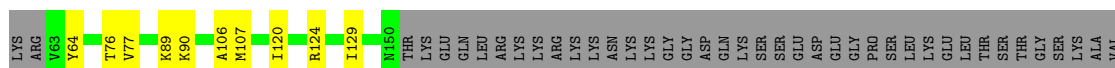


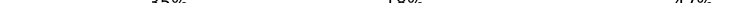
Category	Percentage
Very bad	44%
Bad	34%
Average	20%
Good	2%

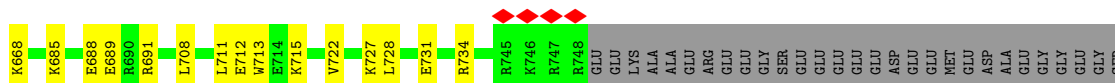
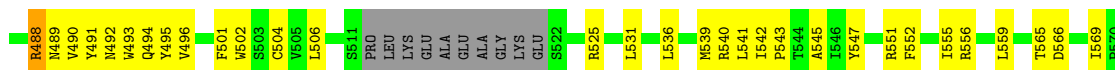
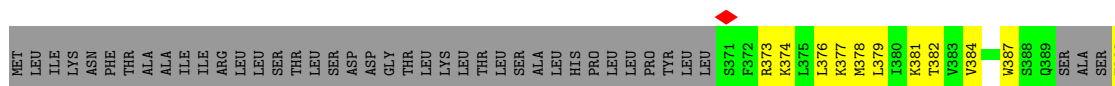
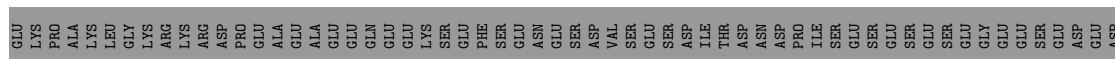
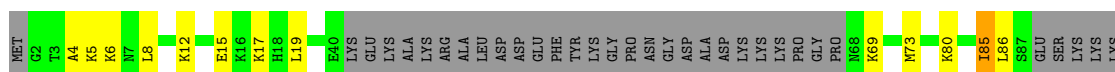




- Chain CX: 

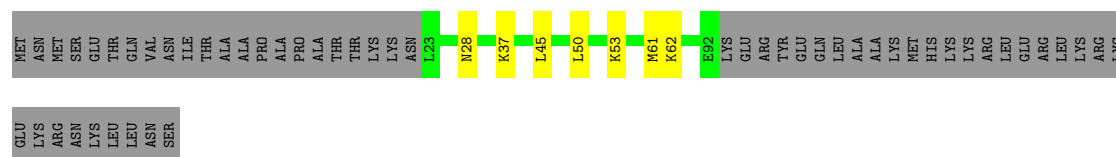


- Chain CY: 



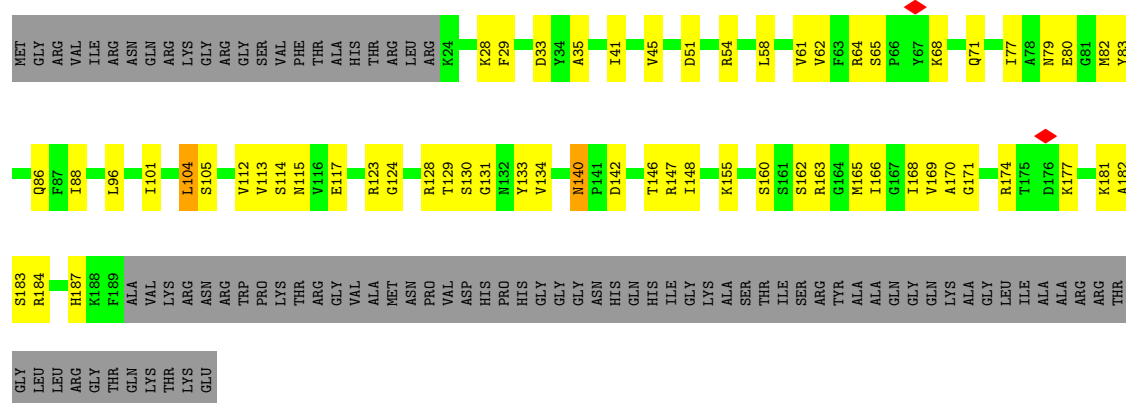
- Molecule 30: rRNA-processing protein

Chain Cz:  51% 6% 43%



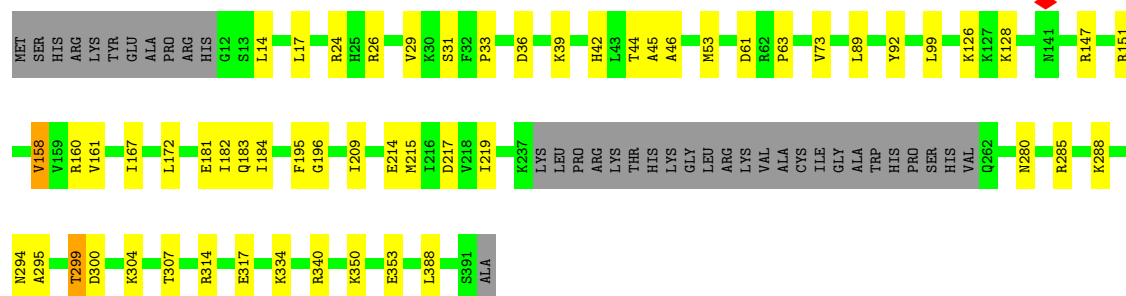
- Molecule 31: 60S ribosomal protein L2-like protein

Chain LA:  41% 23% 35%



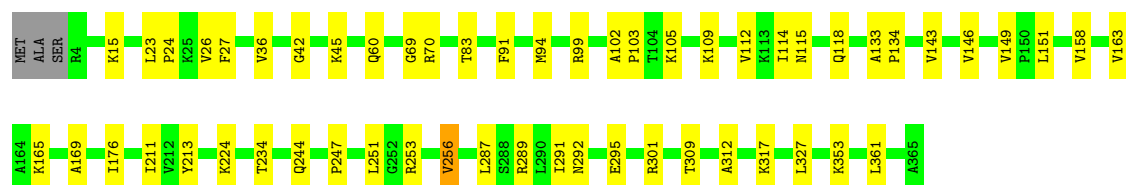
- Molecule 32: 60S ribosomal protein L3-like protein

Chain LB:  77% 14% 9%



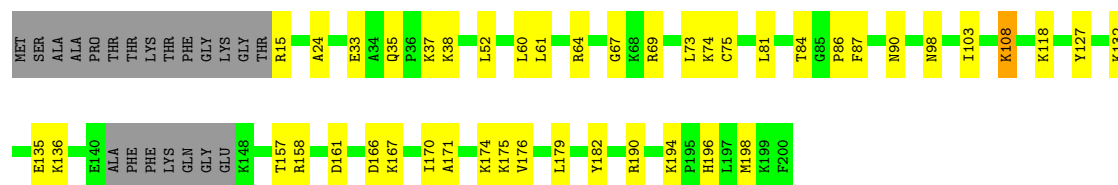
- Molecule 33: 60S ribosomal protein L4-like protein

Chain LC:  84% 15% 1%



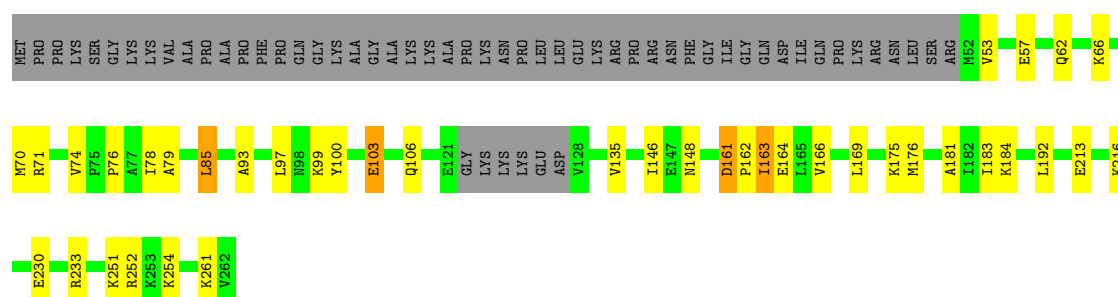
- Molecule 34: 60S ribosomal protein L6

Chain LE:  68% 22% 10%



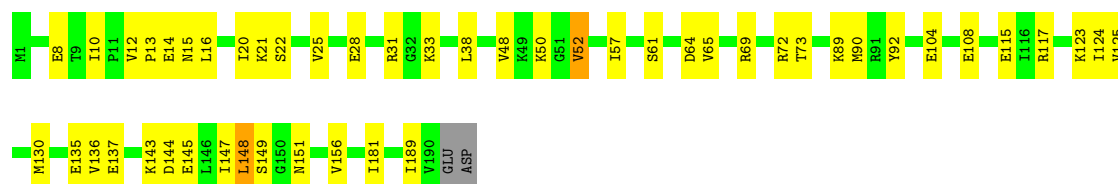
- Molecule 35: 60S ribosomal protein L8

Chain LG:  63% 14% 22%



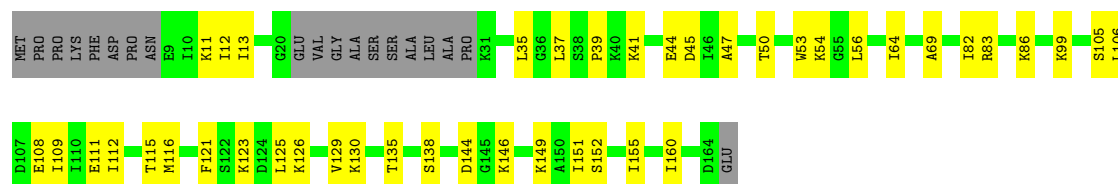
- Molecule 36: 60S ribosomal protein l9-like protein

Chain LH:  73% 24% 3%

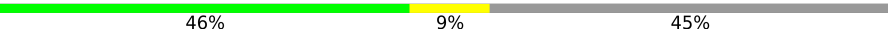


- Molecule 37: 60S ribosomal protein L12-like protein

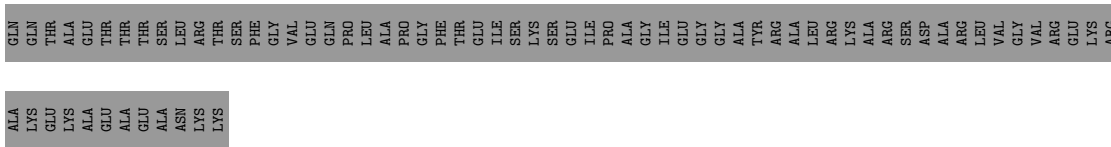
Chain LK:  62% 26% 12%



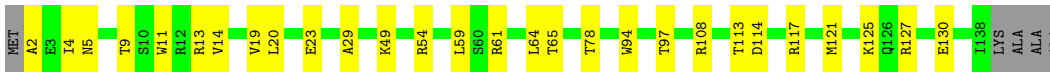
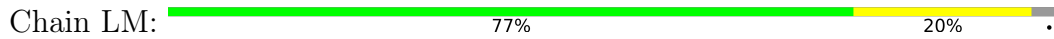
- Molecule 38: 60S ribosomal protein L13

Chain LL:  46% 9% 45%

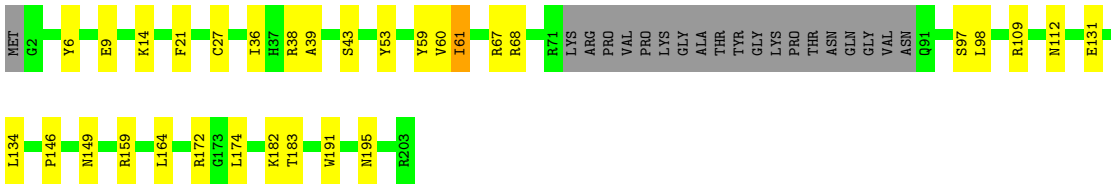
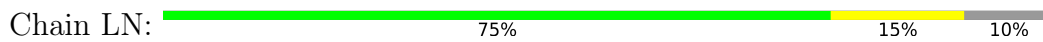




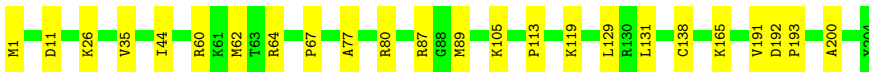
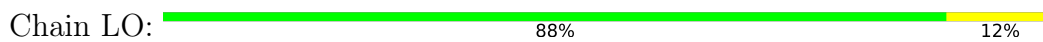
- Molecule 39: 60S ribosomal protein L14-like protein



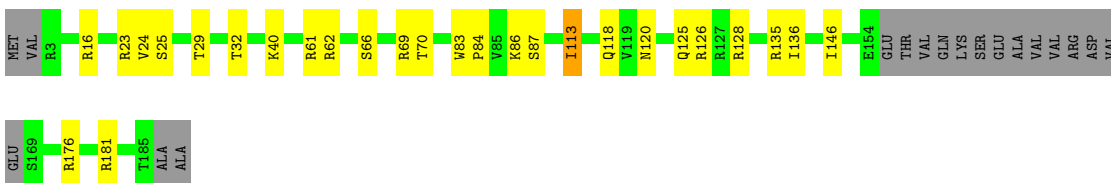
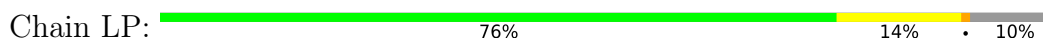
- Molecule 40: Ribosomal protein L15



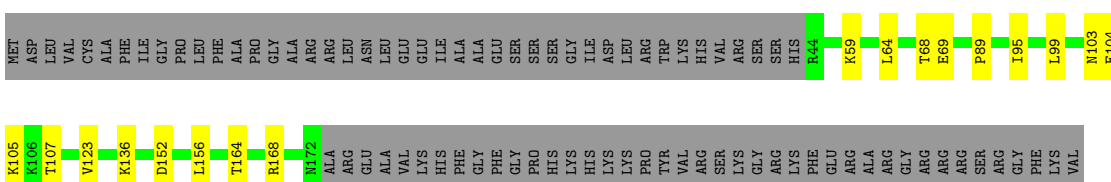
- Molecule 41: 60S ribosomal protein L16-like protein



- Molecule 42: 60S ribosomal protein l17-like protein



- Molecule 43: Ribosomal protein L18-like protein



Chain LR: 95%



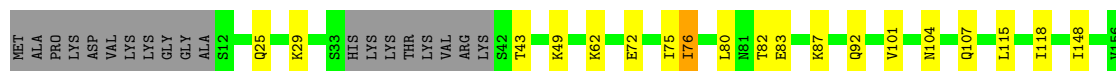


Chain LV:  83% 14%



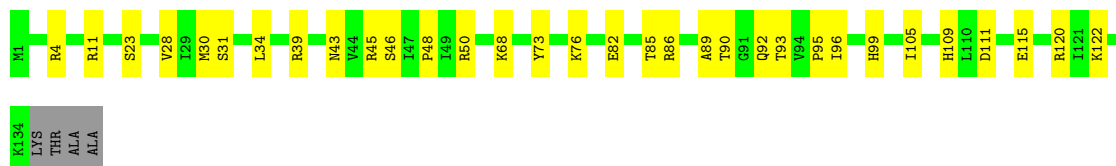
- Molecule 49: 60S ribosomal protein L25-like protein

Chain LX:  76% 12% 12%



- Molecule 50: 60S ribosomal protein L26-like protein

Chain LY:  74% 23%



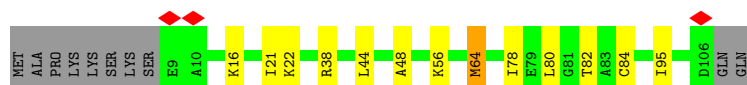
- Molecule 51: 60S ribosomal protein L27

Chain LZ:  63% 37%



- Molecule 52: 60S ribosomal protein l30-like protein

Chain Lc:  79% 11% 9%



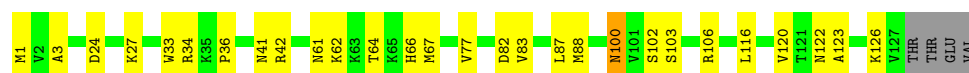
- Molecule 53: Putative 60S ribosomal protein

Chain Ld:  78% 12% 9%



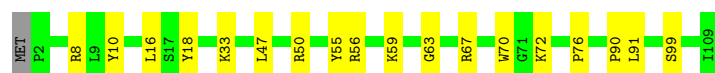
- Molecule 54: 60S ribosomal protein L32-like protein

Chain Le:  76% 21% ..



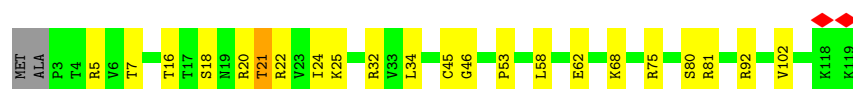
- Molecule 55: 60S ribosomal protein l33-like protein

Chain Lf:  83% 17% .



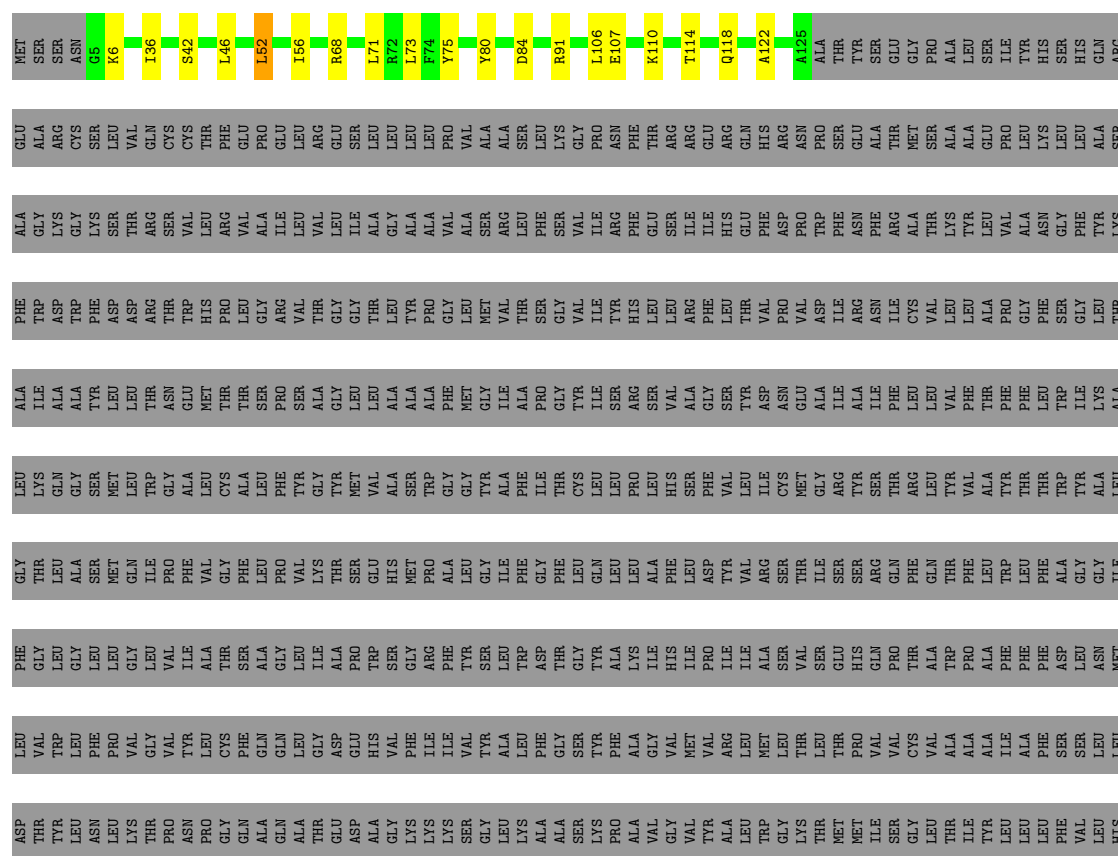
- Molecule 56: Ribosomal protein l34-like protein

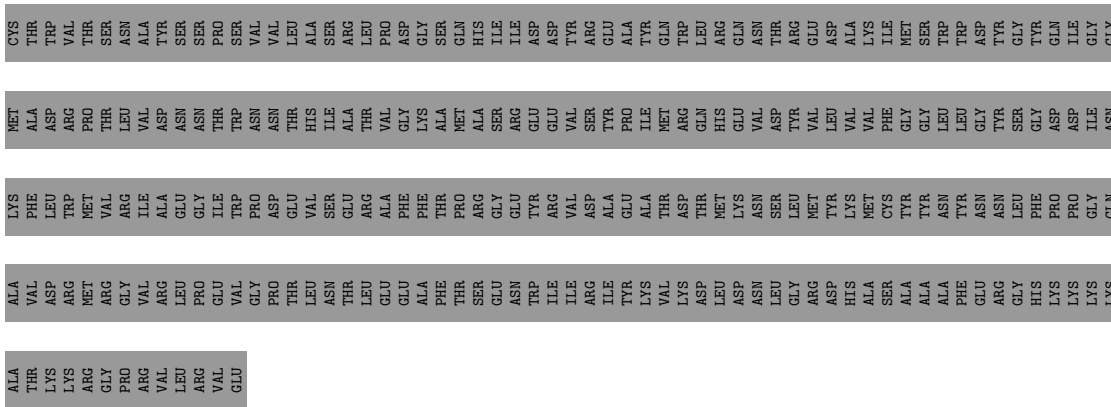
Chain Lg:  80% 18% ..



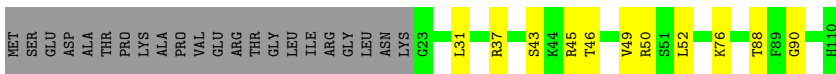
- Molecule 57: dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh:  11% 87% .





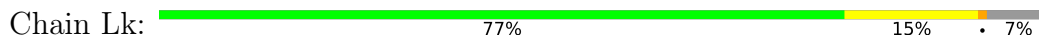
- Molecule 58: 60S ribosomal protein L36



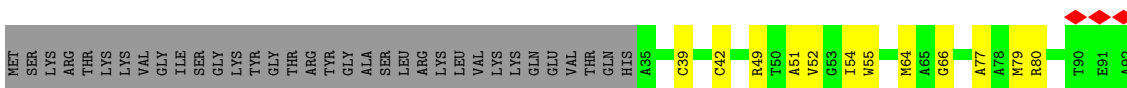
- Molecule 59: Ribosomal protein L37



- Molecule 60: 60S ribosomal protein L38-like protein



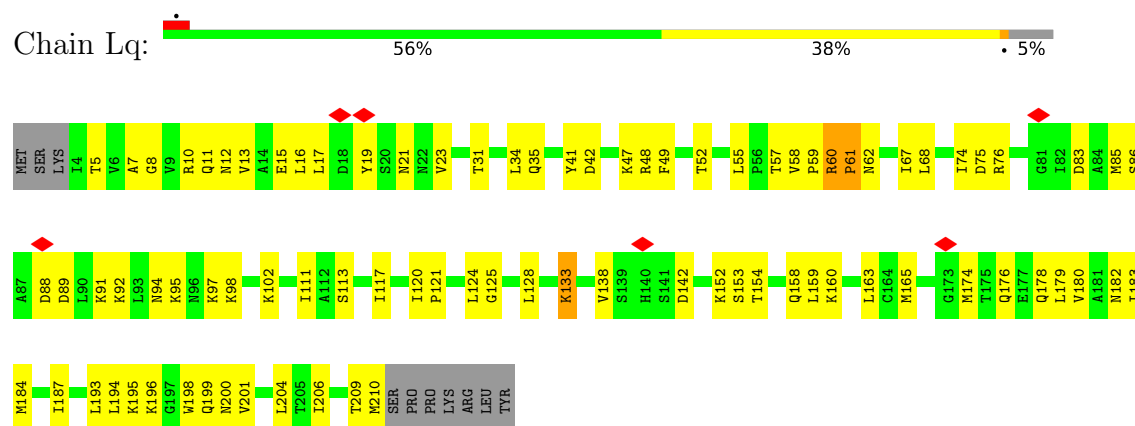
- Molecule 61: 60S ribosomal protein L43-like protein



- Molecule 62: 60S ribosomal protein L39



- Molecule 63: Ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	170689	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.772	Depositor
Minimum map value	-0.289	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	508.32, 508.32, 508.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, TPO, SEP, GTP, 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	C1	0.14	0/70087	0.27	0/109235
2	C2	0.12	0/6097	0.25	0/9499
3	CA	0.14	0/2115	0.33	0/2840
4	CB	0.15	0/2109	0.43	0/2866
5	CC	0.14	0/5423	0.33	0/7380
6	CD	0.15	0/3543	0.42	0/4824
7	CE	0.14	0/3743	0.36	0/5045
8	CF	0.13	0/1982	0.35	0/2671
9	CG	0.14	0/1422	0.29	0/1920
10	CH	0.13	0/4468	0.32	0/6029
11	CI	0.13	0/1225	0.34	0/1645
12	CJ	0.14	0/4125	0.33	0/5548
13	CK	0.13	0/1863	0.30	0/2494
14	CL	0.12	0/2247	0.35	0/3076
15	CM	0.13	0/1851	0.31	0/2481
15	LF	0.13	0/2055	0.30	0/2758
16	CN	0.14	0/1881	0.36	1/2560 (0.0%)
17	CO	0.11	0/470	0.25	0/619
18	CP	0.18	0/2859	0.45	1/3870 (0.0%)
19	CQ	0.14	0/1507	0.34	0/1996
20	CR	0.13	0/1369	0.24	0/1828
21	CS	0.17	0/5162	0.39	0/6904
22	CT	0.15	0/3974	0.38	1/5357 (0.0%)
23	CU	0.12	0/1428	0.30	0/1910
24	CV	0.12	0/1091	0.29	0/1468
25	CW	0.28	0/4397	0.63	9/5951 (0.2%)
26	CX	0.11	0/705	0.24	0/938
27	CY	0.22	0/3470	0.51	1/4659 (0.0%)
28	CZ	0.16	0/4025	0.44	0/5467
29	Ca	0.13	0/988	0.35	0/1302
30	Cz	0.10	0/598	0.24	0/785
31	LA	0.16	0/1286	0.42	0/1734

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LB	0.15	0/2885	0.33	0/3872
33	LC	0.13	0/2809	0.32	0/3787
34	LE	0.13	0/1428	0.31	0/1921
35	LG	0.13	0/1674	0.28	0/2240
36	LH	0.13	0/1516	0.31	0/2038
37	LK	0.14	0/1124	0.39	0/1507
38	LL	0.14	0/983	0.29	0/1318
39	LM	0.13	0/1120	0.27	0/1507
40	LN	0.14	0/1595	0.29	0/2132
41	LO	0.15	0/1652	0.34	0/2215
42	LP	0.12	0/1367	0.27	0/1838
43	LQ	0.13	0/1033	0.29	0/1391
44	LR	0.12	0/1235	0.29	0/1644
45	LS	0.14	0/1468	0.31	0/1975
46	LT	0.13	0/1033	0.33	0/1389
47	LU	0.11	0/863	0.25	0/1155
48	LV	0.14	0/1013	0.31	0/1361
49	LX	0.12	0/1078	0.27	0/1451
50	LY	0.11	0/1079	0.26	0/1443
51	LZ	0.15	0/1135	0.32	0/1519
52	Lc	0.12	0/740	0.27	0/995
53	Ld	0.12	0/904	0.25	0/1209
54	Le	0.12	0/1043	0.28	0/1389
55	Lf	0.15	0/883	0.35	0/1187
56	Lg	0.12	0/943	0.29	0/1258
57	Lh	0.10	0/1006	0.24	0/1338
58	Li	0.11	0/738	0.22	0/971
59	Lj	0.13	0/606	0.30	0/803
60	Lk	0.14	0/628	0.35	0/835
61	Lp	0.10	0/441	0.32	0/590
62	Ll	0.10	0/329	0.27	0/440
63	Lq	0.19	0/1621	0.53	0/2180
All	All	0.15	0/187537	0.33	13/268557 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	CC	0	1
63	Lq	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	CP	289	PRO	CA-N-CD	-12.47	94.54	112.00
22	CT	159	PRO	CA-N-CD	-11.68	95.64	112.00
27	CY	85	ILE	N-CA-C	-8.27	105.85	113.71
25	CW	429	PRO	CA-N-CD	-7.14	102.00	112.00
25	CW	168	GLY	CA-C-N	6.59	130.69	120.68

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	CC	519	GLU	Peptide
63	Lq	60	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	62650	0	31592	939	0
2	C2	5456	0	2762	70	0
3	CA	2069	0	2109	44	0
4	CB	2063	0	2131	64	0
5	CC	5297	0	5220	89	0
6	CD	3468	0	3428	133	0
7	CE	3673	0	3778	79	0
8	CF	1945	0	1965	37	0
9	CG	1396	0	1420	24	0
10	CH	4388	0	4454	82	0
11	CI	1196	0	1202	31	0
12	CJ	4040	0	4087	78	0
13	CK	1835	0	1935	38	0
14	CL	2239	0	1495	20	0
15	CM	1820	0	1938	38	0
15	LF	2017	0	2130	24	0
16	CN	1856	0	1856	31	0
17	CO	468	0	503	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	CP	2798	0	2812	69	0
19	CQ	1485	0	1549	22	0
20	CR	1354	0	1400	24	0
21	CS	5082	0	5244	113	0
22	CT	3911	0	4023	47	0
23	CU	1415	0	1457	30	0
24	CV	1073	0	1130	14	0
25	CW	4310	0	4444	197	0
26	CX	701	0	742	9	0
27	CY	3413	0	3584	131	0
28	CZ	3975	0	3497	100	0
29	Ca	982	0	1044	27	0
30	Cz	592	0	640	8	0
31	LA	1259	0	1300	57	0
32	LB	2829	0	2933	42	0
33	LC	2752	0	2878	44	0
34	LE	1403	0	1503	34	0
35	LG	1651	0	1802	32	0
36	LH	1496	0	1575	35	0
37	LK	1112	0	1190	33	0
38	LL	964	0	1041	19	0
39	LM	1101	0	1170	27	0
40	LN	1563	0	1618	22	0
41	LO	1618	0	1714	22	0
42	LP	1345	0	1389	21	0
43	LQ	1021	0	1118	13	0
44	LR	1219	0	1291	29	0
45	LS	1433	0	1496	29	0
46	LT	1014	0	1073	20	0
47	LU	850	0	894	13	0
48	LV	995	0	1055	14	0
49	LX	1062	0	1145	16	0
50	LY	1065	0	1156	22	0
51	LZ	1112	0	1181	33	0
52	Lc	731	0	772	10	0
53	Ld	890	0	940	11	0
54	Le	1025	0	1104	23	0
55	Lf	862	0	891	15	0
56	Lg	930	0	1011	17	0
57	Lh	995	0	1110	14	0
58	Li	731	0	797	9	0
59	Lj	595	0	625	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	Lk	620	0	680	10	0
61	Lp	436	0	448	9	0
62	Ll	322	0	346	5	0
63	Lq	1600	0	1703	68	0
64	CH	32	0	12	4	0
65	CQ	1	0	0	0	0
65	Lj	1	0	0	0	0
65	Lp	1	0	0	0	0
66	CW	27	0	12	0	0
67	CW	1	0	0	0	0
All	All	177631	0	146544	2952	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 9.

The worst 5 of 2952 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1886:C:H42	1:C1:2294:A:N6	1.34	1.23
1:C1:1886:C:N4	1:C1:2294:A:H61	1.36	1.23
1:C1:3118:A:N6	1:C1:3225:C:H42	1.40	1.18
1:C1:3118:A:H61	1:C1:3225:C:N4	1.41	1.18
27:CY:525:ARG:NH2	27:CY:565:THR:HG23	1.62	1.14

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	CA	247/316 (78%)	232 (94%)	15 (6%)	0	100	100
4	CB	256/391 (66%)	239 (93%)	17 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CC	648/801 (81%)	623 (96%)	24 (4%)	1 (0%)	43	68
6	CD	450/495 (91%)	425 (94%)	25 (6%)	0	100	100
7	CE	459/598 (77%)	449 (98%)	10 (2%)	0	100	100
8	CF	243/270 (90%)	234 (96%)	9 (4%)	0	100	100
9	CG	175/184 (95%)	165 (94%)	10 (6%)	0	100	100
10	CH	538/661 (81%)	522 (97%)	16 (3%)	0	100	100
11	CI	144/414 (35%)	140 (97%)	4 (3%)	0	100	100
12	CJ	484/679 (71%)	473 (98%)	11 (2%)	0	100	100
13	CK	223/261 (85%)	214 (96%)	9 (4%)	0	100	100
14	CL	393/558 (70%)	368 (94%)	23 (6%)	2 (0%)	24	48
15	CM	219/249 (88%)	212 (97%)	7 (3%)	0	100	100
15	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
16	CN	244/246 (99%)	233 (96%)	11 (4%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	354/751 (47%)	336 (95%)	18 (5%)	0	100	100
19	CQ	173/225 (77%)	167 (96%)	6 (4%)	0	100	100
20	CR	159/237 (67%)	158 (99%)	1 (1%)	0	100	100
21	CS	609/834 (73%)	584 (96%)	25 (4%)	0	100	100
22	CT	478/688 (70%)	461 (96%)	17 (4%)	0	100	100
23	CU	174/451 (39%)	170 (98%)	4 (2%)	0	100	100
24	CV	137/147 (93%)	135 (98%)	2 (2%)	0	100	100
25	CW	534/679 (79%)	479 (90%)	54 (10%)	1 (0%)	43	68
26	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100
27	CY	406/788 (52%)	380 (94%)	25 (6%)	1 (0%)	43	68
28	CZ	572/697 (82%)	552 (96%)	20 (4%)	0	100	100
29	Ca	111/227 (49%)	109 (98%)	2 (2%)	0	100	100
30	Cz	68/123 (55%)	66 (97%)	2 (3%)	0	100	100
31	LA	164/254 (65%)	155 (94%)	9 (6%)	0	100	100
32	LB	352/392 (90%)	335 (95%)	17 (5%)	0	100	100
33	LC	360/365 (99%)	346 (96%)	14 (4%)	0	100	100
34	LE	175/200 (88%)	169 (97%)	6 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	LG	201/262 (77%)	197 (98%)	4 (2%)	0	100	100
36	LH	188/192 (98%)	180 (96%)	8 (4%)	0	100	100
37	LK	142/165 (86%)	136 (96%)	6 (4%)	0	100	100
38	LL	115/213 (54%)	112 (97%)	3 (3%)	0	100	100
39	LM	135/142 (95%)	129 (96%)	6 (4%)	0	100	100
40	LN	179/203 (88%)	170 (95%)	9 (5%)	0	100	100
41	LO	202/204 (99%)	195 (96%)	7 (4%)	0	100	100
42	LP	165/187 (88%)	160 (97%)	5 (3%)	0	100	100
43	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
44	LR	144/2898 (5%)	143 (99%)	1 (1%)	0	100	100
45	LS	172/174 (99%)	165 (96%)	7 (4%)	0	100	100
46	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	16	37
47	LU	103/127 (81%)	100 (97%)	3 (3%)	0	100	100
48	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
49	LX	133/156 (85%)	131 (98%)	2 (2%)	0	100	100
50	LY	132/138 (96%)	127 (96%)	5 (4%)	0	100	100
51	LZ	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
52	Lc	96/108 (89%)	96 (100%)	0	0	100	100
53	Ld	107/120 (89%)	105 (98%)	2 (2%)	0	100	100
54	Le	125/131 (95%)	123 (98%)	2 (2%)	0	100	100
55	Lf	106/109 (97%)	104 (98%)	2 (2%)	0	100	100
56	Lg	115/119 (97%)	114 (99%)	1 (1%)	0	100	100
57	Lh	119/935 (13%)	116 (98%)	3 (2%)	0	100	100
58	Li	86/110 (78%)	86 (100%)	0	0	100	100
59	Lj	72/95 (76%)	71 (99%)	1 (1%)	0	100	100
60	Lk	73/81 (90%)	68 (93%)	5 (7%)	0	100	100
61	Lp	56/92 (61%)	52 (93%)	4 (7%)	0	100	100
62	Ll	36/51 (71%)	35 (97%)	1 (3%)	0	100	100
63	Lq	205/217 (94%)	183 (89%)	21 (10%)	1 (0%)	24	48
All	All	13660/21629 (63%)	13103 (96%)	550 (4%)	7 (0%)	49	73

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	CW	393	ARG
27	CY	457	GLN
14	CL	439	ASP
14	CL	446	ASP
46	LT	44	VAL

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	CA	223/276 (81%)	221 (99%)	2 (1%)	70	87
4	CB	222/329 (68%)	221 (100%)	1 (0%)	81	92
5	CC	578/708 (82%)	568 (98%)	10 (2%)	53	79
6	CD	381/410 (93%)	375 (98%)	6 (2%)	55	80
7	CE	398/517 (77%)	394 (99%)	4 (1%)	68	86
8	CF	214/236 (91%)	209 (98%)	5 (2%)	44	73
9	CG	150/155 (97%)	147 (98%)	3 (2%)	48	76
10	CH	481/575 (84%)	475 (99%)	6 (1%)	63	84
11	CI	121/336 (36%)	120 (99%)	1 (1%)	73	88
12	CJ	428/579 (74%)	422 (99%)	6 (1%)	59	82
13	CK	195/225 (87%)	191 (98%)	4 (2%)	47	75
14	CL	72/458 (16%)	72 (100%)	0	100	100
15	CM	191/215 (89%)	190 (100%)	1 (0%)	81	92
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	87
16	CN	206/206 (100%)	204 (99%)	2 (1%)	68	86
17	CO	48/99 (48%)	47 (98%)	1 (2%)	47	75
18	CP	302/632 (48%)	299 (99%)	3 (1%)	68	86
19	CQ	150/192 (78%)	150 (100%)	0	100	100
20	CR	144/206 (70%)	143 (99%)	1 (1%)	76	90
21	CS	532/716 (74%)	522 (98%)	10 (2%)	50	77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	CT	427/600 (71%)	425 (100%)	2 (0%)	81	92
23	CU	149/376 (40%)	149 (100%)	0	100	100
24	CV	109/112 (97%)	108 (99%)	1 (1%)	70	87
25	CW	476/577 (82%)	459 (96%)	17 (4%)	31	60
26	CX	76/172 (44%)	75 (99%)	1 (1%)	61	83
27	CY	369/686 (54%)	363 (98%)	6 (2%)	55	80
28	CZ	310/581 (53%)	301 (97%)	9 (3%)	37	67
29	Ca	101/195 (52%)	101 (100%)	0	100	100
30	Cz	60/107 (56%)	60 (100%)	0	100	100
31	LA	131/198 (66%)	128 (98%)	3 (2%)	44	73
32	LB	301/331 (91%)	296 (98%)	5 (2%)	53	79
33	LC	283/285 (99%)	278 (98%)	5 (2%)	51	78
34	LE	151/166 (91%)	149 (99%)	2 (1%)	61	83
35	LG	176/222 (79%)	169 (96%)	7 (4%)	28	56
36	LH	167/169 (99%)	165 (99%)	2 (1%)	63	84
37	LK	121/136 (89%)	120 (99%)	1 (1%)	73	88
38	LL	99/176 (56%)	98 (99%)	1 (1%)	68	86
39	LM	115/117 (98%)	114 (99%)	1 (1%)	70	87
40	LN	164/180 (91%)	161 (98%)	3 (2%)	51	78
41	LO	163/163 (100%)	162 (99%)	1 (1%)	78	91
42	LP	137/152 (90%)	135 (98%)	2 (2%)	57	81
43	LQ	110/178 (62%)	109 (99%)	1 (1%)	70	87
44	LR	128/2396 (5%)	127 (99%)	1 (1%)	73	88
45	LS	154/154 (100%)	151 (98%)	3 (2%)	50	77
46	LT	109/135 (81%)	108 (99%)	1 (1%)	70	87
47	LU	93/108 (86%)	93 (100%)	0	100	100
48	LV	99/102 (97%)	99 (100%)	0	100	100
49	LX	114/129 (88%)	113 (99%)	1 (1%)	70	87
50	LY	117/119 (98%)	114 (97%)	3 (3%)	40	70
51	LZ	121/121 (100%)	120 (99%)	1 (1%)	73	88
52	Lc	79/88 (90%)	77 (98%)	2 (2%)	42	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	Ld	95/105 (90%)	94 (99%)	1 (1%)	65	85
54	Le	110/114 (96%)	109 (99%)	1 (1%)	70	87
55	Lf	89/90 (99%)	89 (100%)	0	100	100
56	Lg	101/102 (99%)	100 (99%)	1 (1%)	68	86
57	Lh	108/781 (14%)	105 (97%)	3 (3%)	38	68
58	Li	75/93 (81%)	75 (100%)	0	100	100
59	Lj	61/78 (78%)	61 (100%)	0	100	100
60	Lk	71/76 (93%)	70 (99%)	1 (1%)	59	82
61	Lp	45/74 (61%)	45 (100%)	0	100	100
62	Ll	34/46 (74%)	34 (100%)	0	100	100
63	Lq	179/189 (95%)	177 (99%)	2 (1%)	65	85
All	All	11426/18264 (63%)	11267 (99%)	159 (1%)	57	82

5 of 159 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	LE	108	LYS
49	LX	76	ILE
35	LG	57	GLU
39	LM	20	LEU
53	Ld	104	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
21	CS	383	ASN
56	Lg	15	ASN
25	CW	287	GLN
54	Le	72	HIS
36	LH	171	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2903/3341 (86%)	554 (19%)	22 (0%)
2	C2	254/319 (79%)	54 (21%)	1 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3157/3660 (86%)	608 (19%)	23 (0%)

5 of 608 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	16	A
1	C1	22	G
1	C1	26	A
1	C1	41	G
1	C1	49	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3162	A
1	C1	3229	G
1	C1	3216	U
1	C1	3257	U
1	C1	1077	U

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

2 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$
5	SEP	CC	160	5	8,9,10	1.58	1 (12%)	7,12,14	1.22	1 (14%)
5	TPO	CC	163	5	8,10,11	1.71	1 (12%)	10,14,16	1.23	1 (10%)

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
5	SEP	CC	160	5	-	0/6/8/10	-
5	TPO	CC	163	5	-	6/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	CC	163	TPO	P-O1P	3.55	1.61	1.50
5	CC	160	SEP	P-O1P	3.47	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	P-OG1-CB	-2.77	115.79	123.33
5	CC	160	SEP	OG-CB-CA	2.53	110.61	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	163	TPO	N-CA-CB-CG2
5	CC	163	TPO	N-CA-CB-OG1
5	CC	163	TPO	C-CA-CB-CG2
5	CC	163	TPO	O-C-CA-CB
5	CC	163	TPO	CG2-CB-OG1-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	CC	160	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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
66	ADP	CW	1001	67	28,29,29	0.44	0	43,45,45	0.56	0
64	GTP	CH	1001	-	33,34,34	0.97	1 (3%)	50,54,54	1.61	8 (16%)

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
66	ADP	CW	1001	67	-	5/16/32/32	0/3/3/3
64	GTP	CH	1001	-	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	CH	1001	GTP	C2-N3	2.03	1.38	1.33

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	CH	1001	GTP	C5-C4-N3	-4.92	120.56	128.39
64	CH	1001	GTP	C2-N3-C4	4.68	120.36	112.30
64	CH	1001	GTP	N9-C4-N3	3.05	132.05	125.95
64	CH	1001	GTP	C2-N1-C6	-2.88	119.88	125.11
64	CH	1001	GTP	N9-C8-N7	-2.74	108.31	113.40

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

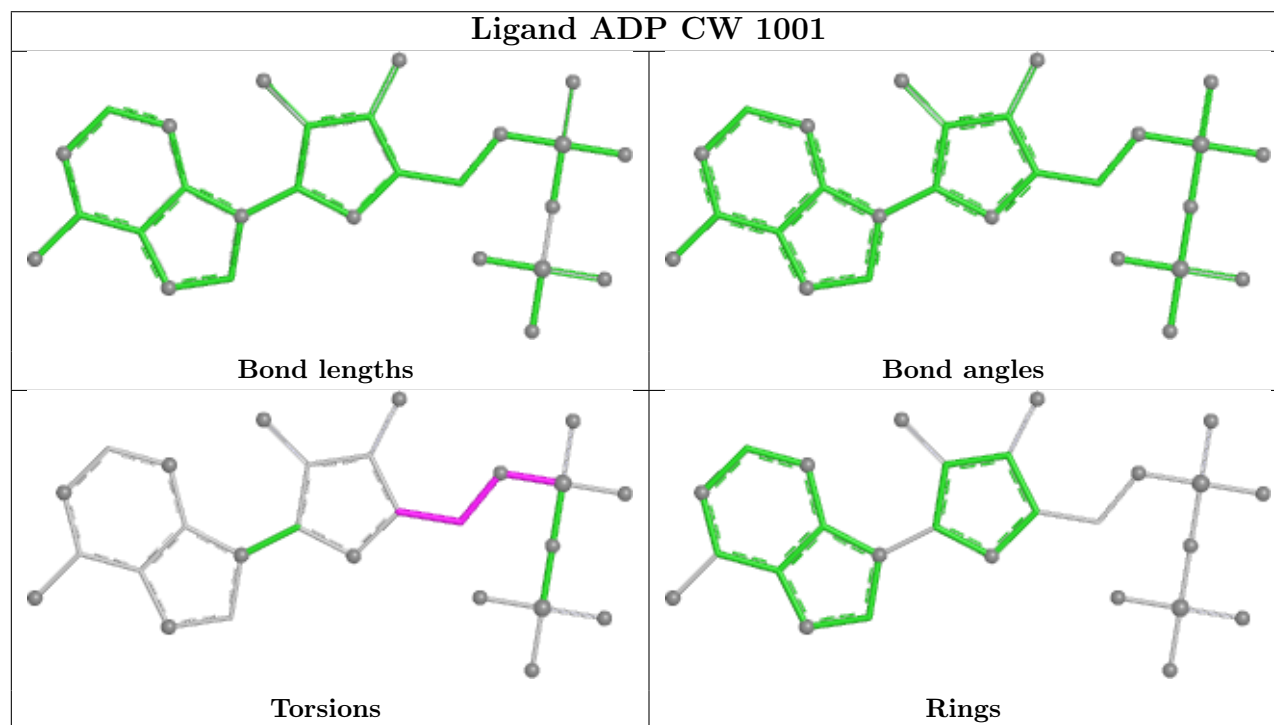
Mol	Chain	Res	Type	Atoms
66	CW	1001	ADP	C5'-O5'-PA-O2A
66	CW	1001	ADP	C5'-O5'-PA-O3A
66	CW	1001	ADP	C4'-C5'-O5'-PA
66	CW	1001	ADP	O4'-C4'-C5'-O5'
66	CW	1001	ADP	C3'-C4'-C5'-O5'

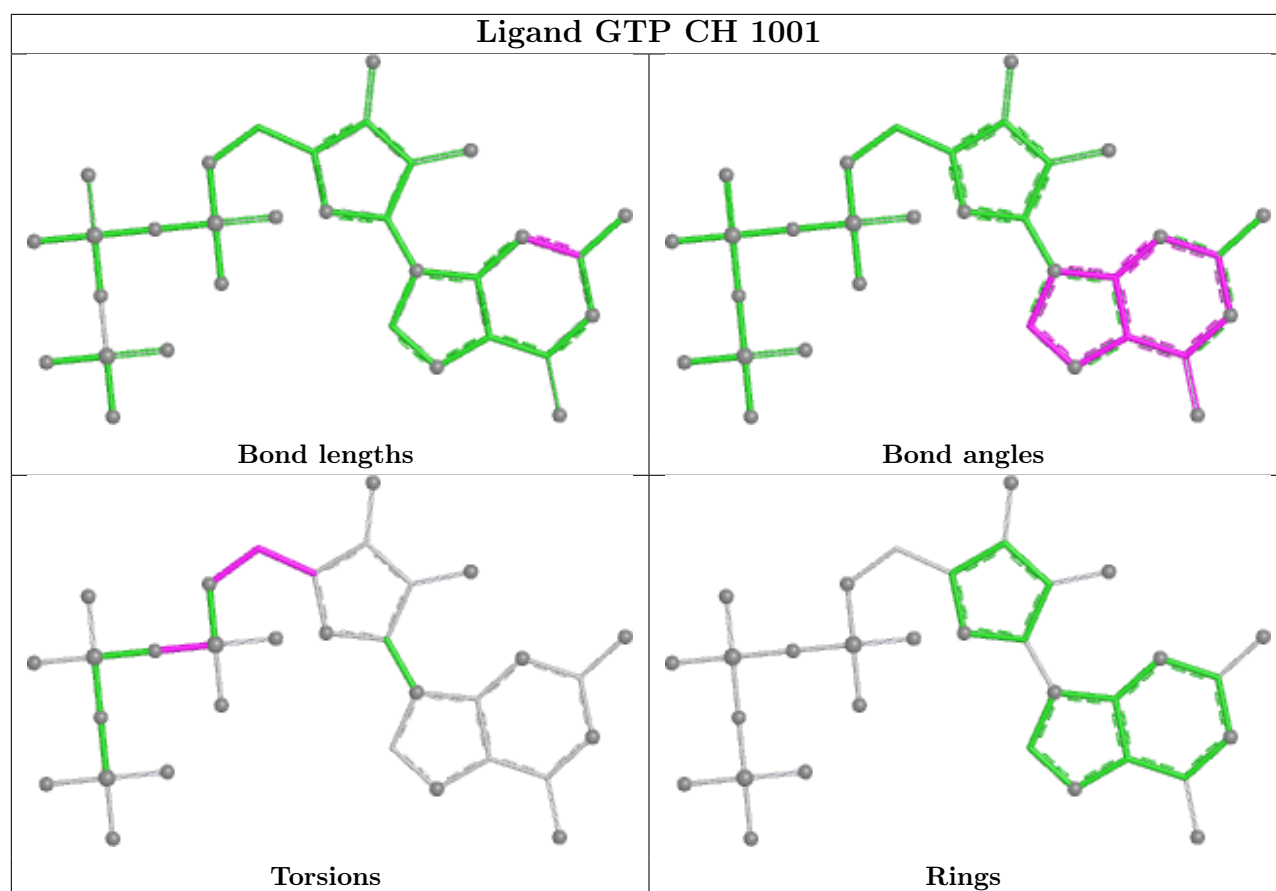
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	CH	1001	GTP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

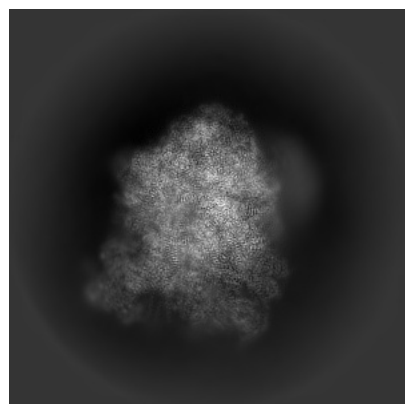
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35290. These allow visual inspection of the internal detail of the map and identification of artifacts.

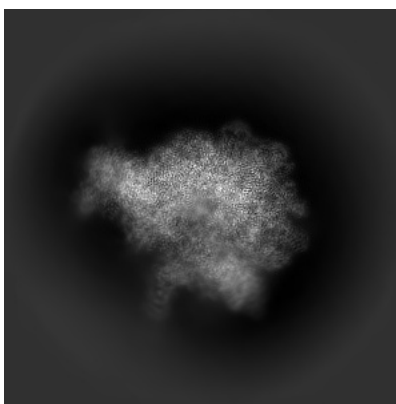
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

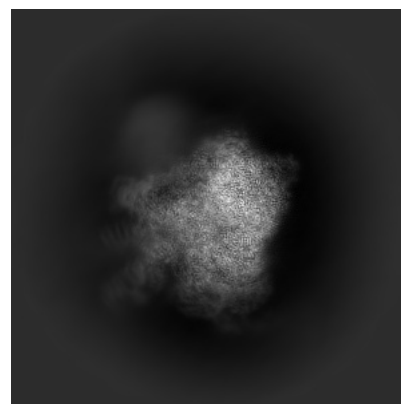
6.1.1 Primary map



X

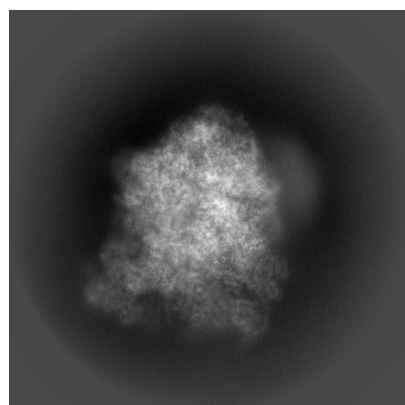


Y

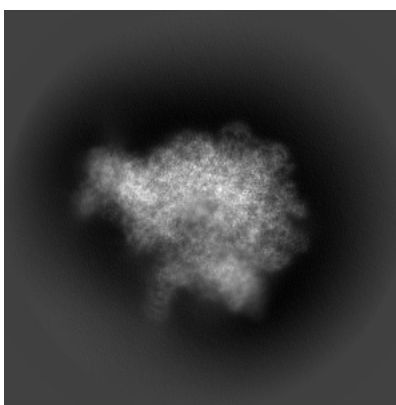


Z

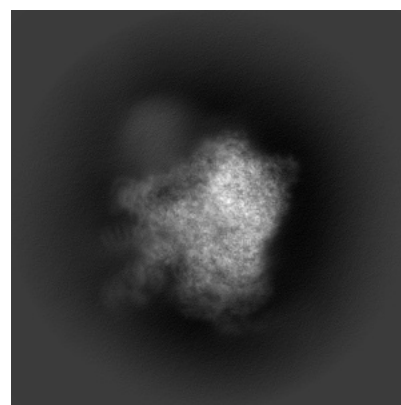
6.1.2 Raw map



X



Y

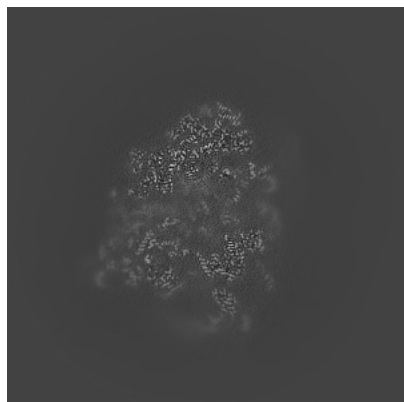


Z

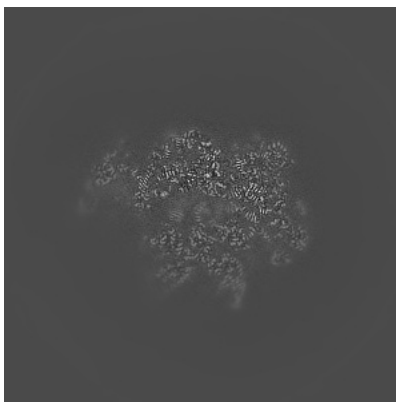
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

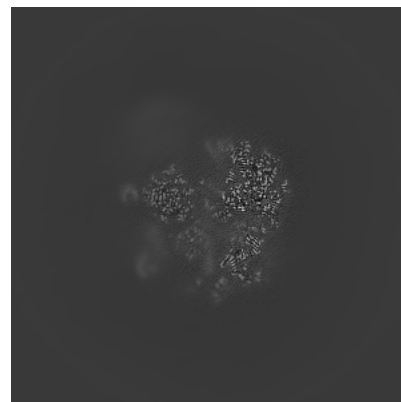
6.2.1 Primary map



X Index: 240

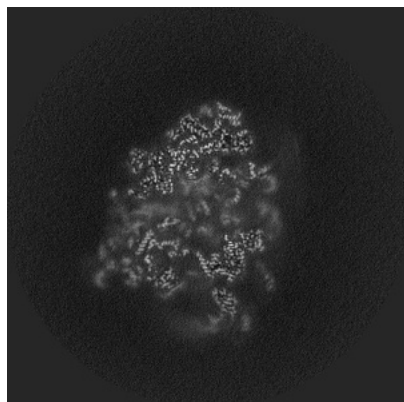


Y Index: 240

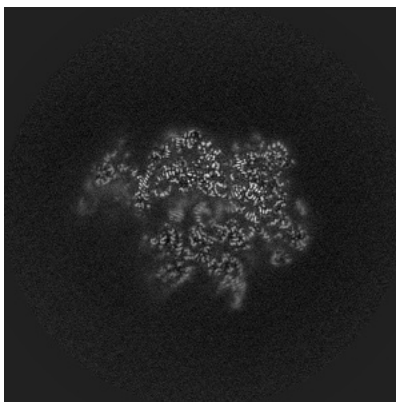


Z Index: 240

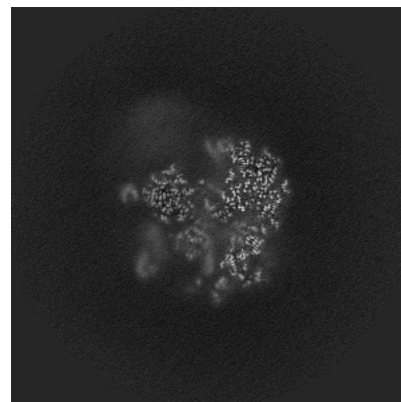
6.2.2 Raw map



X Index: 240



Y Index: 240

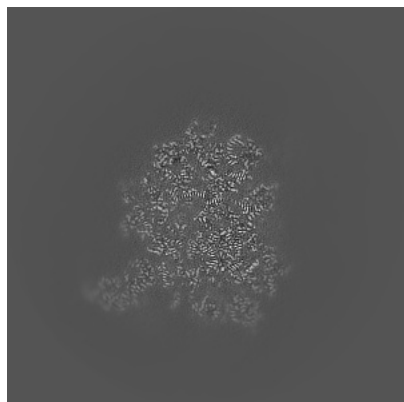


Z Index: 240

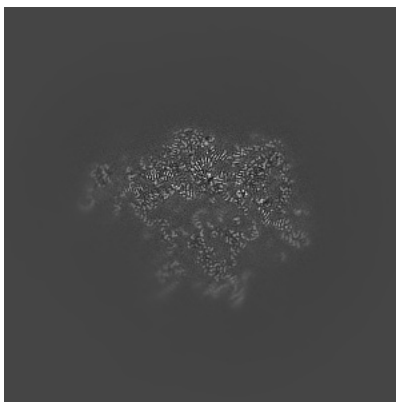
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

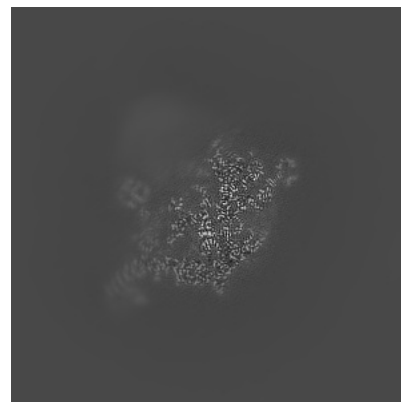
6.3.1 Primary map



X Index: 276

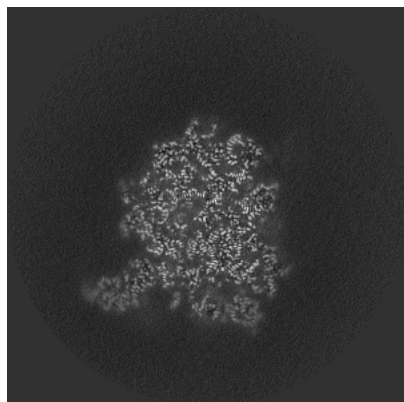


Y Index: 247

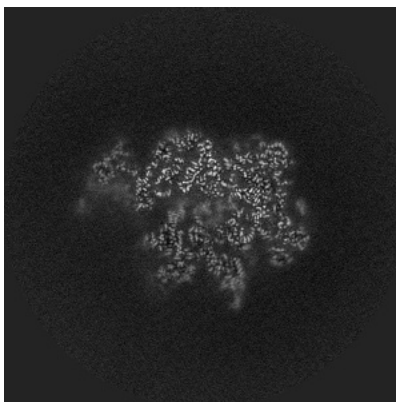


Z Index: 289

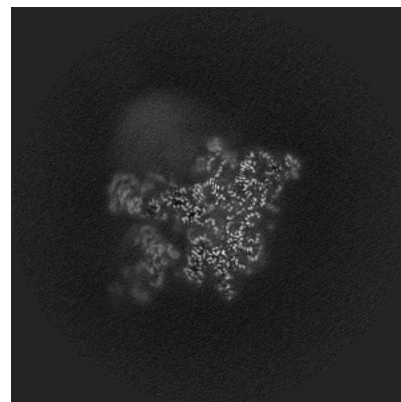
6.3.2 Raw map



X Index: 276



Y Index: 238

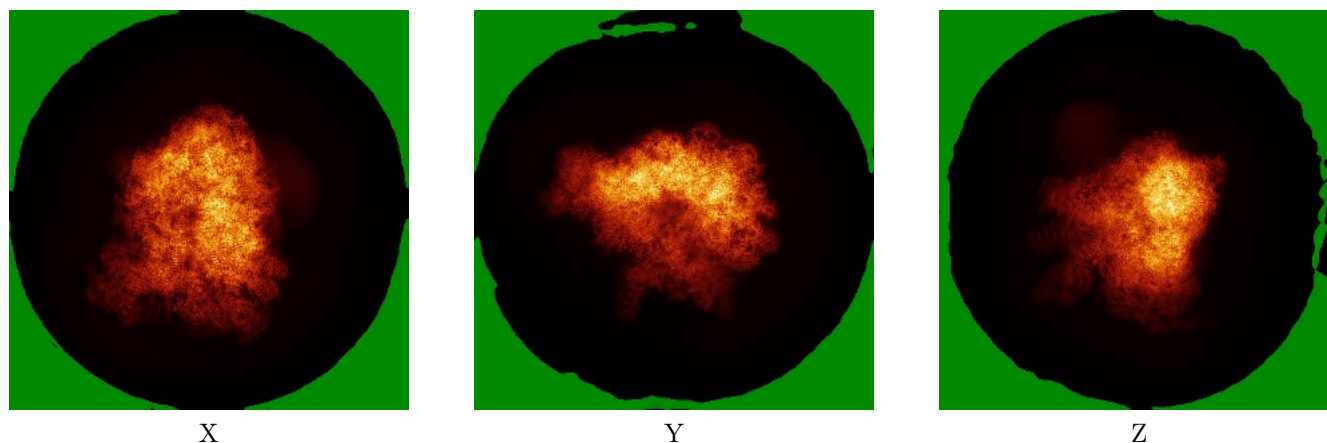


Z Index: 276

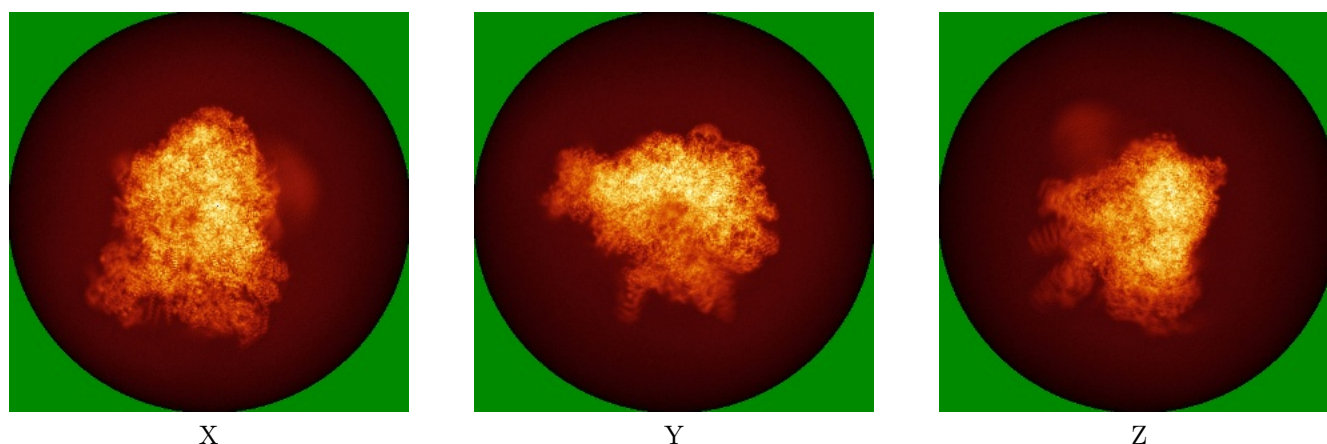
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

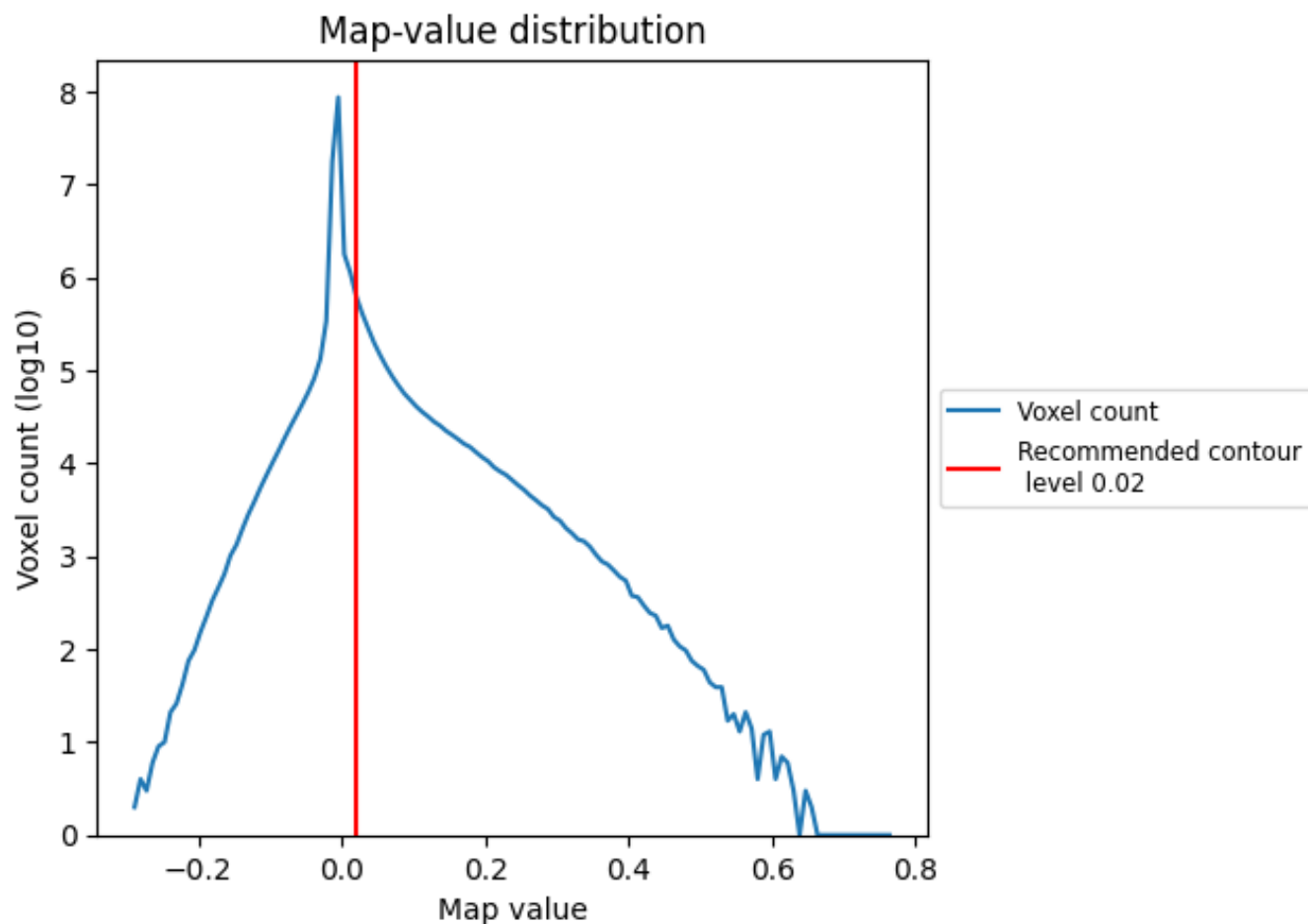
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

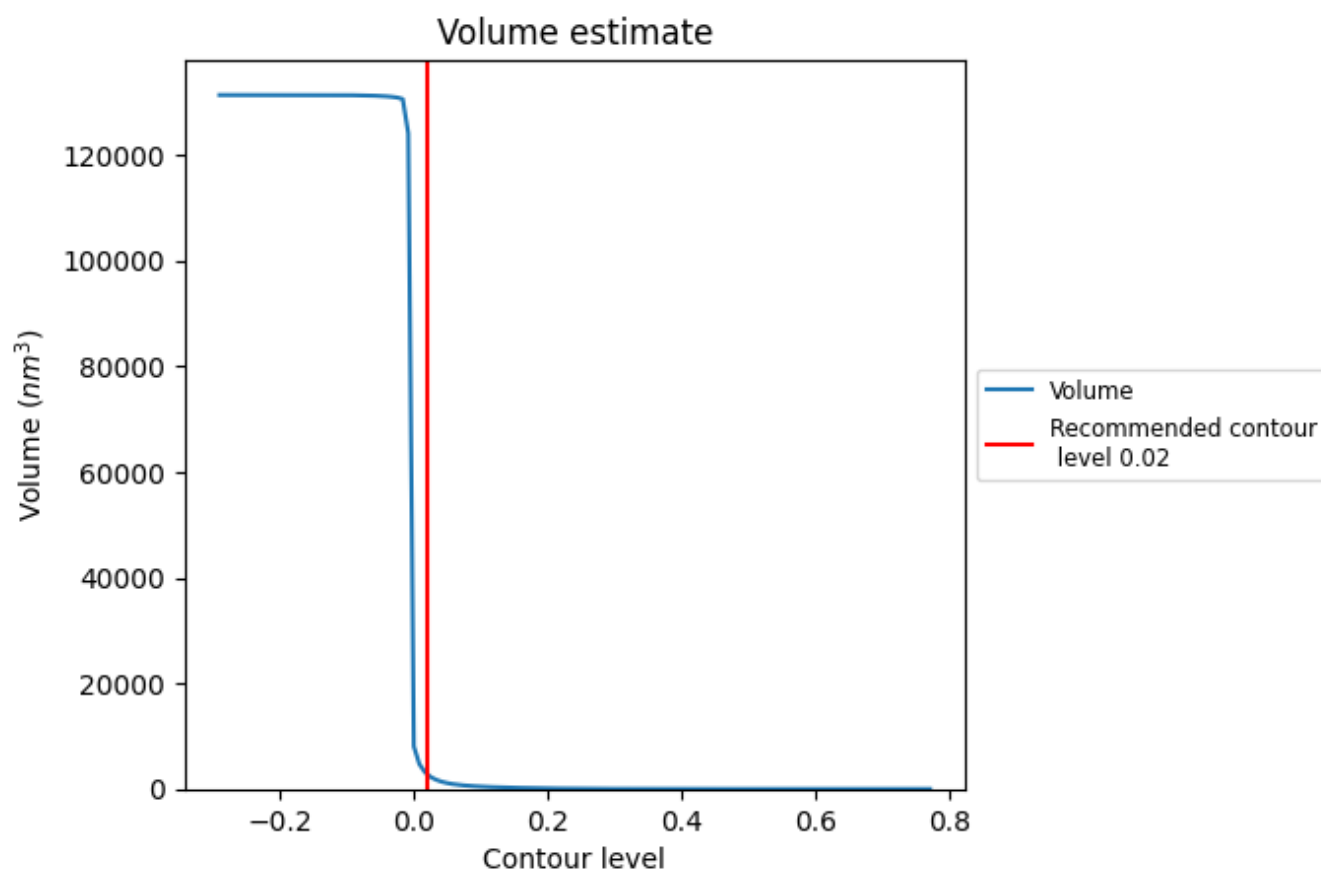
This section contains the results of statistical analysis of the map.

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.

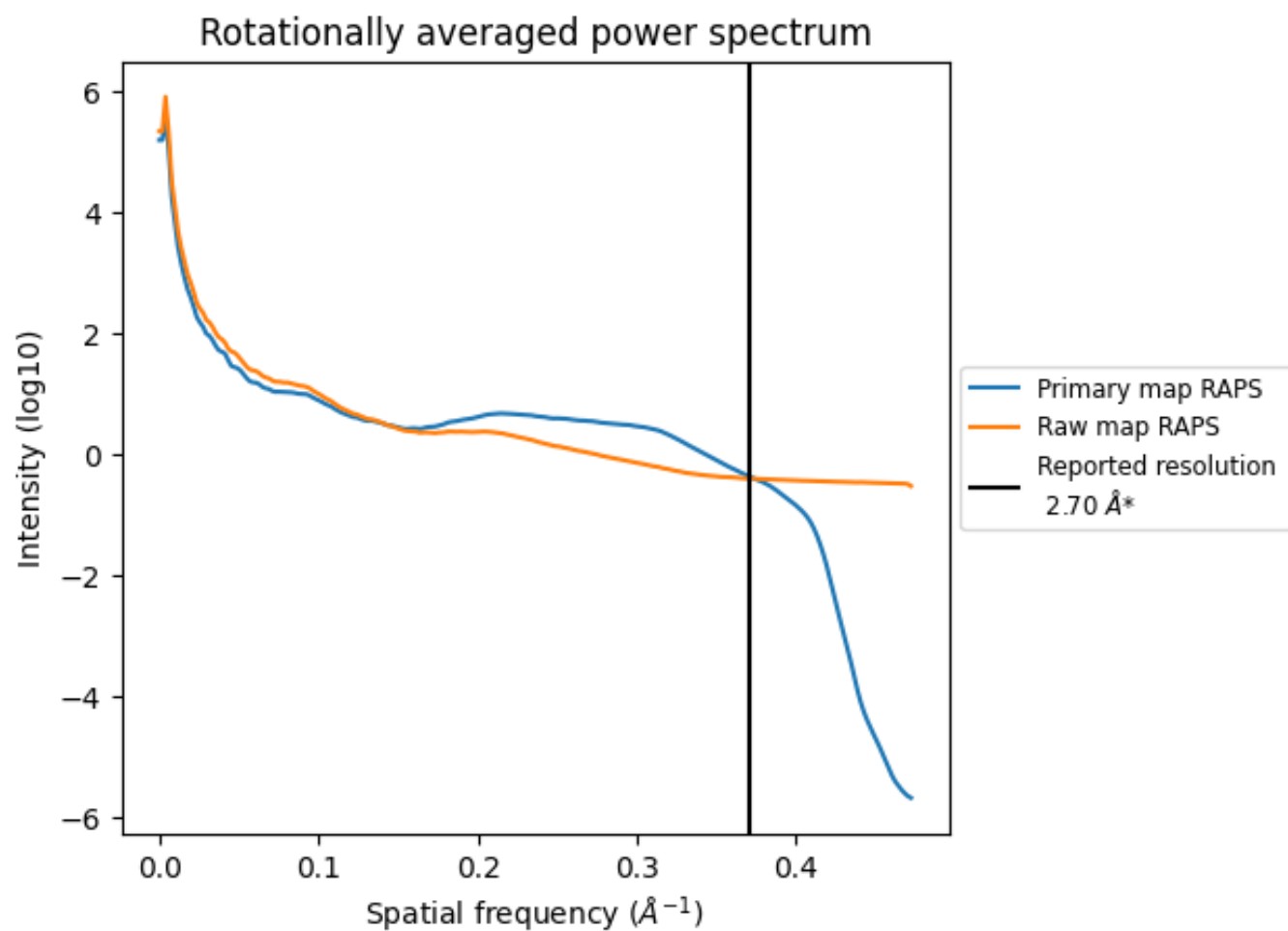
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2911 nm^3 ; this corresponds to an approximate mass of 2630 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 ⓘ

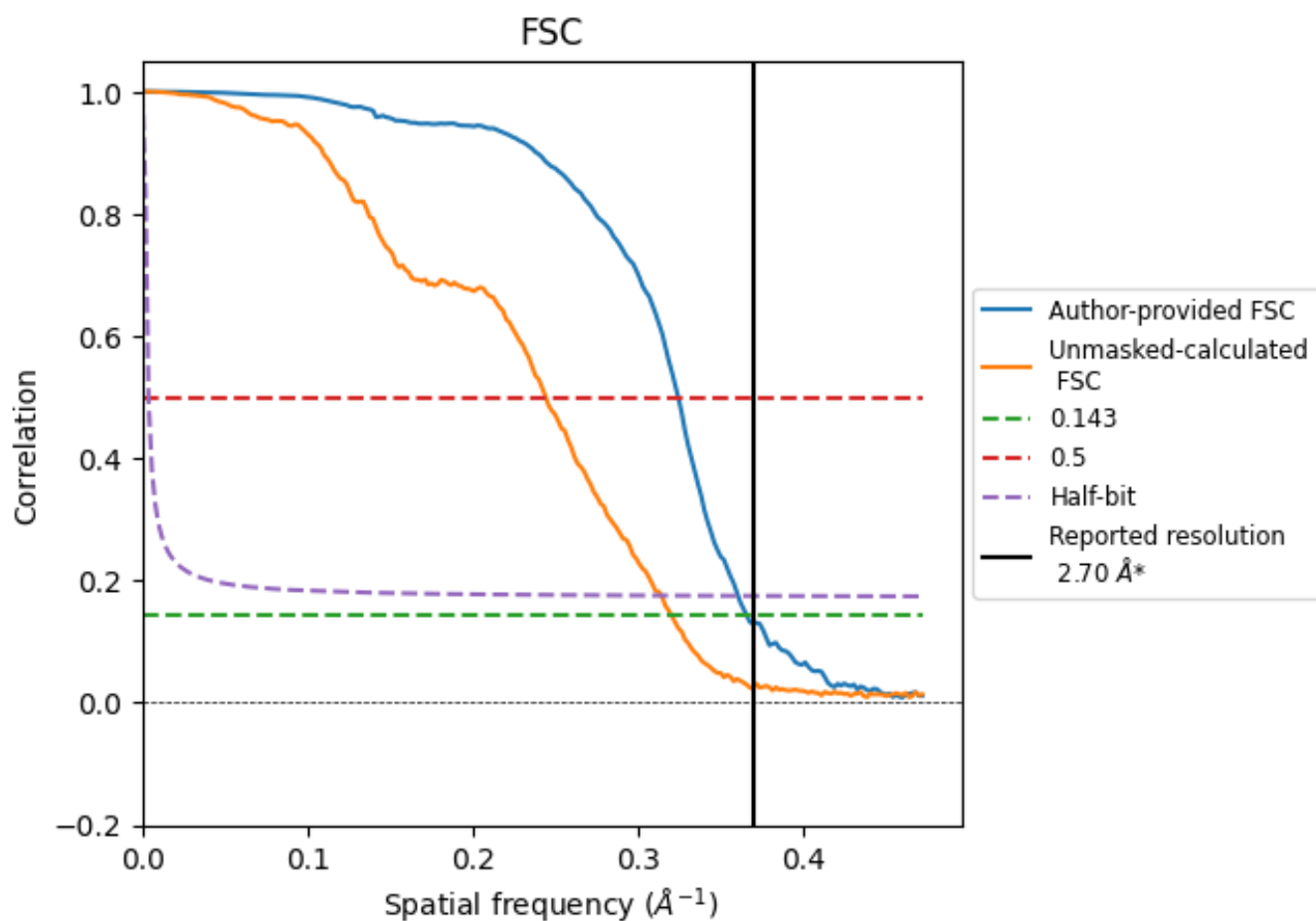


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

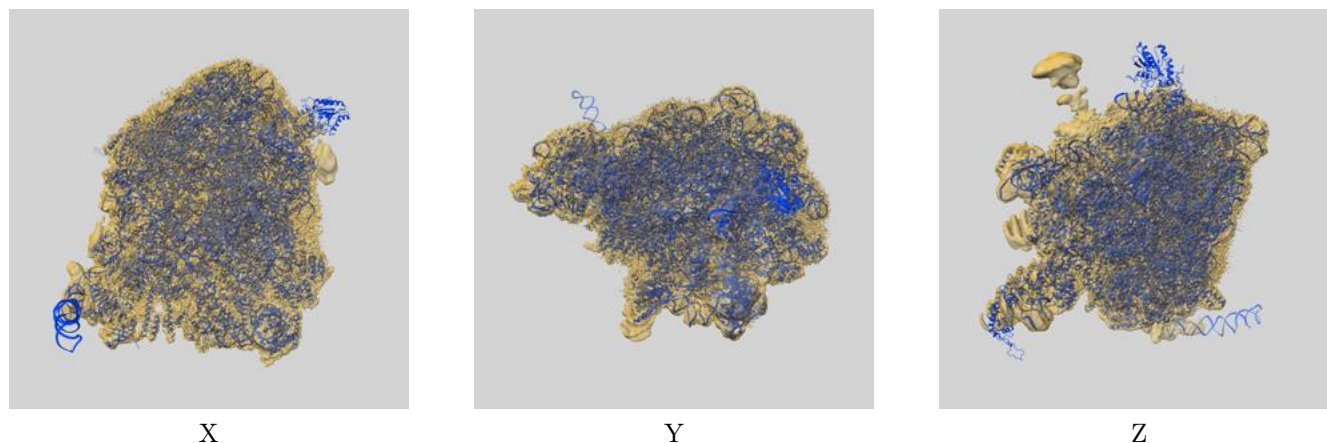
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.73	3.08	2.77
Unmasked-calculated*	3.12	4.09	3.18

*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 3.12 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

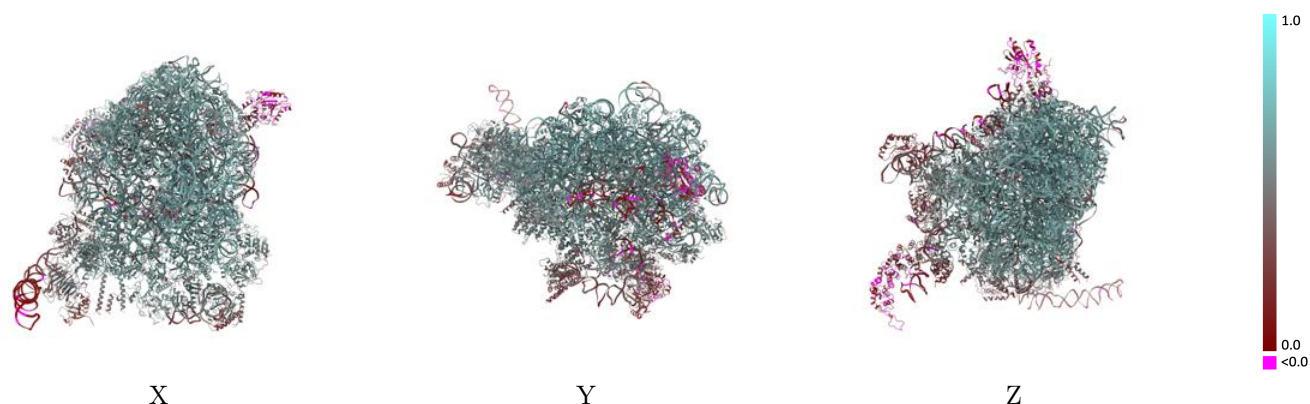
This section contains information regarding the fit between EMDB map EMD-35290 and PDB model 8IA0. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



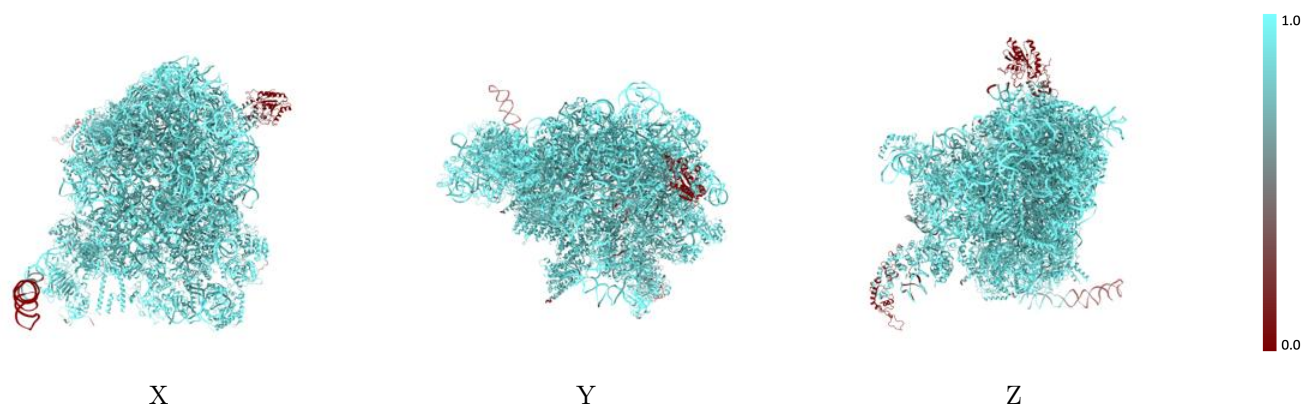
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



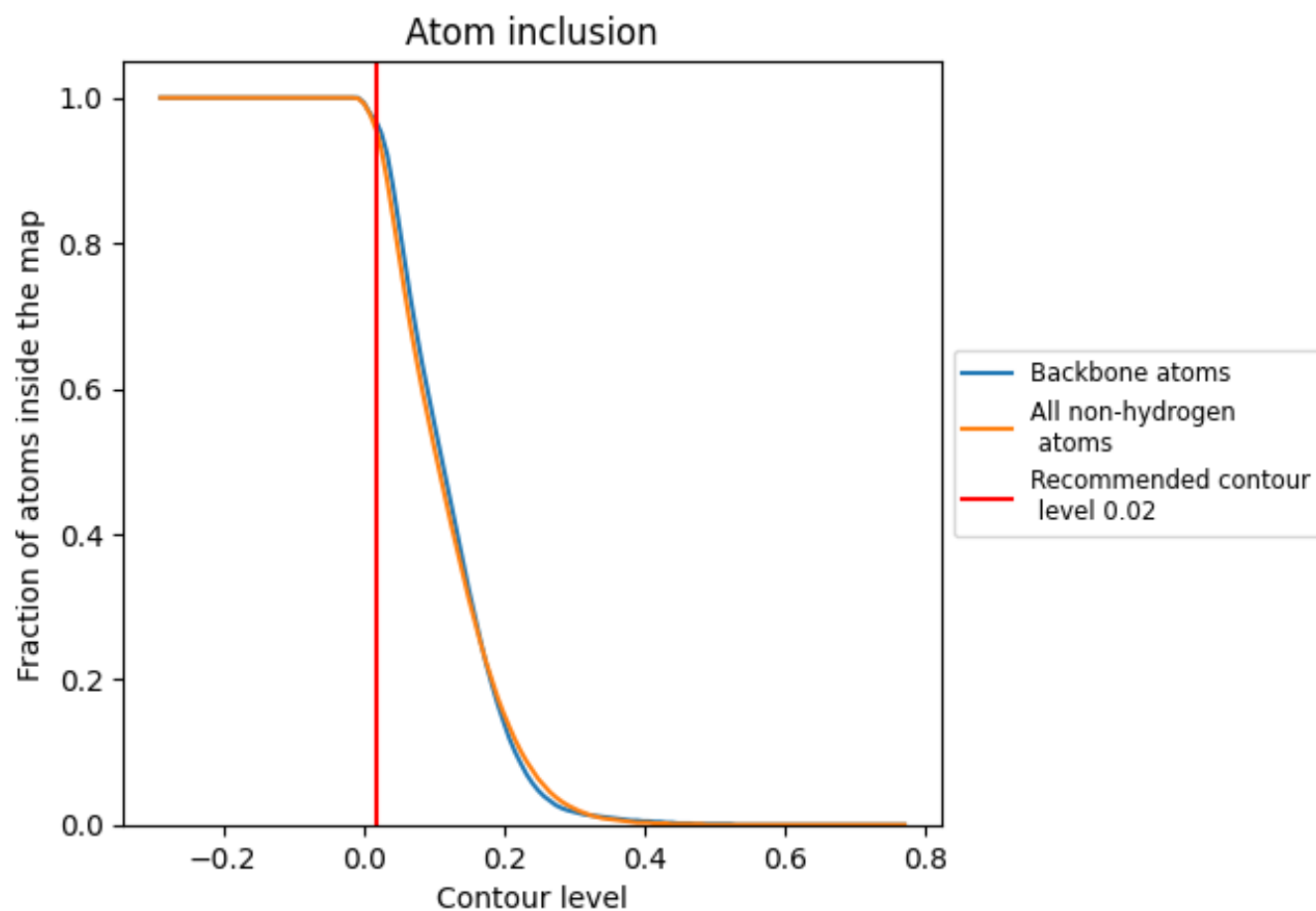
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9520	 0.5310
C1	 0.9590	 0.5350
C2	 0.9740	 0.5430
CA	 0.9820	 0.6050
CB	 0.9430	 0.4610
CC	 0.9730	 0.5670
CD	 0.9330	 0.4020
CE	 0.9580	 0.5390
CF	 0.9740	 0.5520
CG	 0.9770	 0.5990
CH	 0.9740	 0.5750
CI	 0.9470	 0.4850
CJ	 0.9690	 0.5480
CK	 0.9720	 0.5790
CL	 0.4030	 0.2400
CM	 0.9540	 0.5100
CN	 0.9730	 0.5890
CO	 0.9890	 0.6280
CP	 0.9750	 0.5550
CQ	 0.9610	 0.5570
CR	 0.9790	 0.6090
CS	 0.9670	 0.5170
CT	 0.9770	 0.5510
CU	 0.9750	 0.5740
CV	 0.9880	 0.6470
CW	 0.9410	 0.3990
CX	 0.9550	 0.5450
CY	 0.9270	 0.4090
CZ	 0.7470	 0.2500
Ca	 0.9210	 0.4000
Cz	 0.9090	 0.3960
LA	 0.9200	 0.3540
LB	 0.9820	 0.6200
LC	 0.9830	 0.6380
LE	 0.9800	 0.6080



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LF	 0.9830	 0.6290
LG	 0.9800	 0.6220
LH	 0.9790	 0.6120
LK	 0.9520	 0.4670
LL	 0.9950	 0.6520
LM	 0.9870	 0.6290
LN	 0.9950	 0.6680
LO	 0.9900	 0.6470
LP	 0.9820	 0.6060
LQ	 0.9830	 0.6010
LR	 0.9510	 0.5120
LS	 0.9810	 0.6200
LT	 0.9230	 0.3850
LU	 0.9750	 0.5490
LV	 0.9910	 0.6280
LX	 0.9710	 0.5840
LY	 0.9780	 0.6210
LZ	 0.9770	 0.5890
Lc	 0.9570	 0.5300
Ld	 0.9720	 0.6140
Le	 0.9840	 0.6450
Lf	 0.9900	 0.6620
Lg	 0.9620	 0.5960
Lh	 0.9800	 0.5850
Li	 0.9780	 0.6070
Lj	 0.9950	 0.6710
Lk	 0.9740	 0.5390
Ll	 0.9810	 0.5580
Lp	 0.8500	 0.2560
Lq	 0.8990	 0.2370