



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:23 AM UTC

PDB ID : 8I9Z / pdb_00008i9z
EMDB ID : EMD-35289
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Spb4
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.70 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:

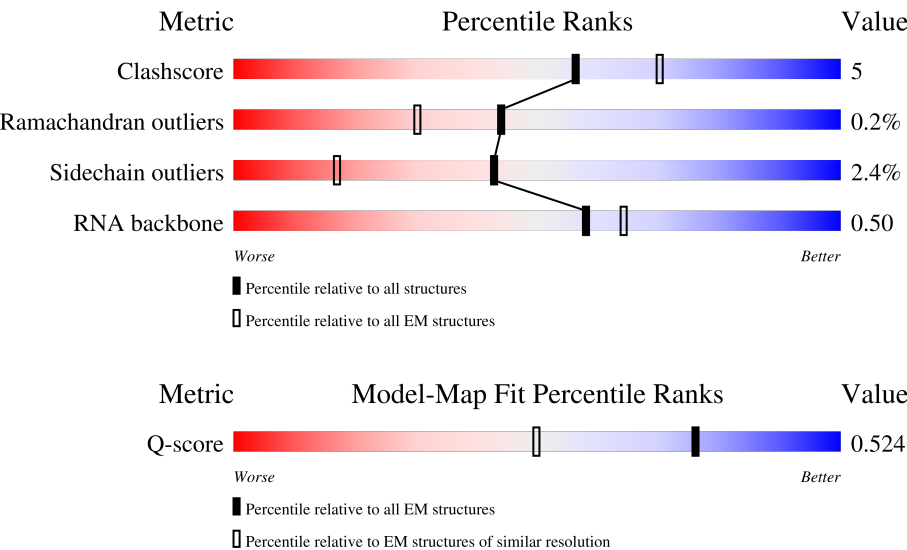
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 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.



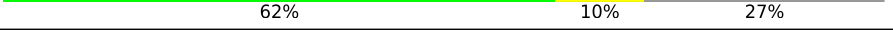
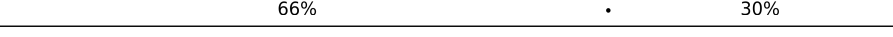
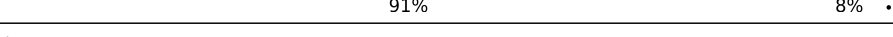
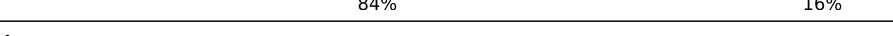
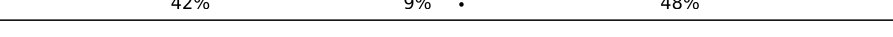
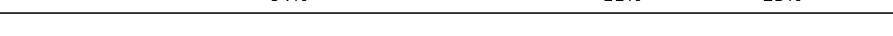
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	

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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	

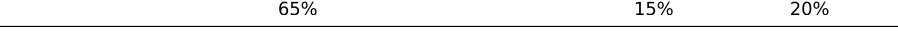
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Mol	Chain	Length	Quality of chain
28	Cz	123	
29	LB	392	
30	LC	365	
31	LE	200	
32	LG	262	
33	LH	192	
34	LK	165	
35	LL	213	
36	LM	142	
37	LN	203	
38	LO	204	
39	LP	187	
40	LQ	213	
41	LR	2898	
42	LS	174	
43	LT	160	
44	LU	127	
45	LV	139	
46	LX	156	
47	LY	138	
48	LZ	135	
49	Lc	108	
50	Ld	120	
51	Le	131	
52	Lf	109	

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Mol	Chain	Length	Quality of chain
53	Lg	119	
54	Lh	935	
55	Li	110	
56	Lj	95	
57	Lk	81	
58	Ll	51	
59	Lq	217	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 167255 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	2787	Total	C	N	O	P	0	0
			59633	26611	10807	19428	2787		

- 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	S	0	0
			5289	3368	931	977	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	465	Total	C	N	O	S	0	0
			3689	2362	646	670	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

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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	390	Total	C	N	O		0	0
			2173	1307	446	420			

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	324	Total	C	N	O	S	0	0
			2535	1618	445	457	15		

- 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	625	Total	C	N	O	S	0	0
			5036	3190	917	910	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	537	Total	C	N	O	S	0	0
			4284	2733	760	777	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	382	Total	C	N	O	S	0	0
			3035	1943	558	523	11		

- Molecule 28 is a protein called rRNA-processing protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 30 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 31 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LE	189	Total	C	N	O	S	0	0
			1475	944	267	261	3		

- Molecule 32 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LG	204	Total	C	N	O	S	0	0
			1644	1060	297	282	5		

- Molecule 33 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 34 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 35 is a protein called 60S ribosomal protein L13.

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

- Molecule 36 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 37 is a protein called Ribosomal protein L15.

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

- Molecule 38 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 39 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 40 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 41 is a protein called Ribosomal protein L19.

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

- Molecule 42 is a protein called 60S ribosomal protein L20.

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

- Molecule 43 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L22-like protein.

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

- Molecule 45 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 46 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 47 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 48 is a protein called 60S ribosomal protein L27.

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

- Molecule 49 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 50 is a protein called Putative 60S ribosomal protein.

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

- Molecule 51 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 52 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 53 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 54 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 55 is a protein called 60S ribosomal protein L36.

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

- Molecule 56 is a protein called Ribosomal protein L37.

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

- Molecule 57 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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

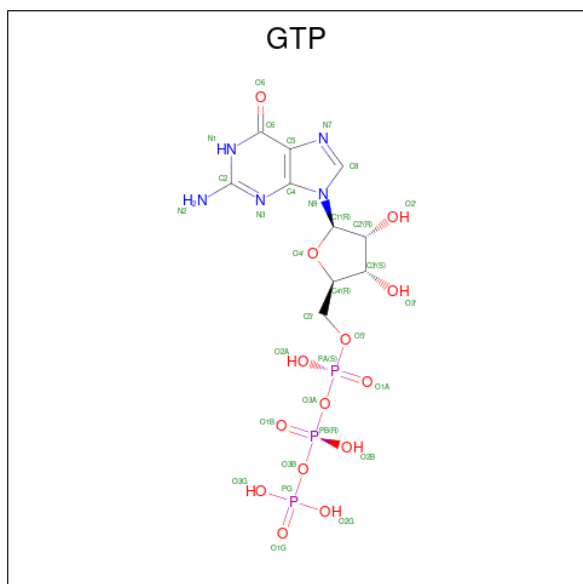
- Molecule 58 is a protein called 60S ribosomal protein L39.

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

- Molecule 59 is a protein called Ribosomal protein.

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

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

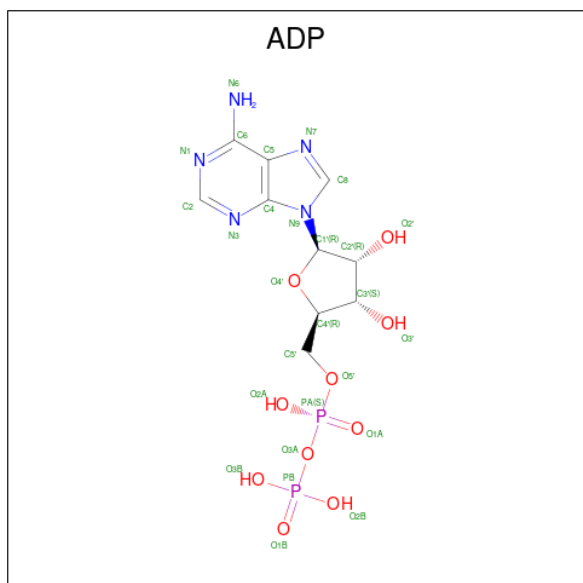


Mol	Chain	Residues	Atoms					AltConf
60	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	CQ	1	Total	Zn	0
			1	1	
61	Lj	1	Total	Zn	0
			1	1	

- Molecule 62 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

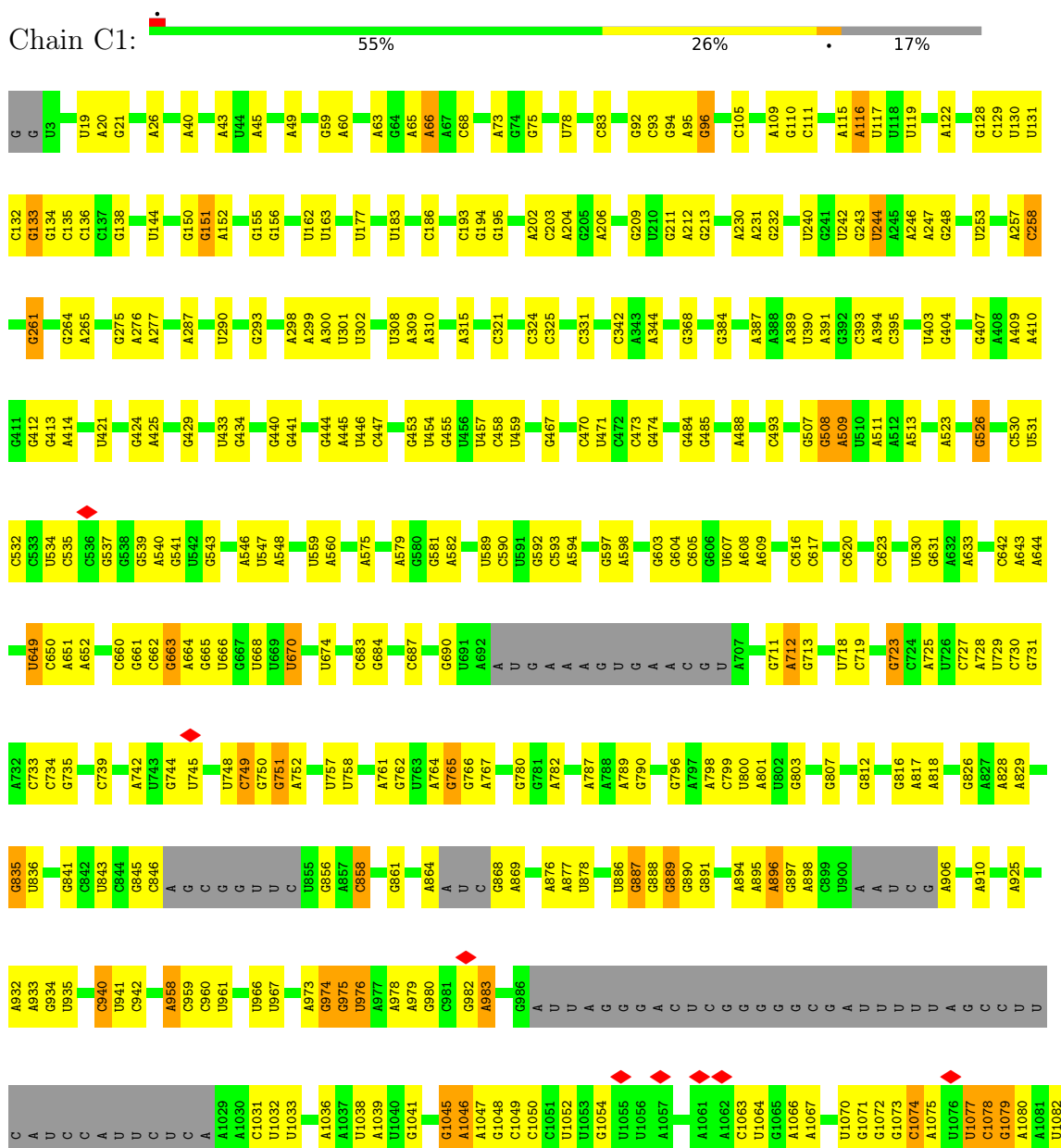
- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	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.

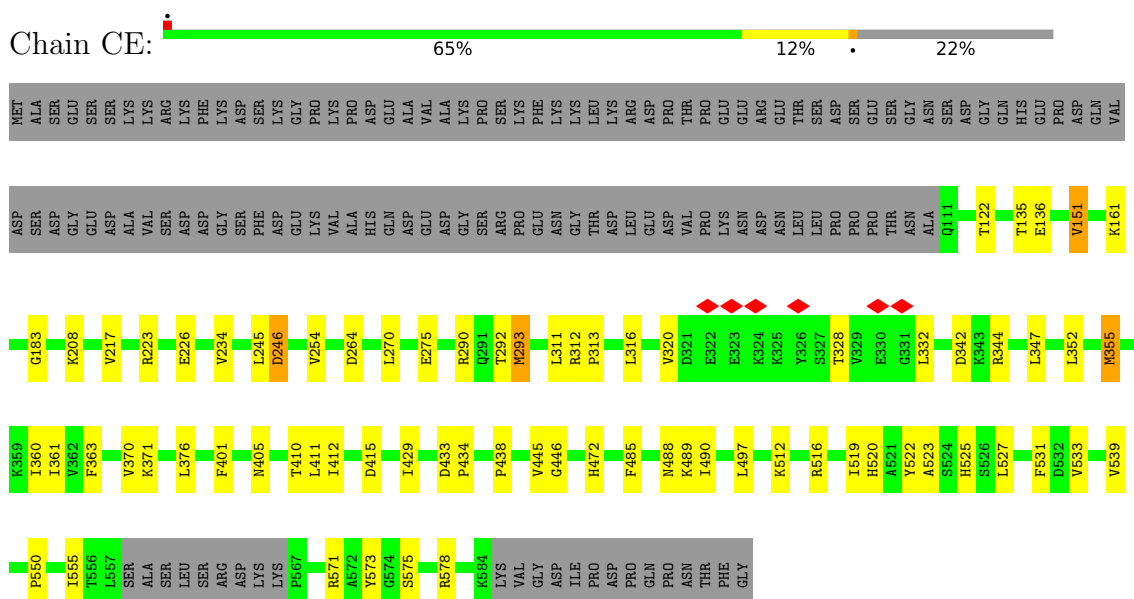
• Molecule 1: RNA (3341-MER)



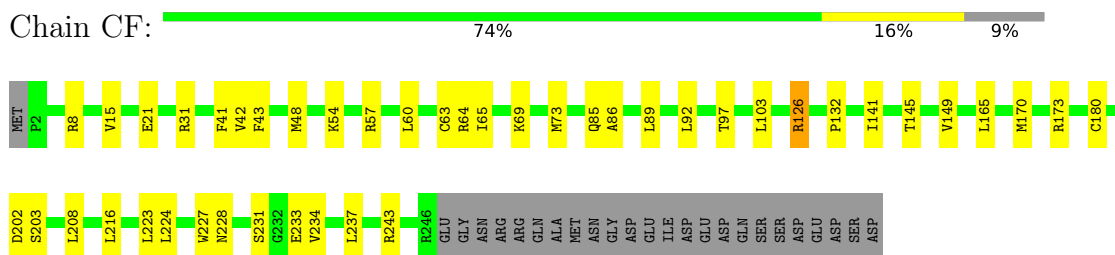




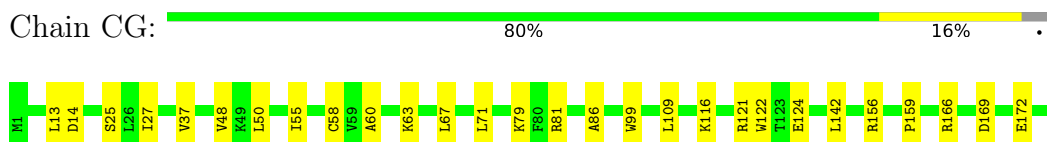
- Molecule 7: RNA helicase

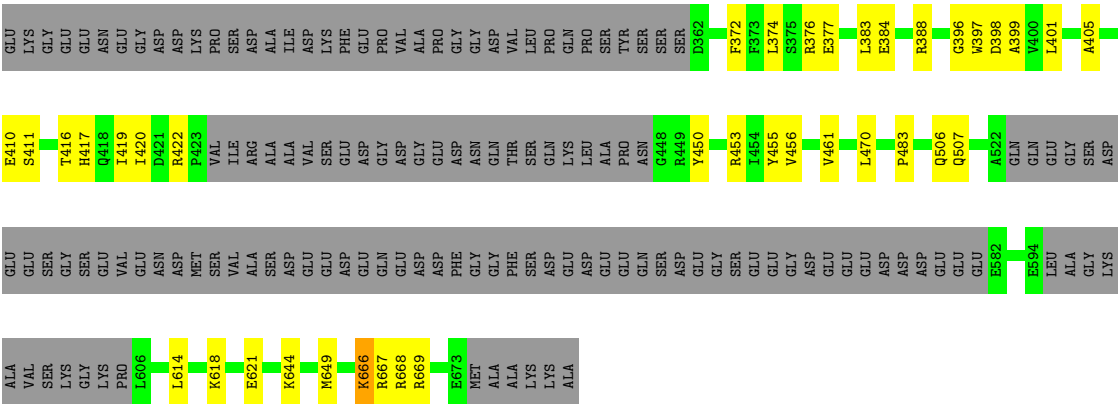


- Molecule 8: Ribosome assembly factor mrt4

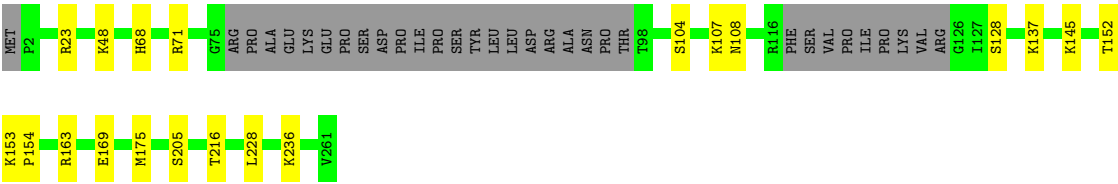
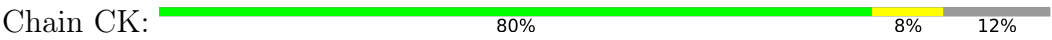


- Molecule 9: 60S ribosome subunit biogenesis protein NIP7

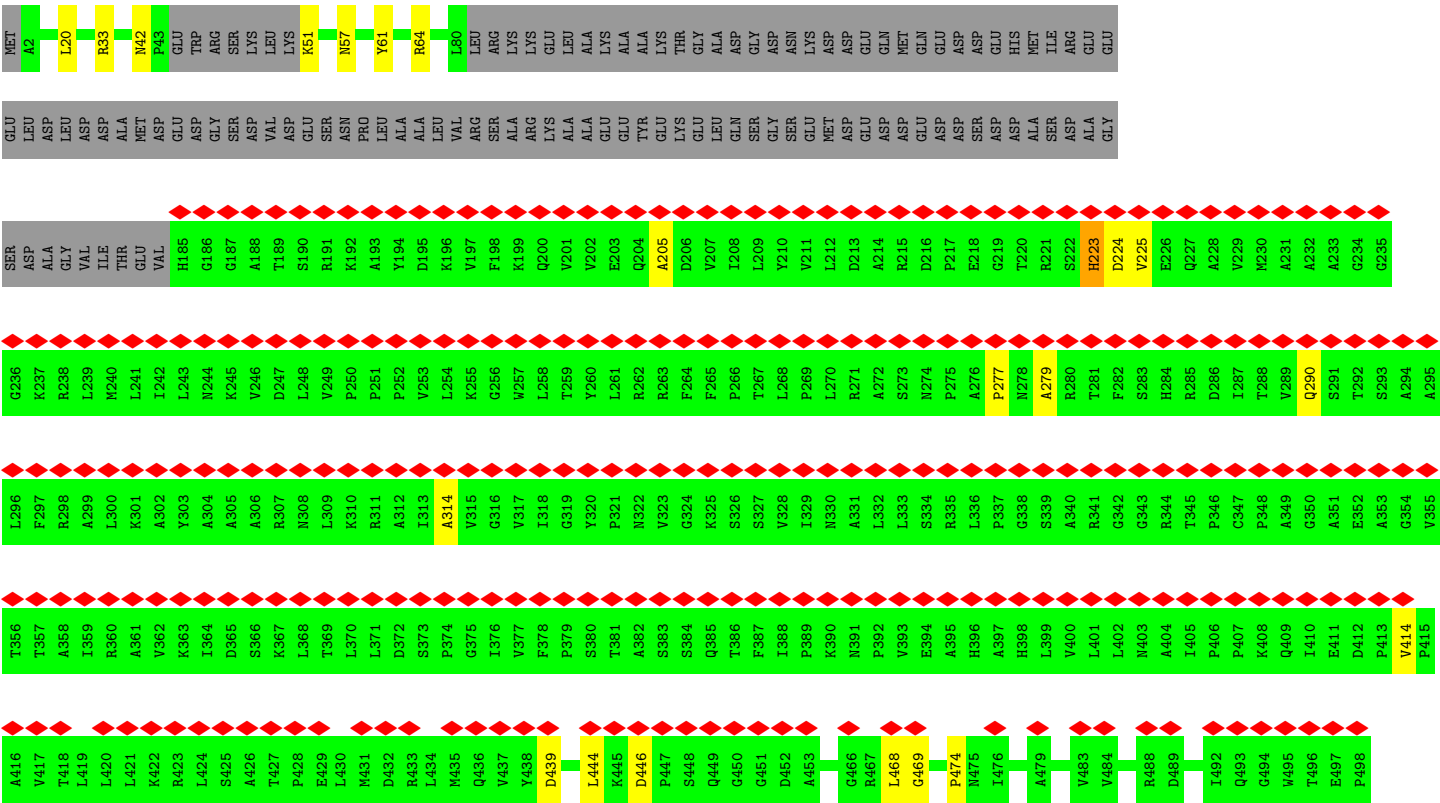


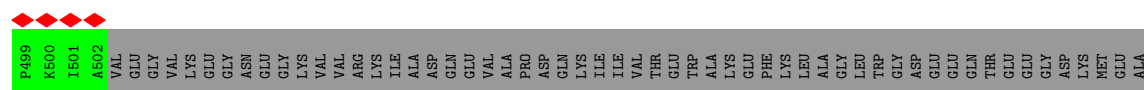


• Molecule 13: Ribosome biogenesis protein NSA2 homolog

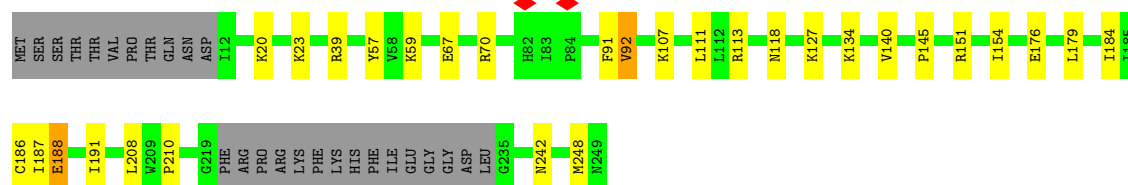
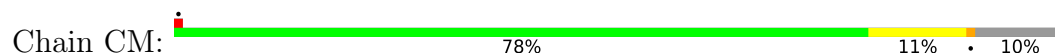


• Molecule 14: Putative GTP binding protein

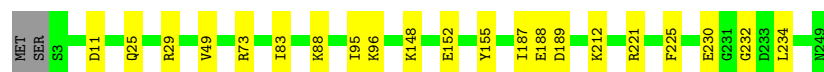




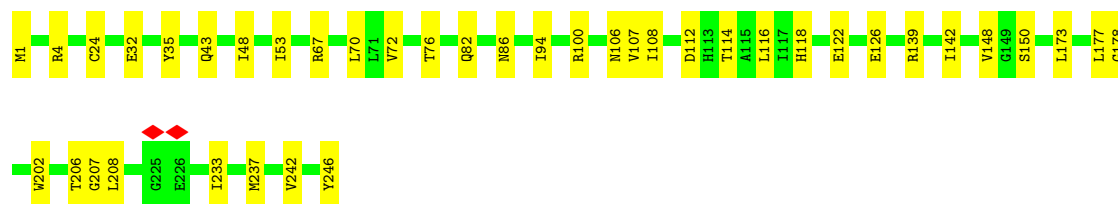
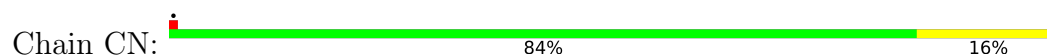
- Molecule 15: 60S ribosomal protein l7-like protein



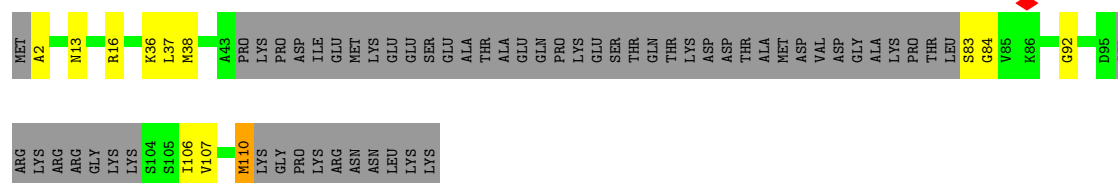
- Molecule 15: 60S ribosomal protein l7-like protein



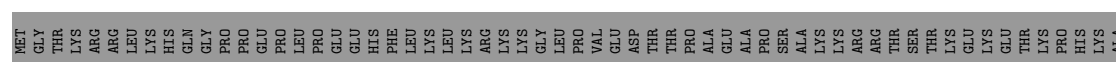
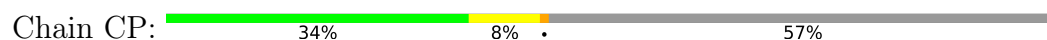
- Molecule 16: Eukaryotic translation initiation factor 6

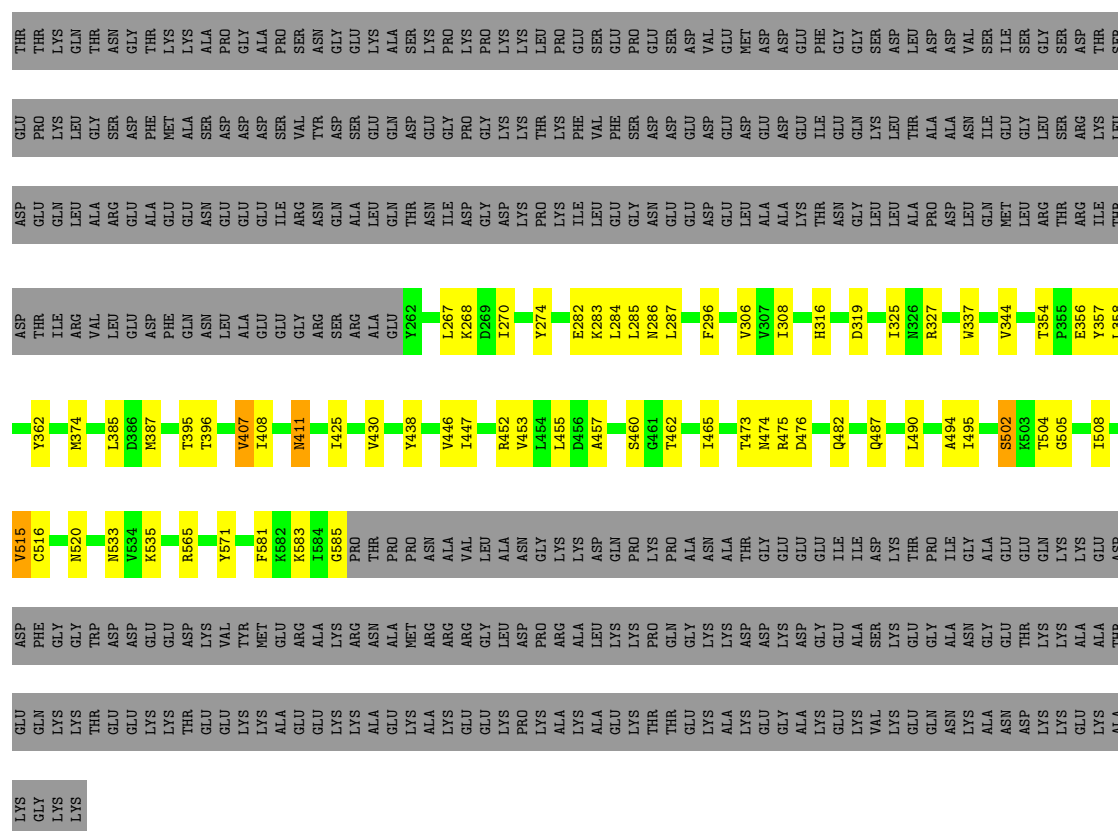


- Molecule 17: DUF2423 domain-containing protein

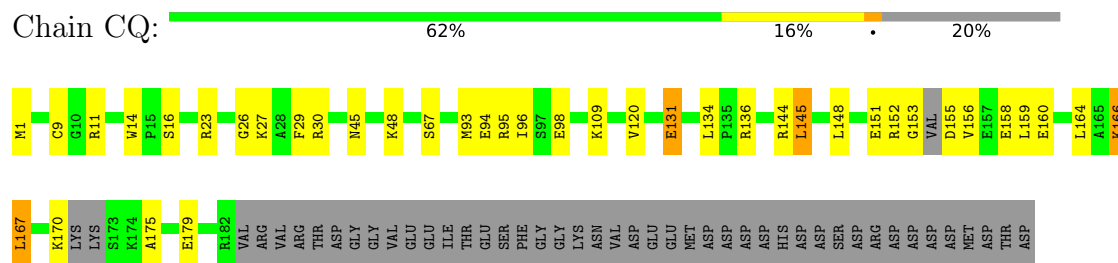


- Molecule 18: RNA methyltransferase nop2-like protein

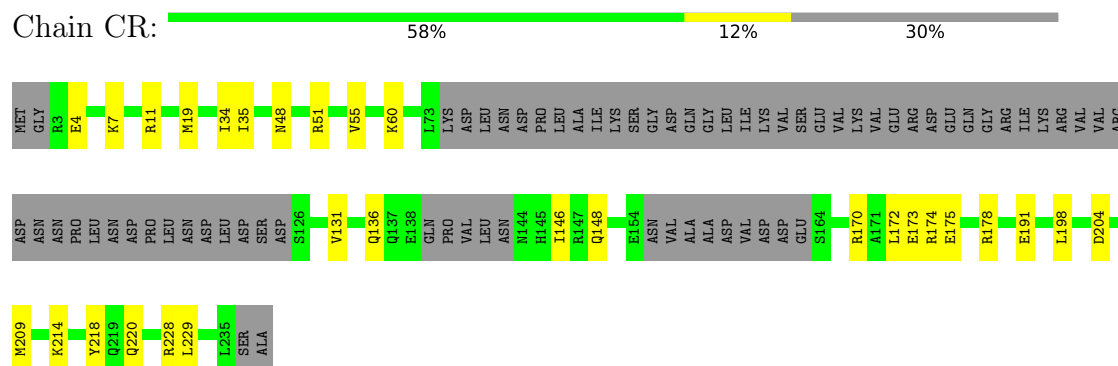




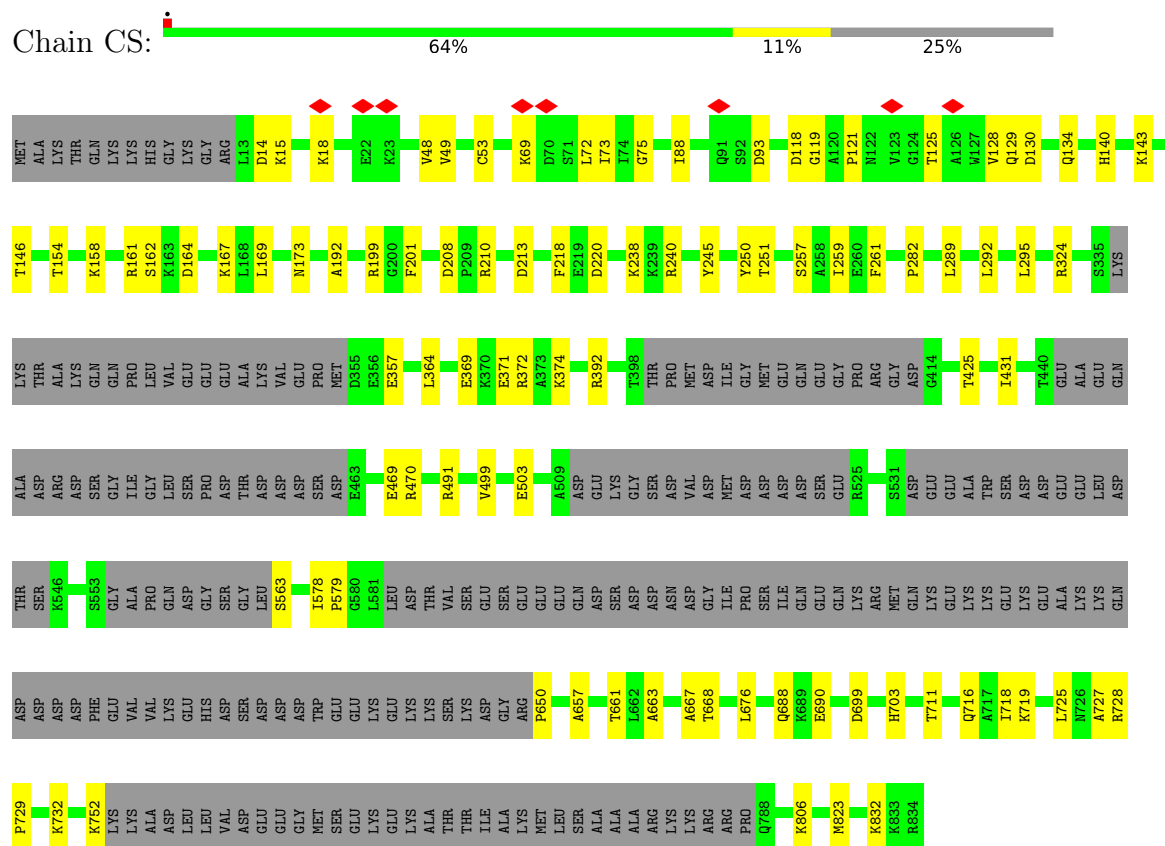
- Molecule 19: Ribosome biogenesis protein RLP24



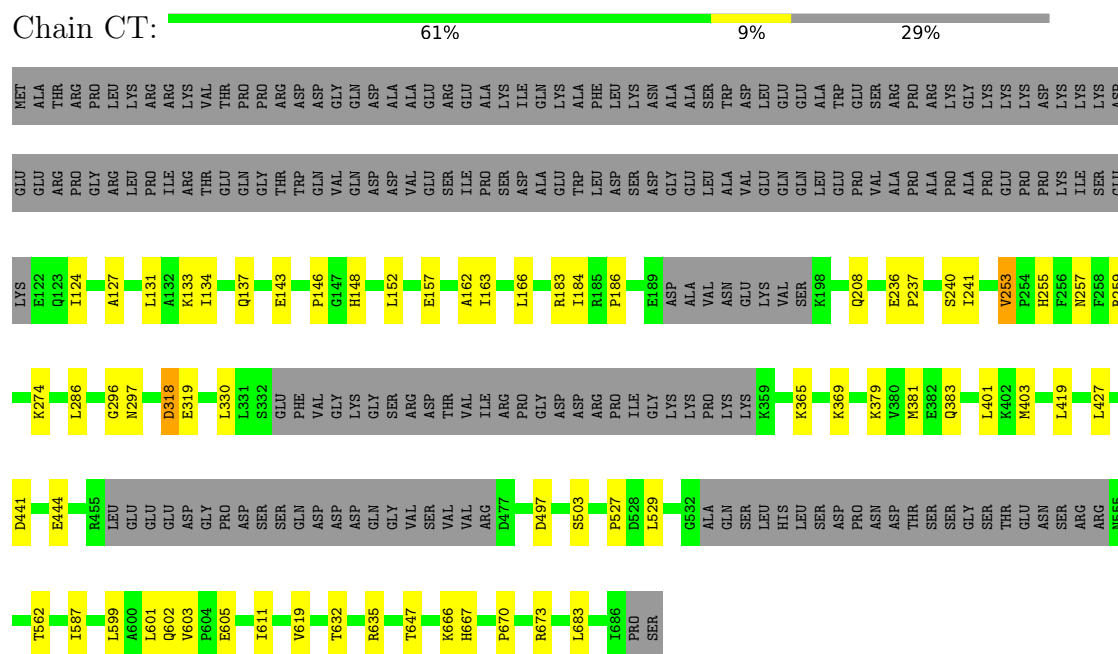
- Molecule 20: Nucleolar protein 16



- Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

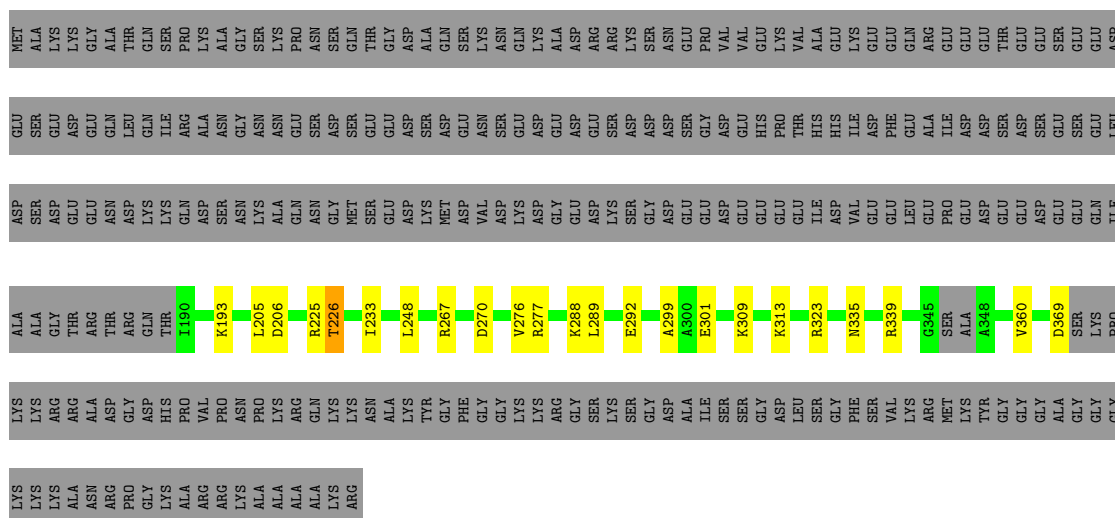


• Molecule 22: Nucleolar complex-associated protein 3

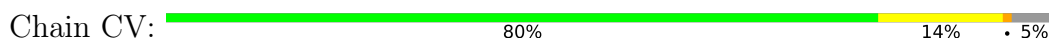


• Molecule 23: rRNA-processing protein EBP2

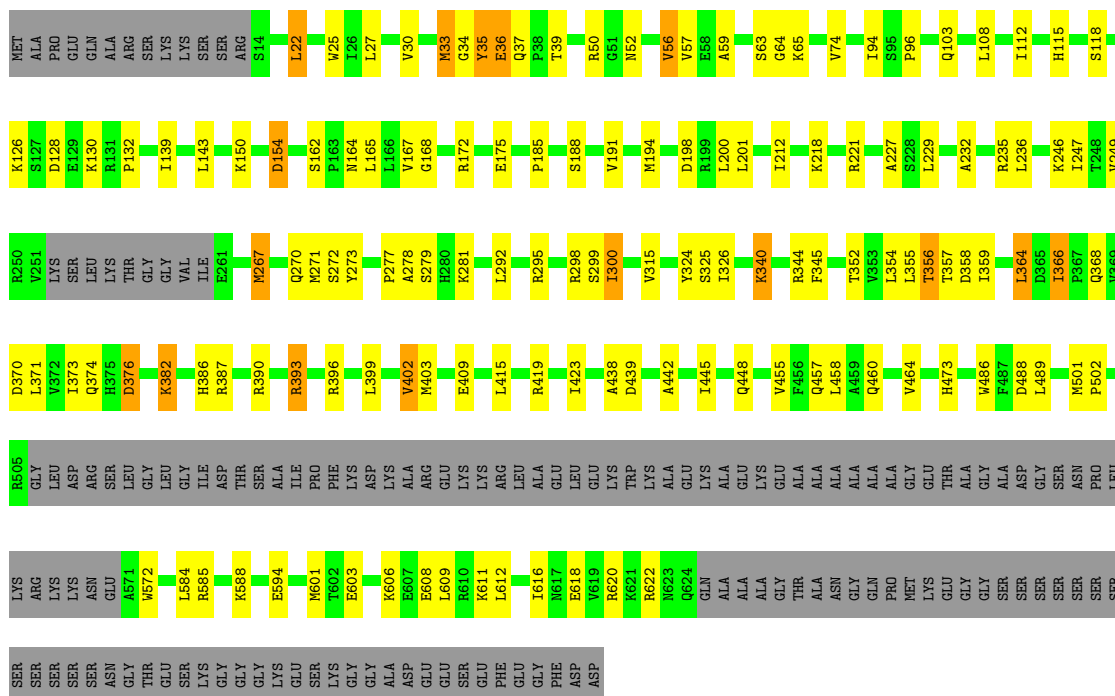




- Molecule 24: Putative 60S ribosomal protein

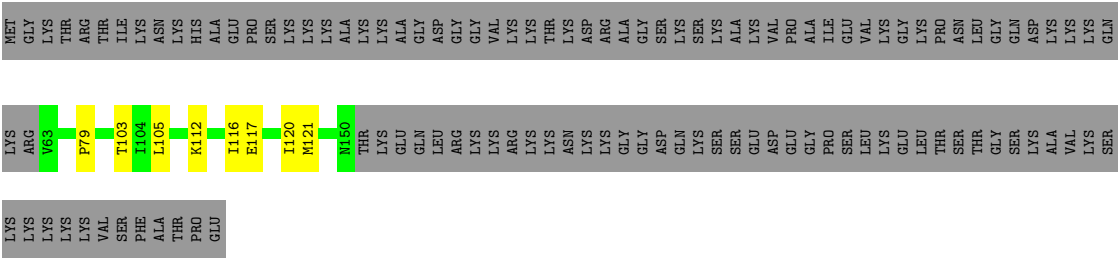


- Molecule 25: ATP-dependent RNA helicase

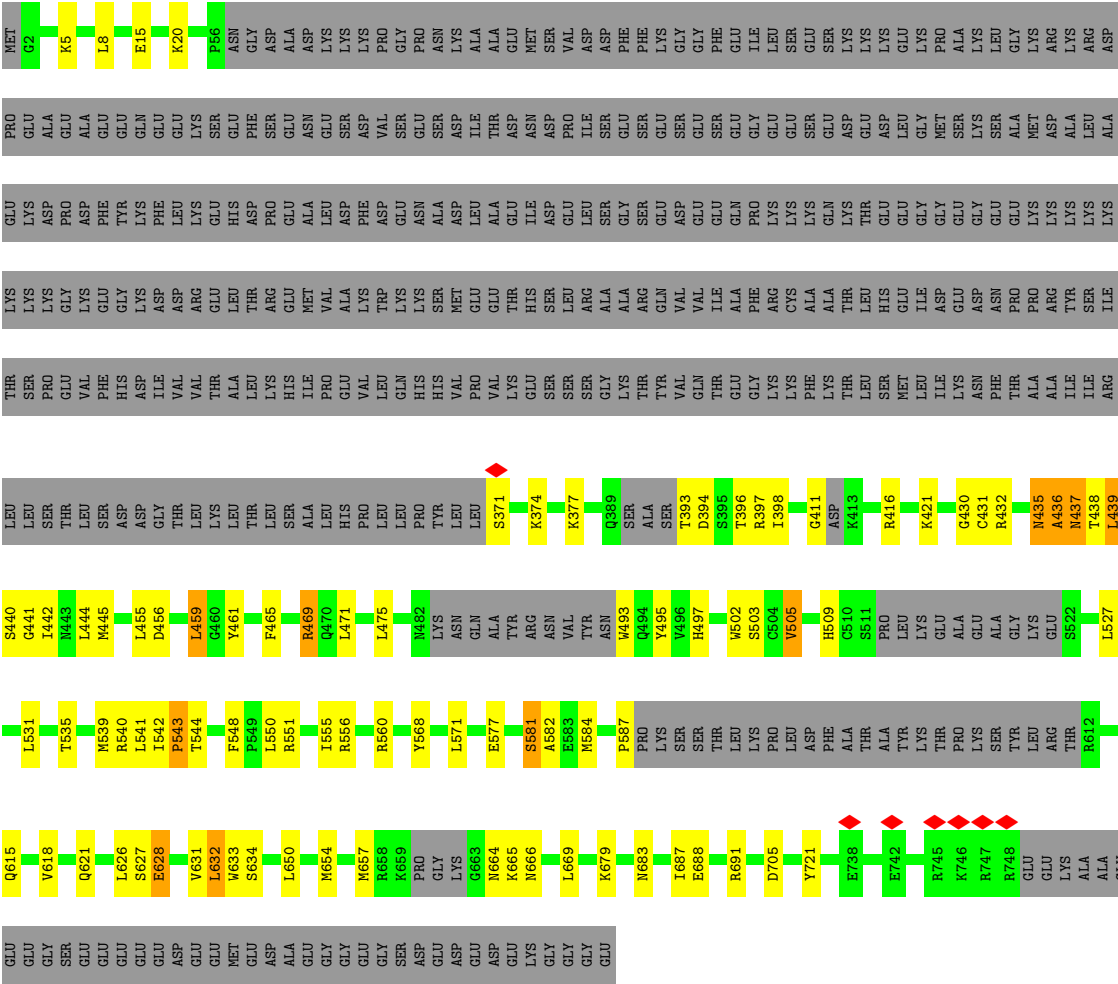
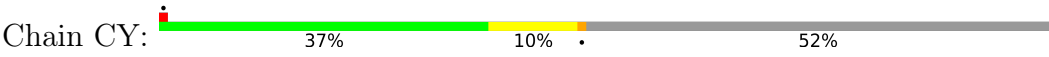


- Molecule 26: 60S ribosomal subunit-like protein

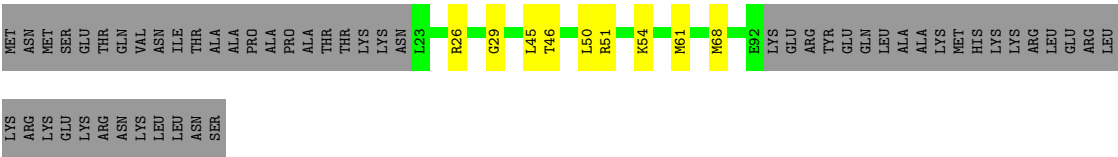




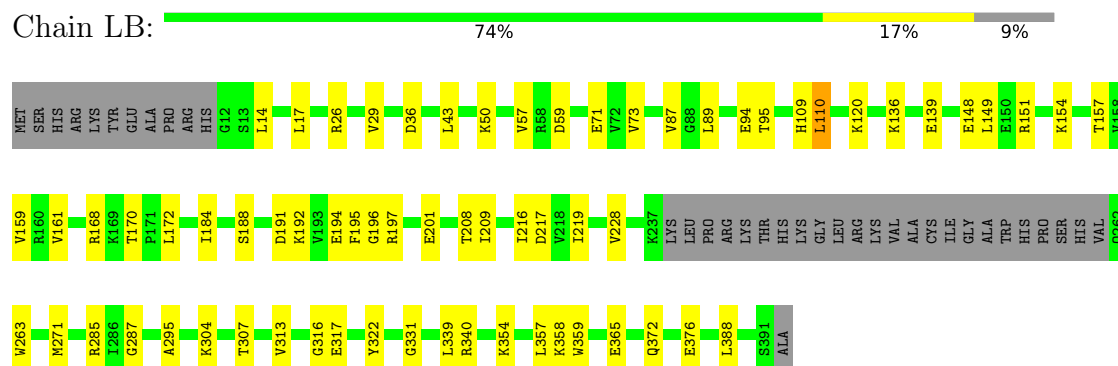
● Molecule 27: Putative NOC2 family protein



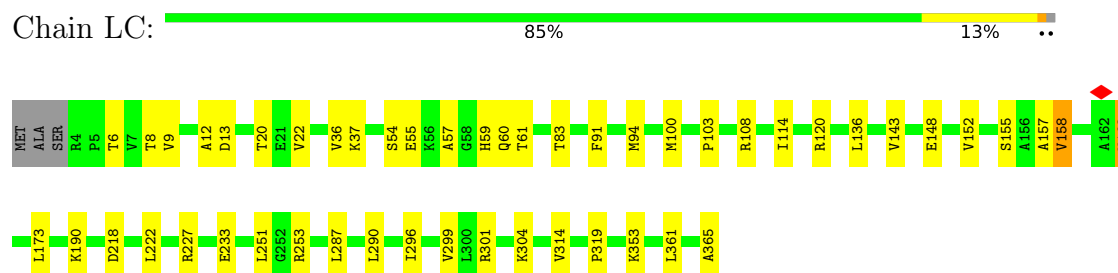
● Molecule 28: rRNA-processing protein



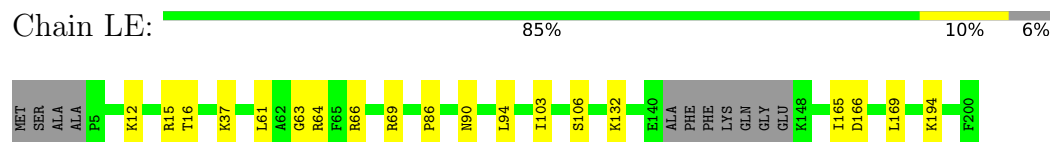
- Molecule 29: 60S ribosomal protein L3-like protein



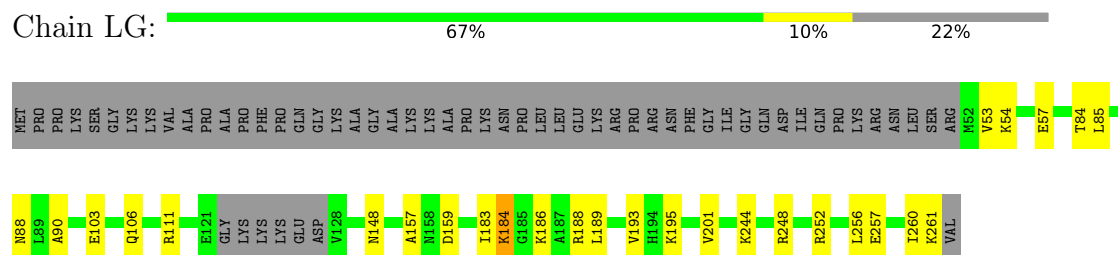
- Molecule 30: 60S ribosomal protein L4-like protein



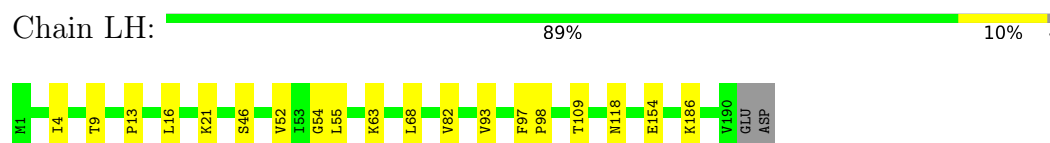
- Molecule 31: 60S ribosomal protein L6



- Molecule 32: 60S ribosomal protein L8

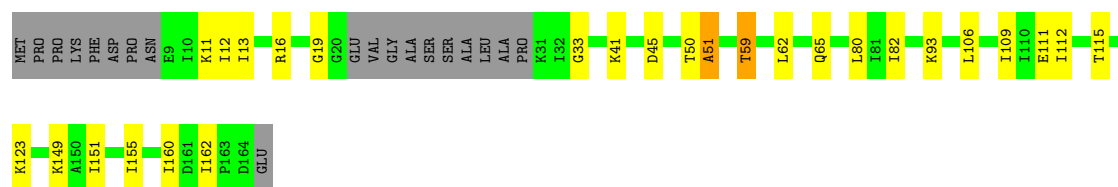


- Molecule 33: 60S ribosomal protein L9-like protein

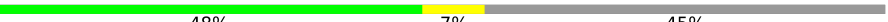


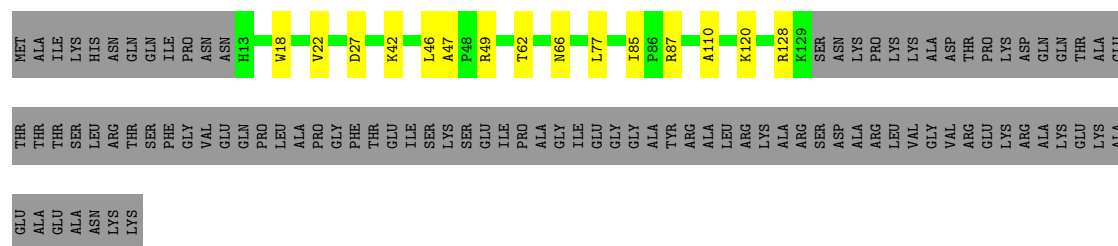
- Molecule 34: 60S ribosomal protein L12-like protein

Chain LK:  72% 15% 12%



- Molecule 35: 60S ribosomal protein L13

Chain LL:  48% 7% 45%



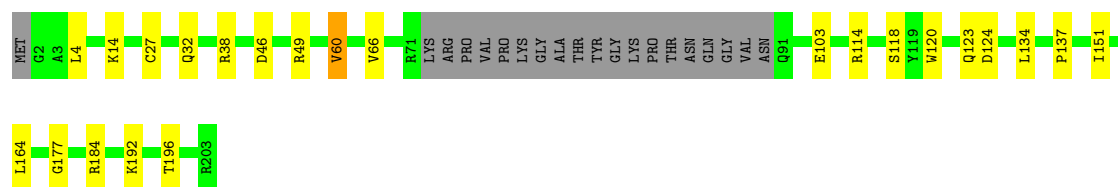
- Molecule 36: 60S ribosomal protein L14-like protein

Chain LM:  88% 8% 4%



- Molecule 37: Ribosomal protein L15

Chain LN:  79% 11% 10%



- Molecule 38: 60S ribosomal protein L16-like protein

Chain LO:  88% 12%

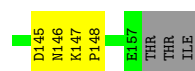


- Molecule 39: 60S ribosomal protein L17-like protein

Chain LP:  82% 9% 10%







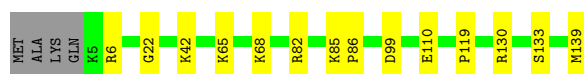
- Molecule 44: 60S ribosomal protein L22-like protein

Chain LU: 75% 8% 17%



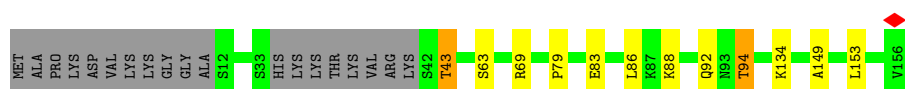
- Molecule 45: 60S ribosomal protein l23-like protein

Chain LV: 87% 10%



- Molecule 46: 60S ribosomal protein L25-like protein

Chain LX: 80% 6% 12%



- Molecule 47: 60S ribosomal protein L26-like protein

Chain LY: 87% 10%



- Molecule 48: 60S ribosomal protein L27

Chain LZ: 80% 20%



- Molecule 49: 60S ribosomal protein l30-like protein

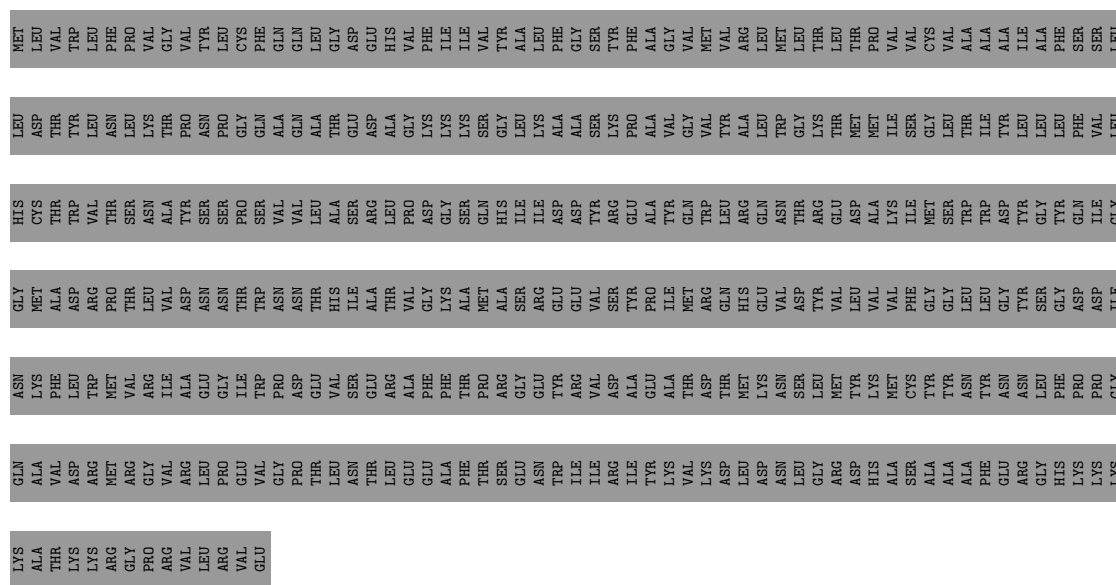
Chain Lc: 80% 10% 9%



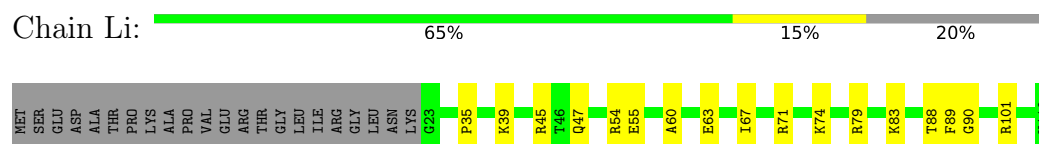
- Molecule 50: Putative 60S ribosomal protein

Chain Ld: 82% 8% 9%

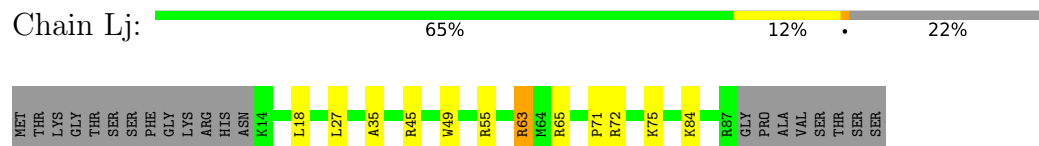




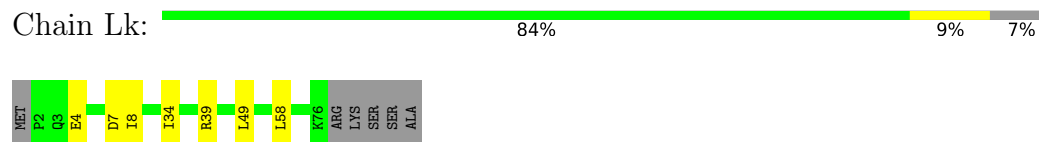
- Molecule 55: 60S ribosomal protein L36



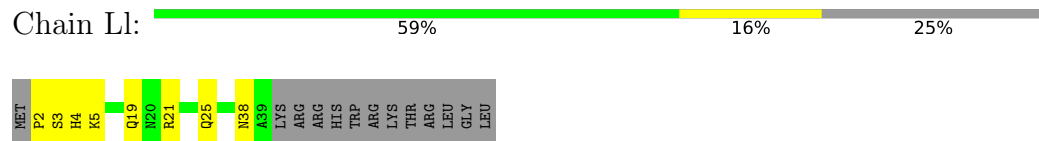
- Molecule 56: Ribosomal protein L37



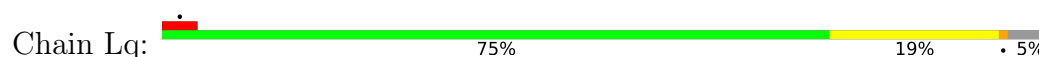
- Molecule 57: 60S ribosomal protein L38-like protein

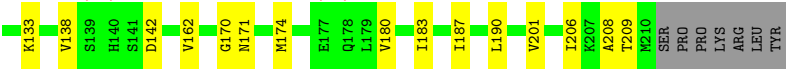
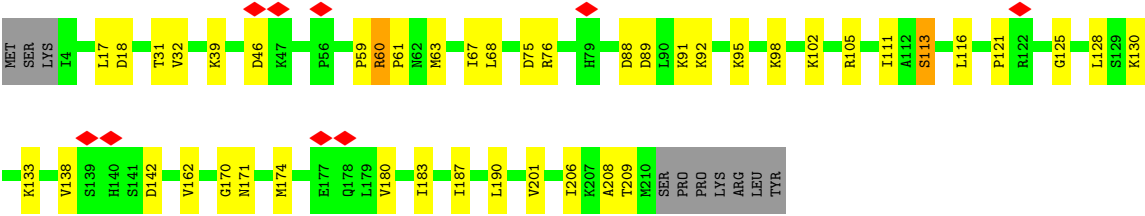


- Molecule 58: 60S ribosomal protein L39



- Molecule 59: Ribosomal protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	173028	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	0.758	Depositor
Minimum map value	-0.259	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	444.78, 444.78, 444.78	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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, ZN, GTP

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	0.24	0/66718	0.36	1/104004 (0.0%)
2	C2	0.21	0/6097	0.32	0/9499
3	CA	0.23	0/2115	0.43	0/2840
4	CB	0.26	0/2109	0.64	4/2866 (0.1%)
5	CC	0.23	0/5438	0.46	0/7404
6	CD	0.22	0/3543	0.57	2/4824 (0.0%)
7	CE	0.21	0/3760	0.49	2/5068 (0.0%)
8	CF	0.23	0/1982	0.50	0/2671
9	CG	0.24	0/1422	0.44	0/1920
10	CH	0.26	0/4468	0.54	1/6029 (0.0%)
11	CI	0.19	0/1225	0.44	0/1645
12	CJ	0.24	0/4125	0.51	0/5548
13	CK	0.25	1/1863 (0.1%)	0.43	0/2494
14	CL	0.20	0/2178	0.52	0/2983
15	CM	0.21	0/1851	0.49	0/2481
15	LF	0.25	0/2055	0.44	0/2758
16	CN	0.23	0/1881	0.52	0/2560
17	CO	0.20	0/470	0.46	1/619 (0.2%)
18	CP	0.23	0/2594	0.50	1/3514 (0.0%)
19	CQ	0.43	0/1507	0.75	0/1996
20	CR	0.20	0/1369	0.39	0/1828
21	CS	0.19	0/5115	0.48	0/6841
22	CT	0.26	0/3974	0.57	4/5357 (0.1%)
23	CU	0.19	0/1428	0.46	3/1910 (0.2%)
24	CV	0.22	0/1091	0.45	2/1468 (0.1%)
25	CW	0.34	0/4371	0.81	9/5917 (0.2%)
26	CX	0.20	0/705	0.48	0/938
27	CY	0.34	0/3079	0.74	3/4136 (0.1%)
28	Cz	0.15	0/598	0.29	0/785
29	LB	0.24	0/2885	0.48	0/3872
30	LC	0.23	0/2809	0.43	0/3787
31	LE	0.22	0/1502	0.44	0/2020

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LG	0.28	0/1667	0.56	1/2230 (0.0%)
33	LH	0.22	0/1516	0.43	0/2038
34	LK	0.20	0/1124	0.55	0/1507
35	LL	0.22	0/983	0.43	0/1318
36	LM	0.21	0/1120	0.38	0/1507
37	LN	0.24	0/1595	0.41	0/2132
38	LO	0.22	0/1652	0.43	0/2215
39	LP	0.19	0/1367	0.36	0/1838
40	LQ	0.21	0/1033	0.42	0/1391
41	LR	0.25	0/1235	0.49	0/1644
42	LS	0.23	0/1468	0.46	0/1975
43	LT	0.18	0/1033	0.44	0/1389
44	LU	0.17	0/863	0.32	0/1155
45	LV	0.20	0/1013	0.41	0/1361
46	LX	0.18	0/1078	0.34	0/1451
47	LY	0.19	0/1079	0.41	0/1443
48	LZ	0.22	0/1135	0.42	0/1519
49	Lc	0.21	0/740	0.48	0/995
50	Ld	0.21	0/904	0.40	0/1209
51	Le	0.20	0/1043	0.38	0/1389
52	Lf	0.25	0/883	0.41	0/1187
53	Lg	0.24	0/943	0.45	0/1258
54	Lh	0.17	0/1006	0.36	0/1338
55	Li	0.23	0/738	0.43	0/971
56	Lj	0.25	0/606	0.45	0/803
57	Lk	0.28	0/628	0.54	0/835
58	Ll	0.19	0/329	0.47	0/440
59	Lq	0.20	0/1621	0.59	0/2180
All	All	0.24	1/176729 (0.0%)	0.45	34/253300 (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
14	CL	0	1
22	CT	0	1
59	Lq	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	CK	152	THR	C-N	-6.27	1.23	1.33

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	CW	277	PRO	CA-N-CD	-11.12	96.43	112.00
22	CT	146	PRO	CA-N-CD	-10.08	97.88	112.00
7	CE	320	VAL	N-CA-C	-7.55	106.13	113.53
4	CB	103	ASP	CB-CA-C	6.99	123.93	110.17
4	CB	104	PRO	CA-N-CD	-6.31	103.17	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	CL	223	HIS	Peptide
22	CT	253	VAL	Peptide
59	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	59633	0	30064	410	0
2	C2	5456	0	2762	38	0
3	CA	2069	0	2109	22	0
4	CB	2063	0	2131	36	0
5	CC	5289	0	5222	68	0
6	CD	3468	0	3428	59	0
7	CE	3689	0	3794	43	0
8	CF	1945	0	1965	29	0
9	CG	1396	0	1420	18	0
10	CH	4388	0	4454	66	0
11	CI	1196	0	1202	19	0
12	CJ	4040	0	4087	44	0
13	CK	1835	0	1935	12	0
14	CL	2173	0	1423	11	0
15	CM	1820	0	1938	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	LF	2017	0	2130	15	0
16	CN	1856	0	1856	28	0
17	CO	468	0	503	10	0
18	CP	2535	0	2549	45	0
19	CQ	1485	0	1549	30	0
20	CR	1354	0	1400	20	0
21	CS	5036	0	5202	64	0
22	CT	3911	0	4023	37	0
23	CU	1415	0	1457	15	0
24	CV	1073	0	1130	10	0
25	CW	4284	0	4419	85	0
26	CX	701	0	742	8	0
27	CY	3035	0	3134	50	0
28	Cz	592	0	640	8	0
29	LB	2829	0	2933	42	0
30	LC	2752	0	2878	32	0
31	LE	1475	0	1580	11	0
32	LG	1644	0	1793	19	0
33	LH	1496	0	1575	13	0
34	LK	1112	0	1190	15	0
35	LL	964	0	1041	10	0
36	LM	1101	0	1170	8	0
37	LN	1563	0	1618	14	0
38	LO	1618	0	1714	16	0
39	LP	1345	0	1389	11	0
40	LQ	1021	0	1118	12	0
41	LR	1219	0	1291	8	0
42	LS	1433	0	1496	25	0
43	LT	1014	0	1073	8	0
44	LU	850	0	894	7	0
45	LV	995	0	1055	13	0
46	LX	1062	0	1145	9	0
47	LY	1065	0	1156	8	0
48	LZ	1112	0	1181	18	0
49	Lc	731	0	772	8	0
50	Ld	890	0	940	9	0
51	Le	1025	0	1104	7	0
52	Lf	862	0	891	9	0
53	Lg	930	0	1011	12	0
54	Lh	995	0	1110	14	0
55	Li	731	0	797	13	0
56	Lj	595	0	625	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	Lk	620	0	680	5	0
58	Ll	322	0	346	5	0
59	Lq	1600	0	1703	29	0
60	CH	32	0	12	0	0
61	CQ	1	0	0	0	0
61	Lj	1	0	0	0	0
62	CW	27	0	12	1	0
63	CW	1	0	0	0	0
All	All	167255	0	137961	1469	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 5.

The worst 5 of 1469 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CQ:153:GLY:O	19:CQ:155:ASP:CB	1.66	1.39
10:CH:544:ILE:HD11	10:CH:546:LEU:CG	1.75	1.15
19:CQ:153:GLY:O	19:CQ:155:ASP:HB3	1.48	1.09
10:CH:544:ILE:CD1	10:CH:546:LEU:HG	1.83	1.08
10:CH:544:ILE:CG1	10:CH:546:LEU:HG	1.84	1.08

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%)	235 (95%)	12 (5%)	0	100	100
4	CB	256/391 (66%)	242 (94%)	12 (5%)	2 (1%)	16	37
5	CC	650/801 (81%)	625 (96%)	24 (4%)	1 (0%)	43	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	CD	450/495 (91%)	429 (95%)	21 (5%)	0	100	100
7	CE	461/598 (77%)	440 (95%)	20 (4%)	1 (0%)	43	68
8	CF	243/270 (90%)	232 (96%)	10 (4%)	1 (0%)	30	54
9	CG	175/184 (95%)	169 (97%)	6 (3%)	0	100	100
10	CH	538/661 (81%)	517 (96%)	21 (4%)	0	100	100
11	CI	144/414 (35%)	139 (96%)	5 (4%)	0	100	100
12	CJ	484/679 (71%)	468 (97%)	16 (3%)	0	100	100
13	CK	223/261 (85%)	216 (97%)	7 (3%)	0	100	100
14	CL	384/558 (69%)	353 (92%)	25 (6%)	6 (2%)	7	20
15	CM	219/249 (88%)	208 (95%)	11 (5%)	0	100	100
15	LF	245/249 (98%)	236 (96%)	9 (4%)	0	100	100
16	CN	244/246 (99%)	229 (94%)	15 (6%)	0	100	100
17	CO	56/120 (47%)	55 (98%)	1 (2%)	0	100	100
18	CP	322/751 (43%)	309 (96%)	13 (4%)	0	100	100
19	CQ	173/225 (77%)	169 (98%)	4 (2%)	0	100	100
20	CR	159/237 (67%)	154 (97%)	5 (3%)	0	100	100
21	CS	607/834 (73%)	577 (95%)	29 (5%)	1 (0%)	43	68
22	CT	478/688 (70%)	454 (95%)	23 (5%)	1 (0%)	43	68
23	CU	174/451 (39%)	169 (97%)	4 (2%)	1 (1%)	21	44
24	CV	137/147 (93%)	131 (96%)	5 (4%)	1 (1%)	18	41
25	CW	531/679 (78%)	495 (93%)	34 (6%)	2 (0%)	30	54
26	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100
27	CY	366/788 (46%)	346 (94%)	19 (5%)	1 (0%)	36	60
28	Cz	68/123 (55%)	65 (96%)	3 (4%)	0	100	100
29	LB	352/392 (90%)	338 (96%)	14 (4%)	0	100	100
30	LC	360/365 (99%)	345 (96%)	15 (4%)	0	100	100
31	LE	185/200 (92%)	172 (93%)	13 (7%)	0	100	100
32	LG	200/262 (76%)	189 (94%)	11 (6%)	0	100	100
33	LH	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
34	LK	142/165 (86%)	132 (93%)	8 (6%)	2 (1%)	9	23
35	LL	115/213 (54%)	109 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LM	135/142 (95%)	129 (96%)	6 (4%)	0	100	100
37	LN	179/203 (88%)	173 (97%)	6 (3%)	0	100	100
38	LO	202/204 (99%)	200 (99%)	2 (1%)	0	100	100
39	LP	165/187 (88%)	162 (98%)	3 (2%)	0	100	100
40	LQ	127/213 (60%)	122 (96%)	5 (4%)	0	100	100
41	LR	144/2898 (5%)	143 (99%)	1 (1%)	0	100	100
42	LS	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
43	LT	124/160 (78%)	118 (95%)	5 (4%)	1 (1%)	16	37
44	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
45	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
46	LX	133/156 (85%)	130 (98%)	3 (2%)	0	100	100
47	LY	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
48	LZ	133/135 (98%)	125 (94%)	8 (6%)	0	100	100
49	Lc	96/108 (89%)	95 (99%)	1 (1%)	0	100	100
50	Ld	107/120 (89%)	104 (97%)	3 (3%)	0	100	100
51	Le	125/131 (95%)	123 (98%)	2 (2%)	0	100	100
52	Lf	106/109 (97%)	103 (97%)	3 (3%)	0	100	100
53	Lg	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
54	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
55	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
56	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
57	Lk	73/81 (90%)	70 (96%)	3 (4%)	0	100	100
58	Ll	36/51 (71%)	36 (100%)	0	0	100	100
59	Lq	205/217 (94%)	184 (90%)	21 (10%)	0	100	100
All	All	12684/20359 (62%)	12128 (96%)	535 (4%)	21 (0%)	44	68

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CB	103	ASP
4	CB	104	PRO
7	CE	313	PRO
14	CL	224	ASP
14	CL	414	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%)	219 (98%)	4 (2%)	51	78
4	CB	222/329 (68%)	212 (96%)	10 (4%)	24	52
5	CC	580/710 (82%)	569 (98%)	11 (2%)	50	77
6	CD	381/410 (93%)	374 (98%)	7 (2%)	51	78
7	CE	400/517 (77%)	390 (98%)	10 (2%)	42	71
8	CF	214/236 (91%)	213 (100%)	1 (0%)	81	92
9	CG	150/155 (97%)	146 (97%)	4 (3%)	39	69
10	CH	481/575 (84%)	467 (97%)	14 (3%)	37	67
11	CI	121/336 (36%)	118 (98%)	3 (2%)	42	71
12	CJ	428/579 (74%)	420 (98%)	8 (2%)	50	77
13	CK	195/225 (87%)	192 (98%)	3 (2%)	57	81
14	CL	65/458 (14%)	64 (98%)	1 (2%)	57	81
15	CM	191/215 (89%)	186 (97%)	5 (3%)	40	70
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	87
16	CN	206/206 (100%)	206 (100%)	0	100	100
17	CO	48/99 (48%)	47 (98%)	1 (2%)	47	75
18	CP	273/632 (43%)	267 (98%)	6 (2%)	45	74
19	CQ	150/192 (78%)	136 (91%)	14 (9%)	8	21
20	CR	144/206 (70%)	142 (99%)	2 (1%)	59	82
21	CS	527/716 (74%)	522 (99%)	5 (1%)	70	87
22	CT	427/600 (71%)	411 (96%)	16 (4%)	30	59
23	CU	149/376 (40%)	146 (98%)	3 (2%)	48	76
24	CV	109/112 (97%)	105 (96%)	4 (4%)	30	59
25	CW	473/577 (82%)	448 (95%)	25 (5%)	20	46
26	CX	76/172 (44%)	75 (99%)	1 (1%)	61	83
27	CY	315/686 (46%)	293 (93%)	22 (7%)	14	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Cz	60/107 (56%)	58 (97%)	2 (3%)	33	63
29	LB	301/331 (91%)	298 (99%)	3 (1%)	68	86
30	LC	283/285 (99%)	276 (98%)	7 (2%)	42	71
31	LE	159/166 (96%)	156 (98%)	3 (2%)	50	77
32	LG	175/222 (79%)	170 (97%)	5 (3%)	37	67
33	LH	167/169 (99%)	165 (99%)	2 (1%)	63	84
34	LK	121/136 (89%)	116 (96%)	5 (4%)	27	56
35	LL	99/176 (56%)	98 (99%)	1 (1%)	68	86
36	LM	115/117 (98%)	114 (99%)	1 (1%)	70	87
37	LN	164/180 (91%)	160 (98%)	4 (2%)	43	72
38	LO	163/163 (100%)	162 (99%)	1 (1%)	78	91
39	LP	137/152 (90%)	134 (98%)	3 (2%)	45	74
40	LQ	110/178 (62%)	109 (99%)	1 (1%)	70	87
41	LR	128/2396 (5%)	123 (96%)	5 (4%)	28	57
42	LS	154/154 (100%)	146 (95%)	8 (5%)	21	47
43	LT	109/135 (81%)	102 (94%)	7 (6%)	16	38
44	LU	93/108 (86%)	93 (100%)	0	100	100
45	LV	99/102 (97%)	99 (100%)	0	100	100
46	LX	114/129 (88%)	112 (98%)	2 (2%)	51	78
47	LY	117/119 (98%)	115 (98%)	2 (2%)	53	79
48	LZ	121/121 (100%)	121 (100%)	0	100	100
49	Lc	79/88 (90%)	77 (98%)	2 (2%)	42	71
50	Ld	95/105 (90%)	93 (98%)	2 (2%)	47	75
51	Le	110/114 (96%)	108 (98%)	2 (2%)	51	78
52	Lf	89/90 (99%)	87 (98%)	2 (2%)	45	74
53	Lg	101/102 (99%)	101 (100%)	0	100	100
54	Lh	108/781 (14%)	107 (99%)	1 (1%)	70	87
55	Li	75/93 (81%)	74 (99%)	1 (1%)	61	83
56	Lj	61/78 (78%)	58 (95%)	3 (5%)	22	49
57	Lk	71/76 (93%)	71 (100%)	0	100	100
58	Ll	34/46 (74%)	33 (97%)	1 (3%)	37	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	Lq	179/189 (95%)	177 (99%)	2 (1%)	65	85
All	All	10752/17218 (62%)	10492 (98%)	260 (2%)	43	72

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	LS	163	LYS
43	LT	146	ASN
19	CQ	158	GLU
19	CQ	151	GLU
47	LY	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
25	CW	414	GLN
37	LN	95	GLN
25	CW	623	ASN
32	LG	92	GLN
38	LO	27	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2770/3341 (82%)	564 (20%)	21 (0%)
2	C2	254/319 (79%)	54 (21%)	1 (0%)
All	All	3024/3660 (82%)	618 (20%)	22 (0%)

5 of 618 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A
1	C1	59	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3078	U
1	C1	3204	G
1	C1	3162	A
1	C1	3209	U
1	C1	1046	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 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	$\# Z > 2$
62	ADP	CW	1001	63	28,29,29	0.45	0	43,45,45	0.50	0
60	GTP	CH	701	-	33,34,34	0.90	0	50,54,54	1.60	9 (18%)

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
62	ADP	CW	1001	63	-	4/16/32/32	0/3/3/3
60	GTP	CH	701	-	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	CH	701	GTP	C5-C4-N3	-4.91	120.57	128.39
60	CH	701	GTP	C2-N3-C4	4.58	120.19	112.30
60	CH	701	GTP	N9-C4-N3	3.10	132.14	125.95
60	CH	701	GTP	C2-N1-C6	-2.90	119.85	125.11
60	CH	701	GTP	N9-C8-N7	-2.70	108.39	113.40

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

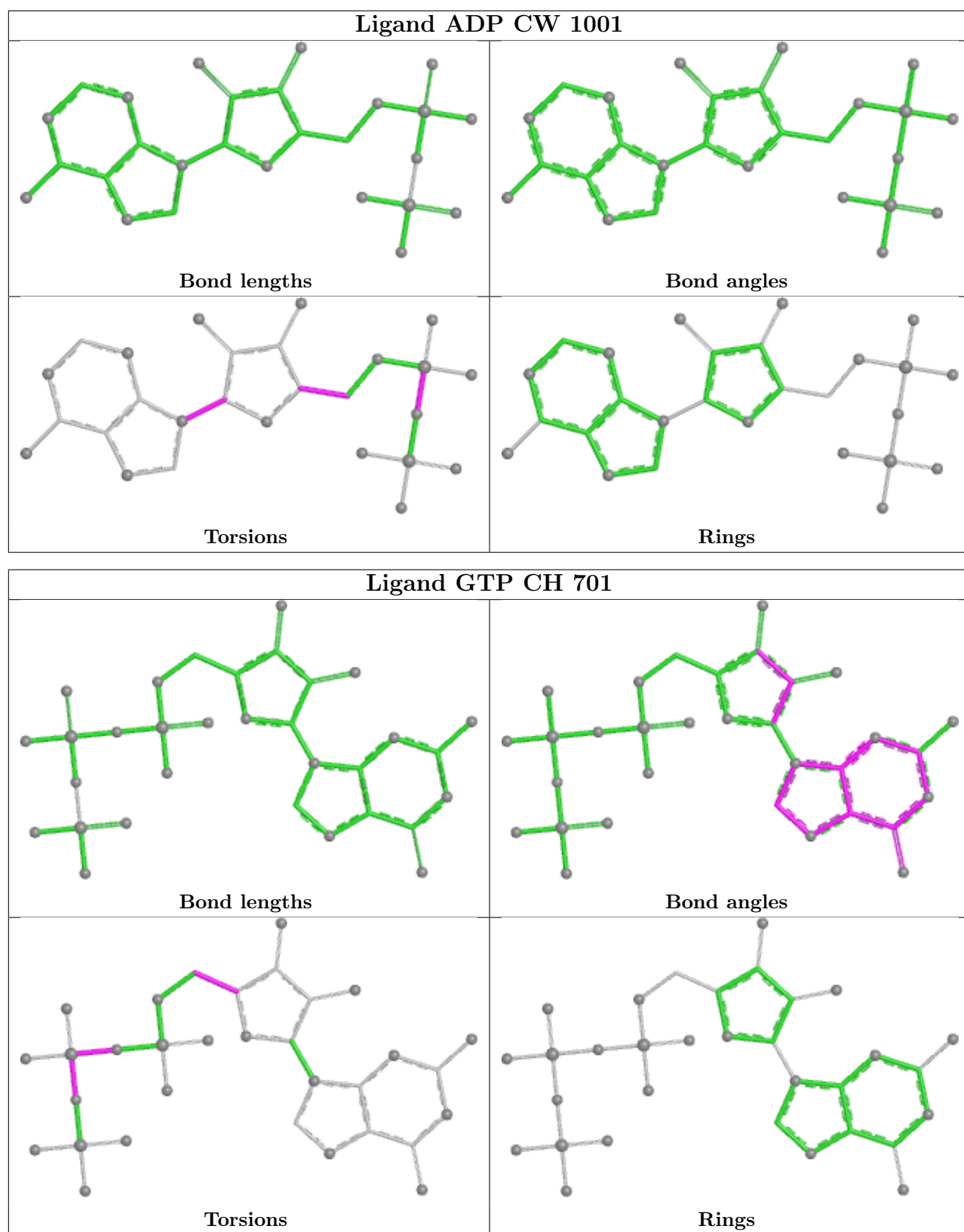
Mol	Chain	Res	Type	Atoms
62	CW	1001	ADP	C3'-C4'-C5'-O5'
62	CW	1001	ADP	O4'-C4'-C5'-O5'
60	CH	701	GTP	PG-O3B-PB-O2B
62	CW	1001	ADP	PB-O3A-PA-O1A
60	CH	701	GTP	PA-O3A-PB-O3B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	CW	1001	ADP	1	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

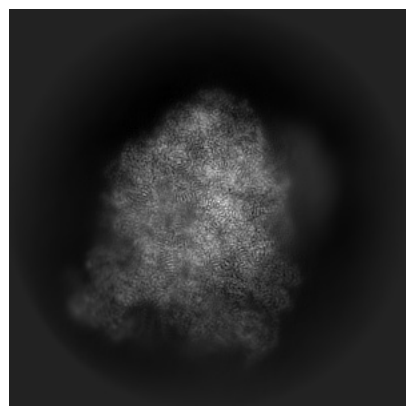
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35289. These allow visual inspection of the internal detail of the map and identification of artifacts.

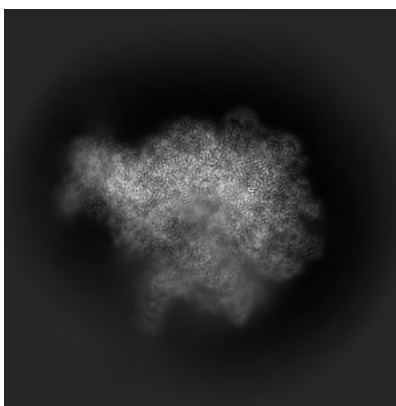
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

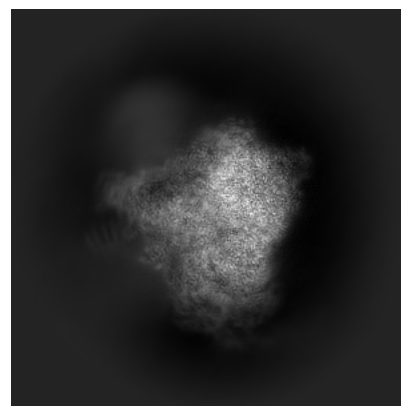
6.1.1 Primary map



X

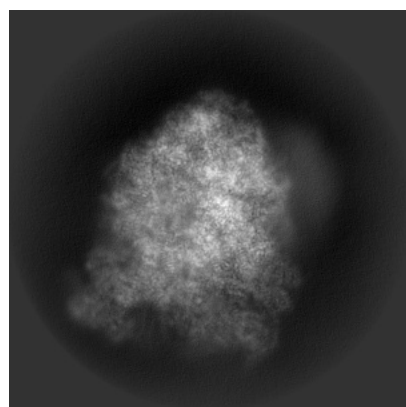


Y

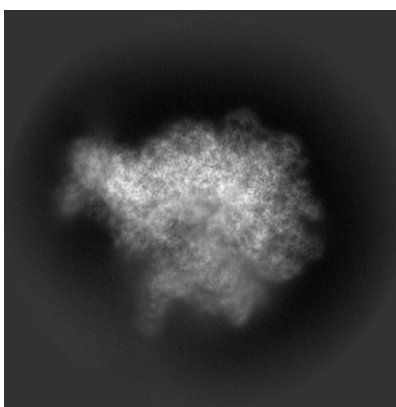


Z

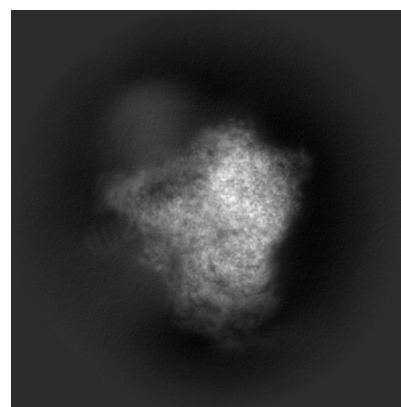
6.1.2 Raw map



X



Y

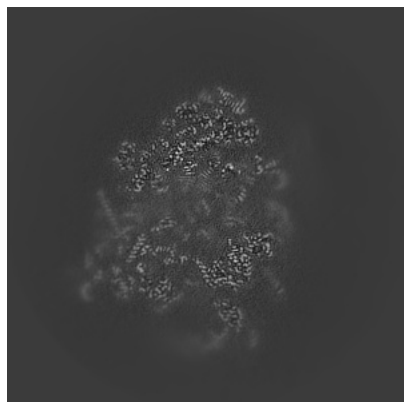


Z

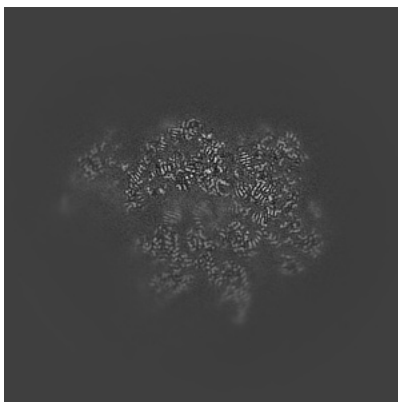
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

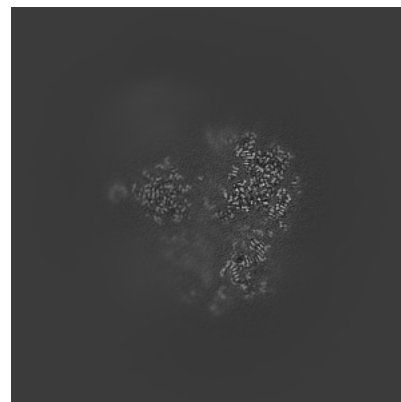
6.2.1 Primary map



X Index: 210

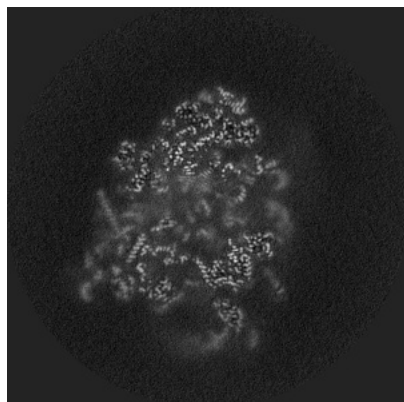


Y Index: 210

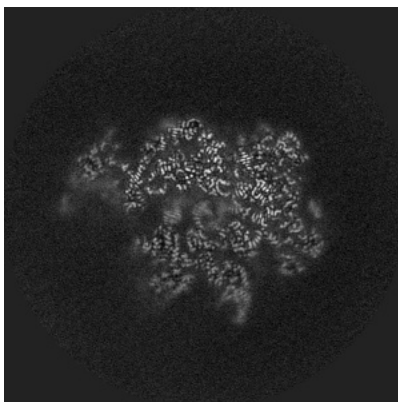


Z Index: 210

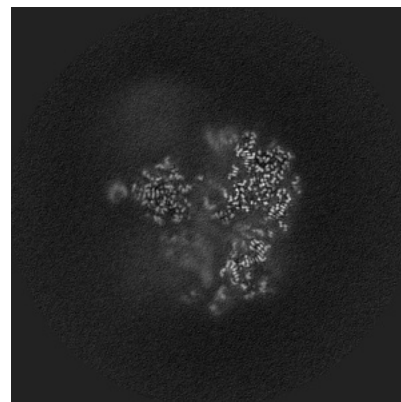
6.2.2 Raw map



X Index: 210



Y Index: 210

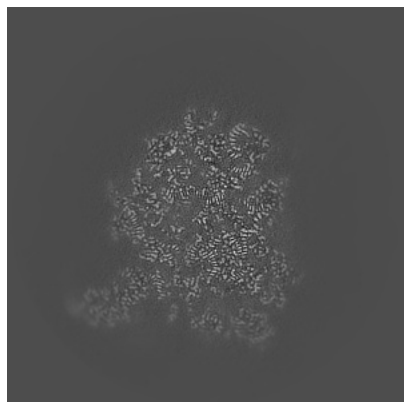


Z Index: 210

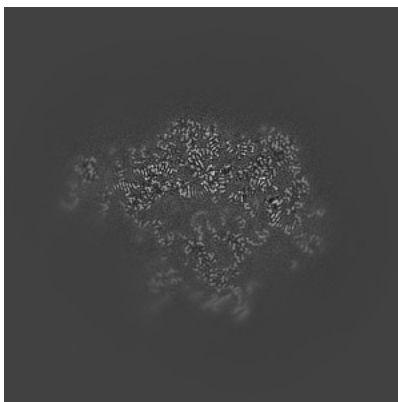
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

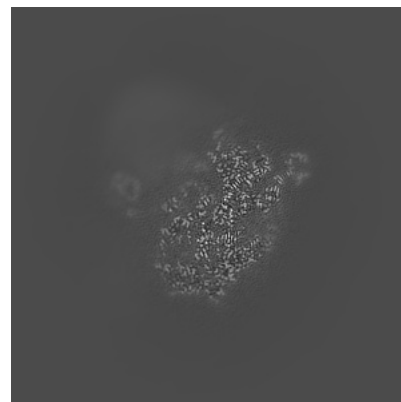
6.3.1 Primary map



X Index: 246

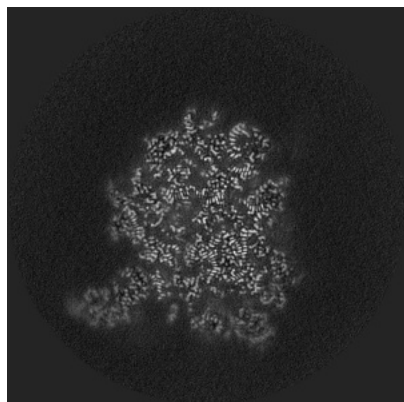


Y Index: 219

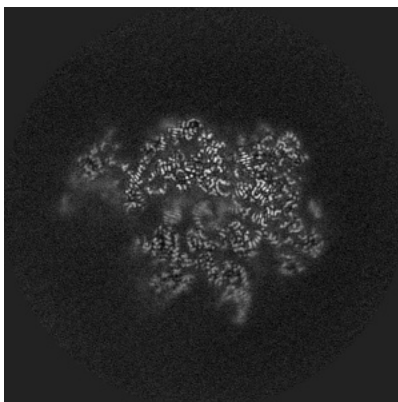


Z Index: 261

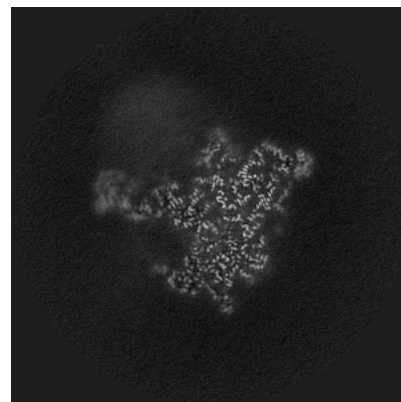
6.3.2 Raw map



X Index: 246



Y Index: 210

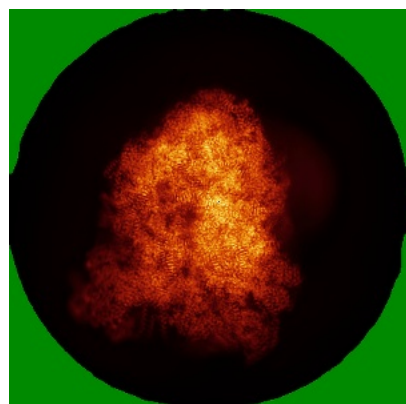


Z Index: 249

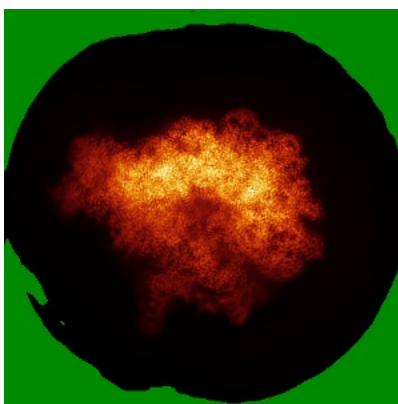
The images above show the largest variance slices of the map in three orthogonal directions.

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

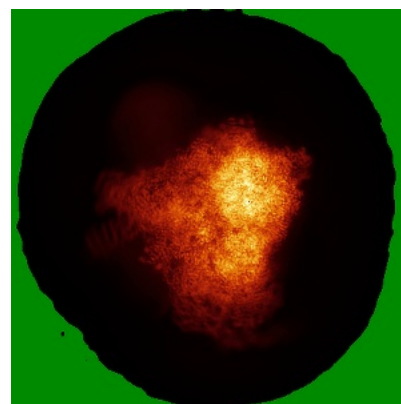
6.4.1 Primary map



X

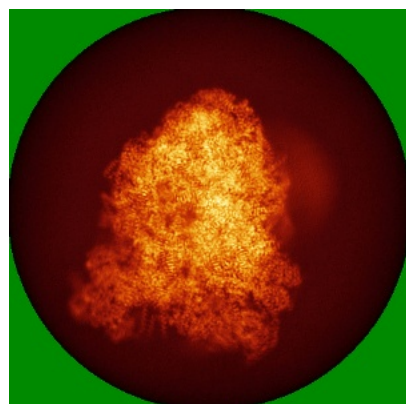


Y

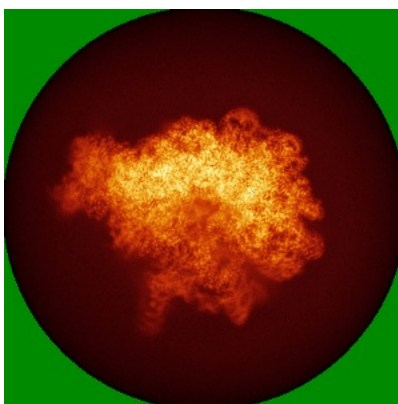


Z

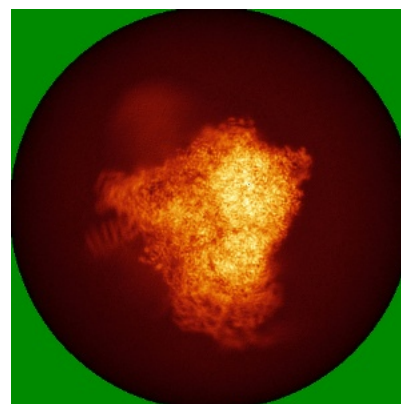
6.4.2 Raw map



X



Y



Z

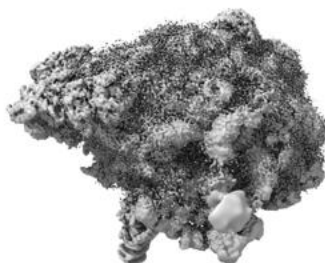
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

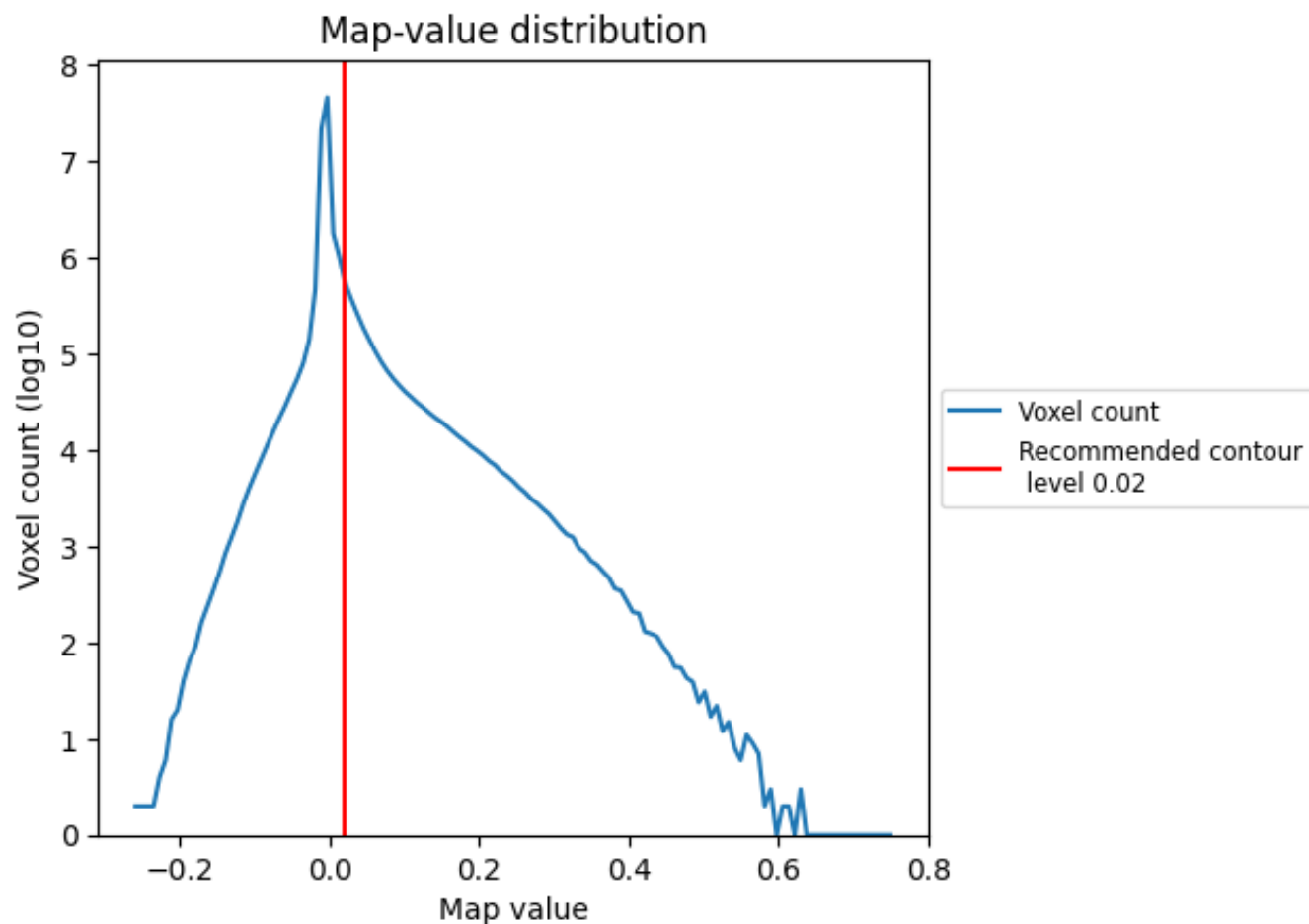
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

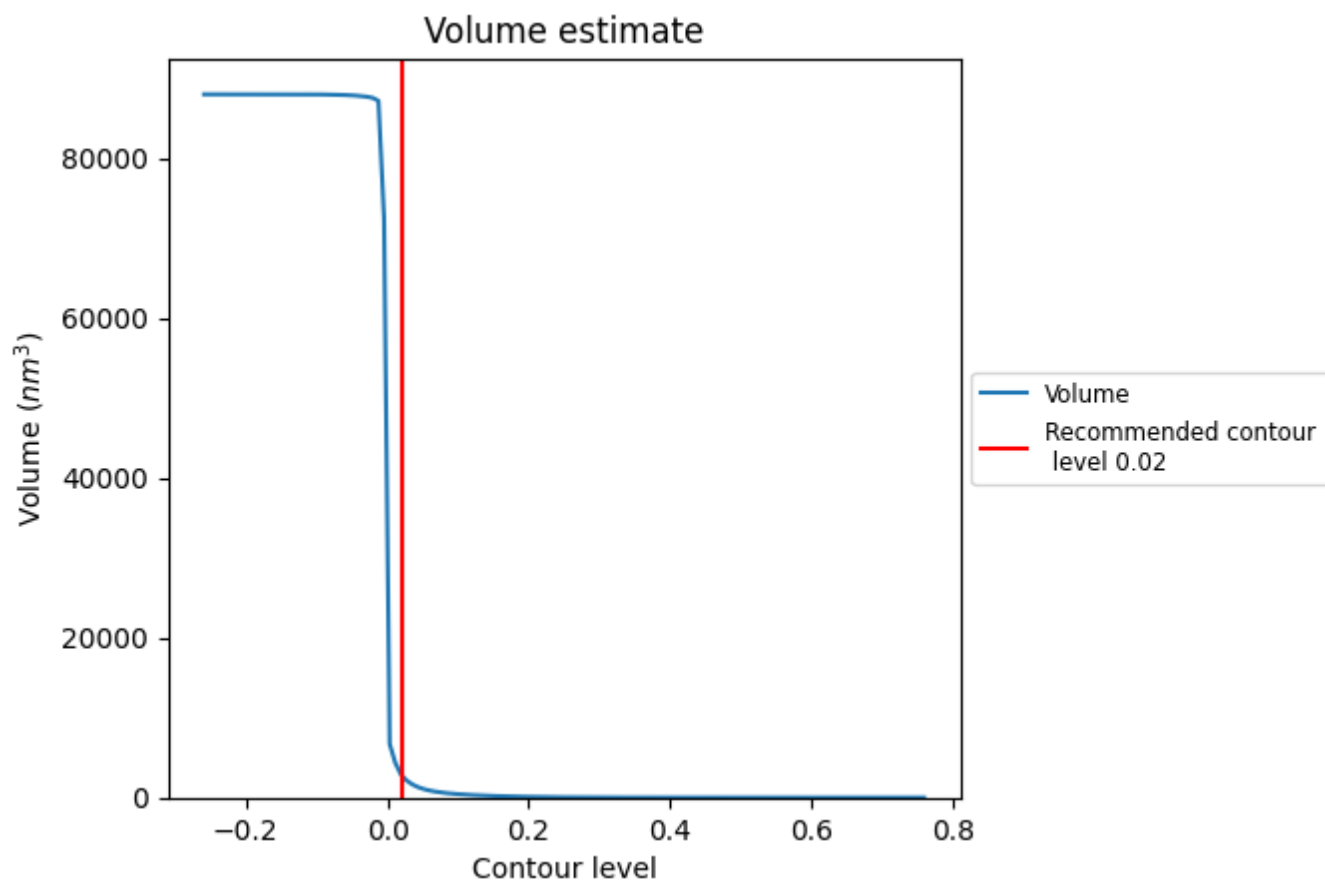
This section contains the results of statistical analysis of the map.

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.

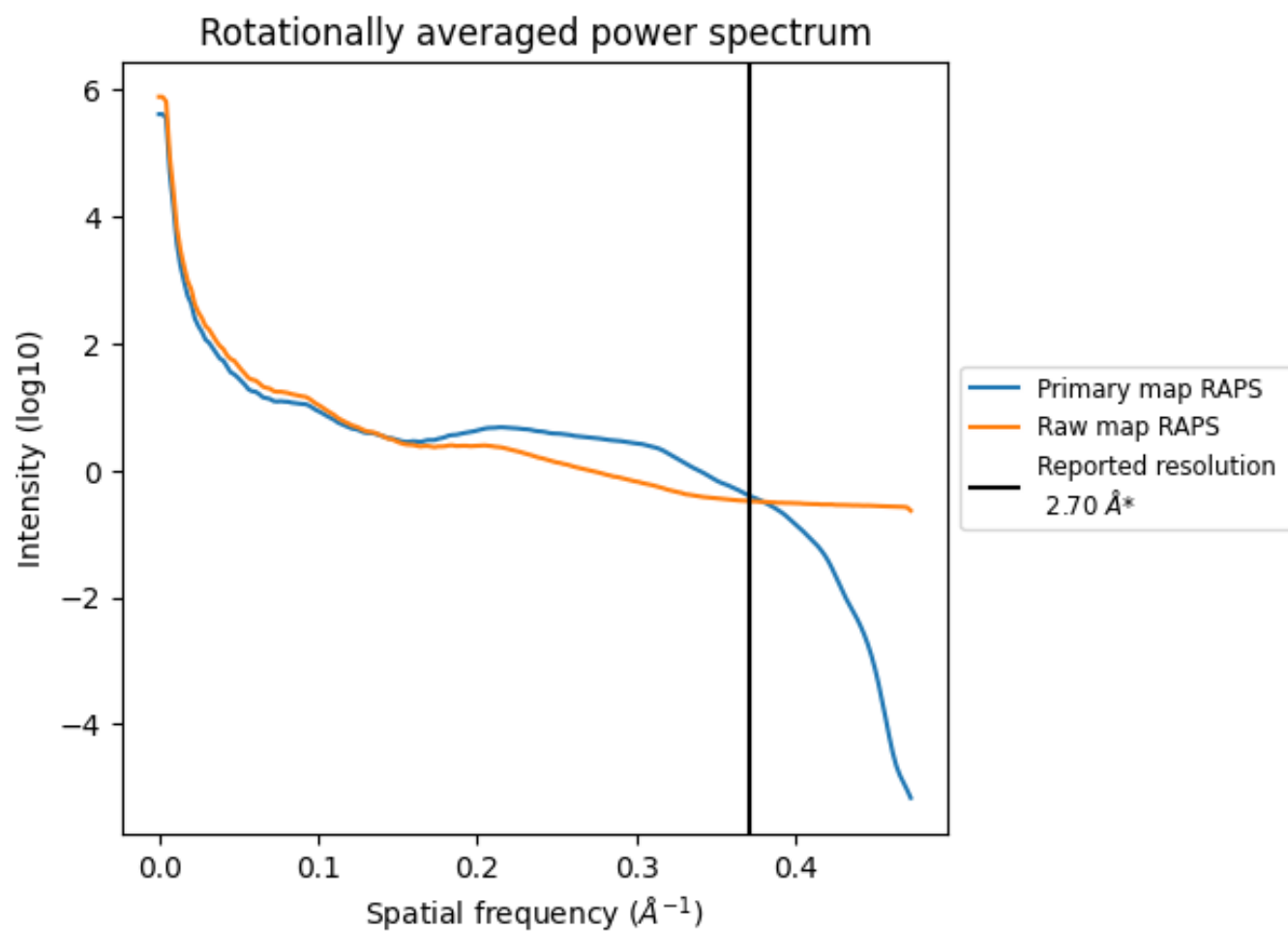
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2816 nm^3 ; this corresponds to an approximate mass of 2544 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 ⓘ

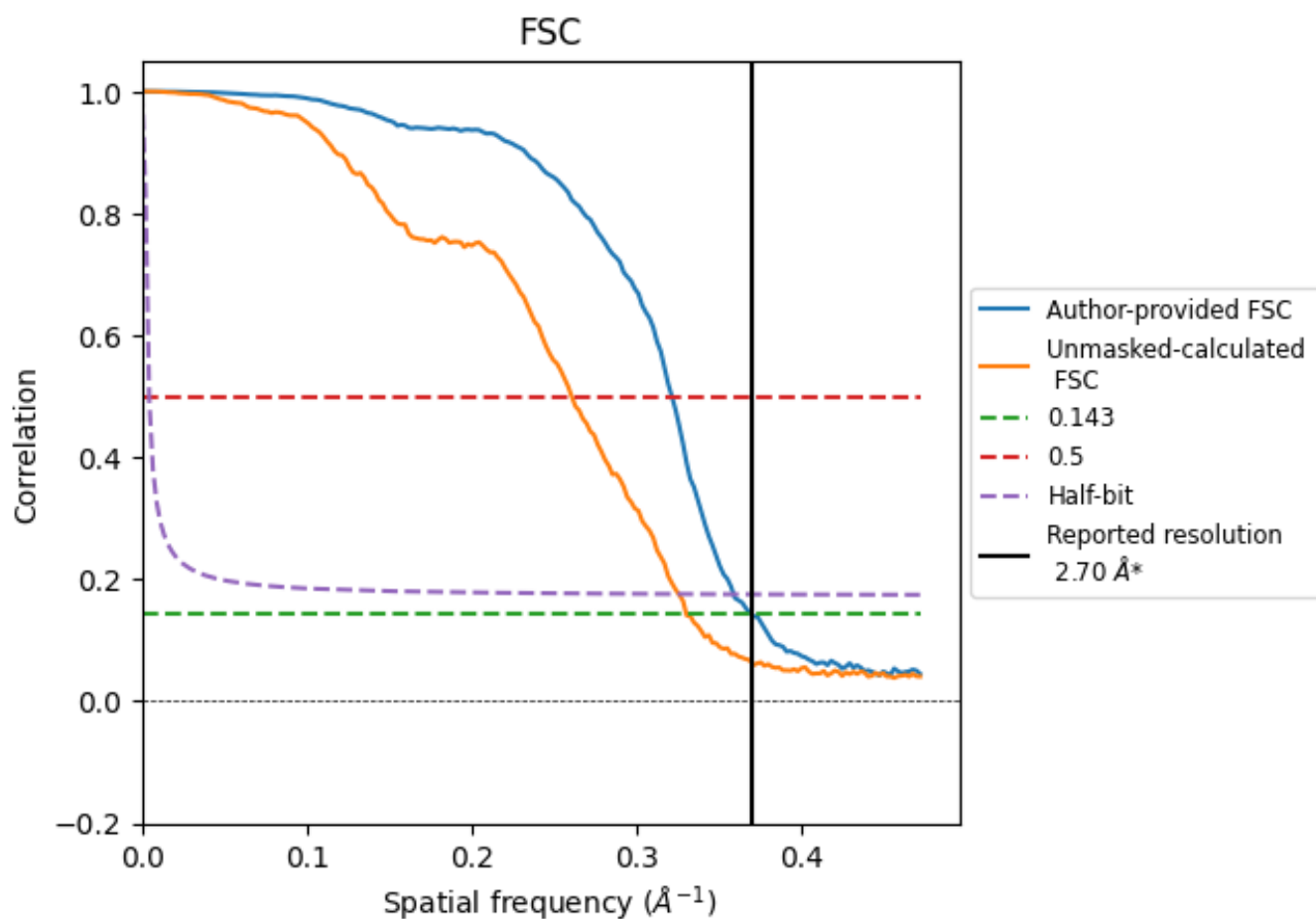


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

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

8.2 Resolution estimates [i](#)

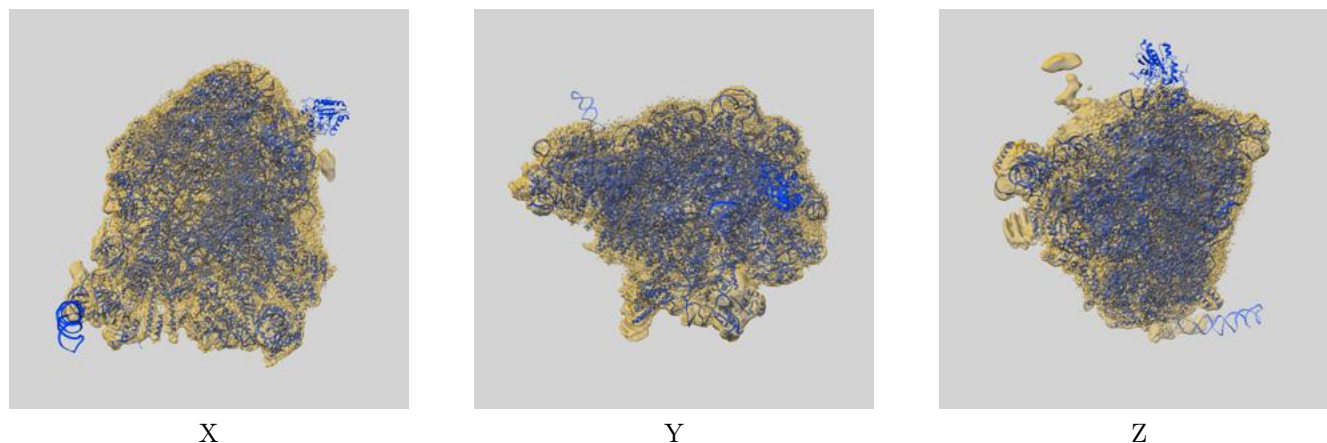
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.71	3.11	2.79
Unmasked-calculated*	3.03	3.84	3.07

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

9 Map-model fit [i](#)

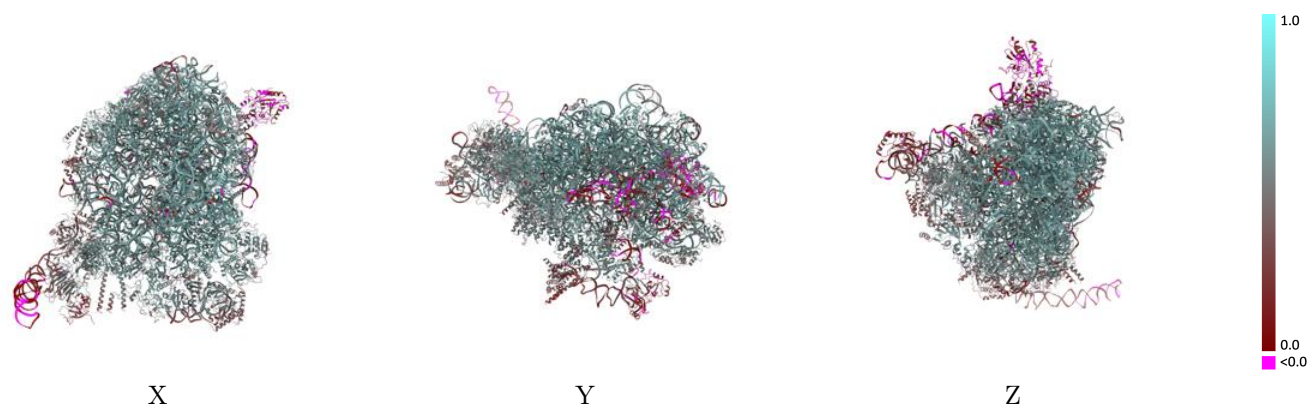
This section contains information regarding the fit between EMDB map EMD-35289 and PDB model 8I9Z. Per-residue inclusion information can be found in section [3](#) on page [19](#).

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](#)

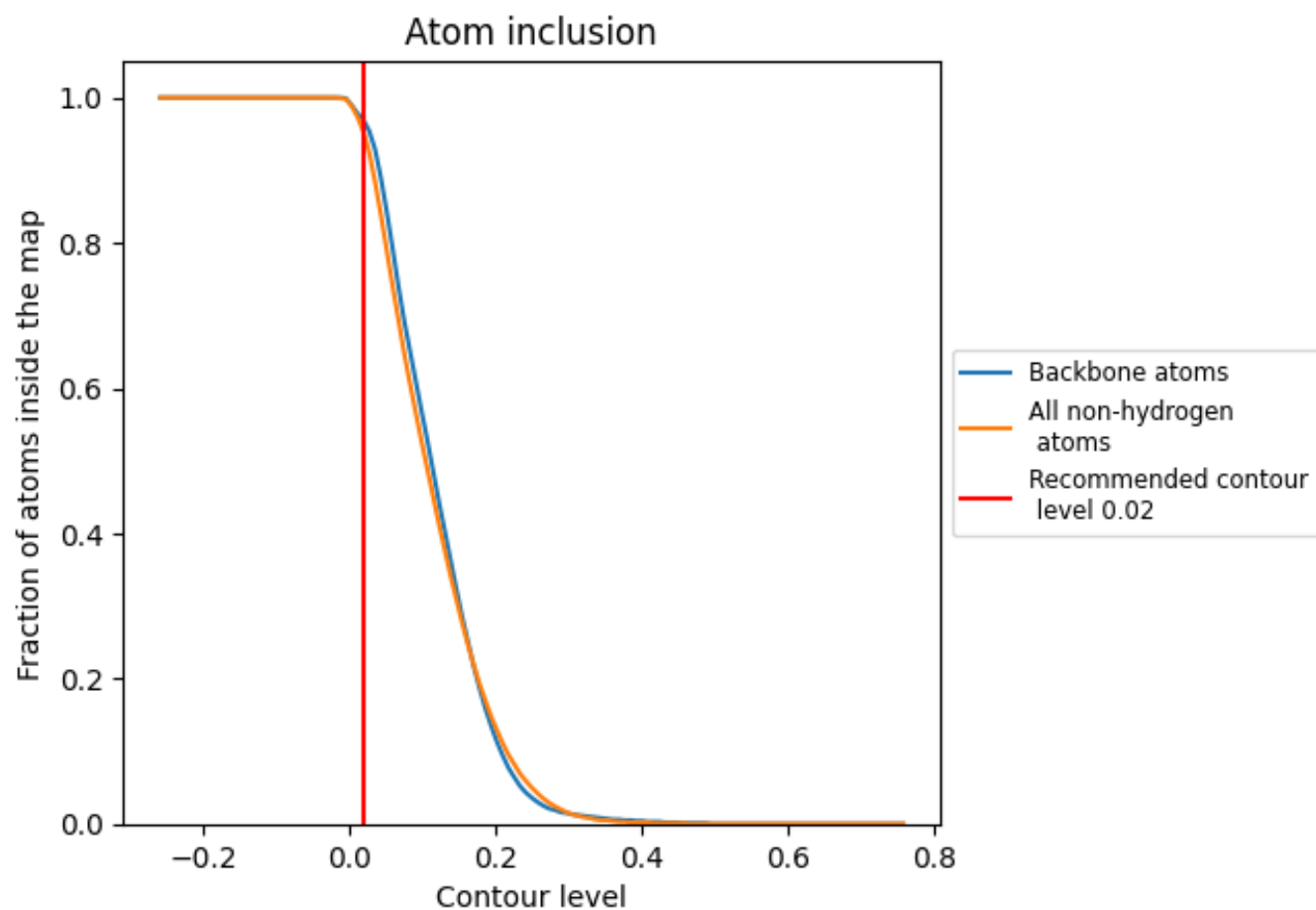


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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	 0.9510	 0.5240
C1	 0.9610	 0.5300
C2	 0.9790	 0.5420
CA	 0.9810	 0.5940
CB	 0.9340	 0.4530
CC	 0.9670	 0.5520
CD	 0.9330	 0.3950
CE	 0.9450	 0.5220
CF	 0.9540	 0.5110
CG	 0.9690	 0.5750
CH	 0.9640	 0.5440
CI	 0.9280	 0.4660
CJ	 0.9510	 0.5260
CK	 0.9660	 0.5600
CL	 0.3380	 0.2040
CM	 0.9450	 0.4760
CN	 0.9630	 0.5610
CO	 0.9540	 0.5600
CP	 0.9720	 0.5530
CQ	 0.9490	 0.5230
CR	 0.9650	 0.5790
CS	 0.9240	 0.4080
CT	 0.9660	 0.5230
CU	 0.9650	 0.5490
CV	 0.9790	 0.6210
CW	 0.9330	 0.3830
CX	 0.9240	 0.4990
CY	 0.9060	 0.3620
Cz	 0.9060	 0.3840
LB	 0.9800	 0.6080
LC	 0.9790	 0.6320
LE	 0.9670	 0.5790
LF	 0.9710	 0.6050
LG	 0.9760	 0.6100
LH	 0.9730	 0.5960



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Chain	Atom inclusion	Q-score
LK	 0.9390	 0.4380
LL	 0.9850	 0.6300
LM	 0.9760	 0.6110
LN	 0.9980	 0.6700
LO	 0.9860	 0.6440
LP	 0.9730	 0.5830
LQ	 0.9800	 0.5950
LR	 0.9520	 0.5090
LS	 0.9830	 0.6110
LT	 0.9320	 0.3910
LU	 0.9610	 0.5410
LV	 0.9820	 0.5820
LX	 0.9670	 0.5730
LY	 0.9720	 0.6020
LZ	 0.9750	 0.5790
Lc	 0.9620	 0.5250
Ld	 0.9620	 0.6020
Le	 0.9830	 0.6420
Lf	 0.9870	 0.6500
Lg	 0.9610	 0.5850
Lh	 0.9580	 0.5680
Li	 0.9570	 0.5740
Lj	 0.9880	 0.6440
Lk	 0.9420	 0.5120
Ll	 0.9810	 0.5260
Lq	 0.8570	 0.1750