



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:39 PM UTC

PDB ID : 8I9X / pdb_00008i9x
EMDB ID : EMD-35287
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- Ytm1-1
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 2.80 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 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

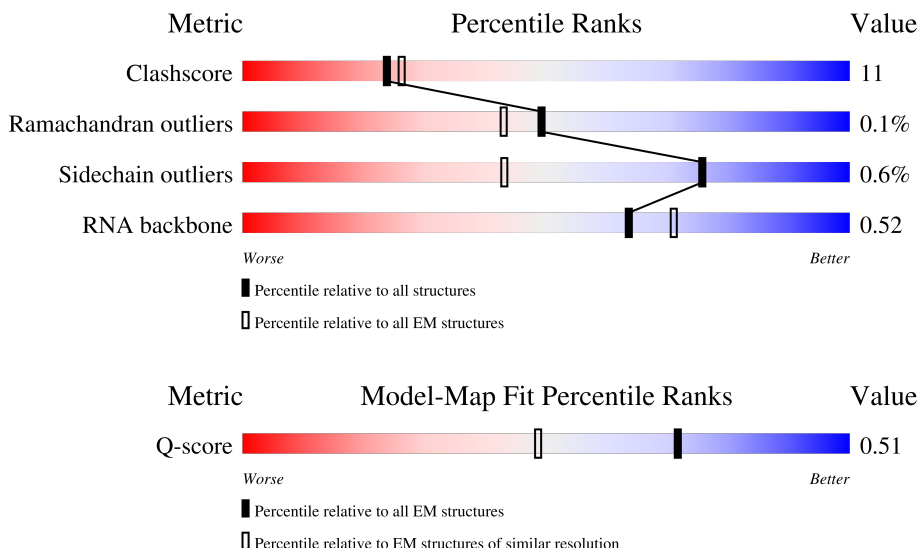
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



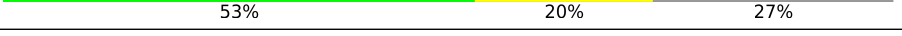
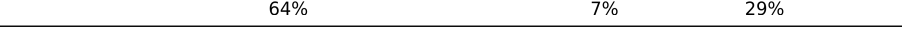
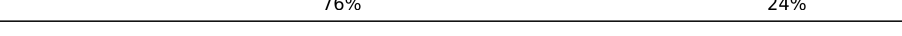
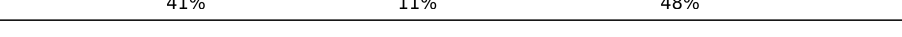
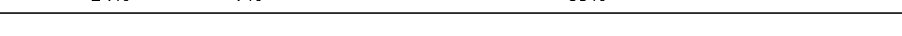
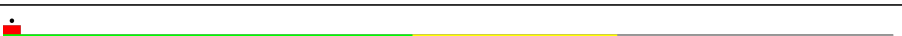
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	CX	203	
26	CY	788	
27	Cb	924	

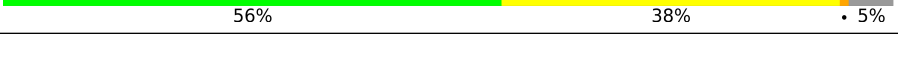
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Mol	Chain	Length	Quality of chain
28	Cz	123	
29	LB	392	
30	LC	365	
31	LE	200	
32	LG	262	
33	LH	192	
34	LK	165	
35	LL	213	
36	LM	142	
37	LN	203	
38	LO	204	
39	LP	187	
40	LQ	213	
41	LR	2898	
42	LS	174	
43	LT	160	
44	LU	127	
45	LV	139	
46	LX	156	
47	LY	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 61 unique types of molecules in this entry. The entry contains 162633 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	2658	Total	C	N	O	P	0	0
			56864	25379	10296	18531	2658		

- 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	462	Total	C	N	O	S	0	0
			3669	2350	642	666	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	238	Total	C	N	O	S	0	0
			1908	1199	375	330	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	262	Total	C	N	O	S	0	0
			2105	1322	399	377	7		

- 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 60S ribosomal subunit-like protein.

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

- Molecule 26 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	CY	410	Total	C	N	O	S	0
			3313	2127	597	577	12	0

- Molecule 27 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Cb	642	Total	C	N	O	S	0
			5058	3216	918	911	13	0

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

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

- 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
			2829	1798	518	501	12	0

- 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
			2752	1738	526	479	9	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LE	179	Total	C	N	O	S	0	0
			1403	898	255	247	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	145	Total	C	N	O	S	0	0
			1103	695	201	205	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	118	Total	C	N	O	S	0	0
			964	607	195	158	4		

- 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

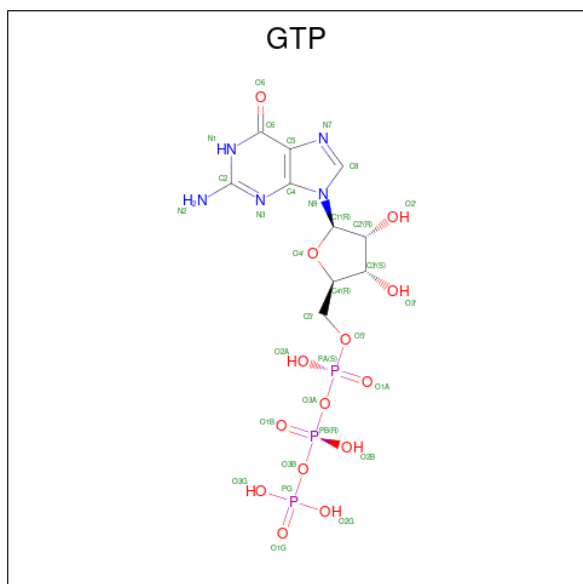
- Molecule 58 is a protein called 60S ribosomal protein L39.

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: $C_{10}H_{16}N_5O_{14}P_3$).



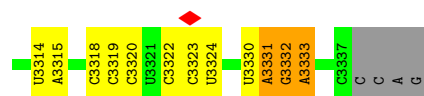
Mol	Chain	Residues	Atoms					AltConf
60	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	

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

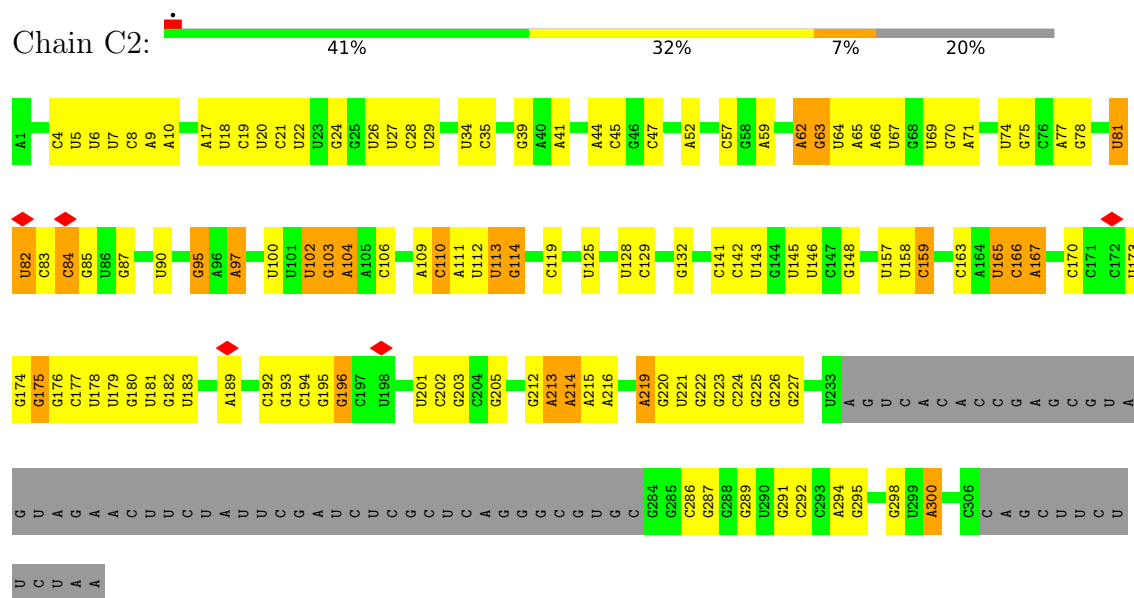
Mol	Chain	Residues	Atoms		AltConf
61	CQ	1	Total 1	Zn 1	0
61	Lj	1	Total 1	Zn 1	0

C871	A958	C	G1088	A1186	A1268	G1362	G1475	C1594	A1697	A1788	G1877	G
C874	C959	C	A1089	A1187	A1269	A1363	U1476	U1595	G1698	G1791	G1878	C
A875	C960	A	A1090	G1188	G1270	G1364	C1479	G1596	U1699	C1791	A1879	C
A876	U961	U	U1091	G1189	G1271	G1365	A1480	G1597	U1700	C1794	A1880	C
C963	U962	U	U1094	C1190	U1272	A1368	U1483	U1598	G1709	U1794	U1881	U
A964	G965	U	U1095	G1191	C1274	A1371	U1484	U1599	C1715	A1795	U1882	C
U878	U966	U	U1096	U1196	U1275	A1372	G1489	U1600	G1716	A1796	C1883	C
G881	U967	A	G1097	A1197	A1276	G1377	G1490	U1601	U1720	U1797	G1884	U
U886	U968	U	G1098	C1198	A1277	G1378	G1491	G1602	U1721	U1798	G1885	U
G887	U969	U	G1099	C1199	U1287	A1381	G1492	G1603	U1722	U1799	C1886	C
G888	G972	U	U1103	U1201	G1288	G1386	G1502	U1607	G1723	C1801	A	
G890	A973	U	U1104	U1202	G1289	G1387	G1503	U1608	C1724	C1805	A	
G891	G974	U	U1105	U1203	G1290	A1389	C1509	U1609	G1725	G1809	A	
A894	G975	U	G1108	A1205	U1291	A1400	U1516	G1610	U1726	U1810	A	
A895	U976	U	G1116	A1208	G1292	A1401	A1517	G1611	A1728	U1813	A	
A896	A977	U	A1117	C1209	G1293	U1409	G1526	G1614	A1729	C1817	A	
A897	A978	U	A1120	A1210	G1294	U1410	U1527	G1615	G1730	A1818	A	
A898	A979	U	U1121	A1213	G1295	U1411	G1528	A1616	G1736	U1819	A	
C899	C981	U	G1122	A1214	U1297	U1412	G1529	A1617	A1737	A1820	A	
U900	G982	U	G1123	C1215	G1302	A1416	G1533	C1618	U1741	A1821	A	
A	A983	U	G1124	G1216	G1303	U1417	U1534	A1621	U1742	C1822	A	
A	G986	U	G1125	U1217	G1304	U1418	U1535	A1622	C1743	C1823	A	
U	A	U	U1126	G1218	C1305	C1419	U1537	G1623	U1744	G1824	A	
C	A	U	U1135	G1219	G1310	G1426	C1538	G1625	U1745	C1825	A	
G	A	U	A1135	A1227	C1311	U1427	A1539	G1634	G1749	C1828	A	
A906	U	U	A1141	G1228	A1312	U1428	A1540	A1635	G1750	A1829	A	
C909	G	U	C1142	G1231	U1313	U1429	A1541	C1636	U1751	C1837	A	
A910	G	U	G1143	G1232	C1314	A1434	G1545	G1637	G1757	U1841	A	
G915	C	U	U1055	U1233	C1315	A1435	C1546	G1645	C1758	U1842	A	
U916	C	U	U1056	A1233	C1316	A1436	U1547	G1646	G1759	A1843	A	
A917	U	U	A1057	A1234	C1317	U1437	U1548	G1657	C1760	C1844	A	
G918	U	U	C1059	U1237	G1318	A1438	U1549	U1657	U1763	C1845	A	
C919	C	U	U1060	G1238	C1319	U1441	C1550	C1662	G1764	G1857	A	
U920	C	U	A1061	C1239	C1321	C1442	U1551	U1665	G1765	U1858	A	
G921	C	U	A1062	U1240	C1322	C1443	U1552	U1666	A1766	U1859	A	
A925	G	U	C1063	U1243	C1323	G1448	G1553	U1667	C1767	A1860	A	
C926	C	U	U1064	G1244	U1324	U1452	C1556	U1668	G1775	C1861	A	
C927	C	U	G1065	A1245	A1330	U1453	C1557	U1669	A1776	U1862	A	
A932	A	U	A1066	U1247	A1331	G1454	U1558	C1672	U1777	C1863	A	
A933	U	U	A1067	U1251	A1332	A1455	G1560	C1673	A1778	C1864	A	
G934	U	U	G1071	C1254	A1333	A1456	U1561	U1674	U1779	A1865	A	
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C942	U	U	A1074	A1260	G1336	A1464	A1567	U1683	G1781	C1868	A	
A943	C	U	A1075	U1263	U1337	G1465	A1568	C1692	C1784	U1869	A	
G944	C	U	U1076	G1264	U1338	U1466	C1575	A1693	G1785	A1870	A	
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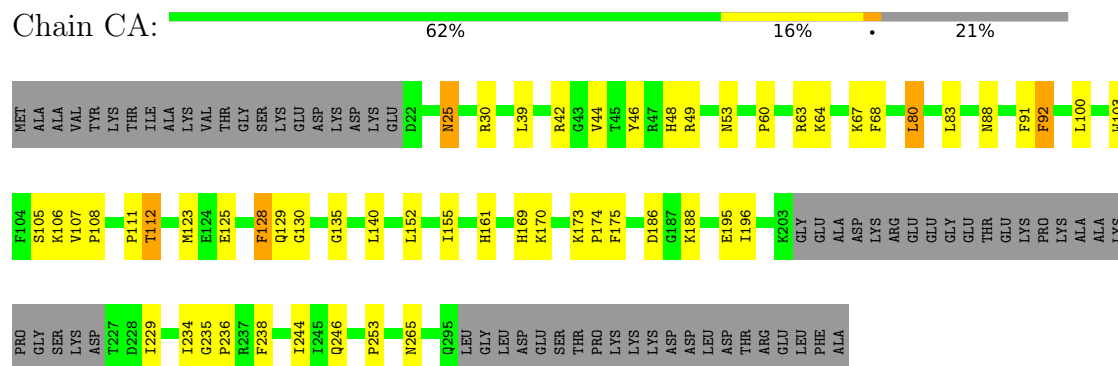




• Molecule 2: RNA (319-MER)



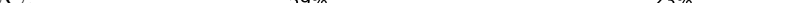
• Molecule 3: Brix domain-containing protein



• Molecule 4: Ribosome biogenesis protein C8F11.04

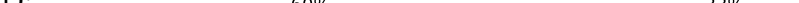


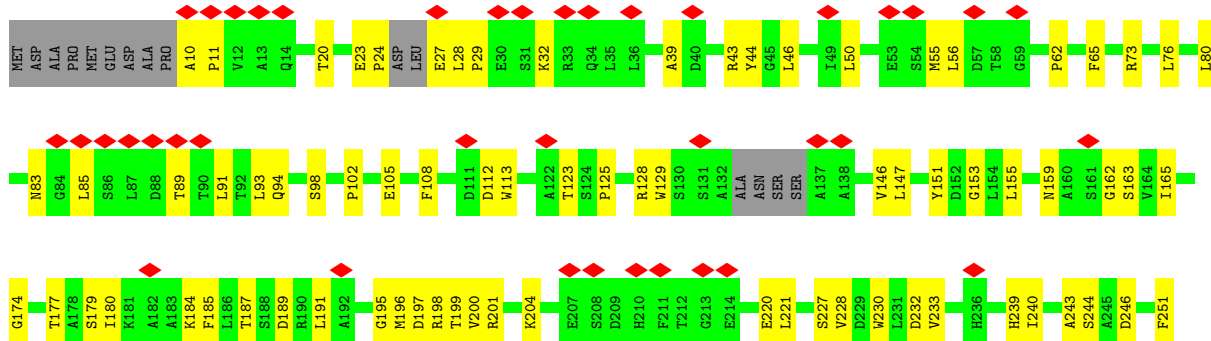
- Molecule 5: Ribosome biogenesis protein ERB1

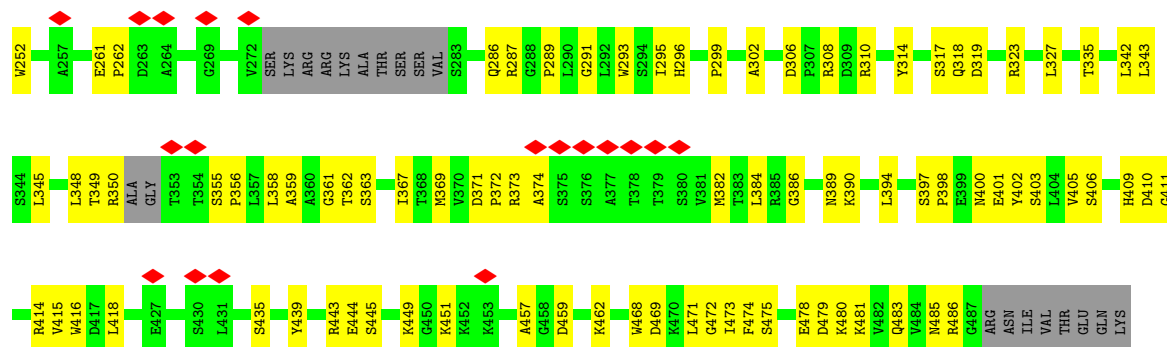
Chain CC:  59% 23% 18%



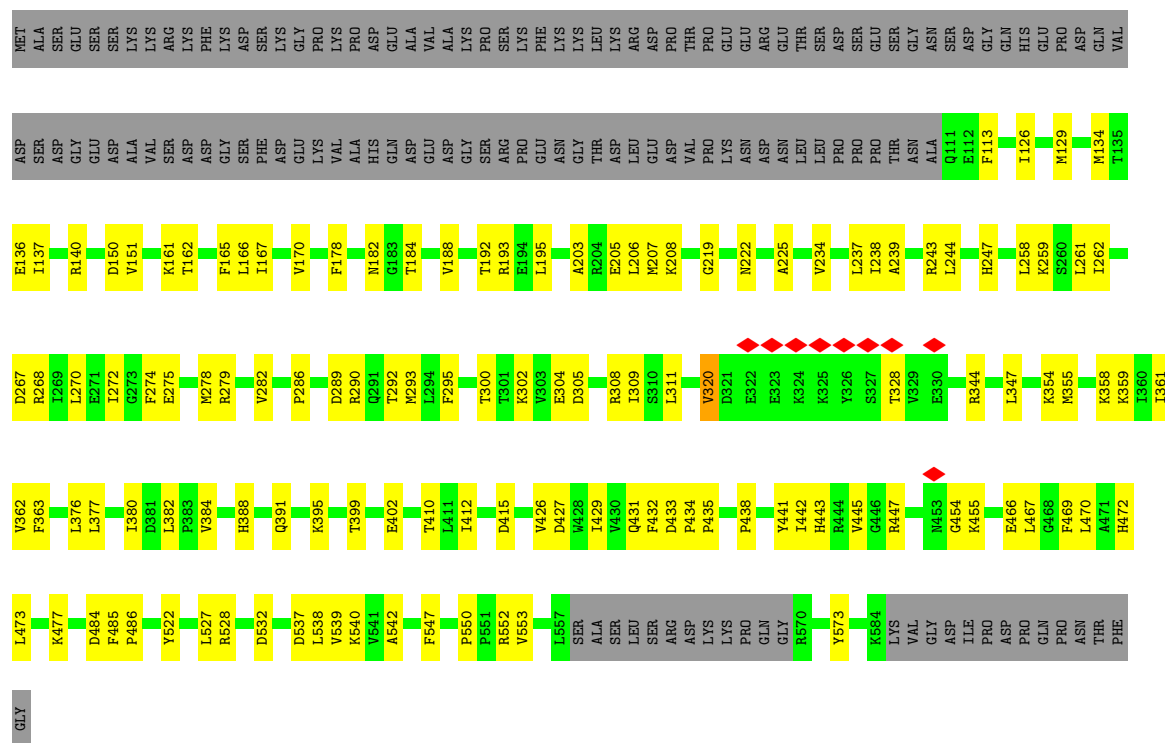
- Molecule 6: Ribosome biogenesis protein YTM1

Chain CD: 

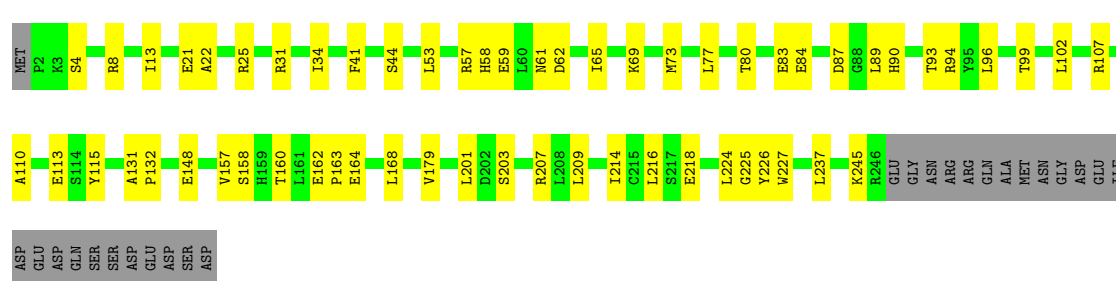




• Molecule 7: RNA helicase

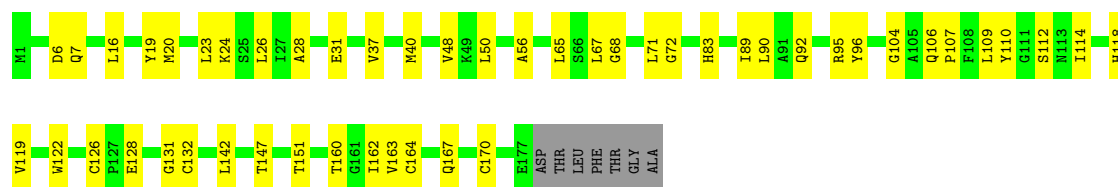


• Molecule 8: Ribosome assembly factor mrt4



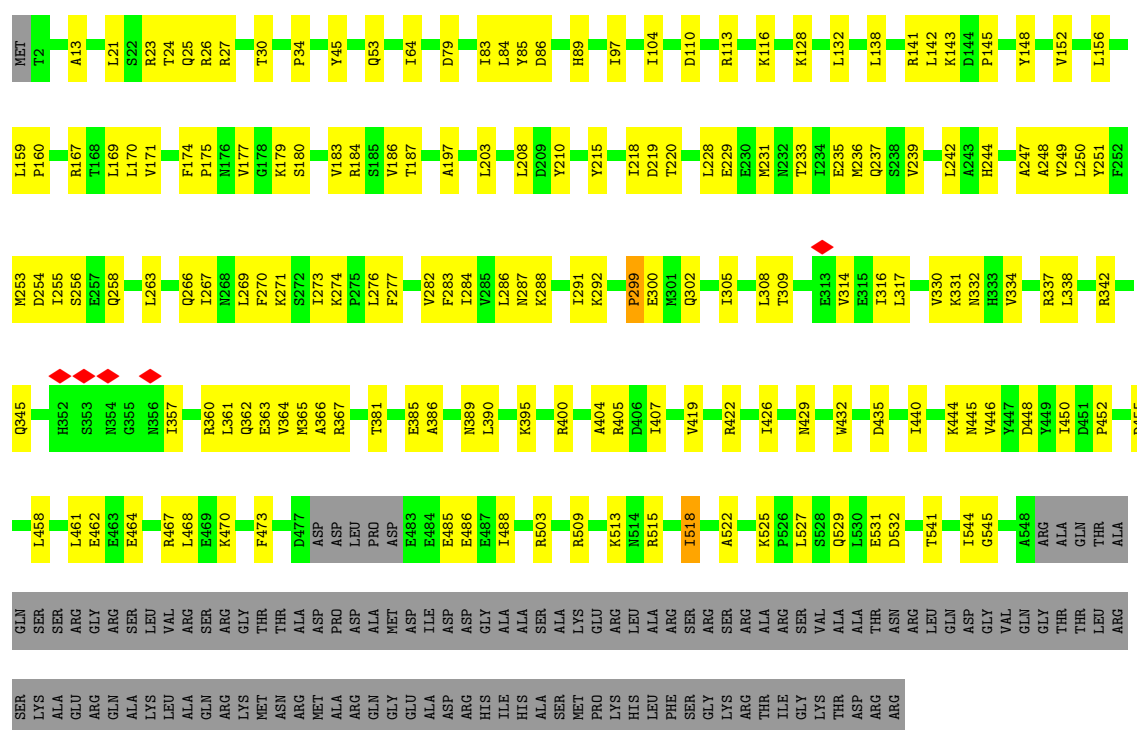
• Molecule 9: 60S ribosome subunit biogenesis protein NIP7

Chain CG:  70% 27% .



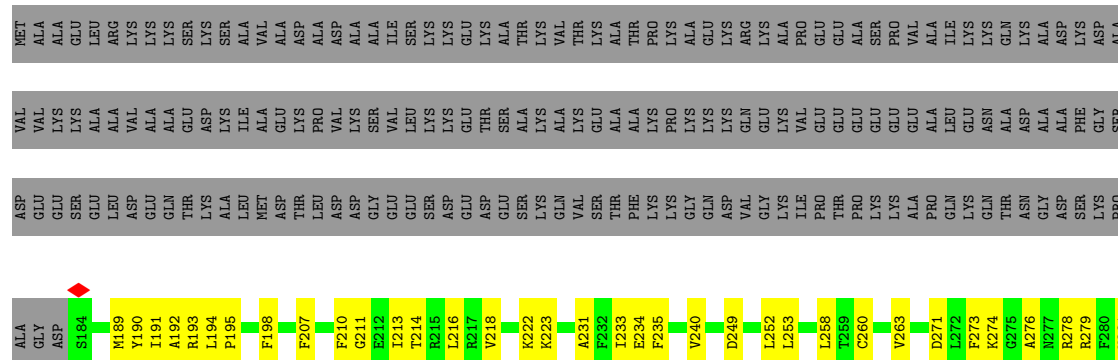
• Molecule 10: Nucleolar GTP-binding protein 1

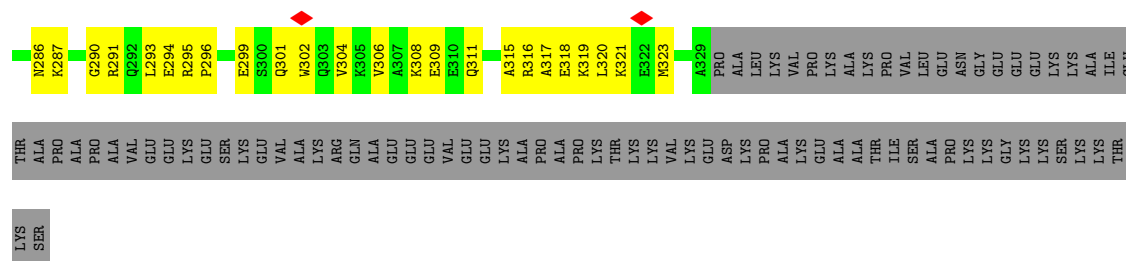
Chain CH:  56% 25% 18%



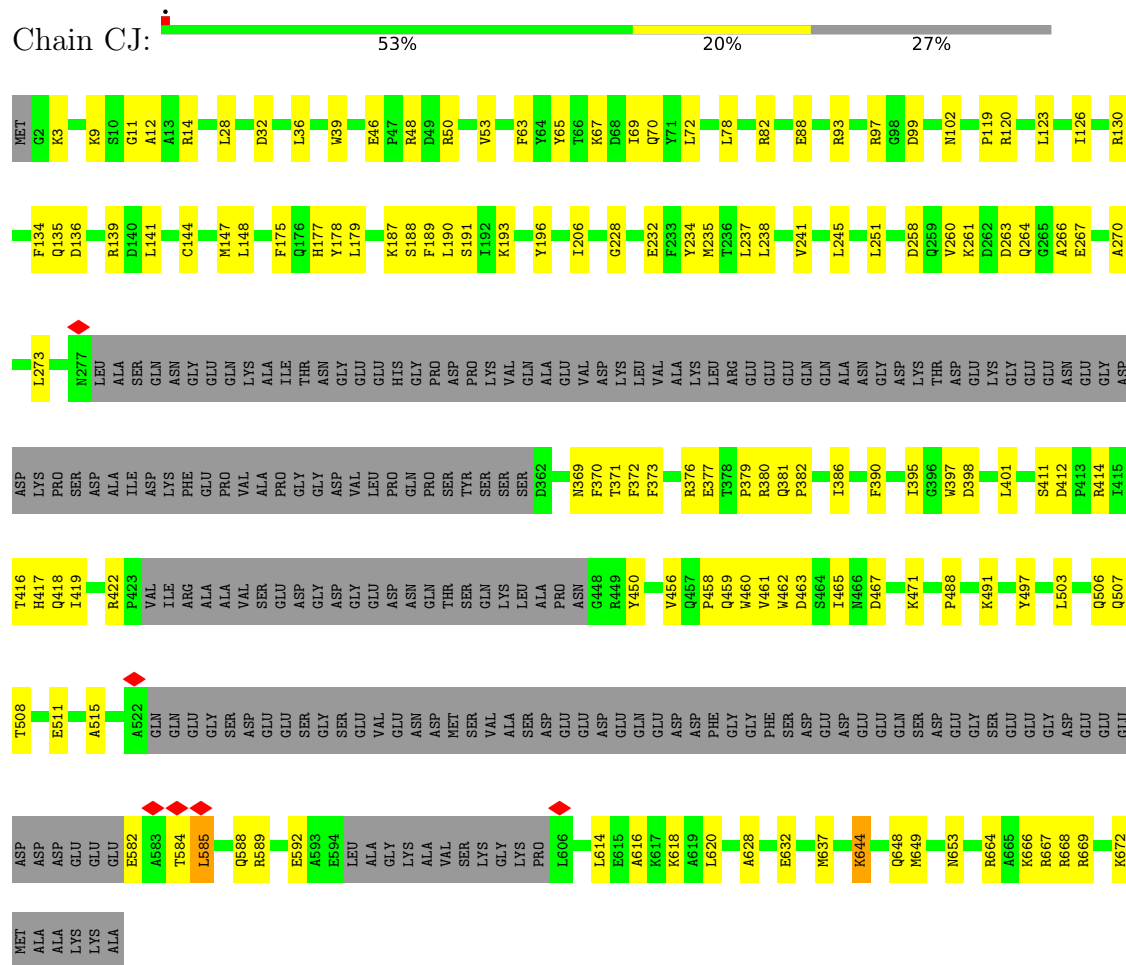
• Molecule 11: Putative RNA-binding protein

Chain CI:  21% 14% 65%

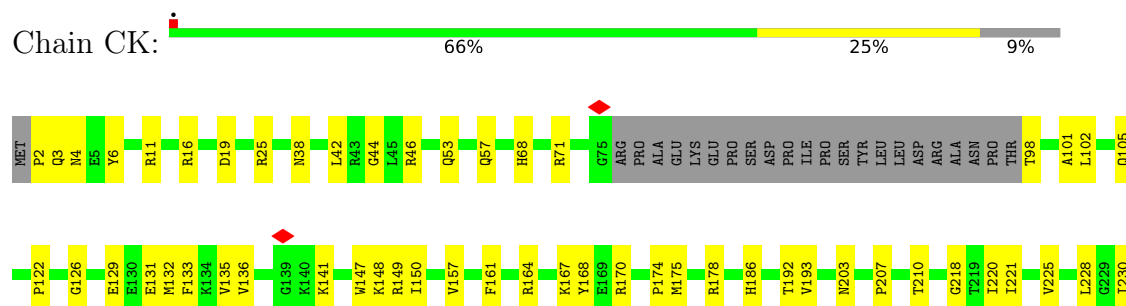


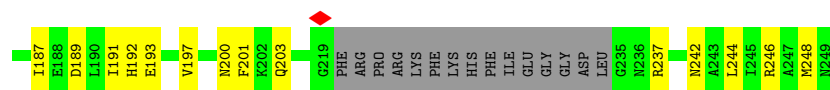


• Molecule 12: Pescadillo homolog



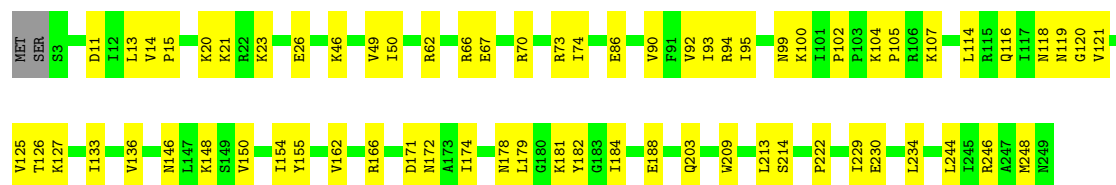
• Molecule 13: Ribosome biogenesis protein NSA2 homolog





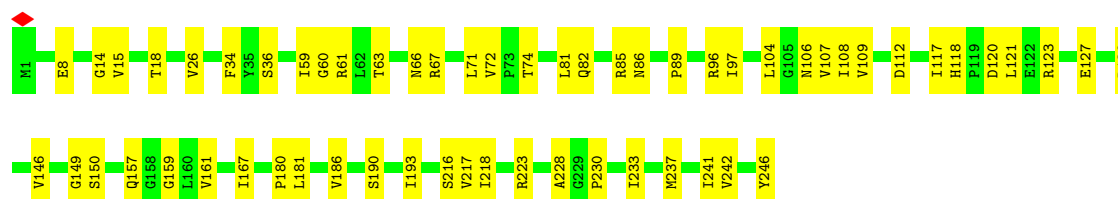
- Molecule 15: 60S ribosomal protein l7-like protein

Chain LF: 72% 27%



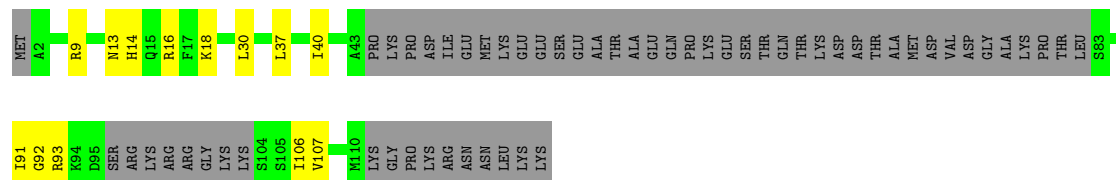
- Molecule 16: Eukaryotic translation initiation factor 6

Chain CN: 76% 24%



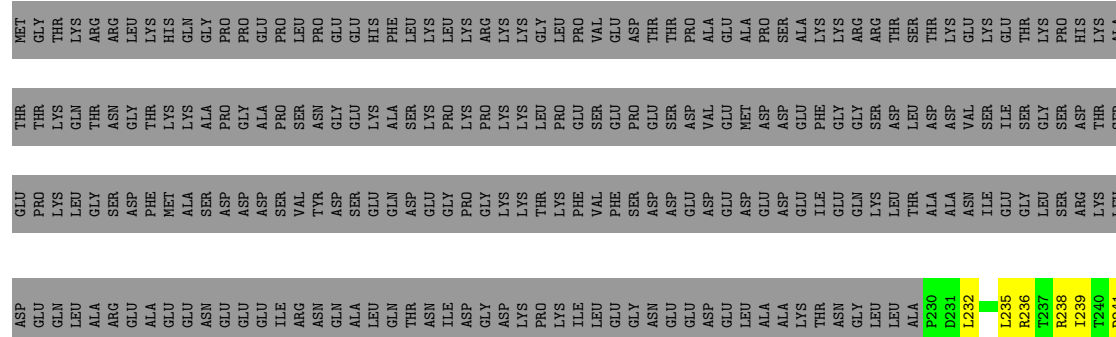
- Molecule 17: DUF2423 domain-containing protein

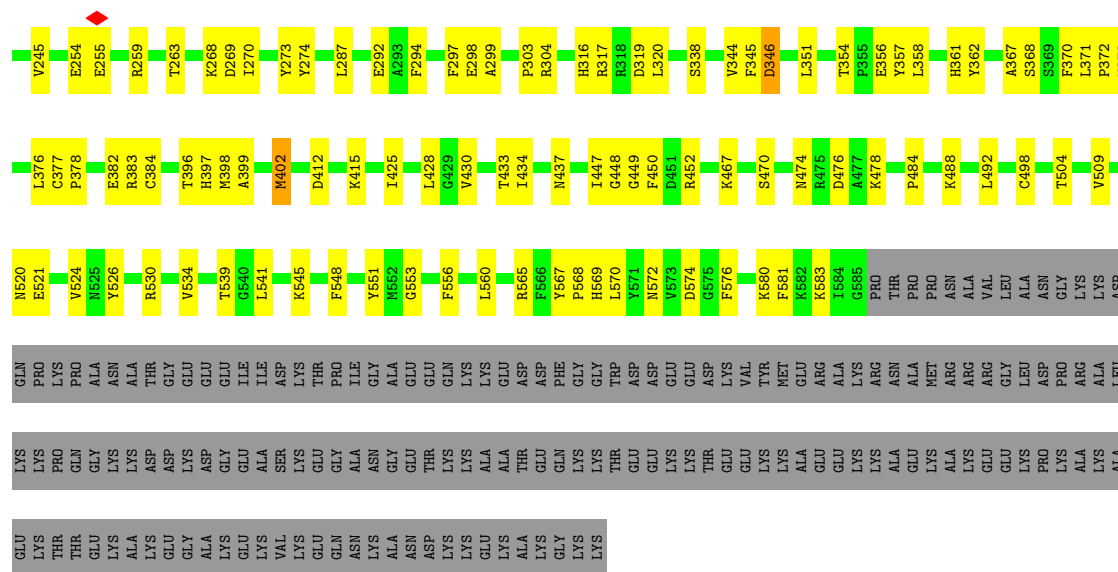
Chain CO: 41% 11% 48%



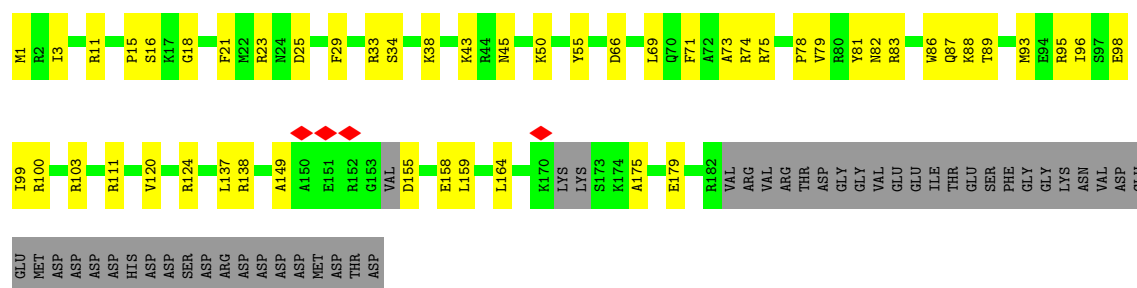
- Molecule 18: RNA methyltransferase nop2-like protein

Chain CP: 33% 14% 53%

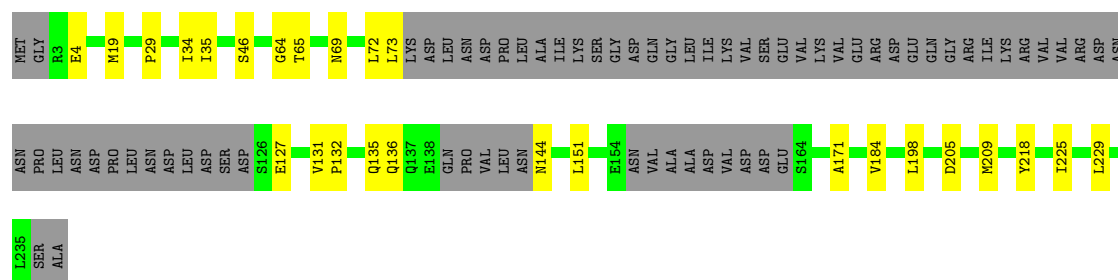




• Molecule 19: Ribosome biogenesis protein RLP24

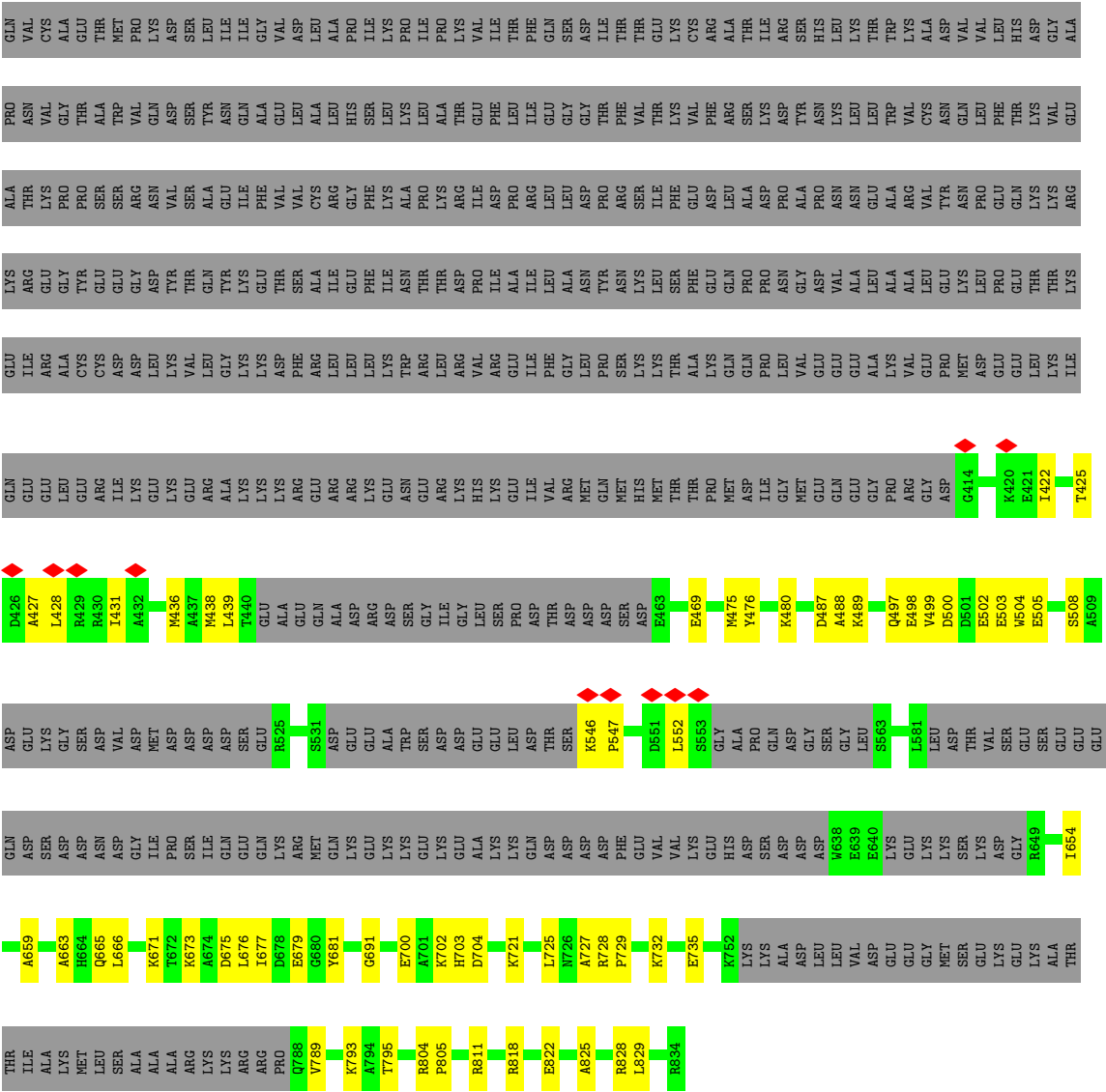


• Molecule 20: Nucleolar protein 16

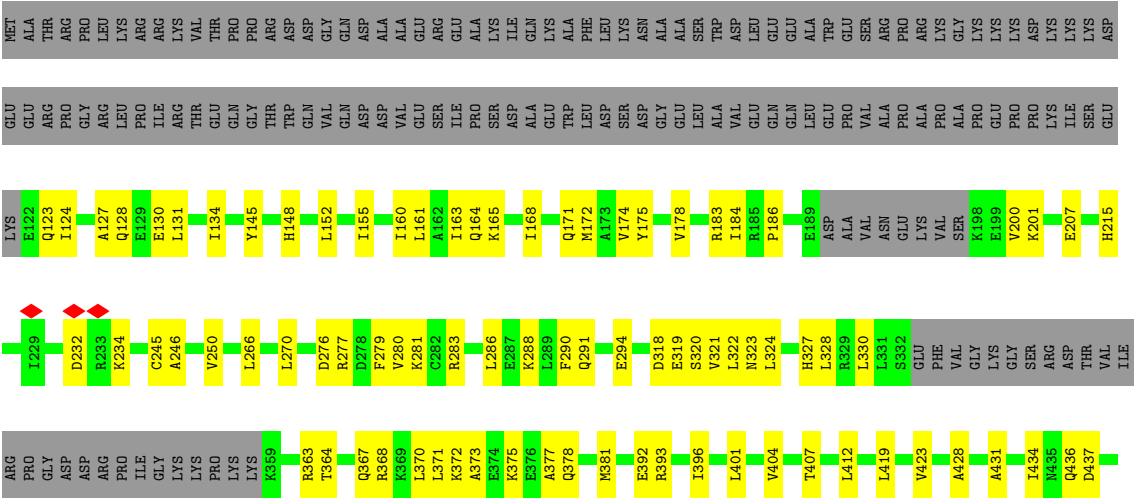


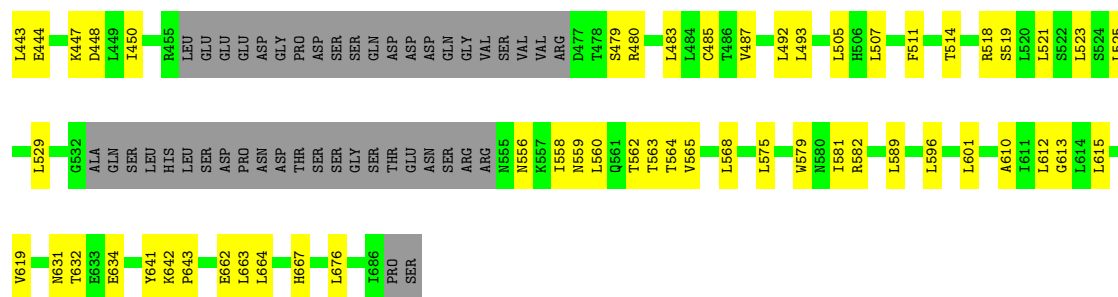
• Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1



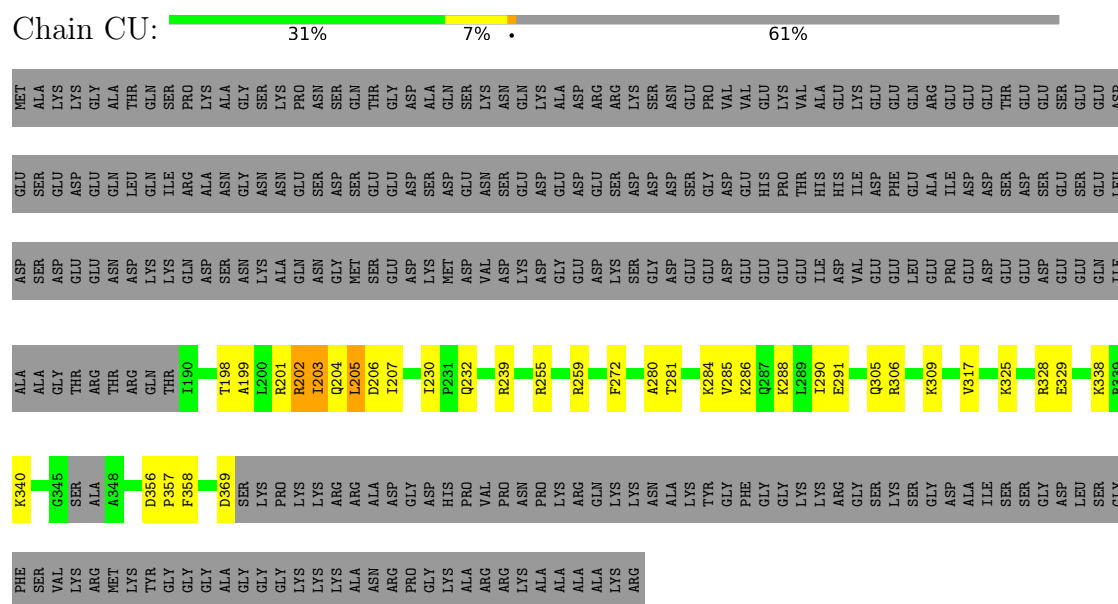


● Molecule 22: Nucleolar complex-associated protein 3

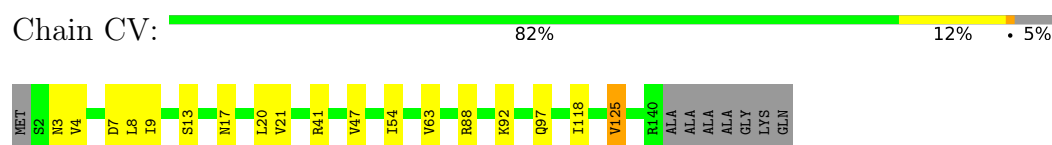




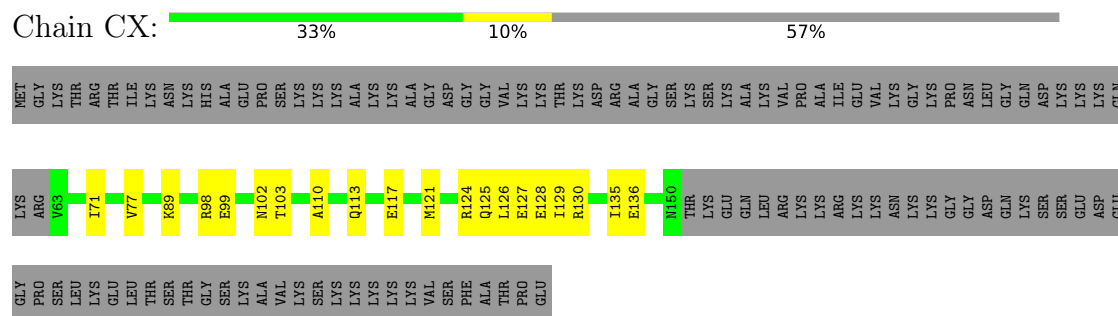
• Molecule 23: rRNA-processing protein EBP2



• Molecule 24: Putative 60S ribosomal protein

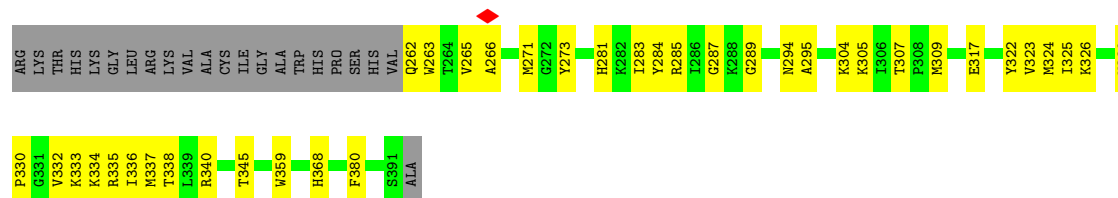


• Molecule 25: 60S ribosomal subunit-like protein



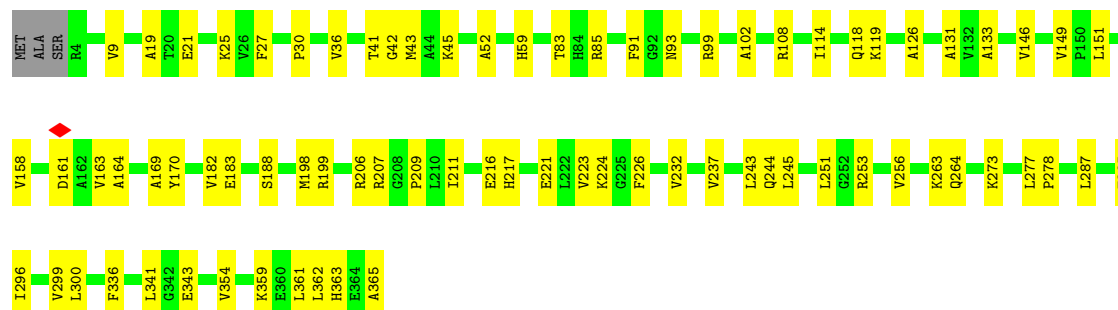
• Molecule 26: Putative NOC2 family protein





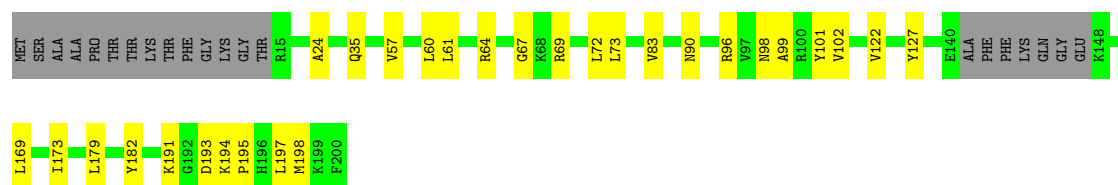
- Molecule 30: 60S ribosomal protein L4-like protein

Chain LC: 78% 21%



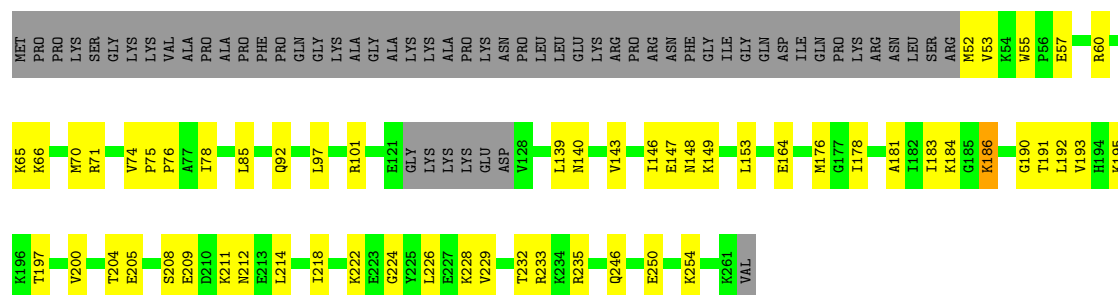
- Molecule 31: 60S ribosomal protein L6

Chain LE: 75% 14% 10%



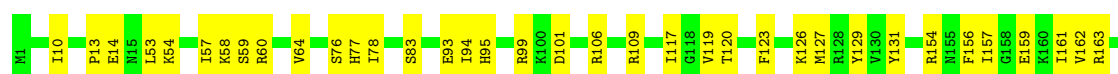
- Molecule 32: 60S ribosomal protein L8

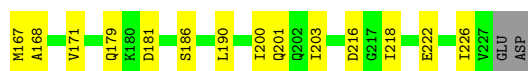
Chain LG: 56% 22% 22%



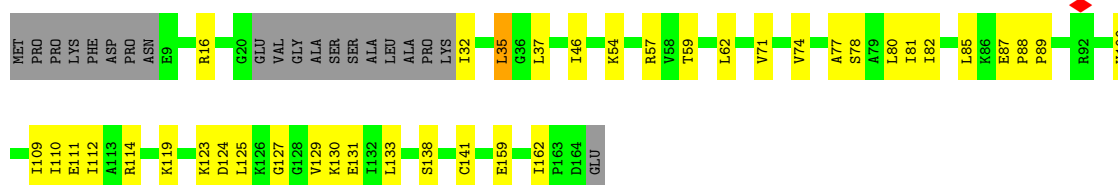
- Molecule 33: 60S ribosomal protein l9-like protein

Chain LH: 73% 26%

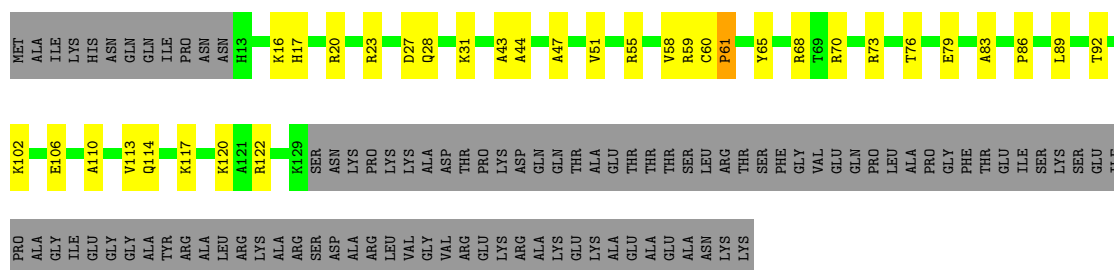




- Molecule 34: 60S ribosomal protein L12-like protein



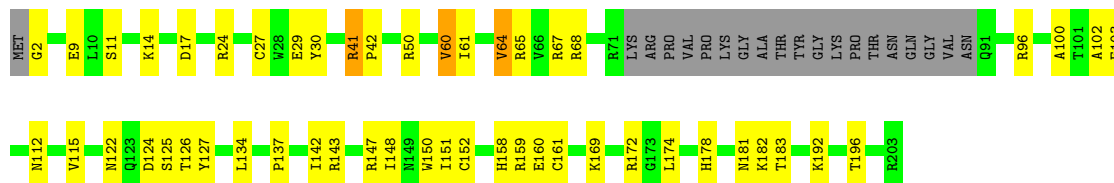
- Molecule 35: 60S ribosomal protein L13



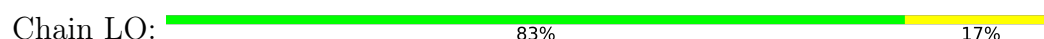
- Molecule 36: 60S ribosomal protein L14-like protein

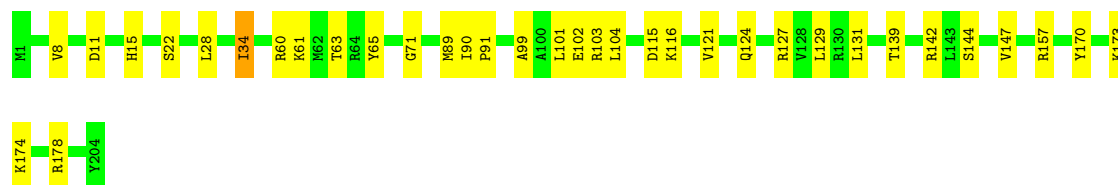


- Molecule 37: Ribosomal protein L15

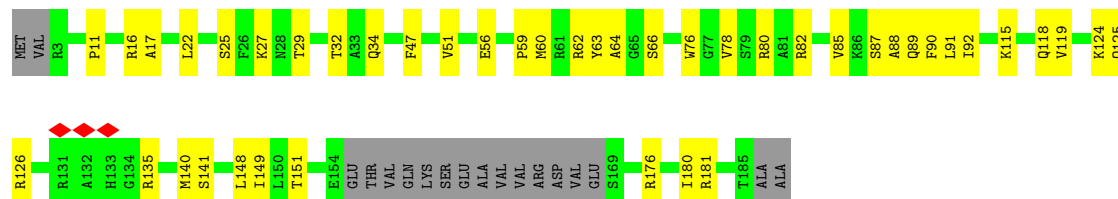


- Molecule 38: 60S ribosomal protein L16-like protein

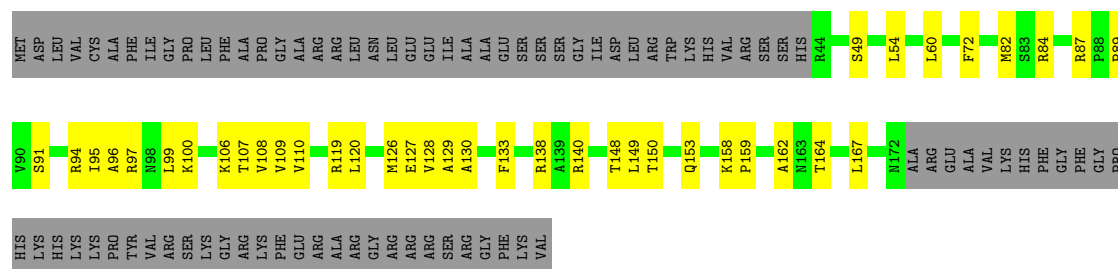




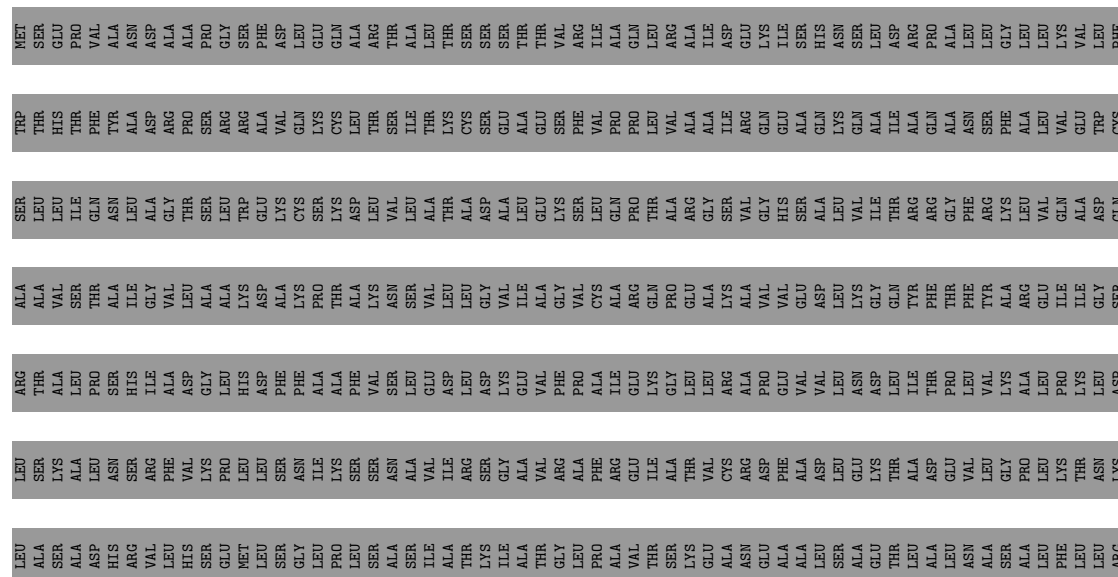
- Molecule 39: 60S ribosomal protein l17-like protein



- Molecule 40: Ribosomal protein L18-like protein



- Molecule 41: Ribosomal protein L19







ARG
ASN
ALA
LEU
LEU
GLY
GLU
GLU
GLU
SER
SER
LYS

• Molecule 42: 60S ribosomal protein L20

Chain LS: 71% 29%

M1 Q5 E6 Y7 Q8 H13 M27 R28 I29 F30 F41 F44 L45 R46 K50 T55 N62 V63 I64 H68 P69 K73 I77 W78 L79 R80 R84 N89 K92 V100 V103 M110 A111 A112 R115 A116 R117 F118 R119 L124 K125

V126 E133 Y139 I140 K141 Q142 V144 F150 P151 L152 R155 T161 K162 R169 P170 S171 T172 F173 S174

• Molecule 43: 60S ribosomal protein l21-like protein

Chain LT: 60% 19% 21%

MET GLY HIS ALA ALA GLY LEU ARG SER THR TYR ALA PHE SER ARG GLY PHE ARG LYS HIS GLY GLN ILE PRO LEU SER THR TYR LEU R32 K43 V44 M45 G46 A47 V48 Q49 K50 F56 G59 K60 V64 K69 S70 A71 V74 R79 H82 R83 Y84

R92 I93 E94 H95 W96 K97 R100 S101 S102 E103 L106 R107 R108 M112 L128 M134 P135 R136 P148 Y156 F157 THR THR ILE

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

Chain LU: 65% 18% 17%

MET ALA PRO LYS VAL ALA LYS LYS SER GLY ALA LYS GLY LYS GLY PRO K16 I22 K41 E45 L56 V59 I60 I65 G66 K69 L78 R81 K84 K89 F90 N94 D98 V99 L100 R101 V102 S106 V109 K113 F114 Y115 M116 I117 V118

H119 D120 ALA ALA GLU GLU GLU ASP

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

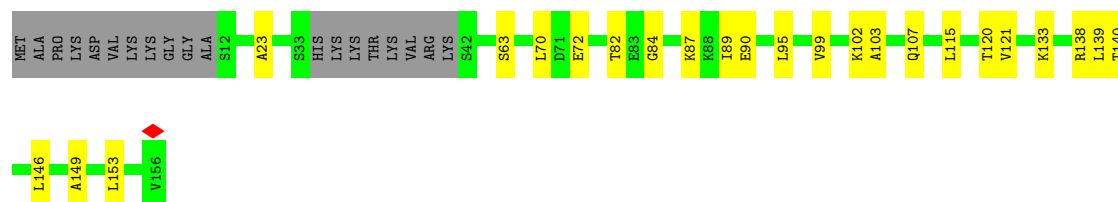
Chain LV: 72% 25%

MET ALA LYS GLN K5 L19 P20 V21 G22 M25 A28 R34 N35 L36 Y37 I38 V41 A44 R47 L48 M49 R50 A53 V56 V60 V64 K65 K66 L71 R72 K73 K74 V75 V79 I80 V81 R82 Q83 R89 F90 D91 G92 N100 V105

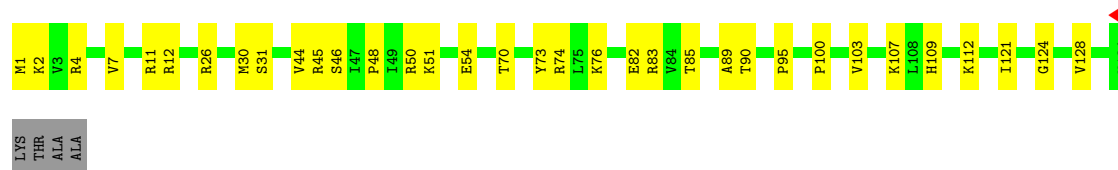
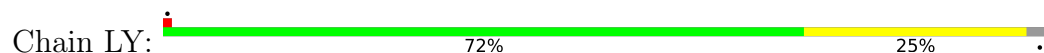
T117 V120 R130 V137 V138 M139

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

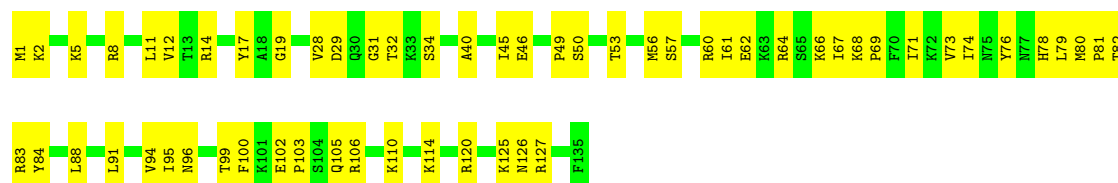
Chain LX: 72% 15% 12%



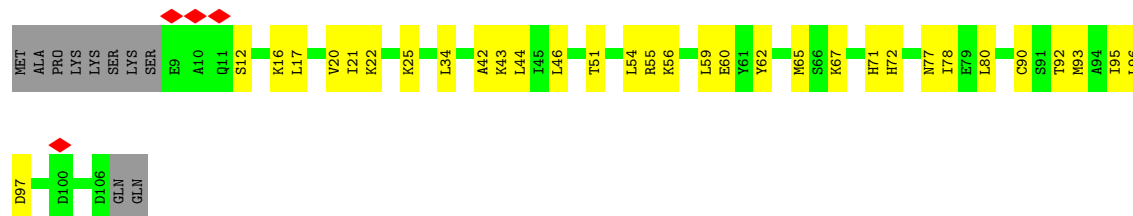
- Molecule 47: 60S ribosomal protein L26-like protein



- Molecule 48: 60S ribosomal protein L27



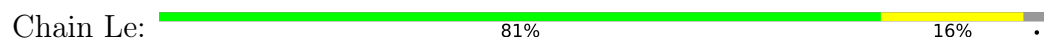
- Molecule 49: 60S ribosomal protein l30-like protein

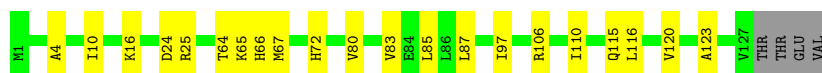


- Molecule 50: Putative 60S ribosomal protein



- Molecule 51: 60S ribosomal protein L32-like protein





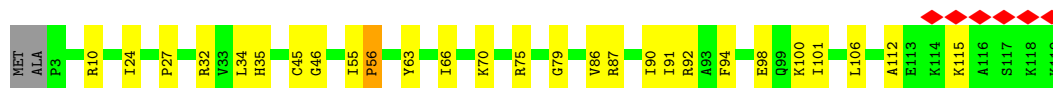
- Molecule 52: 60S ribosomal protein l33-like protein

Chain Lf: 81% 18%



- Molecule 53: Ribosomal protein l34-like protein

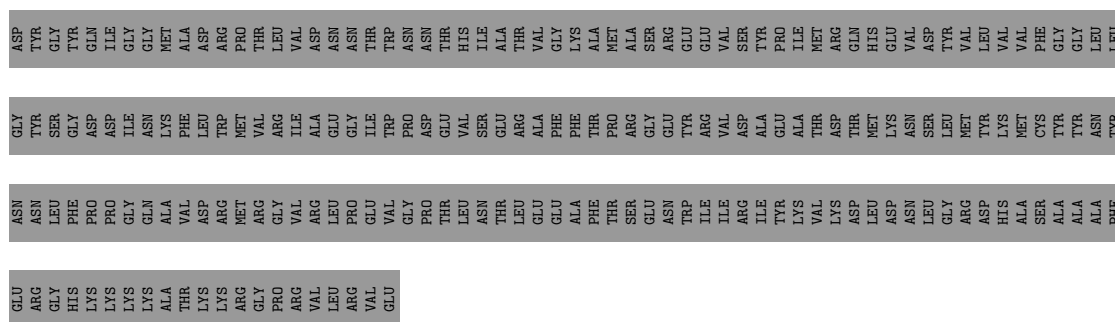
Chain Lg: 5% 76% 22%



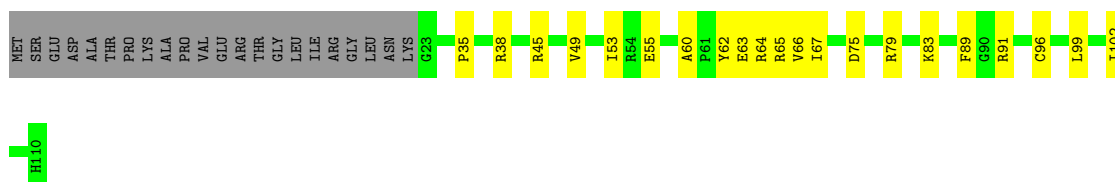
- Molecule 54: dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh: 10% 87%





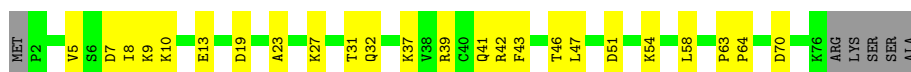
- Molecule 55: 60S ribosomal protein L36



- Molecule 56: Ribosomal protein L37



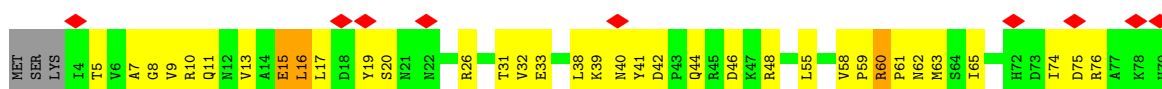
- Molecule 57: 60S ribosomal protein L38-like protein

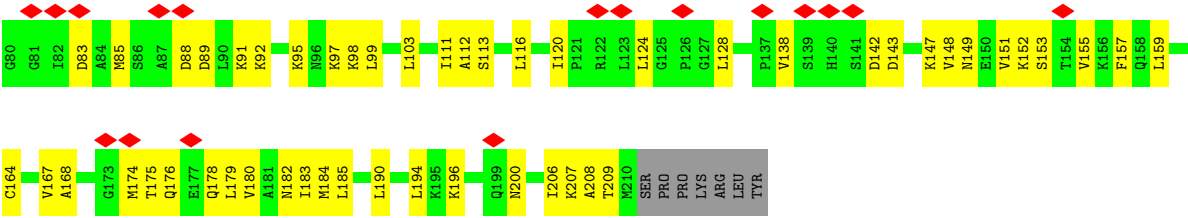


- Molecule 58: 60S ribosomal protein L39



- 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	77844	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	0.706	Depositor
Minimum map value	-0.294	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, GTP, TPO, 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	0.21	0/63619	0.35	2/99165 (0.0%)
2	C2	0.15	0/6097	0.27	0/9499
3	CA	0.58	0/2115	0.96	5/2840 (0.2%)
4	CB	0.28	0/2109	0.58	0/2866
5	CC	0.33	0/5423	0.60	3/7380 (0.0%)
6	CD	0.17	0/3543	0.49	0/4824
7	CE	0.20	0/3739	0.50	1/5040 (0.0%)
8	CF	0.30	0/1982	0.57	0/2671
9	CG	0.31	0/1422	0.59	0/1920
10	CH	0.33	0/4468	0.63	2/6029 (0.0%)
11	CI	0.19	0/1225	0.53	0/1645
12	CJ	0.24	0/4125	0.55	1/5548 (0.0%)
13	CK	0.22	0/1940	0.48	0/2601
14	CL	0.20	0/2247	0.49	0/3076
15	CM	0.20	0/1851	0.51	0/2481
15	LF	0.32	0/2055	0.60	0/2758
16	CN	0.32	0/1881	0.61	0/2560
17	CO	0.17	0/470	0.40	0/619
18	CP	0.34	0/2859	0.63	0/3870
19	CQ	0.24	0/1507	0.52	1/1996 (0.1%)
20	CR	0.28	0/1369	0.50	0/1828
21	CS	0.20	0/2127	0.49	0/2817
22	CT	0.21	0/3974	0.51	0/5357
23	CU	0.47	4/1428 (0.3%)	0.64	4/1910 (0.2%)
24	CV	0.42	0/1091	0.75	2/1468 (0.1%)
25	CX	0.17	0/705	0.47	0/938
26	CY	0.33	0/3368	0.72	2/4525 (0.0%)
27	Cb	0.19	0/5150	0.51	5/6936 (0.1%)
28	Cz	0.17	0/598	0.43	0/785
29	LB	0.36	0/2885	0.63	2/3872 (0.1%)
30	LC	0.18	0/2809	0.40	0/3787
31	LE	0.38	0/1428	0.65	0/1921

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LG	0.33	0/1667	0.61	1/2230 (0.0%)
33	LH	0.20	0/1516	0.47	0/2038
34	LK	0.45	0/1115	0.76	1/1496 (0.1%)
35	LL	0.45	0/983	0.72	0/1318
36	LM	0.18	0/1120	0.41	0/1507
37	LN	0.35	0/1595	0.57	0/2132
38	LO	0.37	0/1652	0.59	0/2215
39	LP	0.15	0/1367	0.38	0/1838
40	LQ	0.19	0/1033	0.42	0/1391
41	LR	0.20	0/980	0.46	0/1311
42	LS	0.24	0/1468	0.49	0/1975
43	LT	0.12	0/1033	0.36	0/1389
44	LU	0.24	0/863	0.52	0/1155
45	LV	0.20	0/1013	0.47	0/1361
46	LX	0.14	0/1078	0.34	0/1451
47	LY	0.16	0/1079	0.40	0/1443
48	LZ	0.16	0/1135	0.41	0/1519
49	Lc	0.14	0/740	0.41	0/995
50	Ld	0.16	0/904	0.35	0/1209
51	Le	0.26	0/1043	0.51	0/1389
52	Lf	0.40	0/883	0.58	0/1187
53	Lg	0.35	0/943	0.55	0/1258
54	Lh	0.15	0/1006	0.37	0/1338
55	Li	0.22	0/738	0.46	0/971
56	Lj	0.33	0/606	0.65	0/803
57	Lk	0.19	0/628	0.54	0/835
58	Ll	0.16	0/329	0.37	0/440
59	Lq	0.25	0/1621	0.63	1/2180 (0.0%)
All	All	0.26	4/171747 (0.0%)	0.48	33/245906 (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
29	LB	0	1
59	Lq	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CU	204	GLN	C-O	-6.90	1.15	1.24
23	CU	202	ARG	C-O	-6.60	1.15	1.24
23	CU	204	GLN	CA-C	-6.28	1.45	1.52
23	CU	201	ARG	C-N	-5.41	1.26	1.33

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CU	201	ARG	O-C-N	-7.34	114.34	122.12
7	CE	320	VAL	N-CA-C	-7.05	105.74	113.43
1	C1	3257	U	C2'-C3'-O3'	6.82	119.72	109.50
1	C1	468	C	C2'-C3'-O3'	6.51	119.27	109.50
29	LB	213	ASP	CB-CA-C	6.42	119.74	110.04

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	LB	17	LEU	Peptide
59	Lq	60	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	56864	0	28664	897	0
2	C2	5456	0	2762	105	0
3	CA	2069	0	2109	40	0
4	CB	2063	0	2131	70	0
5	CC	5297	0	5220	141	0
6	CD	3468	0	3428	134	0
7	CE	3669	0	3775	94	0
8	CF	1945	0	1965	39	0
9	CG	1396	0	1420	38	0
10	CH	4388	0	4454	136	0
11	CI	1196	0	1202	47	0
12	CJ	4040	0	4087	110	0
13	CK	1908	0	2019	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	CL	2239	0	1495	28	0
15	CM	1820	0	1938	58	0
15	LF	2017	0	2130	48	0
16	CN	1856	0	1856	45	0
17	CO	468	0	503	14	0
18	CP	2798	0	2812	75	0
19	CQ	1485	0	1549	39	0
20	CR	1354	0	1400	22	0
21	CS	2105	0	2183	54	0
22	CT	3911	0	4023	112	0
23	CU	1415	0	1457	26	0
24	CV	1073	0	1130	13	0
25	CX	701	0	742	15	0
26	CY	3313	0	3449	150	0
27	Cb	5058	0	5223	181	0
28	Cz	592	0	640	22	0
29	LB	2829	0	2933	71	0
30	LC	2752	0	2878	61	0
31	LE	1403	0	1503	21	0
32	LG	1644	0	1793	41	0
33	LH	1496	0	1575	37	0
34	LK	1103	0	1177	25	0
35	LL	964	0	1041	33	0
36	LM	1101	0	1170	27	0
37	LN	1563	0	1618	37	0
38	LO	1618	0	1714	24	0
39	LP	1345	0	1389	34	0
40	LQ	1021	0	1118	29	0
41	LR	964	0	1022	24	0
42	LS	1433	0	1496	45	0
43	LT	1014	0	1073	20	0
44	LU	850	0	894	18	0
45	LV	995	0	1055	23	0
46	LX	1062	0	1145	17	0
47	LY	1065	0	1156	31	0
48	LZ	1112	0	1181	55	0
49	Lc	731	0	772	21	0
50	Ld	890	0	940	19	0
51	Le	1025	0	1104	15	0
52	Lf	862	0	891	13	0
53	Lg	930	0	1011	26	0
54	Lh	995	0	1110	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	Li	731	0	797	20	0
56	Lj	595	0	625	18	0
57	Lk	620	0	680	18	0
58	Ll	322	0	346	8	0
59	Lq	1600	0	1703	63	0
60	CH	32	0	12	1	0
61	CQ	1	0	0	0	0
61	Lj	1	0	0	0	0
All	All	162633	0	134688	3208	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 11.

The worst 5 of 3208 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)
42:LS:6:GLU:HB2	42:LS:64:ILE:O	1.48	1.13
1:C1:891:G:H1	1:C1:898:A:N6	1.57	1.01
1:C1:1156:G:H21	1:C1:1157:C:H41	1.01	1.00
1:C1:529:G:O6	1:C1:543:G:C2	2.16	0.99
6:CD:369:MET:HB2	6:CD:382:MET:HB3	1.45	0.95

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%)	233 (94%)	14 (6%)	0	100	100
4	CB	256/391 (66%)	241 (94%)	15 (6%)	0	100	100
5	CC	648/801 (81%)	611 (94%)	35 (5%)	2 (0%)	36	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	CD	450/495 (91%)	426 (95%)	24 (5%)	0	100	100
7	CE	458/598 (77%)	441 (96%)	17 (4%)	0	100	100
8	CF	243/270 (90%)	232 (96%)	11 (4%)	0	100	100
9	CG	175/184 (95%)	168 (96%)	7 (4%)	0	100	100
10	CH	538/661 (81%)	514 (96%)	23 (4%)	1 (0%)	43	72
11	CI	144/414 (35%)	134 (93%)	10 (7%)	0	100	100
12	CJ	484/679 (71%)	470 (97%)	14 (3%)	0	100	100
13	CK	234/261 (90%)	222 (95%)	11 (5%)	1 (0%)	30	60
14	CL	393/558 (70%)	362 (92%)	28 (7%)	3 (1%)	16	44
15	CM	219/249 (88%)	209 (95%)	10 (5%)	0	100	100
15	LF	245/249 (98%)	239 (98%)	6 (2%)	0	100	100
16	CN	244/246 (99%)	230 (94%)	14 (6%)	0	100	100
17	CO	56/120 (47%)	54 (96%)	2 (4%)	0	100	100
18	CP	354/751 (47%)	336 (95%)	17 (5%)	1 (0%)	36	66
19	CQ	173/225 (77%)	165 (95%)	7 (4%)	1 (1%)	21	51
20	CR	159/237 (67%)	157 (99%)	2 (1%)	0	100	100
21	CS	246/834 (30%)	238 (97%)	8 (3%)	0	100	100
22	CT	478/688 (70%)	460 (96%)	18 (4%)	0	100	100
23	CU	174/451 (39%)	173 (99%)	1 (1%)	0	100	100
24	CV	137/147 (93%)	133 (97%)	4 (3%)	0	100	100
25	CX	86/203 (42%)	85 (99%)	1 (1%)	0	100	100
26	CY	396/788 (50%)	365 (92%)	29 (7%)	2 (0%)	24	55
27	Cb	630/924 (68%)	604 (96%)	25 (4%)	1 (0%)	43	72
28	Cz	68/123 (55%)	66 (97%)	2 (3%)	0	100	100
29	LB	352/392 (90%)	332 (94%)	18 (5%)	2 (1%)	21	51
30	LC	360/365 (99%)	342 (95%)	18 (5%)	0	100	100
31	LE	175/200 (88%)	165 (94%)	10 (6%)	0	100	100
32	LG	200/262 (76%)	191 (96%)	9 (4%)	0	100	100
33	LH	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
34	LK	141/165 (86%)	127 (90%)	13 (9%)	1 (1%)	18	47
35	LL	115/213 (54%)	107 (93%)	7 (6%)	1 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LM	135/142 (95%)	127 (94%)	8 (6%)	0	100	100
37	LN	179/203 (88%)	171 (96%)	8 (4%)	0	100	100
38	LO	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
39	LP	165/187 (88%)	161 (98%)	4 (2%)	0	100	100
40	LQ	127/213 (60%)	121 (95%)	6 (5%)	0	100	100
41	LR	114/2898 (4%)	114 (100%)	0	0	100	100
42	LS	172/174 (99%)	167 (97%)	5 (3%)	0	100	100
43	LT	124/160 (78%)	118 (95%)	5 (4%)	1 (1%)	16	44
44	LU	103/127 (81%)	101 (98%)	2 (2%)	0	100	100
45	LV	133/139 (96%)	128 (96%)	5 (4%)	0	100	100
46	LX	133/156 (85%)	129 (97%)	4 (3%)	0	100	100
47	LY	132/138 (96%)	127 (96%)	5 (4%)	0	100	100
48	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
49	Lc	96/108 (89%)	96 (100%)	0	0	100	100
50	Ld	107/120 (89%)	105 (98%)	2 (2%)	0	100	100
51	Le	125/131 (95%)	120 (96%)	5 (4%)	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%)	114 (96%)	5 (4%)	0	100	100
55	Li	86/110 (78%)	85 (99%)	1 (1%)	0	100	100
56	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
57	Lk	73/81 (90%)	68 (93%)	5 (7%)	0	100	100
58	Ll	36/51 (71%)	34 (94%)	2 (6%)	0	100	100
59	Lq	205/217 (94%)	179 (87%)	26 (13%)	0	100	100
All	All	12458/20604 (60%)	11891 (95%)	550 (4%)	17 (0%)	49	77

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	CY	523	PRO
27	Cb	85	THR
26	CY	508	GLU
14	CL	224	ASP
14	CL	439	ASP

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%)	217 (97%)	6 (3%)	39	74
4	CB	222/329 (68%)	217 (98%)	5 (2%)	44	78
5	CC	578/708 (82%)	569 (98%)	9 (2%)	55	83
6	CD	381/410 (93%)	381 (100%)	0	100	100
7	CE	398/517 (77%)	398 (100%)	0	100	100
8	CF	214/236 (91%)	214 (100%)	0	100	100
9	CG	150/155 (97%)	149 (99%)	1 (1%)	76	91
10	CH	481/575 (84%)	477 (99%)	4 (1%)	73	90
11	CI	121/336 (36%)	121 (100%)	0	100	100
12	CJ	428/579 (74%)	427 (100%)	1 (0%)	87	96
13	CK	204/225 (91%)	204 (100%)	0	100	100
14	CL	72/458 (16%)	70 (97%)	2 (3%)	38	73
15	CM	191/215 (89%)	191 (100%)	0	100	100
15	LF	213/215 (99%)	211 (99%)	2 (1%)	70	89
16	CN	206/206 (100%)	205 (100%)	1 (0%)	81	93
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	302/632 (48%)	300 (99%)	2 (1%)	76	91
19	CQ	150/192 (78%)	150 (100%)	0	100	100
20	CR	144/206 (70%)	143 (99%)	1 (1%)	76	91
21	CS	209/716 (29%)	209 (100%)	0	100	100
22	CT	427/600 (71%)	427 (100%)	0	100	100
23	CU	149/376 (40%)	147 (99%)	2 (1%)	61	86
24	CV	109/112 (97%)	109 (100%)	0	100	100
25	CX	76/172 (44%)	76 (100%)	0	100	100
26	CY	355/686 (52%)	349 (98%)	6 (2%)	53	83
27	Cb	540/779 (69%)	539 (100%)	1 (0%)	87	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Cz	60/107 (56%)	60 (100%)	0	100	100
29	LB	301/331 (91%)	298 (99%)	3 (1%)	68	88
30	LC	283/285 (99%)	283 (100%)	0	100	100
31	LE	151/166 (91%)	151 (100%)	0	100	100
32	LG	175/222 (79%)	173 (99%)	2 (1%)	65	87
33	LH	167/169 (99%)	166 (99%)	1 (1%)	78	92
34	LK	120/136 (88%)	117 (98%)	3 (2%)	42	76
35	LL	99/176 (56%)	99 (100%)	0	100	100
36	LM	115/117 (98%)	115 (100%)	0	100	100
37	LN	164/180 (91%)	160 (98%)	4 (2%)	43	77
38	LO	163/163 (100%)	161 (99%)	2 (1%)	63	87
39	LP	137/152 (90%)	137 (100%)	0	100	100
40	LQ	110/178 (62%)	110 (100%)	0	100	100
41	LR	104/2396 (4%)	104 (100%)	0	100	100
42	LS	154/154 (100%)	154 (100%)	0	100	100
43	LT	109/135 (81%)	109 (100%)	0	100	100
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%)	114 (100%)	0	100	100
47	LY	117/119 (98%)	117 (100%)	0	100	100
48	LZ	121/121 (100%)	121 (100%)	0	100	100
49	Lc	79/88 (90%)	79 (100%)	0	100	100
50	Ld	95/105 (90%)	95 (100%)	0	100	100
51	Le	110/114 (96%)	110 (100%)	0	100	100
52	Lf	89/90 (99%)	89 (100%)	0	100	100
53	Lg	101/102 (99%)	100 (99%)	1 (1%)	68	88
54	Lh	108/781 (14%)	108 (100%)	0	100	100
55	Li	75/93 (81%)	74 (99%)	1 (1%)	61	86
56	Lj	61/78 (78%)	60 (98%)	1 (2%)	55	83
57	Lk	71/76 (93%)	71 (100%)	0	100	100
58	Ll	34/46 (74%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	Lq	179/189 (95%)	176 (98%)	3 (2%)	53	83
All	All	10549/17418 (61%)	10485 (99%)	64 (1%)	76	92

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	LO	102	GLU
55	Li	75	ASP
10	CH	544	ILE
10	CH	518	ILE
56	Lj	20	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
51	Le	41	ASN
53	Lg	15	ASN
16	CN	86	ASN
16	CN	82	GLN
54	Lh	50	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2640/3341 (79%)	537 (20%)	36 (1%)
2	C2	254/319 (79%)	52 (20%)	1 (0%)
All	All	2894/3660 (79%)	589 (20%)	37 (1%)

5 of 589 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	14	U
1	C1	22	G
1	C1	26	A
1	C1	41	G
1	C1	49	A

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3125	A
1	C1	3297	U
1	C1	3131	A
1	C1	3209	U
1	C1	1085	A

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

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	TPO	CC	163	5	8,10,11	0.68	0	10,14,16	1.04	1 (10%)
5	SEP	CC	160	5	8,9,10	0.64	0	7,12,14	0.73	0

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	TPO	CC	163	5	-	1/9/11/13	-
5	SEP	CC	160	5	-	0/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CC	163	TPO	O-C-CA	-2.56	118.19	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	CC	163	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	CC	163	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
60	GTP	CH	1001	-	33,34,34	0.52	0	50,54,54	0.69	0

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
60	GTP	CH	1001	-	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

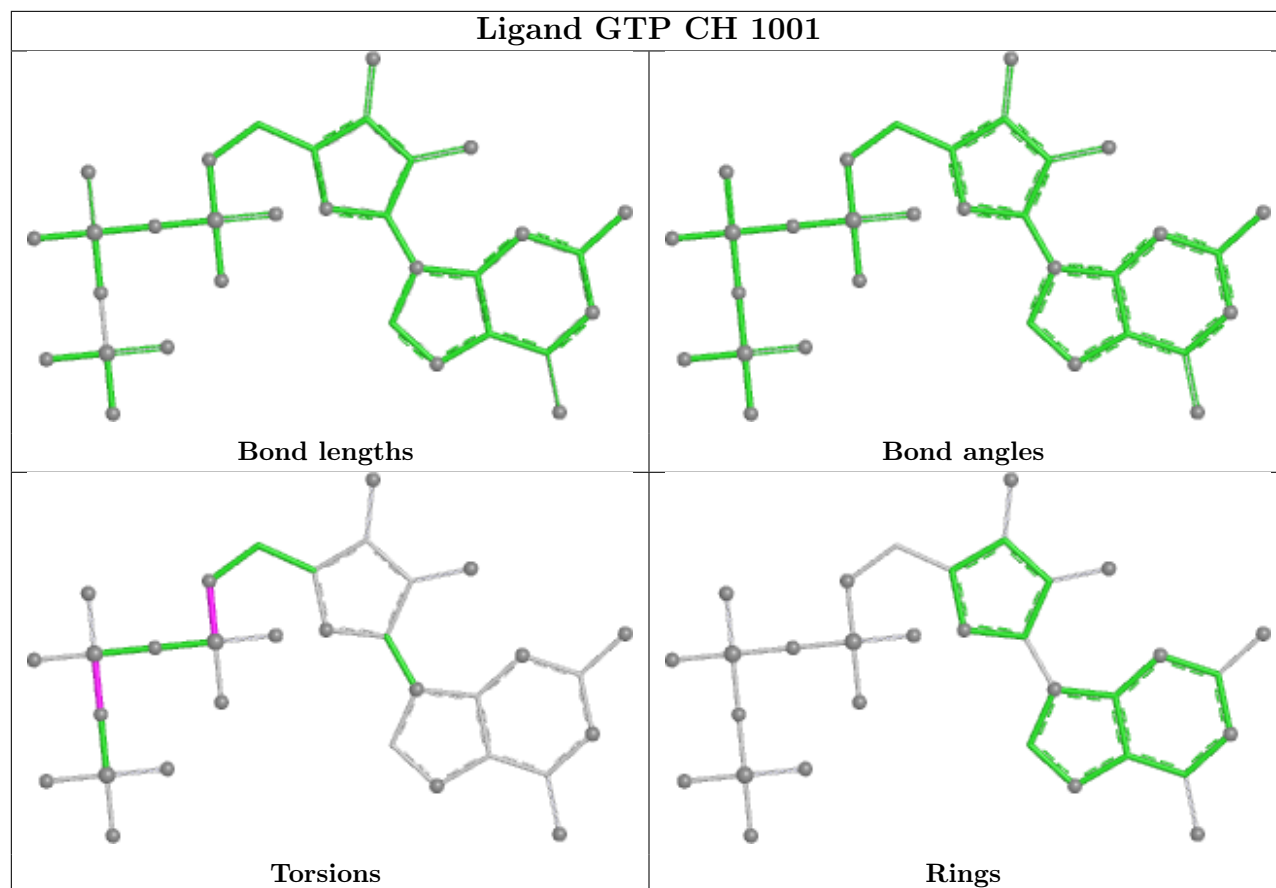
Mol	Chain	Res	Type	Atoms
60	CH	1001	GTP	PG-O3B-PB-O1B
60	CH	1001	GTP	C5'-O5'-PA-O1A
60	CH	1001	GTP	PG-O3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	CH	1001	GTP	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

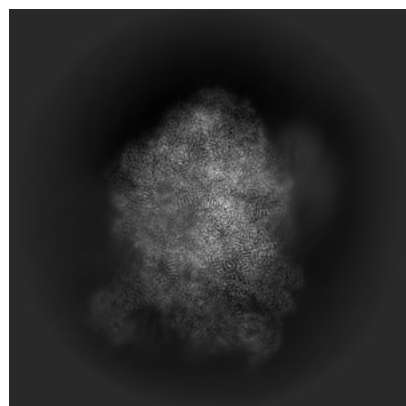
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35287. These allow visual inspection of the internal detail of the map and identification of artifacts.

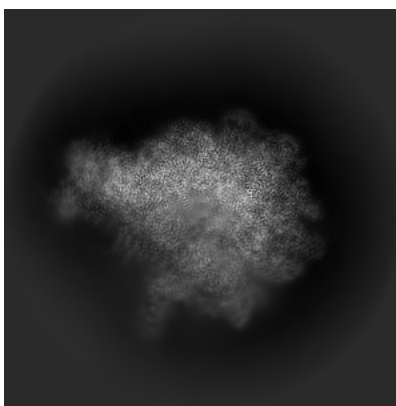
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

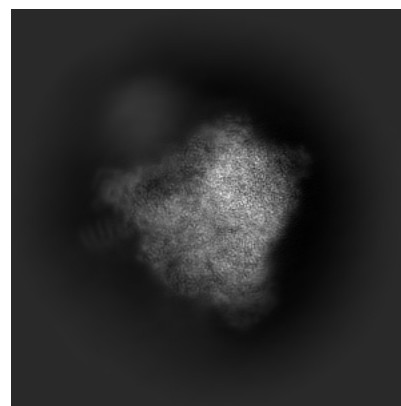
6.1.1 Primary map



X

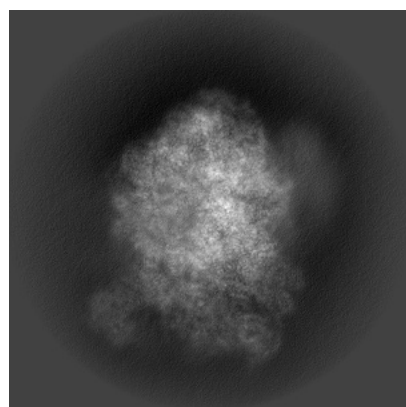


Y

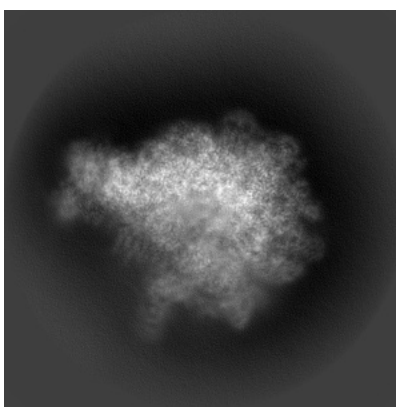


Z

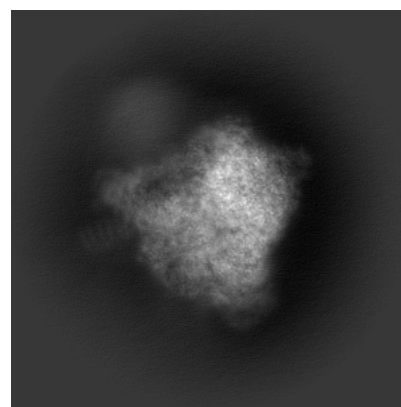
6.1.2 Raw map



X



Y

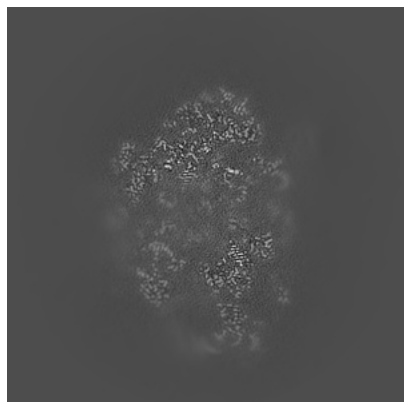


Z

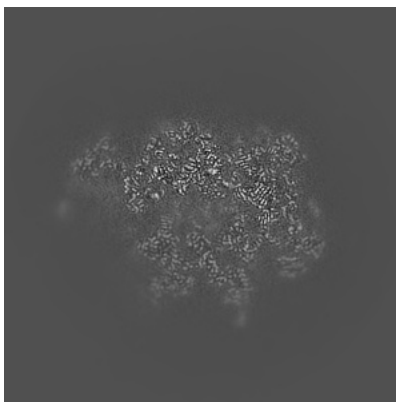
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

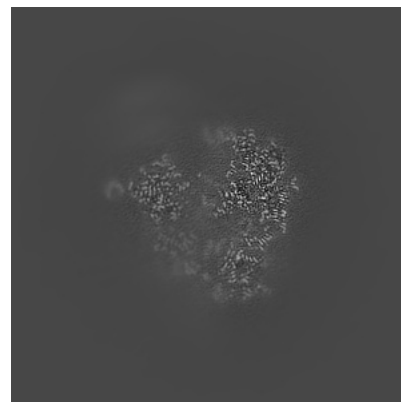
6.2.1 Primary map



X Index: 210

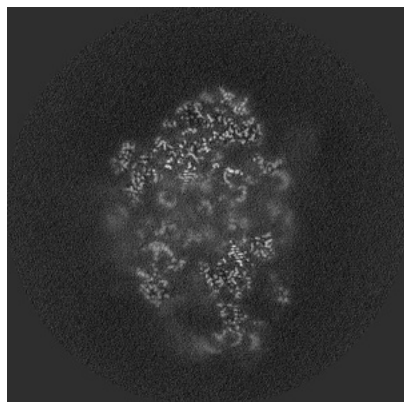


Y Index: 210

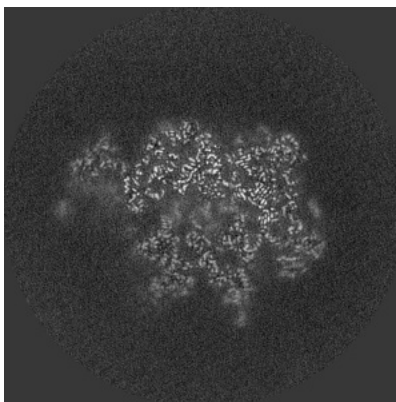


Z Index: 210

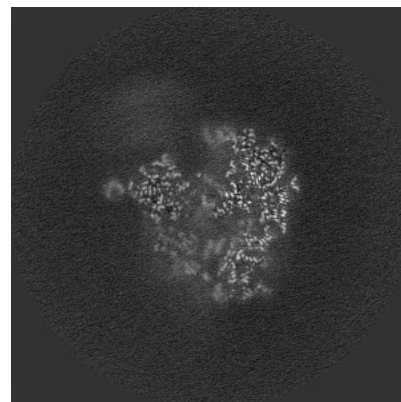
6.2.2 Raw map



X Index: 210



Y Index: 210

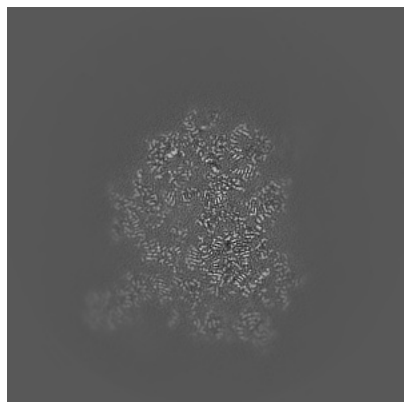


Z Index: 210

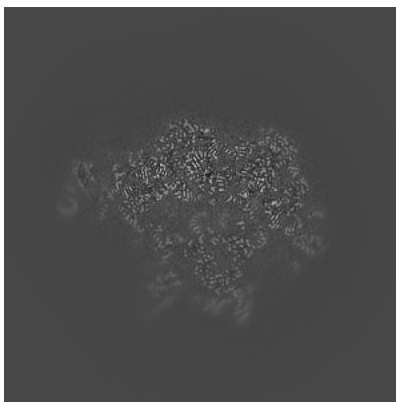
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

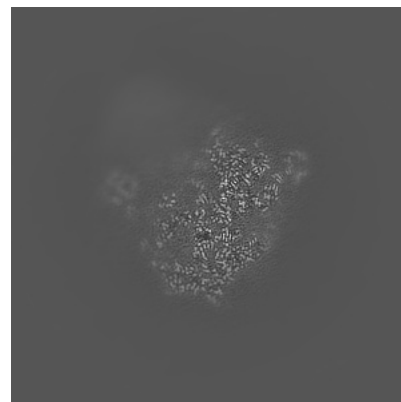
6.3.1 Primary map



X Index: 244

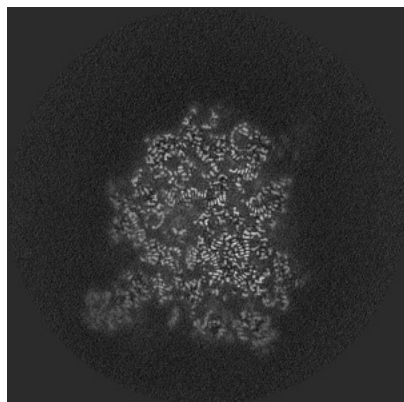


Y Index: 220

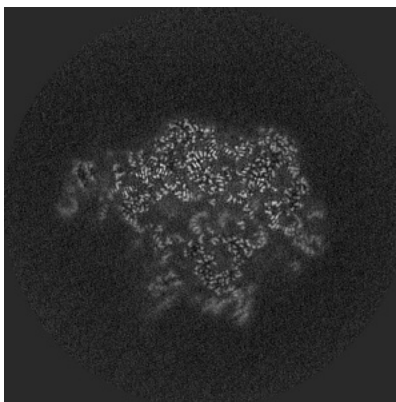


Z Index: 259

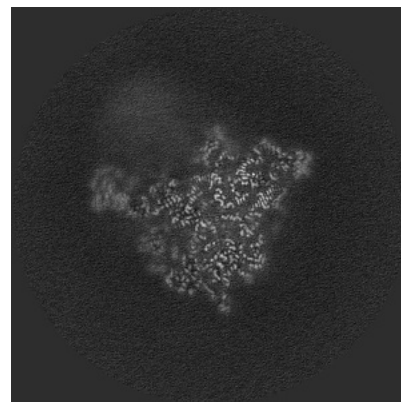
6.3.2 Raw map



X Index: 243



Y Index: 220

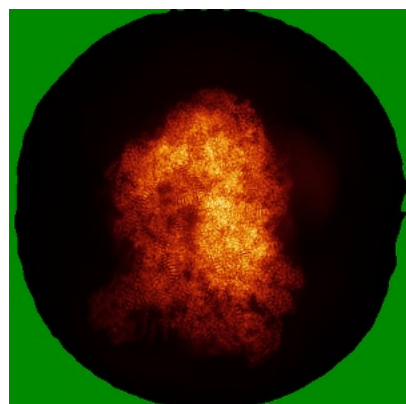


Z Index: 248

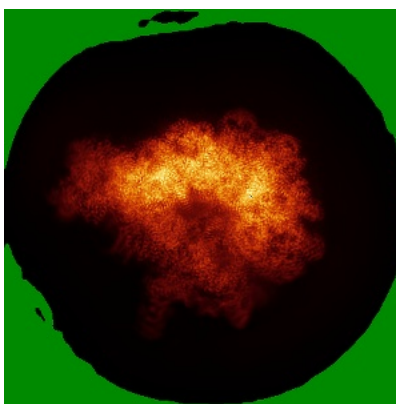
The images above show the largest variance slices of the map in three orthogonal directions.

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

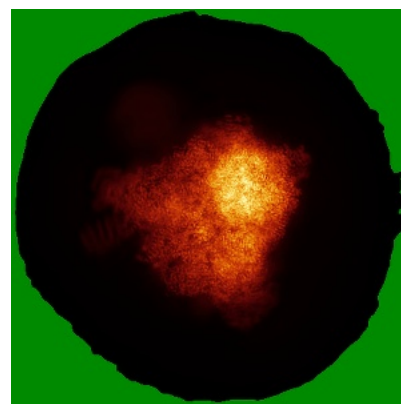
6.4.1 Primary map



X

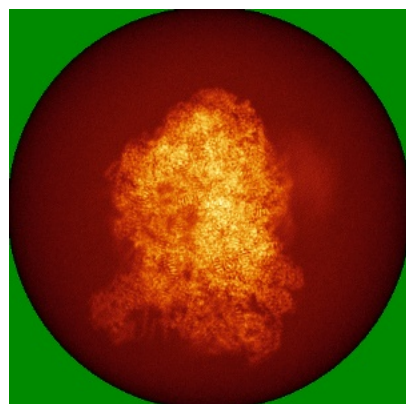


Y

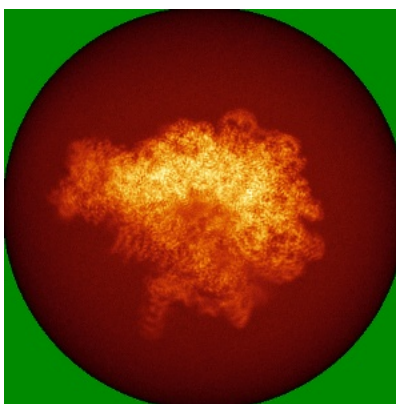


Z

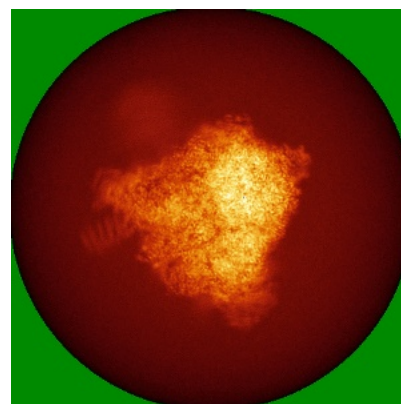
6.4.2 Raw map



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



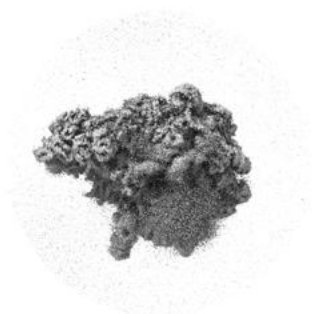
Z

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.

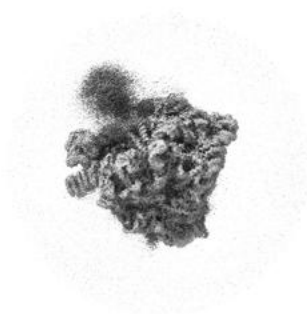
6.5.2 Raw map



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.

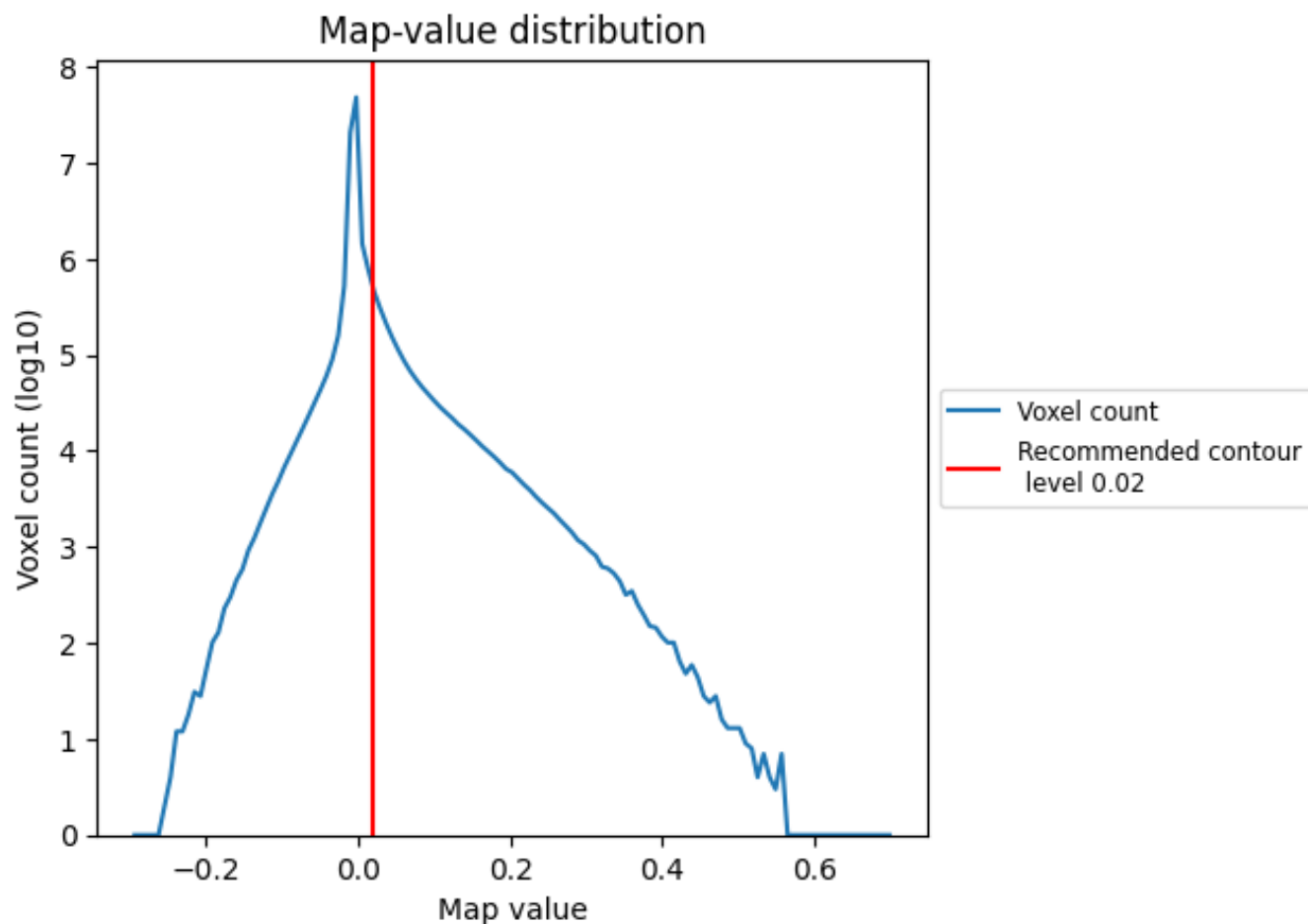
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

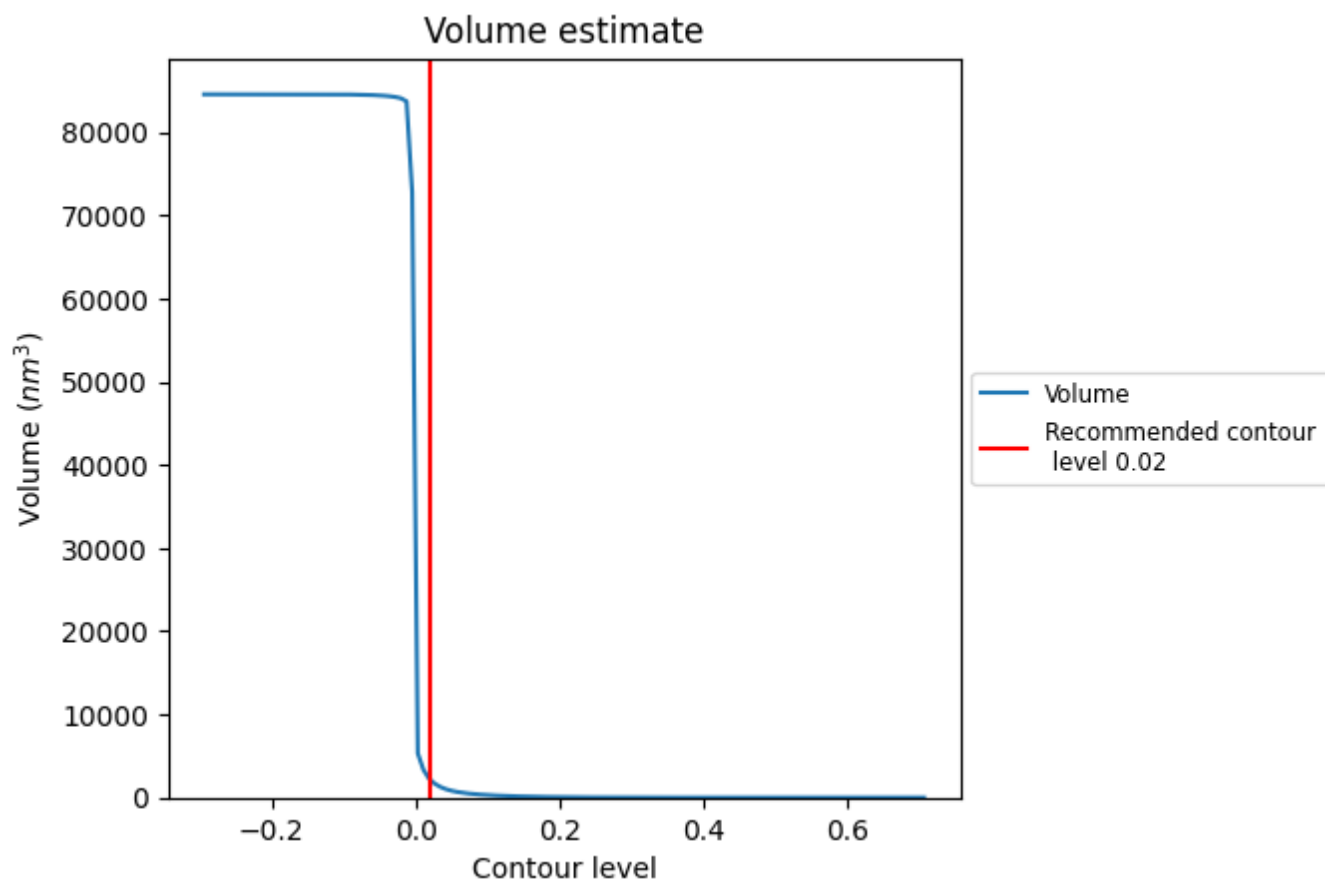
This section contains the results of statistical analysis of the map.

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.

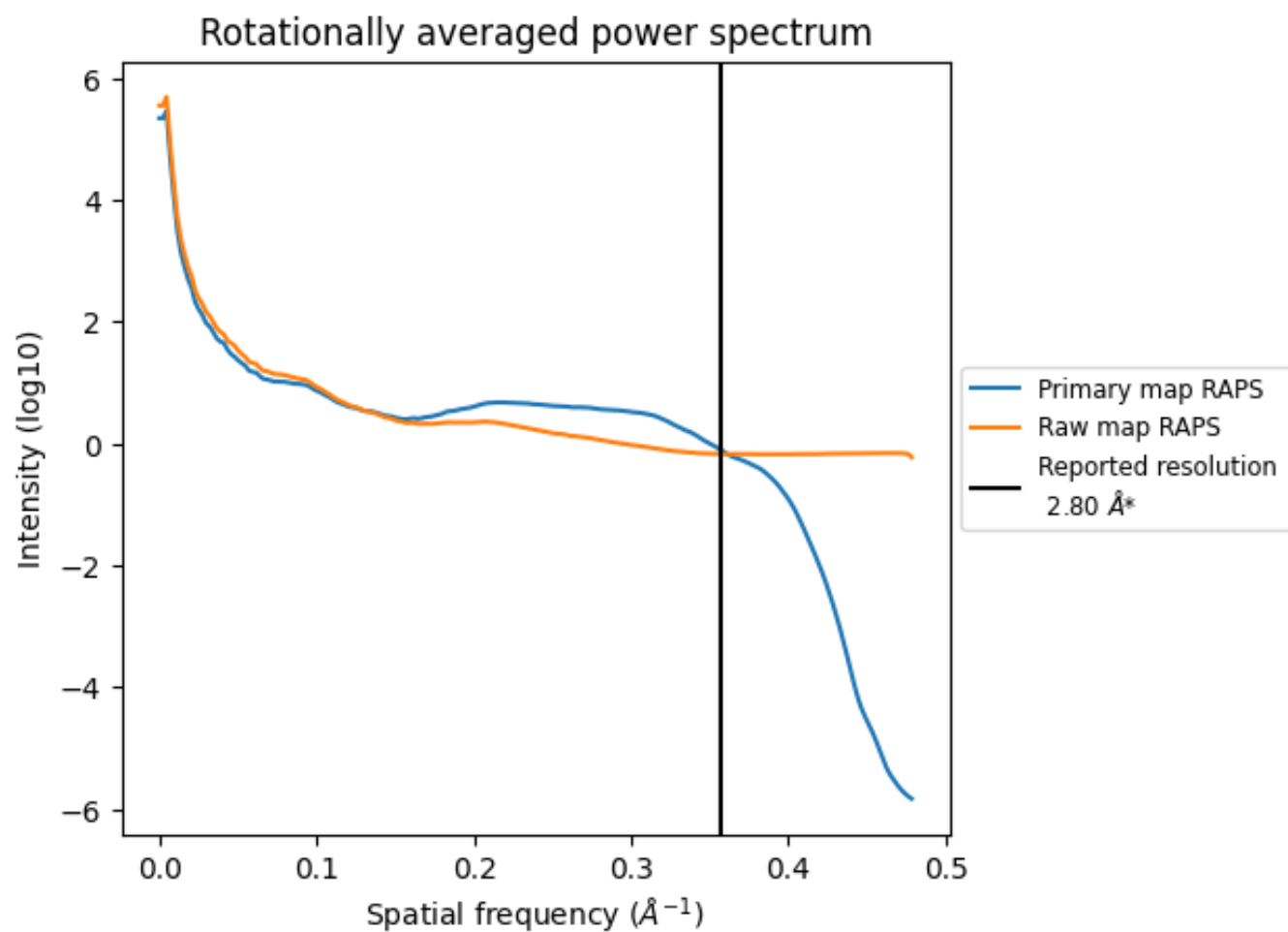
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2160 nm^3 ; this corresponds to an approximate mass of 1951 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 ⓘ

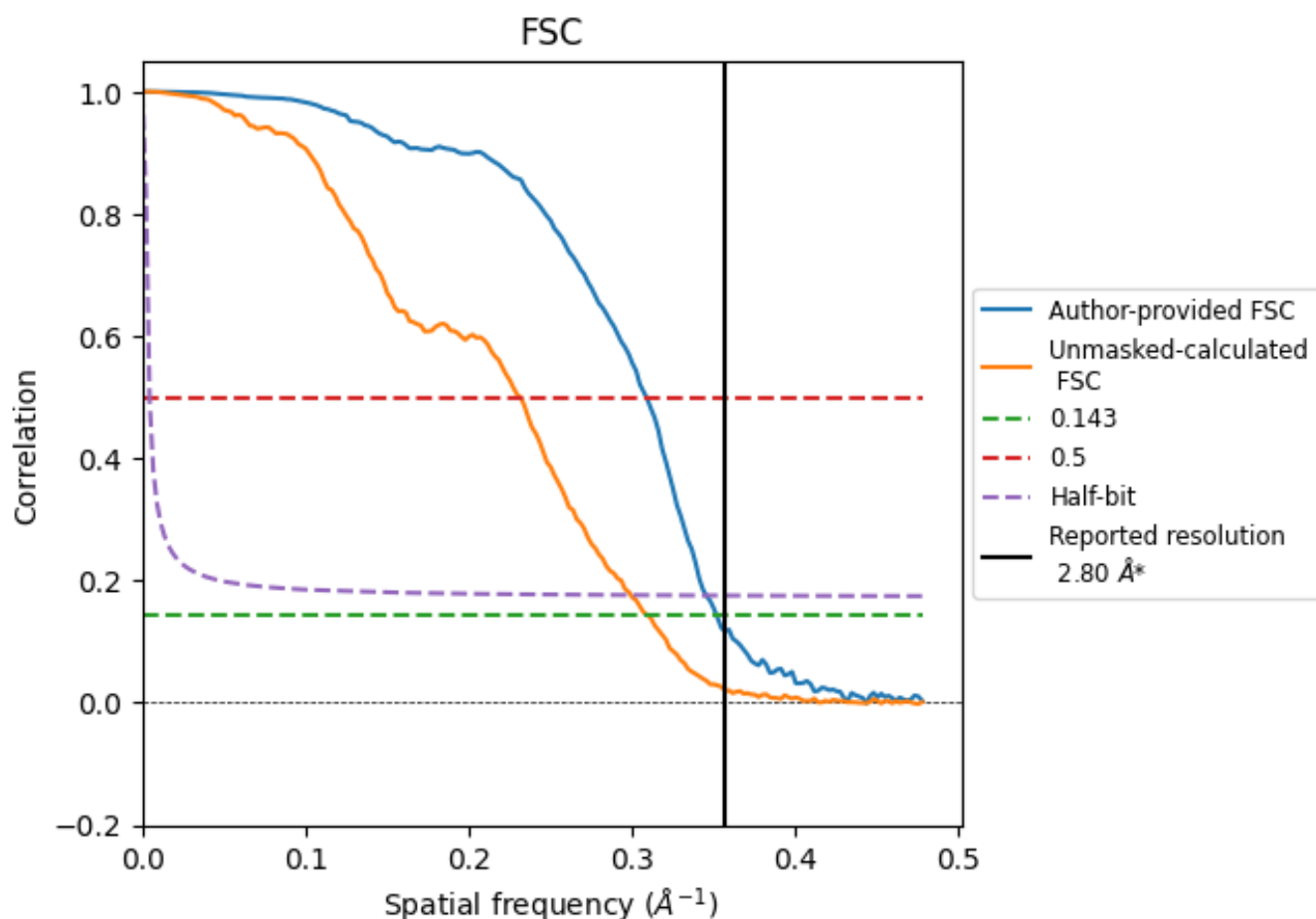


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

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 $0.357 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

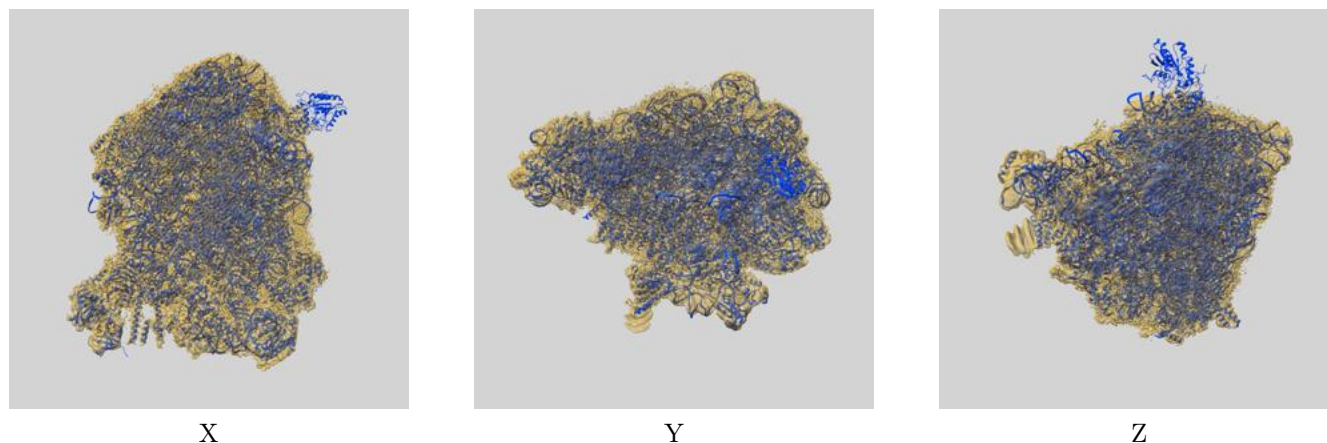
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.23	2.89
Unmasked-calculated*	3.22	4.31	3.34

*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 3.22 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

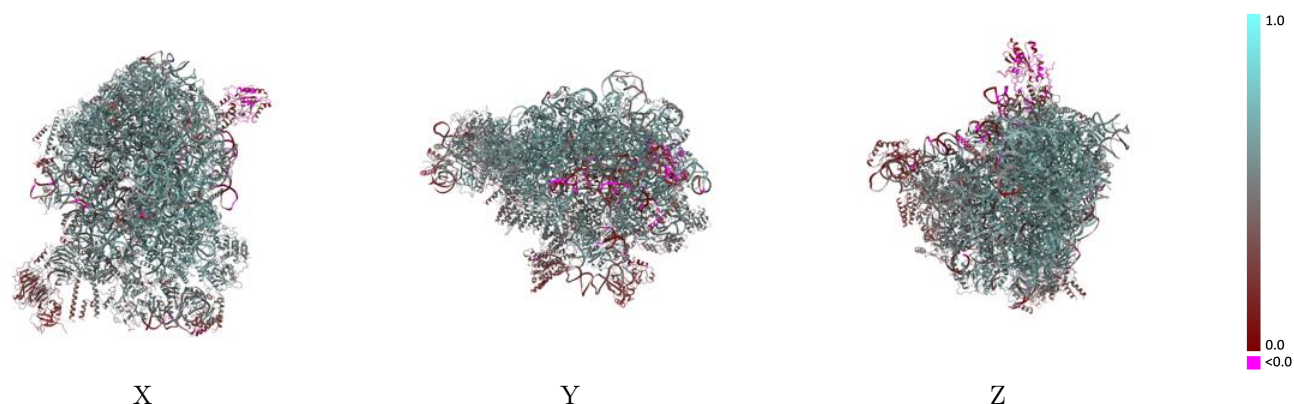
This section contains information regarding the fit between EMDB map EMD-35287 and PDB model 8I9X. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



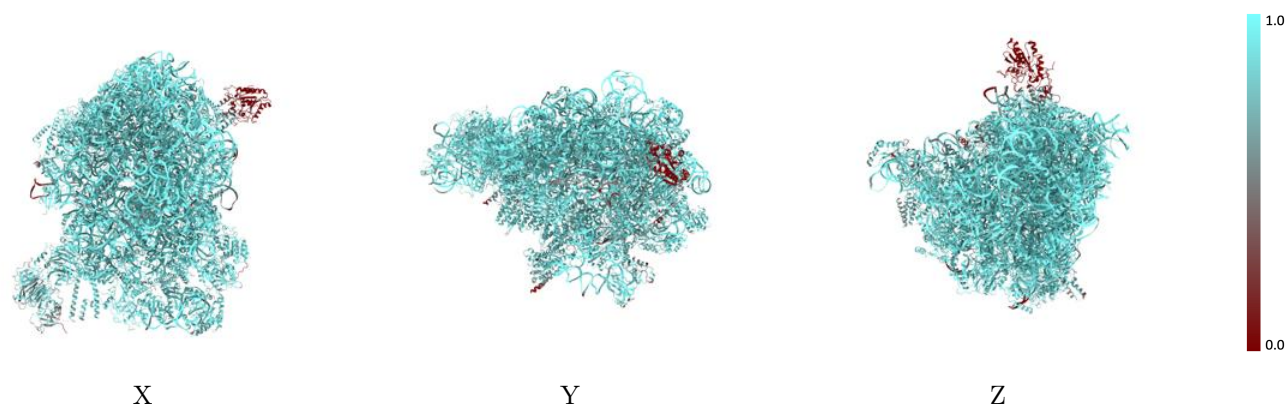
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



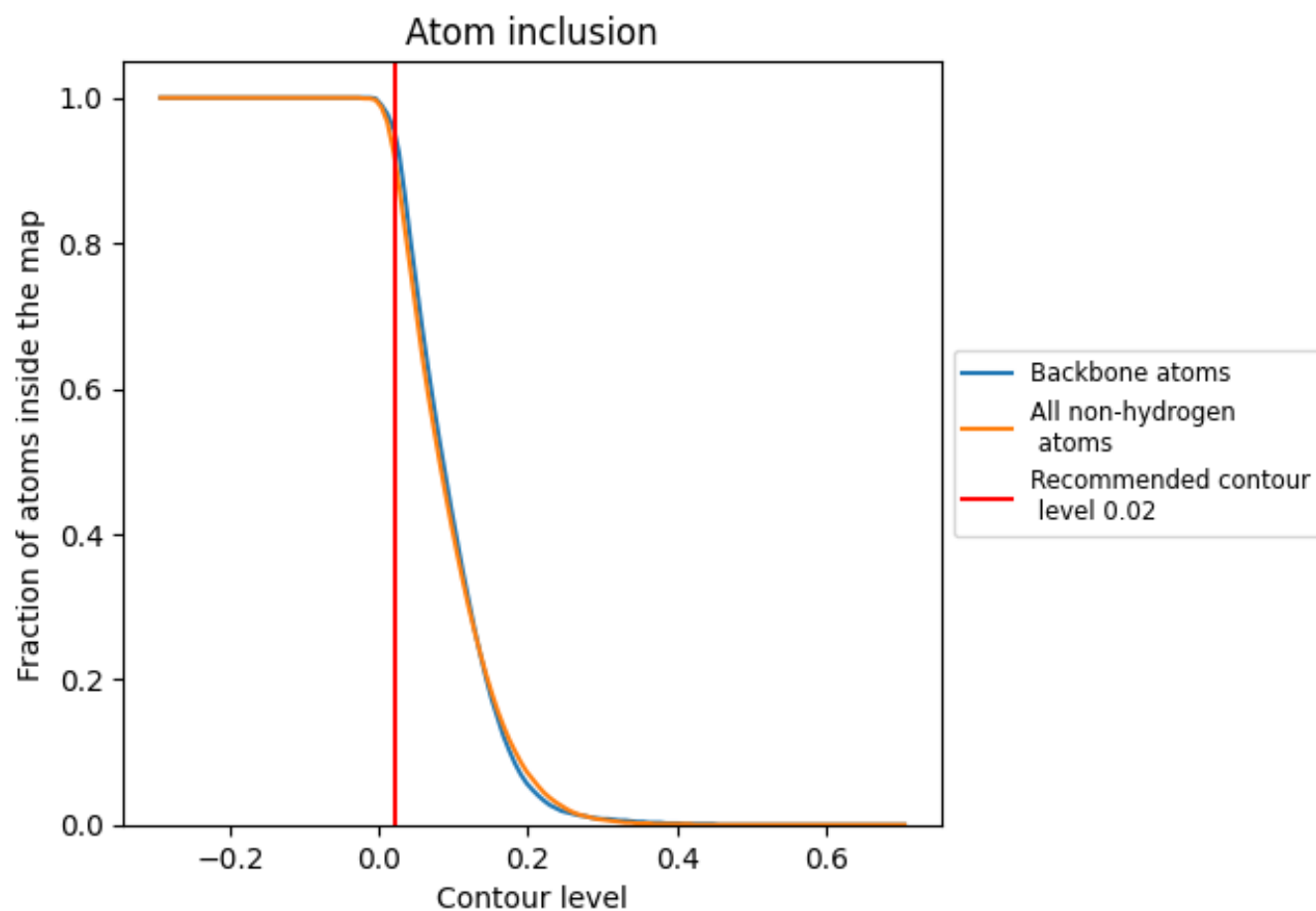
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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, 92% 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	 0.9230	 0.5100
C1	 0.9620	 0.5330
C2	 0.9560	 0.5250
CA	 0.9650	 0.5880
CB	 0.8770	 0.4350
CC	 0.9190	 0.4980
CD	 0.7160	 0.2940
CE	 0.9120	 0.5220
CF	 0.9180	 0.4920
CG	 0.9590	 0.5500
CH	 0.9210	 0.5160
CI	 0.8830	 0.4590
CJ	 0.9080	 0.4920
CK	 0.9420	 0.5280
CL	 0.3510	 0.2110
CM	 0.8870	 0.4600
CN	 0.9580	 0.5610
CO	 0.9630	 0.5830
CP	 0.9490	 0.5390
CQ	 0.9110	 0.5060
CR	 0.9460	 0.5800
CS	 0.8710	 0.4630
CT	 0.9210	 0.4850
CU	 0.9440	 0.5460
CV	 0.9680	 0.6000
CX	 0.9210	 0.5140
CY	 0.8150	 0.3390
Cb	 0.8500	 0.3790
Cz	 0.7450	 0.3270
LB	 0.9520	 0.5710
LC	 0.9640	 0.6040
LE	 0.9470	 0.5630
LF	 0.9600	 0.5880
LG	 0.9470	 0.5890
LH	 0.9480	 0.5600



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Chain	Atom inclusion	Q-score
LK	 0.8580	 0.3800
LL	 0.9830	 0.6150
LM	 0.9690	 0.5910
LN	 0.9850	 0.6500
LO	 0.9760	 0.6200
LP	 0.9550	 0.5550
LQ	 0.9570	 0.5560
LR	 0.9330	 0.4670
LS	 0.9640	 0.5760
LT	 0.8440	 0.3240
LU	 0.9140	 0.4990
LV	 0.9420	 0.5230
LX	 0.9430	 0.5510
LY	 0.9470	 0.5760
LZ	 0.9240	 0.4980
Lc	 0.8540	 0.4250
Ld	 0.9380	 0.5570
Le	 0.9720	 0.6150
Lf	 0.9830	 0.6290
Lg	 0.9060	 0.5300
Lh	 0.9410	 0.5440
Li	 0.9520	 0.5620
Lj	 0.9820	 0.6330
Lk	 0.8810	 0.4580
Ll	 0.9480	 0.4850
Lq	 0.7320	 0.2120