



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:07 PM UTC

PDB ID : 9QLP / pdb_00009qlp
EMDB ID : EMD-53231
Title : NMT1-NAC bound human RNC with full length ARF1 - State 2
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-03-21
Resolution : 2.75 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:

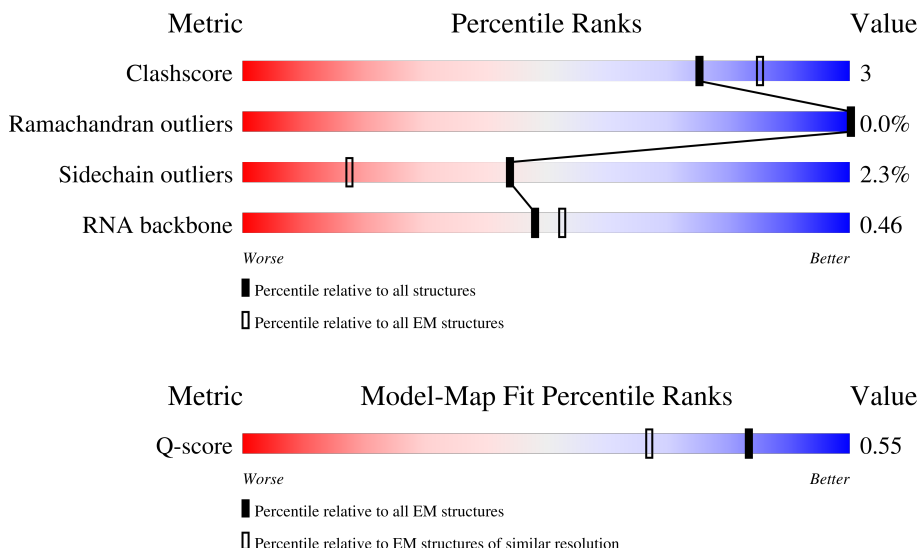
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 2.75 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.



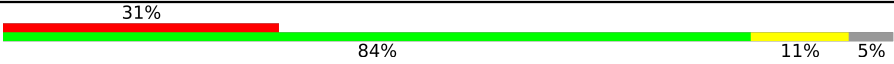

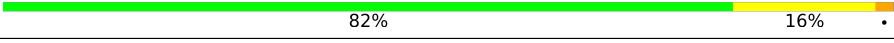




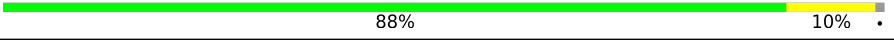










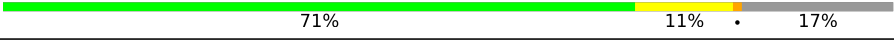




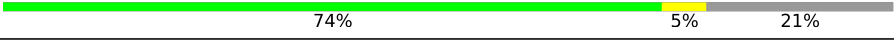

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10570 (2.25 - 3.25)

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	CM	952	
2	CP	75	
3	CR	437	







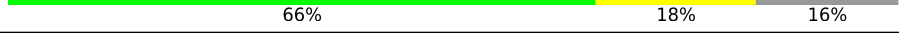
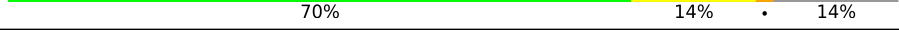
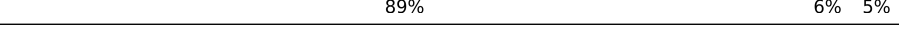
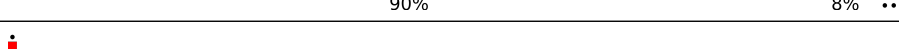
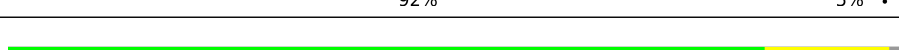

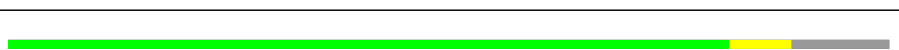







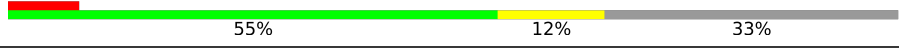
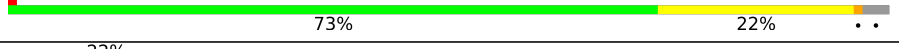



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Mol	Chain	Length	Quality of chain
4	CZ	217	
5	L5	5070	
6	L7	121	
7	L8	157	
8	LA	257	
9	LB	403	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	

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Mol	Chain	Length	Quality of chain
29	LW	157	
30	LX	156	
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Ln	25	
47	Lo	106	
48	Lp	91	
49	Lr	137	
50	Ls	317	
51	Lt	165	
52	NA	215	
53	NB	162	




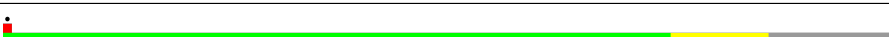
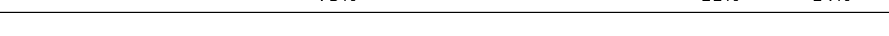
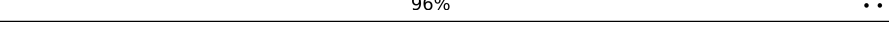




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Mol	Chain	Length	Quality of chain
54	NM	496	
55	S2	1869	
56	SA	295	
57	SB	264	
58	SC	293	
59	SD	243	
60	SE	263	
61	SF	204	
62	SG	249	
63	SH	194	
64	SI	208	
65	SJ	194	
66	SK	165	
67	SL	158	
68	SM	132	
69	SN	151	
70	SO	151	
71	SP	145	
72	SQ	146	
73	SR	135	
74	SS	152	
75	ST	145	
76	SU	119	
77	SV	83	
78	SW	130	

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Mol	Chain	Length	Quality of chain
79	SX	143	 87% 10% ..
80	SY	133	 80% 11% • 8%
81	SZ	125	 53% 7% 40%
82	Sa	115	 75% 11% 14%
83	Sb	84	 96% ..
84	Sc	69	 78% 12% • 9%
85	Sd	56	 88% 7% 5%
86	Se	133	 36% 5% 59%
87	Sf	156	 35% • • 60%
88	Sg	317	 83% 13% • •

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 223418 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 Full length ARF1-V5-hCMV staller mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CM	12	Total	C	N	O	P	0	0
			247	111	37	87	12		

- Molecule 2 is a RNA chain called prolyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CP	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 3 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CR	414	Total	C	N	O	S	0	0
			3269	2080	557	621	11		

- Molecule 4 is a protein called ADP-ribosylation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CZ	206	Total	C	N	O	S	0	0
			1491	947	250	286	8		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CZ	1	GLN	-	expression tag	UNP P84077
CZ	4	SER	ILE	conflict	UNP P84077
CZ	6	SER	ALA	conflict	UNP P84077
CZ	7	LYS	ASN	conflict	UNP P84077
CZ	8	PRO	LEU	conflict	UNP P84077
CZ	9	ARG	PHE	conflict	UNP P84077
CZ	182	GLY	-	expression tag	UNP P84077
CZ	183	LYS	-	expression tag	UNP P84077
CZ	184	PRO	-	expression tag	UNP P84077

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Chain	Residue	Modelled	Actual	Comment	Reference
CZ	185	ILE	-	expression tag	UNP P84077
CZ	186	PRO	-	expression tag	UNP P84077
CZ	187	ASN	-	expression tag	UNP P84077
CZ	188	PRO	-	expression tag	UNP P84077
CZ	189	LEU	-	expression tag	UNP P84077
CZ	190	LEU	-	expression tag	UNP P84077
CZ	191	GLY	-	expression tag	UNP P84077
CZ	192	LEU	-	expression tag	UNP P84077
CZ	193	ASP	-	expression tag	UNP P84077
CZ	194	SER	-	expression tag	UNP P84077
CZ	195	THR	-	expression tag	UNP P84077
CZ	196	MET	-	expression tag	UNP P84077
CZ	197	GLU	-	expression tag	UNP P84077
CZ	198	PRO	-	expression tag	UNP P84077
CZ	199	LEU	-	expression tag	UNP P84077
CZ	200	VAL	-	expression tag	UNP P84077
CZ	201	LEU	-	expression tag	UNP P84077
CZ	202	SER	-	expression tag	UNP P84077
CZ	203	ALA	-	expression tag	UNP P84077
CZ	204	LYS	-	expression tag	UNP P84077
CZ	205	LYS	-	expression tag	UNP P84077
CZ	206	LEU	-	expression tag	UNP P84077
CZ	207	SER	-	expression tag	UNP P84077
CZ	208	SER	-	expression tag	UNP P84077
CZ	209	LEU	-	expression tag	UNP P84077
CZ	210	LEU	-	expression tag	UNP P84077
CZ	211	THR	-	expression tag	UNP P84077
CZ	212	CYS	-	expression tag	UNP P84077
CZ	213	LYS	-	expression tag	UNP P84077
CZ	214	TYR	-	expression tag	UNP P84077
CZ	215	ILE	-	expression tag	UNP P84077
CZ	216	PRO	-	expression tag	UNP P84077
CZ	217	PRO	-	expression tag	UNP P84077

- Molecule 5 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L5	3648	Total	C	N	O	P	0	0
			78199	34823	14307	25422	3647		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 7 is a RNA chain called RNA (156-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 12 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 15 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 16 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	207	Total	C	N	O	S	0	0
			1666	1059	323	270	14		

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 20 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 21 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 22 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 23 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 25 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 26 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 27 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LU	101	Total	C	N	O	S	0	0
			806	520	141	143	2		

- Molecule 28 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

- Molecule 29 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 30 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 31 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 32 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 33 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 34 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 36 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 37 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 38 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 39 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 40 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 42 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 46 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 48 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ls	212	Total	C	N	O	S	0	0
			1640	1042	284	305	9		

- Molecule 51 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lt	160	Total	C	N	O	S	0	0
			1208	749	226	229	4		

- Molecule 52 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	NA	73	Total	C	N	O	S	0	0
			573	361	105	106	1		

- Molecule 53 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	NB	127	Total	C	N	O	S	0	0
			980	606	178	193	3		

- Molecule 54 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	NM	380	Total	C	N	O	S	3	0
			3122	2024	527	555	16		

- Molecule 55 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S2	1713	Total	C	N	O	P	0	0
			36562	16320	6564	11966	1712		

- Molecule 56 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 57 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 58 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 59 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SD	223	Total	C	N	O	S	0	0
			1594	1023	291	273	7		

- Molecule 60 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 61 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SF	181	Total	C	N	O	S	0	0
			1403	879	269	248	7		

- Molecule 62 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 63 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- Molecule 64 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 65 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 66 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 67 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 68 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SM	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 69 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 70 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 71 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SP	129	Total	C	N	O	S	0	0
			990	626	190	168	6		

- Molecule 72 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SQ	142	Total	C	N	O	S	0	0
			1075	689	204	179	3		

- Molecule 73 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 74 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SS	141	Total	C	N	O	S	0	0
			1130	712	232	185	1		

- Molecule 75 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 77 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 78 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 79 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 80 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 81 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 82 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 83 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 84 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

- Molecule 85 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

- Molecule 86 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Se	55	Total	C	N	O	S	0	0
			416	254	93	68	1		

- Molecule 87 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sf	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

- Molecule 88 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	Sg	308	Total	C	N	O	S	0	0
			2180	1393	381	395	11		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

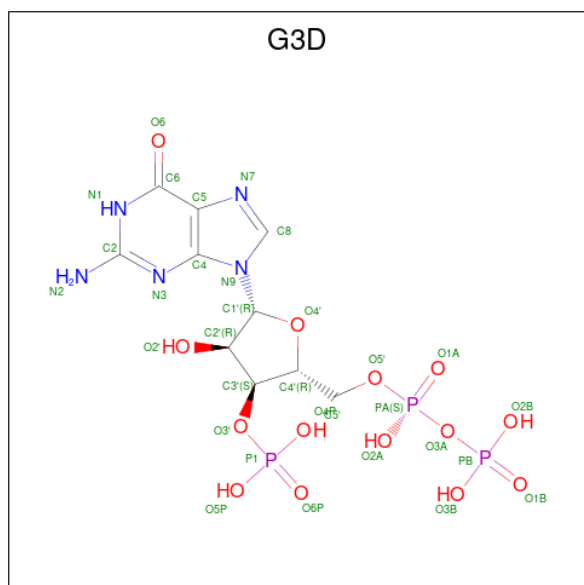
Mol	Chain	Residues	Atoms		AltConf
89	CM	1	Total	Mg	0
			1	1	
89	L5	126	Total	Mg	0
			126	126	
89	L7	3	Total	Mg	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
89	L8	3	Total	Mg	0
			3	3	
89	LA	1	Total	Mg	0
			1	1	
89	LC	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	
89	LN	1	Total	Mg	0
			1	1	
89	LP	1	Total	Mg	0
			1	1	
89	LV	1	Total	Mg	0
			1	1	
89	S2	51	Total	Mg	0
			51	51	
89	ST	1	Total	Mg	0
			1	1	

- Molecule 90 is GUANOSINE-3'-MONOPHOSPHATE-5'-DIPHOSPHATE (CCD ID: G3D) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

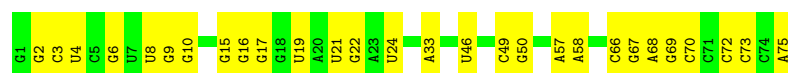
- Molecule 91 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
91	Lg	1	Total 1	Zn 1	0
91	Lj	1	Total 1	Zn 1	0
91	Lm	1	Total 1	Zn 1	0
91	Lo	1	Total 1	Zn 1	0
91	Lp	1	Total 1	Zn 1	0
91	Sa	1	Total 1	Zn 1	0
91	Sd	1	Total 1	Zn 1	0
91	Sf	1	Total 1	Zn 1	0


- Molecule 92 is water.

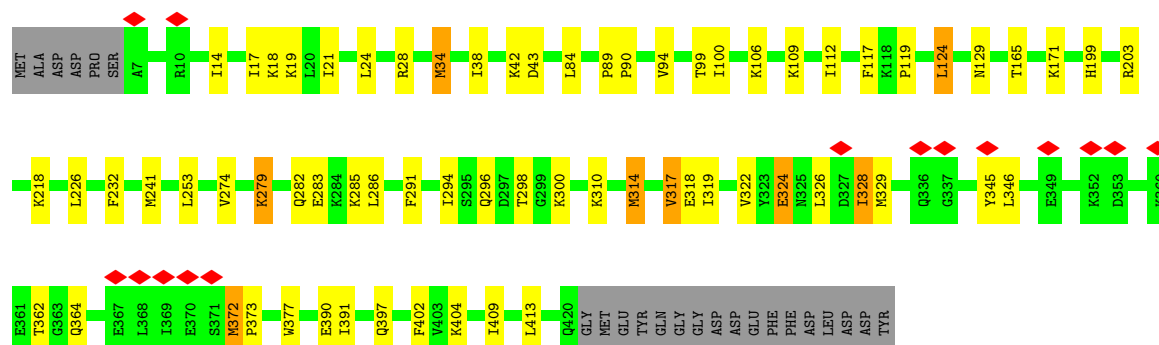
Mol	Chain	Residues	Atoms		AltConf
92	L5	3	Total 3	O 3	0
92	L7	1	Total 1	O 1	0
92	LI	1	Total 1	O 1	0
92	LN	1	Total 1	O 1	0
92	La	1	Total 1	O 1	0
92	Lp	1	Total 1	O 1	0
92	S2	3	Total 3	O 3	0

Chain CP:  63% 37%




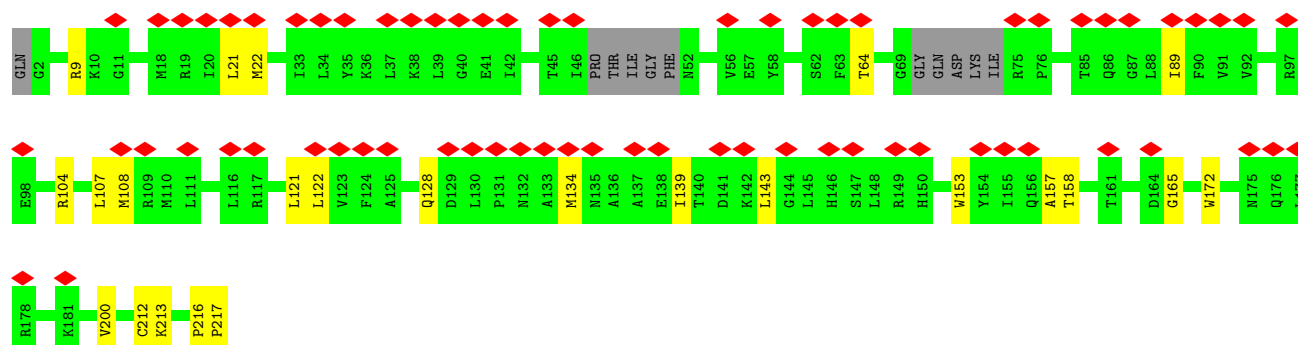
- Molecule 3: Eukaryotic peptide chain release factor subunit 1

Chain CR:  79% 14% 5%



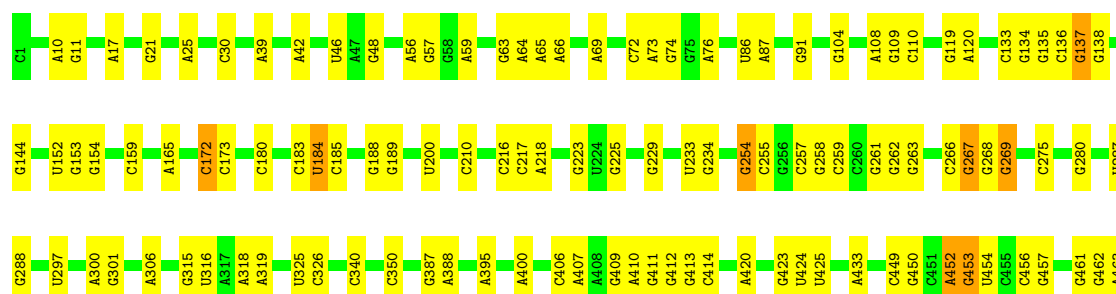
- Molecule 4: ADP-ribosylation factor 1

Chain CZ:  31% 84% 11% 5%



- Molecule 5: 28S rRNA

Chain L5:  51% 20% 28%







C4990	U4882	G4735	U4574	U4438	U4306	G4175	G4089	G	G	U3848	A3711	C3585
U4991	C4863	C4736	G4575	C4444	U4301	G4178	G4093	G	U	A3849	A3712	C3586
G4993	U4888	G4737	A4584	U4449	U4302	C4179	G4094	G	U	A3861	U3713	C3588
U5006	G4889	G4740	G4580	G4448	G4303	G4183	G4097	C	A	A3862	A3717	C3591
A5007	A4894	C4741	A4590	A4449	G4302	G4184	A4098	C	A	A3867	A3718	C3592
A5011	C4895	G4742	U4591	U4452	A4304	U4189	A4099	C	A	A3868	A3719	C3593
A5014	G4896	G4743	C4592	U4453	U4306	U4188	C4102	C	U	A3869	U3721	C3594
A5015	C4900	G4745	G4600	C4453	G4309	U4190	G4103	C	A	A3877	G3722	A3596
A5016	G4901	G4754	U4601	U4457	G4314	G4191	A4105	C	U	A3878	A3723	G3597
G5017	C4906	C4757	G4608	C4458	C4319	A4203	A4106	C	G	A3726	C3598	C3599
G5018	G4907	U4758	G4617	U4460	G4320	C4206	G4107	C	G	A3727	A3599	G3600
A5019	C4908	G4759	G4618	C4461	U4321	C4207	U4113	C	G	A3728	A3604	A3604
U5022	G4910	G4760	C4621	U4464	G4322	U4208	C4114	C	A	U3729	C3605	C3605
C5023	A4911	G4761	A4622	U4465	G4329	U4209	C4115	C	G	A3733	U3606	U3607
C5024	G4912	G4765	U4626	U4466	G4330	A4219	C4116	C	C	U3734	C3612	C3612
U5026	C4913	C4771	U4627	U4467	G4331	C4220	C4119	C	C	G3735	U3613	U3614
C5027	G4914	C4772	U4632	U4468	G4332	C4221	C4122	C	C	A3746	C3614	C3615
G5028	U4925	C4773	U4633	U4469	G4338	G4222	G4125	C	C	A3747	C3615	C3615
C5029	G4926	C4774	U4636	U4470	U4344	G4225	C4128	C	C	A3748	C3616	C3616
U5030	A4927	C4775	G4637	U4471	C4345	G4228	A4128	C	C	C3749	C3617	C3617
C5031	C4928	G4776	U4638	U4472	U4346	U4229	C4129	C	C	A3751	C3618	C3618
A5034	G4931	C	G4639	U4473	G4347	U4233	C4130	C	C	G3753	C3619	C3619
U5037	A4934	U	G4652	U4474	A4348	A4233	G4131	C	C	U3915	A3624	A3624
C4936	C4935	C	A4656	U4475	U4349	G4238	G4135	C	C	A3760	C3625	C3625
G4937	G4936	C	A4657	U4476	C4354	A4239	G4136	C	C	C3761	C3626	C3626
G5041	C4937	C	A4658	U4477	A4354	C4240	C4137	C	C	C3771	A3630	A3630
C5050	C4940	C	A4659	U4478	A4355	G4243	C4138	C	C	A3775	A3635	A3635
C5054	G4941	C	C4670	U4479	C4363	U4249	G4139	C	C	G3776	U3641	U3641
C5057	A4942	C	C4671	U4480	G4373	G4250	C4140	C	C	G3777	U3642	U3642
A5058	C4943	C	U4685	U4481	A4376	G4251	C4141	C	C	A3784	U3644	U3644
G5062	C4944	C	G4686	U4482	G4377	A4251	C4142	C	C	A3785	U3645	U3645
U5069	G4949	C	A4687	U4483	A4378	G4254	C4143	C	C	U3786	A3646	A3646
C	G4954	C	A4691	U4484	A4379	U4254	C4144	C	C	C3810	A3647	A3647
C	A4955	C	A4692	U4485	C4387	C4258	G4145	C	C	U3814	A3648	A3648
U4959	G4959	C	C4693	U4486	A4388	C4259	C4154	C	C	A3817	A3662	A3662
G4960	C4960	C	G4694	U4487	C4389	U4260	C4155	C	C	U3818	A3663	A3663
G4963	A4963	C	U4699	U4488	A4390	C4261	G4156	C	C	G3819	G3665	G3665
A4966	A4966	C	A4700	U4489	G4391	A4268	C4162	C	C	A3947	C3673	C3673
A4967	A4967	C	C4704	U4490	A4394	U4273	C4164	C	C	A3948	G3674	G3674
A4968	A4968	C	A4705	U4491	A4422	A4274	U4169	C	C	U	U3697	U3697
U4976	U4976	C	U4708	U4492	C4426	G4275	A4170	C	C	A	G3698	G3698
A4979	A4979	C	U4709	U4493	C4426	A4281	C4171	C	C	A	U3707	U3707
U4988	U4988	C	G4732	U4494	C4434	G4291	U4174	C	C	A	C3708	C3708
U4989	U4989	C	A4734	U4495	U4436	U4292		C	C	A		
		C	A4734	U4496	U4437	U4293		C	C	A		

• Molecule 6: 5S rRNA

Chain L7:

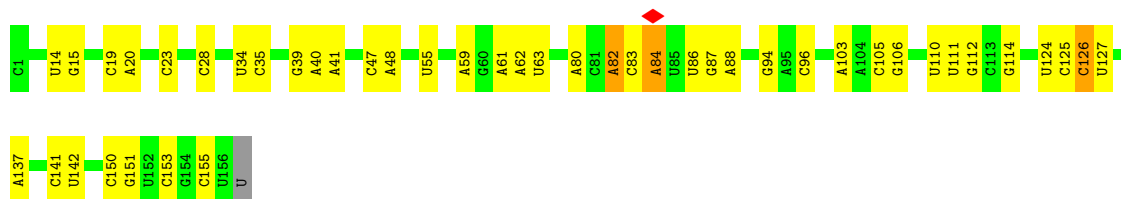
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16%

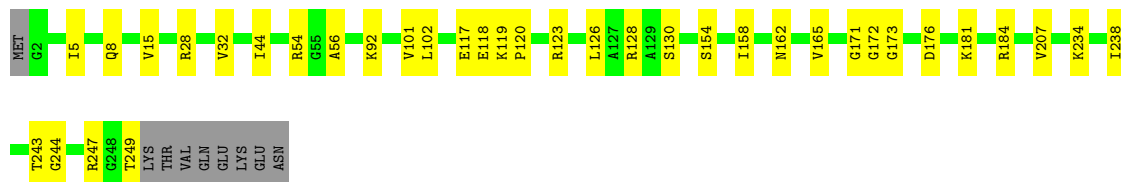
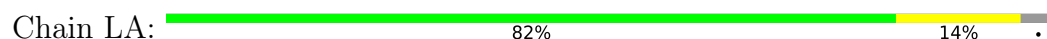
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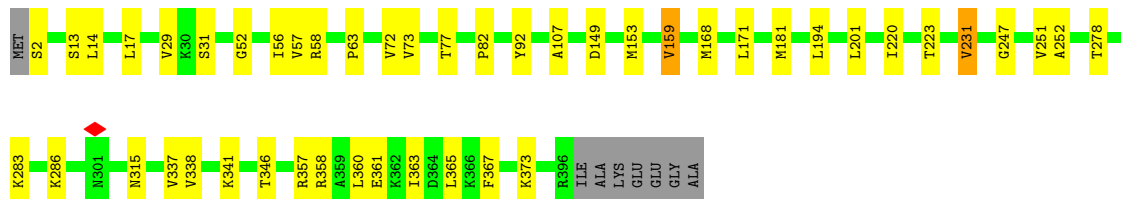
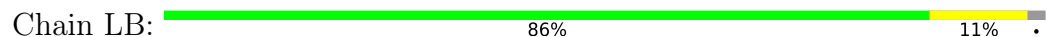
- Molecule 7: RNA (156-MER)



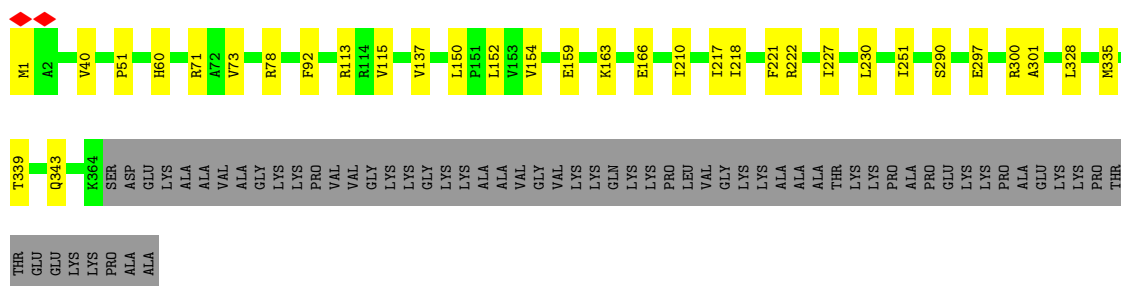
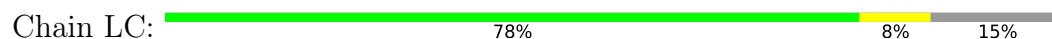
- Molecule 8: 60S ribosomal protein L8



- Molecule 9: 60S ribosomal protein L3



- Molecule 10: 60S ribosomal protein L4



- Molecule 11: 60S ribosomal protein L5

A294	ALA	GLU	SER	MET	G2	K41	K48	I60	I61	G62	A80	H91	E82	L83	P84	K89	T93	Y99	L105	I118	V125	T126	Y145	L146	L163	K164	L211	Y219	F223	Y226	M236	M239	I247	K256	V261	M271	D278	Q282
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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|
| L271 | K100 | T278 | K108 | K111 | R114 | E119 | R123 | K124 | L125 | H128 | T145 | P146 | G147 | T148 | I149 | F164 | L165 | V175 | T176 | R183 | V184 | H190 | F193 | I203 | K221 | L271 | A176 | SER | LYS | VAL | GLU | ILE | PHE | ASP | THR | GLU | K237 | D254 | I257 | MET | | | | |
| ALA | GLY | GLU | LYS | VAL | GLU | PRO | ASP | THR | LYS | GLU | LYS | LYS | LYS | LYS | LYS | LYS | LYS | LYS | LYS | LYS | ASN | LEU | ALA | LYS | LYS | PRO | LYS | LYS | GLY | K41 | V49 | A76 | SER | LYS | VAL | GLU | LYS | LYS | LYS | GLU | VAL | LEU | ALA | T51 |

- | | |
|------|--|
| K222 | |
| H226 | |
| G231 | |
| D232 | |
| A233 | |
| R236 | |
| E237 | |
| D238 | |
| Q239 | |
| I240 | |
| N241 | |
| R245 | |
| B246 | |
| M247 | |
| N248 | |

- [illegible]

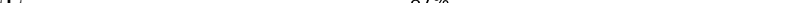
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|------|
| M1 |
| Q8 |
| T9 |
| V10 |
| D11 |
| I12 |
| K28 |
| L34 |
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| K52 |
| K53 |
| R54 |
| L55 |
| K59 |
| R71 |
| C74 |
| S75 |
| H76 |
| M80 |
| M92 |
| R93 |
| Q140 |
| E143 |
| D150 |
| I179 |
| A190 |
| ASP |
| STU |

- WORLDWIDE
PDB
PROTEIN DATA BANK

Amino Acid	Percentage (%)	Color
MET	~2	Grey
C2	~3	Green
I31	~4	Yellow
R38	~5	Yellow
A41	~6	Yellow
L48	~7	Yellow
S61	~8	Yellow
S62	~9	Yellow
R69	~10	Yellow
M76	~11	Yellow
L91	~12	Yellow
I99	~13	Yellow
L103	~14	Red
SER	~15	Yellow
CYS	~16	Yellow
ALA	~17	Yellow
GLY	~18	Yellow
ALA	~19	Yellow
ASP	~20	Yellow
M10	~21	Yellow
Q123	~22	Yellow
V126	~23	Yellow
I136	~24	Yellow
M136	~25	Yellow
S137	~26	Yellow
I138	~27	Yellow
R139	~28	Yellow
K208	~29	Yellow
V211	~30	Yellow
S214	~31	Yellow

- Chain LJ: 85% 10% 5%

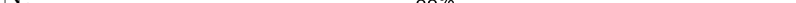
MET
ALA
GLN
ASP
ASN
GLY
GLU
LYS
N10
R35
T56
V57
R58
R63
E66
K67
I68
V74
A79
R90
R95
N98
G108
I109
Q110
I123
I141
K144
K145
R146
R147
E160
V17e

- Chain LL:  87% 9% .

MET	A2	R5	L10	K16	D17	W18	Q19	V22	I33	R36	I46	A47	A51	I58	V59	V70	S106	S109	S122	L124	K145	L146	V157	E164	D206	VAL	GUJ	LVS	LVS	LVS
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- Chain LM:  61% . 35%

[illegible]

- Chain LN:  88% 10%

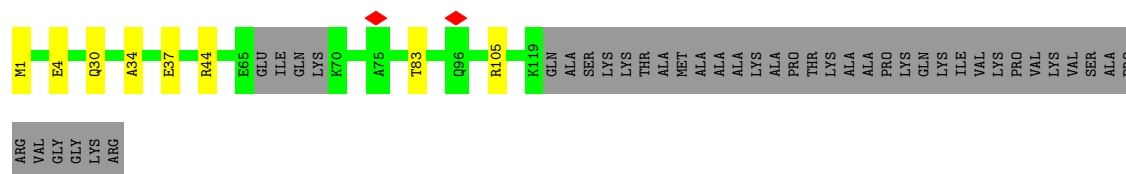
Met	G2	Q15	V18	Y53	V60	P84	H87	G88	Y89	E103	V115	W120	E123 D124	Y127	I133	F138	H139	K140	R143	P154	H178	H181	H182	T183	I184	R194	R204
-----	----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	--------------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Chain LO:  88% 10%

MET	ALA	GLU	V4	L9	L16	V34	F47	R61	P70	F80	P89	K103	G107	M118	V126	V127	K130	R133	E144	K161	E186	D190	E194	T198	V203
-----	-----	-----	----	----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Chain LP:  71% 11% 17%

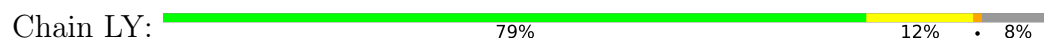
MET	V2	P8	K16	S20	N21	K27	N28	T32	Q64	C57	V68	Y63	T79	W63	M94	L95	K96	Q118	P123	H133	M140	M148	I149	E154	G1N	I1E	VAL	PRO	LVS	LVS	GUJ	GUJ	VAL	ALA	GLN	LVS	LVS	LVS	LVS	SEN	SEN
-----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



- Molecule 30: 60S ribosomal protein L23a



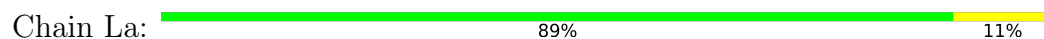
- Molecule 31: 60S ribosomal protein L26



- Molecule 32: 60S ribosomal protein L27



- Molecule 33: 60S ribosomal protein L27a

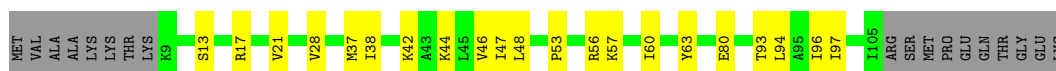


- Molecule 34: 60S ribosomal protein L29

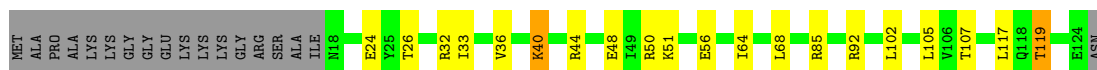


- Molecule 35: 60S ribosomal protein L30

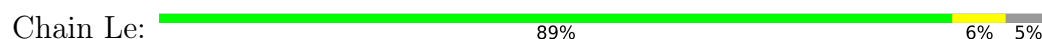




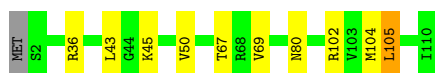
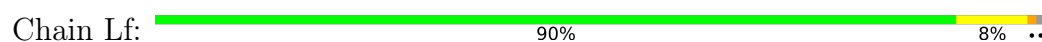
- Molecule 36: 60S ribosomal protein L31



- Molecule 37: 60S ribosomal protein L32



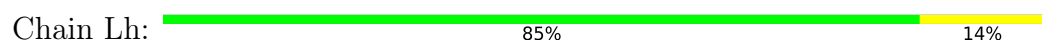
- Molecule 38: 60S ribosomal protein L35a



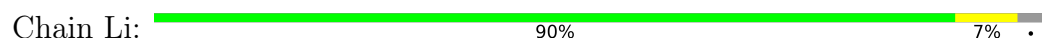
- Molecule 39: 60S ribosomal protein L34



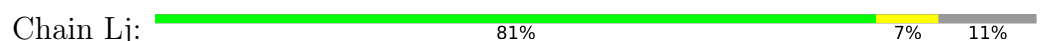
- Molecule 40: 60S ribosomal protein L35



- Molecule 41: 60S ribosomal protein L36



- Molecule 42: Large ribosomal subunit protein eL37





- Molecule 43: 60S ribosomal protein L38

Chain Lk: 83% 16%



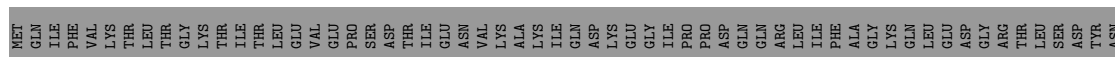
- Molecule 44: 60S ribosomal protein L39

Chain Ll: 90% 6%



- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain Lm: 38% 59%



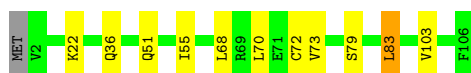
- Molecule 46: 60S ribosomal protein L41

Chain Ln: 92%



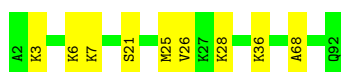
- Molecule 47: 60S ribosomal protein L36a

Chain Lo: 89% 9%



- Molecule 48: 60S ribosomal protein L37a

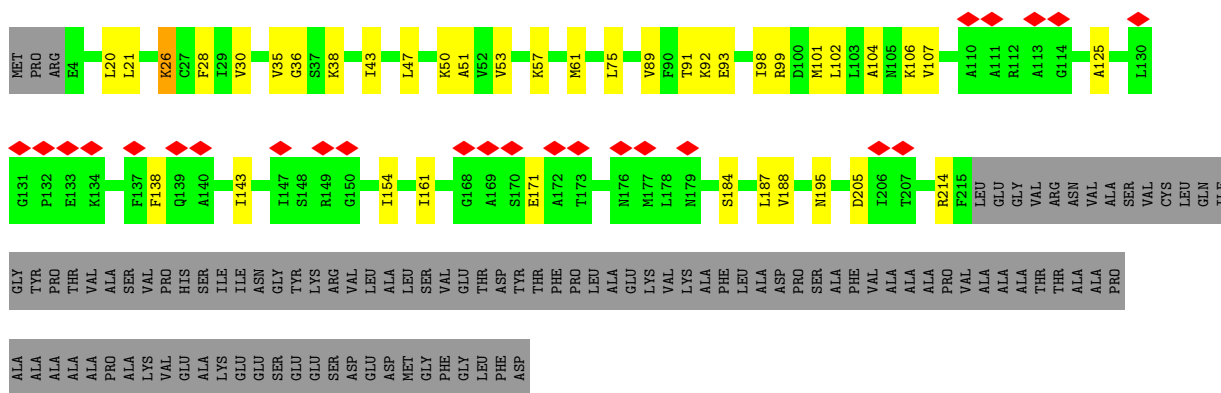
Chain Lp: 90% 10%



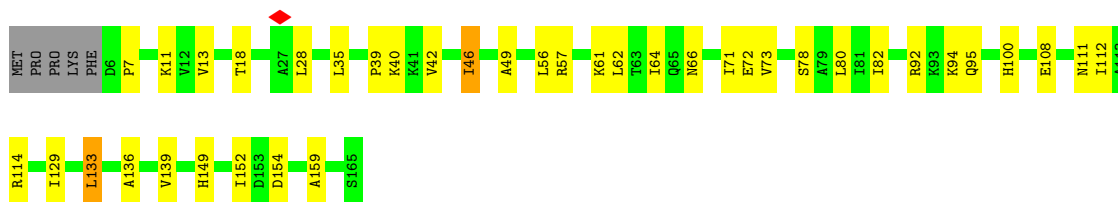
- Molecule 49: 60S ribosomal protein L28

[illegible]

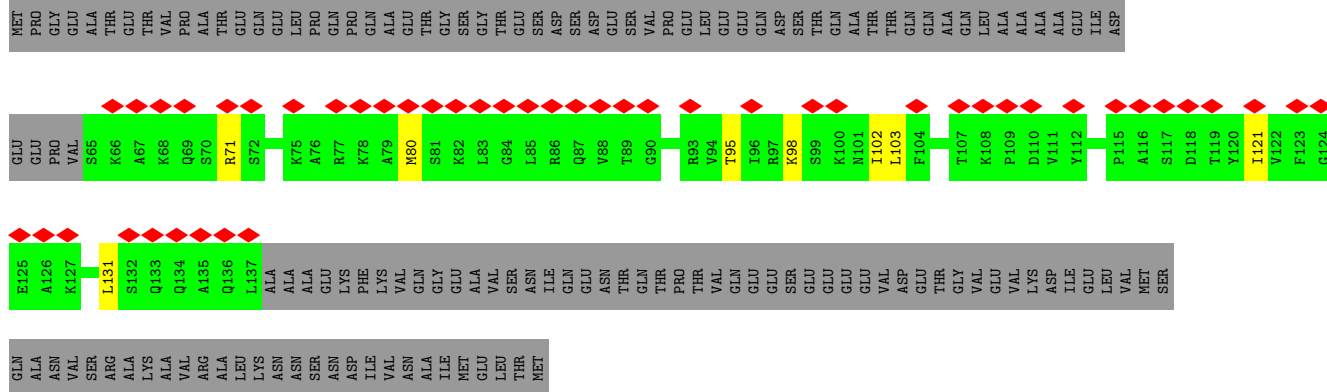
- Chain Ls: 



- Chain Lt:  73% 22% ..

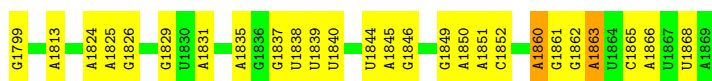


- Chain NA: 



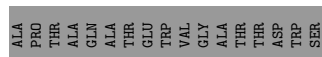
- 

C1670	C1562	A1454	U1342	A1228	A1113	A992	U893	A802	C	A669	A560	A473	C353
G1671	G1563	U1462	U1347	G1229	U1114	A996	G894	C803	C	A670	A561	G474	A360
A1675	G1567	U1463	U1348	U1232	U1115	A997	U896	U804	U	A671	U562	G482	U361
A1678	G1570	A1474	G1348	G1233	C1116		U897	G807	G	A672	C567	C483	A362
A1679	G1570	G1475	G1351	A1240	A1119	A1001	U898	A808	C745	U686	U566	U487	A363
U1692	A1579	G1476	G1356	A1241	U1120	U1002	U899	A809	C746	C687	C567	U488	A364
G1693	A1580	A1477	G1357	U1242	U1121	U1003	G900	A810	U747	U688	A575	U489	U367
U1694	A1580	A1357	G1357	U1243	G1124	U1004	G901	A811	C748	C689	A576	U490	U368
A1695	U1585	A1487	G1365	U1243	C1125	G1005	G902	A812	U749	U689	A576	C491	U369
C1705	U1586	G1488	G1366	C1252	C1126	C1006	A903	A813	C750	G591	U582	C492	G370
G1706	G1587	A1489	G1366	C1252	C1127	C1007	A904	A818	G751	G592	A583	A493	A371
A1719	A1588	A1490	G1371	A1253	C	A1008	C905		G752	A583			
U1720	A1589	G1495	U1372	G1256	G1129	G1010	G909	G821	G	C694	A587	C496	G377
U1721	G1597	U1496	U1378	G1257	A1133	A1011	C912	A830	C	G695	G588	A500	G380
G1722	G1598	A1498	A1378	A1259	G1134	U1012	A913	A837	C	G696	G589	A501	G381
G1736	U1599	U1499	G1381	A1260	C1139	U1013	A920	C834	C	G697	G590	C502	G382
G1737	G1600	U1505	C1384	A1265	U1017	U1018	A921	C835	C	C698	C592	C503	G383
G1743	U1601	A1506	C1395	A1268	U1019	A1020	A922	G836	U	G	C593	G506	U394
G1744	G1603	G1507	A1396	C1268	A1142	A1021	G825	G837	C	G	C594	G507	G385
A1745	G1604	A1508	U1397	C1271	A1143	U1022	G826	C838	C	G	C595	G508	G386
G1748	U1605	U1509	U1407	C1272	A1144	A1023	A927	C839	A	G	U596	A508	C387
C1752	G1613	U1511	A1402	C1273	U1145	A1027	G828	G841	U	G	A604	G509	U388
C1753	U1614	C1512	U1403	G1274	C1153	A1060	G829	C842	C	G	A605	A516	A389
G1754	U1615	A1405	U1406	A1275	U1154	U1061	C830	C847	U	G	G606	C517	A388
C1755	U1616	G1406	U1407	A1276	U1155	A1062	C831	U848	C	G	U607	C399	A398
U	A1620	U1408	U1408	G1281	U1156	U1069	C832	U849	U	G	C608	A525	C400
C	U1621	G1413	G1413	A1282	G1157	U1078	C833	C851	C	G	U609	A526	G409
G	U1622	A1414	A1414	C1283	G1158	C1079	G834	G852	C	G	G610	C527	
C	U1623	C1415	C1415	G1284	G1168	A1080	U940	A858	G	A	C615	A528	G413
C	U1624			G1285	U1168	C1079	U943	G859	A	G	A616	A529	A433
G	G1639	C1419	C1419	G1286	A1183	A1083	A944	G860	G	G	G617	C532	G434
C	C1644	G1420	G1420	U1297	U1184	A1084	C948	G867	U	C	A628	A536	C441
C	C1645	A1421	A1421	G1298	G1184	A1084	G949	G868	G	A	U631	C537	C442
A	A1647	G1422	G1422	U1300	A1189	C1085	G952	A869	C	C	U631	C539	A445
C	G1648	C1423	C1423	A1301	A1195	G1089	C953	A870	C	C	C639	U540	A448
G	U1649	G1428	G1428	C1302	A1204	C1090	U954	A872	C	A	A640	U541	A449
C	A1650	U1432	U1432	C1303	A1204	G1096	A955	G874	C	C	A641	U542	A450
C1772	U1653	C	C	U1304	G1207	G1097	G958	A875	G	C	A643	G545	G451
C1773	G1654	C	C	U1305	G1212	C1098	A963	G878	G	C	A648	G546	G452
A1781	G1655	C	C	U1307	C1215	G1099	A963	G879	C	C	U649	G547	A455
G1782	G1656	U1549	U1549	U1308	C1216	A1100	G970	G880	U	C	A650	C548	C456
C1783	G1657	G1436	G1436	U1309	G1217	U1101	G971	G881	C	C	U651	C549	A64
G1784	U1658	G1437	G1437	A1313	A1217	G1102	A972	U883	C	C	U652	U551	A465
U1785	A1663	A1438	A1438	U1314	C1218	G1105	A981	U888	A	C	A655	A554	G467
U1786	G1664	G1449	G1449	G1321	C1218	C1106	A982	U889	C	C	A655	A555	A468
A1791	G1665	G1450	G1450	U1326	G1221	G1107	G982	U890	C	C	C660	U556	G471
C1798	U1668	G1451	G1451	U1326	G1224	G1108	A990	G891	U	C	A668	G559	C472
		A1452	A1452	A1332		U1112	G991	U892	U801				



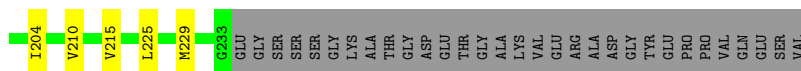
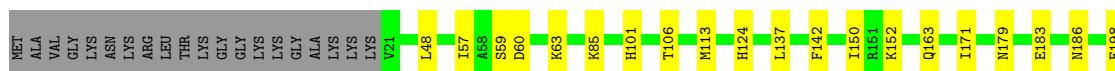
- Molecule 56: 40S ribosomal protein SA

Chain SA: 62% 12% 27%



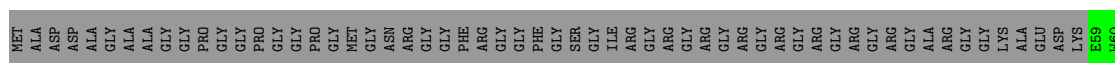
- Molecule 57: 40S ribosomal protein S3a

Chain SB: 71% 9% 19%



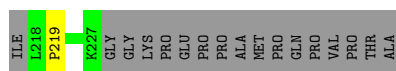
- Molecule 58: 40S ribosomal protein S2

Chain SC: 67% 6% 25%




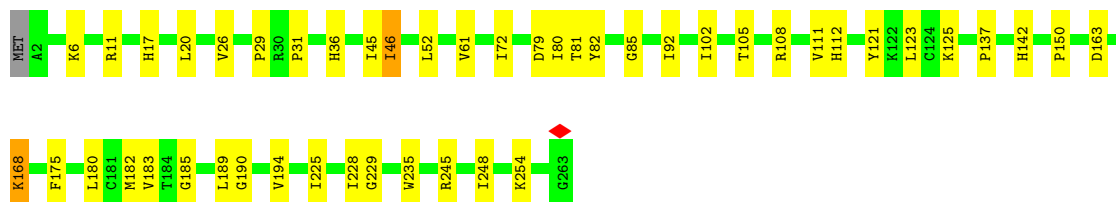
- Molecule 59: 40S ribosomal protein S3

Chain SD: 79% 12% 8%




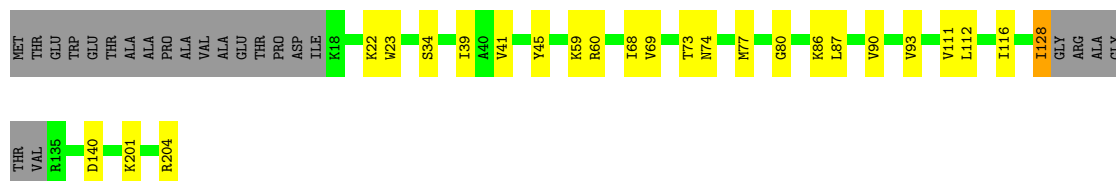
- Molecule 60: Small ribosomal subunit protein eS4, X isoform

Chain SE:  82% 17% .




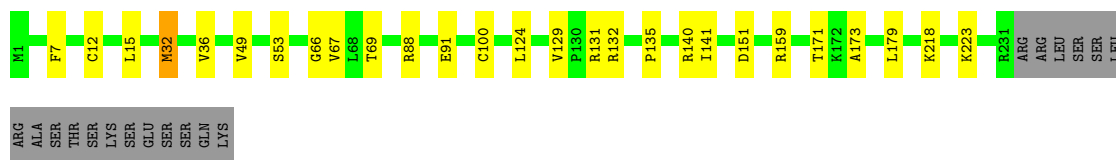
- Molecule 61: 40S ribosomal protein S5

Chain SF:  76% 12% 11%




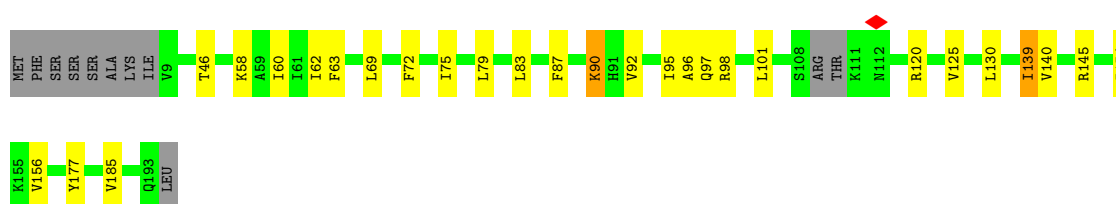
- Molecule 62: 40S ribosomal protein S6

Chain SG:  82% 10% 7%




- Molecule 63: 40S ribosomal protein S7

Chain SH:  80% 13% 6%



- Molecule 64: 40S ribosomal protein S8

Chain SI:  91% 8% .



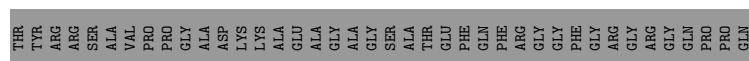
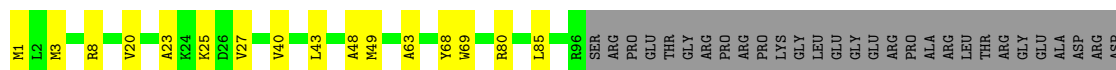
- Molecule 65: 40S ribosomal protein S9

Chain SJ:  85% 8% 8%



- Molecule 66: 40S ribosomal protein S10

Chain SK: 48% 10% 42%



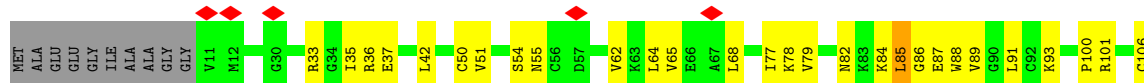
- Molecule 67: 40S ribosomal protein S11

Chain SL: 81% 10% 9%



- Molecule 68: 40S ribosomal protein S12

Chain SM: 6% 67% 24% 8%



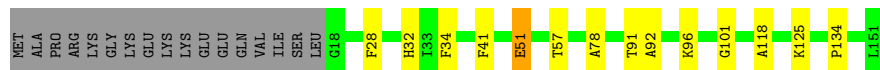
- Molecule 69: 40S ribosomal protein S13

Chain SN: 93% 7%



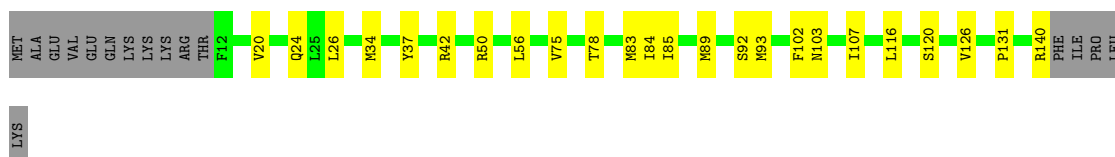
- Molecule 70: 40S ribosomal protein S14

Chain SO: 79% 9% 11%

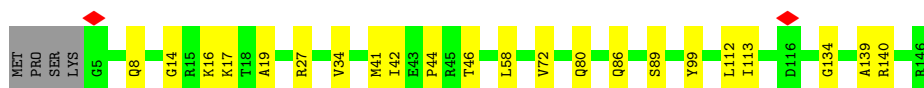
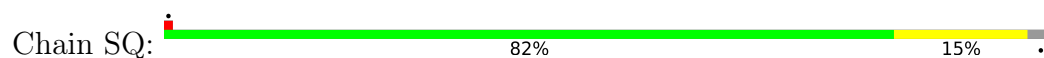


- Molecule 71: 40S ribosomal protein S15

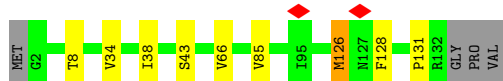
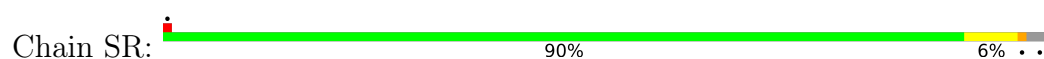
Chain SP: 72% 17% 11%



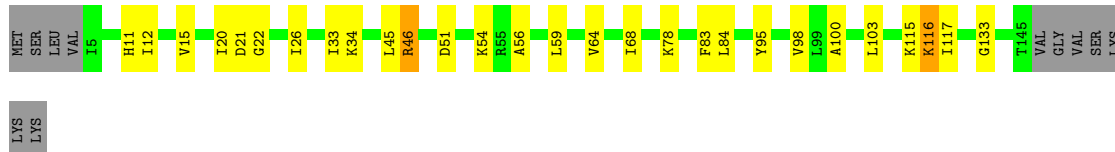
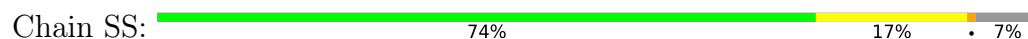
- Molecule 72: 40S ribosomal protein S16



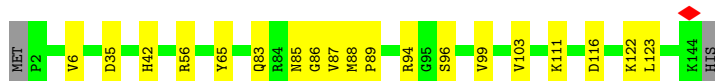
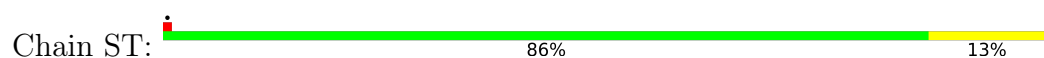
- Molecule 73: 40S ribosomal protein S17



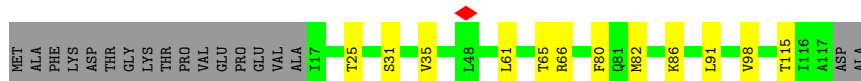
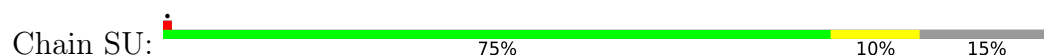
- Molecule 74: 40S ribosomal protein S18



- Molecule 75: 40S ribosomal protein S19



- Molecule 76: 40S ribosomal protein S20



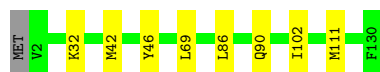
- Molecule 77: 40S ribosomal protein S21





- Molecule 78: 40S ribosomal protein S15a

Chain SW: 93% 6%



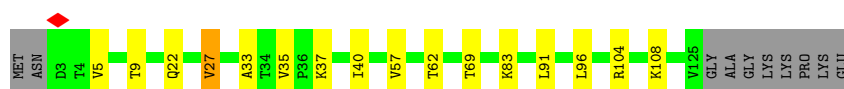
- Molecule 79: 40S ribosomal protein S23

Chain SX: 87% 10%



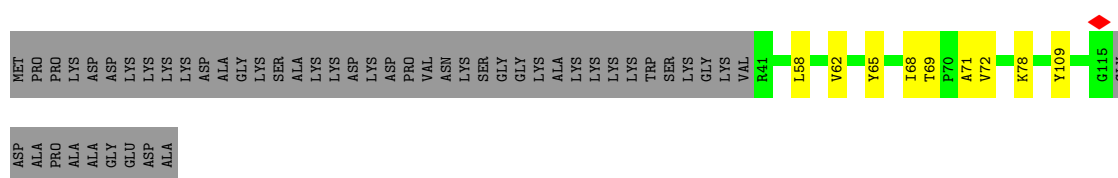
- Molecule 80: 40S ribosomal protein S24

Chain SY: 80% 11% 8%



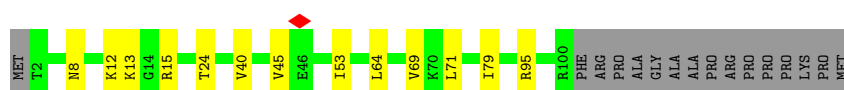
- Molecule 81: 40S ribosomal protein S25

Chain SZ: 53% 7% 40%



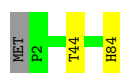
- Molecule 82: 40S ribosomal protein S26

Chain Sa: 75% 11% 14%



- Molecule 83: 40S ribosomal protein S27

Chain Sb: 96%



- Molecule 84: 40S ribosomal protein S28

Category	Count
MET	1
ASP	1
THR	1
SER	1
ARG	1
V6	1
L18	1
T28	1
V32	1
S41	1
I42	1
I43	1
V46	1
V50	1
V55	1
L56	1
T57	1
L68	1
ARG	1

-
- Diagram illustrating the structure of the C-terminal domain of the human histone H4. The structure is shown as a yellow cylinder with a grey cap. The cap is labeled with 'MET', 'GLY', and 'HIS'. The cylinder is labeled with 'Q4', 'W8', 'S25', 'L36', 'F52', and 'D56'.

- [illegible]

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ILE | GLN | LYS | GLU | SER | THR | LEU | HIS | LEU | LEU | VAL | LEU | LYS | THR | ARG | LEU | THR | ARG | GLY | GLU | ALA | GLY | LYS | GLU | VAL | ASP | LYS | THR | ASN | GLN | LYS | ALA | LYS | ILE | GLN | PHE | VAL | THR | LYS | GLN | ILE | MET |
| K89 | R95 | K96 | K97 | V98 | K107 | K113 | C121 | M132 | H135 | Y148 | M151 | PRO | GLU | ASP | LYS | THR | LEU | SER | ASP | TYR | ... | | | | | | | | | | | | | | | | | | | | |

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21642	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.803	Depositor
Minimum map value	-2.734	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.119	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G3D, LYO, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CM	0.20	0/273	0.42	0/421
2	CP	0.19	0/1789	0.44	0/2788
3	CR	0.25	0/3311	0.60	5/4452 (0.1%)
4	CZ	0.22	0/1515	0.60	0/2063
5	L5	0.20	0/87471	0.35	1/136443 (0.0%)
6	L7	0.19	0/2858	0.32	0/4455
7	L8	0.19	0/3701	0.33	0/5766
8	LA	0.23	0/1936	0.56	0/2596
9	LB	0.22	0/3251	0.51	0/4352
10	LC	0.20	0/2938	0.47	0/3947
11	LD	0.22	0/2407	0.54	0/3227
12	LE	0.24	0/1788	0.57	1/2399 (0.0%)
13	LF	0.21	0/1905	0.48	0/2539
14	LG	0.21	0/1849	0.52	2/2496 (0.1%)
15	LH	0.23	0/1529	0.54	0/2058
16	LI	0.21	0/1705	0.51	0/2277
17	LJ	0.19	0/1352	0.48	0/1813
18	LL	0.20	0/1661	0.51	0/2229
19	LM	0.20	0/1145	0.46	0/1536
20	LN	0.20	0/1746	0.42	0/2338
21	LO	0.21	0/1665	0.49	0/2229
22	LP	0.21	0/1260	0.49	0/1692
23	LQ	0.20	0/1526	0.46	0/2038
24	LR	0.20	0/1468	0.47	0/1945
25	LS	0.19	0/1492	0.45	0/2003
26	LT	0.21	0/1310	0.54	0/1752
27	LU	0.19	0/820	0.54	0/1102
28	LV	0.21	0/985	0.53	0/1323
29	LW	0.20	0/820	0.47	0/1104
30	LX	0.22	0/998	0.49	0/1341
31	LY	0.21	0/1128	0.47	0/1500
32	LZ	0.20	0/1130	0.44	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.18	0/1183	0.40	0/1582
34	Lb	0.20	0/600	0.47	0/796
35	Lc	0.20	0/752	0.49	0/1011
36	Ld	0.21	0/889	0.49	0/1198
37	Le	0.21	0/1067	0.48	0/1425
38	Lf	0.23	0/891	0.53	0/1194
39	Lg	0.20	0/899	0.48	0/1200
40	Lh	0.17	0/1014	0.41	0/1340
41	Li	0.22	0/824	0.54	0/1093
42	Lj	0.21	0/720	0.50	0/952
43	Lk	0.25	0/548	0.61	0/730
44	Ll	0.22	0/454	0.49	0/599
45	Lm	0.18	0/431	0.46	0/570
46	Ln	0.20	0/231	0.37	0/294
47	Lo	0.18	0/876	0.44	0/1156
48	Lp	0.19	0/706	0.51	0/939
49	Lr	0.23	0/1012	0.50	0/1358
50	Ls	0.24	0/1666	0.62	2/2250 (0.1%)
51	Lt	0.29	0/1224	0.80	4/1651 (0.2%)
52	NA	0.13	0/578	0.38	0/771
53	NB	0.15	0/989	0.40	0/1327
54	NM	0.28	0/3211	0.71	1/4365 (0.0%)
55	S2	0.20	0/40882	0.39	2/63715 (0.0%)
56	SA	0.23	0/1708	0.55	0/2324
57	SB	0.19	0/1745	0.49	0/2337
58	SC	0.21	0/1697	0.48	1/2301 (0.0%)
59	SD	0.21	0/1620	0.52	0/2198
60	SE	0.19	0/2014	0.51	2/2726 (0.1%)
61	SF	0.20	0/1423	0.53	0/1913
62	SG	0.27	0/1657	0.55	0/2247
63	SH	0.21	0/1295	0.47	0/1763
64	SI	0.20	0/1603	0.49	0/2161
65	SJ	0.18	0/1456	0.48	0/1957
66	SK	0.20	0/750	0.49	0/1026
67	SL	0.19	0/1163	0.43	0/1562
68	SM	0.21	0/960	0.59	1/1286 (0.1%)
69	SN	0.21	0/1206	0.49	1/1626 (0.1%)
70	SO	0.22	0/982	0.58	0/1320
71	SP	0.18	0/1010	0.48	0/1362
72	SQ	0.21	0/1093	0.61	0/1470
73	SR	0.21	0/955	0.56	0/1294
74	SS	0.24	0/1148	0.62	0/1542
75	ST	0.19	0/1100	0.44	0/1479

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SU	0.17	0/722	0.45	0/983
77	SV	0.18	0/625	0.42	0/837
78	SW	0.20	0/1043	0.43	0/1396
79	SX	0.22	0/1096	0.56	0/1467
80	SY	0.18	0/944	0.50	0/1271
81	SZ	0.21	0/565	0.54	0/764
82	Sa	0.20	0/794	0.47	0/1065
83	Sb	0.22	0/632	0.51	0/851
84	Sc	0.21	0/474	0.61	0/638
85	Sd	0.17	0/443	0.44	0/589
86	Se	0.18	0/420	0.56	0/554
87	Sf	0.18	0/525	0.52	0/695
88	Sg	0.23	0/2235	0.65	0/3068
All	All	0.20	0/239482	0.43	23/351319 (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
4	CZ	0	1
18	LL	0	1
62	SG	0	2
74	SS	0	1
77	SV	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	S2	1145	A	O4'-C1'-N9	9.02	122.04	108.50
50	Ls	26	LYS	CB-CG-CD	5.92	124.91	111.30
54	NM	169	LEU	CA-CB-CG	5.88	136.90	116.30
14	LG	164	ILE	CA-C-N	5.82	130.84	122.23
14	LG	164	ILE	C-N-CA	5.82	130.84	122.23

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	CZ	9	ARG	Peptide
18	LL	47	ALA	Peptide
62	SG	140	ARG	Sidechain
62	SG	32	MET	Peptide
74	SS	11	HIS	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	CM	247	0	128	1	0
2	CP	1602	0	809	3	0
3	CR	3269	0	3312	39	0
4	CZ	1491	0	1365	14	0
5	L5	78199	0	39524	259	0
6	L7	2558	0	1296	9	0
7	L8	3314	0	1683	13	0
8	LA	1898	0	1993	17	0
9	LB	3183	0	3316	30	0
10	LC	2884	0	3050	19	0
11	LD	2361	0	2378	19	0
12	LE	1754	0	1899	14	0
13	LF	1870	0	1996	15	0
14	LG	1818	0	1911	11	0
15	LH	1510	0	1579	14	0
16	LI	1666	0	1711	9	0
17	LJ	1329	0	1348	10	0
18	LL	1630	0	1715	15	0
19	LM	1122	0	1174	4	0
20	LN	1701	0	1749	13	0
21	LO	1633	0	1771	12	0
22	LP	1234	0	1254	15	0
23	LQ	1502	0	1616	14	0
24	LR	1452	0	1580	8	0
25	LS	1452	0	1490	10	0
26	LT	1282	0	1336	16	0
27	LU	806	0	826	3	0
28	LV	971	0	1024	7	0
29	LW	808	0	726	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	LX	981	0	1055	8	0
31	LY	1111	0	1194	11	0
32	LZ	1107	0	1182	9	0
33	La	1154	0	1198	10	0
34	Lb	590	0	613	9	0
35	Lc	742	0	774	9	0
36	Ld	874	0	918	12	0
37	Le	1049	0	1136	6	0
38	Lf	872	0	901	5	0
39	Lg	889	0	968	3	0
40	Lh	1006	0	1132	11	0
41	Li	813	0	887	4	0
42	Lj	705	0	737	3	0
43	Lk	542	0	590	7	0
44	Ll	444	0	483	2	0
45	Lm	425	0	462	0	0
46	Ln	230	0	276	0	0
47	Lo	862	0	929	4	0
48	Lp	696	0	744	6	0
49	Lr	997	0	1054	6	0
50	Ls	1640	0	1687	22	0
51	Lt	1208	0	1257	21	0
52	NA	573	0	620	6	0
53	NB	980	0	994	5	0
54	NM	3122	0	3103	48	0
55	S2	36562	0	18472	161	0
56	SA	1671	0	1672	16	0
57	SB	1718	0	1786	16	0
58	SC	1661	0	1710	12	0
59	SD	1594	0	1568	17	0
60	SE	1972	0	2012	24	0
61	SF	1403	0	1421	17	0
62	SG	1634	0	1568	14	0
63	SH	1274	0	1196	16	0
64	SI	1574	0	1540	11	0
65	SJ	1431	0	1497	11	0
66	SK	726	0	674	12	0
67	SL	1143	0	1177	8	0
68	SM	950	0	987	17	0
69	SN	1182	0	1249	6	0
70	SO	969	0	982	9	0
71	SP	990	0	974	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	SQ	1075	0	1110	13	0
73	SR	942	0	913	4	0
74	SS	1130	0	1167	15	0
75	ST	1081	0	1093	11	0
76	SU	713	0	692	6	0
77	SV	618	0	617	2	0
78	SW	1026	0	1072	6	0
79	SX	1078	0	1130	8	0
80	SY	927	0	914	10	0
81	SZ	559	0	594	6	0
82	Sa	781	0	831	9	0
83	Sb	618	0	604	1	0
84	Sc	472	0	484	4	0
85	Sd	433	0	415	3	0
86	Se	416	0	439	4	0
87	Sf	515	0	521	5	0
88	Sg	2180	0	1968	23	0
89	CM	1	0	0	0	0
89	L5	126	0	0	0	0
89	L7	3	0	0	0	0
89	L8	3	0	0	0	0
89	LA	1	0	0	0	0
89	LC	1	0	0	0	0
89	LI	1	0	0	0	0
89	LN	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	S2	51	0	0	0	0
89	ST	1	0	0	0	0
90	CZ	32	0	10	0	0
91	Lg	1	0	0	0	0
91	Lj	1	0	0	0	0
91	Lm	1	0	0	0	0
91	Lo	1	0	0	0	0
91	Lp	1	0	0	0	0
91	Sa	1	0	0	0	0
91	Sd	1	0	0	0	0
91	Sf	1	0	0	0	0
92	L5	3	0	0	0	0
92	L7	1	0	0	0	0
92	LI	1	0	0	0	0
92	LN	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	La	1	0	0	0	0
92	Lp	1	0	0	0	0
92	S2	3	0	0	0	0
All	All	223418	0	165512	1205	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 3.

The worst 5 of 1205 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)
55:S2:1748:G:H1	55:S2:1786:U:H3	1.21	0.85
55:S2:529:A:H61	55:S2:556:U:H3	1.29	0.79
54:NM:182:GLU:HB3	54:NM:189:ARG:HH21	1.48	0.79
5:L5:1443:A:N6	5:L5:2103:G:C6	2.51	0.77
54:NM:278:GLN:HG3	54:NM:480:ASN:HB3	1.68	0.76

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	CR	411/437 (94%)	397 (97%)	14 (3%)	0	100	100
4	CZ	200/217 (92%)	190 (95%)	10 (5%)	0	100	100
8	LA	246/257 (96%)	230 (94%)	16 (6%)	0	100	100
9	LB	393/403 (98%)	378 (96%)	15 (4%)	0	100	100
10	LC	362/427 (85%)	336 (93%)	26 (7%)	0	100	100
11	LD	291/297 (98%)	275 (94%)	16 (6%)	0	100	100
12	LE	213/288 (74%)	194 (91%)	19 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
14	LG	225/266 (85%)	210 (93%)	15 (7%)	0	100	100
15	LH	188/192 (98%)	179 (95%)	9 (5%)	0	100	100
16	LI	203/214 (95%)	191 (94%)	12 (6%)	0	100	100
17	LJ	167/178 (94%)	162 (97%)	5 (3%)	0	100	100
18	LL	203/211 (96%)	192 (95%)	11 (5%)	0	100	100
19	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
20	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
21	LO	198/203 (98%)	194 (98%)	4 (2%)	0	100	100
22	LP	151/184 (82%)	142 (94%)	8 (5%)	1 (1%)	18	34
23	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
24	LR	174/196 (89%)	173 (99%)	1 (1%)	0	100	100
25	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
26	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
27	LU	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
28	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
29	LW	111/157 (71%)	103 (93%)	8 (7%)	0	100	100
30	LX	118/156 (76%)	114 (97%)	4 (3%)	0	100	100
31	LY	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
32	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
33	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
34	Lb	73/159 (46%)	69 (94%)	4 (6%)	0	100	100
35	Lc	95/115 (83%)	91 (96%)	4 (4%)	0	100	100
36	Ld	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
37	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
38	Lf	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
39	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
40	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
41	Li	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
42	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
43	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
45	Lm	50/128 (39%)	50 (100%)	0	0	100	100
46	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
48	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
49	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
50	Ls	210/317 (66%)	204 (97%)	6 (3%)	0	100	100
51	Lt	158/165 (96%)	154 (98%)	4 (2%)	0	100	100
52	NA	71/215 (33%)	70 (99%)	1 (1%)	0	100	100
53	NB	123/162 (76%)	123 (100%)	0	0	100	100
54	NM	381/496 (77%)	365 (96%)	16 (4%)	0	100	100
56	SA	214/295 (72%)	201 (94%)	11 (5%)	2 (1%)	14	28
57	SB	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
58	SC	217/293 (74%)	208 (96%)	9 (4%)	0	100	100
59	SD	219/243 (90%)	209 (95%)	10 (5%)	0	100	100
60	SE	260/263 (99%)	254 (98%)	6 (2%)	0	100	100
61	SF	177/204 (87%)	170 (96%)	6 (3%)	1 (1%)	21	38
62	SG	229/249 (92%)	211 (92%)	18 (8%)	0	100	100
63	SH	179/194 (92%)	170 (95%)	9 (5%)	0	100	100
64	SI	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
65	SJ	177/194 (91%)	173 (98%)	4 (2%)	0	100	100
66	SK	94/165 (57%)	88 (94%)	6 (6%)	0	100	100
67	SL	140/158 (89%)	130 (93%)	10 (7%)	0	100	100
68	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
69	SN	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
70	SO	132/151 (87%)	118 (89%)	14 (11%)	0	100	100
71	SP	127/145 (88%)	117 (92%)	10 (8%)	0	100	100
72	SQ	140/146 (96%)	129 (92%)	11 (8%)	0	100	100
73	SR	129/135 (96%)	118 (92%)	11 (8%)	0	100	100
74	SS	139/152 (91%)	120 (86%)	19 (14%)	0	100	100
75	ST	141/145 (97%)	135 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	SU	99/119 (83%)	92 (93%)	7 (7%)	0	100	100
77	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
78	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
79	SX	139/143 (97%)	127 (91%)	12 (9%)	0	100	100
80	SY	121/133 (91%)	115 (95%)	6 (5%)	0	100	100
81	SZ	73/125 (58%)	69 (94%)	4 (6%)	0	100	100
82	Sa	97/115 (84%)	90 (93%)	7 (7%)	0	100	100
83	Sb	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
84	Sc	61/69 (88%)	54 (88%)	7 (12%)	0	100	100
85	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
86	Se	53/133 (40%)	52 (98%)	1 (2%)	0	100	100
87	Sf	61/156 (39%)	55 (90%)	6 (10%)	0	100	100
88	Sg	304/317 (96%)	275 (90%)	29 (10%)	0	100	100
All	All	12679/14770 (86%)	12037 (95%)	638 (5%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
56	SA	196	GLU
61	SF	80	GLY
22	LP	20	SER
56	SA	11	LYS

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	CR	356/375 (95%)	346 (97%)	10 (3%)	38	61
4	CZ	139/189 (74%)	139 (100%)	0	100	100
8	LA	190/199 (96%)	181 (95%)	9 (5%)	23	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	LB	343/349 (98%)	337 (98%)	6 (2%)	53	71
10	LC	299/348 (86%)	294 (98%)	5 (2%)	53	71
11	LD	241/250 (96%)	237 (98%)	4 (2%)	53	71
12	LE	191/252 (76%)	185 (97%)	6 (3%)	35	59
13	LF	194/215 (90%)	191 (98%)	3 (2%)	57	74
14	LG	188/223 (84%)	184 (98%)	4 (2%)	47	67
15	LH	167/171 (98%)	167 (100%)	0	100	100
16	LI	174/181 (96%)	174 (100%)	0	100	100
17	LJ	136/149 (91%)	135 (99%)	1 (1%)	76	86
18	LL	164/177 (93%)	160 (98%)	4 (2%)	43	65
19	LM	114/161 (71%)	111 (97%)	3 (3%)	40	63
20	LN	171/172 (99%)	167 (98%)	4 (2%)	44	66
21	LO	170/174 (98%)	169 (99%)	1 (1%)	78	88
22	LP	132/163 (81%)	129 (98%)	3 (2%)	44	66
23	LQ	161/165 (98%)	158 (98%)	3 (2%)	50	70
24	LR	150/175 (86%)	148 (99%)	2 (1%)	61	76
25	LS	156/157 (99%)	153 (98%)	3 (2%)	50	70
26	LT	135/140 (96%)	133 (98%)	2 (2%)	57	74
27	LU	86/115 (75%)	85 (99%)	1 (1%)	63	78
28	LV	99/107 (92%)	99 (100%)	0	100	100
29	LW	61/126 (48%)	61 (100%)	0	100	100
30	LX	107/133 (80%)	106 (99%)	1 (1%)	70	82
31	LY	123/135 (91%)	121 (98%)	2 (2%)	55	73
32	LZ	117/118 (99%)	115 (98%)	2 (2%)	53	71
33	La	118/121 (98%)	116 (98%)	2 (2%)	53	71
34	Lb	59/126 (47%)	56 (95%)	3 (5%)	21	40
35	Lc	79/97 (81%)	74 (94%)	5 (6%)	16	30
36	Ld	94/110 (86%)	91 (97%)	3 (3%)	34	58
37	Le	113/121 (93%)	112 (99%)	1 (1%)	70	82
38	Lf	87/89 (98%)	85 (98%)	2 (2%)	44	66
39	Lg	93/100 (93%)	92 (99%)	1 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Lh	108/110 (98%)	106 (98%)	2 (2%)	50	70
41	Li	81/89 (91%)	78 (96%)	3 (4%)	30	54
42	Lj	73/80 (91%)	70 (96%)	3 (4%)	27	49
43	Lk	57/65 (88%)	56 (98%)	1 (2%)	51	71
44	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	47
45	Lm	47/116 (40%)	44 (94%)	3 (6%)	16	29
46	Ln	23/24 (96%)	22 (96%)	1 (4%)	26	47
47	Lo	93/94 (99%)	88 (95%)	5 (5%)	20	38
48	Lp	71/74 (96%)	69 (97%)	2 (3%)	38	61
49	Lr	107/121 (88%)	102 (95%)	5 (5%)	23	45
50	Ls	180/258 (70%)	175 (97%)	5 (3%)	38	61
51	Lt	132/137 (96%)	130 (98%)	2 (2%)	57	74
52	NA	64/183 (35%)	64 (100%)	0	100	100
53	NB	107/136 (79%)	106 (99%)	1 (1%)	70	82
54	NM	345/443 (78%)	340 (99%)	5 (1%)	59	75
56	SA	170/243 (70%)	163 (96%)	7 (4%)	27	49
57	SB	191/231 (83%)	189 (99%)	2 (1%)	68	81
58	SC	175/225 (78%)	169 (97%)	6 (3%)	32	57
59	SD	148/202 (73%)	145 (98%)	3 (2%)	48	69
60	SE	196/225 (87%)	189 (96%)	7 (4%)	31	55
61	SF	142/170 (84%)	139 (98%)	3 (2%)	47	67
62	SG	138/218 (63%)	132 (96%)	6 (4%)	26	47
63	SH	109/174 (63%)	106 (97%)	3 (3%)	38	61
64	SI	149/180 (83%)	149 (100%)	0	100	100
65	SJ	143/168 (85%)	142 (99%)	1 (1%)	76	86
66	SK	65/136 (48%)	64 (98%)	1 (2%)	57	74
67	SL	121/142 (85%)	118 (98%)	3 (2%)	42	64
68	SM	104/108 (96%)	100 (96%)	4 (4%)	29	52
69	SN	123/131 (94%)	122 (99%)	1 (1%)	73	84
70	SO	95/119 (80%)	94 (99%)	1 (1%)	65	79
71	SP	98/130 (75%)	96 (98%)	2 (2%)	48	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SQ	103/121 (85%)	101 (98%)	2 (2%)	50	70
73	SR	84/122 (69%)	79 (94%)	5 (6%)	17	32
74	SS	112/132 (85%)	107 (96%)	5 (4%)	24	46
75	ST	105/115 (91%)	103 (98%)	2 (2%)	50	70
76	SU	68/107 (64%)	64 (94%)	4 (6%)	18	33
77	SV	62/67 (92%)	59 (95%)	3 (5%)	23	44
78	SW	110/113 (97%)	110 (100%)	0	100	100
79	SX	109/115 (95%)	104 (95%)	5 (5%)	24	45
80	SY	86/115 (75%)	83 (96%)	3 (4%)	32	56
81	SZ	56/103 (54%)	56 (100%)	0	100	100
82	Sa	83/98 (85%)	82 (99%)	1 (1%)	63	78
83	Sb	65/76 (86%)	64 (98%)	1 (2%)	57	74
84	Sc	51/62 (82%)	47 (92%)	4 (8%)	11	21
85	Sd	44/49 (90%)	43 (98%)	1 (2%)	44	66
86	Se	39/104 (38%)	37 (95%)	2 (5%)	21	40
87	Sf	56/140 (40%)	53 (95%)	3 (5%)	20	38
88	Sg	201/275 (73%)	193 (96%)	8 (4%)	28	50
All	All	10343/12577 (82%)	10108 (98%)	235 (2%)	44	66

5 of 235 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	Lo	103	VAL
85	Sd	25	SER
57	SB	106	THR
84	Sc	50	VAL
75	ST	87	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
47	Lo	102	GLN
85	Sd	26	ASN
54	NM	317	ASN
84	Sc	7	GLN

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Mol	Chain	Res	Type
70	SO	32	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CM	11/952 (1%)	2 (18%)	0
2	CP	74/75 (98%)	21 (28%)	2 (2%)
5	L5	3633/5070 (71%)	772 (21%)	14 (0%)
55	S2	1704/1869 (91%)	465 (27%)	17 (0%)
6	L7	119/121 (98%)	11 (9%)	0
7	L8	155/157 (98%)	29 (18%)	1 (0%)
All	All	5696/8244 (69%)	1300 (22%)	34 (0%)

5 of 1300 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CM	804	C
1	CM	809	U
2	CP	2	G
2	CP	4	U
2	CP	6	G

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	S2	1273	C
55	S2	1519	U
55	S2	1664	A
5	L5	3673	C
5	L5	3614	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
3	LYO	CR	63	3	7,9,10	0.80	0	7,10,12	1.05	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
3	LYO	CR	63	3	-	2/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	CR	63	LYO	N-CA-CB-CG
3	CR	63	LYO	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 200 ligands modelled in this entry, 199 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
90	G3D	CZ	301	-	33,34,34	3.26	15 (45%)	52,54,54	1.90	11 (21%)

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
90	G3D	CZ	301	-	-	2/21/37/37	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	CZ	301	G3D	C3'-C4'	-8.34	1.31	1.52
90	CZ	301	G3D	O4'-C4'	7.85	1.62	1.45
90	CZ	301	G3D	C4-N3	6.63	1.49	1.34
90	CZ	301	G3D	C2-N3	5.44	1.46	1.33
90	CZ	301	G3D	PA-O3A	5.16	1.65	1.59

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	CZ	301	G3D	C1'-N9-C8	-5.83	110.17	126.73
90	CZ	301	G3D	C5-C4-N3	-4.52	121.19	128.39
90	CZ	301	G3D	C2-N3-C4	4.31	119.73	112.30
90	CZ	301	G3D	C1'-N9-C4	4.23	139.00	126.49
90	CZ	301	G3D	N9-C8-N7	-4.10	105.80	113.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

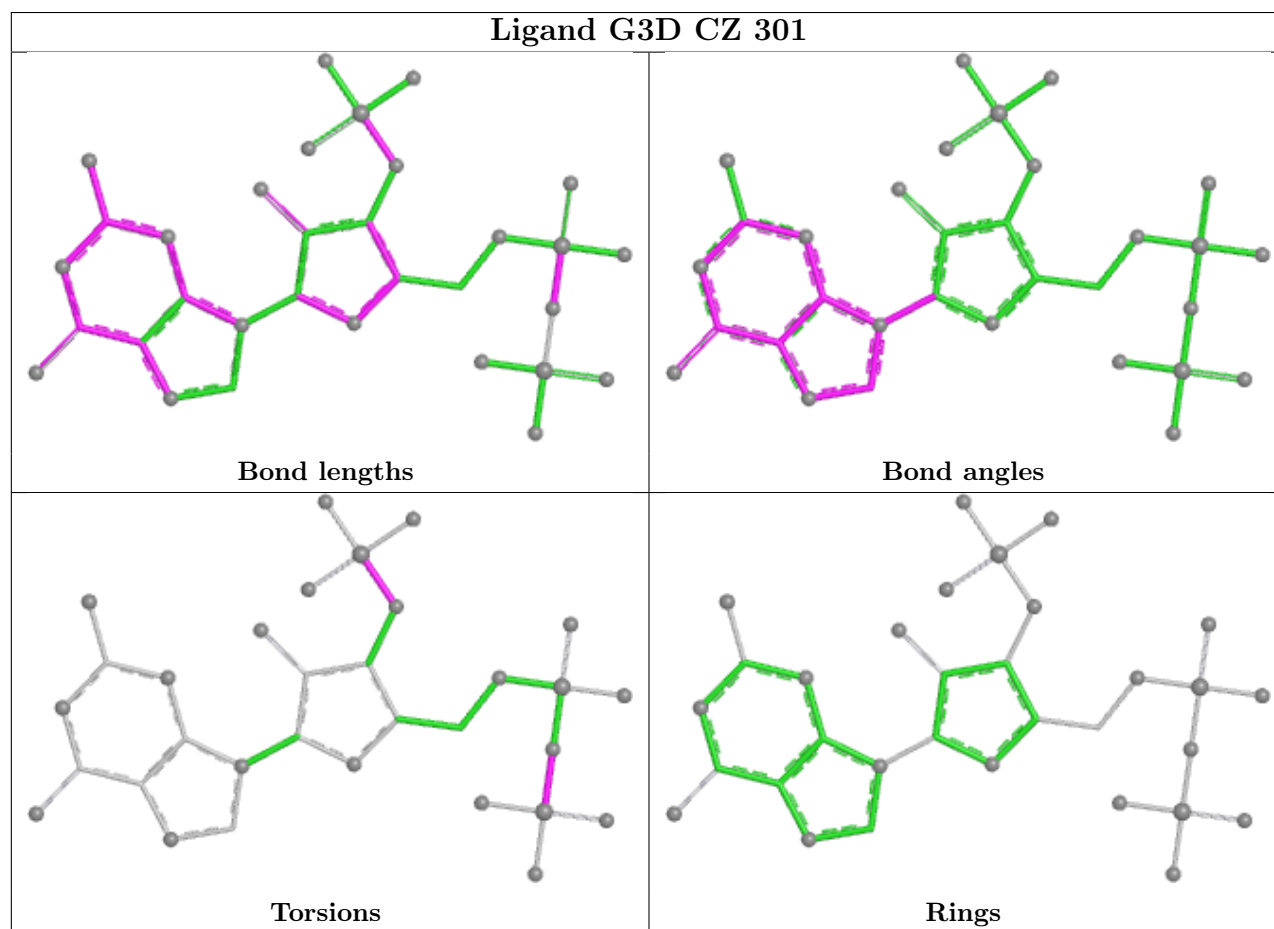
Mol	Chain	Res	Type	Atoms
90	CZ	301	G3D	PA-O3A-PB-O1B
90	CZ	301	G3D	C3'-O3'-P1-O5P

There are no ring outliers.

No monomer is involved in short contacts.

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.

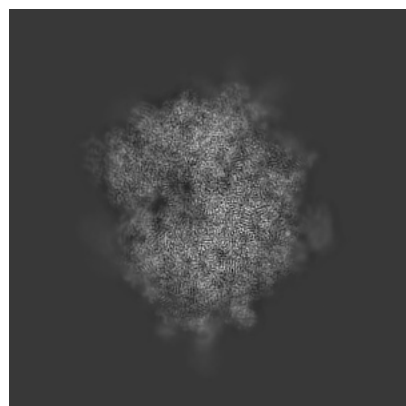
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53231. These allow visual inspection of the internal detail of the map and identification of artifacts.

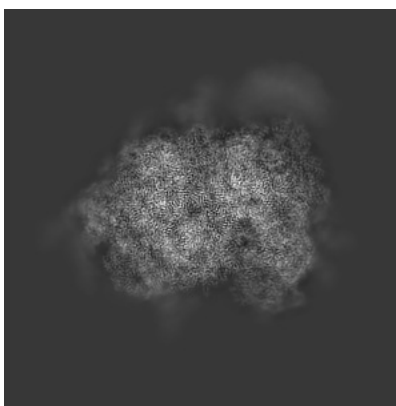
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

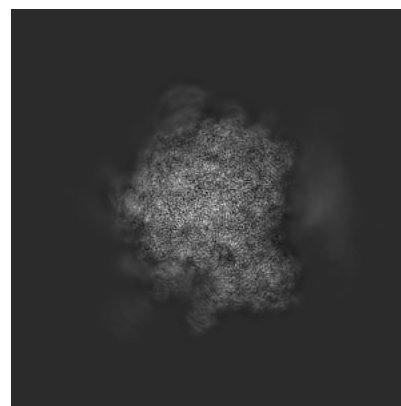
6.1.1 Primary map



X

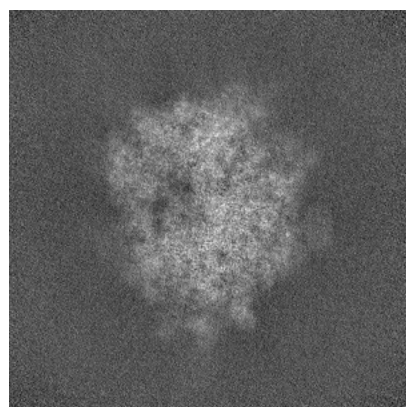


Y

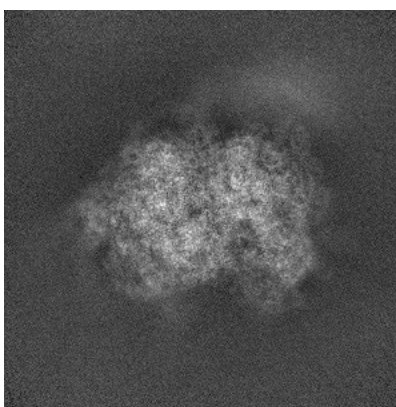


Z

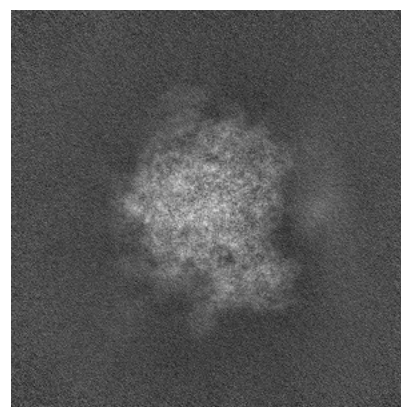
6.1.2 Raw map



X



Y

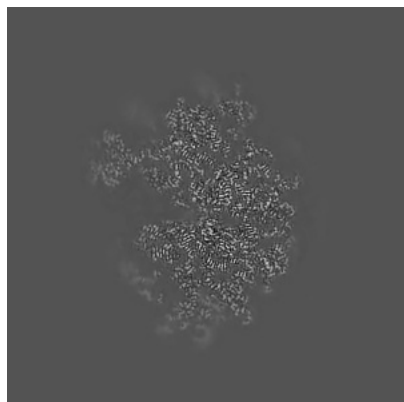


Z

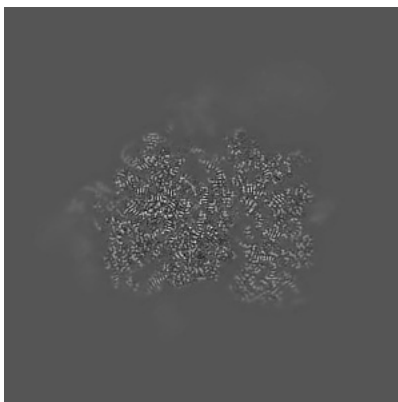
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

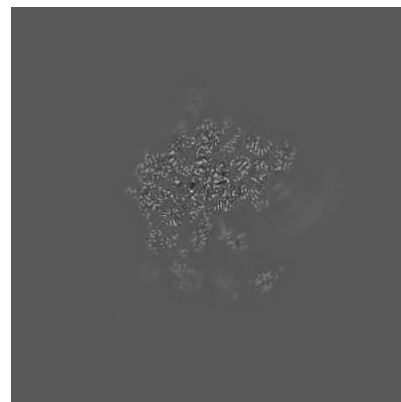
6.2.1 Primary map



X Index: 320

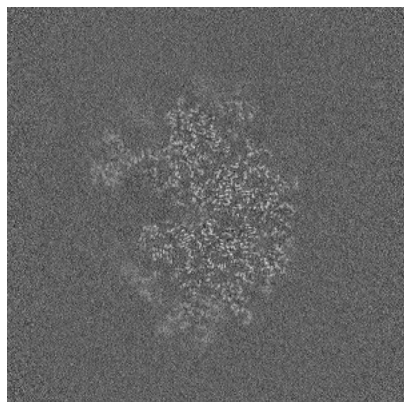


Y Index: 320

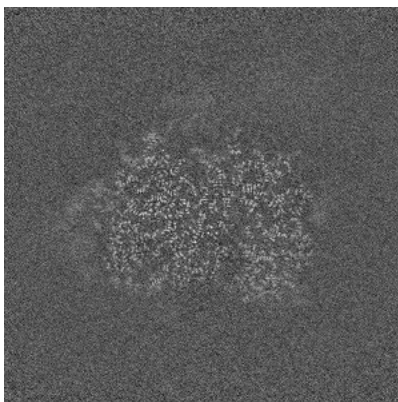


Z Index: 320

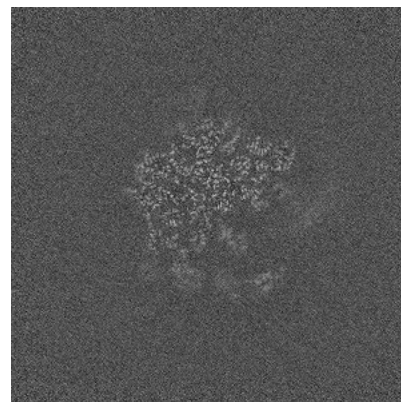
6.2.2 Raw map



X Index: 320



Y Index: 320

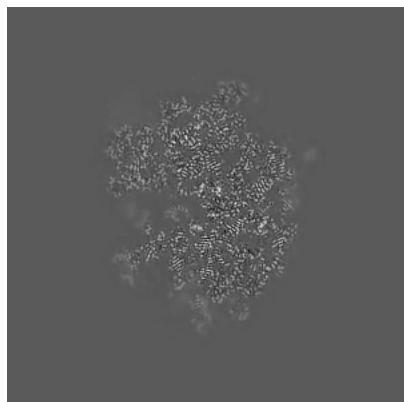


Z Index: 320

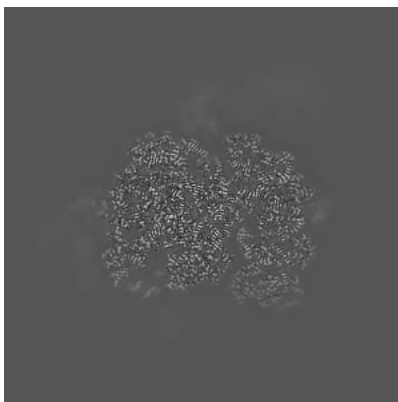
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

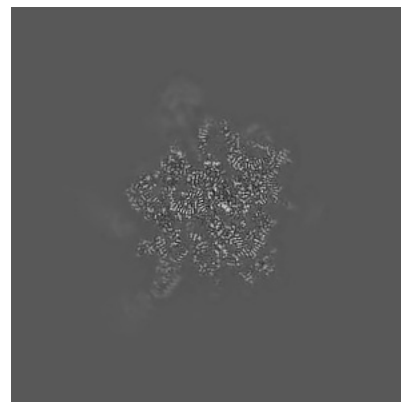
6.3.1 Primary map



X Index: 344

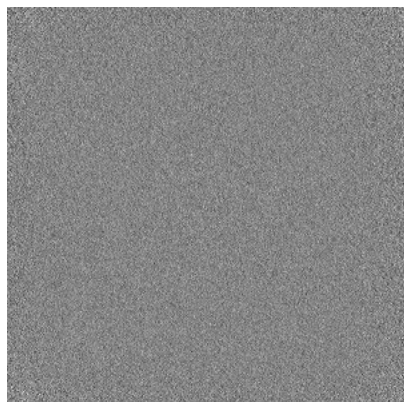


Y Index: 329

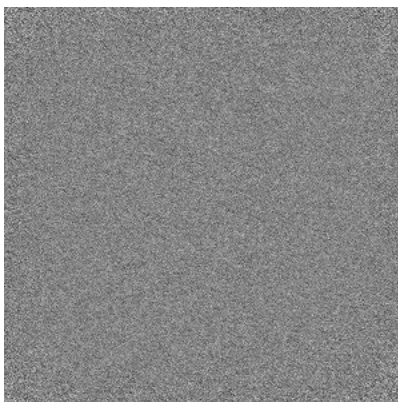


Z Index: 267

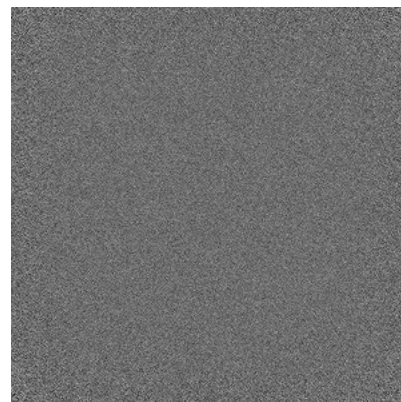
6.3.2 Raw map



X Index: 0



Y Index: 0

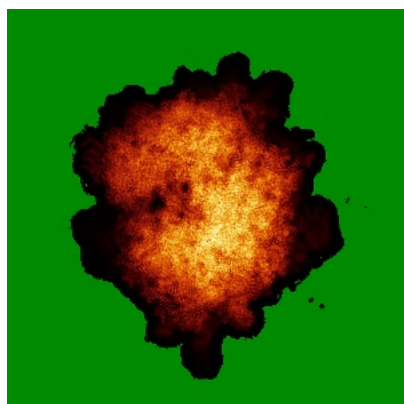


Z Index: 0

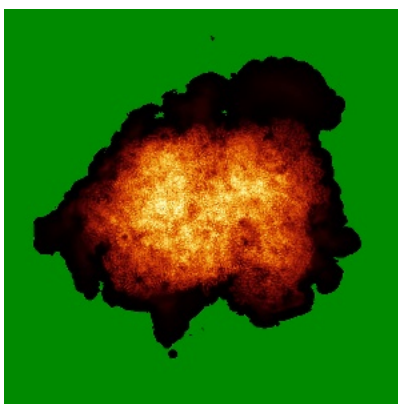
The images above show the largest variance slices of the map in three orthogonal directions.

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

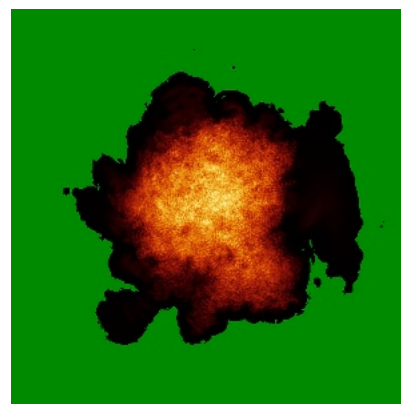
6.4.1 Primary map



X

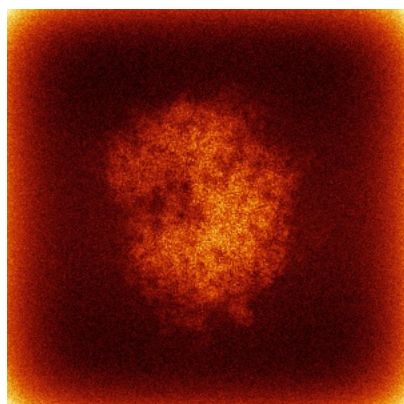


Y

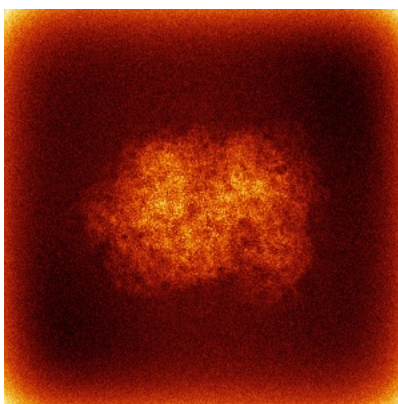


Z

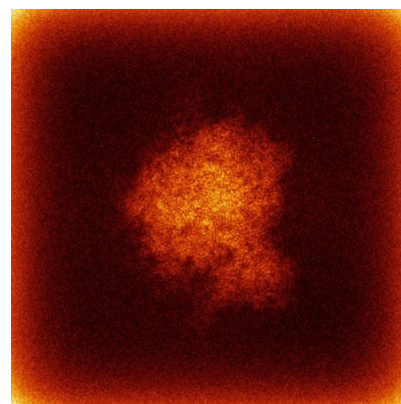
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



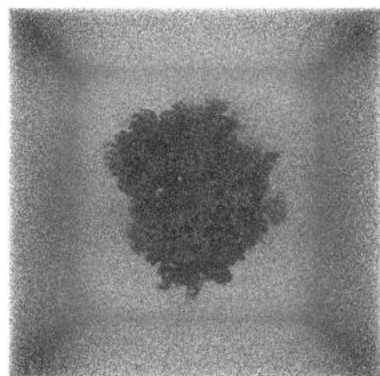
Y



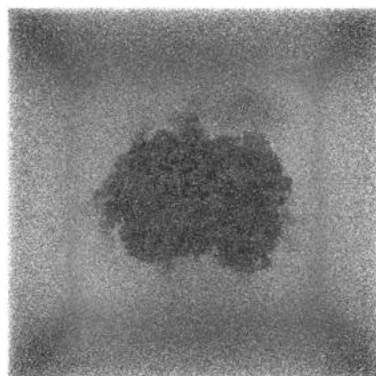
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

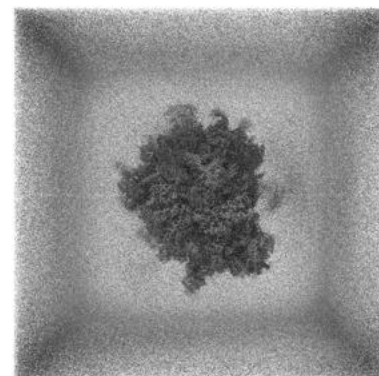
6.5.2 Raw map



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.

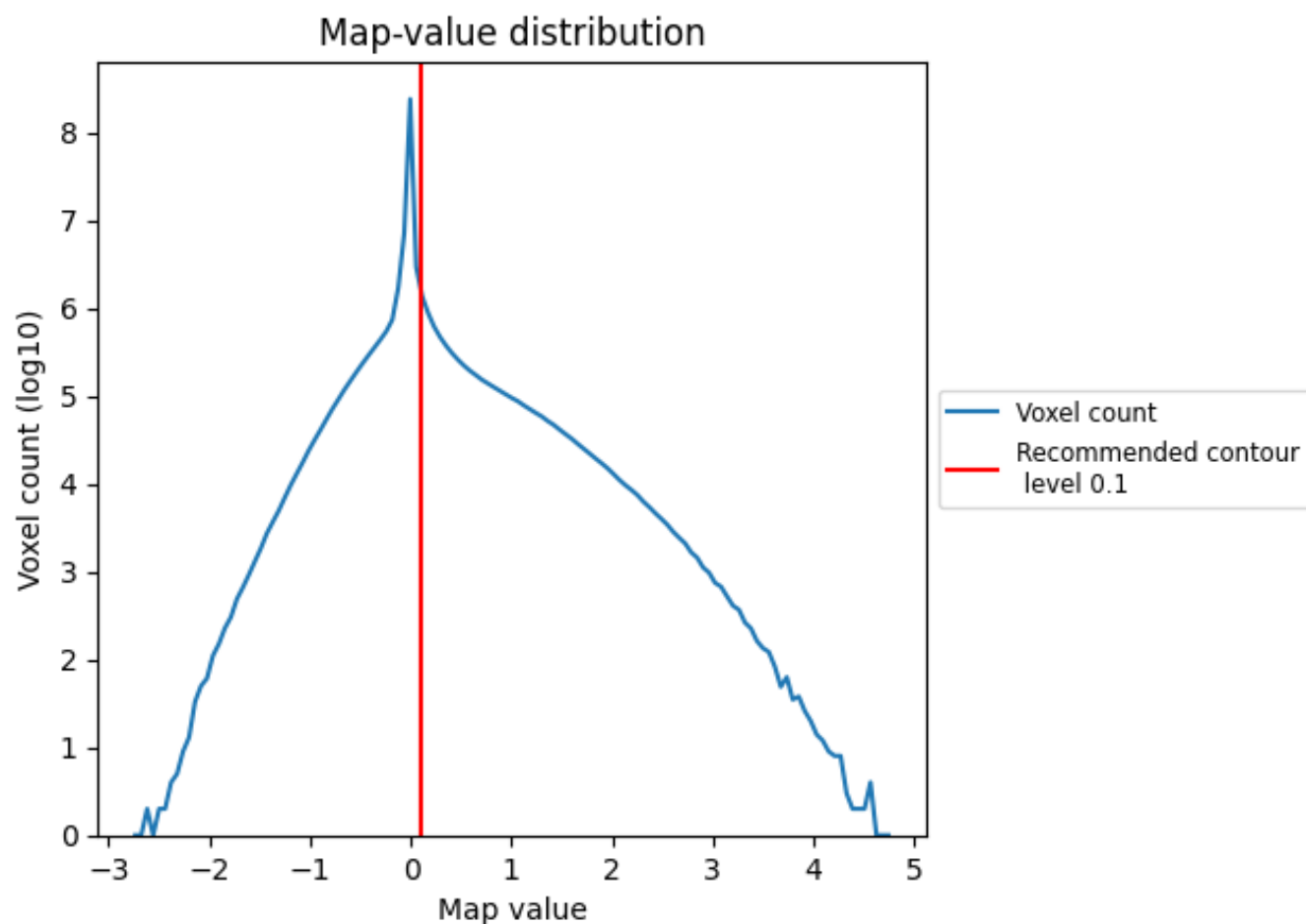
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

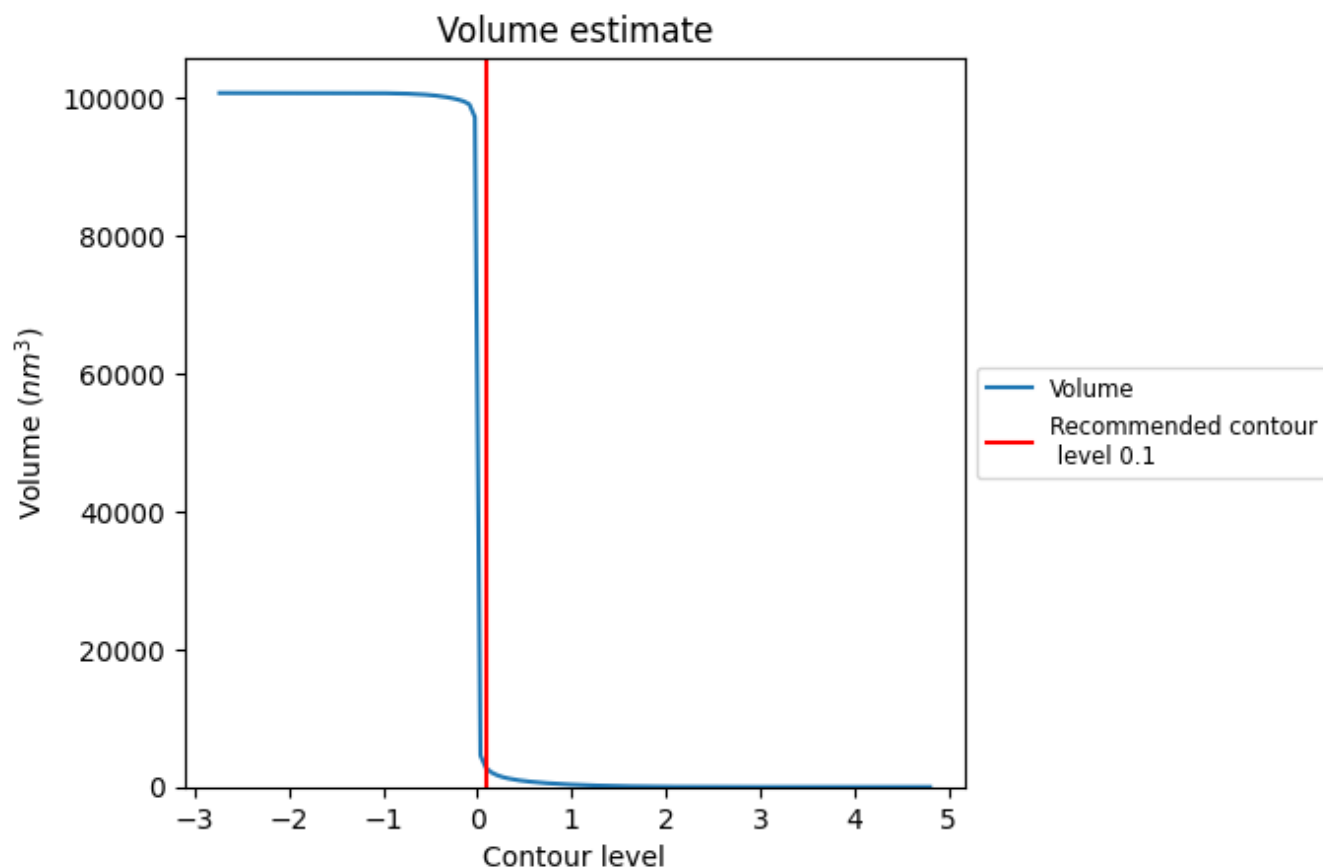
This section contains the results of statistical analysis of the map.

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.

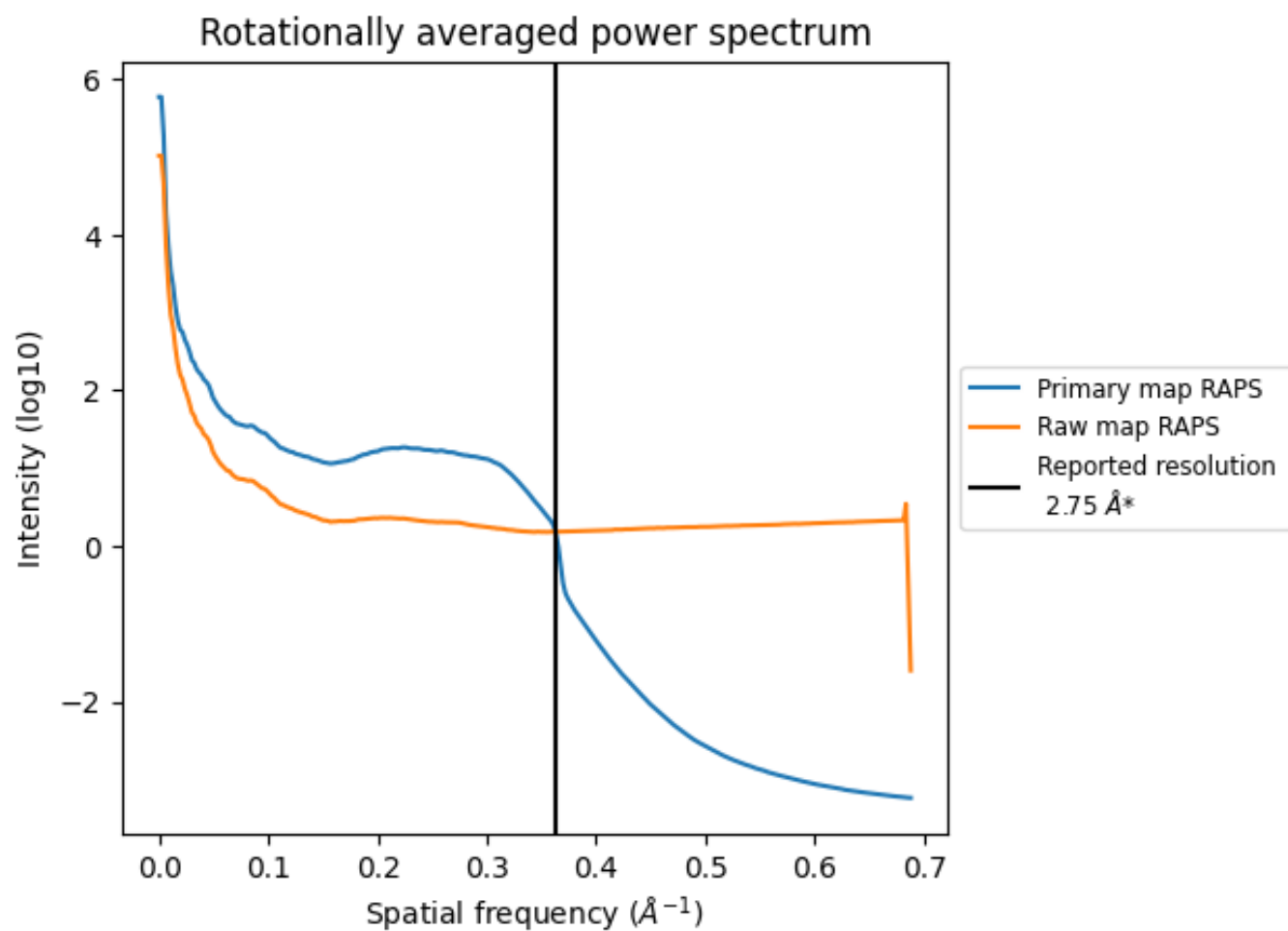
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2667 nm^3 ; this corresponds to an approximate mass of 2409 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 ⓘ

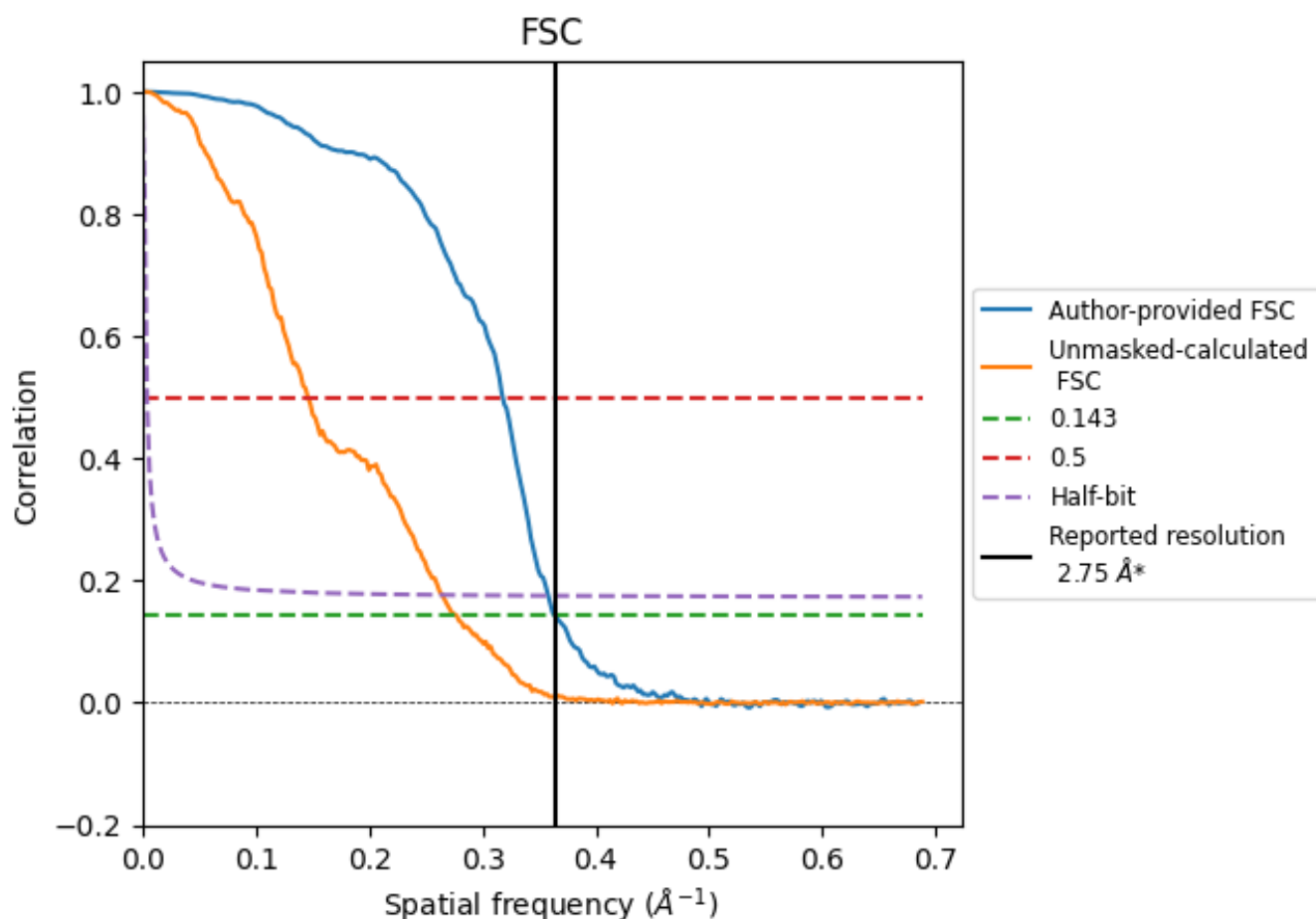


*Reported resolution corresponds to spatial frequency of 0.364 \AA^{-1}

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 0.364 \AA^{-1}

8.2 Resolution estimates [i](#)

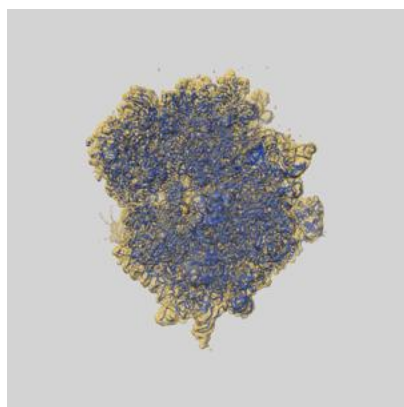
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	2.75	3.15	2.79
Unmasked-calculated*	3.61	6.84	3.78

*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 3.61 differs from the reported value 2.75 by more than 10 %

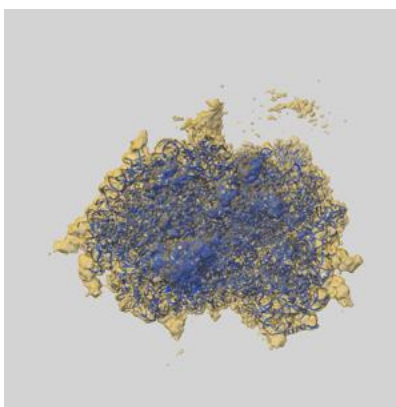
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53231 and PDB model 9QLP. Per-residue inclusion information can be found in section [3](#) on page [23](#).

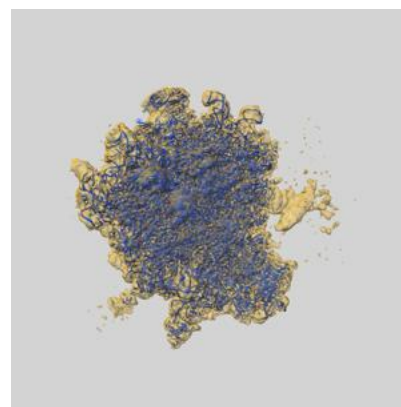
9.1 Map-model overlay [i](#)



X



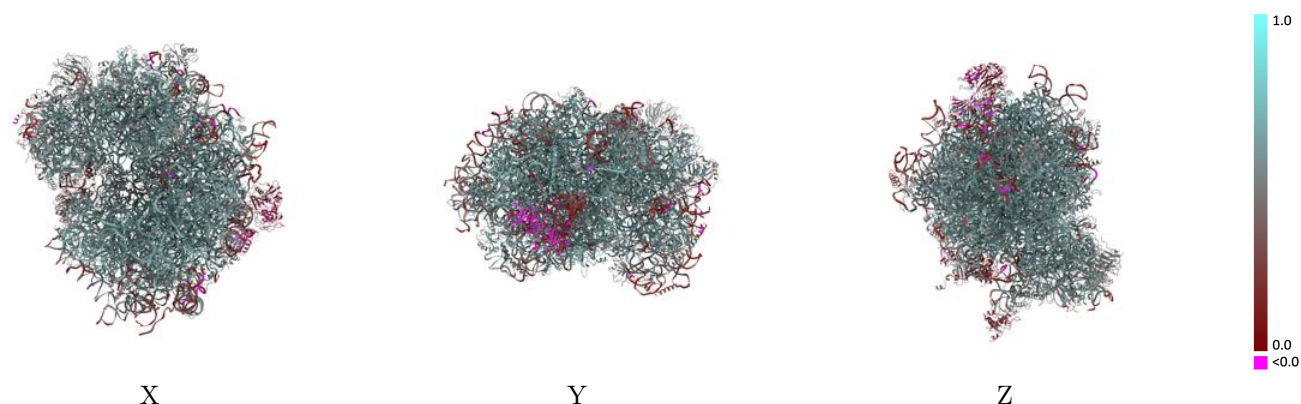
Y



Z

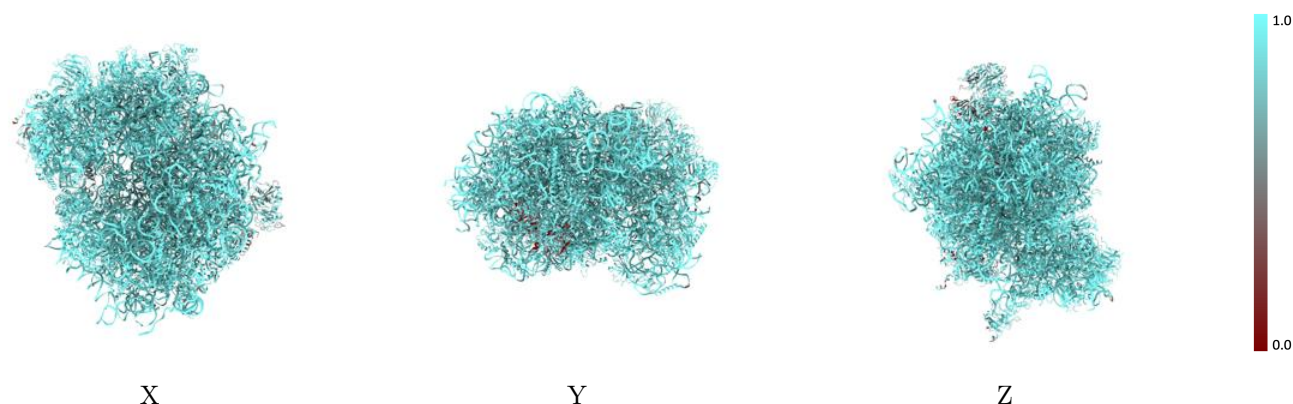
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



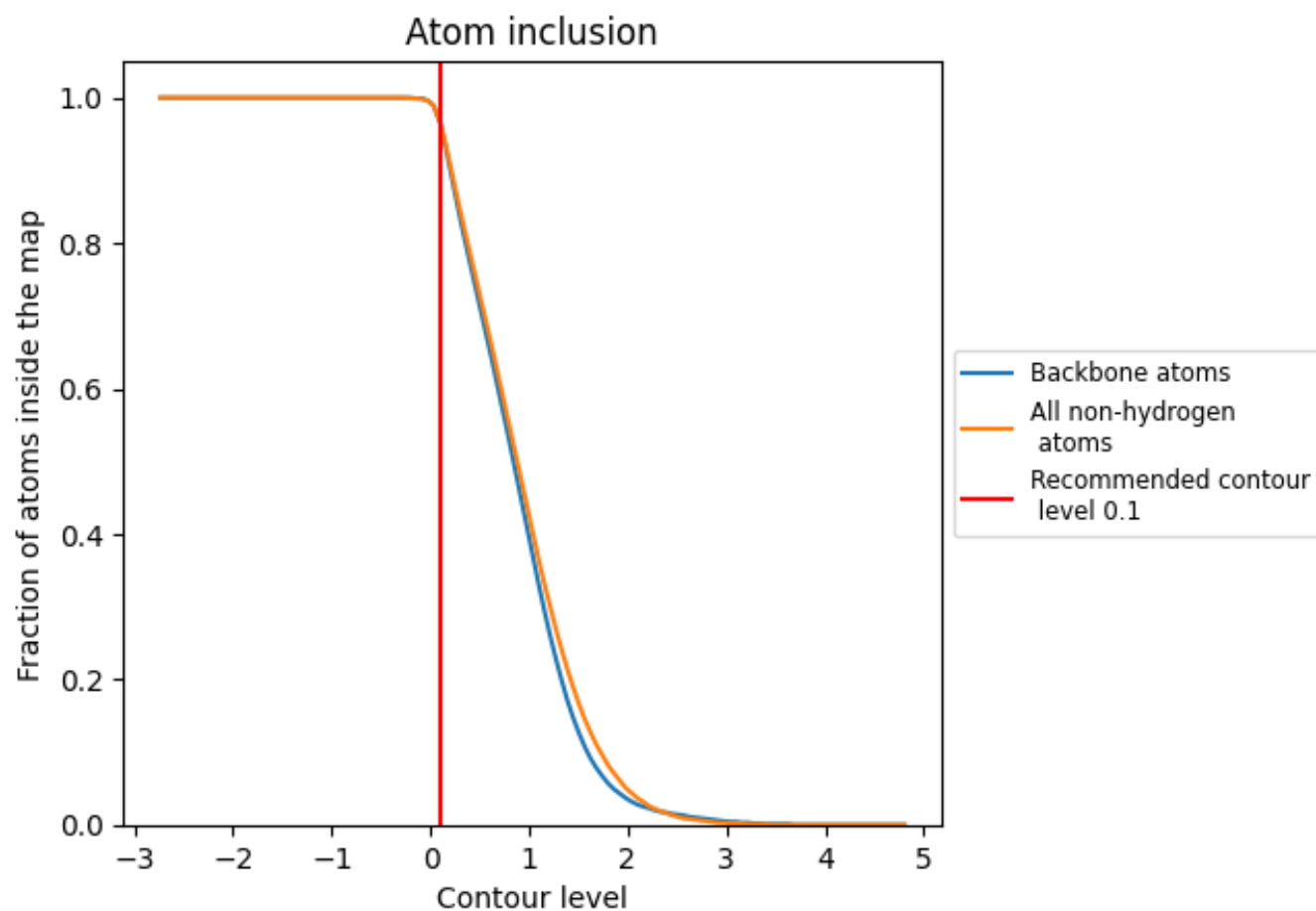
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9660	 0.5500
CM	 0.9600	 0.5400
CP	 0.9580	 0.5000
CR	 0.8870	 0.4450
CZ	 0.5950	 0.0830
L5	 0.9840	 0.5660
L7	 0.9960	 0.6220
L8	 0.9850	 0.5880
LA	 0.9900	 0.6370
LB	 0.9840	 0.6200
LC	 0.9850	 0.6150
LD	 0.9760	 0.5690
LE	 0.9770	 0.5590
LF	 0.9830	 0.6180
LG	 0.9640	 0.5550
LH	 0.9790	 0.5830
LI	 0.9710	 0.5900
LJ	 0.9660	 0.5570
LL	 0.9710	 0.5840
LM	 0.9910	 0.5920
LN	 0.9960	 0.6440
LO	 0.9850	 0.6270
LP	 0.9850	 0.6250
LQ	 0.9910	 0.6310
LR	 0.9860	 0.6050
LS	 0.9890	 0.6250
LT	 0.9680	 0.5830
LU	 0.9570	 0.4950
LV	 0.9870	 0.6230
LW	 0.9570	 0.4840
LX	 0.9650	 0.5950
LY	 0.9830	 0.5940
LZ	 0.9820	 0.5930
La	 0.9910	 0.6320
Lb	 0.9480	 0.5450



























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Chain	Atom inclusion	Q-score
Lc	 0.9810	 0.6040
Ld	 0.9830	 0.6020
Le	 0.9940	 0.6340
Lf	 0.9830	 0.6340
Lg	 0.9740	 0.6050
Lh	 0.9750	 0.5900
Li	 0.9800	 0.5790
Lj	 0.9840	 0.6290
Lk	 0.9340	 0.5230
Ll	 0.9810	 0.6110
Lm	 0.9730	 0.6000
Ln	 0.9950	 0.6330
Lo	 0.9860	 0.6150
Lp	 0.9910	 0.6330
Lr	 0.9810	 0.6050
Ls	 0.7980	 0.2570
Lt	 0.8740	 0.2670
NA	 0.3350	 0.0570
NB	 0.4800	 0.1730
NM	 0.8000	 0.1440
S2	 0.9790	 0.5500
SA	 0.9800	 0.5800
SB	 0.9660	 0.5800
SC	 0.9840	 0.5970
SD	 0.9640	 0.5370
SE	 0.9810	 0.5650
SF	 0.9560	 0.5520
SG	 0.9680	 0.4910
SH	 0.9690	 0.5130
SI	 0.9820	 0.5770
SJ	 0.9830	 0.5730
SK	 0.9610	 0.5090
SL	 0.9850	 0.6070
SM	 0.8110	 0.2230
SN	 0.9800	 0.6080
SO	 0.9760	 0.5930
SP	 0.9670	 0.5180
SQ	 0.9530	 0.5560
SR	 0.9440	 0.5150
SS	 0.9630	 0.5360
ST	 0.9670	 0.5550
SU	 0.9610	 0.4940

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Chain	Atom inclusion	Q-score
SV	 0.9820	 0.5790
SW	 0.9800	 0.6150
SX	 0.9780	 0.5940
SY	 0.9800	 0.5360
SZ	 0.9560	 0.5330
Sa	 0.9680	 0.5830
Sb	 0.9600	 0.5420
Sc	 0.9300	 0.5040
Sd	 0.9760	 0.5810
Se	 0.9630	 0.5500
Sf	 0.8150	 0.2630
Sg	 0.9520	 0.4780