



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:34 AM UTC

PDB ID : 6ZMI / pdb_00006zmi
EMDB ID : EMD-11292
Title : SARS-CoV-2 Nsp1 bound to the human LYAR-80S ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-02
Resolution : 2.60 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:

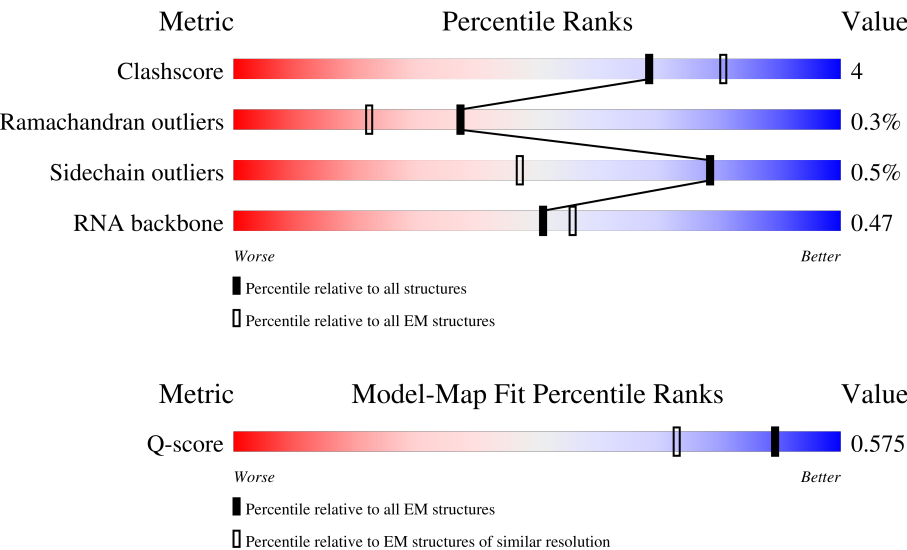
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.60 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.



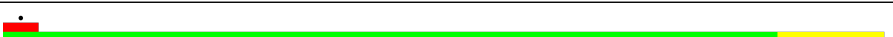
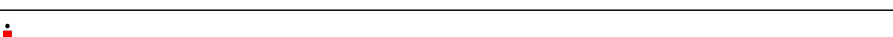
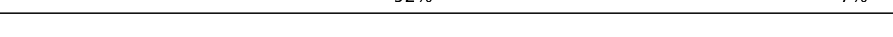
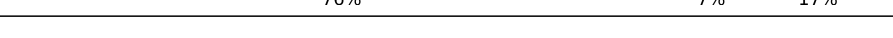
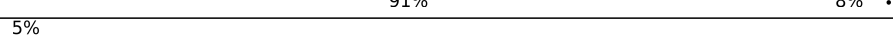
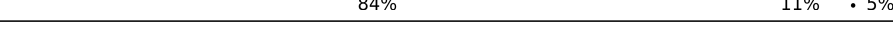
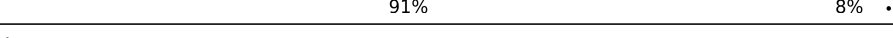
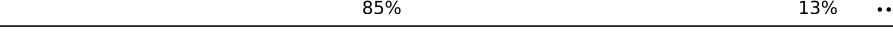
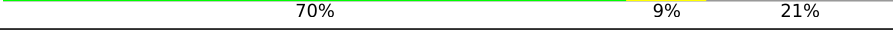
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	L5	5066	
2	L7	121	
3	L8	157	

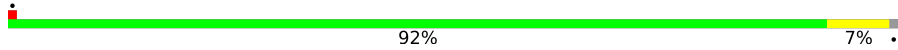
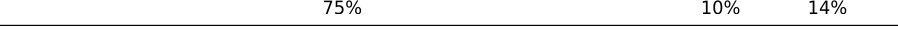
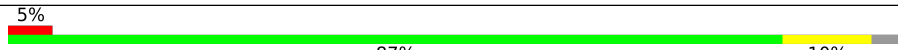
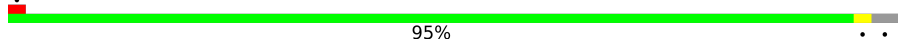
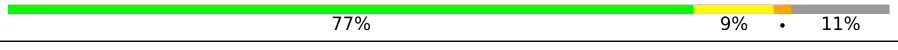
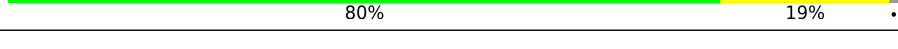
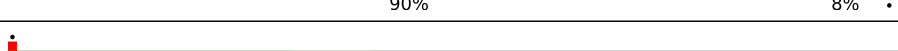
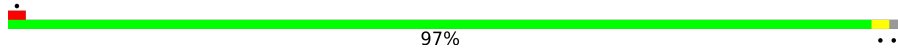
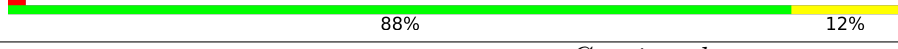
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

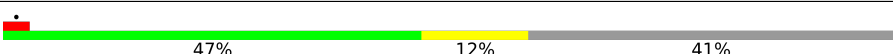
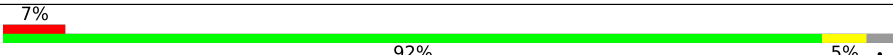
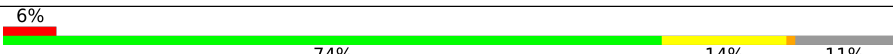
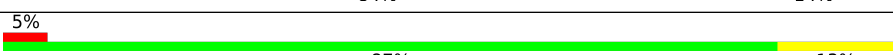
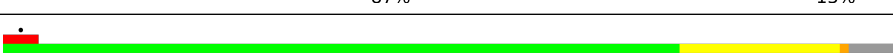
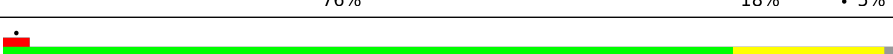
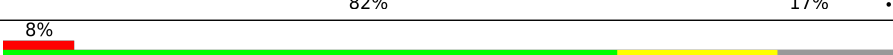
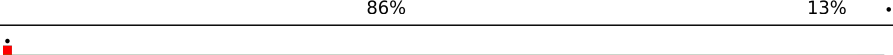
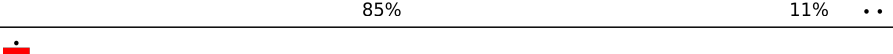
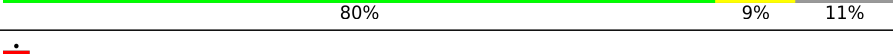
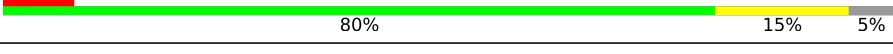
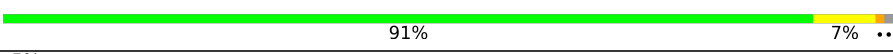
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	Lz	217	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SH	194	
56	SI	208	
57	SK	165	
58	SL	158	
59	SP	145	
60	SQ	146	
61	SR	135	
62	SS	152	
63	ST	145	
64	SU	119	
65	SV	83	
66	SX	143	
67	Sa	115	
68	Sc	69	
69	Sd	56	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	46%13%40%
80	Sb	84	85%14%
81	Se	59	15%95%
82	Sf	156	17%34%9%57%
83	CA	394	86%66%24%10%
84	CC	75	7%49%40%11%
85	CE	379	17%81%
86	i	180	18%82%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 225122 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3773	Total	C	N	O	P	0	0
			80138	35655	14589	26122	3772		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

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

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 47 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 48 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1740	Total	C	N	O	P	0	0
			36899	16459	6598	12103	1739		

- Molecule 50 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 52 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 59 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	129	Total	C	N	O	S	0	0
			1061	672	202	180	7		

- Molecule 60 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 61 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 62 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 63 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 64 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 65 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 66 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 67 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 68 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 69 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 70 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 71 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 72 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 73 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 74 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 75 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 76 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 77 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 80 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			443	271	98	73	1		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 83 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 84 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 85 is a protein called Cell growth-regulating nucleolar protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	CE	72	Total	C	N	O	0	0
			603	395	105	103		

- Molecule 86 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	i	33	Total	C	N	O	S	0	0
			263	160	47	55	1		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	L5	212	Total	Mg	0
			212	212	
87	L7	3	Total	Mg	0
			3	3	
87	L8	4	Total	Mg	0
			4	4	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lg	1	Total	Mg	0
			1	1	
87	Lj	1	Total	Mg	0
			1	1	
87	S2	30	Total	Mg	0
			30	30	

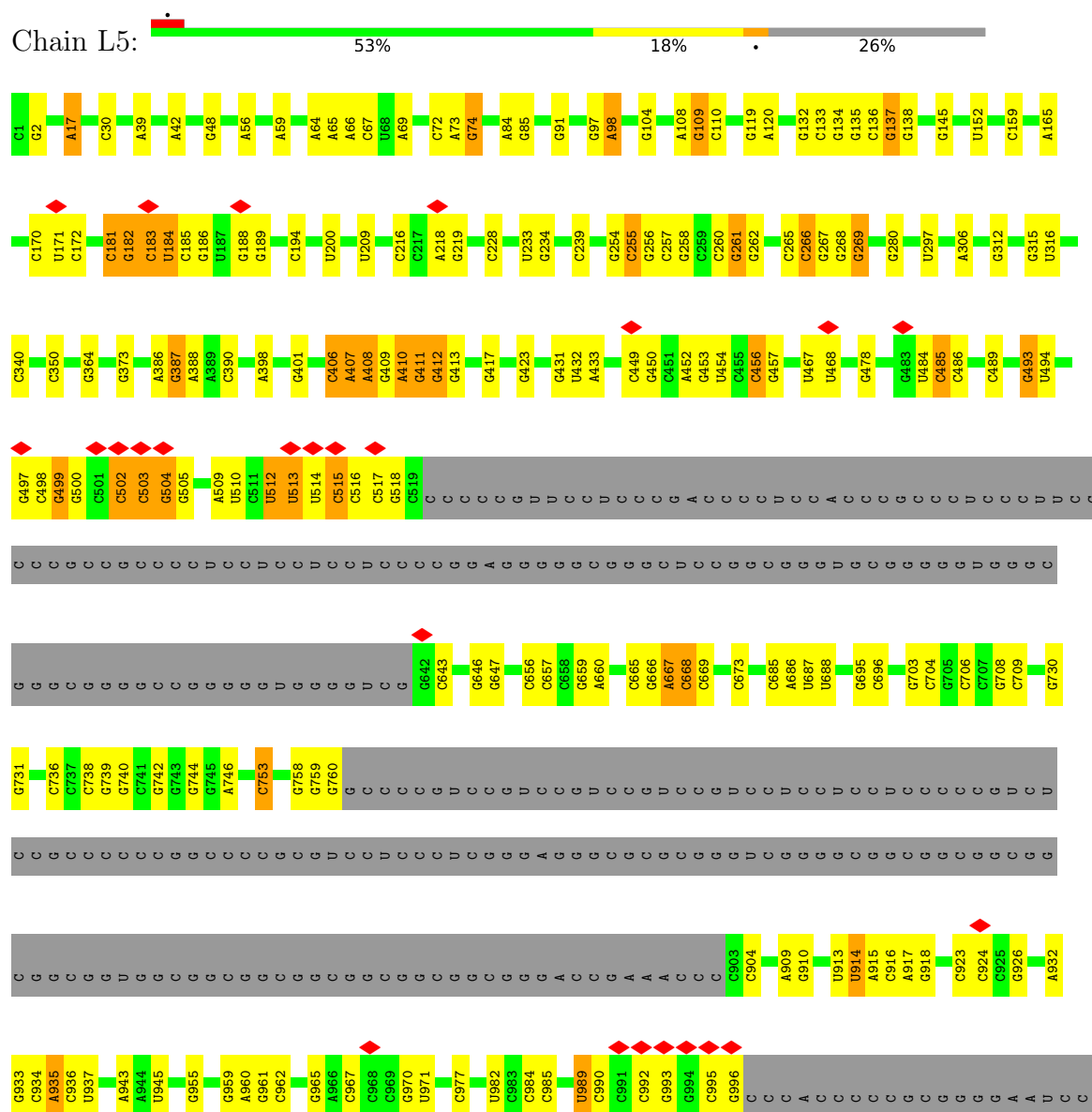
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

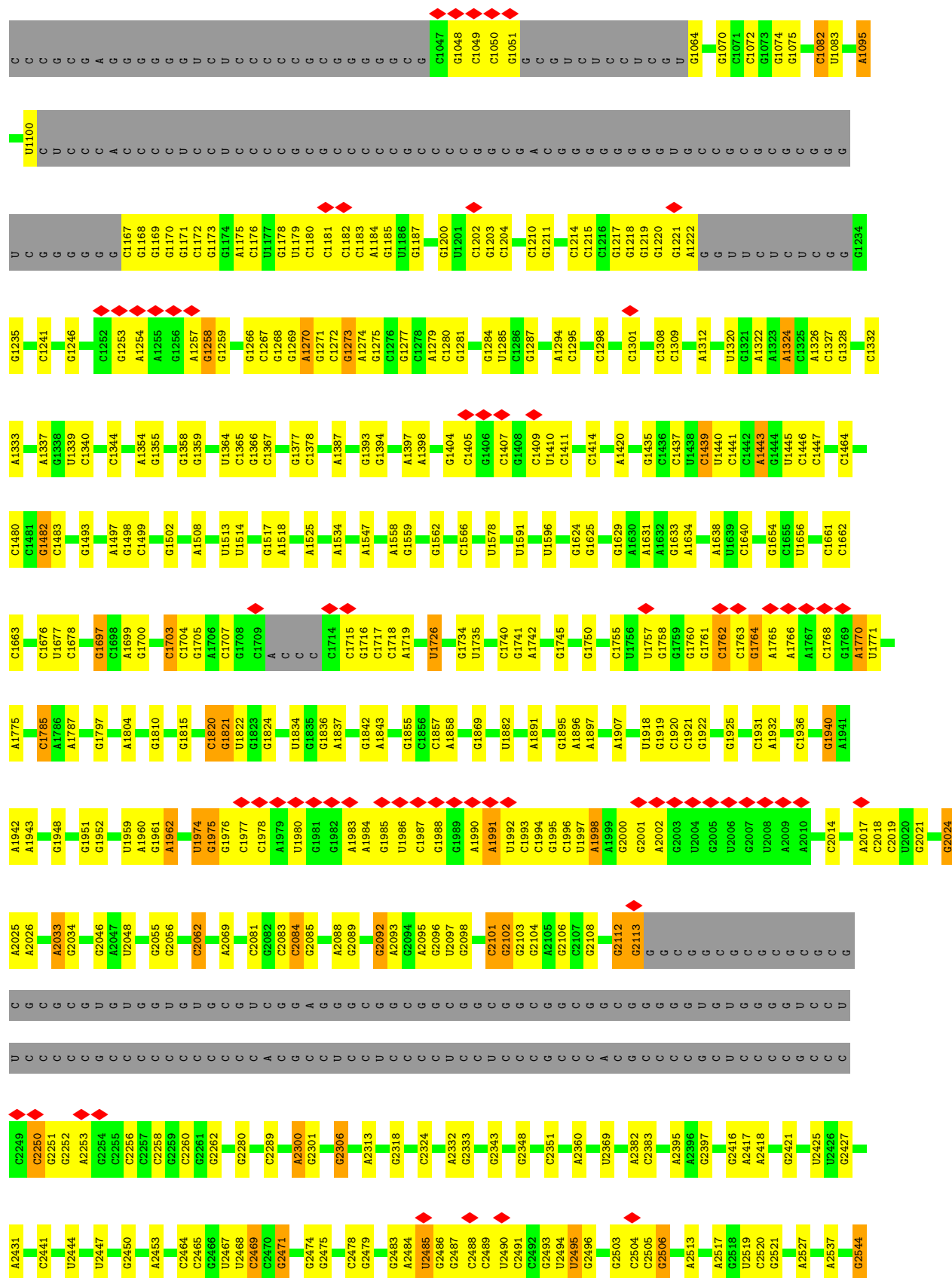
Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0
88	Sf	1	Total 1	Zn 1	0

3 Residue-property plots

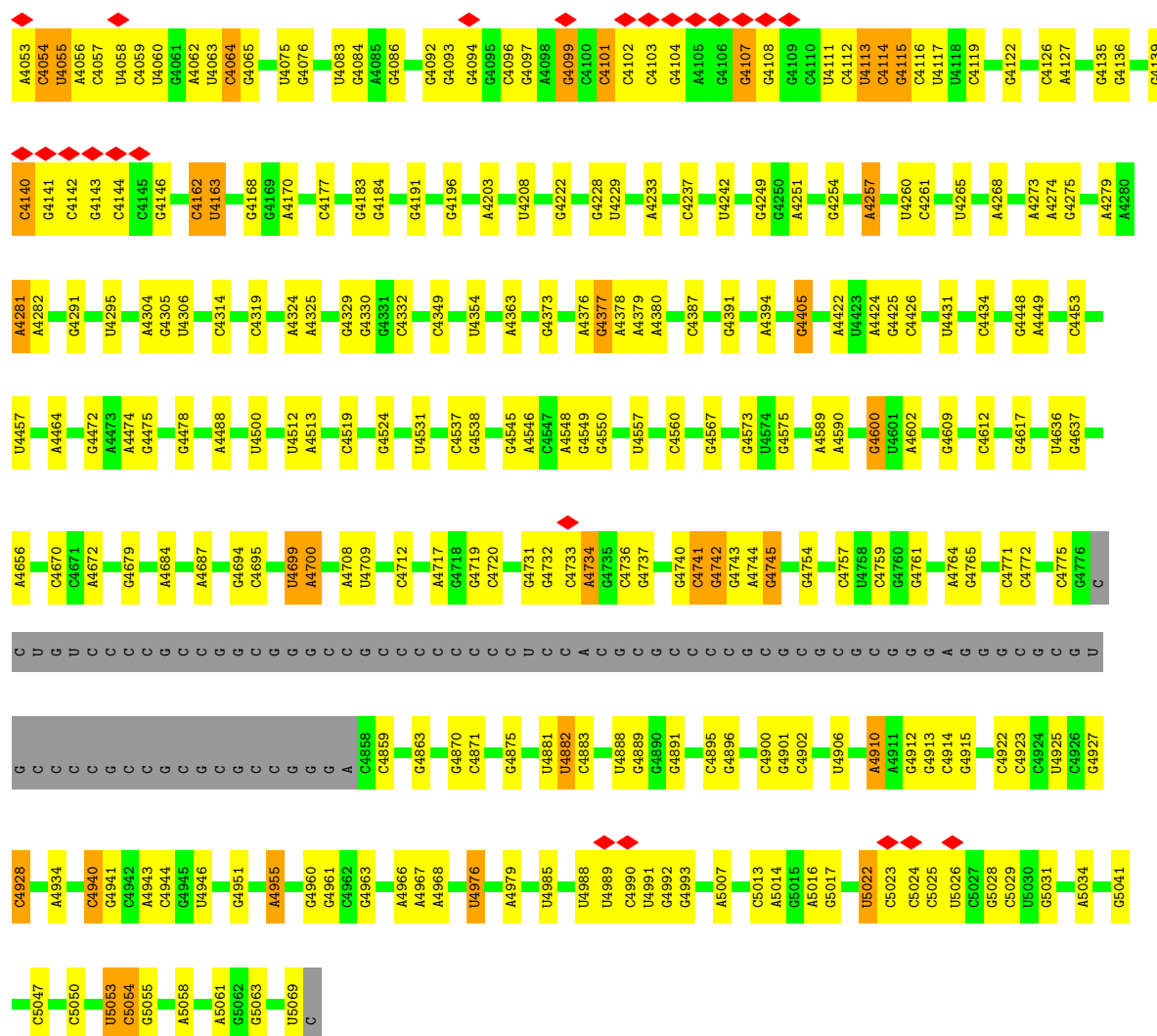
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 28S ribosomal RNA

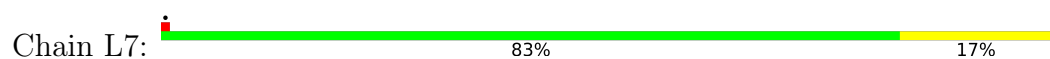




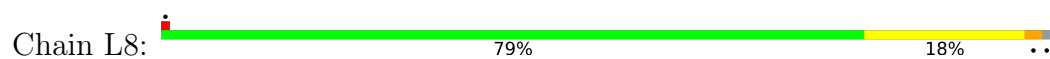
U3993	U3994	U3995	U3996	C3997	C3998	C3999	G4000	G4001	G4002	A4003	G4004	G4005	G4006	G4007	C4008	C4009	C4010	G4011	G4012	G4013	G4014	C4015	G4016	G4017	G4018	G4019	U4020	C4021	C4022	G4023	C4024	C4025	G4026	G4027	C4028	C4029	C4030	U4031	G4032	C4033	G4034	G4035	G4036	C4037	C4038	G4039	C4040	C4041	G4042	G4043	U4044	G4045	A4046	A4047	U4048	U4049	A4050	C4051	C4052																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
U3771	U3616	G3617	G3618	C3619	C3620	C3621	C3622	C3623	C3624	C3625	C3626	C3627	C3628	C3629	C3630	C3631	C3632	C3633	C3634	C3635	C3636	C3637	C3638	C3639	C3640	C3641	C3642	C3643	C3644	C3645	C3646	C3647	C3648	C3649	C3650	C3651	C3652	C3653	C3654	C3655	C3656	C3657	C3658	C3659	C3660	C3661	C3662	C3663	C3664	C3665	C3666	C3667	C3668	C3669	C3670	C3671	C3672	C3673	C3674	C3675	C3676	C3677	C3678	C3679	C3680	C3681	C3682	C3683	C3684	C3685	C3686	C3687	C3688	C3689	C3690	C3691	C3692	C3693	C3694	C3695	C3696	C3697	C3698	C3699	C3700	C3701	C3702	C3703	C3704	C3705	C3706	C3707	C3708	C3709	C3710	C3711	C3712	C3713	C3714	C3715	C3716	C3717	C3718	C3719	C3720	C3721	C3722	C3723	C3724	C3725	C3726	C3727	C3728	C3729	C3730	C3731	C3732	C3733	C3734	C3735	C3736	C3737	C3738	C3739	C3740	C3741	C3742	C3743	C3744	C3745	C3746	C3747	C3748	C3749	C3750	C3751	C3752	C3753	C3754	C3755	C3756	C3757	C3758	C3759	C3760	C3761	C3762	C3763	C3764	C3765	C3766	C3767	C3768	C3769	C3770	C3771	C3772	C3773	C3774	C3775	C3776	C3777	C3778	C3779	C3780	C3781	C3782	C3783	C3784	C3785	C3786	C3787	C3788	C3789	C3790	C3791	C3792	C3793	C3794	C3795	C3796	C3797	C3798	C3799	C3800	C3801	C3802	C3803	C3804	C3805	C3806	C3807	C3808	C3809	C3810	C3811	C3812	C3813	C3814	C3815	C3816	C3817	C3818	C3819	C3820	C3821	C3822	C3823	C3824	C3825	C3826	C3827	C3828	C3829	C3830	C3831	C3832	C3833	C3834	C3835	C3836	C3837	C3838	C3839	C3840	C3841	C3842	C3843	C3844	C3845	C3846	C3847	C3848	C3849	C3850	C3851	C3852	C3853	C3854	C3855	C3856	C3857	C3858	C3859	C3860	C3861	C3862	C3863	C3864	C3865	C3866	C3867	C3868	C3869	C3870	C3871	C3872	C3873	C3874	C3875	C3876	C3877	C3878	C3879	C3880	C3881	C3882	C3883	C3884	C3885	C3886	C3887	C3888	C3889	C3890	C3891	C3892	C3893	C3894	C3895	C3896	C3897	C3898	C3899	C3900	C3901	C3902	C3903	C3904	C3905	C3906	C3907	C3908	C3909	C3910	C3911	C3912	C3913	C3914	C3915	C3916	C3917	C3918	C3919	C3920	C3921	C3922	C3923	C3924	C3925	C3926	C3927	C3928	C3929	C3930	C3931	C3932	C3933	C3934	C3935	C3936	C3937	C3938	C3939	C3940	C3941	C3942	C3943	C3944	C3945	C3946	C3947	C3948	C3949	C3950	C3951	C3952	C3953	C3954	C3955	C3956	C3957	C3958	C3959	C3960	C3961	C3962	C3963	C3964	C3965	C3966	C3967	C3968	C3969	C3970	C3971	C3972	C3973	C3974	C3975	C3976	C3977	C3978	C3979	C3980	C3981	C3982	C3983	C3984	C3985	C3986	C3987	C3988	C3989	C3990	C3991	C3992	C3993	C3994	C3995	C3996	C3997	C3998	C3999	C4000	C4001	C4002	C4003	C4004	C4005	C4006	C4007	C4008	C4009	C4010	C4011	C4012	C4013	C4014	C4015	C4016	C4017	C4018	C4019	C4020	C4021	C4022	C4023	C4024	C4025	C4026	C4027	C4028	C4029	C4030	C4031	C4032	C4033	C4034	C4035	C4036	C4037	C4038	C4039	C4040	C4041	C4042	C4043	C4044	C4045	C4046	C4047	C4048	C4049	C4050	C4051	C4052																																																																																																																																																																																																																																																																																																																																																																																																																																				
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- Molecule 2: 5S ribosomal RNA

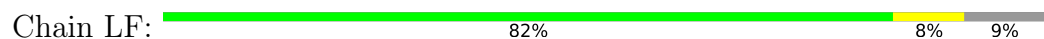


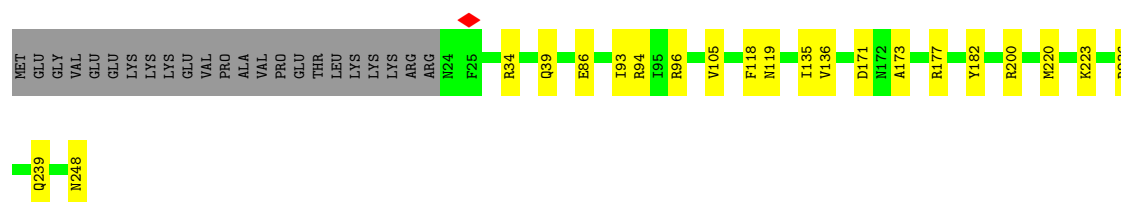
- Molecule 3: 5.8S ribosomal RNA



- Molecule 4: 60S ribosomal protein L8

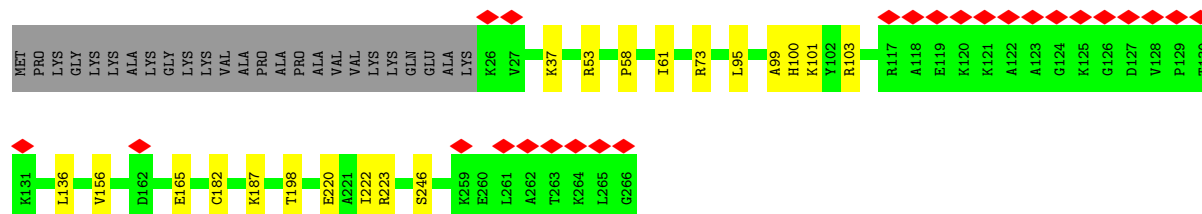






- Molecule 10: 60S ribosomal protein L7a

Chain LG: 9% 83% 8% 9%



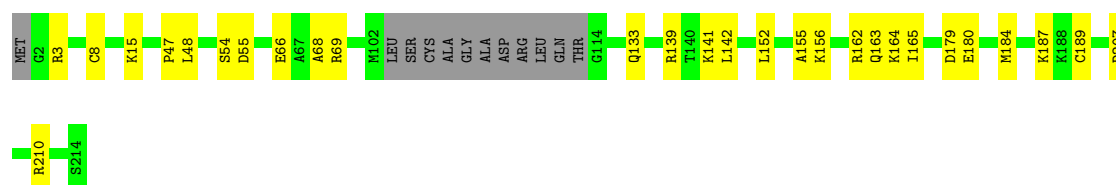
- Molecule 11: 60S ribosomal protein L9

Chain LH: 84% 14% ..



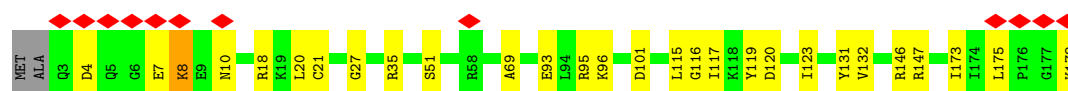
- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 81% 13% 6%



- Molecule 13: 60S ribosomal protein L11

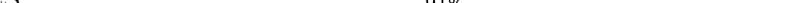
Chain LJ: 7% 83% 15% ..

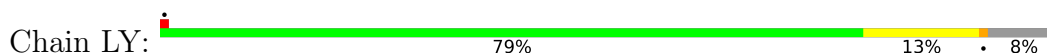


- Molecule 14: 60S ribosomal protein L13

Chain LL: 87% 12%



- Chain LS:  91% 8%





- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  85% 13% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg:  5% 87% 10% .

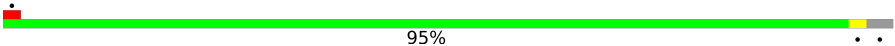


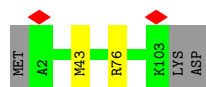
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  90% 8% ..



- Molecule 37: 60S ribosomal protein L36

Chain Li:  95% ..



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  77% 9% . 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  80% 19% .

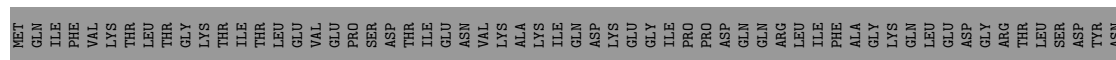
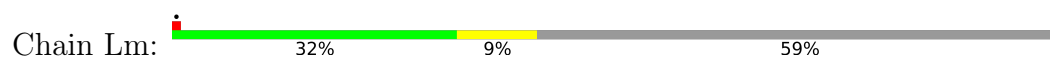


- Molecule 40: 60S ribosomal protein L39

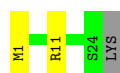
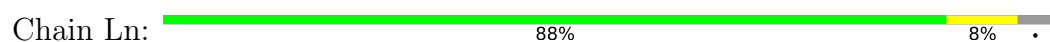
Chain Ll:  90% 8% .



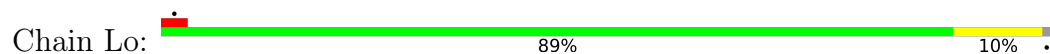
- Molecule 41: Ubiquitin-60S ribosomal protein L40



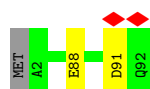
- Molecule 42: 60S ribosomal protein L41



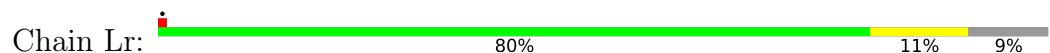
- Molecule 43: 60S ribosomal protein L36a



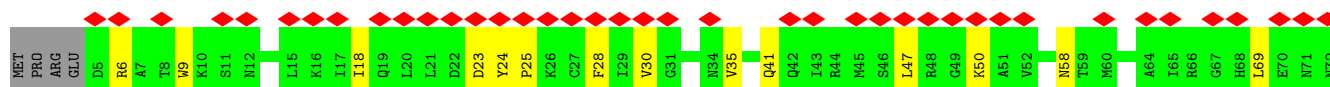
- Molecule 44: 60S ribosomal protein L37a

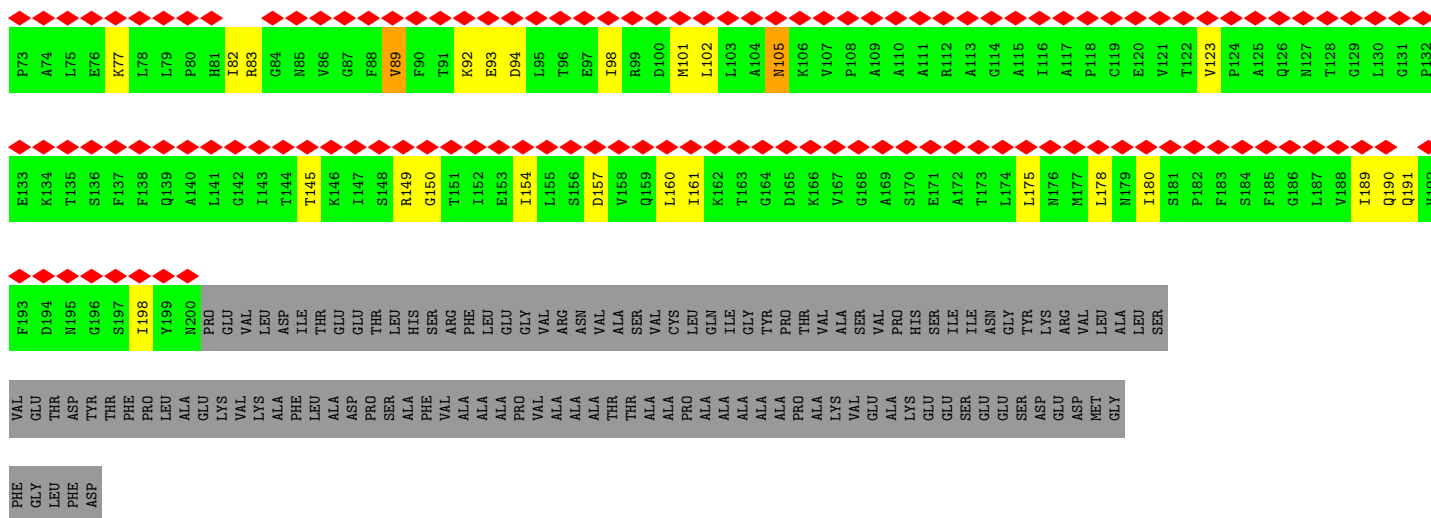


- Molecule 45: 60S ribosomal protein L28

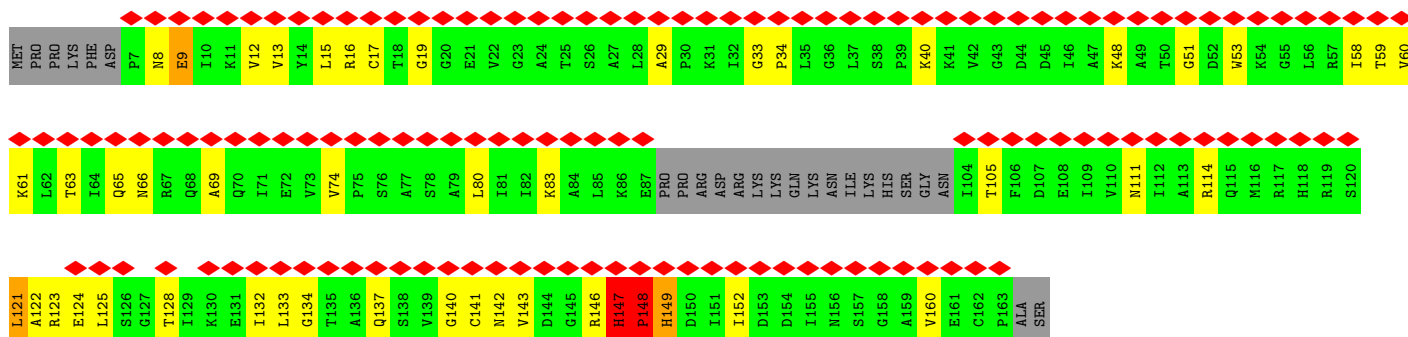
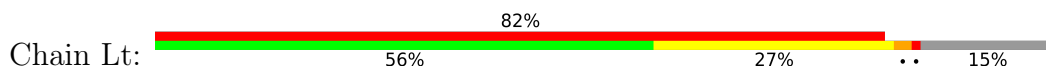


- Molecule 46: 60S acidic ribosomal protein P0

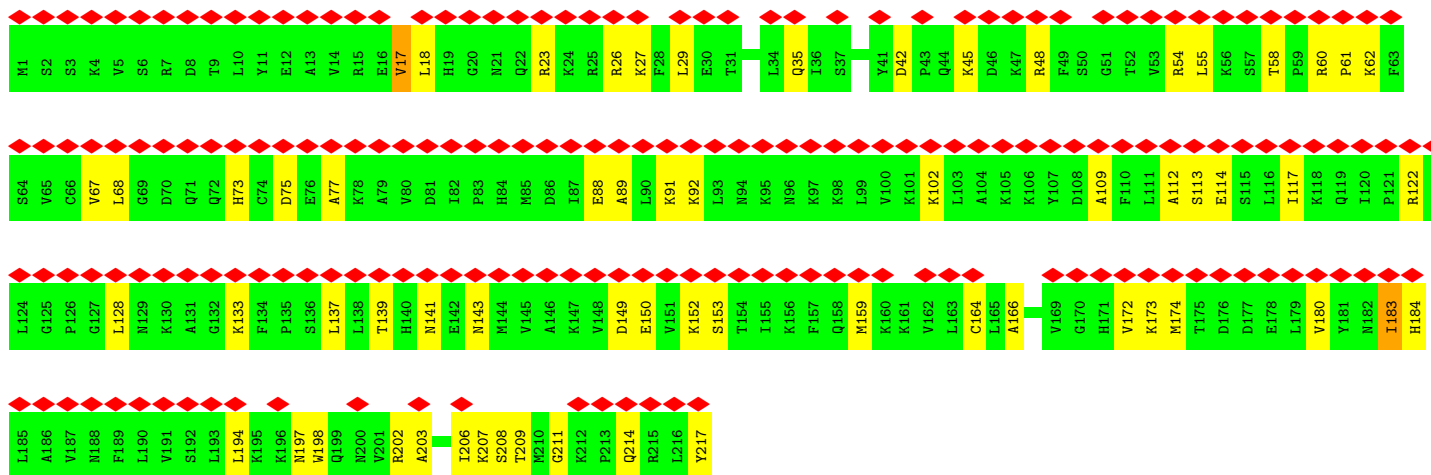
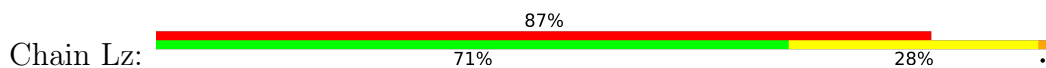




• Molecule 47: 60S ribosomal protein L12

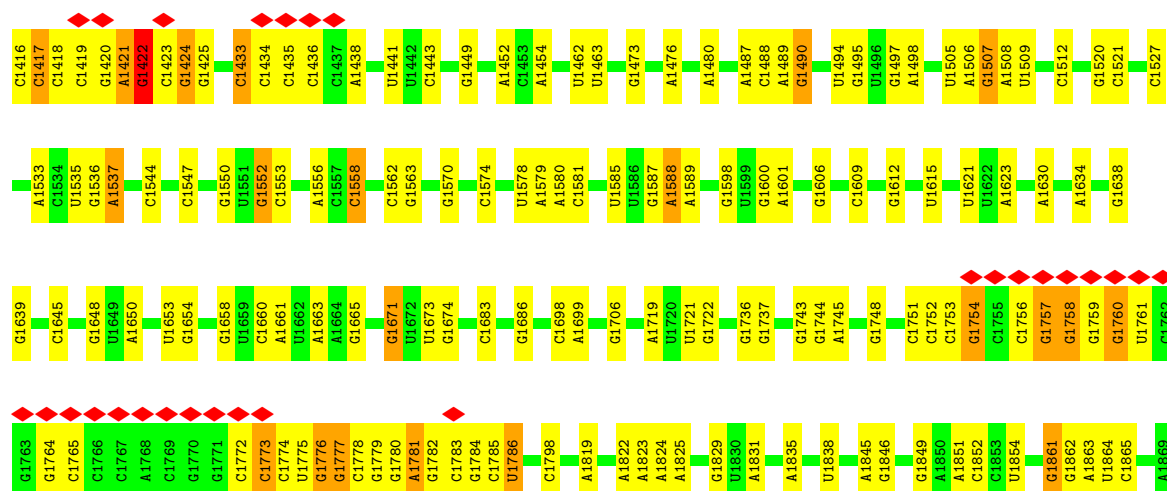


• Molecule 48: 60S ribosomal protein L10a

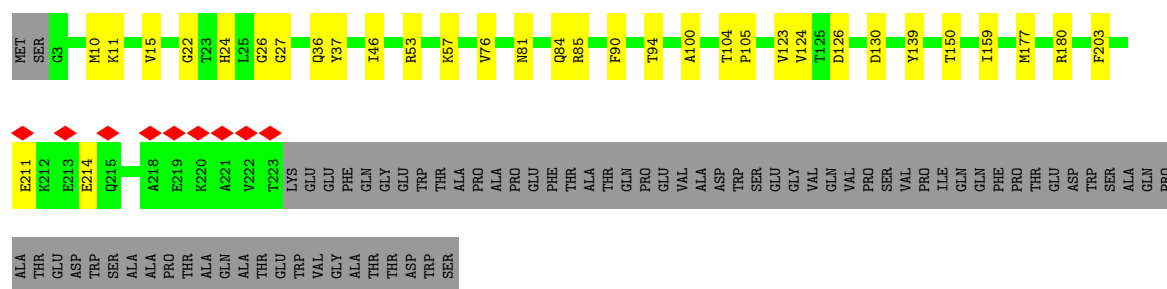


• Molecule 49: 18S ribosomal RNA

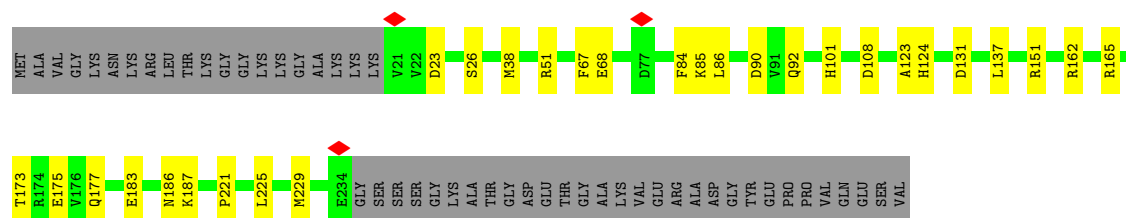




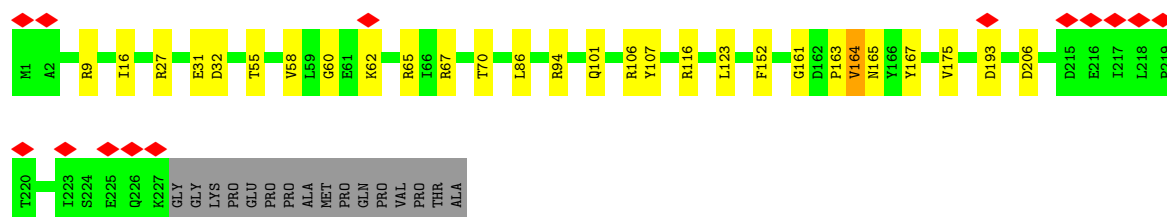
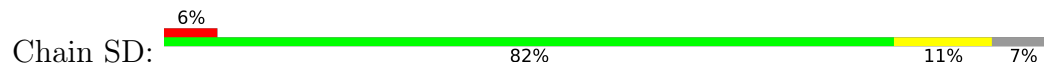
• Molecule 50: 40S ribosomal protein SA



• Molecule 51: 40S ribosomal protein S3a

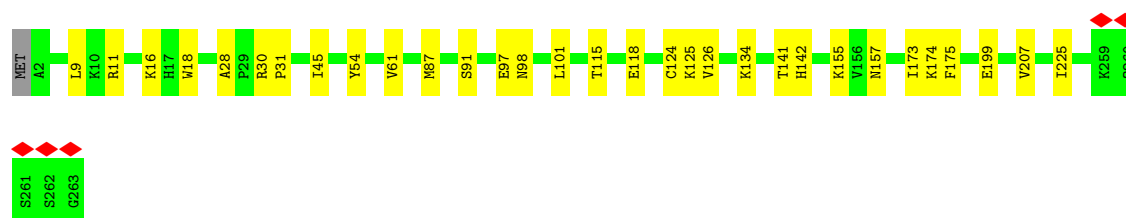


• Molecule 52: 40S ribosomal protein S3



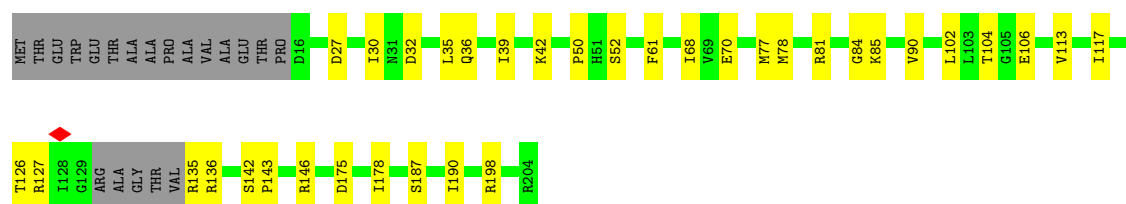
- Molecule 53: 40S ribosomal protein S4, X isoform

Chain SE:  88% 12%



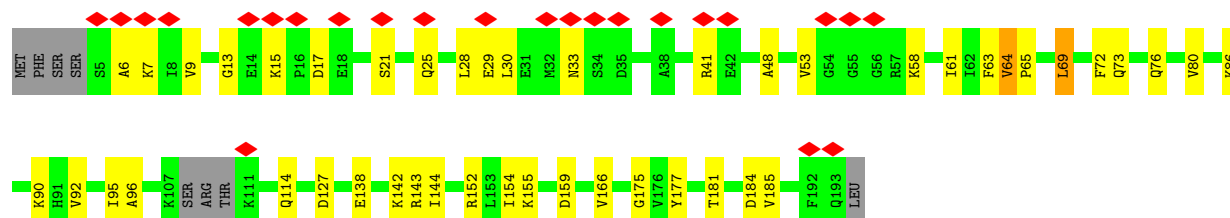
- Molecule 54: 40S ribosomal protein S5

Chain SF:  73% 17% 10%



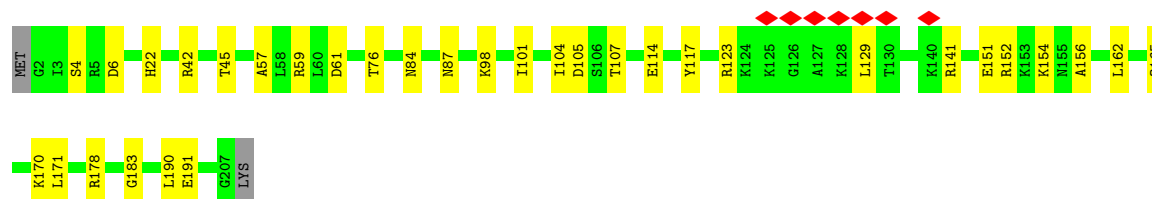
- Molecule 55: 40S ribosomal protein S7

Chain SH:  12% 72% 23%



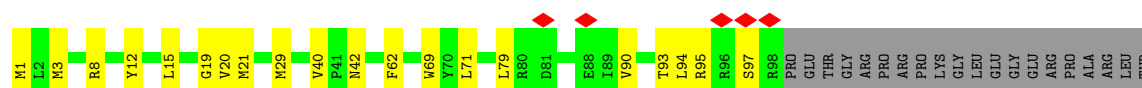
- Molecule 56: 40S ribosomal protein S8

Chain SI:  83% 16%



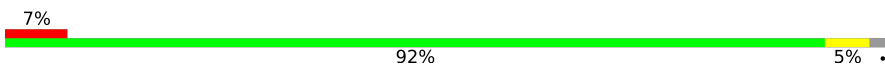
- Molecule 57: 40S ribosomal protein S10

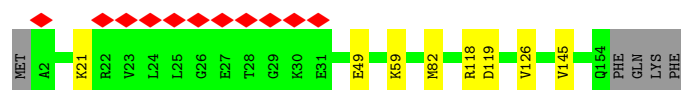
Chain SK:  47% 12% 41%



ARG GLY GLU ALA ASP ARG ASP THR TYR ARG ARG SER ALA VAL PRO PRO GLY ALA ASP LYS LYS ALA GLU ALA GLY ALA GLY SER SER THR ALA PHE GLN PHE PHE GLY PHE GLY ARG ARG GLN GLN PRO PRO GLN

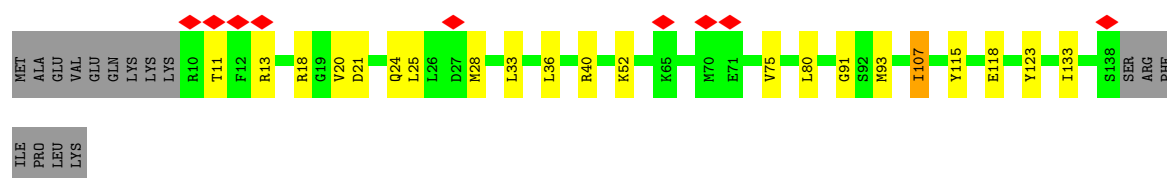
- Molecule 58: 40S ribosomal protein S11

Chain SL:  7% 92% 5% .



- Molecule 59: 40S ribosomal protein S15

Chain SP:  6% 74% 14% . 11%



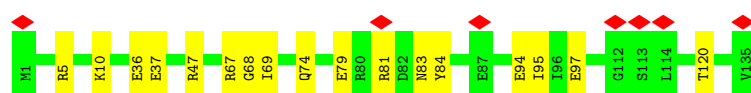
- Molecule 60: 40S ribosomal protein S16

Chain SQ:  1% 84% 14% ..



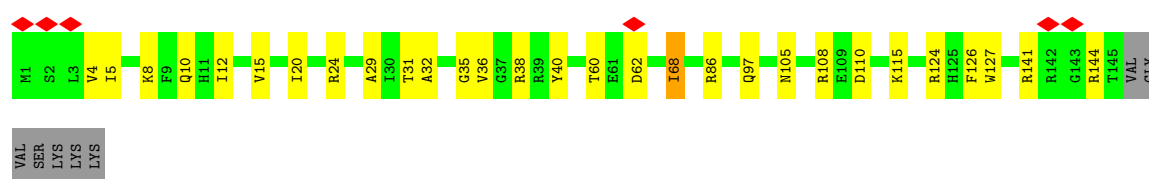
- Molecule 61: 40S ribosomal protein S17

Chain SR:  5% 87% 13%



- Molecule 62: 40S ribosomal protein S18

Chain SS:  1% 76% 18% . 5%

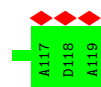
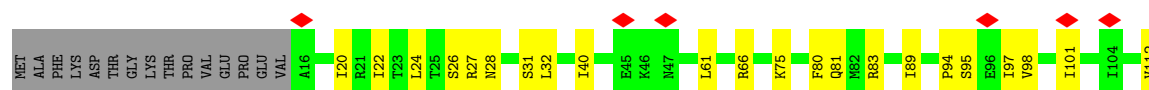


- Molecule 63: 40S ribosomal protein S19

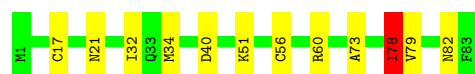
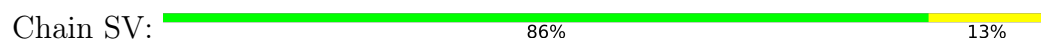
Chain ST:  1% 82% 17% .



- Molecule 64: 40S ribosomal protein S20



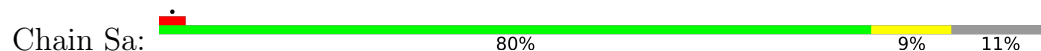
- Molecule 65: 40S ribosomal protein S21



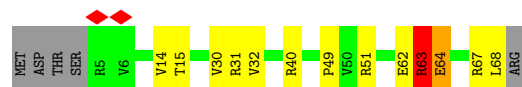
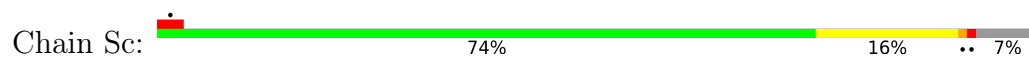
- Molecule 66: 40S ribosomal protein S23



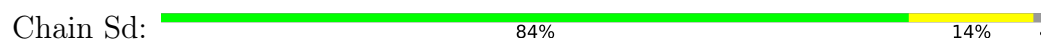
- Molecule 67: 40S ribosomal protein S26



- Molecule 68: 40S ribosomal protein S28

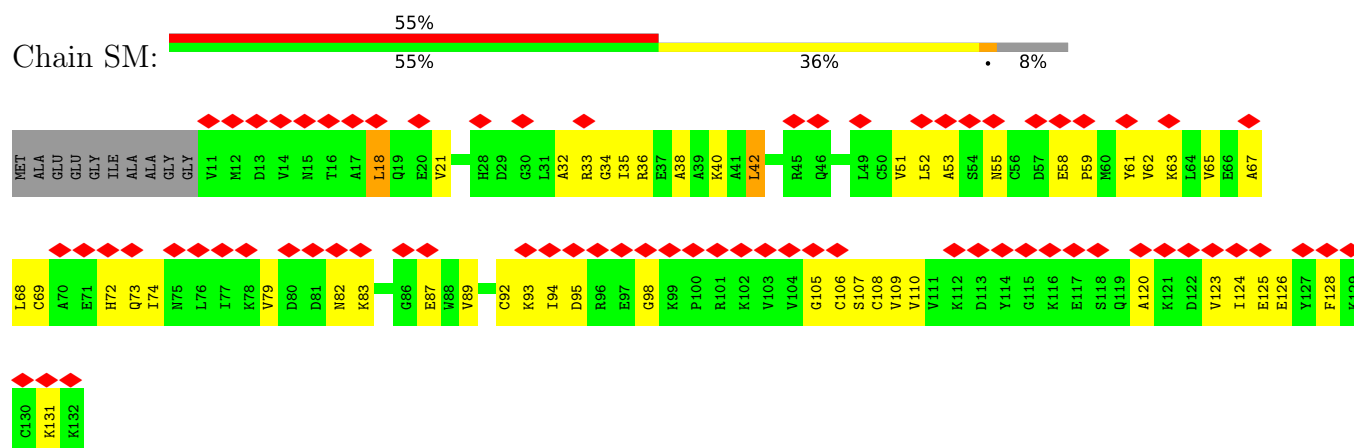


- Molecule 69: 40S ribosomal protein S29

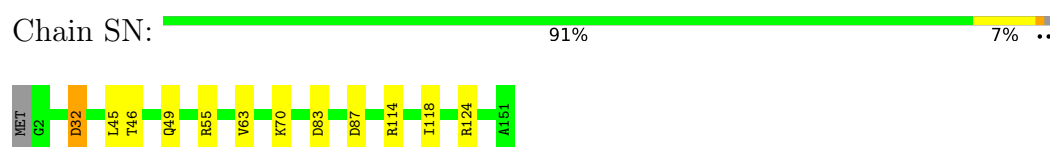




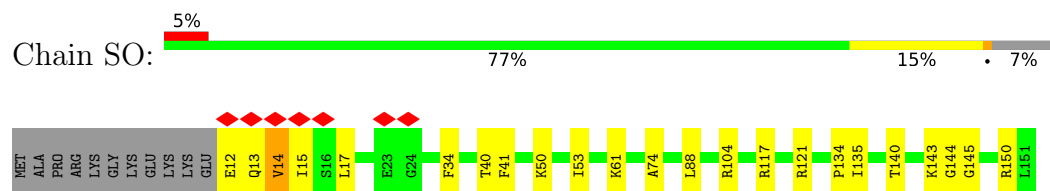
- Molecule 74: 40S ribosomal protein S12



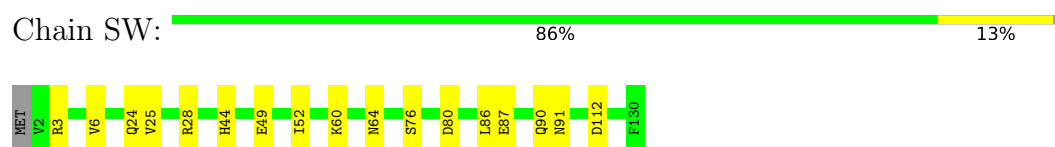
- Molecule 75: 40S ribosomal protein S13



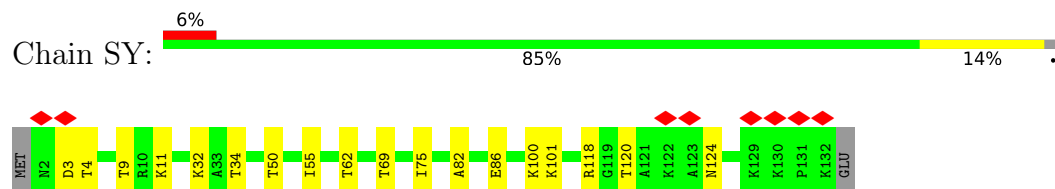
- Molecule 76: 40S ribosomal protein S14



- Molecule 77: 40S ribosomal protein S15a

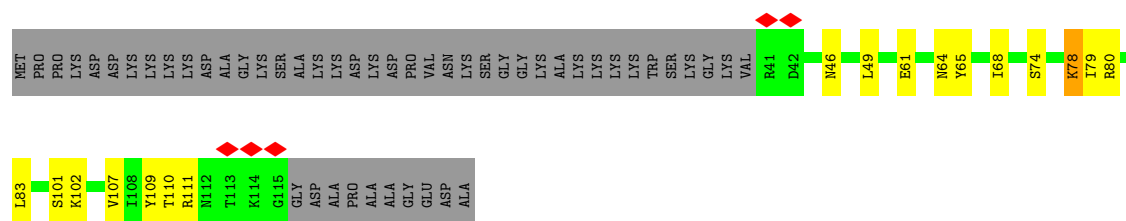


- Molecule 78: 40S ribosomal protein S24

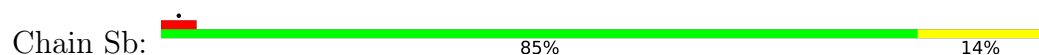


- Molecule 79: 40S ribosomal protein S25

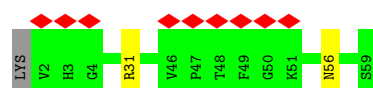




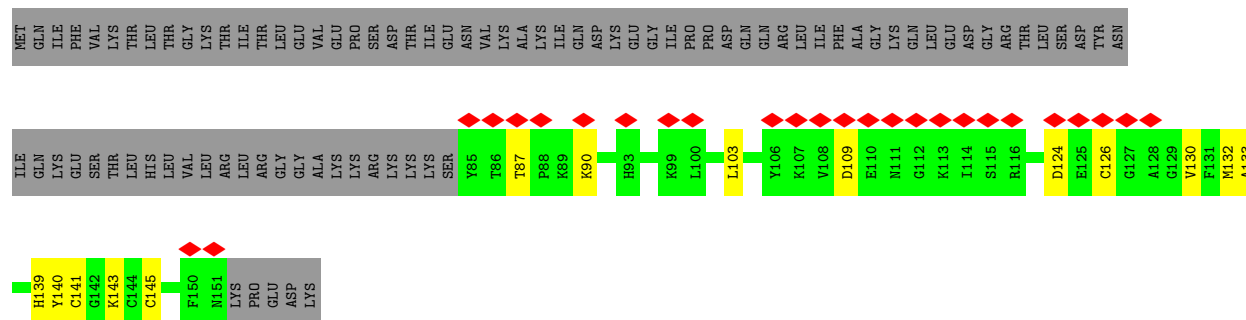
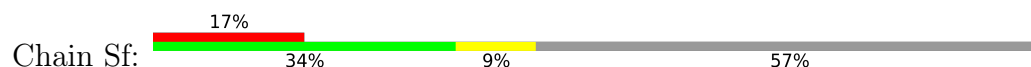
- Molecule 80: 40S ribosomal protein S27



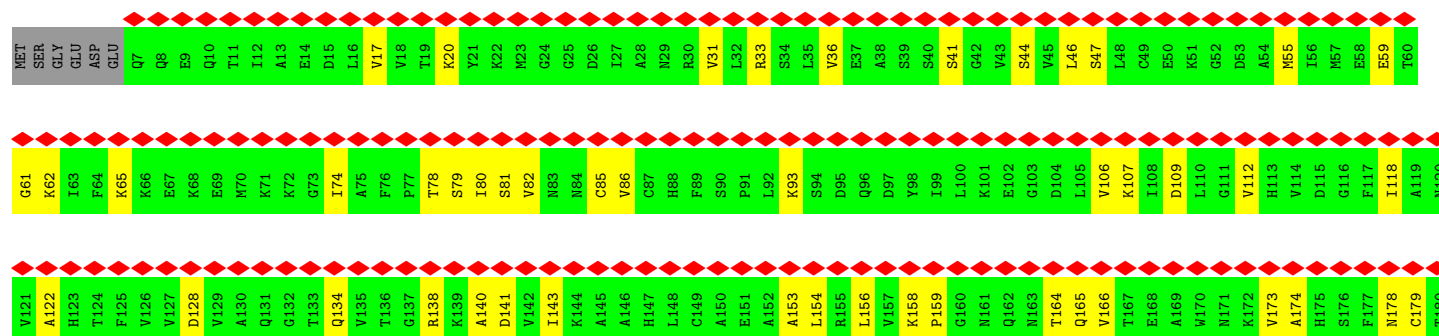
- Molecule 81: 40S ribosomal protein S30



- Molecule 82: Ubiquitin-40S ribosomal protein S27a



- Molecule 83: Proliferation-associated protein 2G4



VAL	LEU	LEU	ARG	LYS	ASN	GLY	ASN	LYS	GLY	ALA	GLY	GLY	HIS	SER	TYR	GLY	ALA	ASP	LEU	LYS	SER	PHE	ASP	LEU	GLY	ASP	E148	D152	G180
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107149	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.518	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.41	0/89595	0.44	8/139686 (0.0%)
2	L7	0.38	0/2861	0.38	0/4459
3	L8	0.41	0/3701	0.39	0/5766
4	LA	0.43	0/1936	0.73	2/2596 (0.1%)
5	LB	0.38	0/3306	0.62	0/4424
6	LC	0.39	0/2981	0.65	4/4002 (0.1%)
7	LD	0.31	0/2428	0.57	0/3252
8	LE	0.31	0/1942	0.64	0/2606
9	LF	0.39	0/1905	0.65	2/2539 (0.1%)
10	LG	0.35	0/1960	0.65	0/2637
11	LH	0.35	0/1537	0.57	0/2066
12	LI	0.37	0/1673	0.59	0/2233
13	LJ	0.29	0/1433	0.74	3/1915 (0.2%)
14	LL	0.36	0/1732	0.65	0/2315
15	LM	0.36	0/1161	0.68	2/1554 (0.1%)
16	LN	0.42	0/1746	0.68	2/2338 (0.1%)
17	LO	0.37	0/1682	0.53	0/2250
18	LP	0.37	0/1268	0.57	0/1701
19	LQ	0.40	0/1537	0.58	0/2052
20	LR	0.35	0/1582	0.59	2/2091 (0.1%)
21	LS	0.37	0/1493	0.52	0/2003
22	LT	0.37	0/1326	0.60	0/1770
23	LU	0.30	0/839	0.68	0/1126
24	LV	0.35	0/993	0.57	0/1332
25	LW	0.33	0/1030	0.64	0/1364
26	LX	0.34	0/1002	0.55	0/1345
27	LY	0.37	0/1132	0.62	0/1504
28	LZ	0.34	0/1130	0.59	1/1507 (0.1%)
29	La	0.39	0/1191	0.59	0/1591
30	Lb	0.31	0/889	0.63	0/1175
31	Lc	0.37	0/774	0.63	0/1038
32	Ld	0.36	0/903	0.60	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.40	0/1071	0.64	0/1429
34	Lf	0.40	0/895	0.65	0/1198
35	Lg	0.36	0/916	0.56	0/1220
36	Lh	0.32	0/1023	0.49	0/1351
37	Li	0.30	0/843	0.53	0/1115
38	Lj	0.43	0/720	0.69	0/952
39	Lk	0.29	0/575	0.56	0/761
40	Ll	0.39	0/454	0.60	0/599
41	Lm	0.37	0/435	0.60	0/575
42	Ln	0.33	0/231	0.56	0/294
43	Lo	0.35	0/876	0.56	0/1156
44	Lp	0.38	0/718	0.55	0/953
45	Lr	0.37	0/1017	0.60	0/1364
46	Ls	0.30	0/1519	0.77	2/2052 (0.1%)
47	Lt	0.41	1/1058 (0.1%)	0.96	3/1430 (0.2%)
48	Lz	0.28	0/1769	0.76	0/2371
49	S2	0.36	0/41245	0.44	8/64265 (0.0%)
50	SA	0.34	0/1778	0.62	0/2416
51	SB	0.32	0/1765	0.59	0/2362
52	SD	0.30	0/1793	0.65	2/2414 (0.1%)
53	SE	0.33	0/2118	0.64	0/2849
54	SF	0.29	0/1481	0.62	0/1988
55	SH	0.34	0/1519	0.72	0/2033
56	SI	0.34	0/1715	0.62	2/2287 (0.1%)
57	SK	0.26	0/851	0.55	0/1147
58	SL	0.36	0/1268	0.58	0/1696
59	SP	0.26	0/1082	0.69	2/1446 (0.1%)
60	SQ	0.31	0/1160	0.65	0/1553
61	SR	0.28	0/1105	0.72	0/1484
62	SS	0.27	0/1216	0.59	0/1628
63	ST	0.27	0/1131	0.57	0/1515
64	SU	0.30	0/831	0.67	0/1115
65	SV	0.34	0/643	0.68	0/860
66	SX	0.36	0/1116	0.65	1/1490 (0.1%)
67	Sa	0.37	0/836	0.66	0/1121
68	Sc	0.32	0/508	0.76	2/680 (0.3%)
69	Sd	0.31	0/470	0.63	0/623
70	Sg	0.28	0/2493	0.69	0/3394
71	SC	0.37	0/1762	0.67	2/2381 (0.1%)
72	SG	0.29	0/1946	0.62	2/2590 (0.1%)
73	SJ	0.33	0/1550	0.60	0/2069
74	SM	0.30	0/950	0.90	2/1275 (0.2%)
75	SN	0.33	0/1232	0.55	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.34	0/1062	0.66	2/1425 (0.1%)
77	SW	0.36	0/1051	0.55	0/1406
78	SY	0.28	0/1083	0.56	0/1438
79	SZ	0.33	0/604	0.79	0/810
80	Sb	0.31	0/665	0.57	0/891
81	Se	0.27	0/448	0.55	0/592
82	Sf	0.24	0/560	0.78	2/745 (0.3%)
83	CA	0.30	0/2810	0.78	2/3780 (0.1%)
84	CC	0.21	0/1773	0.40	1/2759 (0.0%)
85	CE	0.23	0/613	0.57	0/819
86	i	0.27	0/268	0.51	0/361
All	All	0.37	1/241289 (0.0%)	0.52	61/353636 (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	LA	0	2
5	LB	0	2
8	LE	0	1
11	LH	0	2
12	LI	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	1
22	LT	0	3
29	La	0	1
32	Ld	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
46	Ls	0	1
47	Lt	0	6
48	Lz	0	1
51	SB	0	1
52	SD	0	1
54	SF	0	2
55	SH	0	2
60	SQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
61	SR	0	1
63	ST	0	1
65	SV	0	1
66	SX	0	4
68	Sc	0	1
73	SJ	0	1
79	SZ	0	2
80	Sb	0	1
All	All	0	49

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Lt	29	ALA	C-N	6.34	1.40	1.34

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SP	107	ILE	CA-C-N	9.35	151.06	121.98
59	SP	107	ILE	C-N-CA	9.35	151.06	121.98
74	SM	98	GLY	CA-C-N	8.89	143.50	121.80
74	SM	98	GLY	C-N-CA	8.89	143.50	121.80
47	Lt	149	HIS	N-CA-C	6.82	121.87	112.04

There are no chirality outliers.

5 of 49 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
8	LE	129	GLY	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	L5	80138	0	40380	321	0
2	L7	2561	0	1295	6	0
3	L8	3314	0	1683	6	0
4	LA	1898	0	1993	9	0
5	LB	3238	0	3376	29	0
6	LC	2927	0	3104	16	0
7	LD	2382	0	2410	15	0
8	LE	1904	0	2055	22	0
9	LF	1870	0	1996	15	0
10	LG	1927	0	2074	13	0
11	LH	1518	0	1601	17	0
12	LI	1634	0	1671	17	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	17	0
15	LM	1138	0	1204	12	0
16	LN	1701	0	1749	8	0
17	LO	1650	0	1794	9	0
18	LP	1242	0	1269	9	0
19	LQ	1513	0	1628	10	0
20	LR	1566	0	1729	14	0
21	LS	1453	0	1490	10	0
22	LT	1298	0	1366	16	0
23	LU	825	0	850	7	0
24	LV	979	0	1039	4	0
25	LW	1015	0	1079	15	0
26	LX	985	0	1066	8	0
27	LY	1115	0	1205	13	0
28	LZ	1107	0	1182	8	0
29	La	1162	0	1213	7	0
30	Lb	876	0	948	6	0
31	Lc	764	0	804	8	0
32	Ld	888	0	930	7	0
33	Le	1053	0	1147	7	0
34	Lf	876	0	912	9	0
35	Lg	906	0	998	7	0
36	Lh	1015	0	1148	8	0
37	Li	832	0	917	2	0
38	Lj	705	0	736	8	0
39	Lk	569	0	637	9	0
40	Ll	444	0	483	3	0
41	Lm	429	0	465	9	0
42	Ln	230	0	276	2	0
43	Lo	862	0	929	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	708	0	756	1	0
45	Lr	1002	0	1068	10	0
46	Ls	1496	0	1540	25	0
47	Lt	1046	0	1076	22	0
48	Lz	1741	0	1854	41	0
49	S2	36899	0	18602	188	0
50	SA	1741	0	1746	23	0
51	SB	1738	0	1809	20	0
52	SD	1765	0	1865	17	0
53	SE	2076	0	2177	16	0
54	SF	1461	0	1511	22	0
55	SH	1497	0	1590	28	0
56	SI	1686	0	1772	21	0
57	SK	827	0	854	13	0
58	SL	1247	0	1323	6	0
59	SP	1061	0	1107	14	0
60	SQ	1142	0	1213	13	0
61	SR	1090	0	1149	10	0
62	SS	1198	0	1261	18	0
63	ST	1112	0	1146	15	0
64	SU	821	0	883	16	0
65	SV	636	0	637	9	0
66	SX	1098	0	1167	9	0
67	Sa	821	0	870	8	0
68	Sc	506	0	536	9	0
69	Sd	459	0	452	6	0
70	Sg	2436	0	2393	51	0
71	SC	1725	0	1813	12	0
72	SG	1923	0	2089	26	0
73	SJ	1525	0	1640	12	0
74	SM	940	0	965	49	0
75	SN	1208	0	1294	9	0
76	SO	1049	0	1073	16	0
77	SW	1034	0	1080	10	0
78	SY	1065	0	1142	13	0
79	SZ	598	0	656	11	0
80	Sb	651	0	672	7	0
81	Se	443	0	469	2	0
82	Sf	548	0	553	11	0
83	CA	2764	0	2779	59	0
84	CC	1589	0	810	20	0
85	CE	603	0	660	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	i	263	0	234	1	0
87	L5	212	0	0	0	0
87	L7	3	0	0	0	0
87	L8	4	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	S2	30	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
All	All	225122	0	168376	1408	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 4.

The worst 5 of 1408 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)
74:SM:52:LEU:CD2	74:SM:108:CYS:HB3	1.68	1.22
74:SM:52:LEU:HD23	74:SM:108:CYS:HB3	1.23	1.11
49:S2:1756:C:H42	49:S2:1776:G:N2	1.49	1.09
49:S2:1756:C:N4	49:S2:1776:G:H22	1.52	1.06
74:SM:52:LEU:HD23	74:SM:108:CYS:CB	1.86	1.05

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	225 (92%)	20 (8%)	1 (0%)	30	51
5	LB	400/403 (99%)	380 (95%)	17 (4%)	3 (1%)	16	34
6	LC	366/427 (86%)	341 (93%)	25 (7%)	0	100	100
7	LD	291/297 (98%)	267 (92%)	24 (8%)	0	100	100
8	LE	232/288 (81%)	211 (91%)	21 (9%)	0	100	100
9	LF	223/248 (90%)	214 (96%)	9 (4%)	0	100	100
10	LG	239/266 (90%)	224 (94%)	15 (6%)	0	100	100
11	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
12	LI	198/214 (92%)	183 (92%)	14 (7%)	1 (0%)	24	46
13	LJ	174/178 (98%)	157 (90%)	16 (9%)	1 (1%)	21	42
14	LL	208/211 (99%)	191 (92%)	17 (8%)	0	100	100
15	LM	137/215 (64%)	130 (95%)	6 (4%)	1 (1%)	18	38
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	28
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	10 (7%)	1 (1%)	18	38
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
22	LT	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	21	42
23	LU	99/128 (77%)	86 (87%)	13 (13%)	0	100	100
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	111 (91%)	11 (9%)	0	100	100
26	LX	118/156 (76%)	116 (98%)	2 (2%)	0	100	100
27	LY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	98 (93%)	7 (7%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	119 (94%)	6 (5%)	1 (1%)	16	34
34	Lf	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	6	13
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
38	Lj	84/97 (87%)	75 (89%)	8 (10%)	1 (1%)	10	23
39	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Ls	194/317 (61%)	166 (86%)	27 (14%)	1 (0%)	24	46
47	Lt	137/165 (83%)	100 (73%)	33 (24%)	4 (3%)	3	6
48	Lz	215/217 (99%)	160 (74%)	55 (26%)	0	100	100
50	SA	219/295 (74%)	202 (92%)	17 (8%)	0	100	100
51	SB	212/264 (80%)	201 (95%)	11 (5%)	0	100	100
52	SD	225/243 (93%)	201 (89%)	24 (11%)	0	100	100
53	SE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
54	SF	180/204 (88%)	164 (91%)	16 (9%)	0	100	100
55	SH	182/194 (94%)	161 (88%)	21 (12%)	0	100	100
56	SI	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
57	SK	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	119 (94%)	8 (6%)	0	100	100
60	SQ	142/146 (97%)	128 (90%)	13 (9%)	1 (1%)	18	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SR	133/135 (98%)	116 (87%)	16 (12%)	1 (1%)	16	34
62	SS	143/152 (94%)	131 (92%)	12 (8%)	0	100	100
63	ST	141/145 (97%)	130 (92%)	10 (7%)	1 (1%)	18	38
64	SU	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
65	SV	81/83 (98%)	74 (91%)	5 (6%)	2 (2%)	4	8
66	SX	139/143 (97%)	131 (94%)	4 (3%)	4 (3%)	3	6
67	Sa	100/115 (87%)	92 (92%)	7 (7%)	1 (1%)	12	28
68	Sc	62/69 (90%)	52 (84%)	9 (14%)	1 (2%)	7	16
69	Sd	53/56 (95%)	50 (94%)	2 (4%)	1 (2%)	6	13
70	Sg	311/317 (98%)	269 (86%)	41 (13%)	1 (0%)	36	58
71	SC	220/293 (75%)	205 (93%)	15 (7%)	0	100	100
72	SG	235/249 (94%)	222 (94%)	13 (6%)	0	100	100
73	SJ	183/194 (94%)	169 (92%)	12 (7%)	2 (1%)	11	25
74	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
75	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
76	SO	138/151 (91%)	127 (92%)	9 (6%)	2 (1%)	9	19
77	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
78	SY	129/133 (97%)	123 (95%)	6 (5%)	0	100	100
79	SZ	73/125 (58%)	60 (82%)	13 (18%)	0	100	100
80	Sb	81/84 (96%)	71 (88%)	10 (12%)	0	100	100
81	Se	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
82	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
83	CA	350/394 (89%)	328 (94%)	22 (6%)	0	100	100
85	CE	70/379 (18%)	67 (96%)	3 (4%)	0	100	100
86	i	31/180 (17%)	29 (94%)	2 (6%)	0	100	100
All	All	12323/14340 (86%)	11364 (92%)	922 (8%)	37 (0%)	37	58

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
47	Lt	147	HIS
66	SX	127	ASN

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Mol	Chain	Res	Type
47	Lt	142	ASN
47	Lt	148	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	189 (100%)	1 (0%)	81	92
5	LB	348/349 (100%)	345 (99%)	3 (1%)	70	87
6	LC	306/348 (88%)	306 (100%)	0	100	100
7	LD	246/250 (98%)	245 (100%)	1 (0%)	84	93
8	LE	209/252 (83%)	209 (100%)	0	100	100
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	92
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	147 (99%)	1 (1%)	76	89
14	LL	176/177 (99%)	172 (98%)	4 (2%)	44	71
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	88
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	172 (99%)	1 (1%)	78	91
18	LP	134/163 (82%)	133 (99%)	1 (1%)	76	89
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	91
20	LR	166/175 (95%)	164 (99%)	2 (1%)	63	83
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	86
25	LW	103/126 (82%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	122 (98%)	2 (2%)	55	79
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	88/126 (70%)	86 (98%)	2 (2%)	44	71
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	86
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	84
35	Lg	98/100 (98%)	96 (98%)	2 (2%)	48	74
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	93 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Ls	162/258 (63%)	160 (99%)	2 (1%)	63	83
47	Lt	112/137 (82%)	108 (96%)	4 (4%)	31	58
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	92
50	SA	183/243 (75%)	182 (100%)	1 (0%)	81	92
51	SB	195/231 (84%)	195 (100%)	0	100	100
52	SD	190/202 (94%)	190 (100%)	0	100	100
53	SE	224/225 (100%)	223 (100%)	1 (0%)	84	93
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	162 (98%)	4 (2%)	43	70
56	SI	178/180 (99%)	178 (100%)	0	100	100
57	SK	89/136 (65%)	88 (99%)	1 (1%)	65	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SL	137/142 (96%)	137 (100%)	0	100	100
59	SP	115/130 (88%)	115 (100%)	0	100	100
60	SQ	119/121 (98%)	119 (100%)	0	100	100
61	SR	122/122 (100%)	122 (100%)	0	100	100
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	88
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	94 (100%)	0	100	100
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	113 (100%)	0	100	100
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	267 (98%)	5 (2%)	51	76
71	SC	188/225 (84%)	185 (98%)	3 (2%)	55	79
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	160 (99%)	1 (1%)	78	91
74	SM	102/108 (94%)	99 (97%)	3 (3%)	37	65
75	SN	130/131 (99%)	128 (98%)	2 (2%)	57	80
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	110 (98%)	2 (2%)	51	76
78	SY	113/115 (98%)	112 (99%)	1 (1%)	70	87
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100
81	Se	43/48 (90%)	43 (100%)	0	100	100
82	Sf	60/140 (43%)	60 (100%)	0	100	100
83	CA	303/336 (90%)	302 (100%)	1 (0%)	86	94
85	CE	68/338 (20%)	68 (100%)	0	100	100
86	i	28/151 (18%)	28 (100%)	0	100	100
All	All	10729/12217 (88%)	10670 (100%)	59 (0%)	78	92

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	Lt	74	VAL
77	SW	25	VAL
55	SH	29	GLU
75	SN	63	VAL
73	SJ	137	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 183 such sidechains are listed below:

Mol	Chain	Res	Type
51	SB	202	GLN
63	ST	42	HIS
53	SE	188	ASN
56	SI	84	ASN
68	Sc	26	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	830 (22%)	18 (0%)
2	L7	119/121 (98%)	11 (9%)	0
3	L8	155/157 (98%)	27 (17%)	0
49	S2	1715/1869 (91%)	406 (23%)	11 (0%)
84	CC	74/75 (98%)	23 (31%)	2 (2%)
All	All	5768/7288 (79%)	1297 (22%)	31 (0%)

5 of 1297 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	30	C
1	L5	39	A
1	L5	42	A

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3876	A
49	S2	688	U
1	L5	4913	G
84	CC	35	U

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Mol	Chain	Res	Type
49	S2	420	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 264 ligands modelled in this entry, 264 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

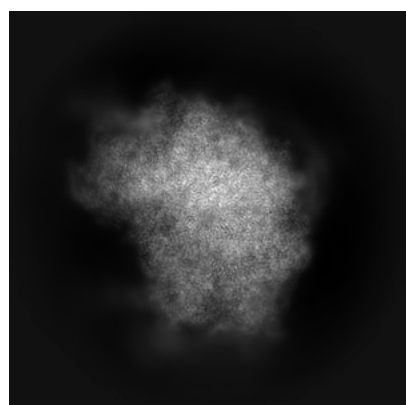
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11292. These allow visual inspection of the internal detail of the map and identification of artifacts.

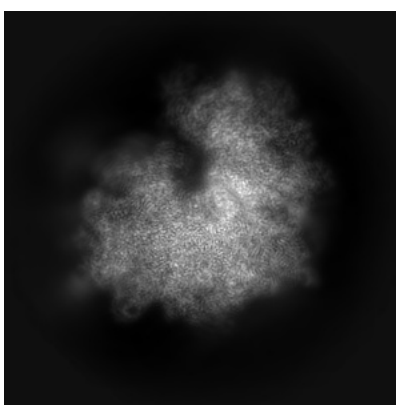
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

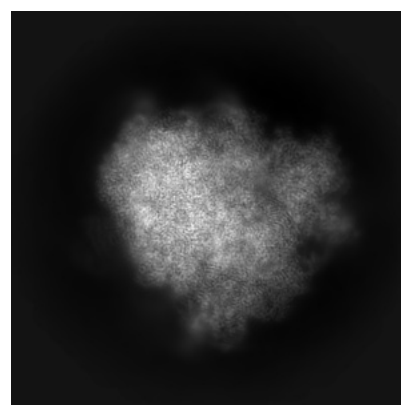
6.1.1 Primary map



X



Y

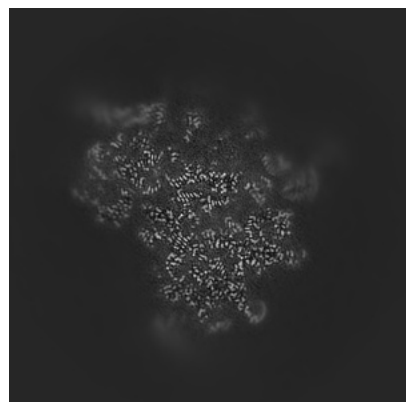


Z

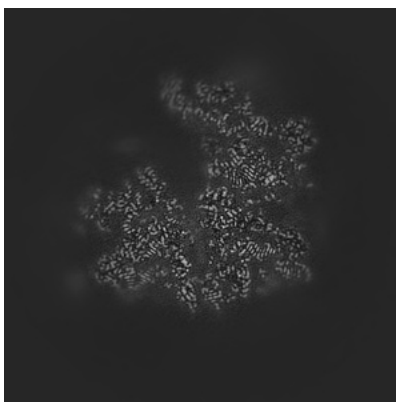
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

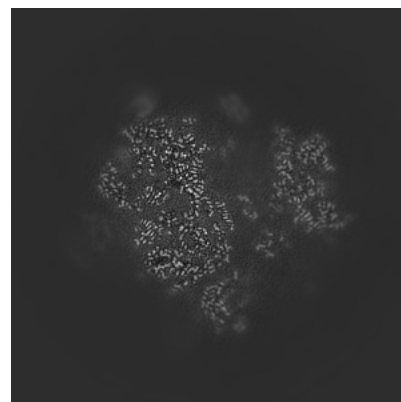
6.2.1 Primary map



X Index: 200



Y Index: 200

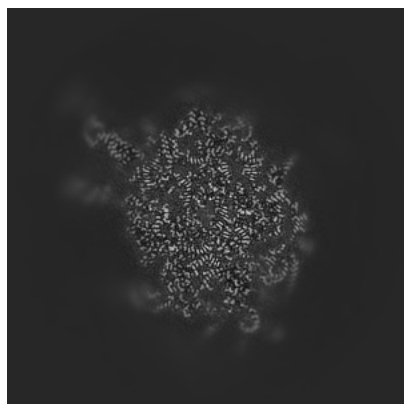


Z Index: 200

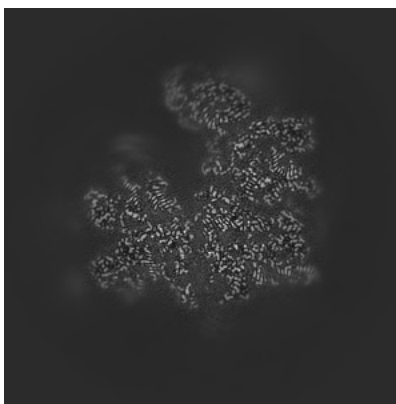
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

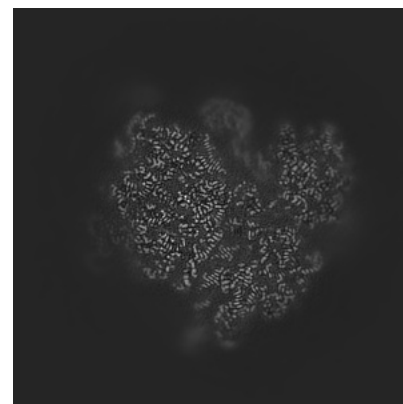
6.3.1 Primary map



X Index: 178



Y Index: 194

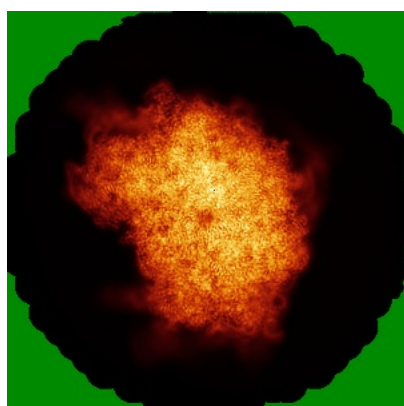


Z Index: 224

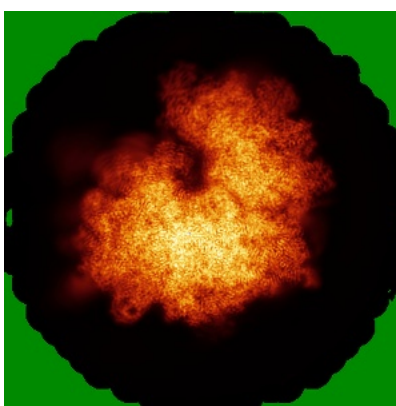
The images above show the largest variance slices of the map in three orthogonal directions.

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

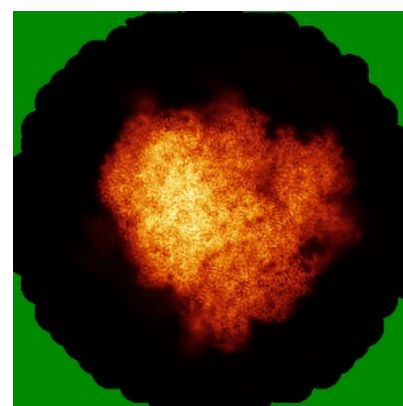
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

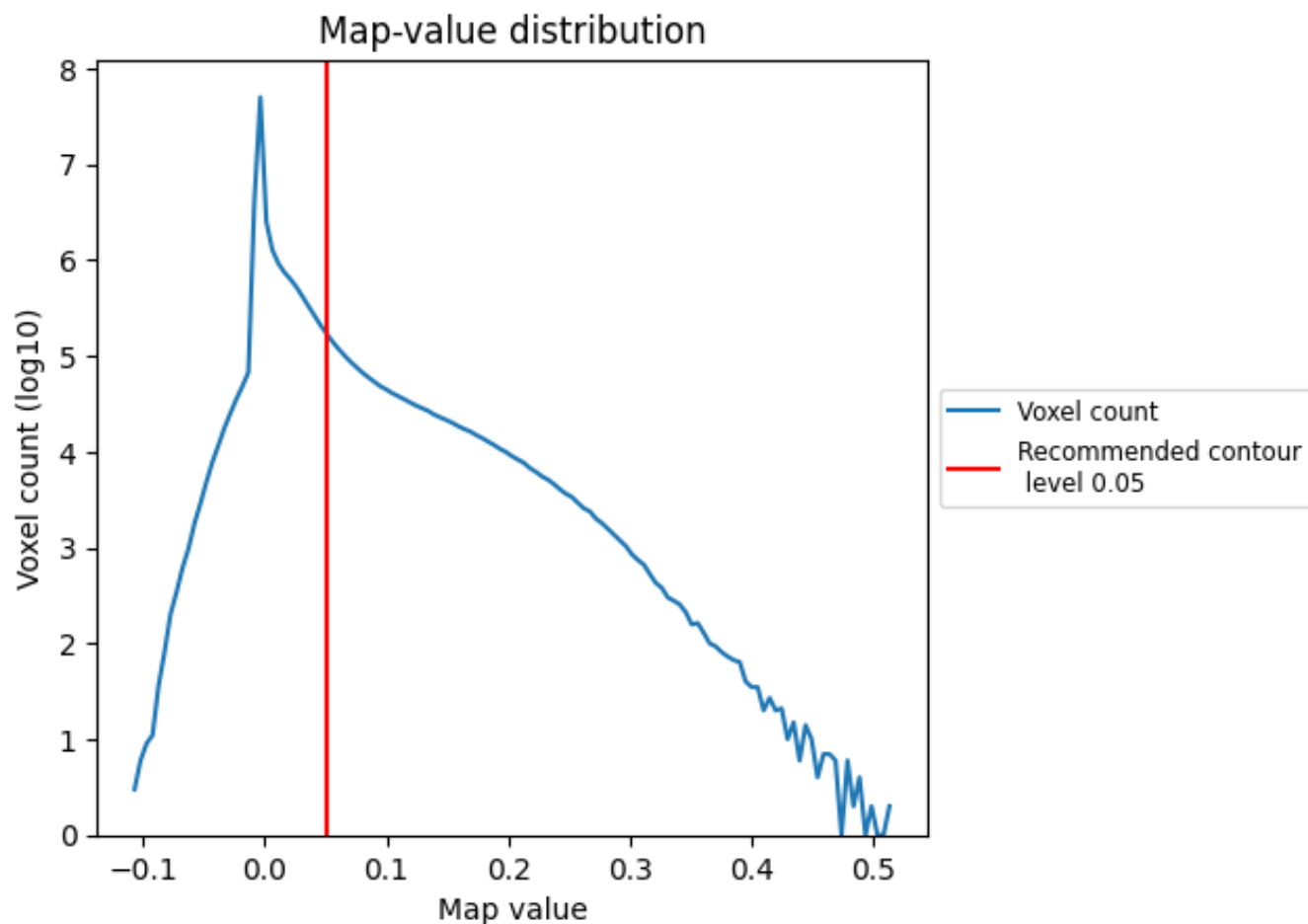
6.6 Mask visualisation

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

7 Map analysis [i](#)

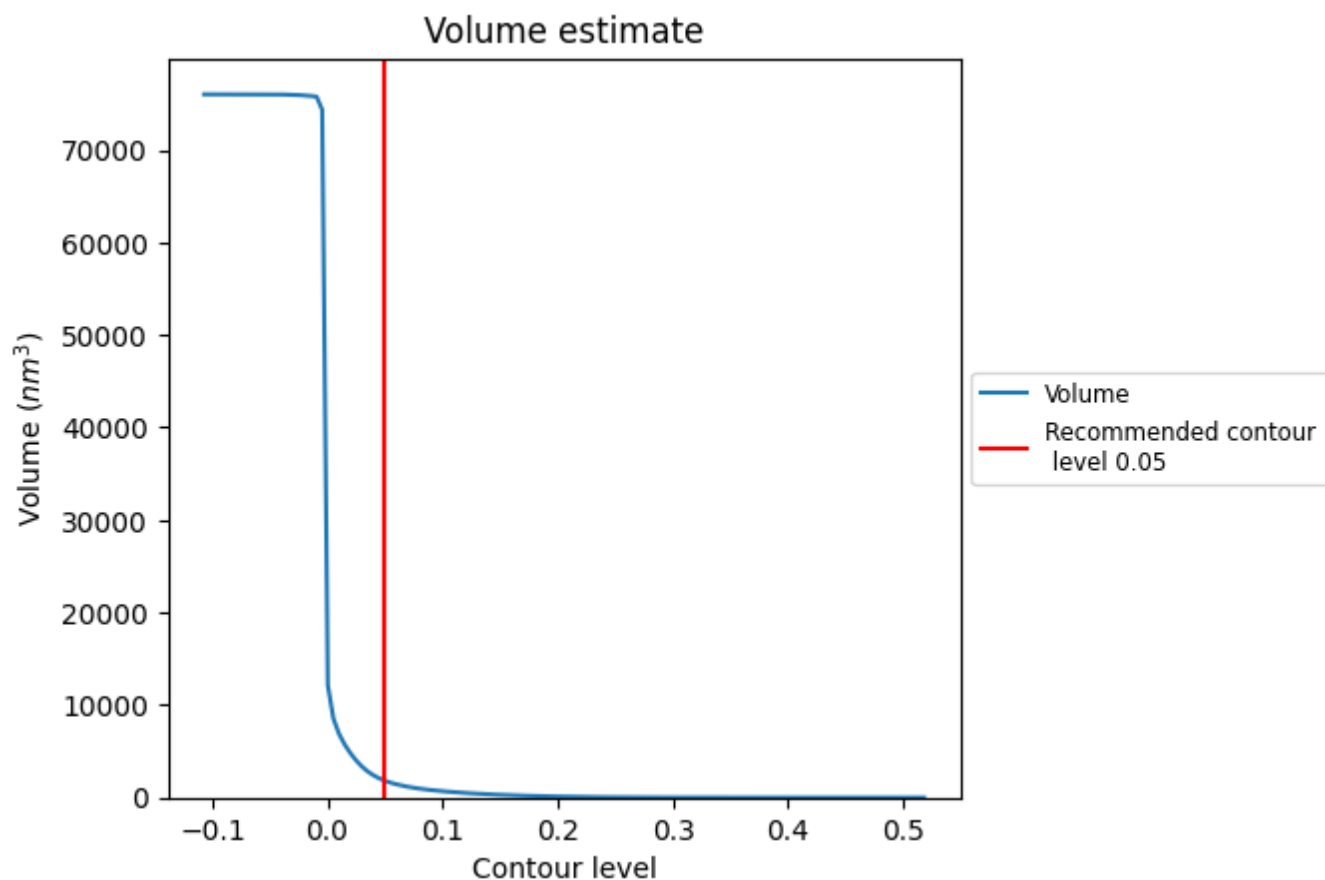
This section contains the results of statistical analysis of the map.

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.

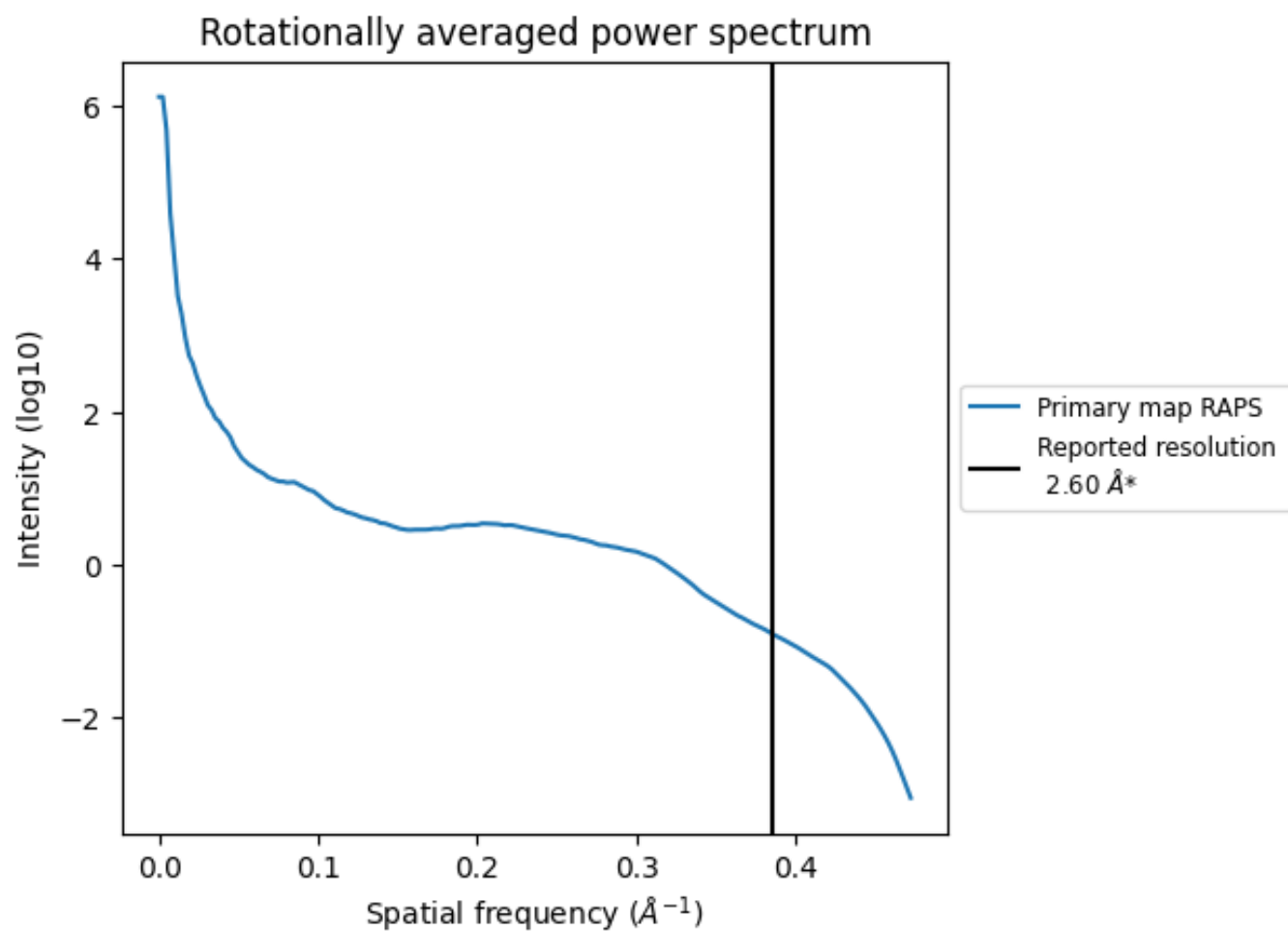
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1822 nm³; this corresponds to an approximate mass of 1646 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 ⓘ

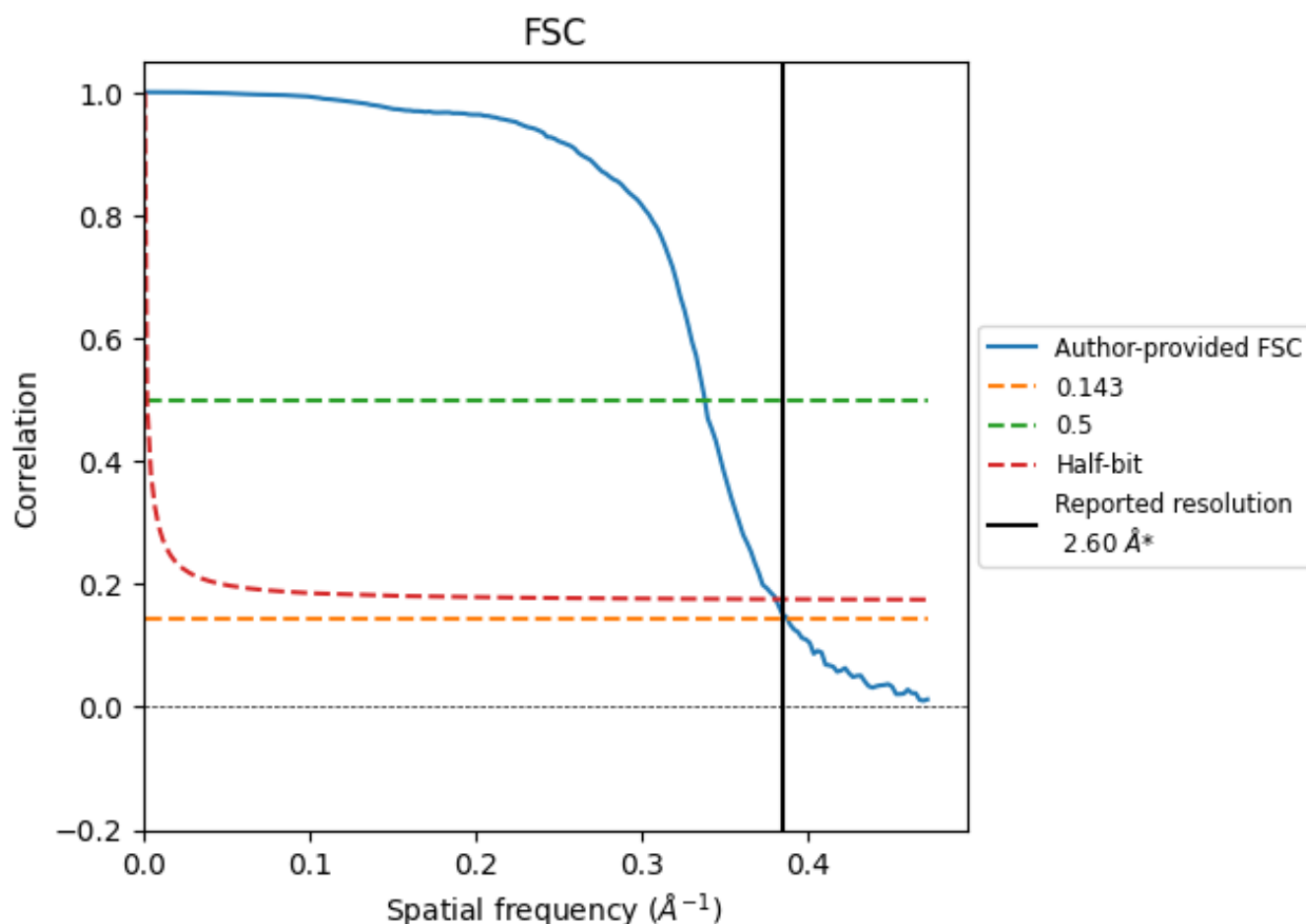


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	2.96	2.63
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

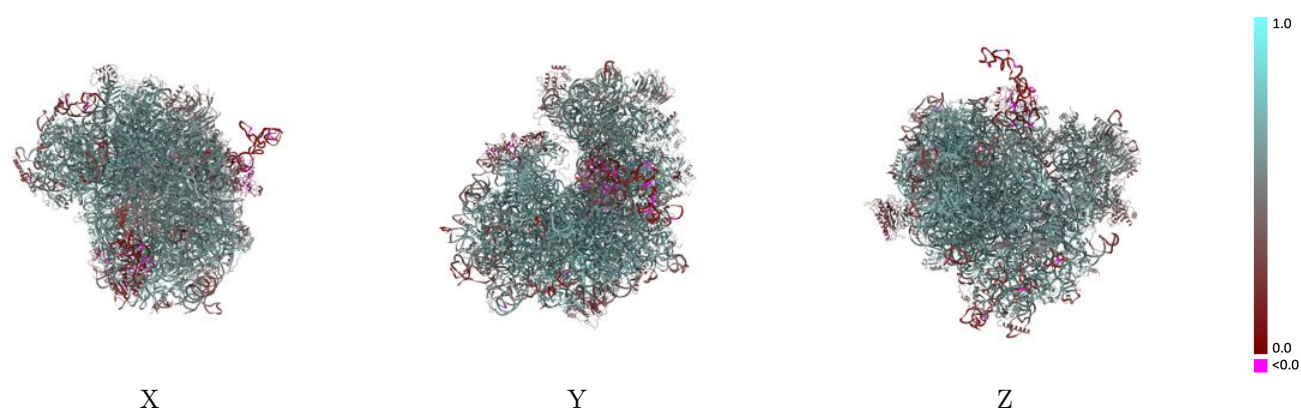
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11292 and PDB model 6ZMI. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

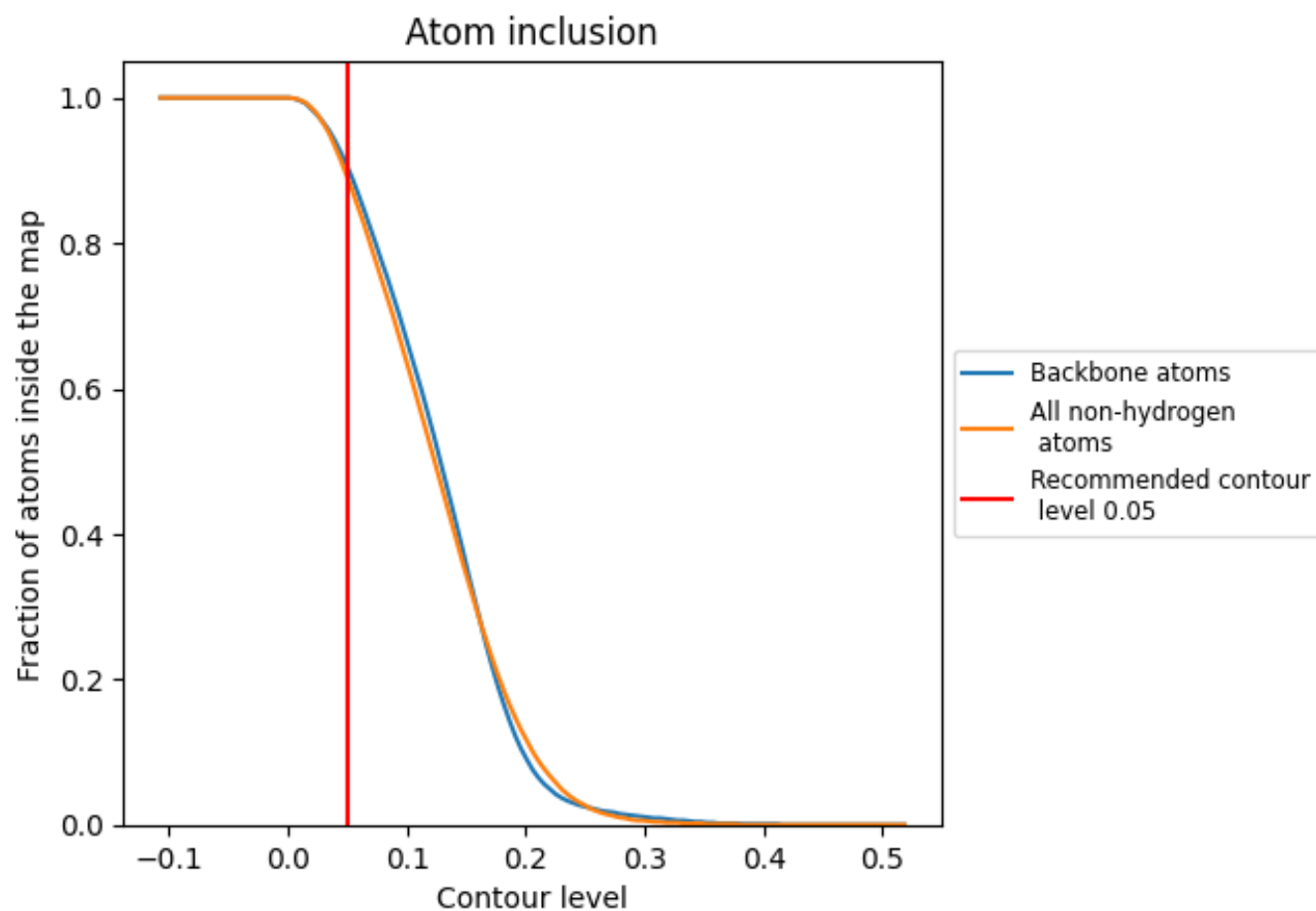


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.5750
CA	 0.0380	 0.3190
CC	 0.8400	 0.3510
CE	 0.7730	 0.5450
L5	 0.9300	 0.5890
L7	 0.9930	 0.6360
L8	 0.9670	 0.6210
LA	 0.9870	 0.6800
LB	 0.9410	 0.6450
LC	 0.9450	 0.6340
LD	 0.9100	 0.5870
LE	 0.8540	 0.5600
LF	 0.9640	 0.6440
LG	 0.8450	 0.5730
LH	 0.9320	 0.6090
LI	 0.9470	 0.6230
LJ	 0.8180	 0.5110
LL	 0.8970	 0.6040
LM	 0.9360	 0.6020
LN	 0.9940	 0.6820
LO	 0.9570	 0.6500
LP	 0.9610	 0.6610
LQ	 0.9770	 0.6630
LR	 0.8910	 0.6040
LS	 0.9790	 0.6520
LT	 0.9370	 0.6170
LU	 0.8430	 0.5310
LV	 0.9660	 0.6550
LW	 0.7010	 0.4780
LX	 0.9310	 0.6250
LY	 0.9260	 0.6210
LZ	 0.9390	 0.6170
La	 0.9710	 0.6630
Lb	 0.8620	 0.5650
Lc	 0.9300	 0.6230



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Chain	Atom inclusion	Q-score
Ld	 0.9210	 0.6190
Le	 0.9770	 0.6620
Lf	 0.9810	 0.6610
Lg	 0.9260	 0.6430
Lh	 0.9270	 0.6080
Li	 0.9220	 0.6050
Lj	 0.9820	 0.6680
Lk	 0.8470	 0.5640
Ll	 0.9760	 0.6380
Lm	 0.9280	 0.6240
Ln	 0.9860	 0.6670
Lo	 0.9310	 0.6350
Lp	 0.9590	 0.6680
Lr	 0.9600	 0.6310
Ls	 0.1440	 0.1380
Lt	 0.0350	 0.0940
Lz	 0.1310	 0.1510
S2	 0.9430	 0.5820
SA	 0.8890	 0.5810
SB	 0.9120	 0.5940
SC	 0.9370	 0.6100
SD	 0.8390	 0.5240
SE	 0.9290	 0.5940
SF	 0.8920	 0.5370
SG	 0.7920	 0.5060
SH	 0.7540	 0.4980
SI	 0.8970	 0.5850
SJ	 0.9060	 0.5760
SK	 0.7910	 0.4830
SL	 0.8940	 0.6120
SM	 0.3120	 0.2690
SN	 0.9570	 0.6320
SO	 0.8990	 0.5910
SP	 0.7810	 0.4850
SQ	 0.8640	 0.5450
SR	 0.8070	 0.5240
SS	 0.8140	 0.5060
ST	 0.8610	 0.5300
SU	 0.7790	 0.4950
SV	 0.9150	 0.5870
SW	 0.9640	 0.6400
SX	 0.9510	 0.6340

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Chain	Atom inclusion	Q-score
SY	 0.8170	 0.5290
SZ	 0.7270	 0.4700
Sa	 0.9210	 0.6060
Sb	 0.8860	 0.5710
Sc	 0.8170	 0.5250
Sd	 0.9460	 0.5890
Se	 0.8060	 0.5460
Sf	 0.4720	 0.3380
Sg	 0.6880	 0.4630
i	 0.9260	 0.6210