



## wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 10:04 pm BST

PDB ID : 6Z6N  
EMDB ID : EMD-11100  
Title : Cryo-EM structure of human EBP1-80S ribosomes (focus on EBP1)  
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.  
Deposited on : 2020-05-28  
Resolution : 2.90 Å(reported)  
Based on initial model : 6EK0

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

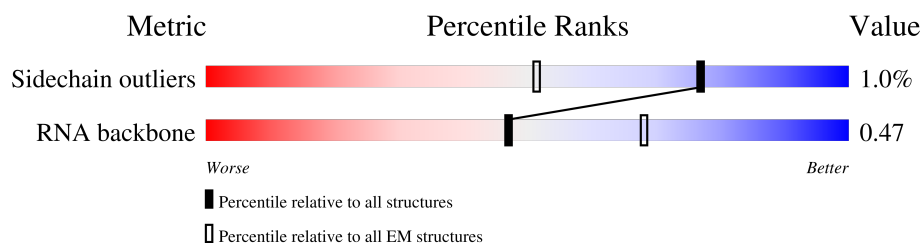
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 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.



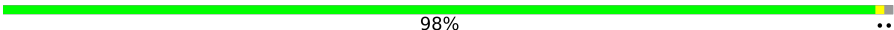
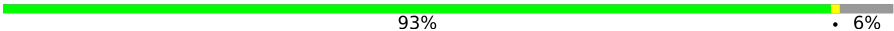
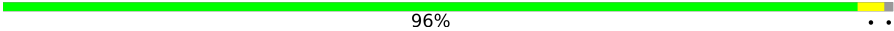
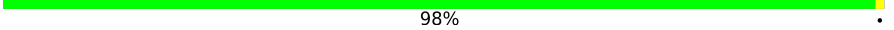

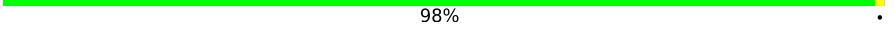
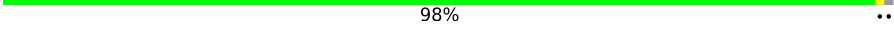

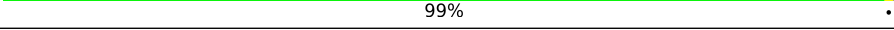
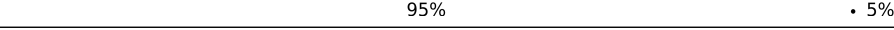
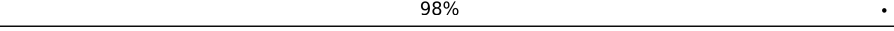
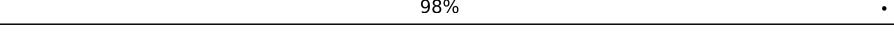

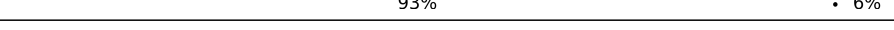



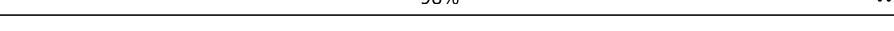
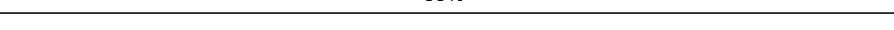
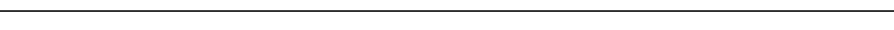

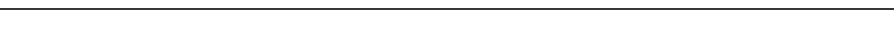
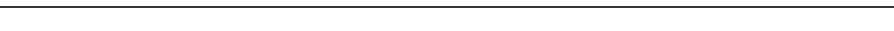


Metric	Whole archive (#Entries)	EM structures (#Entries)
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	L5	5070	53% 20% • 26%
2	L7	121	86% 13% •
3	L8	157	77% 21% ••
4	LA	257	94% • •
5	LB	403	99% •
6	LC	427	86% 14%
7	LD	297	98% •
8	LE	288	81% • 18%
9	LF	248	90% 9%
10	LG	266	89% • 9%

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Mol	Chain	Length	Quality of chain
11	LH	192	 98% ..
12	LI	214	 93% • 6%
13	LJ	178	 96% ..
14	LL	211	 98% •
15	LM	215	 63% • 35%
16	LN	204	 98% •
17	LO	203	 98% ..
18	LP	184	 83% • 17%
19	LQ	188	 99% ..
20	LR	196	 95% • 5%
21	LS	176	 98% ..
22	LT	160	 98% ..
23	LU	128	 78% • 21%
24	LV	140	 93% • 6%
25	LW	157	 78% • 21%
26	LX	156	 77% 23%
27	LY	145	 91% • 8%
28	LZ	136	 98% ..
29	La	148	 99% ..
30	Lb	159	 69% 31%
31	Lc	115	 83% • 15%
32	Ld	125	 84% • 14%
33	Le	135	 93% • 5%
34	Lf	110	 97% ..
35	Lg	117	 96% • •

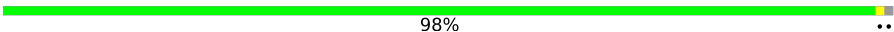

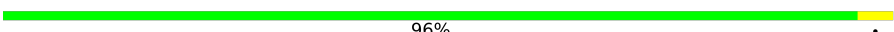
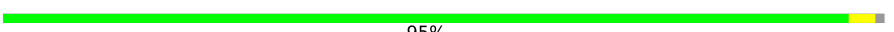









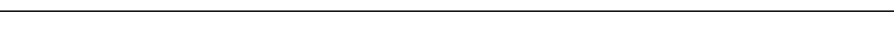

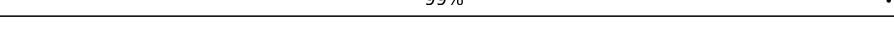
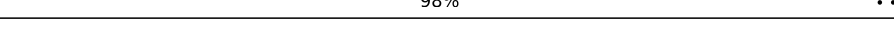
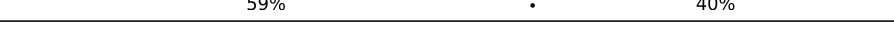
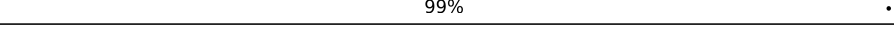
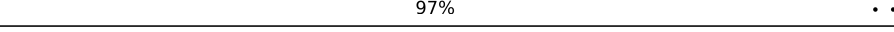


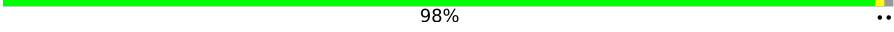

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Mol	Chain	Length	Quality of chain
36	Lh	123	98% ..
37	Li	105	97% .
38	Lj	97	87% . 11%
39	Lk	70	99% .
40	Ll	51	96% ..
41	Lm	128	40% . 59%
42	Ln	25	96% .
43	Lo	106	99% .
44	Lp	92	99% .
45	Lr	137	90% . 9%
46	Lz	217	98% .
47	S2	1869	65% 26% . 7%
48	SA	295	74% . 25%
49	SB	264	79% . 19%
50	SD	243	91% . 7%
51	SE	263	99%
52	SF	204	92% . 7%
53	SH	194	93% . .
54	SI	208	99% .
55	SK	165	58% . 41%
56	SL	158	94% . .
57	SP	145	88% 12%
58	SQ	146	95% ..
59	SR	135	99% .
60	SS	152	95% . 5%

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Mol	Chain	Length	Quality of chain
61	ST	145	 98% ..
62	SU	119	 87% . 13%
63	SV	83	 96% .
64	SX	143	 95% ..
65	Sa	115	 89% 11%
66	Sc	69	 91% . 7%
67	Sd	56	 96% ..
68	Sg	317	 98% .
69	SC	293	 75% . 24%
70	SG	249	 94% . 5%
71	SJ	194	 95% . 5%
72	SM	132	 87% 5% 8%
73	SN	151	 99% .
74	SO	151	 91% . 7%
75	SW	130	 99% .
76	SY	133	 98% ..
77	SZ	125	 59% . 40%
78	Sb	84	 99% .
79	Se	59	 97% ..
80	Sf	156	 42% . 57%
81	CA	394	 90% 10%
82	CB	858	 98% ..
83	CC	75	 57% 36% 7%
84	CD	408	 7% 92%

## 2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228566 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3772	Total	C	N	O	P	0	0
			80116	35645	14585	26115	3771		

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

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 rRNA.

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 ribosomal protein L10a.

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

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 48 is a protein called 40S ribosomal protein SA.

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

- Molecule 49 is a protein called 40S ribosomal protein S3a.

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

- Molecule 50 is a protein called 40S ribosomal protein S3.

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

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 53 is a protein called 40S ribosomal protein S7.

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

- Molecule 54 is a protein called 40S ribosomal protein S8.

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

- Molecule 55 is a protein called 40S ribosomal protein S10.

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

- Molecule 56 is a protein called 40S ribosomal protein S11.

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

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 58 is a protein called 40S ribosomal protein S16.

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

- Molecule 59 is a protein called 40S ribosomal protein S17.

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

- Molecule 60 is a protein called 40S ribosomal protein S18.

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

- Molecule 61 is a protein called 40S ribosomal protein S19.

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

- Molecule 62 is a protein called 40S ribosomal protein S20.

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

- Molecule 63 is a protein called 40S ribosomal protein S21.

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

- Molecule 64 is a protein called 40S ribosomal protein S23.

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

- Molecule 65 is a protein called 40S ribosomal protein S26.

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

- Molecule 66 is a protein called 40S ribosomal protein S28.

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

- Molecule 67 is a protein called 40S ribosomal protein S29.

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

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S2.

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

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S12.

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

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called 40S ribosomal protein S14.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called 40S ribosomal protein S25.



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

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 81 is a protein called Proliferation-associated protein 2G4.

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

- Molecule 82 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CB	846	Total	C	N	O	S	0	0
			6609	4195	1136	1234	44		

- Molecule 83 is a RNA chain called tRNA.

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

- Molecule 84 is a protein called Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CD	32	Total	C	N	O	S	0	0
			232	135	59	37	1		

- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	L5	211	Total	Mg	0
			211	211	
85	L7	3	Total	Mg	0
			3	3	
85	L8	4	Total	Mg	0
			4	4	
85	LA	1	Total	Mg	0
			1	1	
85	LI	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	2	Total	Mg	0
			2	2	
85	Lg	1	Total	Mg	0
			1	1	
85	S2	30	Total	Mg	0
			30	30	
85	SG	1	Total	Mg	0
			1	1	

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	Lg	1	Total	Zn	0
			1	1	
86	Lj	1	Total	Zn	0
			1	1	
86	Lm	1	Total	Zn	0
			1	1	
86	Lo	1	Total	Zn	0
			1	1	
86	Lp	1	Total	Zn	0
			1	1	
86	Sa	1	Total	Zn	0
			1	1	

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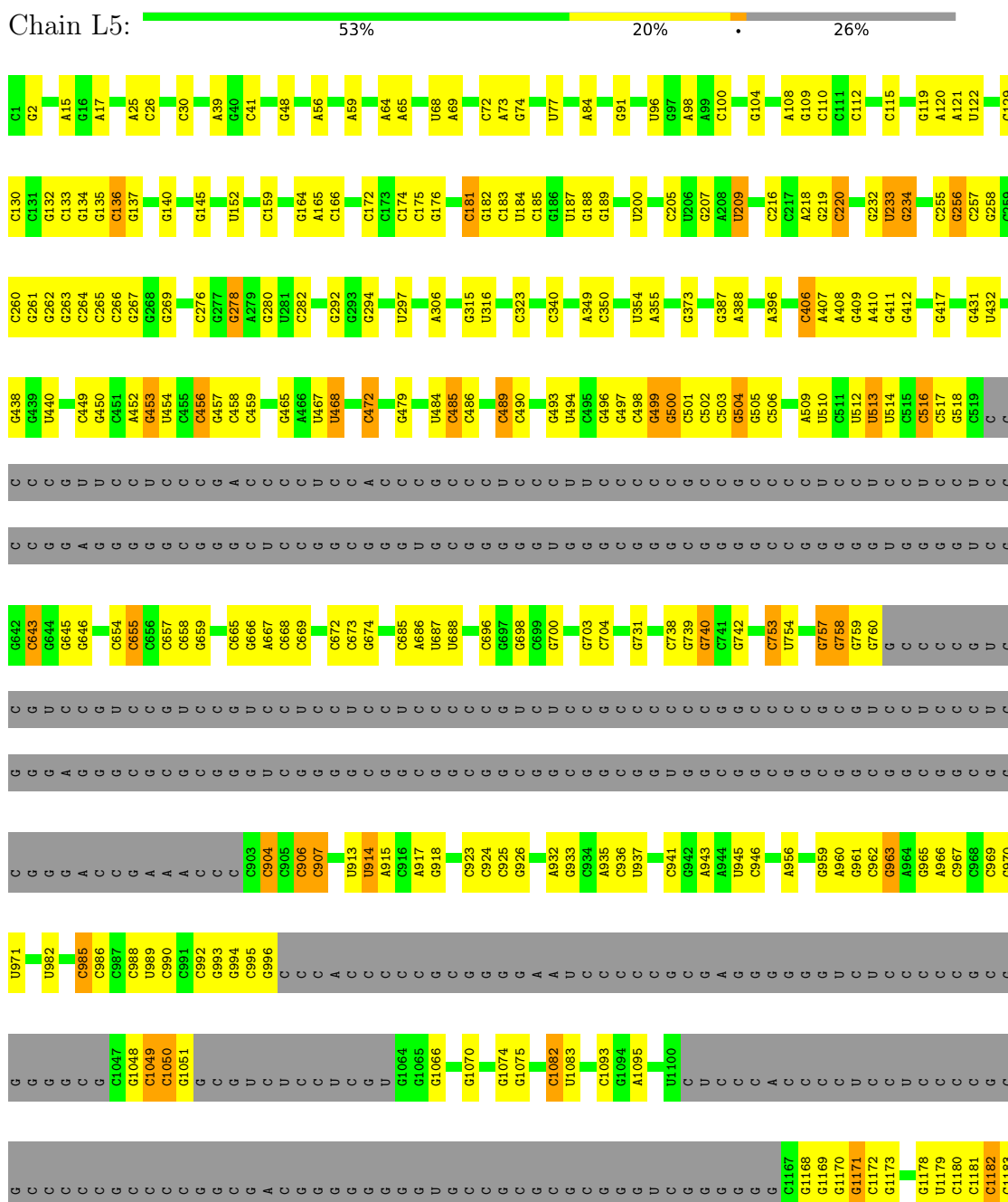
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Mol	Chain	Residues	Atoms		AltConf
86	Sd	1	Total 1	Zn 1	0
86	Sf	1	Total 1	Zn 1	0

### 3 Residue-property plots [i](#)

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. 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. 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 rRNA

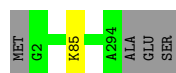


C2909	U2763	A2601	C2465	G2262	U2048	U1974	G1842	G	U1620	C1413	G1275	A1184
G2910	A2764	G2606	G2466	A2263	U2054	G1975	A1843	G	G1624	C1414	C1276	
G		G2606	C	C	G2055	G1976	G1853	G	G1625	G1415	G1277	C1191
C	U2769	G2618	C	C	G2056	C1977	G1854	C	G1741	G1416	C1280	C1203
A	C2770		A	C	C	C1978	G1855	C	A1631	C1417	G1284	C1204
C	A2783		C	C	A2069	U1980	A1868	C	A1632	A1420	G1287	
C			G	G	C	G1981	G1969	G	G1633	A1433	G1287	C1210
C			C	C	C2084	G1982	G1969	C	A1634	A1437	A1294	G1211
C			C	C	G2085	A1983	G1878	C	A1638	C1437	A1294	
C			C	C	G2089	G1985	G1878	C	A1638	U1438	C1295	C1214
C			C	C	U2090	U1986	U1882	C	G1755	C1439	G1296	C1215
C			C	C	C2091	C1987	U1882	C	G1756	U1440	C1301	C1216
C			C	C	G2092	G1988	A1892	C	U1757	C1441	C1301	C1217
C			C	C	A2093	G1989	A1893	C	G1758	C1442	G1324	G1218
C			C	C	G2094	A1990	A1897	C	G1759	A1443	G1324	G1219
C			C	C	A2095	A1991	A1897	C	G1760	C1446	G1325	
C			C	C	G2096	U1992	C1915	C	C1762	C1447	A1326	A1222
C			C	C	U2097	C1993	C1915	C	G1763	C1472	C1327	G
C			C	C	G2098	C1994	C1915	C	G1764	G1482	A1337	G
C			C	C	U2099	G1995	G1918	C	A1765	C1483	C1340	U
C			C	C	A2100	G1996	G1919	C	A1766	G1482	C1340	U
C			C	C	C2101	U1997	C1920	C	A1767	C1483	C1340	U
C			C	C	G2102	A1998	C1921	C	G1768	G1493	A1354	C
C			C	C		A1999	G1922	C	U1677	C1497	C1358	U
C			C	C	C2107	G2000		C	C1678	G1498	G1359	C
C			C	C	G2108	G2001	G1925	C	C1678	G1498	G1360	C
C			C	C	C2111	A2002	A1929	C	G1681	G1498	C1360	G
C			C	C	G2112	G2003	U1930	C	G1681	G1498	C1360	G
C			C	C		U2004	C1931	C	G1691	G1502	G1365	G1234
C			C	C	G	G2005	A1932	C	C1694	G1502	G1365	G1235
C			C	C	G	U2006	C1932	C	G1694	A1515	G1366	
C			C	C	G	G2007	C1935	C	G1697	A1515	G1366	C1241
C			C	C	G	U2008	C1935	C	C1698	G1516	G1367	C1241
C			C	C	G	A2009	C1936	C	A1699	G1517	C1368	C1243
C			C	C	G	A2010	C1936	C	G1700	A1518	G1377	G1244
C			C	C	G	C2011	G1940	C	U1792	C1519	C1378	C1245
C			C	C	G	A2012		C	G1797	G1534	G1379	G1246
C			C	C	G	A2013	G1945	C	C1701	A1534	U1381	U1247
C			C	C	G	C2014	G1946	C	C1702	A1547	A1387	
C			C	C	G	U2015	U1947	C	C1703	G1552	G1253	G1253
C			C	C	G		G1948	C	G1704	A1254	A1254	A1254
C			C	C	G	C2018	U1949	C	G1705	A1255	G1256	G1256
C			C	C	G	C2019	U1950	C	C1707	C1566	A1257	G1257
C			C	C	G	U2020	G1951	C	G1708	C1566	G1258	G1258
C			C	C	G	G2021		C	C1709	U1578	G1259	G1259
C			C	C	G	C2022	U1959	C	A	C	G1260	G1260
C			C	C	G	C2023	A1960	C	C	U1582	G1261	G1261
C			C	C	G	G2024	G1961	C	C	G1582	G1262	G1262
C			C	C	G	A2025	A1962	C	C	G1582	G1263	G1263
C			C	C	G	A2026		C	C	G1582	G1264	G1264
C			C	C	G		C1966	C	C	G1582	G1265	G1265
C			C	C	G	A2033	A1967	C	C	G1582	G1266	G1266
C			C	C	G	G2034	G1968	C	C	G1582	G1267	G1267
C			C	C	G	G2034	G1969	C	C	G1582	G1268	G1268
C			C	C	G		A1970	C	C	G1582	G1269	G1269
C			C	C	G	U2044	C1971	C	C	G1582	G1270	G1270
C			C	C	G	G2045	G1972	C	C	G1582	G1271	G1271
C			C	C	G	C2046	G1972	C	C	G1582	G1272	G1272
C			C	C	G	A2047	G1973	C	C	G1582	G1273	G1273
C			C	C	G			C	C	G1582	G1274	G1274
C			C	C	G			C	C	G1582	G1275	G1275
C			C	C	G			C	C	G1582	G1276	G1276
C			C	C	G			C	C	G1582	G1277	G1277
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C			C	C	G			C	C	G1582	G1344	G1344
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C			C	C	G			C	C	G1582	G1346	G1346
C			C	C	G			C	C	G1582	G1347	G1347
C			C	C	G			C	C	G1582	G1348	G1348
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C			C	C	G			C	C	G1582	G1357	G1357
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C			C	C	G			C	C	G1582	G1359	G1359
C			C	C	G			C	C	G1582	G1360	G1360
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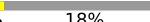


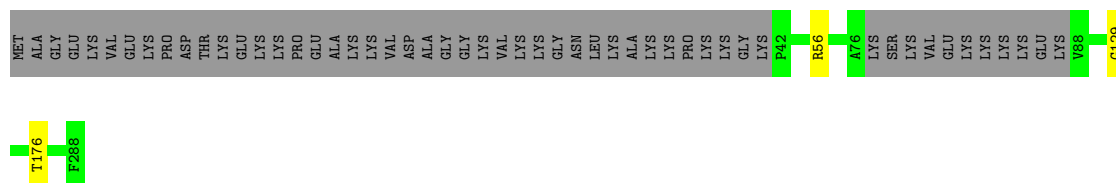


Chain LD:  98%



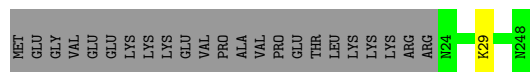
- Molecule 8: 60S ribosomal protein L6

Chain LE:  81%  18%



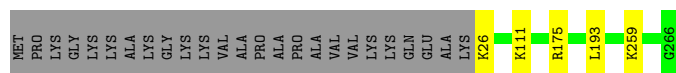
- Molecule 9: 60S ribosomal protein L7

Chain LF:  90%  9%



- Molecule 10: 60S ribosomal protein L7a

Chain LG:  89%  9%



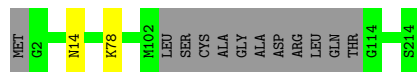
- Molecule 11: 60S ribosomal protein L9

Chain LH:  98%  2%



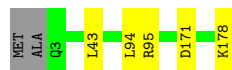
- Molecule 12: 60S ribosomal protein L10-like

Chain LI:  93%  6%



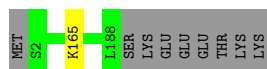
- Molecule 13: 60S ribosomal protein L11

Chain LJ:  96%  4%





- Chain LR:  95% . 5



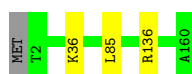
- Molecule 21: 60S ribosomal protein L18a

Chain LS: 98%



- Molecule 22: 60S ribosomal protein L21

Chain LT: 98%



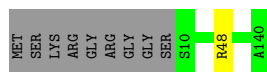
- Molecule 23: 60S ribosomal protein L22

Chain LU: 78% 21%



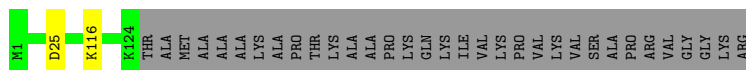
- Molecule 24: 60S ribosomal protein L23

Chain LV: 93% 6%



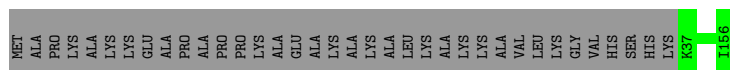
- Molecule 25: 60S ribosomal protein L24

Chain LW: 78% 21%



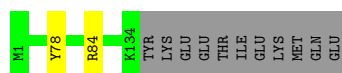
- Molecule 26: 60S ribosomal protein L23a

Chain LX: 77% 23%



- Molecule 27: 60S ribosomal protein L26

Chain LY: 91% 8%



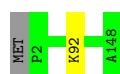
- Molecule 28: 60S ribosomal protein L27

Chain LZ: 98% ..



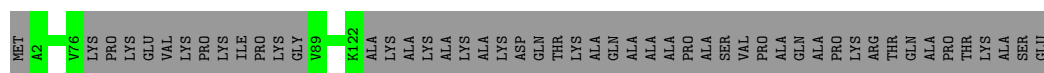
- Molecule 29: 60S ribosomal protein L27a

Chain La: 99% ..



- Molecule 30: 60S ribosomal protein L29

Chain Lb: 69% 31%



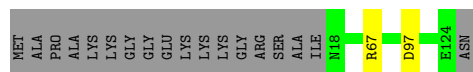
- Molecule 31: 60S ribosomal protein L30

Chain Lc: 83% • 15%



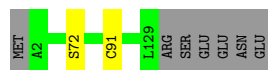
- Molecule 32: 60S ribosomal protein L31

Chain Ld: 84% • 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 93% • 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 97% • 5%



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 96% ..



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 98% ..



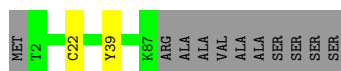
- Molecule 37: 60S ribosomal protein L36

Chain Li: 97% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 87% . 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 99% .



- Molecule 40: 60S ribosomal protein L39

Chain Ll: 96% ..



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 40% . 59%

MET GLN ILE PHE VAL THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS LYS ILE ASP LYS GLU ILE ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA LYS LYS LEU GLU ASP GLY THR SER TYR ASN

ILE GLN LYS SER THR LEU HIS VAL ARG LEU ARG GLY I77 V127 K128

- Molecule 42: 60S ribosomal protein L41

Chain Ln: 96%

M1 S24 LYS

- Molecule 43: 60S ribosomal protein L36a

Chain Lo: 99%

MET Y2 F106

- Molecule 44: 60S ribosomal protein L37a

Chain Lp: 99%

MET A2 Q92

- Molecule 45: 60S ribosomal protein L28

Chain Lr: 90% 9%

MET S2 R20 R103 Y126 LYS ARG LYS ARG ARG ARG PRO THR LYS SER SER

- Molecule 46: 60S ribosomal protein L10a

Chain Lz: 98%

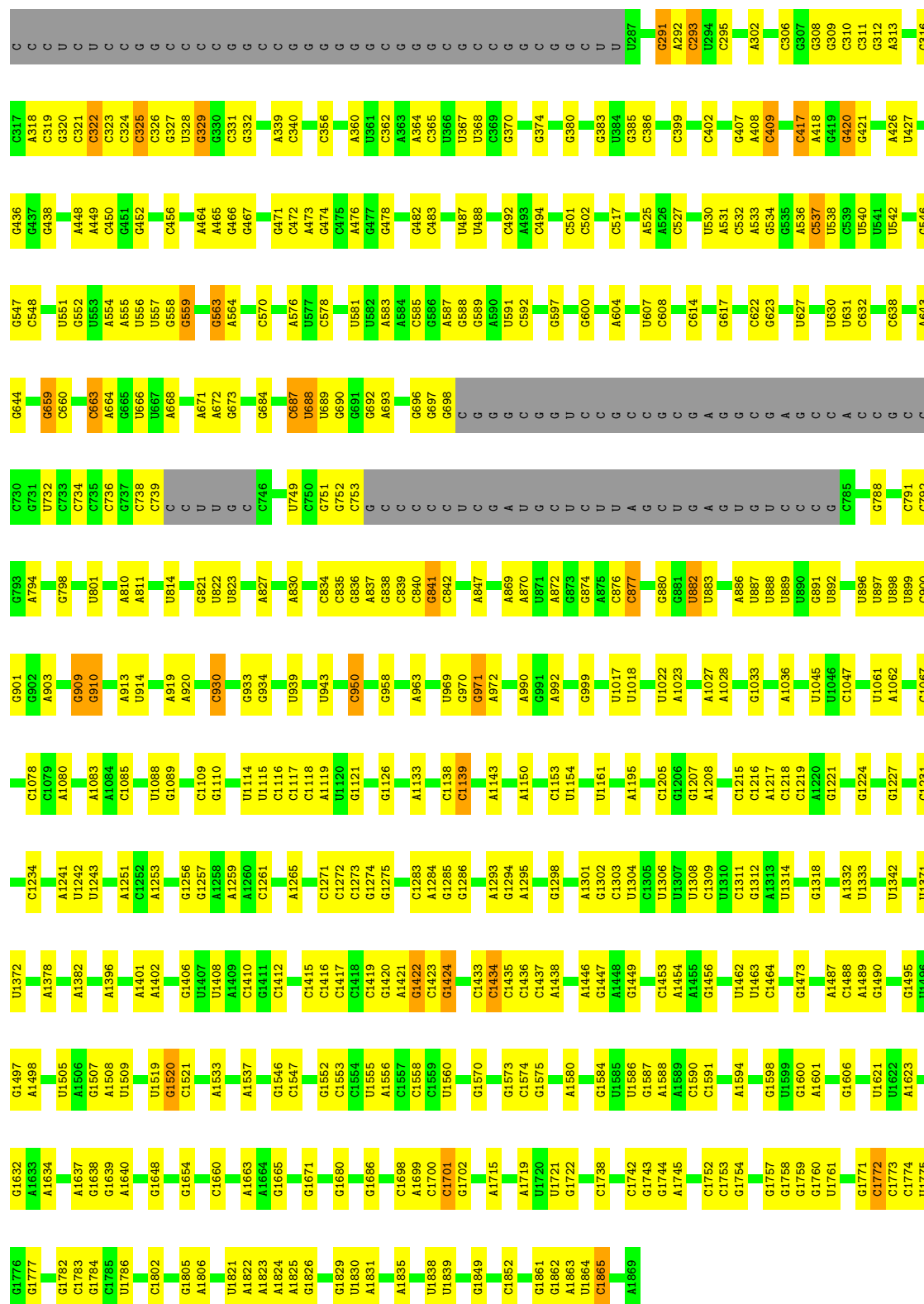
M1 R7 R122 K161 L194 R215 L216 Y217

- Molecule 47: 18S rRNA

Chain S2: 65% 26% 7%

U1 C14 C17 G20 A25 G33 G41 A42 A46 G47 C48 C49 G56 U59 G62 G63 A64 G67 G204 A68 C72 C73 G74 G75 U76 A92 A103 U112 G113 G114 U115 U116 C117 C118 G126 C129 G130 C139 U143 A147 U148

A149 U154 A158 A159 U160 U161 C162 U163 A175 C178 C179 G184 C188 U189 G190 C196 U197 U198 C199 G200 G203 G204 G205 G206 G207 G208 G213 U214 G225 A U C A A A A C C A A C C C G G U C A G C

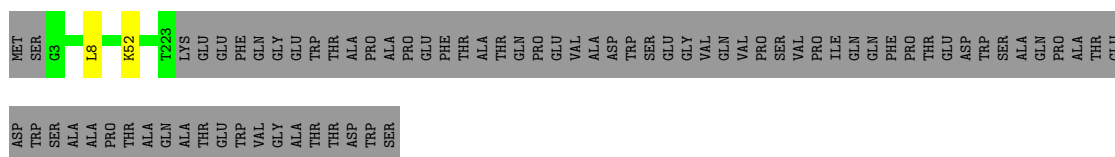


• Molecule 48: 40S ribosomal protein SA

Chain SA:

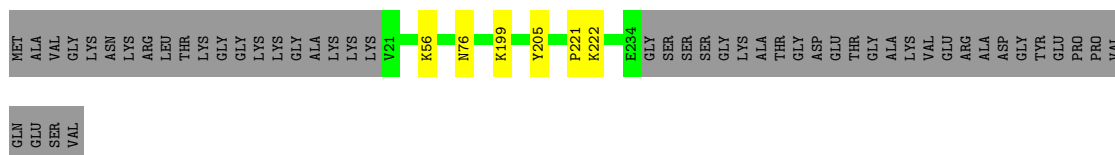
74%

25%



- Molecule 49: 40S ribosomal protein S3a

Chain SB: 79% 19%



- Molecule 50: 40S ribosomal protein S3

Chain SD: 91% 7%



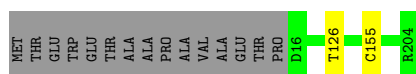
- Molecule 51: 40S ribosomal protein S4, X isoform

Chain SE: 99%



- Molecule 52: 40S ribosomal protein S5

Chain SF: 92% 7%



- Molecule 53: 40S ribosomal protein S7

Chain SH: 93% 2%



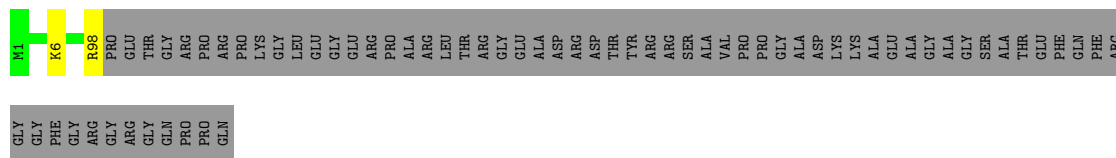
- Molecule 54: 40S ribosomal protein S8

Chain SI: 99%



- Molecule 55: 40S ribosomal protein S10

Chain SK:  58% 41%




- Molecule 56: 40S ribosomal protein S11

Chain SL:  94%



- Molecule 57: 40S ribosomal protein S15

Chain SP:  88% 12%



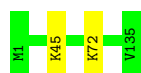
- Molecule 58: 40S ribosomal protein S16

Chain SQ:  95%



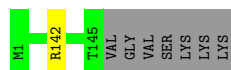
- Molecule 59: 40S ribosomal protein S17

Chain SR:  99%



- Molecule 60: 40S ribosomal protein S18

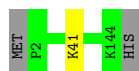
Chain SS:  95% 5%



- Molecule 61: 40S ribosomal protein S19

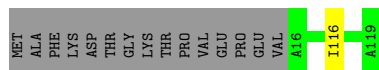
Chain ST:  98%





- Molecule 62: 40S ribosomal protein S20

Chain SU: 87% 13%



- Molecule 63: 40S ribosomal protein S21

Chain SV: 96%



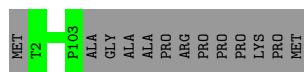
- Molecule 64: 40S ribosomal protein S23

Chain SX: 95%



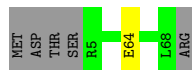
- Molecule 65: 40S ribosomal protein S26

Chain Sa: 89% 11%



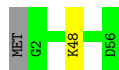
- Molecule 66: 40S ribosomal protein S28

Chain Sc: 91% 7%



- Molecule 67: 40S ribosomal protein S29

Chain Sd: 96%



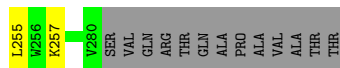
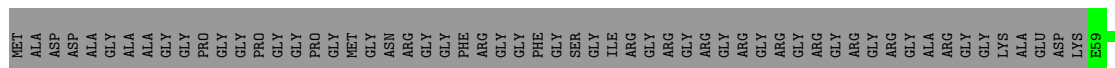
- Molecule 68: Receptor of activated protein C kinase 1

Chain Sg: 98%



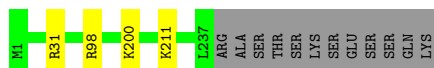
- Molecule 69: 40S ribosomal protein S2

Chain SC: 75% 24%



- Molecule 70: 40S ribosomal protein S6

Chain SG: 94% 5%



- Molecule 71: 40S ribosomal protein S9

Chain SJ: 95% 5%



- Molecule 72: 40S ribosomal protein S12

Chain SM: 87% 5% 8%



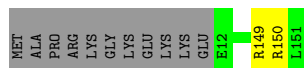
- Molecule 73: 40S ribosomal protein S13

Chain SN: 99% 0%



- Molecule 74: 40S ribosomal protein S14

Chain SO: 91% 7%



- Molecule 75: 40S ribosomal protein S15a

MET V2 F130

- MET N2 K132 GLU

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | PRO | PRO | LYS | ASP | ASP | LYS | LYS | LYS | ASP | ALA | GLY | LYS | SER | LYS | LYS | VAL | ASN | LYS | SER | GLY | GLY | LYS | ALA | LYS | LYS | LYS | LYS | TRP | SER | LYS | GLY | GLY | VAL | R41 | L44 | GLY | GLY | ASP | ALA | PRO | ALA | ALA | ALA | GLY | GLY | ASP |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- MET  
 P2  
 H84

- LYS  
V2  
K26  
S59

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ILE | GLN | GLN | LYS | GLU | THR | LEU | HIS | LEU | VAL | GLY | ARG | LEU | THR | LYS | THR | LEU | GLY | ASP | GLU | ASP | GLY | LEU | GLN | ASP | GLN | ARG | LEU | THR | LEU | GLY | ASP | THR | TYR |
| ILE | GLN | GLN | LYS | GLU | THR | LEU | HIS | LEU | VAL | GLY | ARG | LEU | THR | LYS | THR | LEU | GLY | ASP | GLU | ASP | GLY | LEU | GLN | ASP | GLN | ARG | LEU | THR | LEU | GLY | ASP | THR |     |

- |     |     |     |     |     |     |    |      |     |     |      |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|----|------|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | SER | GLY | GLU | ASP | GLU | Q7 | F283 | GLU | ASP | E286 | A362 | SER | ARG | LYS | THR | GLN | LYS | LYS | LYS | LYS | LYS | LYS | ALA | SER | SER | LYS | THR | ALA | ALA | ASN | GLU | THR | THR | SER | GLY | GLU | THR | LEU | GLU | GLU | ASN | GLU | ALA | GLY | ASP |
|-----|-----|-----|-----|-----|-----|----|------|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	127706	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 ( $e^-/\text{\AA}^2$ )	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	L5	1.18	10/89570 (0.0%)	1.10	478/139647 (0.3%)
2	L7	1.17	0/2861	0.97	1/4459 (0.0%)
3	L8	1.18	0/3701	1.00	9/5766 (0.2%)
4	LA	0.60	1/1936 (0.1%)	0.65	1/2596 (0.0%)
5	LB	0.55	0/3306	0.62	2/4424 (0.0%)
6	LC	0.53	0/2981	0.60	0/4002
7	LD	0.49	0/2428	0.54	0/3252
8	LE	0.45	0/1942	0.56	0/2606
9	LF	0.59	0/1905	0.57	0/2539
10	LG	0.47	0/1960	0.56	1/2637 (0.0%)
11	LH	0.52	0/1537	0.58	0/2066
12	LI	0.54	0/1673	0.57	0/2233
13	LJ	0.42	0/1433	0.65	0/1915
14	LL	0.47	0/1732	0.56	0/2315
15	LM	0.50	0/1161	0.57	1/1554 (0.1%)
16	LN	0.61	0/1746	0.60	1/2338 (0.0%)
17	LO	0.56	0/1682	0.52	0/2250
18	LP	0.55	0/1268	0.56	0/1701
19	LQ	0.57	0/1537	0.57	0/2052
20	LR	0.47	0/1582	0.55	0/2091
21	LS	0.59	0/1493	0.53	0/2003
22	LT	0.57	0/1326	0.59	0/1770
23	LU	0.47	0/839	0.64	0/1126
24	LV	0.56	0/993	0.59	0/1332
25	LW	0.47	0/1030	0.52	0/1364
26	LX	0.49	0/1002	0.54	0/1345
27	LY	0.52	0/1132	0.54	0/1504
28	LZ	0.53	0/1130	0.56	0/1507
29	La	0.56	0/1191	0.55	0/1591
30	Lb	0.43	0/889	0.57	0/1175
31	Lc	0.53	0/774	0.57	0/1038
32	Ld	0.55	0/903	0.60	1/1216 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.59	1/1071 (0.1%)	0.59	0/1429
34	Lf	0.61	0/895	0.62	0/1198
35	Lg	0.55	0/916	0.58	0/1220
36	Lh	0.45	0/1023	0.53	0/1351
37	Li	0.42	0/843	0.51	0/1115
38	Lj	0.60	0/720	0.61	0/952
39	Lk	0.43	0/575	0.56	0/761
40	Ll	0.53	0/454	0.52	0/599
41	Lm	0.53	0/435	0.57	0/575
42	Ln	0.42	0/231	0.54	0/294
43	Lo	0.54	0/876	0.55	0/1156
44	Lp	0.55	0/718	0.55	0/953
45	Lr	0.52	0/1017	0.57	0/1364
46	Lz	0.31	0/1769	0.63	1/2371 (0.0%)
47	S2	0.67	1/41244 (0.0%)	1.08	186/64263 (0.3%)
48	SA	0.38	0/1778	0.60	1/2416 (0.0%)
49	SB	0.35	0/1765	0.56	0/2362
50	SD	0.33	0/1793	0.62	1/2414 (0.0%)
51	SE	0.33	0/2118	0.57	1/2849 (0.0%)
52	SF	0.31	0/1516	0.54	0/2037
53	SH	0.34	0/1519	0.63	2/2033 (0.1%)
54	SI	0.36	0/1715	0.58	0/2287
55	SK	0.28	0/851	0.53	0/1147
56	SL	0.40	0/1268	0.55	0/1696
57	SP	0.29	0/1065	0.54	0/1423
58	SQ	0.29	0/1160	0.58	2/1553 (0.1%)
59	SR	0.31	0/1105	0.56	0/1484
60	SS	0.29	0/1216	0.56	0/1628
61	ST	0.30	0/1131	0.53	0/1515
62	SU	0.29	0/831	0.59	0/1115
63	SV	0.36	0/643	0.61	0/860
64	SX	0.40	0/1116	0.63	0/1490
65	Sa	0.39	0/836	0.58	0/1121
66	Sc	0.33	0/508	0.63	0/680
67	Sd	0.34	0/470	0.52	0/623
68	Sg	0.29	0/2493	0.59	0/3394
69	SC	0.42	0/1762	0.58	1/2381 (0.0%)
70	SG	0.29	0/1946	0.53	0/2590
71	SJ	0.34	0/1550	0.57	0/2069
72	SM	0.31	0/950	0.72	3/1275 (0.2%)
73	SN	0.36	0/1232	0.52	0/1656
74	SO	0.36	0/1062	0.62	0/1425
75	SW	0.38	0/1051	0.53	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	SY	0.32	0/1083	0.53	0/1438
77	SZ	0.30	0/604	0.67	1/810 (0.1%)
78	Sb	0.34	0/665	0.54	0/891
79	Se	0.35	0/465	0.56	0/612
80	Sf	0.30	0/560	0.63	0/745
81	CA	0.34	0/2810	0.58	0/3780
82	CB	0.32	0/6738	0.61	1/9099 (0.0%)
83	CC	0.55	0/1773	1.15	12/2759 (0.4%)
84	CD	0.30	0/233	0.73	0/302
All	All	0.84	13/244811 (0.0%)	0.93	707/358380 (0.2%)

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	3
8	LE	0	2
11	LH	0	2
12	LI	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
16	LN	0	1
17	LO	0	1
21	LS	0	1
22	LT	0	1
33	Le	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
49	SB	0	1
50	SD	0	1
52	SF	0	1
53	SH	0	1
58	SQ	0	3
63	SV	0	1
64	SX	0	3
66	Sc	0	1

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
82	CB	0	2
84	CD	0	1
All	All	0	39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L5	3646	A	N7-C5	-5.98	1.35	1.39
1	L5	4764	A	N9-C4	-5.94	1.34	1.37
47	S2	1422	G	C6-N1	-5.87	1.35	1.39
1	L5	4355	G	C2-N3	-5.82	1.28	1.32
33	Le	72	SER	CA-CB	-5.82	1.44	1.52

The worst 5 of 707 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	S2	1417	C	N3-C4-N4	-27.49	98.76	118.00
47	S2	1422	G	N1-C6-O6	-24.74	105.05	119.90
47	S2	1417	C	C5-C4-N4	21.24	135.07	120.20
47	S2	1422	G	C5-C6-O6	21.20	141.32	128.60
47	S2	1772	C	N1-C2-O2	14.69	127.71	118.90

There are no chirality outliers.

5 of 39 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	2	SER	Peptide
5	LB	258	HIS	Peptide

## 5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

### 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%)	187 (98%)	3 (2%)	62	86
5	LB	348/349 (100%)	345 (99%)	3 (1%)	78	93
6	LC	306/348 (88%)	305 (100%)	1 (0%)	92	98
7	LD	246/250 (98%)	245 (100%)	1 (0%)	91	97
8	LE	209/252 (83%)	208 (100%)	1 (0%)	88	96
9	LF	194/215 (90%)	193 (100%)	1 (0%)	88	96
10	LG	203/223 (91%)	199 (98%)	4 (2%)	55	82
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	171 (99%)	1 (1%)	86	96
13	LJ	148/149 (99%)	144 (97%)	4 (3%)	44	77
14	LL	176/177 (99%)	174 (99%)	2 (1%)	73	92
15	LM	118/161 (73%)	117 (99%)	1 (1%)	81	94
16	LN	171/172 (99%)	170 (99%)	1 (1%)	86	96
17	LO	173/174 (99%)	171 (99%)	2 (1%)	71	91
18	LP	134/163 (82%)	133 (99%)	1 (1%)	84	95
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	86	96
20	LR	166/175 (95%)	165 (99%)	1 (1%)	86	96
21	LS	156/157 (99%)	154 (99%)	2 (1%)	69	90
22	LT	139/140 (99%)	137 (99%)	2 (1%)	67	89
23	LU	91/115 (79%)	90 (99%)	1 (1%)	73	92
24	LV	101/107 (94%)	100 (99%)	1 (1%)	76	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LW	103/126 (82%)	101 (98%)	2 (2%)	57	84
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	122 (98%)	2 (2%)	62	86
28	LZ	117/118 (99%)	115 (98%)	2 (2%)	60	86
29	La	120/121 (99%)	119 (99%)	1 (1%)	81	94
30	Lb	88/126 (70%)	88 (100%)	0	100	100
31	Lc	83/97 (86%)	80 (96%)	3 (4%)	35	69
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	76	92
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	96 (98%)	2 (2%)	55	82
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%)	72 (99%)	1 (1%)	67	89
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	53	81
41	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	81
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%)	108 (99%)	1 (1%)	78	93
46	Lz	195/196 (100%)	191 (98%)	4 (2%)	53	81
48	SA	183/243 (75%)	182 (100%)	1 (0%)	88	96
49	SB	195/231 (84%)	190 (97%)	5 (3%)	46	77
50	SD	190/202 (94%)	187 (98%)	3 (2%)	62	86
51	SE	224/225 (100%)	224 (100%)	0	100	100
52	SF	159/170 (94%)	158 (99%)	1 (1%)	86	96
53	SH	166/174 (95%)	163 (98%)	3 (2%)	59	85
54	SI	178/180 (99%)	177 (99%)	1 (1%)	86	96
55	SK	89/136 (65%)	87 (98%)	2 (2%)	52	81
56	SL	137/142 (96%)	133 (97%)	4 (3%)	42	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SP	113/130 (87%)	113 (100%)	0	100	100
58	SQ	119/121 (98%)	119 (100%)	0	100	100
59	SR	122/122 (100%)	120 (98%)	2 (2%)	62	86
60	SS	126/132 (96%)	125 (99%)	1 (1%)	81	94
61	ST	113/115 (98%)	112 (99%)	1 (1%)	78	93
62	SU	94/107 (88%)	93 (99%)	1 (1%)	73	92
63	SV	67/67 (100%)	65 (97%)	2 (3%)	41	75
64	SX	113/115 (98%)	111 (98%)	2 (2%)	59	85
65	Sa	89/98 (91%)	89 (100%)	0	100	100
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	48/49 (98%)	47 (98%)	1 (2%)	53	81
68	Sg	272/275 (99%)	271 (100%)	1 (0%)	91	97
69	SC	188/225 (84%)	187 (100%)	1 (0%)	88	96
70	SG	207/218 (95%)	203 (98%)	4 (2%)	57	84
71	SJ	161/168 (96%)	160 (99%)	1 (1%)	86	96
72	SM	102/108 (94%)	98 (96%)	4 (4%)	32	66
73	SN	130/131 (99%)	130 (100%)	0	100	100
74	SO	110/119 (92%)	108 (98%)	2 (2%)	59	85
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SY	113/115 (98%)	112 (99%)	1 (1%)	78	93
77	SZ	66/103 (64%)	66 (100%)	0	100	100
78	Sb	75/76 (99%)	75 (100%)	0	100	100
79	Se	47/48 (98%)	46 (98%)	1 (2%)	53	81
80	Sf	60/140 (43%)	58 (97%)	2 (3%)	38	72
81	CA	303/336 (90%)	303 (100%)	0	100	100
82	CB	723/730 (99%)	719 (99%)	4 (1%)	86	96
84	CD	19/328 (6%)	18 (95%)	1 (5%)	22	54
All	All	11106/12391 (90%)	10999 (99%)	107 (1%)	77	92

5 of 107 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	SB	76	ASN

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Mol	Chain	Res	Type
56	SL	19	ASN
79	Se	26	LYS
49	SB	205	TYR
53	SH	27	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 132 such sidechains are listed below:

Mol	Chain	Res	Type
81	CA	7	GLN
81	CA	178	ASN
82	CB	270	ASN
38	Lj	66	HIS
38	Lj	57	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5070 (73%)	969 (26%)	19 (0%)
2	L7	119/121 (98%)	15 (12%)	0
3	L8	155/157 (98%)	33 (21%)	1 (0%)
47	S2	1717/1869 (91%)	469 (27%)	8 (0%)
83	CC	74/75 (98%)	29 (39%)	3 (4%)
All	All	5770/7292 (79%)	1515 (26%)	31 (0%)

5 of 1515 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	15	A
1	L5	17	A
1	L5	25	A
1	L5	26	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3614	G
47	S2	1434	C
1	L5	4378	A
83	CC	37	A

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Mol	Chain	Res	Type
47	S2	563	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 monosaccharides 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

This section contains visualisations of the EMDB entry EMD-11100. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 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 ⓘ

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

### 7.1 Map-value distribution ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.



## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.