

# wwPDB EM Validation Summary Report (i)

#### Mar 16, 2024 - 09:37 am GMT

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EMDB ID	:	EMD-16880
Title	:	60S ribosomal subunit bound to the E3-UFM1 complex - state 3 (native)
Authors	:	Penchev, I.; DaRosa, P.A.; Becker, T.; Beckmann, R.; Kopito, R.
Deposited on	:	2023-03-21
Resolution	:	3.10 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 (i) 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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 3.10 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	EM structures (#Entries)		
Ramachandran outliers	154571	4023		
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  $\leq=5\%$  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	5	5070	61% 7%	31	%
2	7	121	95%		• •
3	8	157	85%		10% 6%
4	А	794	86%		• 13%
5	В	506	77%	•	20%
6	С	314	9% 59% •	40%	
7	D	85	18%		• 8%
8	K	245	89%		• 9%



Mol	Chain	Length	Quality of chain	
9	LA	257	96%	•
10	LB	403	99%	-
11	LC	427	85% • 14%	-
12	LD	297	96% •	•
13	LE	288	76% • 24%	_
14	$\operatorname{LF}$	248	90% • 9%	
15	LG	266	89% • 9%	
16	LH	192	98%	
17	LI	214	92% • 6	%
18	LJ	178	97%	•••
19	$\operatorname{LL}$	211	91% • 8%	-
20	LM	215	• 37%	-
21	LN	204	99%	-
22	LO	203	97%	•••
23	LP	184	82% · 17%	
24	LQ	188	98%	••
25	LR	196	• 78% • 21%	_
26	LS	176	97%	
27	LT	160	97%	
28	LU	128	74% 5% 21%	-
29	LV	140	93% • 6%	6
30	LW	157	39% 61%	-
31	LX	156	75% • 24%	-
32	LY	145	91% • 8%	-
33	LZ	136	99%	•



Mol	Chain	Length	Quality of chain	
34	La	148	99%	••
35	Lb	159	<b>67%</b> • 31%	
36	Lc	115	82% ·	15%
37	Ld	125	84%	14%
38	Le	135	95%	5%
39	Lf	110	95%	• •
40	Lg	117	97%	• •
41	Lh	123	98%	••
42	Li	105	96%	••
43	Lj	97	86%	11%
44	Lk	70	96%	••
45	Ll	51	94%	••
46	Lm	128	40% • 59%	
47	Lo	106	97%	••
48	Lp	92	98%	••
49	Lr	137	90%	• 9%
50	Lz	217	98%	•



# 2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 146745 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			AltConf	Trace			
1	5	3474	Total 74502	C 33181	N 13653	O 24195	Р 3473	0	0

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

Mol	Chain	Residues		A	AltConf	Trace			
2	7	120	Total 2561	C 1141	N 456	0 844	Р 120	0	0

• Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues		A	AltConf	Trace			
3	8	148	Total 3152	C 1407	N 563	O 1035	Р 147	0	0

• Molecule 4 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues		A	AltConf	Trace			
4	Δ	692	Total	С	Ν	0	$\mathbf{S}$	0	0
т	11	052	5479	3453	957	1050	19	0	0

• Molecule 5 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues		At	AltConf	Trace			
5	В	403	Total 3234	C 2049	N 545	0 624	S 16	0	0

• Molecule 6 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	С	188	Total 1547	C 954	N 279	O 313	S 1	0	0



• Molecule 7 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
7	D	78	Total	C 200	N 06	0	S 1	0	0
			986	382	90	109	T		

• Molecule 8 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues		At	AltConf	Trace			
8	K	224	Total 1704	C 1061	N 293	O 338	S 12	0	0

• Molecule 9 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues		Ate	AltConf	Trace			
9	LA	248	Total 1898	C 1189	N 389	0 314	S 6	0	0

• Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues		At	AltConf	Trace			
10	LB	402	Total 3239	C 2060	N 608	O 557	S 14	0	0

• Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues		At	AltConf	Trace			
11	LC	368	Total 2927	C 1840	N 583	0 489	S 15	0	0

• Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues		At	AltConf	Trace			
12	LD	293	Total 2382	C 1507	N 434	0 427	S 14	0	0

• Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues		Ate	AltConf	Trace			
13	LE	220	Total 1765	C 1136	N 334	O 291	${S \atop 4}$	0	0

• Molecule 14 is a protein called 60S ribosomal protein L7.



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

• Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues		At	AltConf	Trace			
15	LG	241	Total 1927	C 1228	N 371	0 324	$\frac{S}{4}$	0	0

• Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues		At	oms	AltConf	Trace		
16	LH	190	Total 1518	C 956	N 284	0 272	S 6	0	0

• Molecule 17 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues		At	AltConf	Trace			
17	LI	202	Total 1634	C 1038	N 314	O 269	S 13	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

• Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues		At	oms	AltConf	Trace		
18	LJ	175	Total 1401	C 882	N 261	O 252	S 6	0	0

• Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues		At	$\mathbf{oms}$			AltConf	Trace
19	$\operatorname{LL}$	194	Total 1573	C 987	N 327	O 255	${f S}$ $4$	0	0

• Molecule 20 is a protein called 60S ribosomal protein L14.



Mol	Chain	Residues		At	oms			AltConf	Trace
20	LM	136	Total 1120	C 719	N 215	O 179	${ m S} 7$	0	0

• Molecule 21 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues		Ate	AltConf	Trace			
21	LN	203	Total 1701	C 1072	N 359	O 266	${S \atop 4}$	0	0

• Molecule 22 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues		Ate	AltConf	Trace			
22	LO	201	Total 1650	C 1063	N 321	0 261	$\frac{S}{5}$	0	0

• Molecule 23 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues		At	oms	AltConf	Trace		
23	LP	153	Total 1242	C 776	N 241	0 216	S 9	0	0

• Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues		At	oms	AltConf	Trace		
24	LQ	187	Total 1513	C 944	N 314	O 250	${ m S}{ m 5}$	0	0

• Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues		At	oms			AltConf	Trace
25	LR	155	Total 1294	C 808	N 278	O 199	${ m S} 9$	0	0

• Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues		$\mathbf{A}$	toms		AltConf	Trace	
26	LS	175	Total 1453	C 925	N 283	0 235	S 10	0	0

• Molecule 27 is a protein called 60S ribosomal protein L21.



Mol	Chain	Residues		At	oms			AltConf	Trace
27	LT	159	Total 1298	C 823	N 252	O 217	S 6	0	0

• Molecule 28 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues		At	oms	AltConf	Trace		
28	LU	101	Total 825	C 529	N 144	O 150	${S \over 2}$	0	0

• Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues		At	oms	AltConf	Trace		
29	LV	131	Total 979	C 618	N 184	0 172	${ m S}{ m 5}$	0	0

• Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
30	IW	62	Total	С	Ν	Ο	$\mathbf{S}$	0	0
- 50		02	519	332	101	83	3	0	0

• Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
31	LX	118	Total 967	C 618	N 181	O 167	S 1	0	0

• Molecule 32 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues		At	oms	AltConf	Trace		
32	LY	134	Total 1115	C 700	N 226	0 186	${ m S} { m 3}$	0	0

• Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	LZ	135	Total 1107	С 714	N 208	0 182	${ m S} { m 3}$	0	0

• Molecule 34 is a protein called 60S ribosomal protein L27a.



Mol	Chain	Residues		At	oms			AltConf	Trace
34	La	147	Total 1162	C 736	N 237	0 186	${ m S} { m 3}$	0	0

• Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues		At	oms	AltConf	Trace		
35	Lb	109	Total 876	С 546	N 189	0 137	$\frac{S}{4}$	0	0

• Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues		At	oms			AltConf	Trace
36	Lc	98	Total 764	C 485	N 135	0 138	S 6	0	0

• Molecule 37 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues		At	oms			AltConf	Trace
37	Ld	107	Total 888	C 560	N 171	0 155	${ m S} { m 2}$	0	0

• Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	Le	128	Total 1053	C 667	N 216	0 165	${ m S}{ m 5}$	0	0

• Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
39	Lf	109	Total 876	C 555	N 174	0 144	${ m S} { m 3}$	0	0

• Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues		At	oms	AltConf	Trace		
40	Lg	114	Total 906	C 566	N 187	0 147	S 6	0	0

• Molecule 41 is a protein called 60S ribosomal protein L35.



Mol	Chain	Residues		At	oms			AltConf	Trace
41	Lh	122	Total 1015	C 641	N 205	0 168	S 1	0	0

• Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace	
42	Li	102	Total 832	C 521	N 177	0 129	${ m S}{ m 5}$	0	0

• Molecule 43 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms			AltConf	Trace		
43	Lj	86	Total 705	C 434	N 155	0 111	${f S}{5}$	0	0

• Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms			AltConf	Trace		
44	Lk	69	Total	С	N	0	S	0	0
			569	366	103	99	1	Ŭ	Ŭ

• Molecule 45 is a protein called 60S ribosomal protein L39.

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

• Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

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

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

Mol	Chain	Residues	Atoms			AltConf	Trace		
47	Lo	105	Total 863	C 542	N 175	0 140	S 6	0	0

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



Mol	Chain	Residues	Atoms				AltConf	Trace	
48	Lp	91	Total 708	$\begin{array}{c} \mathrm{C} \\ 445 \end{array}$	N 136	O 120	${ m S} 7$	0	0

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

Mol	Chain	Residues	Atoms			AltConf	Trace		
49	Lr	125	Total 1002	C 622	N 207	0 168	${ m S}{ m 5}$	0	0

• Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms			AltConf	Trace		
50	Lz	217	Total 1744	C 1114	N 314	O 307	S 9	0	0

• Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
51	5	208	Total         Mg           208         208	0
51	7	2	Total Mg 2 2	0
51	8	5	Total Mg 5 5	0
51	LI	1	Total Mg 1 1	0
51	LP	1	Total Mg 1 1	0
51	LV	1	Total Mg 1 1	0
51	Le	1	Total Mg 1 1	0
51	Lj	1	Total Mg 1 1	0

• Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
52	Lg	1	Total Zn 1 1	0
52	Lj	1	Total Zn 1 1	0



Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
52	Lm	1	Total Zn 1 1	0
52	Lo	1	Total Zn 1 1	0
52	Lp	1	Total Zn 1 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 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 rRNA











MET G2 T249 LYS LYS LYS GLU GLU ASN		
• Molecule 10: 60S	ribosomal protein L3	
Chain LB:	99%	
MET S2 C134 R200 R200 R396 E400 6401 6401		
• Molecule 11: 60S	ribosomal protein L4	
Chain LC:	85%	• 14%
M1 A2 X122 X122 K348 E367 A1A A1A A1A A1A A1A A1A	LY LYS LYS VAL VAL VAL USS CLY CLYS CLY ALA ALA ALA ALA ALA CLY CLY CLY CLY CLY CLY CLN CLN	dLYS LYS LYS ALA ALA ALA ALA ALA PRO PRO PRO CYS CYS CYS CYS CYS CYS CYS CYS CYS CYS
THR GLU GLU LYS LYS PRO ALA ALA		
• Molecule 12: 60S	ribosomal protein L5	
Chain LD:	96%	
MET 62 62 73 74 74 75 75 75 75 75 75 75 75 75 75 75 75 75	K262 A294 GLU SER	
• Molecule 13: 60S	ribosomal protein L6	
Chain LE:	76%	• 24%
MET ALA ALA ALA CLY CLY CLY CLYS CLYS ARD ARD ARD ARD ARD CLYS CLYS CLYS	LYS PRO GLU GLU LYS LYS VAL ASP GLY GLY GLY GLY GLY GLY CYS CYS CYS CYS CYS CYS CYS CYS CYS CY	LITS LITS LITS LITS LITS LITS LITS LITS
K221 LEU ARG ARG ARG ARG GLU GLU GLU GLU TLE FHE	ASP THR GLU E1238 F238 F238	
• Molecule 14: 60S	ribosomal protein L7	
Chain LF:	90%	• 9%
MET GLU GLU GLU GLU CLU GLU CLV GLU GLU GLU GLU ALL ALL	PR0 CLU CLU CLS CLS CS CS CS CS CS CS CS CS CS CS CS CS CS	
• Molecule 15: 60S	ribosomal protein L7a	
Chain LG:	89%	• 9%





• Molecule 22: 60S ribosomal protein L13a



Chain LO:	97%		••
MET ALA E3 K53 K53 M18 M18 M173 C173	N176 V 203		
• Molecule 23	: 60S ribosomal protein L17		
Chain LP:	82%	·	17%
MET V2 E9 C57 C57 K153 E164 G1N	LLE PRO PRO PRO PRO PRO CLU CLU CLU CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV		
• Molecule 24	: 60S ribosomal protein L18		
Chain LQ:	98%		
MET 62 66 66 69 4 0188			
• Molecule 25	: 60S ribosomal protein L19		
Chain LR:	78%	·	21%
MET S2 K114 K149 K153 A156	ASP ALA ALA ALA ALA ALA ARG SER ARG CUU CVS ARG ARG ARG CUU CVS ARG CUU CUU CUU CUU CUU CUU CUU CUU CUU CU	LYS GLU GLU THR LYS	LYS
• Molecule 26	: 60S ribosomal protein L18a		
Chain LS:	97%		•••
MET K2 D85 S86 T169			
• Molecule 27	: 60S ribosomal protein L21		
Chain LT:	97%		
MET T2 R17 M52 M52 T68 T68 q114	A160		
• Molecule 28	: 60S ribosomal protein L22		
Chain LU:	74%	5%	21%
MET ALA PRO VAL LYS LYS VAL VAL VAL	GLY CLY CLYS CLYS CLYS CLYS CLYS CLYS CC2 CC2 CC2 CC2 CC2 CC2 CC2 CC2 CC2 CC		
• Molecule 90	609 mil agornal protain I 22		

• Molecule 29: 60S ribosomal protein L23



Chain LV:	93% • 6%	
MET SER LYS ARG GLY GLY GLY	SER 10 140 140 140	
• Molecule	2 30: 60S ribosomal protein L24	
Chain LW:	39% 61%	
M1 682 GLN GLU GLU TLE	GLN LYS LYS LYS ARG ARG ARG ARG ALA CYS GLN GLN ALA ALA ALA ALA ALA ALA ALA ALA ALA A	LYS ALA LYS
GLN ALA SER LYS LYS THR ALA MET	ALA ALA ALA ALA ALA PRO PRO THR ALA ALA ALA ALA ALA ALA PRO CTN CTN CTN CTN CTN CTN CTN CTN CTN CTN	
• Molecule	e 31: 60S ribosomal protein L23a	
Chain LX:	75% • 24%	
MET ALA PRO LYS ALA LYS LYS LYS GLU	PR0 ALA ALA PR0 CLYS CLYS CLYS CLYS CLYS CLYS CLYS CLYS	
• Molecule	e 32: 60S ribosomal protein L26	
Chain LY:	91% • 8%	
M1 Y74 E120 K134 TYR	LYS GLUU GLUU CLUU CLYS MART GLU GLU	
• Molecule	= 33: 60S ribosomal protein L27	
Chain LZ:	99% •	
MET G2 F136		
• Molecule	e 34: 60S ribosomal protein L27a	
Chain La:	99% ••	
MET P2 K92 A148		
• Molecule	e 35: 60S ribosomal protein L29	
Chain Lb:	• 67% • 31%	
MET A2 K63 E70 K73	A 4 177 177 177 177 177 177 177 17	THR GLN ALA PRO



#### THR LYS ALA SER GLU

 $\bullet$  Molecule 36: 60S ribosomal protein L30

Chain Lc:	82%	• 15%
MET MLA ALA ALA ALA ALA ALA ALA ALA CYS CYS	SY5 SY5 C92 S102 S102 C114 C114 C114 C114 C114 C114	
• Molecule 37:	60S ribosomal protein L31	
Chain Ld:	84%	• 14%
MET ALA PRO ALA LYS LYS GLY GLY CJU LYS LYS	LVIS CLVS ARG ARG AILA ILLE M18 ASA ASN ASN	
• Molecule 38:	60S ribosomal protein L32	
Chain Le:	95%	5%
MET A2 L129 ARG SER GLU ASN GLU GLU GLU		
• Molecule 39:	60S ribosomal protein L35a	
Chain Lf:	95%	· ·
MET S2 D37 K63 K63 S90 S90		
• Molecule 40:	60S ribosomal protein L34	
Chain Lg:	97%	•••
MET V2 H73 H73 A15 ALA LYS		
• Molecule 41:	60S ribosomal protein L35	
Chain Lh:	98%	
MET A2 K87 A123		
• Molecule 42:	60S ribosomal protein L36	
Chain Li:	96%	





• Molecule 43: 60S ribosomal protein L37

Chain Lj:	86% • 11%
MET T2 S7 R65 R63	ARA ALA VAL ALA ALA ALA SER SER SER SER SER
• Molecule	4: 60S ribosomal protein L38
Chain Lk:	96%
MET P2 K21 E68 L69 K70	
• Molecule 4	5: 60S ribosomal protein L39
Chain Ll:	94% •••
MET 82 747 T47 L51	
• Molecule 4	6: Ubiquitin-60S ribosomal protein L40
Chain Lm:	40% • 59%
MET GLN ILE PHE VAL LYS THR LEU THR	
	NET CONTRACT OF CO
LLE GLN CLYS CLYS CLY SER LEU LEU LEU	LEU LEU LEU LEU CIIO CIIO CIIO CIIO CIIO CIIO CIIO CII
• Molecule 4	534149535488449553231583148895349142555958549449884 7: 60S ribosomal protein L36a
HBSBBBBBB • Molecule 4 Chain Lo:	3 * H H H H H H H H H H H H H H H H H H
H 5 X 5 5 5 H A A A • Molecule 4 Chain Lo: H 5 F 6 F	534144555555555555555555555555555555555
H H H H H H H         • Molecule 4         Chain Lo:         H H H H H H H         H H H H H H H         • Molecule 4         • Molecule 4	3 S H H H H H H H H H H H H H H H H H H
H       H	3 S H H H H H H H H H H H H H H H H H H

• Molecule 49: 60S ribosomal protein L28



• 9%

Chain Lr:



 $\bullet$  Molecule 50: 60S ribosomal protein L10a

Chain Lz: 98%

90%



# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	123096	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0055	Depositor
Map size (Å)	392.58, 392.58, 392.58	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor



# 5 Model quality (i)

# 5.1 Standard geometry (i)

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	Bond lengths		Bond angles	
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	5	0.15	0/83342	0.65	0/129985	
2	7	0.15	0/2861	0.65	0/4459	
3	8	0.15	0/3520	0.66	1/5481~(0.0%)	
4	А	0.23	0/5549	0.45	0/7469	
5	В	0.24	0/3280	0.43	0/4426	
6	С	0.23	0/1560	0.47	0/2085	
7	D	0.25	0/601	0.45	0/818	
8	Κ	0.23	0/1728	0.48	0/2351	
9	LA	0.25	0/1936	0.56	0/2596	
10	LB	0.24	0/3307	0.50	0/4424	
11	LC	0.23	0/2981	0.52	0/4002	
12	LD	0.24	0/2428	0.49	0/3252	
13	LE	0.24	0/1799	0.51	0/2414	
14	LF	0.24	0/1905	0.51	0/2539	
15	LG	0.24	0/1960	0.50	0/2637	
16	LH	0.24	0/1537	0.51	0/2066	
17	LI	0.25	0/1673	0.51	0/2234	
18	LJ	0.24	0/1424	0.51	0/1904	
19	LL	0.24	0/1604	0.56	0/2149	
20	LM	0.25	0/1142	0.51	0/1527	
21	LN	0.24	0/1746	0.57	0/2338	
22	LO	0.24	0/1682	0.51	0/2250	
23	LP	0.24	0/1268	0.50	0/1701	
24	LQ	0.25	0/1537	0.59	0/2052	
25	LR	0.24	0/1310	0.56	0/1734	
26	LS	0.25	0/1493	0.53	0/2003	
27	LT	0.25	0/1326	0.51	0/1770	
28	LU	0.27	0/839	0.48	0/1126	
29	LV	0.26	0/993	0.52	0/1332	
30	LW	0.26	0/532	0.50	0/708	
31	LX	0.25	0/984	0.51	0/1323	
32	LY	0.25	0/1132	0.54	0/1504	



Mol	Chain	Bond	lengths	В	ond angles
INIOI	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
33	LZ	0.26	0/1130	0.52	0/1507
34	La	0.23	0/1191	0.50	0/1591
35	Lb	0.25	0/889	0.53	0/1175
36	Lc	0.25	0/774	0.49	0/1038
37	Ld	0.24	0/903	0.54	0/1216
38	Le	0.24	0/1071	0.53	0/1429
39	Lf	0.26	0/895	0.57	0/1198
40	Lg	0.24	0/916	0.56	0/1220
41	Lh	0.24	0/1023	0.52	0/1351
42	Li	0.24	0/843	0.56	0/1115
43	Lj	0.24	0/720	0.58	0/952
44	Lk	0.26	0/575	0.52	0/761
45	Ll	0.24	0/454	0.56	0/599
46	Lm	0.24	0/435	0.51	0/575
47	Lo	0.25	0/877	0.53	0/1156
48	Lp	0.25	0/718	0.53	0/953
49	Lr	0.23	0/1017	0.55	0/1364
50	Lz	0.24	0/1772	0.46	0/2375
All	All	0.19	0/157182	0.60	1/230234~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	8	111	U	C2-N1-C1'	5.28	124.04	117.70

There are no chirality outliers.

There are no planarity outliers.

#### 5.2 Too-close contacts (i)

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

# 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

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



Mol	Chain	Analysed	Favoured Allowed		Outliers	Perce	ntiles
4	А	684/794~(86%)	675~(99%)	9~(1%)	0	100	100
5	В	397/506~(78%)	389~(98%)	8 (2%)	0	100	100
6	С	186/314~(59%)	186 (100%)	0	0	100	100
7	D	76/85~(89%)	76 (100%)	0	0	100	100
8	Κ	222/245~(91%)	216 (97%)	6 (3%)	0	100	100
9	LA	246/257~(96%)	241 (98%)	5 (2%)	0	100	100
10	LB	400/403~(99%)	395 (99%)	5 (1%)	0	100	100
11	LC	366/427~(86%)	357 (98%)	9(2%)	0	100	100
12	LD	291/297~(98%)	287 (99%)	3 (1%)	1 (0%)	41	73
13	LE	214/288~(74%)	205 (96%)	9 (4%)	0	100	100
14	LF	223/248~(90%)	219 (98%)	4 (2%)	0	100	100
15	LG	239/266~(90%)	236 (99%)	3 (1%)	0	100	100
16	LH	188/192~(98%)	186 (99%)	2 (1%)	0	100	100
17	LI	198/214~(92%)	196 (99%)	2 (1%)	0	100	100
18	LJ	173/178~(97%)	171 (99%)	2 (1%)	0	100	100
19	LL	192/211~(91%)	187 (97%)	5 (3%)	0	100	100
20	LM	134/215~(62%)	132 (98%)	2 (2%)	0	100	100
21	LN	201/204~(98%)	195 (97%)	6 (3%)	0	100	100
22	LO	199/203~(98%)	198 (100%)	1 (0%)	0	100	100
23	LP	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
24	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
25	LR	153/196~(78%)	152 (99%)	1 (1%)	0	100	100
26	LS	173/176~(98%)	168 (97%)	5 (3%)	0	100	100
27	LT	157/160~(98%)	154 (98%)	3 (2%)	0	100	100
28	LU	99/128~(77%)	95 (96%)	3 (3%)	1 (1%)	15	49
29	LV	129/140~(92%)	127 (98%)	2 (2%)	0	100	100
30	LW	60/157~(38%)	59 (98%)	1 (2%)	0	100	100
31	LX	116/156~(74%)	114 (98%)	2 (2%)	0	100	100
32	LY	132/145~(91%)	131 (99%)	1 (1%)	0	100	100
33	LZ	133/136~(98%)	131 (98%)	2 (2%)	0	100	100

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	Perce	entiles
34	La	145/148~(98%)	139 (96%)	6 (4%)	0	100	100
35	Lb	105/159~(66%)	105 (100%)	0	0	100	100
36	Lc	96/115~(84%)	96 (100%)	0	0	100	100
37	Ld	105/125~(84%)	103 (98%)	2 (2%)	0	100	100
38	Le	126/135~(93%)	125 (99%)	1 (1%)	0	100	100
39	Lf	107/110~(97%)	107 (100%)	0	0	100	100
40	Lg	112/117~(96%)	111 (99%)	1 (1%)	0	100	100
41	Lh	120/123~(98%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/105~(95%)	99~(99%)	1 (1%)	0	100	100
43	Lj	84/97~(87%)	83 (99%)	1 (1%)	0	100	100
44	Lk	67/70~(96%)	67 (100%)	0	0	100	100
45	Ll	48/51~(94%)	47 (98%)	1 (2%)	0	100	100
46	Lm	50/128~(39%)	50 (100%)	0	0	100	100
47	Lo	103/106~(97%)	101 (98%)	2 (2%)	0	100	100
48	Lp	89/92~(97%)	85 (96%)	4 (4%)	0	100	100
49	Lr	123/137~(90%)	123 (100%)	0	0	100	100
50	Lz	215/217~(99%)	208 (97%)	7 (3%)	0	100	100
All	All	8112/9348 (87%)	7976 (98%)	134 (2%)	2(0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	LD	4	VAL
28	LU	67	LYS

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	А	612/704~(87%)	601 (98%)	11 (2%)	59 82





Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	В	360/438~(82%)	348~(97%)	12 (3%)	38	69
6	$\mathbf{C}$	162/254~(64%)	160 (99%)	2(1%)	71	88
7	D	66/72~(92%)	64~(97%)	2(3%)	41	71
8	Κ	194/213~(91%)	188~(97%)	6 (3%)	40	70
9	LA	190/199~(96%)	190 (100%)	0	100	100
10	LB	348/349~(100%)	345~(99%)	3~(1%)	78	91
11	LC	306/348~(88%)	303~(99%)	3 (1%)	76	90
12	LD	246/250~(98%)	240~(98%)	6 (2%)	49	76
13	LE	194/252~(77%)	192~(99%)	2(1%)	76	90
14	$_{ m LF}$	194/215~(90%)	191 (98%)	3(2%)	65	85
15	LG	203/223~(91%)	198~(98%)	5(2%)	47	75
16	LH	169/171~(99%)	167~(99%)	2(1%)	71	88
17	LI	172/181~(95%)	166 (96%)	6 (4%)	36	68
18	LJ	147/149~(99%)	144 (98%)	3~(2%)	55	80
19	LL	164/177~(93%)	161 (98%)	3~(2%)	59	82
20	LM	116/161~(72%)	113~(97%)	3~(3%)	46	74
21	LN	171/172~(99%)	170~(99%)	1 (1%)	86	94
22	LO	173/174~(99%)	169~(98%)	4(2%)	50	77
23	LP	134/163~(82%)	131~(98%)	3~(2%)	52	78
24	LQ	164/165~(99%)	162~(99%)	2(1%)	71	88
25	LR	138/175~(79%)	135~(98%)	3~(2%)	52	78
26	LS	156/157~(99%)	152~(97%)	4 (3%)	46	74
27	LT	139/140~(99%)	135~(97%)	4(3%)	42	72
28	LU	91/115~(79%)	86 (94%)	5~(6%)	21	53
29	LV	101/107~(94%)	100 (99%)	1 (1%)	76	90
30	LW	54/126~(43%)	54 (100%)	0	100	100
31	LX	$106/133$ ( $\overline{80\%}$ )	105 (99%)	1 (1%)	78	91
32	LY	124/135~(92%)	122 (98%)	2(2%)	62	84
33	LZ	117/118 (99%)	117 (100%)	0	100	100
34	La	120/121 (99%)	119 (99%)	1 (1%)	81	92
35	Lb	88/126~(70%)	85 (97%)	3(3%)	37	69



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
36	Lc	83/97~(86%)	79~(95%)	4(5%)	25	58
37	Ld	98/110 (89%)	96~(98%)	2 (2%)	55	80
38	Le	114/121~(94%)	114 (100%)	0	100	100
39	Lf	88/89~(99%)	84 (96%)	4 (4%)	27	60
40	Lg	98/100 (98%)	97~(99%)	1 (1%)	76	90
41	Lh	109/110 (99%)	108 (99%)	1 (1%)	78	91
42	Li	86/89~(97%)	85 (99%)	1 (1%)	71	88
43	Lj	73/80~(91%)	70 (96%)	3 (4%)	30	64
44	Lk	64/65~(98%)	62 (97%)	2 (3%)	40	70
45	Ll	47/48~(98%)	45 (96%)	2 (4%)	29	62
46	Lm	48/116 (41%)	47 (98%)	1 (2%)	53	79
47	Lo	93/94~(99%)	91 (98%)	2 (2%)	52	78
48	Lp	74/75~(99%)	73~(99%)	1 (1%)	67	86
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	59	82
50	Lz	196/196~(100%)	192 (98%)	4 (2%)	55	80
All	All	7099/7994~(89%)	6963~(98%)	136 (2%)	59	81

 $5~{\rm of}~136$  residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
39	Lf	90	SER
43	Lj	7	SER
49	Lr	96	MET
14	LF	134	ARG
14	LF	31	LYS

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such side chains are listed below:

Mol	Chain	Res	Type
27	LT	54	HIS
39	Lf	65	ASN

#### 5.3.3 RNA (i)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3451/5070~(68%)	371 (10%)	4 (0%)
2	7	119/121~(98%)	5~(4%)	0
3	8	145/157~(92%)	14 (9%)	0
All	All	3715/5348~(69%)	390 (10%)	4 (0%)

5 of 390 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	13	U
1	5	39	А
1	5	42	А
1	5	48	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	5	739	G
1	5	1590	С
1	5	1633	G
1	5	3964	U

#### 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 225 ligands modelled in this entry, 225 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-16880. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

# 6.1 Orthogonal projections (i)

#### 6.1.1 Primary map



6.1.2 Raw map



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



# 6.2 Central slices (i)

### 6.2.1 Primary map



X Index: 270



Y Index: 270



Z Index: 270

#### 6.2.2 Raw map



X Index: 270

Y Index: 270



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: 260



Y Index: 276



Z Index: 248

#### 6.3.2 Raw map



X Index: 260

Y Index: 276



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



6.4.2 Raw map



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



### 6.5 Orthogonal surface views (i)

#### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

#### 6.5.2 Raw map



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

#### 6.6 Mask visualisation (i)

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



# 7 Map analysis (i)

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

# 7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



# 7.2 Volume estimate (i)



The volume at the recommended contour level is 2480  $\text{nm}^3$ ; this corresponds to an approximate mass of 2240 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 (i)



\*Reported resolution corresponds to spatial frequency of 0.323  ${\rm \AA^{-1}}$ 



# 8 Fourier-Shell correlation (i)

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

#### 8.1 FSC (i)



\*Reported resolution corresponds to spatial frequency of 0.323  $\mathrm{\AA^{-1}}$ 



# 8.2 Resolution estimates (i)

$\mathbf{Bosolution ostimato}(\mathbf{\hat{A}})$	Estimation criterion (FSC cut-off)		
Resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.15	3.43	3.18

\*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-16880 and PDB model 80HD. Per-residue inclusion information can be found in section 3 on page 14.

# 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



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



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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0055).



### 9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

### 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0055) and Q-score for the entire model and for each chain.

$\mathbf{Chain}$	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.9800	0.5310
5	0.9990	0.5420
7	0.9990	0.5580
8	1.0000	0.5580
А	0.9010	0.3960
В	0.8540	0.3040
С	0.7120	0.2650
D	0.6670	0.1940
Κ	0.7950	0.5090
LA	0.9970	0.5820
LB	0.9830	0.5670
LC	0.9850	0.5610
LD	0.9790	0.5360
LE	0.9940	0.5470
m LF	0.9960	0.5640
LG	0.9640	0.5160
LH	0.9920	0.5580
LI	0.9920	0.5650
LJ	0.9470	0.5100
LL	0.9830	0.5470
LM	0.9950	0.5570
LN	0.9990	0.5860
LO	0.9910	0.5670
LP	0.9940	0.5750
LQ	0.9970	0.5750
LR	0.9770	0.5550
LS	0.9960	0.5770
LT	0.9940	0.5500
LU	0.9770	0.4900
LV	0.9970	0.5660
LW	1.0000	0.5740
LX	0.9930	0.5560
LY	0.9870	0.5590
LZ	0.9940	0.5500
La	0.9910	0.5790



Chain	Atom inclusion	Q-score
Lb	0.9620	0.5180
Lc	0.9710	0.5360
Ld	0.9850	0.5500
Le	0.9980	0.5770
Lf	0.9960	0.5840
Lg	0.9920	0.5590
Lh	0.9870	0.5500
Li	0.9810	0.5420
Lj	0.9990	0.5850
Lk	0.9610	0.5190
Ll	1.0000	0.5680
Lm	0.9930	0.5630
Lo	0.9810	0.5620
Lp	0.9900	0.5560
Lr	0.9990	0.5680
Lz	0.9310	0.4320

