



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:58 AM UTC

PDB ID : 8OHD / pdb_00008ohd
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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

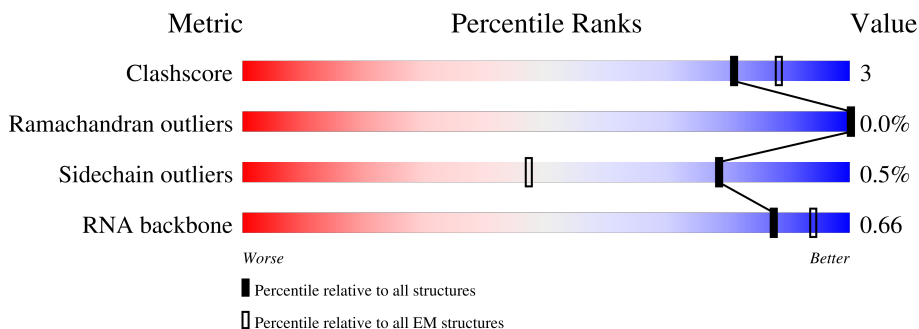
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.



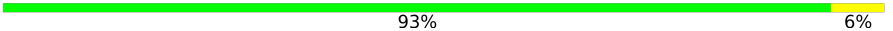
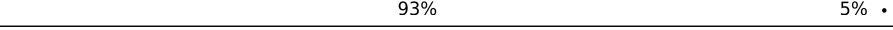
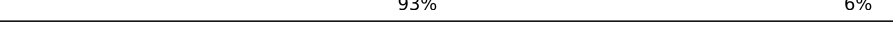
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	5	5070	55% 12% . 31%
2	7	121	87% 12% ..
3	8	157	81% 13% . 6%
4	A	794	78% 9% 13%
5	B	506	75% 5% 20%
6	C	314	55% 5% 40%
7	D	85	92% 8%

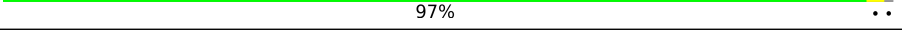
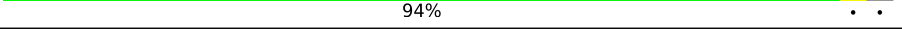
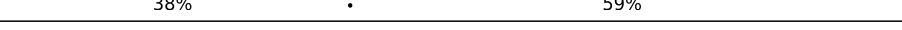
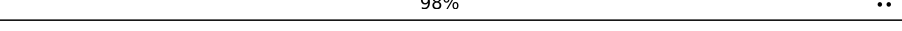
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Mol	Chain	Length	Quality of chain
8	K	245	
9	LA	257	
10	LB	403	
11	LC	427	
12	LD	297	
13	LE	288	
14	LF	248	
15	LG	266	
16	LH	192	
17	LI	214	
18	LJ	178	
19	LL	211	
20	LM	215	
21	LN	204	
22	LO	203	
23	LP	184	
24	LQ	188	
25	LR	196	
26	LS	176	
27	LT	160	
28	LU	128	
29	LV	140	
30	LW	157	
31	LX	156	
32	LY	145	

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Mol	Chain	Length	Quality of chain
33	LZ	136	 88% 12% .
34	La	148	 93% 6% .
35	Lb	159	 62% 7% 31%
36	Lc	115	 75% 10% . 15%
37	Ld	125	 80% 6% 14%
38	Le	135	 90% . . 5%
39	Lf	110	 92% 7% .
40	Lg	117	 91% 6% .
41	Lh	123	 97% ..
42	Li	105	 94% . .
43	Lj	97	 79% 9% 11%
44	Lk	70	 80% 19% .
45	Ll	51	 88% 10% .
46	Lm	128	 38% . 59%
47	Lo	106	 98% ..
48	Lp	92	 88% 10% ..
49	Lr	137	 82% 9% 9%
50	LZ	217	 88% 12%

2 Entry composition

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	Atoms					AltConf	Trace
1	5	3474	Total	C	N	O	P	0	0
			74502	33181	13653	24195	3473		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	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	8	148	Total	C	N	O	P	0	0
			3152	1407	563	1035	147		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	692	Total	C	N	O	S	0	0
			5479	3453	957	1050	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	403	Total	C	N	O	S	0	0
			3234	2049	545	624	16		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	78	Total	C	N	O	S	0	0
			588	382	96	109	1		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	220	Total	C	N	O	S	0	0
			1765	1136	334	291	4		

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

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

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

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

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

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

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

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

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	Atoms					AltConf	Trace
18	LJ	175	Total	C	N	O	S	0	0
			1401	882	261	252	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	194	Total	C	N	O	S	0	0
			1573	987	327	255	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	136	Total	C	N	O	S	0	0
			1120	719	215	179	7		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	155	Total	C	N	O	S	0	0
			1294	808	278	199	9		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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

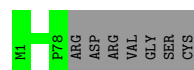
G1404	G1405	G1577	U1578	C	G1890	A1891	G	A2069	C	A	G2296	C2470	C2471	C2583	A2789	U2790	G	G
G	C	U1578	C	C	A1891	G	A	C2072	G	C	A2300	A2587	C2588	C2589	U2789	G	G	G
C	C	C1590	C	C	G1895	C	U	C2084	A	G	A2301	C2588	C2589	C2590	U2790	G	G	G
C	C	U1591	C	C	A1896	C	C	C2084	A	G	C2302	C2474	C2475	C2589	U2810	G	G	G
U	U	U1596	C	C	A1897	C	C	C2089	G	C	C2303	C2476	C2477	C2590	U2811	G	G	G
C	C	C	C	C	G1903	C	C	U2089	C	C	A2313	C2478	C2479	A2601	U2812	G	G	G
C	C	C	C	C	U2090	C	C	C2091	C	C	G2314	C2482	C2483	A2602	A2813	G	G	G
G	G	G1612	C	C	A1907	C	U	C2092	C	C	G2315	C2484	C2485	A2603	C2814	G	G	G
C	C	G1624	C	C	G1912	C	A	A2093	C	C	G2316	C2486	C2487	C2627	U2826	G	G	G
C	C	G1625	C	C	G1913	C	A	G2094	C	C	G2317	C2488	C2489	G2628	U2827	G	G	G
C	C	C	C	C	G1914	C	A	A2095	C	C	G2318	C2490	C2491	G2629	G2838	G	G	G
C	C	C	C	C	G1915	C	A	G2096	C	C	G2319	C2492	C2493	A2630	U2839	G	G	G
C	C	C	C	C	G1916	C	A	G2097	C	C	G2320	C2494	C2495	A2631	U2840	G	G	G
C	C	C	C	C	A1917	C	U	U2098	C	C	G2321	C2496	C2497	A2632	U2841	G	G	G
C	C	C	C	C	U1918	C	U	G2099	C	C	G2322	C2498	C2499	A2633	U2842	G	G	G
C	C	C	C	C	G1919	C	U	G2100	C	C	G2323	C2500	C2501	A2634	U2843	G	G	G
C	C	C	C	C	G1920	C	U	G2101	C	C	G2324	C2502	C2503	A2635	U2844	G	G	G
C	C	C	C	C	G1921	C	U	G2102	C	C	G2325	C2504	C2505	A2636	U2845	G	G	G
C	C	C	C	C	G1922	C	U	G2103	C	C	G2326	C2506	C2507	A2637	U2846	G	G	G
C	C	C	C	C	A1765	C	U	C2107	C	C	G2327	C2508	C2509	A2638	U2847	G	G	G
C	C	C	C	C	A1766	C	U	G	C	C	G2328	C2510	C2511	U2869	U2848	G	G	G
C	C	C	C	C	A1767	C	U	G	C	C	G2329	C2512	C2513	A2881	A2849	G	G	G
C	C	C	C	C	C1768	C	U	G	C	C	G2330	C2514	C2515	G2902	A2850	G	G	G
C	C	C	C	C	U1779	C	U	G	C	C	G2331	C2516	C2517	G	U2851	G	G	G
C	C	C	C	C	A1804	C	U	G	C	C	G2332	C2518	C2519	G	U2852	G	G	G
C	C	C	C	C	U1807	C	U	G	C	C	G2333	C2520	C2521	G	U2853	G	G	G
C	C	C	C	C	G1818	C	U	G	C	C	G2334	C2522	C2523	G	U2854	G	G	G
C	C	C	C	C	U1833	C	U	G	C	C	G2335	C2524	C2525	G	U2855	G	G	G
C	C	C	C	C	U1834	C	U	G	C	C	G2336	C2526	C2527	G	U2856	G	G	G
C	C	C	C	C	G1835	C	U	G	C	C	G2337	C2528	C2529	G	U2857	G	G	G
C	C	C	C	C	A1836	C	U	G	C	C	G2338	C2530	C2531	G	U2858	G	G	G
C	C	C	C	C	G1837	C	U	G	C	C	G2339	C2532	C2533	G	U2859	G	G	G
C	C	C	C	C	U1842	C	U	G	C	C	G2340	C2534	C2535	G	U2860	G	G	G
C	C	C	C	C	G1843	C	U	G	C	C	G2341	C2536	C2537	G	U2861	G	G	G
C	C	C	C	C	U1852	C	U	G	C	C	G2342	C2538	C2539	G	U2862	G	G	G
C	C	C	C	C	G1853	C	U	G	C	C	G2343	C2540	C2541	G	U2863	G	G	G
C	C	C	C	C	A1854	C	U	G	C	C	G2344	C2542	C2543	G	U2864	G	G	G
C	C	C	C	C	G1855	C	U	G	C	C	G2345	C2544	C2545	G	U2865	G	G	G
C	C	C	C	C	U1865	C	U	G	C	C	G2346	C2546	C2547	G	U2866	G	G	G
C	C	C	C	C	U1866	C	U	G	C	C	G2347	C2548	C2549	G	U2867	G	G	G
C	C	C	C	C	A1867	C	U	G	C	C	G2348	C2550	C2551	G	U2868	G	G	G
C	C	C	C	C	G1868	C	U	G	C	C	G2349	C2552	C2553	G	U2869	G	G	G
C	C	C	C	C	U1869	C	U	G	C	C	G2350	C2554	C2555	G	U2870	G	G	G
C	C	C	C	C	G1872	C	U	G	C	C	G2351	C2556	C2557	G	U2871	G	G	G
C	C	C	C	C	U1873	C	U	G	C	C	G2352	C2558	C2559	G	U2872	G	G	G
C	C	C	C	C	C1879	C	U	G	C	C	G2353	C2560	C2561	G	U2873	G	G	G
C	C	C	C	C	U1880	C	U	G	C	C	G2354	C2562	C2563	G	U2874	G	G	G
C	C	C	C	C	A1881	C	U	G	C	C	G2355	C2564	C2565	G	U2875	G	G	G
C	C	C	C	C	G1882	C	U	G	C	C	G2356	C2566	C2567	G	U2876	G	G	G
C	C	C	C	C	U1883	C	U	G	C	C	G2357	C2568	C2569	G	U2877	G	G	G
C	C	C	C	C	A1884	C	U	G	C	C	G2358	C2570	C2571	G	U2878	G	G	G
C	C	C	C	C	G1885	C	U	G	C	C	G2359	C2572	C2573	G	U2879	G	G	G
C	C	C	C	C	U1886	C	U	G	C	C	G2360	C2574	C2575	G	U2880	G	G	G
C	C	C	C	C	A1887	C	U	G	C	C	G2361	C2576	C2577	G	U2881	G	G	G
C	C	C	C	C	G1888	C	U	G	C	C	G2362	C2578	C2579	G	U2882	G	G	G
C	C	C	C	C	U1889	C	U	G	C	C	G2363	C2580	C2581	G	U2883	G	G	G
C	C	C	C	C	A1890	C	U	G	C	C	G2364	C2582	C2583	G	U2884	G	G	G
C	C	C	C	C	G1891	C	U	G	C	C	G2365	C2584	C2585	G	U2885	G	G	G
C	C	C	C	C	U1892	C	U	G	C	C	G2366	C2586	C2587	G	U2886	G	G	G
C	C	C	C	C	A1893	C	U	G	C	C	G2367	C2588	C2589	G	U2887	G	G	G
C	C	C	C	C	U1894	C	U	G	C	C	G2368	C2590	C2591	G	U2888	G	G	G
C	C	C	C	C	A1895	C	U	G	C	C	G2369	C2592	C2593	G	U2889	G	G	G
C	C	C	C	C	G1896	C	U	G	C	C	G2370	C2594	C2595	G	U2890	G	G	G
C	C	C	C	C	A1897	C	U	G	C	C	G2371	C2596	C2597	G	U2891	G	G	G
C	C	C	C	C	G1900	C	U	G	C	C	G2372	C2598	C2599	G	U2892	G	G	G
C	C	C	C	C	U1901	C	U	G	C	C	G2373	C2600	C2601	G	U2893	G	G	G
C	C	C	C	C	A1902	C	U	G	C	C	G2374	C2602	C2603	G	U2894	G	G	G
C	C	C	C	C	U1903	C	U	G	C	C	G2375	C2604	C2605	G	U2895	G	G	G
C	C	C	C	C	A1904	C	U	G	C	C	G2376	C2606	C2607	G	U2896	G	G	G
C	C	C	C	C	U1905	C	U	G	C	C	G2377	C2608	C2609	G	U2897	G	G	G
C	C	C	C	C	A1906	C	U	G	C	C	G2378	C2610	C2611	G	U2898	G	G	G
C	C	C	C	C	G1907	C	U	G	C	C	G2379	C2612	C2613	G	U2899	G	G	G
C	C	C	C	C	U1908	C	U	G	C	C	G2380	C2614	C2615	G	U2900	G	G	G
C	C	C	C	C	A1909	C	U	G	C	C	G2381	C2616	C2617	G	U2901	G	G	G
C	C	C	C	C	U1910	C	U	G	C	C	G2382	C2618	C2619	G	U2902	G	G	G
C	C	C	C	C	A1911	C	U	G	C	C	G2383	C2620	C2621	G	U2903	G	G	G
C	C	C	C	C	U1912	C	U	G	C	C	G2384	C2622	C2623	G	U2904	G	G	G
C	C	C	C	C	A1913	C	U	G	C	C	G2385	C2624	C2625	G	U2905	G	G	G
C	C	C	C	C	U1914	C	U	G	C	C	G2386	C2626	C2627	G	U2906	G	G	G
C	C	C	C	C	A1915	C	U	G	C	C	G2387	C2628	C2629	G	U2907	G	G	G
C	C	C	C	C	U1916	C	U	G	C	C	G2388	C2630	C2631	G	U2908	G	G	G
C	C	C	C	C	A1917	C	U	G	C	C	G2389	C2632	C2633	G	U2909	G	G	G
C	C	C	C	C	U1918	C	U	G	C	C	G2390	C2634	C2635	G	U2910	G	G	G
C	C	C	C	C	A1919	C	U	G	C	C	G2391	C2636	C2637	G	U2911	G	G	G
C	C	C	C	C	U1920	C	U	G	C	C	G2392	C2638	C2639	G	U2912	G	G	G
C	C	C	C	C	A1921	C	U	G	C	C	G2393	C2640	C2641	G	U2913	G	G	G
C	C	C	C	C	U1922	C	U	G	C	C	G2394	C2642	C2643	G	U2914	G	G	G
C	C	C	C	C	A1923	C	U	G	C	C	G2395	C2644	C2645	G	U2915	G	G	G
C	C	C	C	C	U1924	C	U	G	C	C	G2396	C2646	C2647	G	U2916	G	G	G
C	C	C	C	C	A1925	C	U	G	C	C	G2397	C2648	C2649	G	U2917	G	G	G
C	C	C	C	C	U1926	C	U	G	C	C	G2398	C2650	C2651	G	U2918	G	G	G
C	C	C	C	C	A1927	C	U	G	C	C	G2399	C2652	C2653	G	U2919	G	G	G
C	C	C	C	C	U1928	C	U	G	C	C	G2400	C2654	C2655	G	U2920	G	G	G
C	C	C	C	C	A1929	C	U	G	C	C	G2401	C2656	C2657	G	U2921	G	G	G
C	C	C	C	C	U1930	C	U	G	C	C	G2402	C2658	C2659	G	U2922	G	G	G
C	C	C	C	C	A1931	C	U	G	C	C	G2403	C2660	C2661	G	U2923	G	G	G
C	C	C	C	C	U1932	C	U	G	C	C	G2404	C2662	C2663	G	U2924	G	G	G
C	C	C	C	C	A1933	C	U	G	C	C	G2405	C2664	C2665	G	U2925	G	G	G
C	C	C	C	C	U1934	C	U	G	C	C	G2406	C2666	C2667	G	U2926	G	G	G
C	C	C																





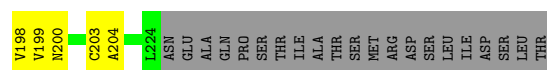
- Molecule 7: Ubiquitin-fold modifier 1

Chain D: 92% 8%



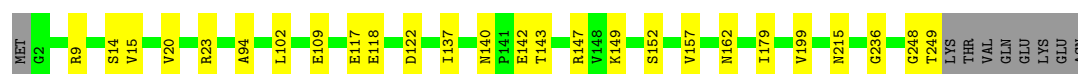
- Molecule 8: Eukaryotic translation initiation factor 6

Chain K: 76% 15% 9%



- Molecule 9: 60S ribosomal protein L8

Chain LA: 86% 10% 4%



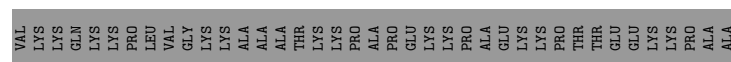
- Molecule 10: 60S ribosomal protein L3

Chain LB: 93% 6%



- Molecule 11: 60S ribosomal protein L4

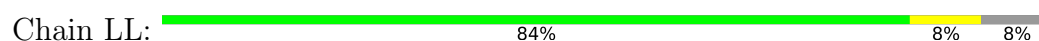
Chain LC: 81% 5% 14%



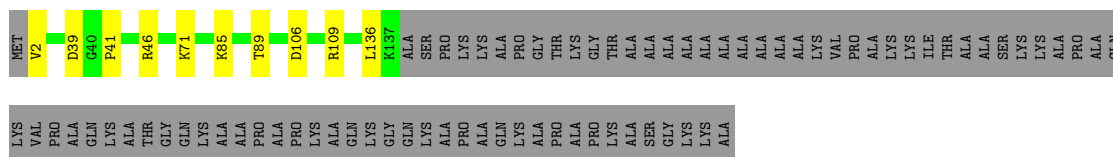
- Molecule 12: 60S ribosomal protein L5

Chain LD: 91% 8%





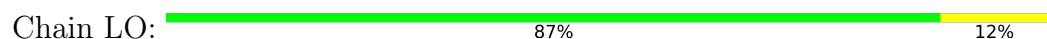
- Molecule 20: 60S ribosomal protein L14



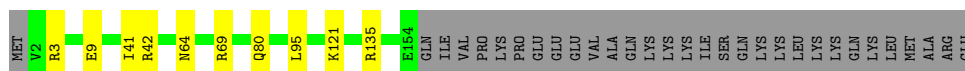
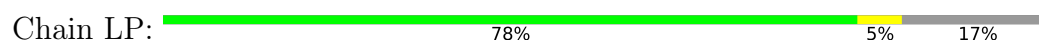
- Molecule 21: 60S ribosomal protein L15



- Molecule 22: 60S ribosomal protein L13a



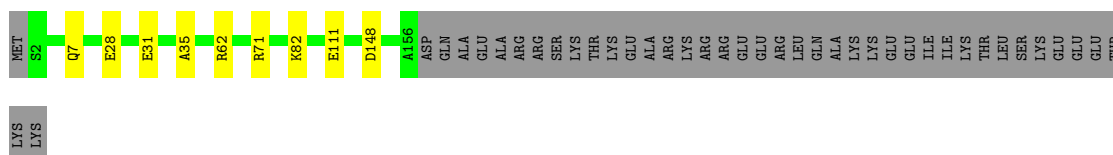
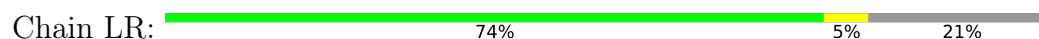
- Molecule 23: 60S ribosomal protein L17



- Molecule 24: 60S ribosomal protein L18



- Molecule 25: 60S ribosomal protein L19



• Molecule 26: 60S ribosomal protein L18a

Chain LS:  91% 8% ..

• Molecule 27: 60S ribosomal protein L21

Chain LT:  89% 9% ..

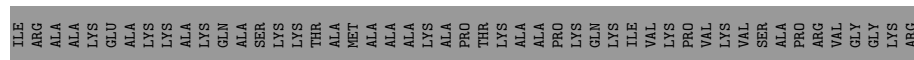
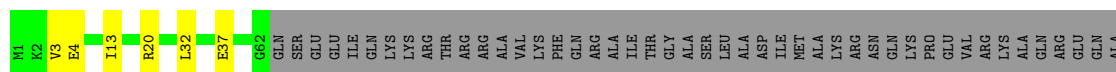
• Molecule 28: 60S ribosomal protein L22

Chain LU:  73% 6% 21%

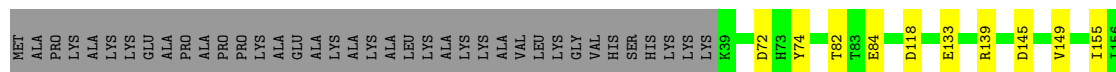
• Molecule 29: 60S ribosomal protein L23

Chain LV:  85% 9% 6%

• Molecule 30: 60S ribosomal protein L24

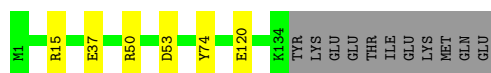
Chain LW:  36% 61%

• Molecule 31: 60S ribosomal protein L23a

Chain LX:  69% 6% 24%

• Molecule 32: 60S ribosomal protein L26

Chain LY:  88% 8%



- Molecule 33: 60S ribosomal protein L27

Chain LZ: 88% 12%



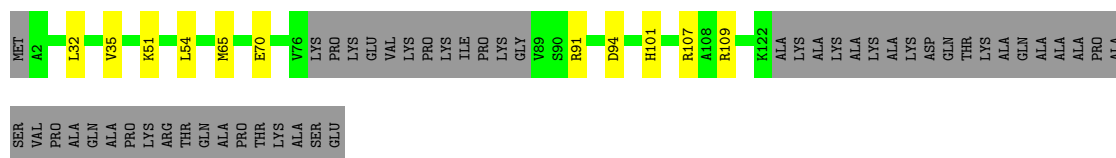
- Molecule 34: 60S ribosomal protein L27a

Chain La: 93% 6%



- Molecule 35: 60S ribosomal protein L29

Chain Lb: 62% 7% 31%



- Molecule 36: 60S ribosomal protein L30

Chain Lc: 75% 10% 15%



- Molecule 37: 60S ribosomal protein L31

Chain Ld: 80% 6% 14%



- Molecule 38: 60S ribosomal protein L32

Chain Le: 90% 5% 5%

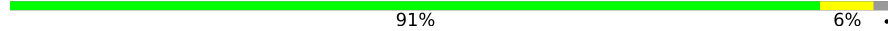


- Molecule 39: 60S ribosomal protein L35a

Chain Lf:  92% 7% .

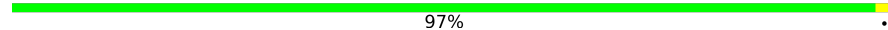


- Molecule 40: 60S ribosomal protein L34

Chain Lg:  91% 6% .

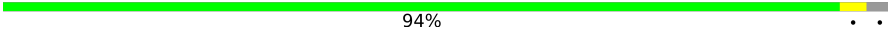


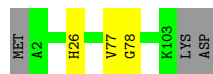
- Molecule 41: 60S ribosomal protein L35

Chain Lh:  97% ..



- Molecule 42: 60S ribosomal protein L36

Chain Li:  94% . .



- Molecule 43: 60S ribosomal protein L37

Chain Lj:  79% 9% 11%



- Molecule 44: 60S ribosomal protein L38

Chain Lk:  80% 19% .



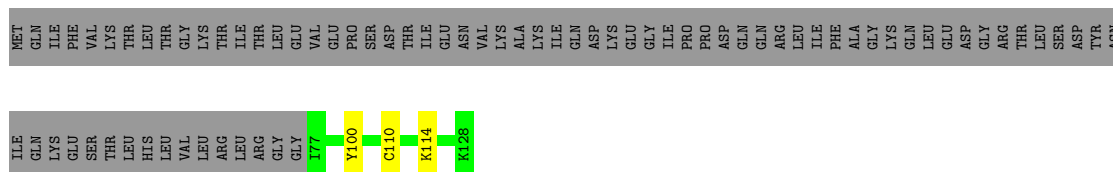
- Molecule 45: 60S ribosomal protein L39

Chain Ll:  88% 10% .

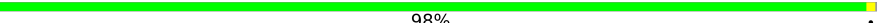


- Molecule 46: Ubiquitin-60S ribosomal protein L40

Chain Lm:  38% 59%



- Molecule 47: 60S ribosomal protein L36a

Chain Lo:  98% ..



- Molecule 48: 60S ribosomal protein L37a

Chain Lp:  88% 10% ..



- Molecule 49: 60S ribosomal protein L28

Chain Lr:  82% 9% 9%



- Molecule 50: 60S ribosomal protein L10a

Chain Lz:  88% 12%



4 Experimental information

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 CORRECTION	Depositor
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

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.06	0/83342	0.14	0/129985
2	7	0.06	0/2861	0.12	0/4459
3	8	0.07	0/3520	0.14	0/5481
4	A	0.07	0/5549	0.19	0/7469
5	B	0.08	0/3280	0.21	0/4426
6	C	0.07	0/1560	0.15	0/2085
7	D	0.10	0/601	0.21	0/818
8	K	0.08	0/1728	0.20	0/2351
9	LA	0.10	0/1936	0.21	0/2596
10	LB	0.08	0/3307	0.20	0/4424
11	LC	0.08	0/2981	0.19	0/4002
12	LD	0.08	0/2428	0.18	0/3252
13	LE	0.07	0/1799	0.20	0/2414
14	LF	0.08	0/1905	0.19	0/2539
15	LG	0.09	0/1960	0.22	0/2637
16	LH	0.09	0/1537	0.20	0/2066
17	LI	0.10	0/1673	0.21	0/2234
18	LJ	0.09	0/1424	0.19	0/1904
19	LL	0.09	0/1604	0.20	0/2149
20	LM	0.09	0/1142	0.20	0/1527
21	LN	0.09	0/1746	0.19	0/2338
22	LO	0.09	0/1682	0.21	0/2250
23	LP	0.09	0/1268	0.21	0/1701
24	LQ	0.11	0/1537	0.23	0/2052
25	LR	0.09	0/1310	0.21	0/1734
26	LS	0.09	0/1493	0.22	0/2003
27	LT	0.09	0/1326	0.23	0/1770
28	LU	0.11	0/839	0.25	0/1126
29	LV	0.10	0/993	0.22	0/1332
30	LW	0.10	0/532	0.19	0/708
31	LX	0.09	0/984	0.22	0/1323
32	LY	0.09	0/1132	0.23	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.10	0/1130	0.20	0/1507
34	La	0.07	0/1191	0.18	0/1591
35	Lb	0.10	0/889	0.23	0/1175
36	Lc	0.11	0/774	0.23	0/1038
37	Ld	0.10	0/903	0.24	0/1216
38	Le	0.09	0/1071	0.19	0/1429
39	Lf	0.11	0/895	0.24	0/1198
40	Lg	0.09	0/916	0.22	0/1220
41	Lh	0.09	0/1023	0.18	0/1351
42	Li	0.09	0/843	0.19	0/1115
43	Lj	0.09	0/720	0.19	0/952
44	Lk	0.11	0/575	0.27	0/761
45	Ll	0.11	0/454	0.20	0/599
46	Lm	0.10	0/435	0.19	0/575
47	Lo	0.09	0/877	0.19	0/1156
48	Lp	0.10	0/718	0.23	0/953
49	Lr	0.09	0/1017	0.21	0/1364
50	Lz	0.08	0/1772	0.20	0/2375
All	All	0.07	0/157182	0.17	0/230234

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	74502	0	37634	272	0
2	7	2561	0	1295	8	0
3	8	3152	0	1601	7	0
4	A	5479	0	5608	46	0
5	B	3234	0	3287	15	0
6	C	1547	0	1543	9	0
7	D	588	0	616	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	K	1704	0	1683	18	0
9	LA	1898	0	1993	21	0
10	LB	3239	0	3376	20	0
11	LC	2927	0	3104	17	0
12	LD	2382	0	2410	17	0
13	LE	1765	0	1917	14	0
14	LF	1870	0	1996	8	0
15	LG	1927	0	2074	9	0
16	LH	1518	0	1601	13	0
17	LI	1634	0	1673	6	0
18	LJ	1401	0	1428	7	0
19	LL	1573	0	1681	14	0
20	LM	1120	0	1187	8	0
21	LN	1701	0	1749	9	0
22	LO	1650	0	1794	16	0
23	LP	1242	0	1269	9	0
24	LQ	1513	0	1628	11	0
25	LR	1294	0	1434	8	0
26	LS	1453	0	1490	11	0
27	LT	1298	0	1366	12	0
28	LU	825	0	850	8	0
29	LV	979	0	1039	9	0
30	LW	519	0	533	4	0
31	LX	967	0	1040	7	0
32	LY	1115	0	1205	5	0
33	LZ	1107	0	1182	10	0
34	La	1162	0	1213	8	0
35	Lb	876	0	948	9	0
36	Lc	764	0	804	12	0
37	Ld	888	0	930	5	0
38	Le	1053	0	1147	5	0
39	Lf	876	0	912	6	0
40	Lg	906	0	998	6	0
41	Lh	1015	0	1148	3	0
42	Li	832	0	917	2	0
43	Lj	705	0	737	6	0
44	Lk	569	0	637	9	0
45	Ll	444	0	483	4	0
46	Lm	429	0	465	2	0
47	Lo	863	0	929	0	0
48	Lp	708	0	756	8	0
49	Lr	1002	0	1068	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Lz	1744	0	1859	20	0
51	5	208	0	0	0	0
51	7	2	0	0	0	0
51	8	5	0	0	0	0
51	LI	1	0	0	0	0
51	LP	1	0	0	0	0
51	LV	1	0	0	0	0
51	Le	1	0	0	0	0
51	Lj	1	0	0	0	0
52	Lg	1	0	0	0	0
52	Lj	1	0	0	0	0
52	Lm	1	0	0	0	0
52	Lo	1	0	0	0	0
52	Lp	1	0	0	0	0
All	All	146745	0	110237	625	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 625 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:29:GLU:N	4:A:32:CYS:HG	1.71	0.89
19:LL:108:GLU:N	19:LL:108:GLU:OE2	2.09	0.86
1:5:3641:U:OP2	1:5:3646:A:N6	2.09	0.85
1:5:3962:A:N6	1:5:3965:A:O2'	2.11	0.83
37:Ld:96:GLU:N	37:Ld:96:GLU:OE2	2.12	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	684/794 (86%)	675 (99%)	9 (1%)	0	100	100
5	B	397/506 (78%)	389 (98%)	8 (2%)	0	100	100
6	C	186/314 (59%)	186 (100%)	0	0	100	100
7	D	76/85 (89%)	76 (100%)	0	0	100	100
8	K	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%)	36	67
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%)	12	41
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
34	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
35	Lb	105/159 (66%)	105 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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	A	612/704 (87%)	607 (99%)	5 (1%)	73	81
5	B	360/438 (82%)	360 (100%)	0	100	100
6	C	162/254 (64%)	161 (99%)	1 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	D	66/72 (92%)	66 (100%)	0	100	100
8	K	194/213 (91%)	190 (98%)	4 (2%)	47	71
9	LA	190/199 (96%)	190 (100%)	0	100	100
10	LB	348/349 (100%)	348 (100%)	0	100	100
11	LC	306/348 (88%)	306 (100%)	0	100	100
12	LD	246/250 (98%)	244 (99%)	2 (1%)	73	81
13	LE	194/252 (77%)	194 (100%)	0	100	100
14	LF	194/215 (90%)	194 (100%)	0	100	100
15	LG	203/223 (91%)	201 (99%)	2 (1%)	68	79
16	LH	169/171 (99%)	169 (100%)	0	100	100
17	LI	172/181 (95%)	171 (99%)	1 (1%)	78	83
18	LJ	147/149 (99%)	146 (99%)	1 (1%)	76	82
19	LL	164/177 (93%)	164 (100%)	0	100	100
20	LM	116/161 (72%)	116 (100%)	0	100	100
21	LN	171/172 (99%)	170 (99%)	1 (1%)	78	83
22	LO	173/174 (99%)	173 (100%)	0	100	100
23	LP	134/163 (82%)	134 (100%)	0	100	100
24	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	83
25	LR	138/175 (79%)	138 (100%)	0	100	100
26	LS	156/157 (99%)	154 (99%)	2 (1%)	61	77
27	LT	139/140 (99%)	137 (99%)	2 (1%)	59	76
28	LU	91/115 (79%)	91 (100%)	0	100	100
29	LV	101/107 (94%)	101 (100%)	0	100	100
30	LW	54/126 (43%)	54 (100%)	0	100	100
31	LX	106/133 (80%)	106 (100%)	0	100	100
32	LY	124/135 (92%)	124 (100%)	0	100	100
33	LZ	117/118 (99%)	117 (100%)	0	100	100
34	La	120/121 (99%)	120 (100%)	0	100	100
35	Lb	88/126 (70%)	88 (100%)	0	100	100
36	Lc	83/97 (86%)	81 (98%)	2 (2%)	43	69
37	Ld	98/110 (89%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Le	114/121 (94%)	113 (99%)	1 (1%)	70	80
39	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	78
40	Lg	98/100 (98%)	98 (100%)	0	100	100
41	Lh	109/110 (99%)	109 (100%)	0	100	100
42	Li	86/89 (97%)	86 (100%)	0	100	100
43	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	76
44	Lk	64/65 (98%)	63 (98%)	1 (2%)	55	75
45	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	71
46	Lm	48/116 (41%)	47 (98%)	1 (2%)	47	71
47	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	78
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	59	76
49	Lr	109/121 (90%)	109 (100%)	0	100	100
50	Lz	196/196 (100%)	196 (100%)	0	100	100
All	All	7099/7994 (89%)	7067 (100%)	32 (0%)	78	85

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	Ll	47	THR
46	Lm	110	CYS
15	LG	159	HIS
12	LD	239	MET
47	Lo	7	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
19	LL	67	HIS
25	LR	40	GLN
39	Lf	99	HIS
20	LM	125	ASN
23	LP	34	GLN

5.3.3 RNA ⓘ

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	A
1	5	42	A
1	5	48	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	739	G
1	5	1590	C
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 oligosaccharides 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

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

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.