



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 02:39 pm GMT

PDB ID : 7OOD
EMDB ID : EMD-11999
Title : Mycoplasma pneumoniae 50S subunit of ribosomes in chloramphenicol-treated cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-05-27
Resolution : 3.40 Å (reported)
Based on initial models : 3J9W, 4YBB, 1DIV, 1ZAV

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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

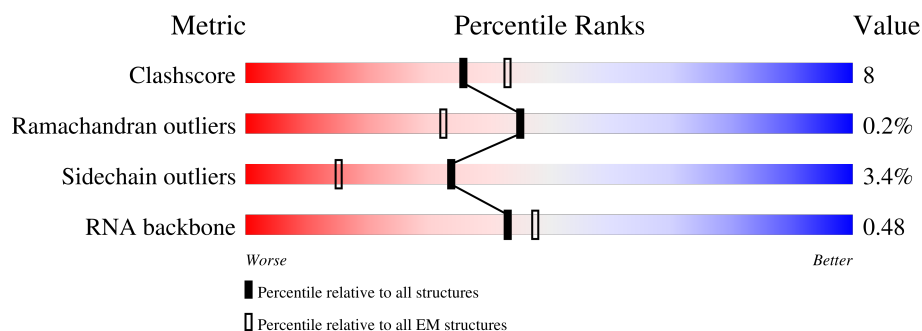
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



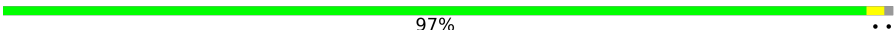
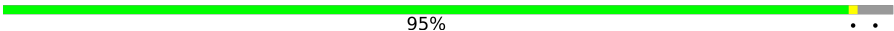
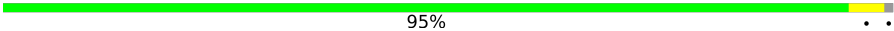









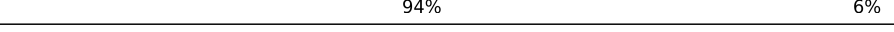
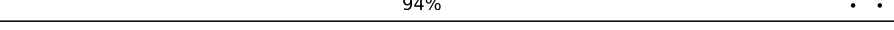

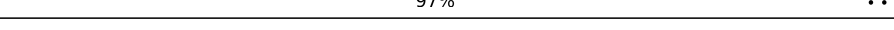

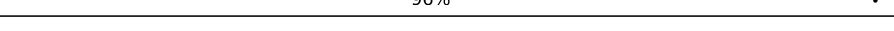
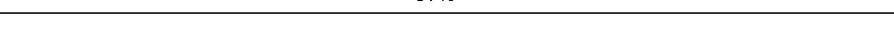


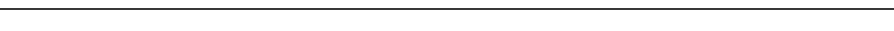


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	3	2907	
2	4	108	
3	w	111	
4	a	287	
5	c	212	
6	e	184	
7	k	151	

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Mol	Chain	Length	Quality of chain
8	i	146	 97% ..
9	m	124	 95% ..
10	q	100	 95% ..
11	u	104	 82% . 17%
12	y	57	 89% 9% .
13	0	48	 75% 23% .
14	2	37	 38% 57% 5%
15	1	59	 64% 32% .
16	o	119	 92% ..
17	s	237	 39% 61%
18	v	65	 89% 8% .
19	x	97	 45% 55%
20	z	53	 94% 6%
21	d	180	 94% ..
22	b	287	 78% . 20%
23	l	139	 97% ..
24	p	127	 87% . 10%
25	j	122	 96% .
26	n	116	 97% .
27	t	111	 86% . 14%
28	r	159	 82% 5% 13%
29	f	149	 96% ..
30	h	137	 92% .. 7%
31	g	161	 75% . 22%

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 89509 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	2879	Total	C	N	O	P	0	0
			61690	27566	11236	20009	2879		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	105	Total	C	N	O	P	0	0
			2245	1003	409	728	105		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	w	99	Total	C	N	O	0	0
			798	505	149	144		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total	C	N	O	S	0	0
			2199	1370	433	390	6		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	210	Total	C	N	O	S	0	0
			1613	1026	294	290	3		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	176	Total	C	N	O	0	0
			1349	867	240	242		

- Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	148	Total	C	N	O	0	0
			1138	722	223	193		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	144	Total	C	N	O	S	0	0
			1158	733	212	208	5		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	119	Total	C	N	O	S	0	0
			957	609	175	170	3		

- Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	99	Total	C	N	O	S	0	0
			809	525	148	133	3		

- Molecule 11 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	u	86	Total	C	N	O	S	0	0
			641	397	127	116	1		

- Molecule 12 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	y	56	Total	C	N	O	S	0	0
			436	262	96	73	5		

- Molecule 13 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0	47	Total	C	N	O	S	0	0
			377	234	81	61	1		

- Molecule 14 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	37	Total	C	N	O	S	0	0
			303	189	65	45	4		

- Molecule 15 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o	115	Total	C	N	O	S	0	0
			895	568	169	157	1		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	92	Total	C	N	O	S	0	0
			714	470	121	122	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	63	Total	C	N	O	S	0	0
			504	312	107	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	44	Total	C	N	O	0	0
			218	130	44	44		

- Molecule 20 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 21 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	175	Total	C	N	O	S	0	0
			1244	797	214	229	4		

- Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	229	Total	C	N	O	S	0	0
			1758	1116	317	318	7		

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	136	Total	C	N	O	S	0	0
			1057	680	193	177	7		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	114	Total	C	N	O	S	0	0
			941	600	185	154	2		

- Molecule 25 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 26 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	n	112	Total	C	N	O	S	0	0
			853	534	169	149	1		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	96	Total	C	N	O	S	0	0
			706	449	132	122	3		

- Molecule 28 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	144	Total	C	N	O	0	0
			713	425	144	144		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	h	128	Total	C	N	O	0	0
			630	374	128	128		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	g	125	Total	C	N	O	0	0
			617	367	125	125		

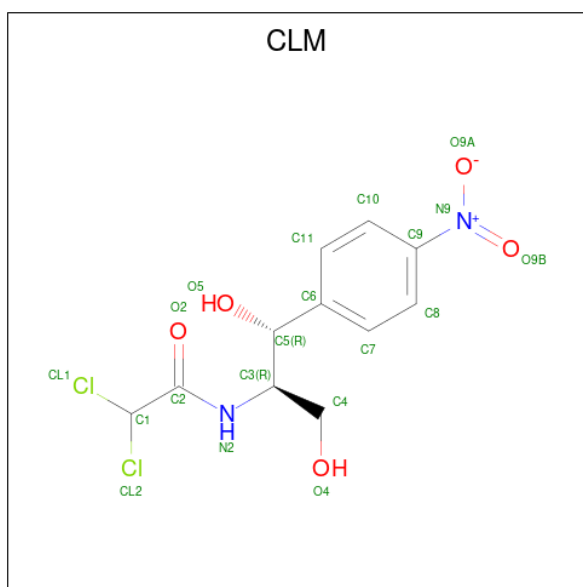
- Molecule 32 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
32	3	1	Total	K	0
			1	1	

- Molecule 33 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	3	24	Total	Mg	0
			24	24	
33	y	1	Total	Mg	0
			1	1	

- Molecule 34 is CHLORAMPHENICOL (three-letter code: CLM) (formula: C₁₁H₁₂Cl₂N₂O₅).



Mol	Chain	Residues	Atoms					AltConf
34	3	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

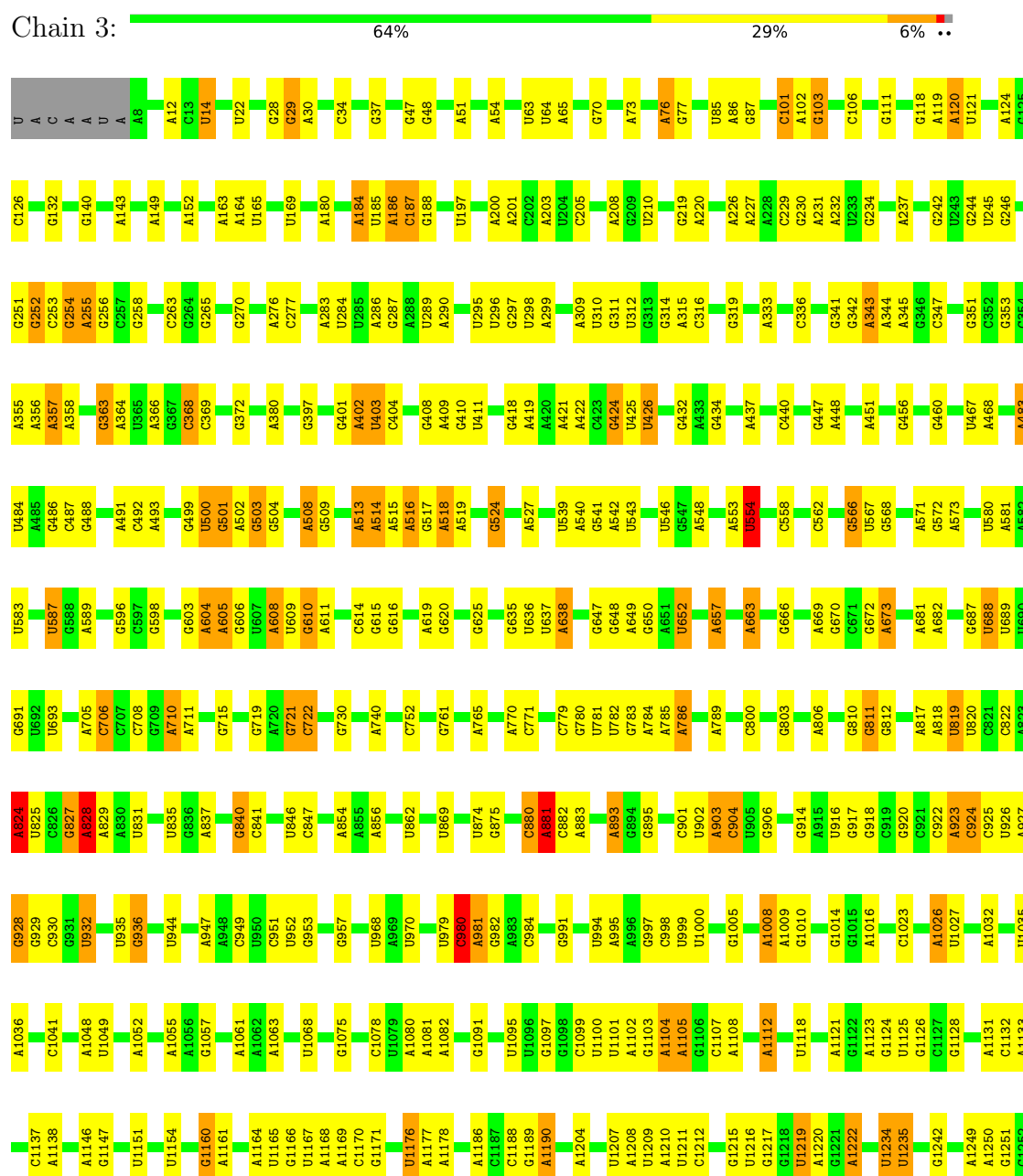
- Molecule 35 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	y	1	Total	Zn	0
			1	1	
35	2	1	Total	Zn	0
			1	1	
35	z	1	Total	Zn	0
			1	1	

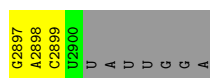
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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: 23S ribosomal RNA

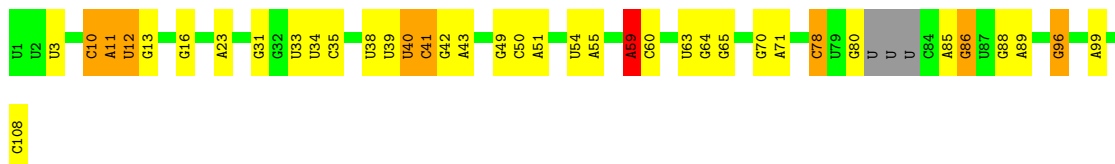


C2796	G2453	G2353	G2259	G2131	A2037	G1815	A1688	U1584	U1481	G1366	G1253
C2797	G2454	A2354	C2266	G2132	A2038	U1816	A1689	A1585	U1482	G1367	U1256
A2798	G2455	C2355	C2267	A2133	G2039	A1935	U1691	U1586	G1483	U1368	G1257
U2799	A2456	U2563	U2273	C2139	A2040	U1820	U1692	U1587	U1486	U1369	G1266
U2800	U2457	U2563	U2274	G2140	A2042	G1821	U1693	A1588	U1487	A1370	G1267
U2801	A2458	U2564	A2275	A2141	C2043	A1822	A1694	A1589	U1494	U1372	U1268
C2802	A2459	A2366	A2276	G2151	G2050	U1824	A1698	A1592	U1497	U1372	U1269
G	C2460	C2367	A2281	C2152	C2054	U1825	A1699	A1601	C1379	U1380	C1270
C	G2463	G2370	A2282	U2153	C2064	A1826	A1699	A1602	C1379	U1380	C1271
A	C2464	A2371	A2283	A2154	A2055	U1958	A1702	A1603	G1383	G1383	A1271
G2807	U2465	G2380	A2286	G2164	A2056	U1958	A1703	A1604	A1503	A1276	A1276
A2808	G2381	G2381	C2289	A2165	C2057	U1962	C1704	A1605	A1504	A1277	A1277
A2809	A2382	G2383	G2290	U2166	G2058	U1970	U1705	G1388	G1388	G1278	G1278
G2810	G2383	G2383	G2291	A2167	G2059	G1706	C1706	G1389	G1389	U1279	U1279
G2811	A2476	U2291	A2292	G2168	G2060	G1707	U1707	G1390	G1390	U1280	U1280
U2812	A2477	A2386	A2293	G2169	A2061	G1708	G1708	G1391	G1391	G1281	G1281
A2813	G2584	C2393	C2294	G2170	C2062	A1836	G1708	G1392	G1392	A1281	A1281
A2814	A2484	G2390	A2295	A2171	G2063	C1837	U1723	G1393	G1393	G1282	G1282
G2815	G2391	G2391	A2296	A2172	G2064	U1841	A1723	A1394	A1394	A1283	A1283
G2816	U2485	C2392	A2297	G2174	A2067	G1842	U1727	A1513	A1513	A1284	A1284
G2817	A2486	G2393	G2298	U2175	G2068	G1843	U1727	U1285	U1285	U1285	U1285
G2818	G2487	A2396	G2299	U2176	A2069	C1845	U1727	G1286	G1286	C1287	C1287
G2819	G2488	G2397	U2299	U2177	A2070	C1845	U1727	G1287	G1287	C1287	C1287
G2820	G2489	G2398	U2300	U2178	A2071	C1845	U1727	G1288	G1288	C1288	C1288
G2821	G2490	G2399	U2301	U2179	A2072	C1845	U1727	G1289	G1289	C1289	C1289
G2822	G2491	G2400	U2302	U2180	A2073	C1845	U1727	G1290	G1290	C1290	C1290
G2823	G2492	A2401	U2303	A2181	C2073	A1854	U1727	G1291	G1291	C1291	C1291
G2824	G2493	A2402	U2304	C2182	A2074	C1855	U1727	G1292	G1292	C1292	C1292
G2825	U2494	A2403	U2305	U2183	G2076	A1856	U1727	G1293	G1293	C1293	C1293
G2826	G2495	C2411	A2306	U2184	A2077	G1857	U1727	G1294	G1294	C1294	C1294
G2827	C2504	G2412	G2312	U2185	A2078	G1858	U1727	G1295	G1295	C1295	C1295
G2828	A2505	U2414	U2313	U2186	U2083	G1859	U1727	G1296	G1296	C1296	C1296
G2829	C2506	A2415	U2314	U2187	A2084	G1860	U1727	G1297	G1297	C1297	C1297
G2830	C2507	U2416	U2315	U2188	U2085	G1861	U1727	G1298	G1298	C1298	C1298
G2831	C2508	A2417	U2316	U2189	A2085	G1862	U1727	G1299	G1299	C1299	C1299
G2832	C2509	G2418	A2317	C2198	A2097	A1873	U1727	G1300	G1300	C1301	C1301
G2833	G2510	G2419	U2318	U2199	G2098	C1874	U1727	G1302	G1302	C1302	C1302
G2834	G2511	G2420	U2319	U2200	U2099	G1875	U1727	G1303	G1303	C1303	C1303
G2835	G2512	G2421	U2320	G2201	G2100	C1876	U1727	G1304	G1304	C1304	C1304
G2836	G2513	G2422	U2321	U2202	G2101	A1877	U1727	G1305	G1305	C1305	C1305
G2837	G2514	G2423	U2322	U2203	G2102	A1878	U1727	G1306	G1306	C1306	C1306
G2838	G2515	G2424	U2323	U2204	G2103	A1879	U1727	G1307	G1307	C1307	C1307
G2839	G2516	G2425	U2324	U2205	G2104	A1880	U1727	G1308	G1308	C1308	C1308
G2840	G2517	G2426	U2325	U2206	G2105	A1881	U1727	G1309	G1309	C1309	C1309
G2841	G2518	G2427	U2326	U2207	G2106	A1882	U1727	G1310	G1310	C1310	C1310
G2842	G2519	G2428	U2327	U2208	G2107	A1883	U1727	G1311	G1311	C1311	C1311
G2843	G2520	G2429	U2328	U2209	A2107	A1884	U1727	G1312	G1312	C1312	C1312
G2844	G2521	G2430	U2329	U2210	U2110	A1885	U1727	G1313	G1313	C1313	C1313
G2845	G2522	G2431	U2330	U2211	U2111	A1886	U1727	G1314	G1314	C1314	C1314
G2846	G2523	G2432	U2331	U2212	A2112	A1887	U1727	G1315	G1315	C1315	C1315
G2847	G2524	G2433	U2332	U2213	U2113	A1888	U1727	G1316	G1316	C1316	C1316
G2848	G2525	G2434	U2333	U2214	C2016	A1889	U1727	G1317	G1317	C1317	C1317
G2849	G2526	G2435	U2334	U2215	G2017	A1890	U1727	G1318	G1318	C1318	C1318
G2850	G2527	G2436	U2335	U2216	G2018	A1891	U1727	G1319	G1319	C1319	C1319
G2851	G2528	G2437	U2336	U2217	U2116	A1892	U1727	G1320	G1320	C1320	C1320
G2852	G2529	G2438	U2337	U2218	G2117	A1893	U1727	G1321	G1321	C1321	C1321
G2853	G2530	G2439	U2338	U2219	U2118	A1894	U1727	G1322	G1322	C1322	C1322
G2854	G2531	G2440	U2339	U2220	U2119	A1895	U1727	G1323	G1323	C1323	C1323
G2855	G2532	G2441	U2340	U2221	U2120	A1896	U1727	G1324	G1324	C1324	C1324
G2856	G2533	G2442	U2341	U2222	U2121	A1897	U1727	G1325	G1325	C1325	C1325
G2857	G2534	G2443	U2342	U2223	U2122	A1898	U1727	G1326	G1326	C1326	C1326
G2858	G2535	G2444	U2343	U2224	G2123	A1899	U1727	G1327	G1327	C1327	C1327
G2859	G2536	G2445	U2344	U2225	A2124	A1899	U1727	G1328	G1328	C1328	C1328
G2860	G2537	G2446	U2345	U2226	U2125	A1899	U1727	G1329	G1329	C1329	C1329
G2861	G2538	G2447	U2346	U2227	U2126	A1899	U1727	G1330	G1330	C1330	C1330
G2862	G2539	G2448	U2347	U2228	U2127	A1899	U1727	G1331	G1331	C1331	C1331
G2863	G2540	G2449	U2348	U2229	U2128	A1899	U1727	G1332	G1332	C1332	C1332
G2864	G2541	G2450	U2349	U2230	U2129	A1899	U1727	G1333	G1333	C1333	C1333
G2865	G2542	G2451	U2350	U2231	U2130	A1899	U1727	G1334	G1334	C1334	C1334
G2866	G2543	G2452	U2351	U2232	U2131	A1899	U1727	G1335	G1335	C1335	C1335
G2867	G2544	G2453	U2352	U2233	U2132	A1899	U1727	G1336	G1336	C1336	C1336
G2868	G2545	G2454	U2353	U2234	U2133	A1899	U1727	G1337	G1337	C1337	C1337
G2869	G2546	G2455	U2354	U2235	U2134	A1899	U1727	G1338	G1338	C1338	C1338
G2870	G2547	G2456	U2355	U2236	U2135	A1899	U1727	G1339	G1339	C1339	C1339
G2871	G2548	G2457	U2356	U2237	U2136	A1899	U1727	G1340	G1340	C1340	C1340
G2872	G2549	G2458	U2357	U2238	U2137	A1899	U1727	G1341	G1341	C1341	C1341
G2873	G2550	G2459	U2358	U2239	U2138	A1899	U1727	G1342	G1342	C1342	C1342
G2874	G2551	G2460	U2359	U2240	U2139	A1899	U1727	G1343	G1343	C1343	C1343
G2875	G2552	G2461	U2360	U2241	U2140	A1899	U1727	G1344	G1344	C1344	C1344
G2876	G2553	G2462	U2361	U2242	U2141	A1899	U1727	G1345	G1345	C1345	C1345
G2877	G2554	G2463	U2362	U2243	U2142	A1899	U1727	G1346	G1346	C1346	C1346
G2878	G2555	G2464	U2363	U2244	U2143	A1899	U1727	G1347	G1347	C1347	C1347
G2879	G2556	G2465	U2364	U2245	U2144	A1899	U1727	G1348	G1348	C1348	C1348
G2880	G2557	G2466	U2365	U2246	U2145	A1899	U1727	G1349	G1349	C1349	C1349
G2881	G2558	G2467	U2366	U2247	U2146	A1899	U1727	G1350	G1350	C1350	C1350
G2882	G2559	G2468	U2367	U2248	U2147	A1899	U1727	G1351	G1351	C1351	C1351
G2883	G2560	G2469	U2368	U2249	U2148	A1899	U1727	G1352	G1352	C1352	C1352
G2884	G2561	G2470	U2369	U2250	U2149	A1899	U1727	G1353	G1353	C1353	C1353
G2885	G2562	G2471	U2370	U2251	U2150	A1899	U1727	G1354	G1354	C1354	C1354
G2886	G2563	G2472	U2371	U2252	U2151	A1899	U1727	G1355	G1355	C1355	C1355
G2887	G2564	G2473	U2372	U2253	U2152	A1899	U1727	G1356	G1356	C1356	C1356
G2888	G2565	G2474	U2373	U2254	U2153	A1899	U1727	G1357	G1357	C1357	C1357
G2889	G2566	G2475	U2374	U2255	U2154	A1899	U1727	G1358	G1358	C1358	C1358
G2890	G2567	G2476	U2375	U2256	U2155	A1899	U1727	G1359	G1359	C1359	C1359
G2891	G2568	G2477	U2376	U2257	U2156	A1899	U1727	G1360	G1360	C1360	C1360
G2892	G2569	G2478	U2377	U2258	U2157	A1899	U1727	G1361	G1361	C1361	C1361
G2893	G2570	G2479	U2378	U2259	U2158	A1899	U1727	G1362	G1362	C1362	C1362
G2894	G2571	G2480	U2379	U2260	U2159	A1899	U1727	G1363	G1363	C1363	C1363
G2895	G2572	G2481	U2380	U2261	U2160	A1899	U1727	G1364	G1364	C1364	C1364
G2896	G2573	G2482	U2381	U2262	U2161	A1899	U1727	G1365	G1365	C1365	C1365
G2897	G2574	G2483	U2382	U2263	U2162	A1899	U1727	G1366	G1366	C1366	C1366
G2898	G2575	G2484	U2383	U2264	U2163	A1899	U1727	G1367	G1367	C1367	C1367
G2899	G2576	G2485	U2384	U2265	U2164	A1899	U1727	G1368	G1368	C1368	C1368
G2900	G2577	G2486	U2385	U2266	U2165	A1899	U1727	G1369	G1369	C1369	C1369
G2901	G2578	G2487	U2386	U2267	U2166	A1899	U1727	G1370	G1370	C1370	C1370
G2902	G2579	G2488	U2387	U2268	U2167	A1899	U1727	G1371	G1371	C1371	C1371
G2903	G2580	G248									



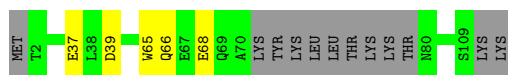
- Molecule 2: 5S ribosomal RNA

Chain 4: 62% 27% 7% ..



- Molecule 3: 50S ribosomal protein L29

Chain w: 85% 5% 11%



- Molecule 4: 50S ribosomal protein L2

Chain a: 97% ..



- Molecule 5: 50S ribosomal protein L4

Chain c: 95% ..



- Molecule 6: 50S ribosomal protein L6

Chain e: 94% ..



- Molecule 7: 50S ribosomal protein L15

Chain k: 95% ..



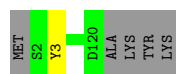
- Molecule 8: 50S ribosomal protein L13

Chain i:  97% ..



- Molecule 9: 50S ribosomal protein L17

Chain m:  95% ..




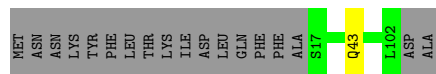
- Molecule 10: 50S ribosomal protein L21

Chain q:  95% ..




- Molecule 11: 50S ribosomal protein L27

Chain u:  82% . 17%



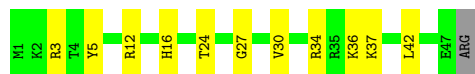
- Molecule 12: 50S ribosomal protein L32

Chain y:  89% 9% .



- Molecule 13: 50S ribosomal protein L34

Chain 0:  75% 23% .

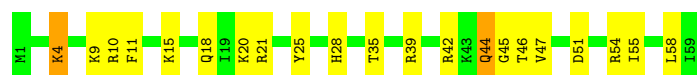


- Molecule 14: 50S ribosomal protein L36

Chain 2:  38% 57% 5%



- Molecule 15: 50S ribosomal protein L35



- MET
LYS
K3
Q80
N83
I86
S87
I88
R117
LYS
GLN

- [illegible]

- | | | | | | | | | |
|-----|----|-----|-----|-----|-----|-----|-----|-----|
| MET | A2 | T45 | T46 | R47 | I48 | L49 | L64 | SER |
|-----|----|-----|-----|-----|-----|-----|-----|-----|

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | LVS | LVS | LVS | F5 | GAS | GLU | LEU | THR | LVS | LVS | GLN | THR | VAL | HIS | GLY | ARG | ALA | GLU | GLU | LVS | LEU | SER | GLY | LVS | PHE | ASN | ALA | GLY | LVS | THR | PRO | LVS | LVS | ALA | GLU | LEU | ASN | LVS | THR | LVS | GLY | LVS | THR | GLU | TVA | THR | LVS | HIS | ARG | SER | LEU | ASN | GLU | LEU |
|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

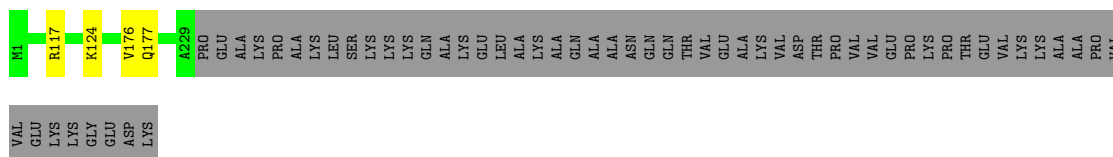
- | | | | | |
|-----|----|-----|-----|-----|
| MET | A2 | K51 | ARG | LYS |
|-----|----|-----|-----|-----|

- 



- Molecule 22: 50S ribosomal protein L3

Chain b: 78% 20%



- Molecule 23: 50S ribosomal protein L16

Chain l: 97% ..



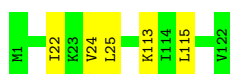
- Molecule 24: 50S ribosomal protein L20

Chain p: 87% 10%



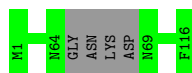
- Molecule 25: 50S ribosomal protein L14

Chain j: 96% .



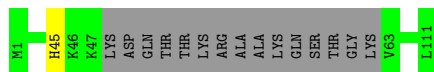
- Molecule 26: 50S ribosomal protein L18

Chain n: 97% .

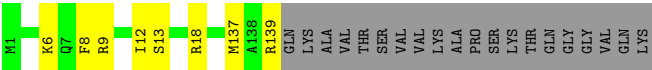
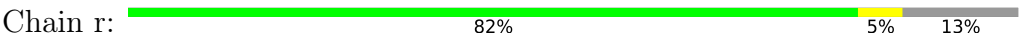


- Molecule 27: 50S ribosomal protein L24

Chain t: 86% 14%



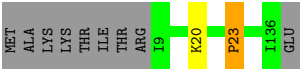
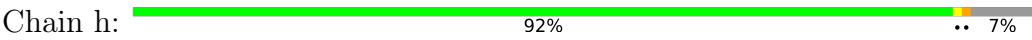
- Molecule 28: 50S ribosomal protein L22



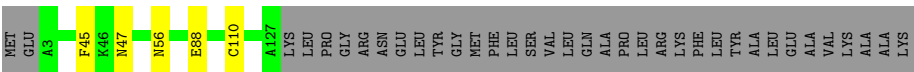
• Molecule 29: 50S ribosomal protein L9



• Molecule 30: 50S ribosomal protein L11



• Molecule 31: 50S ribosomal protein L10



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	17890	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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: MG, K, CLM, 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	3	0.89	68/69100 (0.1%)	0.93	141/107749 (0.1%)
2	4	0.60	0/2511	0.82	1/3910 (0.0%)
3	w	0.41	0/806	0.61	0/1080
4	a	0.46	1/2241 (0.0%)	0.59	0/3013
5	c	0.41	0/1639	0.65	1/2209 (0.0%)
6	e	0.36	0/1373	0.55	0/1854
7	k	0.40	0/1155	0.59	0/1541
8	i	0.43	0/1180	0.54	0/1585
9	m	0.41	0/972	0.55	0/1308
10	q	0.42	0/826	0.59	0/1109
11	u	0.45	0/649	0.55	0/867
12	y	0.48	0/440	0.79	1/582 (0.2%)
13	0	0.41	0/380	0.50	0/501
14	2	0.57	1/305 (0.3%)	0.77	2/401 (0.5%)
15	1	0.44	0/484	0.56	0/637
16	o	0.42	0/905	0.63	1/1211 (0.1%)
17	s	0.39	0/726	0.51	0/981
18	v	0.39	0/510	0.59	0/684
19	x	0.25	0/217	0.48	0/301
20	z	0.39	0/412	0.58	0/547
21	d	0.32	0/1264	0.57	1/1719 (0.1%)
22	b	0.42	0/1791	0.57	0/2408
23	l	0.45	0/1082	0.54	0/1456
24	p	0.49	0/955	0.55	0/1271
25	j	0.49	0/953	0.60	0/1275
26	n	0.35	0/861	0.51	0/1156
27	t	0.35	0/712	0.52	0/954
28	r	0.50	1/1077 (0.1%)	0.57	0/1441
29	f	0.44	0/711	0.78	0/988
30	h	0.62	0/629	1.00	1/873 (0.1%)
31	g	0.76	0/616	1.03	1/856 (0.1%)
All	All	0.79	71/97482 (0.1%)	0.86	150/146467 (0.1%)

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	a	89	ASP	C-N	8.41	1.50	1.34
1	3	2735	G	O3'-P	-7.74	1.51	1.61
1	3	611	A	P-OP2	7.73	1.62	1.49
1	3	1281	A	C5-C6	-7.67	1.34	1.41
1	3	2057	C	O3'-P	-7.63	1.51	1.61

The worst 5 of 150 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3	2506	C	O5'-P-OP1	-12.90	94.09	105.70
1	3	1399	G	O5'-P-OP1	-12.79	94.19	105.70
1	3	205	C	O5'-P-OP1	-12.26	94.67	105.70
1	3	372	G	O5'-P-OP2	-11.34	95.49	105.70
1	3	2060	G	O5'-P-OP1	11.10	124.02	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	61690	0	30961	237	0
2	4	2245	0	1135	7	0
3	w	798	0	838	0	0
4	a	2199	0	2248	0	0
5	c	1613	0	1676	0	0
6	e	1349	0	1373	0	0
7	k	1138	0	1223	0	0
8	i	1158	0	1176	0	0
9	m	957	0	1008	0	0
10	q	809	0	852	0	0
11	u	641	0	650	0	0
12	y	436	0	441	0	0
13	0	377	0	422	14	0
14	2	303	0	348	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	l	477	0	530	30	0
16	o	895	0	932	0	0
17	s	714	0	785	0	0
18	v	504	0	542	0	0
19	x	218	0	90	0	0
20	z	408	0	436	0	0
21	d	1244	0	1160	0	0
22	b	1758	0	1797	0	0
23	l	1057	0	1088	0	0
24	p	941	0	1017	0	0
25	j	944	0	1019	0	0
26	n	853	0	873	0	0
27	t	706	0	726	0	0
28	r	1068	0	1150	0	0
29	f	713	0	313	0	0
30	h	630	0	309	0	0
31	g	617	0	308	0	0
32	3	1	0	0	0	0
33	3	24	0	0	0	0
33	y	1	0	0	0	0
34	3	20	0	10	4	0
35	2	1	0	0	0	0
35	y	1	0	0	0	0
35	z	1	0	0	0	0
All	All	89509	0	57436	272	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 8.

The worst 5 of 272 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)
14:2:11:CYS:SG	14:2:32:HIS:HE1	1.46	1.35
14:2:14:CYS:SG	14:2:27:CYS:HB2	1.99	1.03
1:3:254:G:OP2	15:1:10:ARG:NH2	2.01	0.93
1:3:253:C:O2	15:1:9:LYS:NZ	2.09	0.86
14:2:16:ILE:HG12	14:2:25:VAL:HG12	1.62	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	w	95/111 (86%)	89 (94%)	6 (6%)	0	100	100
4	a	283/287 (99%)	253 (89%)	30 (11%)	0	100	100
5	c	208/212 (98%)	186 (89%)	22 (11%)	0	100	100
6	e	174/184 (95%)	165 (95%)	9 (5%)	0	100	100
7	k	146/151 (97%)	126 (86%)	20 (14%)	0	100	100
8	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
9	m	117/124 (94%)	111 (95%)	6 (5%)	0	100	100
10	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
11	u	84/104 (81%)	76 (90%)	8 (10%)	0	100	100
12	y	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
13	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
14	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
15	1	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
16	o	113/119 (95%)	95 (84%)	18 (16%)	0	100	100
17	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
18	v	61/65 (94%)	53 (87%)	8 (13%)	0	100	100
19	x	42/97 (43%)	31 (74%)	11 (26%)	0	100	100
20	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
21	d	173/180 (96%)	154 (89%)	19 (11%)	0	100	100
22	b	227/287 (79%)	199 (88%)	28 (12%)	0	100	100
23	l	134/139 (96%)	118 (88%)	16 (12%)	0	100	100
24	p	112/127 (88%)	104 (93%)	8 (7%)	0	100	100
25	j	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
26	n	108/116 (93%)	91 (84%)	17 (16%)	0	100	100
27	t	92/111 (83%)	84 (91%)	8 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	r	137/159 (86%)	123 (90%)	14 (10%)	0	100	100
29	f	140/149 (94%)	121 (86%)	18 (13%)	1 (1%)	19	47
30	h	126/137 (92%)	116 (92%)	8 (6%)	2 (2%)	8	29
31	g	123/161 (76%)	115 (94%)	4 (3%)	4 (3%)	3	18
All	All	3383/3879 (87%)	3039 (90%)	337 (10%)	7 (0%)	45	72

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	f	115	ASP
30	h	20	LYS
31	g	45	PHE
31	g	110	CYS
30	h	23	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	w	83/98 (85%)	78 (94%)	5 (6%)	16	41
4	a	233/243 (96%)	226 (97%)	7 (3%)	36	61
5	c	174/184 (95%)	166 (95%)	8 (5%)	23	49
6	e	138/159 (87%)	135 (98%)	3 (2%)	47	68
7	k	118/126 (94%)	114 (97%)	4 (3%)	32	57
8	i	124/128 (97%)	121 (98%)	3 (2%)	44	66
9	m	104/109 (95%)	103 (99%)	1 (1%)	73	83
10	q	88/91 (97%)	84 (96%)	4 (4%)	23	50
11	u	64/85 (75%)	63 (98%)	1 (2%)	58	75
12	y	45/49 (92%)	41 (91%)	4 (9%)	8	27
13	0	39/41 (95%)	39 (100%)	0	100	100
14	2	35/35 (100%)	32 (91%)	3 (9%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	1	51/51 (100%)	47 (92%)	4 (8%)	10	33
16	o	91/105 (87%)	87 (96%)	4 (4%)	24	50
17	s	80/208 (38%)	80 (100%)	0	100	100
18	v	55/60 (92%)	50 (91%)	5 (9%)	7	26
20	z	47/50 (94%)	47 (100%)	0	100	100
21	d	111/154 (72%)	107 (96%)	4 (4%)	30	56
22	b	185/233 (79%)	181 (98%)	4 (2%)	47	68
23	l	107/115 (93%)	106 (99%)	1 (1%)	75	86
24	p	99/108 (92%)	95 (96%)	4 (4%)	27	52
25	j	103/103 (100%)	98 (95%)	5 (5%)	21	48
26	n	85/99 (86%)	85 (100%)	0	100	100
27	t	69/96 (72%)	68 (99%)	1 (1%)	62	77
28	r	116/132 (88%)	109 (94%)	7 (6%)	16	41
All	All	2444/2862 (85%)	2362 (97%)	82 (3%)	34	57

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	d	94	GLU
25	j	25	LEU
21	d	99	PHE
24	p	50	ARG
28	r	6	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
26	n	38	HIS
15	1	28	HIS
6	e	24	HIS
6	e	21	GLN
7	k	134	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	2876/2907 (98%)	667 (23%)	58 (2%)
2	4	103/108 (95%)	32 (31%)	6 (5%)
All	All	2979/3015 (98%)	699 (23%)	64 (2%)

5 of 699 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	12	A
1	3	14	U
1	3	28	G
1	3	37	G
1	3	47	G

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	2897	G
2	4	34	U
1	3	1209	U
1	3	1048	A
2	4	38	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 30 ligands modelled in this entry, 29 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	CLM	3	3026	-	19,20,20	2.42	7 (36%)	23,27,27	1.34	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	CLM	3	3026	-	-	3/20/22/22	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	3	3026	CLM	O9B-N9	-5.97	1.12	1.22
34	3	3026	CLM	C2-N2	4.12	1.43	1.34
34	3	3026	CLM	C1-C2	3.80	1.58	1.53
34	3	3026	CLM	O2-C2	-3.42	1.16	1.23
34	3	3026	CLM	O5-C5	-3.12	1.36	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	3	3026	CLM	C4-C3-N2	-3.06	104.40	109.27
34	3	3026	CLM	C3-N2-C2	-2.79	118.14	123.07

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	3	3026	CLM	C3-C5-C6-C7
34	3	3026	CLM	C3-C5-C6-C11
34	3	3026	CLM	N2-C3-C4-O4

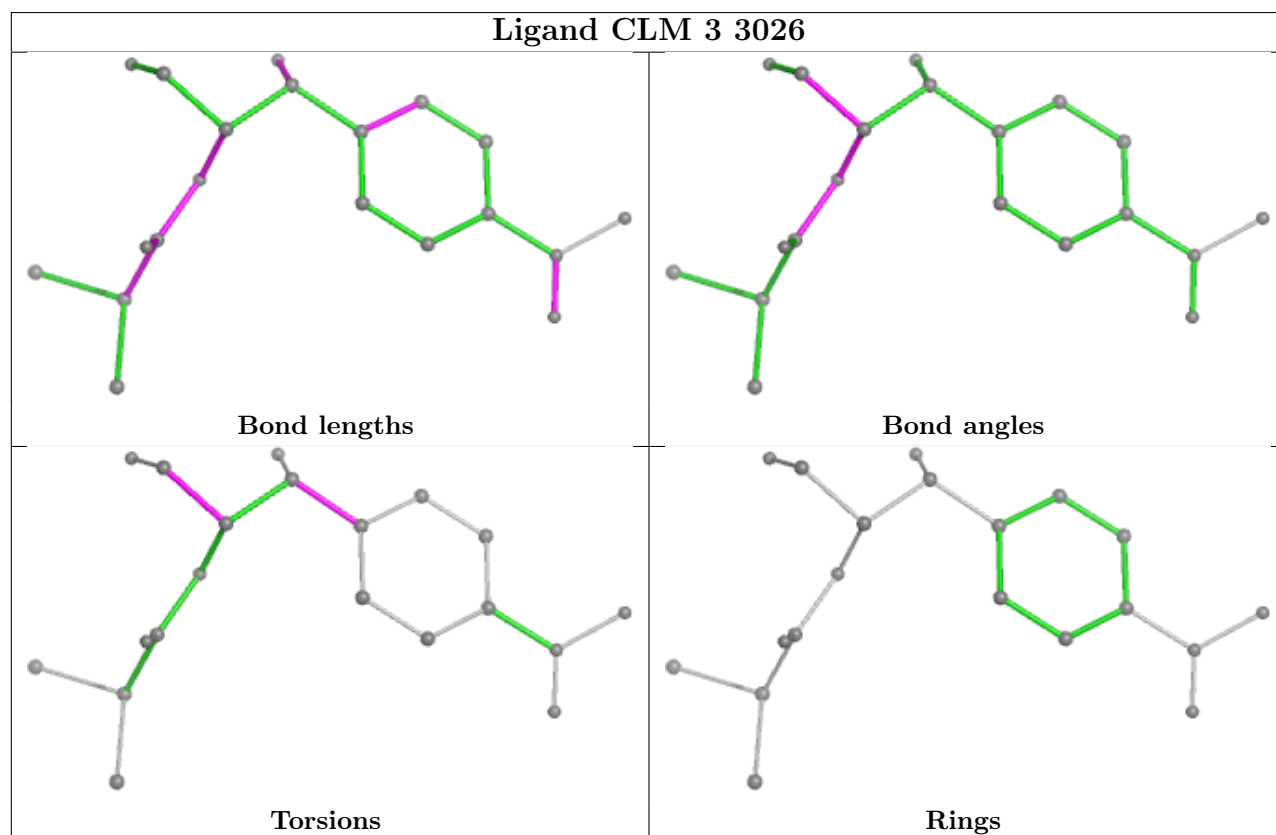
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	3	3026	CLM	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11999. 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.