



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:24 AM UTC

PDB ID : 8B5L / pdb_00008b5l
EMDB ID : EMD-15860
Title : Cryo-EM structure of ribosome-Sec61-TRAP (TRanslocon Associated Protein) translocon complex
Authors : Pauwels, E.; Shewakramani, N.R.; De Wijngaert, B.; Vermeire, K.; Das, K.
Deposited on : 2022-09-23
Resolution : 2.86 Å (reported)
Based on initial models : 3J7Q, 6MTE

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

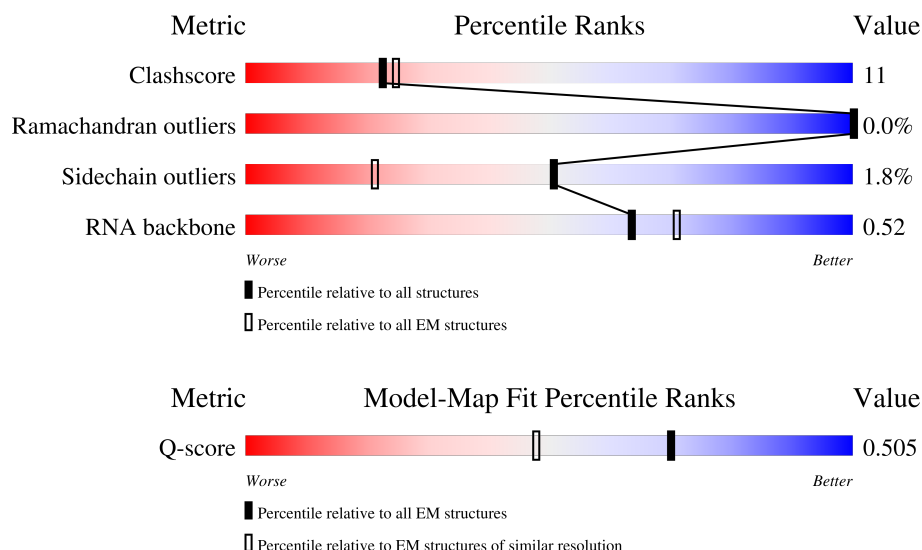
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	h	122	
2	P	153	
3	d	107	

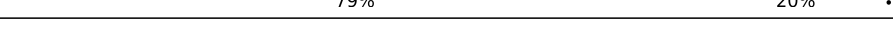
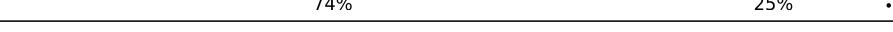
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Mol	Chain	Length	Quality of chain
4	5	4808	
5	G	319	
6	e	128	
7	t	185	
8	S	176	
9	I	214	
10	D	293	
11	V	131	
12	E	291	
13	J	170	
14	q	286	
15	k	70	
16	b	245	
17	m	52	
18	Z	135	
19	T	159	
20	i	105	
21	F	225	
22	n	25	
23	L	211	
24	O	203	
25	8	156	
26	C	362	
27	Y	134	
28	B	394	

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Mol	Chain	Length	Quality of chain
29	R	196	
30	X	118	
31	p	91	
32	M	138	
33	H	190	
34	7	120	
35	r	124	
36	Q	188	
37	f	109	
38	a	147	
39	A	257	
40	g	114	
41	K	173	
42	u	68	
43	v	183	
44	j	86	
45	N	203	
46	o	103	
47	s	476	
48	c	98	
49	W	157	
50	l	50	
51	U	99	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 145148 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 protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 2 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 3 is a protein called 60S ribosomal protein L31.

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

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	3619	Total	C	N	O	P	0	0
			77665	34619	14204	25223	3619		

- Molecule 5 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 6 is a protein called Ribosomal protein L32.

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

- Molecule 7 is a protein called Signal sequence receptor subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	t	181	Total	C	N	O	S	0	0
			1459	951	241	264	3		

- Molecule 8 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 9 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 11 is a protein called 60S ribosomal protein L23.

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

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called Translocon-associated protein subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	q	153	Total	C	N	O	S	0	0
			1222	795	196	228	3		

- Molecule 15 is a protein called 60S ribosomal protein L38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 16 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 17 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	m	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 18 is a protein called 60S ribosomal protein L27.

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

- Molecule 19 is a protein called 60S ribosomal protein L21.

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

- Molecule 20 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 21 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 22 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 23 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 24 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 25 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 26 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	C	362	Total	C	N	O	S	0	0
			2884	1813	577	480	14		

- Molecule 27 is a protein called Ribosomal protein L26.

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

- Molecule 28 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 29 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6
R	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 30 is a protein called Ribosomal_L23eN domain-containing protein.

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

- Molecule 31 is a protein called 60S ribosomal protein L37a.

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

- Molecule 32 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 33 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 34 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 36 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 38 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 39 is a protein called Ribosomal protein L8.

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

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

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

- Molecule 41 is a protein called Translocon-associated protein subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	146	Total	C	N	O	S	0	0
			1159	739	195	223	2		

- Molecule 42 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	67	Total	C	N	O	S	0	0
			535	350	93	88	4		

- Molecule 43 is a protein called Translocon-associated protein subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	158	Total	C	N	O	S	0	0
			1229	792	207	228	2		

- Molecule 44 is a protein called Ribosomal protein L37.

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

- Molecule 45 is a protein called Ribosomal protein L15.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 47 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	464	Total	C	N	O	S	0	0
			3589	2355	578	632	24		

- Molecule 48 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 49 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 50 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 51 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	P	1	Total 1	Mg 1	0
52	5	161	Total 161	Mg 161	0
52	I	1	Total 1	Mg 1	0
52	V	1	Total 1	Mg 1	0
52	8	5	Total 5	Mg 5	0
52	7	7	Total 7	Mg 7	0
52	a	1	Total 1	Mg 1	0
52	A	1	Total 1	Mg 1	0

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

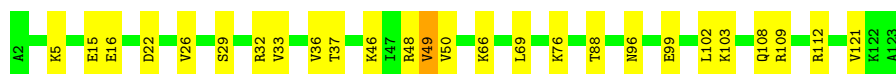
Mol	Chain	Residues	Atoms		AltConf
53	m	1	Total 1	Zn 1	0
53	p	1	Total 1	Zn 1	0
53	g	1	Total 1	Zn 1	0
53	j	1	Total 1	Zn 1	0
53	o	1	Total 1	Zn 1	0

3 Residue-property plots

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

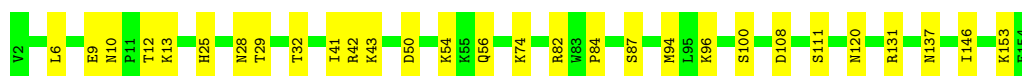
• Molecule 1: 60S ribosomal protein L35

Chain h: 



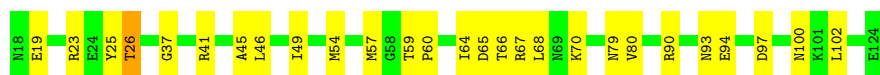
• Molecule 2: 60S ribosomal protein L17

Chain P: 

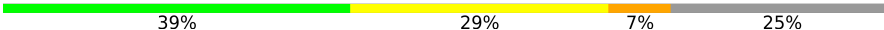


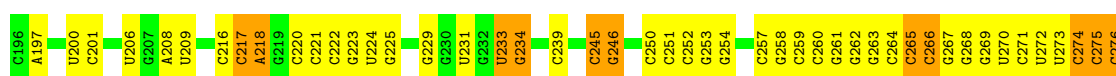
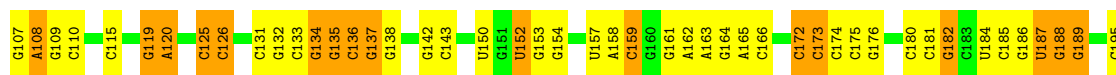
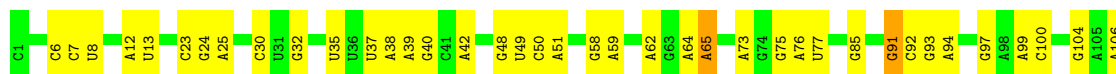
• Molecule 3: 60S ribosomal protein L31

Chain d: 



• Molecule 4: 28S rRNA

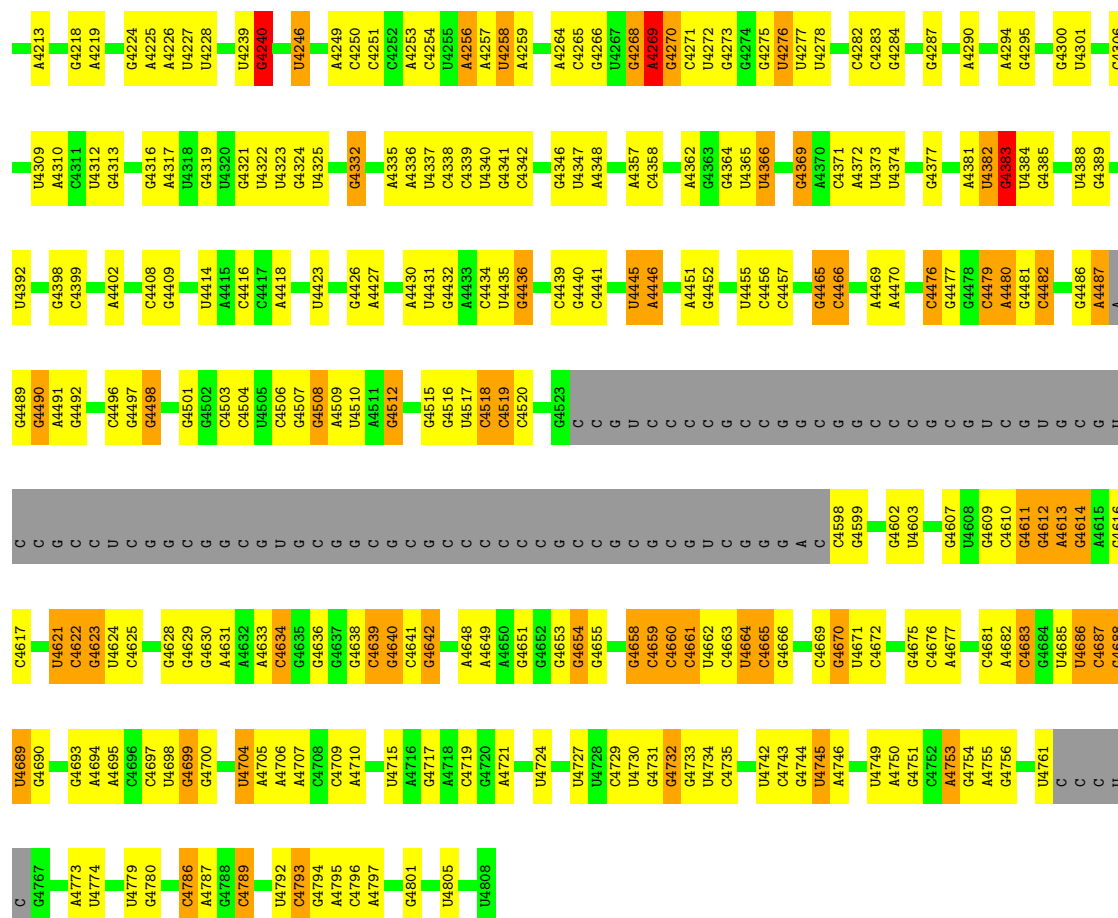
Chain 5: 



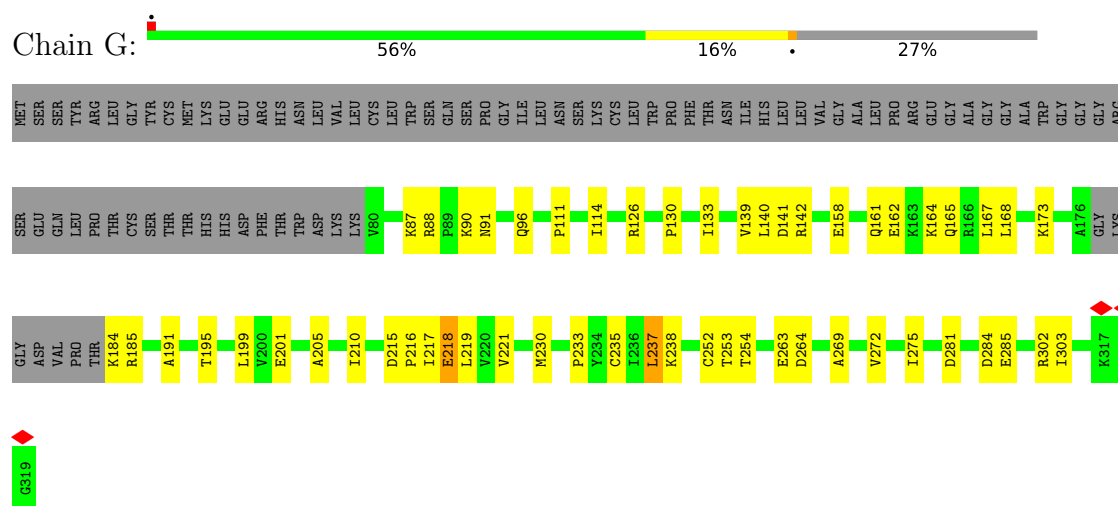


G2689	A2586	G2492	C2391	C2308	A2184	U	G2018	G1924	C1832	G1736	C	C1549
A2700	A2587	G2495	G2392	G2309	G2185	C	U2019	U1925	C1833	G1736	A	U1550
A2701	A2588	G2496	A2396	U2310	G2186	C	C2020	G1926	A1834	A1741	A	U1551
C2704	A2589	G2503	U2397	U2311	A2190	C	U2023	G1927	A1835	G1742	C	G1552
G2706	G2504	A2503	G2400	G2314	G2191	G	G2026	G1928	A1836	A1743	C	C1553
A2707	G2505	U2504	G2401	G2318	G2194	G	A2027	A1929	A1837	A1744	C	G1554
U2708	G2510	G2506	G2403	G2319	G2199	C	U2028	A1930	G1838	G1745	C	A1555
U2712	G2511	G2404	G2405	G2322	A2203	A	U2029	U1931	U1845	C1746	U	U1557
G2718	C2512	G2406	G2407	G2323	G2207	C	C2030	G1932	A1846	G1750	U	C1558
C2718	C2513	G2407	G2422	G2326	G2208	C	G2031	G1933	A1847	G1751	U	G1559
A2724	G2515	U2413	G2425	A2327	A2217	C	G2032	U1934	G1848	U1752	U	G1560
A2737	G2516	G2420	G2426	U2328	A2218	C	A2036	A1935	C1854	G1753	U	G1567
A2738	A2517	G2421	G2429	U2328	A2219	C	G2037	G1936	U1857	G1754	U	A1568
G2741	G2518	G2422	G2430	G2330	A2220	C	U2038	A1941	C1858	G1755	U	A1568
G2742	U2606	G2423	G2431	G2331	G2221	C	A2040	G1942	C1859	U1756	U	G1572
U2743	A2607	G2432	G2432	G2332	A2222	C	G2041	U1943	C1860	U1757	U	G1579
G2744	A2608	G2433	G2433	G2333	G2223	C	A2042	G1946	C1861	G1760	U	G1580
G	U2610	G2434	U2435	G2334	A2224	C	U2043	U1947	U1866	G1765	U	C1583
G	G2611	G2435	G2440	G2335	U2229	C	G2044	A1948	U1869	C1766	U	A1586
G	U2612	G2441	G2441	G2336	A2230	C	U2045	A1949	C1870	C1767	U	A1587
U	C2613	G2444	A2444	U2337	A2231	C	A2046	G1952	A1871	G1774	U	G1588
G	G2616	G2445	G2445	G2338	A2232	C	G2047	A1953	C1872	G1775	U	A1589
G	G2617	G2446	G2446	G2339	A2233	C	A2048	G1954	A1873	A1776	U	C1595
G	A2630	G2447	G2447	G2340	U2234	C	G2049	A1955	C1874	G1781	U	C1600
G	U2631	G2448	G2448	G2341	A2235	C	U2050	A1956	U1888	G1785	U	A1601
G	A2632	G2449	G2449	G2342	U2236	C	G2051	G1957	G1889	C1786	U	U1602
G	U2633	G2450	G2450	G2343	G2237	C	G2052	C1958	A1881	G1794	U	G1609
G	G2639	G2451	G2451	G2344	A2238	C	A	A1965	A1882	G1795	U	C1610
G	G2647	G2452	G2452	G2345	U2239	C	G	A1966	U1887	C1796	U	U1614
G	G2654	G2453	G2453	G2346	A2240	C	G	A1967	U1888	A1806	U	U1615
G	G2657	G2454	G2454	G2347	U2241	C	G	G1970	U1889	A1807	U	C1616
G	G2658	G2455	G2455	G2348	G2242	C	G	U1971	G1890	C1797	U	A1704
G	G2659	G2456	G2456	G2349	A2243	C	G	A1972	G1891	C1798	U	A1705
G	G2665	G2457	G2457	U2350	G2244	C	G	G1985	U1896	U1799	U	C1617
G	G2667	G2458	G2458	U2351	A2245	C	G	A1986	A1897	U1805	U	C1618
G	G2668	G2459	G2459	A2356	G2246	C	G	U1987	G1900	A1806	U	A1624
G	G2669	G2460	G2460	G2357	A2247	C	G	G1991	A1901	A1807	U	U1710
G	G2670	G2461	G2461	G2358	U2248	C	G	U1992	C1902	C1808	U	C1631
G	G2671	G2462	G2462	G2359	G2249	C	G	G1993	A1903	C1809	U	U1632
G	G2672	G2463	G2463	G2360	A2250	C	G	G1994	G1904	A1810	U	C1633
G	G2673	G2464	G2464	G2361	G2251	C	G	A1995	U1910	A1714	U	U1638
G	G2674	G2465	G2465	G2362	G2252	C	G	G1996	G1911	C1715	U	A1639
G	G2675	G2466	G2466	G2363	U2253	C	G	U1997	G1912	C1716	U	G1640
G	G2676	G2467	G2467	G2364	A2254	C	G	C2001	U1913	C1817	U	C1641
G	G2677	G2468	G2468	G2365	G2255	C	G	A2008	G1916	G1818	U	A1719
G	G2678	G2469	G2469	G2366	U2256	C	G	G1997	C1917	C1820	U	C1645
G	G2679	G2470	G2470	G2367	G2257	C	G	U1998	C1918	G1821	U	G1646
G	G2680	G2471	G2471	G2368	A2258	C	G	A2009	G1919	U1822	U	C1647
G	G2681	G2472	G2472	G2369	G2259	C	G	C2010	A1918	U1823	U	A1725
G	G2682	G2473	G2473	U2388	A2260	C	G	G2011	U1919	G1824	U	A1726
G	G2683	G2474	G2474	G2389	G2261	C	G	G2012	G1825	G1825	U	C1728
G	G2684	G2475	G2475	G2390	G2262	C	G	G2013	A1923	G1826	U	G1652
G	G2685	G2476	G2476	G2391	U2263	C	G	G2014				
G	G2686	G2477	G2477	G2392	A2264	C	G	G2015				
G	G2687	G2478	G2478	G2393	G2265	C	G					
G	G2688	G2479	G2479	G2394	A2266	C	G					
G	G2689	G2480	G2480	G2395	G2267	C	G					
G	G2690	G2481	G2481	G2396	G2268	C	G					
G	G2691	G2482	G2482	G2397	U2269	C	G					
G	G2692	G2483	G2483	G2398	A2270	C	G					
G	G2693	G2484	G2484	G2399	G2271	C	G					
G	G2694	G2485	G2485	G2400	U2272	C	G					
G	G2695	G2486	G2486	G2401	G2273	C	G					
G	G2696	G2487	G2487	G2402	A2274	C	G					
G	G2697	G2488	G2488	G2403	G2275	C	G					
G	G2698	G2489	G2489	G2404	G2276	C	G					
G	G2699	G2490	G2490	G2405	G2277	C	G					
G	G2700	G2491	G2491	G2406	G2278	C	G					
G	G2701	G2492	G2492	G2407	G2279	C	G					
G	G2702	G2493	G2493	G2408	G2280	C	G					
G	G2703	G2494	G2494	G2409	G2281	C	G					
G	G2704	G2495	G2495	G2410	G2282	C	G					
G	G2705	G2496	G2496	G2411	G2283	C	G					
G	G2706	G2497	G2497	G2412	G2284	C	G					
G	G2707	G2498	G2498	G2413	G2285	C	G					
G	G2708	G2499	G2499	G2414	G2286	C	G					
G	G2709	G2500	G2500	G2415	G2287	C	G					
G	G2710	G2501	G2501	G2416	G2288	C	G					
G	G2711	G2502	G2502	G2417	G2289	C	G					
G	G2712	G2503	G2503	G2418	G2290	C	G					
G	G2713	G2504	G2504	G2419	G2291	C	G					
G	G2714	G2505	G2505	G2420	G2292	C	G					
G	G2715	G2506	G2506	G2421	G2293	C	G					
G	G2716	G2507	G2507	G2422	G2294	C	G					
G	G2717	G2508	G2508	G2423	G2295	C	G					
G	G2718	G2509	G2509	G2424	G2296	C	G					
G	G2719	G2510	G2510	G2425	G2297	C	G					
G	G2720	G2511	G2511	G2426	G2298	C	G					
G	G2721	G2512	G2512	G2427	G2299	C	G					
G	G2722	G2513	G2513	G2428	G2300	C	G					
G	G2723	G2514	G2514	G2429	G2301	C	G					
G	G2724	G2515	G2515	G2430	G2302	C	G					
G	G2725	G2516	G2516	G2431	G2303	C	G					
G	G2726	G2517	G2517	G2432	G2304	C	G					
G	G2727	G2518	G2518	G2433	G2305	C	G					
G	G2728	G2519	G2519	G2434	G2306	C	G					
G	G2729	G2520	G2520	G2435	G2307	C	G					
G	G2730	G2521	G2521	G2436	G2308	C	G					
G	G2731	G2522	G2522	G2437	G2309	C	G					
G	G2732	G2523	G2523	G2438	G2310	C	G					
G	G2733	G2524	G2524	G2439	G2311	C	G					
G	G2734	G2525	G2525	G2440	G2312	C	G					
G	G2735	G2526	G2526	G2441	G2313	C	G					
G	G2736	G2527	G2527	G2442	G2314	C	G					
G	G2737	G2528	G2528	G2443	G2315	C	G					
G	G2738	G2529	G2529	G2444	G2316	C	G					
G	G2739	G2530	G2530	G2445	G2317	C	G					
G	G2740	G2531	G2531	G2446	G2318	C	G					
G	G2741	G2532	G2532	G2447	G2319	C	G					
G	G2742	G2533	G2533	G2448	G2320	C	G					
G	G2743	G2534	G2534	G2449	G2321	C	G					
G	G2744	G2535	G2535	G2450	G2322	C	G					
G	G2745	G2536	G2536	G2451	G2323	C	G					
G	G2746	G2537	G2537	G2452	G2324	C	G					
G	G2747	G2538	G2538	G2453	G2325	C	G					
G	G2748	G2539	G2539	G2454	G2326	C	G					
G	G2749	G2540	G2540	G2455	G2327	C	G					
G	G2750	G2541	G2541	G2456	G2328	C	G					
G	G2751	G2542	G2542	G2457	G2329	C	G					
G	G2752	G2543	G2543	G2458	G2330	C	G					
G	G2753	G2544	G2544	G2459	G2331	C	G					
G	G2754	G2545	G2545	G2460	G2332	C	G					
G	G2755	G2546	G2546	G2461	G2333	C	G					
G	G2756	G2547	G2547	G2462	G2334	C	G					
G	G2757	G2548	G2548	G2463	G2335	C	G					
G	G2758	G2549	G2549	G2464	G2336	C	G					
G	G2759	G2550	G2550	G2465	G2337	C	G					
G	G2760	G2551	G2551	G2466	G2338	C	G					
G	G2761	G2552	G2552	G2467	G2339	C	G					
G	G											

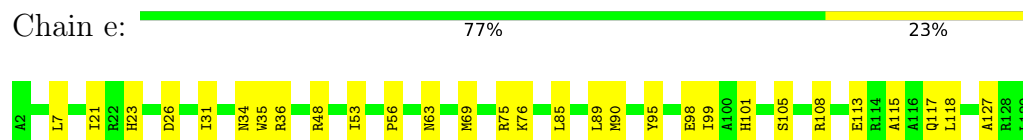




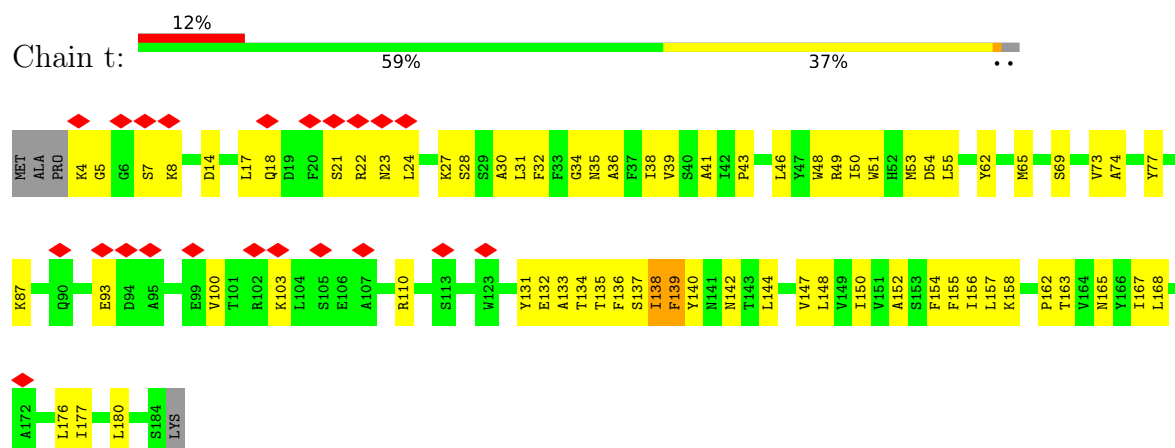
• Molecule 5: 60S ribosomal protein L7a



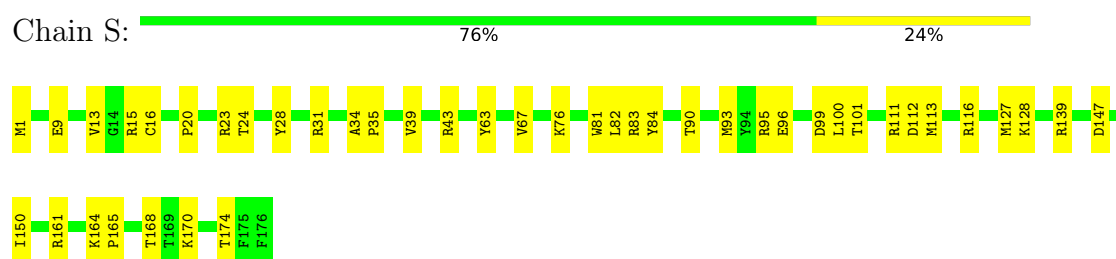
• Molecule 6: Ribosomal protein L32



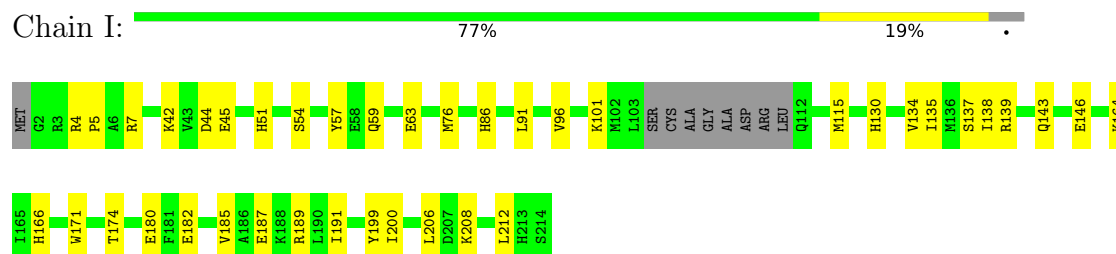
- Molecule 7: Signal sequence receptor subunit 3



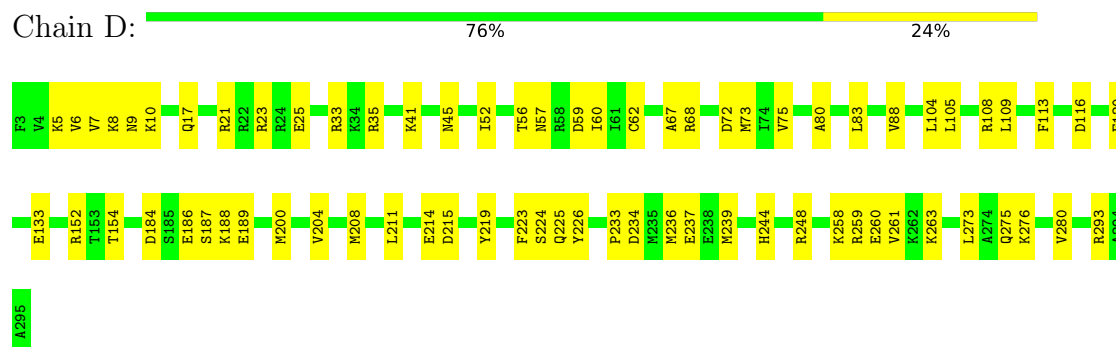
- Molecule 8: 60S ribosomal protein L18a



- Molecule 9: Ribosomal protein L10

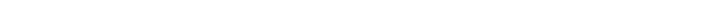


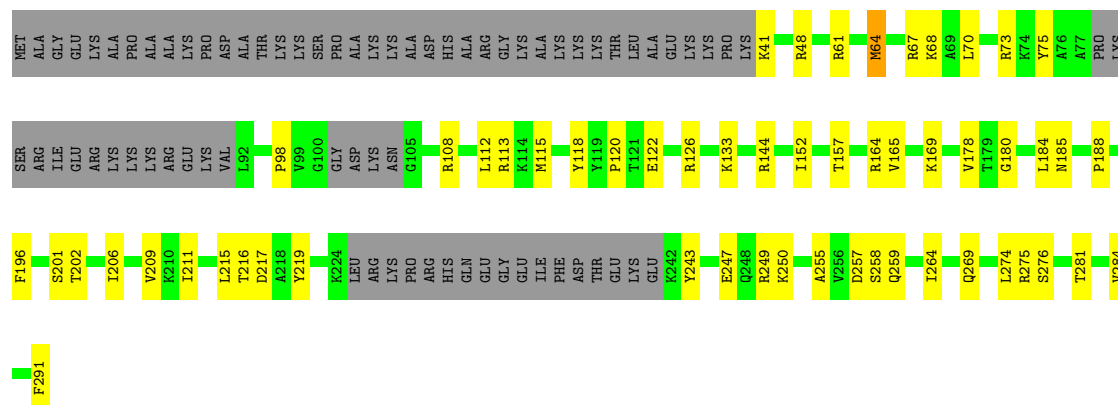
- Molecule 10: Ribosomal_L18_c domain-containing protein

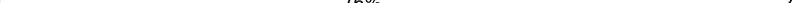


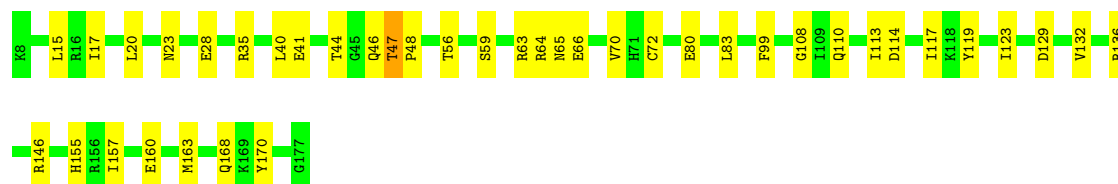
- Molecule 11: 60S ribosomal protein L23

S10	G11	R15	L18	N31	I40	S41	E71	I82	R83	S87	K91	L96	Y97	V106	N107	N108	K109	G110	E111	M112	A116	V121	L128	R131	S134	A140
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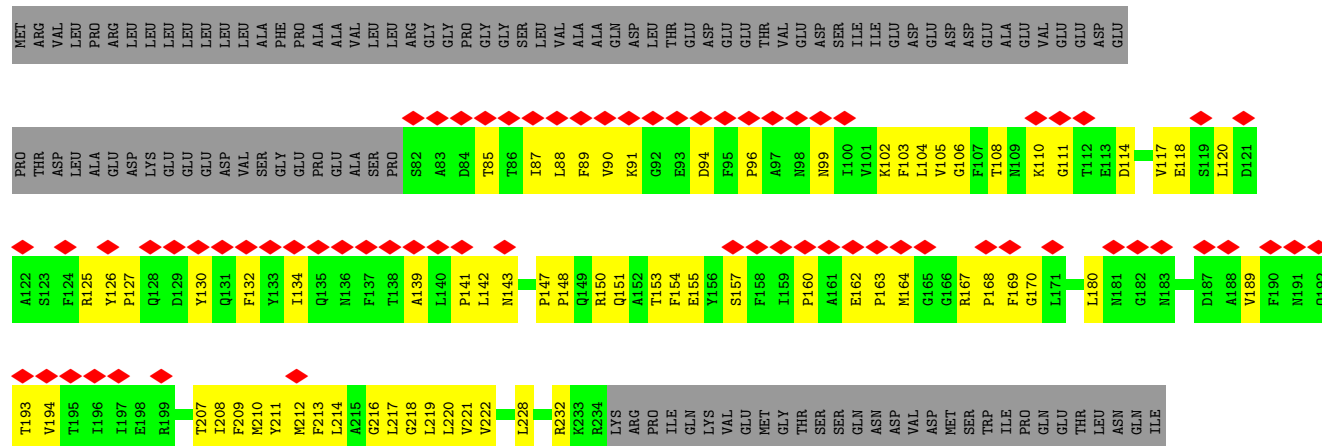
- Chain E:  55% 19% 26%



- Chain J:  76% 23%



- Chain q:





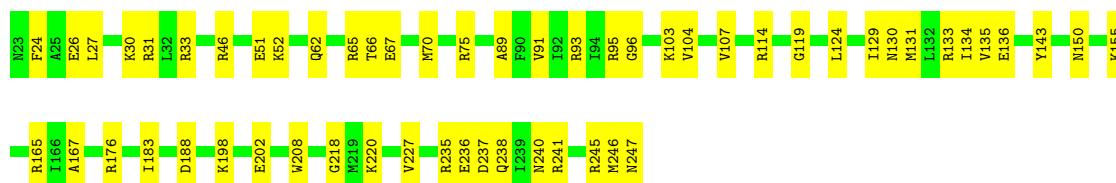
- Molecule 20: 60S ribosomal protein L36

Chain i: 74% 22% ..



- Molecule 21: 60S ribosomal protein L7

Chain F: 75% 25%



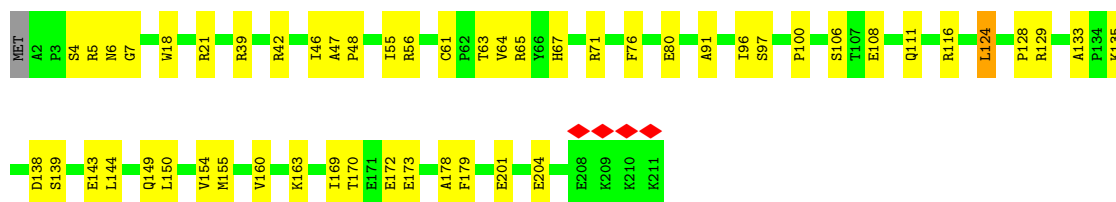
- Molecule 22: 60S ribosomal protein L41

Chain n: 88% 8% .



- Molecule 23: 60S ribosomal protein L13

Chain L: 75% 24%



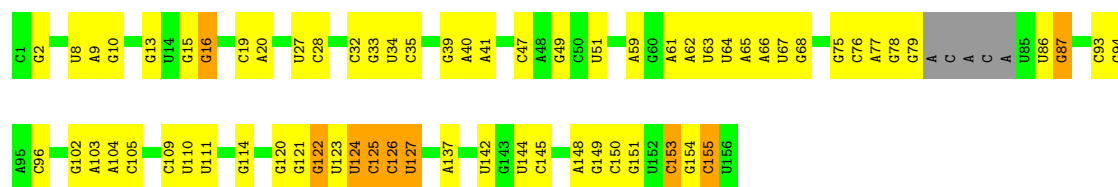
- Molecule 24: 60S ribosomal protein L13a

Chain O: 78% 18% ..



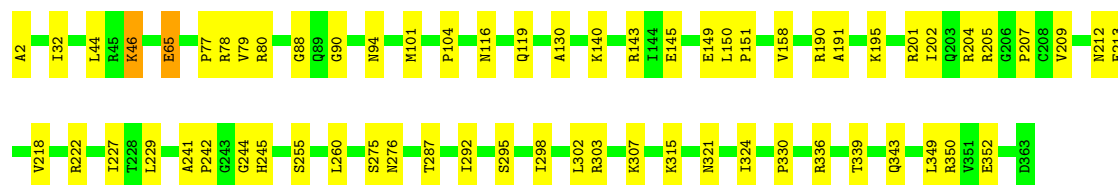
- Molecule 25: 5.8S rRNA

Chain 8:  54% 37% 6% .



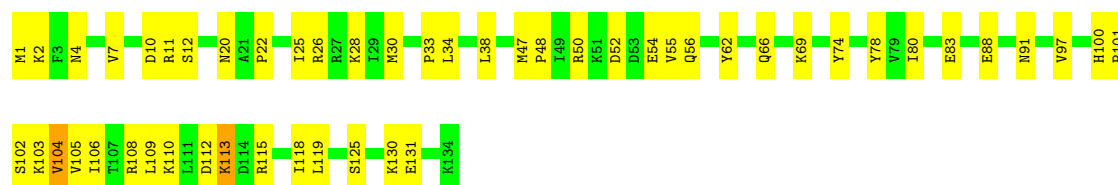
• Molecule 26: 60S ribosomal protein L4

Chain C:  82% 17% .



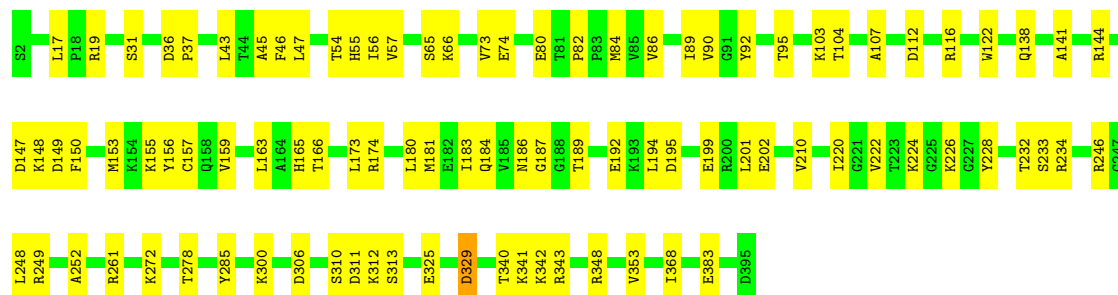
• Molecule 27: Ribosomal protein L26

Chain Y:  62% 37% .



• Molecule 28: Ribosomal protein L3

Chain B:  76% 24% .



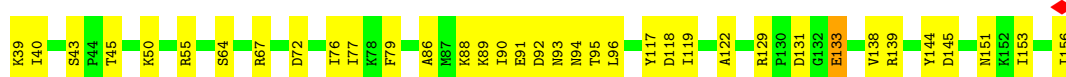
• Molecule 29: Ribosomal protein L19

Chain R:  63% 29% 8% .





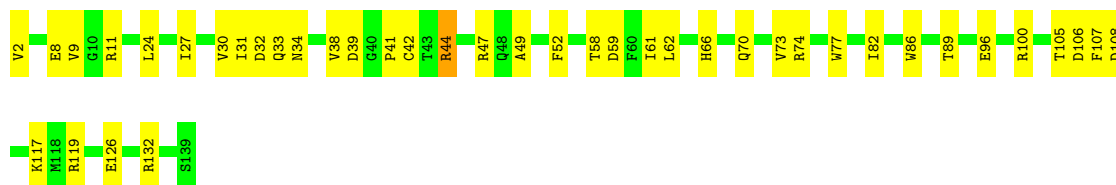
- Molecule 30: Ribosomal_L23eN domain-containing protein



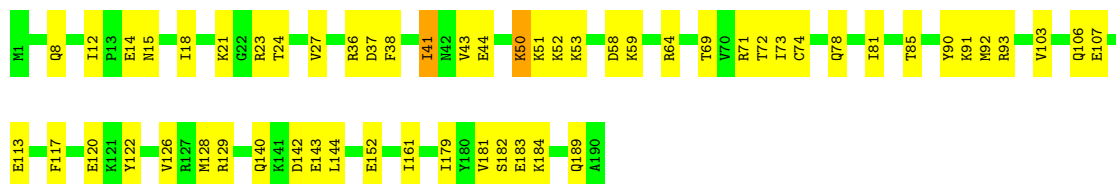
- Molecule 31: 60S ribosomal protein L37a



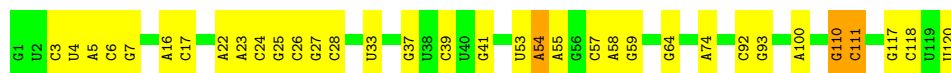
- Molecule 32: 60S ribosomal protein L14



- Molecule 33: 60S ribosomal protein L9



- Molecule 34: 5S rRNA



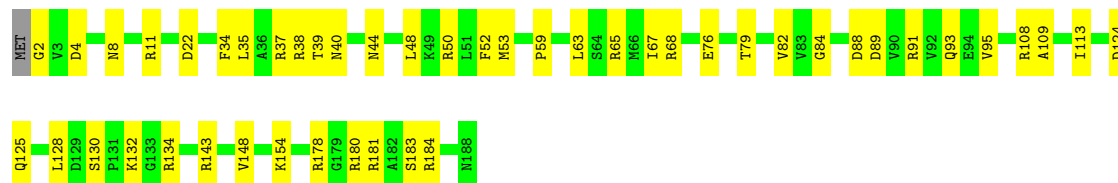
- Molecule 35: 60S ribosomal protein L28





• Molecule 36: Ribosomal protein L18

Chain Q: 74% 25%



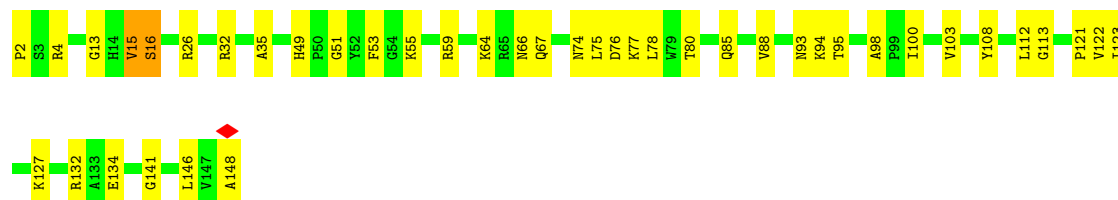
• Molecule 37: 60S ribosomal protein L35a

Chain f: 75% 25%



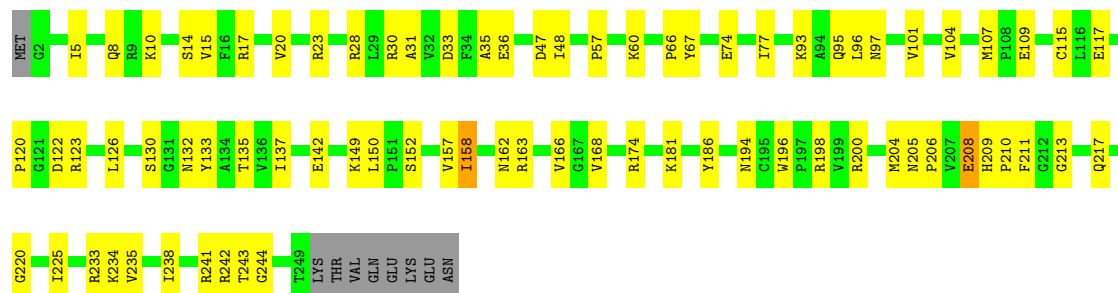
• Molecule 38: 60S ribosomal protein L27a

Chain a: 71% 27%



• Molecule 39: Ribosomal protein L8

Chain A: 67% 29%



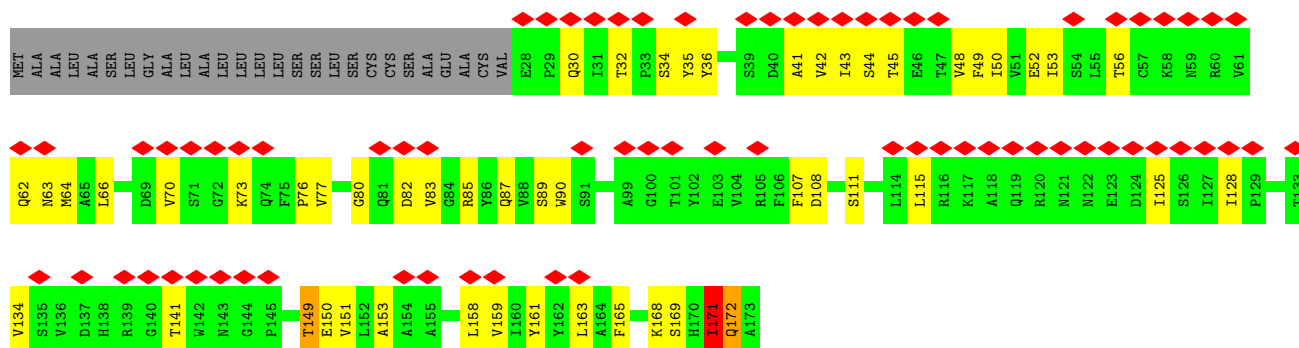
• Molecule 40: 60S ribosomal protein L34

Chain g: 



- Molecule 41: Translocon-associated protein subunit delta

Chain K: 



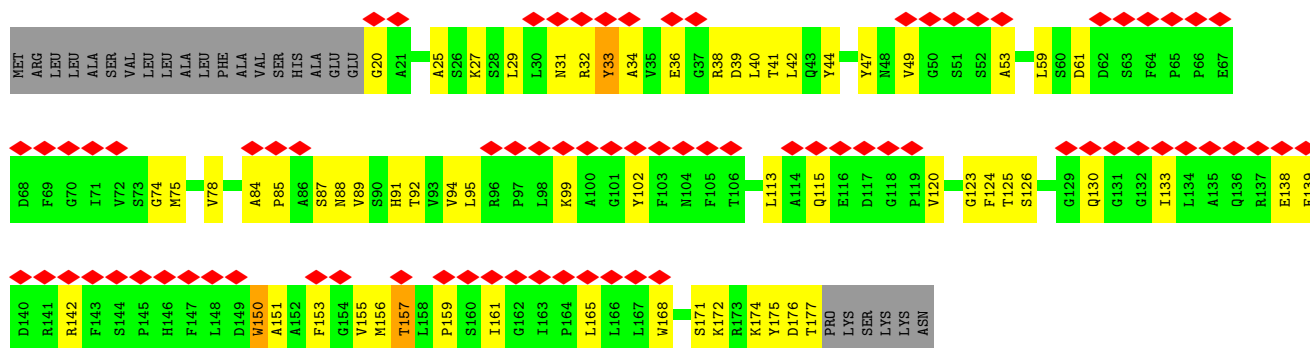
- Molecule 42: Protein transport protein Sec61 subunit gamma

Chain u: 



- Molecule 43: Translocon-associated protein subunit beta

Chain v: 



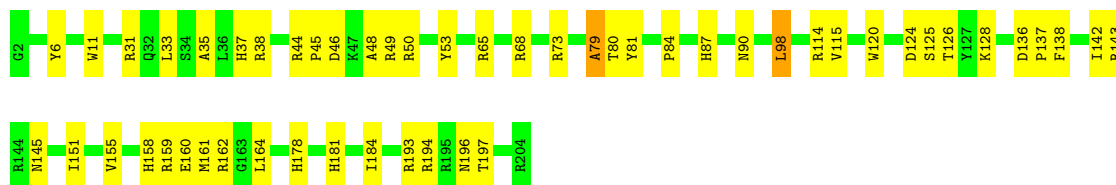
- Molecule 44: Ribosomal protein L37

Chain j: 



- Molecule 45: Ribosomal protein L15

Chain N:  74% 25% .



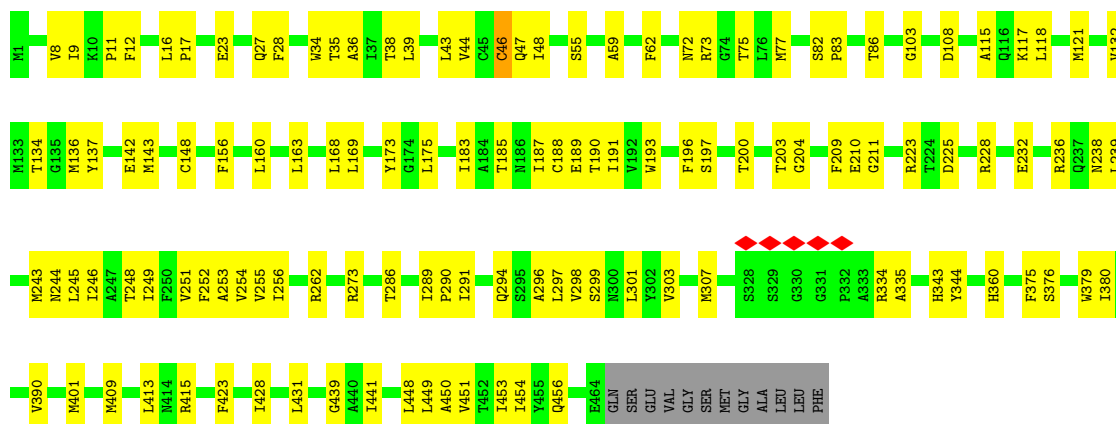
- Molecule 46: 60S ribosomal protein L36a-like

Chain o:  85% 14% .



- Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

Chain s:  71% 26% .



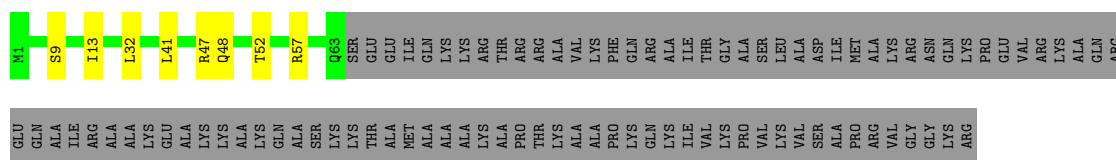
- Molecule 48: 60S ribosomal protein L30

Chain c:  74% 23% .



- Molecule 49: Ribosomal protein L24

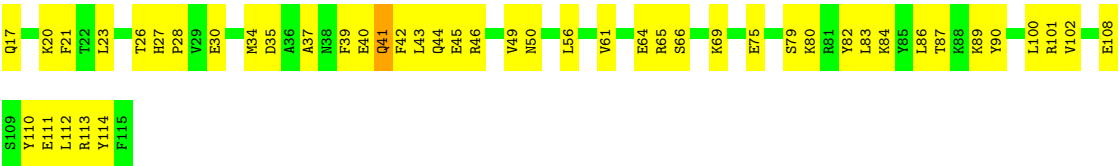
Chain W:  35% 5% 60%



- Molecule 50: 60S ribosomal protein L39-like



● Molecule 51: 60S ribosomal protein L22



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	119208	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.8	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.351	Depositor
Minimum map value	-0.161	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.01527	Depositor
Map size ($\text{\AA}$)	432.96002, 432.96002, 432.96002	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.23, 1.23, 1.23	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, P7G, PSU, UR3, A2M, I4U, OMU, MLZ, 5MC, OMC, OMG, B8H, 7MG, E6G, E7G, BGH, B8K, 1MA, ZN, P4U

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	h	0.17	0/1021	0.37	0/1348
2	P	0.31	0/1268	0.45	0/1700
3	d	0.45	0/903	0.50	0/1216
4	5	0.24	2/85271 (0.0%)	0.31	4/132978 (0.0%)
5	G	0.32	0/1910	0.48	0/2569
6	e	0.19	0/1071	0.35	0/1429
7	t	0.85	2/1489 (0.1%)	1.14	1/2011 (0.0%)
8	S	0.23	0/1501	0.42	0/2012
9	I	0.36	0/1702	0.48	0/2272
10	D	0.24	0/2437	0.40	0/3264
11	V	0.41	0/993	0.41	0/1332
12	E	0.22	0/1762	0.36	0/2362
13	J	0.21	0/1385	0.55	0/1852
14	q	0.49	0/1251	0.65	0/1699
15	k	0.22	0/575	0.66	2/761 (0.3%)
16	b	0.27	0/861	0.52	0/1138
17	m	0.25	0/425	0.49	0/561
18	Z	0.31	0/1130	0.44	0/1507
19	T	0.23	0/1326	0.45	0/1770
20	i	0.16	0/841	0.34	0/1112
21	F	0.20	0/1911	0.33	0/2549
22	n	0.13	0/240	0.38	0/305
23	L	0.29	0/1733	0.44	0/2316
24	O	0.24	0/1662	0.41	0/2222
25	8	0.20	0/3581	0.26	0/5577
26	C	0.36	0/2927	0.45	2/3932 (0.1%)
27	Y	0.22	0/1132	0.45	0/1504
28	B	0.21	0/3240	0.34	0/4339
29	R	0.21	0/1524	0.41	0/2013
30	X	0.24	0/984	0.48	0/1323
31	p	0.29	0/718	0.40	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	M	0.29	0/1158	0.47	0/1547
33	H	0.23	0/1535	0.44	0/2063
34	7	0.18	0/2858	0.22	0/4455
35	r	0.40	0/1010	0.46	0/1354
36	Q	0.24	0/1539	0.40	0/2054
37	f	0.21	0/895	0.39	0/1198
38	a	0.20	0/1191	0.68	3/1590 (0.2%)
39	A	0.37	0/1936	0.48	0/2596
40	g	0.20	0/916	0.36	0/1220
41	K	0.35	0/1188	0.52	1/1619 (0.1%)
42	u	0.22	0/545	0.55	0/728
43	v	0.26	0/1261	0.46	0/1717
44	j	0.20	0/720	0.36	0/952
45	N	0.37	0/1746	0.45	1/2338 (0.0%)
46	o	0.28	0/855	0.46	0/1128
47	s	0.26	0/3668	0.48	1/4974 (0.0%)
48	c	0.19	0/771	0.42	0/1034
49	W	0.20	0/541	0.37	0/720
50	l	0.19	0/459	0.36	0/608
51	U	0.28	0/823	0.76	1/1104 (0.1%)
All	All	0.27	4/154389 (0.0%)	0.38	16/226925 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	5	732	C	O3'-P	19.64	1.90	1.61
4	5	1390	G	O3'-P	18.60	1.89	1.61
7	t	138	ILE	C-N	-7.59	1.24	1.33
7	t	139	PHE	C-N	5.80	1.41	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	a	15	VAL	N-CA-C	-16.57	82.95	109.12
38	a	16	SER	N-CA-CB	15.14	136.08	110.49
4	5	732	C	O3'-P-O5'	8.10	116.14	104.00
4	5	732	C	P-O3'-C3'	-8.10	108.06	120.20
26	C	244	GLY	N-CA-C	-7.25	105.49	114.92

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	h	1013	0	1147	22	0
2	P	1242	0	1274	19	0
3	d	888	0	930	18	0
4	5	77665	0	39155	1283	0
5	G	1879	0	2027	53	0
6	e	1053	0	1147	26	0
7	t	1459	0	1495	176	0
8	S	1462	0	1508	37	0
9	I	1664	0	1712	29	0
10	D	2391	0	2424	54	0
11	V	979	0	1039	19	0
12	E	1729	0	1887	48	0
13	J	1362	0	1399	27	0
14	q	1222	0	1198	115	0
15	k	569	0	637	33	0
16	b	848	0	920	36	0
17	m	430	0	466	12	0
18	Z	1107	0	1182	30	0
19	T	1298	0	1366	40	0
20	i	830	0	916	19	0
21	F	1875	0	1995	46	0
22	n	239	0	289	2	0
23	L	1702	0	1820	46	0
24	O	1630	0	1778	38	0
25	8	3208	0	1629	47	0
26	C	2884	0	3054	48	0
27	Y	1115	0	1205	38	0
28	B	3172	0	3310	68	0
29	R	1508	0	1664	44	0
30	X	967	0	1040	33	0
31	p	708	0	756	20	0
32	M	1137	0	1211	33	0
33	H	1516	0	1597	52	0
34	7	2558	0	1296	20	0
35	r	994	0	1051	41	0
36	Q	1515	0	1634	40	0
37	f	876	0	912	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	a	1162	0	1209	41	0
39	A	1898	0	1993	63	0
40	g	906	0	998	19	0
41	K	1159	0	1125	83	0
42	u	535	0	565	32	0
43	v	1229	0	1211	131	0
44	j	705	0	737	14	0
45	N	1701	0	1749	39	0
46	o	842	0	912	9	0
47	s	3589	0	3714	98	0
48	c	761	0	794	18	0
49	W	528	0	541	4	0
50	l	447	0	480	13	0
51	U	809	0	833	45	0
52	5	161	0	0	0	0
52	7	7	0	0	0	0
52	8	5	0	0	0	0
52	A	1	0	0	0	0
52	I	1	0	0	0	0
52	P	1	0	0	0	0
52	V	1	0	0	0	0
52	a	1	0	0	0	0
53	g	1	0	0	0	0
53	j	1	0	0	0	0
53	m	1	0	0	0	0
53	o	1	0	0	0	0
53	p	1	0	0	0	0
All	All	145148	0	106931	2818	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 11.

The worst 5 of 2818 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)
7:t:132:GLU:HA	41:K:168:LYS:NZ	1.19	1.47
24:O:5:GLN:N	24:O:5:GLN:HE21	1.34	1.21
7:t:35:ASN:HB2	43:v:168:TRP:NE1	1.53	1.21
7:t:147:VAL:HG21	14:q:221:VAL:CG1	1.76	1.15
7:t:22:ARG:HH22	43:v:177:THR:HG22	1.06	1.14

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	
1	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
2	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
3	d	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
5	G	229/319 (72%)	219 (96%)	10 (4%)	0	100	100
6	e	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
7	t	179/185 (97%)	174 (97%)	5 (3%)	0	100	100
8	S	174/176 (99%)	168 (97%)	6 (3%)	0	100	100
9	I	201/214 (94%)	193 (96%)	8 (4%)	0	100	100
10	D	291/293 (99%)	284 (98%)	7 (2%)	0	100	100
11	V	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
12	E	208/291 (72%)	198 (95%)	9 (4%)	1 (0%)	24	42
13	J	168/170 (99%)	159 (95%)	9 (5%)	0	100	100
14	q	151/286 (53%)	150 (99%)	1 (1%)	0	100	100
15	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
16	b	100/245 (41%)	97 (97%)	3 (3%)	0	100	100
17	m	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
18	Z	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
19	T	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
20	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
21	F	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
22	n	23/25 (92%)	23 (100%)	0	0	100	100
23	L	208/211 (99%)	201 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	O	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
26	C	359/362 (99%)	343 (96%)	16 (4%)	0	100	100
27	Y	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
28	B	392/394 (100%)	382 (97%)	10 (3%)	0	100	100
29	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
30	X	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
31	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
32	M	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
33	H	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
35	r	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
36	Q	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
37	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
38	a	145/147 (99%)	138 (95%)	6 (4%)	1 (1%)	18	35
39	A	246/257 (96%)	229 (93%)	17 (7%)	0	100	100
40	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
41	K	144/173 (83%)	143 (99%)	1 (1%)	0	100	100
42	u	65/68 (96%)	65 (100%)	0	0	100	100
43	v	156/183 (85%)	153 (98%)	3 (2%)	0	100	100
44	j	84/86 (98%)	84 (100%)	0	0	100	100
45	N	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
46	o	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
47	s	462/476 (97%)	454 (98%)	8 (2%)	0	100	100
48	c	96/98 (98%)	96 (100%)	0	0	100	100
49	W	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
50	l	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
51	U	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
All	All	7511/8263 (91%)	7267 (97%)	242 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	a	16	SER
12	E	118	TYR

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	
1	h	109/109 (100%)	107 (98%)	2 (2%)	51	73
2	P	134/134 (100%)	131 (98%)	3 (2%)	45	69
3	d	98/98 (100%)	95 (97%)	3 (3%)	35	60
5	G	200/272 (74%)	197 (98%)	3 (2%)	57	77
6	e	114/114 (100%)	114 (100%)	0	100	100
7	t	161/164 (98%)	160 (99%)	1 (1%)	78	89
8	S	157/157 (100%)	155 (99%)	2 (1%)	61	79
9	I	175/181 (97%)	171 (98%)	4 (2%)	44	68
10	D	247/247 (100%)	243 (98%)	4 (2%)	55	76
11	V	101/101 (100%)	97 (96%)	4 (4%)	28	53
12	E	190/251 (76%)	188 (99%)	2 (1%)	65	81
13	J	143/143 (100%)	140 (98%)	3 (2%)	47	70
14	q	133/249 (53%)	131 (98%)	2 (2%)	57	77
15	k	64/65 (98%)	62 (97%)	2 (3%)	35	60
16	b	84/184 (46%)	82 (98%)	2 (2%)	43	67
17	m	47/47 (100%)	47 (100%)	0	100	100
18	Z	117/117 (100%)	114 (97%)	3 (3%)	40	65
19	T	139/139 (100%)	135 (97%)	4 (3%)	37	61
20	i	86/89 (97%)	82 (95%)	4 (5%)	23	47
21	F	196/196 (100%)	196 (100%)	0	100	100
22	n	24/24 (100%)	22 (92%)	2 (8%)	10	22
23	L	175/176 (99%)	172 (98%)	3 (2%)	53	75
24	O	171/173 (99%)	166 (97%)	5 (3%)	37	61
26	C	301/301 (100%)	298 (99%)	3 (1%)	68	83
27	Y	124/124 (100%)	119 (96%)	5 (4%)	28	53
28	B	342/342 (100%)	340 (99%)	2 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	R	159/175 (91%)	156 (98%)	3 (2%)	50	72
30	X	106/106 (100%)	105 (99%)	1 (1%)	70	84
31	p	74/74 (100%)	71 (96%)	3 (4%)	27	52
32	M	117/117 (100%)	115 (98%)	2 (2%)	53	75
33	H	169/169 (100%)	167 (99%)	2 (1%)	63	80
35	r	108/108 (100%)	107 (99%)	1 (1%)	70	84
36	Q	164/165 (99%)	158 (96%)	6 (4%)	30	55
37	f	88/88 (100%)	88 (100%)	0	100	100
38	a	119/119 (100%)	119 (100%)	0	100	100
39	A	190/199 (96%)	185 (97%)	5 (3%)	40	65
40	g	98/98 (100%)	91 (93%)	7 (7%)	13	28
41	K	127/146 (87%)	123 (97%)	4 (3%)	35	60
42	u	58/59 (98%)	58 (100%)	0	100	100
43	v	131/152 (86%)	128 (98%)	3 (2%)	44	68
44	j	73/73 (100%)	72 (99%)	1 (1%)	59	78
45	N	171/171 (100%)	169 (99%)	2 (1%)	63	80
46	o	91/91 (100%)	88 (97%)	3 (3%)	33	58
47	s	389/398 (98%)	389 (100%)	0	100	100
48	c	84/84 (100%)	82 (98%)	2 (2%)	43	67
49	W	55/126 (44%)	53 (96%)	2 (4%)	31	56
50	l	47/47 (100%)	47 (100%)	0	100	100
51	U	89/89 (100%)	89 (100%)	0	100	100
All	All	6539/7051 (93%)	6424 (98%)	115 (2%)	51	73

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	O	194	ASP
46	o	66	ILE
30	X	133	GLU
46	o	33	LEU
41	K	151	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
30	X	151	ASN
36	Q	160	HIS
50	I	25	GLN
45	N	156	HIS
31	p	72	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	8	149/156 (95%)	26 (17%)	1 (0%)
34	7	119/120 (99%)	12 (10%)	0
4	5	3602/4808 (74%)	701 (19%)	56 (1%)
All	All	3870/5084 (76%)	739 (19%)	57 (1%)

5 of 739 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	5	12	A
4	5	13	U
4	5	25	A
4	5	30	C
4	5	39	A

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	1985	G
4	5	4786	C
4	5	2597	G
4	5	4686	U
4	5	4465	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

66 non-standard protein/DNA/RNA residues are modelled in this entry.

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
4	OMG	5	4383	4	23,26,27	2.57	6 (26%)	32,38,41	2.01	10 (31%)
4	A2M	5	1489	4,52	22,25,26	4.02	8 (36%)	30,36,39	2.04	9 (30%)
4	P7G	5	1848	4	24,28,29	5.06	6 (25%)	25,41,44	1.13	1 (4%)
4	A2M	5	3450	4	22,25,26	4.01	8 (36%)	30,36,39	2.01	8 (26%)
4	7MG	5	2365	4	23,26,27	1.41	4 (17%)	27,39,42	2.80	8 (29%)
4	PSU	5	4277	4	18,21,22	1.97	5 (27%)	21,30,33	2.03	4 (19%)
4	OMG	5	1477	4	23,26,27	2.57	6 (26%)	32,38,41	1.99	10 (31%)
4	B8H	5	1799	4	19,22,23	2.05	8 (42%)	21,32,35	2.20	3 (14%)
4	PSU	5	3496	4	18,21,22	2.03	6 (33%)	21,30,33	1.92	5 (23%)
4	A2M	5	398	4	22,25,26	4.01	8 (36%)	30,36,39	2.04	8 (26%)
4	OMG	5	2616	4	23,26,27	2.57	4 (17%)	32,38,41	1.97	10 (31%)
4	PSU	5	1632	4	18,21,22	1.99	5 (27%)	21,30,33	2.12	4 (19%)
4	OMG	5	4240	4	23,26,27	2.56	5 (21%)	32,38,41	1.97	9 (28%)
4	7MG	5	1560	4	23,26,27	4.57	7 (30%)	27,39,42	2.23	8 (29%)
4	BGH	5	3631	4	25,29,30	5.72	12 (48%)	30,43,46	2.44	9 (30%)
4	B8H	5	4042	4	19,22,23	2.06	8 (42%)	21,32,35	2.20	3 (14%)
4	PSU	5	1638	4	18,21,22	2.04	5 (27%)	21,30,33	2.05	4 (19%)
4	5MC	5	4193	4	19,22,23	1.41	3 (15%)	26,32,35	1.38	4 (15%)
4	B8H	5	3494	4	19,22,23	2.03	7 (36%)	21,32,35	2.07	3 (14%)
4	OMG	5	2267	4	23,26,27	1.29	4 (17%)	32,38,41	2.10	7 (21%)
4	OMG	5	3524	4	23,26,27	2.57	5 (21%)	32,38,41	1.96	9 (28%)
4	OMC	5	2265	4,52	19,22,23	2.22	5 (26%)	25,31,34	0.97	2 (8%)
4	OMG	5	4116	4	23,26,27	1.29	4 (17%)	32,38,41	2.19	8 (25%)
4	OMG	5	4369	4	23,26,27	2.56	5 (21%)	32,38,41	1.98	10 (31%)
4	OMC	5	3433	4	19,22,23	2.23	4 (21%)	25,31,34	0.98	3 (12%)
4	E6G	5	4101	4	24,27,28	1.64	5 (20%)	34,39,42	2.49	13 (38%)
17	MLZ	m	72	17	8,9,10	0.49	0	4,9,11	0.52	0
4	B8K	5	4436	4	24,28,29	5.10	7 (29%)	29,42,45	2.41	7 (24%)
4	OMC	5	2647	4	19,22,23	2.25	5 (26%)	25,31,34	0.97	2 (8%)
4	OMC	5	2704	4	19,22,23	2.22	5 (26%)	25,31,34	0.98	2 (8%)
4	A2M	5	1479	4	22,25,26	3.98	8 (36%)	30,36,39	2.18	10 (33%)
4	E7G	5	1736	4	24,27,28	4.30	7 (29%)	28,40,43	2.25	8 (28%)
4	UR3	5	4276	4	19,22,23	1.01	1 (5%)	26,32,35	1.82	5 (19%)
4	P4U	5	1292	4	21,24,25	2.41	7 (33%)	28,33,36	1.61	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	A2M	5	1810	4,52	22,25,26	1.50	4 (18%)	30,36,39	2.17	10 (33%)
4	OMG	5	1260	4	23,26,27	2.55	5 (21%)	32,38,41	1.96	9 (28%)
4	1MA	5	4161	4	21,25,26	2.01	3 (14%)	30,37,40	1.95	7 (23%)
4	I4U	5	1614	4	20,24,25	2.46	5 (25%)	27,34,37	1.94	2 (7%)
4	B8K	5	3629	4	24,28,29	5.16	7 (29%)	29,42,45	2.36	7 (24%)
4	OMU	5	4366	4	19,22,23	3.10	7 (36%)	25,31,34	1.94	6 (24%)
4	A2M	5	3455	4	22,25,26	3.99	8 (36%)	30,36,39	2.04	8 (26%)
4	OMC	5	3619	4	19,22,23	2.25	5 (26%)	25,31,34	0.98	3 (12%)
4	P7G	5	3612	4	24,28,29	5.14	6 (25%)	25,41,44	1.14	1 (4%)
4	PSU	5	4149	4	18,21,22	1.59	5 (27%)	21,30,33	2.27	6 (28%)
26	MLZ	C	333	26	8,9,10	0.46	0	4,9,11	0.65	0
4	OMC	5	2208	4	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
4	A2M	5	4269	4,52	22,25,26	3.99	8 (36%)	30,36,39	2.03	9 (30%)
4	OMC	5	4282	4	19,22,23	0.95	1 (5%)	25,31,34	1.08	1 (4%)
4	PSU	5	4196	4,52	18,21,22	1.99	5 (27%)	21,30,33	2.07	4 (19%)
4	A2M	5	3557	4	22,25,26	4.00	8 (36%)	30,36,39	2.06	8 (26%)
4	OMC	5	3601	4	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
4	PSU	5	3461	4	18,21,22	2.04	5 (27%)	21,30,33	1.96	4 (19%)
4	OMG	5	2207	4	23,26,27	2.56	5 (21%)	32,38,41	1.95	7 (21%)
4	OMU	5	4052	4	19,22,23	3.12	7 (36%)	25,31,34	1.90	6 (24%)
4	PSU	5	4188	4	18,21,22	2.05	6 (33%)	21,30,33	2.11	5 (23%)
4	PSU	5	3447	4	18,21,22	2.00	5 (27%)	21,30,33	1.99	4 (19%)
4	PSU	5	4382	4	18,21,22	2.02	5 (27%)	21,30,33	2.11	5 (23%)
4	PSU	5	4039	4	18,21,22	2.02	5 (27%)	21,30,33	2.06	4 (19%)
4	PSU	5	4246	4	18,21,22	2.02	5 (27%)	21,30,33	2.10	5 (23%)
4	1MA	5	1266	4	21,25,26	2.02	3 (14%)	30,37,40	1.97	7 (23%)
4	PSU	5	1537	4	18,21,22	2.06	6 (33%)	21,30,33	2.00	4 (19%)
4	PSU	5	2351	4	18,21,22	2.03	5 (27%)	21,30,33	1.97	4 (19%)
4	5MC	5	3514	4	19,22,23	2.98	5 (26%)	26,32,35	1.36	3 (11%)
4	PSU	5	4374	4	18,21,22	2.05	5 (27%)	21,30,33	2.10	5 (23%)
4	OMG	5	1580	4,52	23,26,27	1.34	3 (13%)	32,38,41	1.99	6 (18%)
4	A2M	5	1270	4	22,25,26	1.50	5 (22%)	30,36,39	2.13	8 (26%)

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
4	OMG	5	4383	4	-	3/9/27/28	0/3/3/3
4	A2M	5	1489	4,52	-	2/9/27/28	0/3/3/3
4	P7G	5	1848	4	-	0/10/40/41	0/3/3/3
4	A2M	5	3450	4	-	0/9/27/28	0/3/3/3
4	7MG	5	2365	4	-	0/7/37/38	0/3/3/3
4	PSU	5	4277	4	-	0/7/25/26	0/2/2/2
4	OMG	5	1477	4	-	0/9/27/28	0/3/3/3
4	B8H	5	1799	4	-	0/7/25/26	0/2/2/2
4	PSU	5	3496	4	-	3/7/25/26	0/2/2/2
4	A2M	5	398	4	-	1/9/27/28	0/3/3/3
4	OMG	5	2616	4	-	1/9/27/28	0/3/3/3
4	PSU	5	1632	4	-	0/7/25/26	0/2/2/2
4	OMG	5	4240	4	-	3/9/27/28	0/3/3/3
4	7MG	5	1560	4	-	0/7/37/38	0/3/3/3
4	BGH	5	3631	4	-	2/13/43/44	0/3/3/3
4	B8H	5	4042	4	-	2/7/25/26	0/2/2/2
4	PSU	5	1638	4	-	0/7/25/26	0/2/2/2
4	5MC	5	4193	4	-	4/7/25/26	0/2/2/2
4	B8H	5	3494	4	-	2/7/25/26	0/2/2/2
4	OMG	5	2267	4	-	2/9/27/28	0/3/3/3
4	OMG	5	3524	4	-	2/9/27/28	0/3/3/3
4	OMC	5	2265	4,52	-	2/9/27/28	0/2/2/2
4	OMG	5	4116	4	-	1/9/27/28	0/3/3/3
4	OMG	5	4369	4	-	1/9/27/28	0/3/3/3
4	OMC	5	3433	4	-	4/9/27/28	0/2/2/2
4	E6G	5	4101	4	-	4/10/28/29	0/3/3/3
17	MLZ	m	72	17	-	1/7/8/10	-
4	B8K	5	4436	4	-	0/11/41/42	0/3/3/3
4	OMC	5	2647	4	-	1/9/27/28	0/2/2/2
4	OMC	5	2704	4	-	1/9/27/28	0/2/2/2
4	A2M	5	1479	4	-	2/9/27/28	0/3/3/3
4	E7G	5	1736	4	-	3/9/39/40	0/3/3/3
4	UR3	5	4276	4	-	0/7/25/26	0/2/2/2
4	P4U	5	1292	4	-	4/10/29/30	0/2/2/2
4	A2M	5	1810	4,52	-	0/9/27/28	0/3/3/3
4	OMG	5	1260	4	-	1/9/27/28	0/3/3/3
4	1MA	5	4161	4	-	1/7/25/26	0/3/3/3
4	I4U	5	1614	4	-	1/9/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	B8K	5	3629	4	-	3/11/41/42	0/3/3/3
4	OMU	5	4366	4	-	1/9/27/28	0/2/2/2
4	A2M	5	3455	4	-	0/9/27/28	0/3/3/3
4	OMC	5	3619	4	-	1/9/27/28	0/2/2/2
4	P7G	5	3612	4	-	3/10/40/41	0/3/3/3
4	PSU	5	4149	4	-	2/7/25/26	0/2/2/2
26	MLZ	C	333	26	-	0/7/8/10	-
4	OMC	5	2208	4	-	0/9/27/28	0/2/2/2
4	A2M	5	4269	4,52	-	3/9/27/28	0/3/3/3
4	OMC	5	4282	4	-	2/9/27/28	0/2/2/2
4	PSU	5	4196	4,52	-	4/7/25/26	0/2/2/2
4	A2M	5	3557	4	-	1/9/27/28	0/3/3/3
4	OMC	5	3601	4	-	0/9/27/28	0/2/2/2
4	PSU	5	3461	4	-	2/7/25/26	0/2/2/2
4	OMG	5	2207	4	-	2/9/27/28	0/3/3/3
4	OMU	5	4052	4	-	3/9/27/28	0/2/2/2
4	PSU	5	4188	4	-	0/7/25/26	0/2/2/2
4	PSU	5	3447	4	-	0/7/25/26	0/2/2/2
4	PSU	5	4382	4	-	3/7/25/26	0/2/2/2
4	PSU	5	4039	4	-	2/7/25/26	0/2/2/2
4	PSU	5	4246	4	-	5/7/25/26	0/2/2/2
4	1MA	5	1266	4	-	1/7/25/26	0/3/3/3
4	PSU	5	1537	4	-	2/7/25/26	0/2/2/2
4	PSU	5	2351	4	-	0/7/25/26	0/2/2/2
4	5MC	5	3514	4	-	0/7/25/26	0/2/2/2
4	PSU	5	4374	4	-	0/7/25/26	0/2/2/2
4	OMG	5	1580	4,52	-	0/9/27/28	0/3/3/3
4	A2M	5	1270	4	-	3/9/27/28	0/3/3/3

The worst 5 of 355 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	5	3629	B8K	C8-N9	-22.43	1.31	1.45
4	5	3631	BGH	C8-N9	-22.32	1.31	1.45
4	5	4436	B8K	C8-N9	-22.13	1.31	1.45
4	5	3612	P7G	C8-N9	-21.51	1.31	1.45
4	5	1848	P7G	C8-N9	-21.08	1.32	1.45

The worst 5 of 373 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	5	2365	7MG	N9-C4-N3	9.53	139.42	125.46
4	5	1614	I4U	O4-C4-C5	8.28	121.33	115.45
4	5	4101	E6G	C5-C4-N3	-7.27	119.52	127.18
4	5	4149	PSU	N1-C2-N3	6.97	122.52	115.17
4	5	1799	B8H	N3-C2-N1	6.71	121.71	115.22

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	5	1260	OMG	C1'-C2'-O2'-CM2
4	5	1270	A2M	C1'-C2'-O2'-CM'
4	5	1292	P4U	N3-C4-O4-C41
4	5	1292	P4U	O4'-C4'-C5'-O5'
4	5	1537	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

31 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	5	4383	OMG	2	0
4	5	1489	A2M	1	0
4	5	3450	A2M	3	0
4	5	2365	7MG	1	0
4	5	3496	PSU	1	0
4	5	398	A2M	1	0
4	5	2616	OMG	2	0
4	5	1632	PSU	1	0
4	5	4240	OMG	1	0
4	5	1560	7MG	1	0
4	5	1638	PSU	1	0
4	5	4193	5MC	2	0
4	5	2267	OMG	2	0
4	5	2265	OMC	1	0
4	5	4369	OMG	1	0
4	5	4436	B8K	2	0
4	5	2647	OMC	1	0
4	5	2704	OMC	2	0
4	5	4276	UR3	2	0
4	5	1810	A2M	1	0
4	5	1260	OMG	1	0
4	5	4366	OMU	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	5	3455	A2M	1	0
4	5	4149	PSU	1	0
4	5	2208	OMC	1	0
4	5	4269	A2M	1	0
4	5	3557	A2M	3	0
4	5	3601	OMC	1	0
4	5	2207	OMG	1	0
4	5	4052	OMU	1	0
4	5	1270	A2M	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 183 ligands modelled in this entry, 183 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.

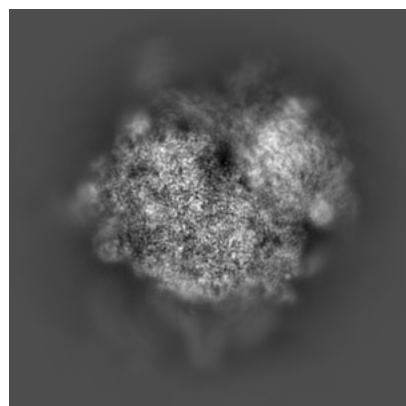
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15860. These allow visual inspection of the internal detail of the map and identification of artifacts.

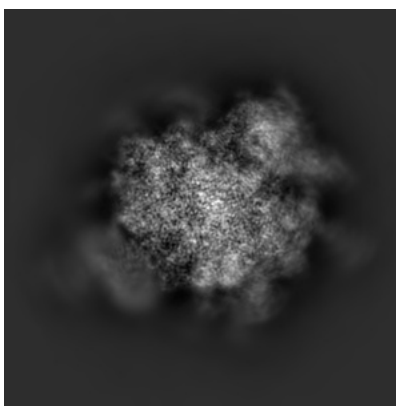
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

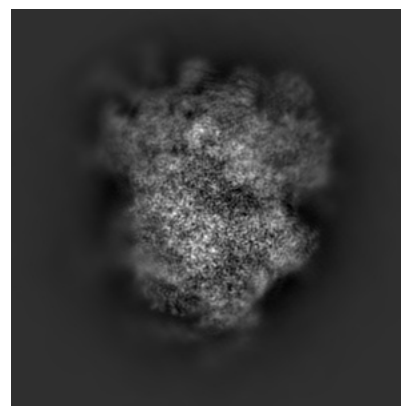
6.1.1 Primary map



X

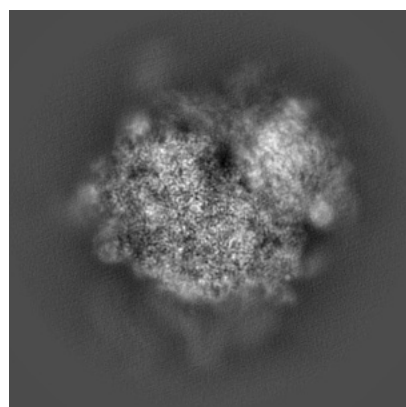


Y

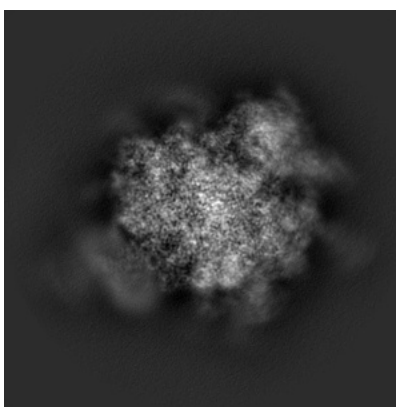


Z

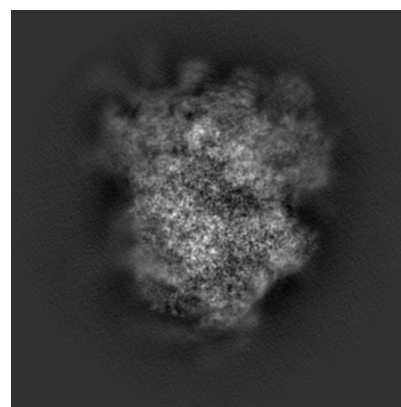
6.1.2 Raw map



X



Y

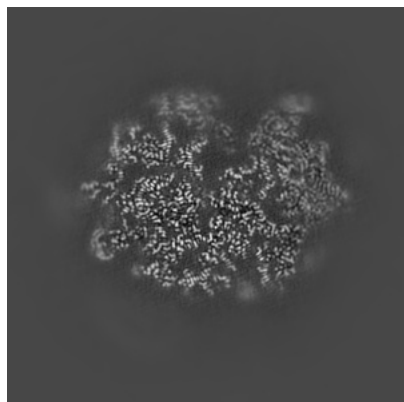


Z

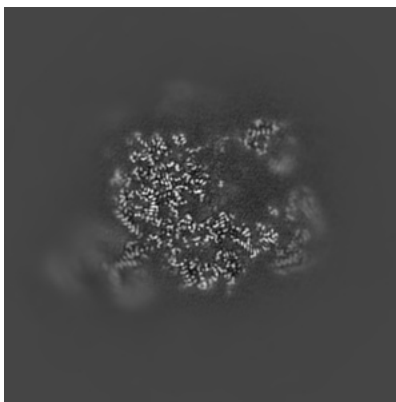
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

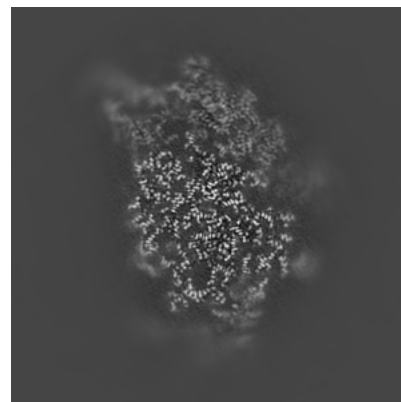
6.2.1 Primary map



X Index: 176

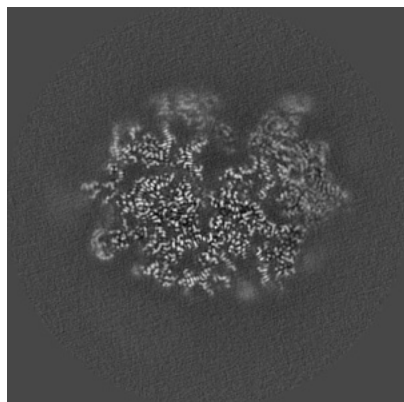


Y Index: 176

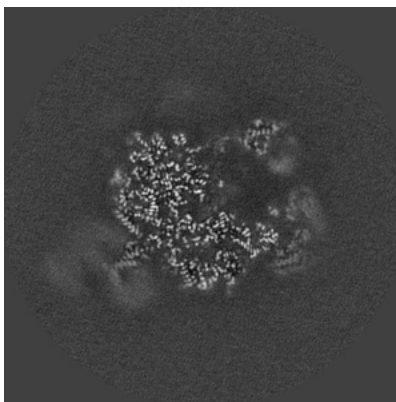


Z Index: 176

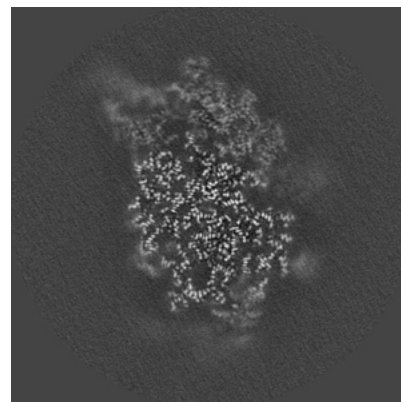
6.2.2 Raw map



X Index: 176



Y Index: 176

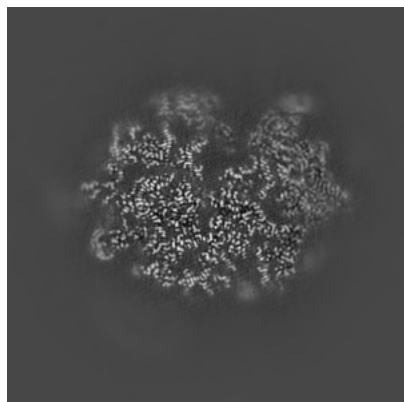


Z Index: 176

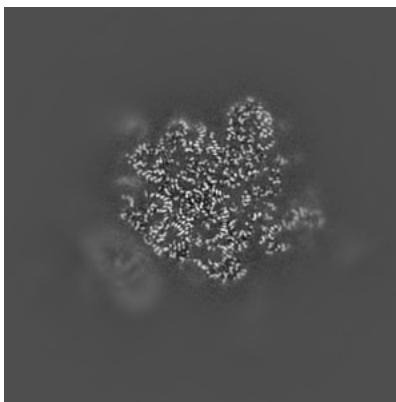
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

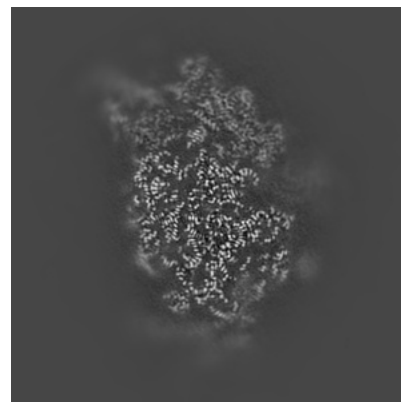
6.3.1 Primary map



X Index: 176

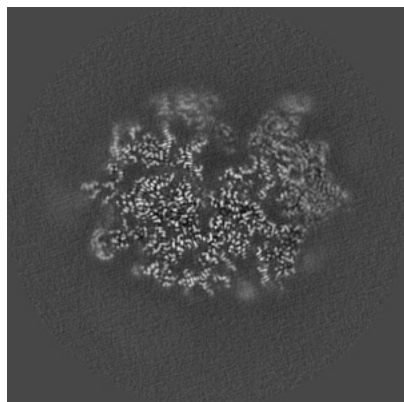


Y Index: 147

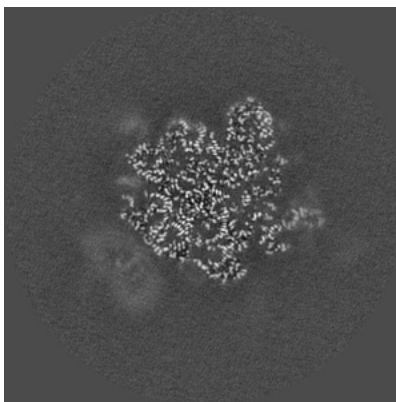


Z Index: 179

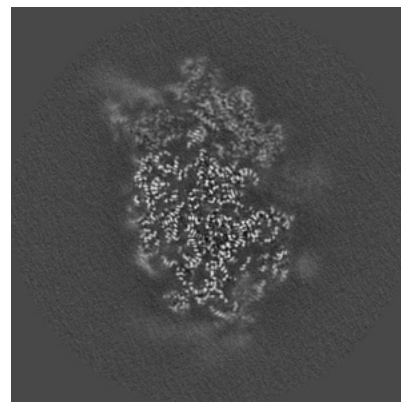
6.3.2 Raw map



X Index: 176



Y Index: 147

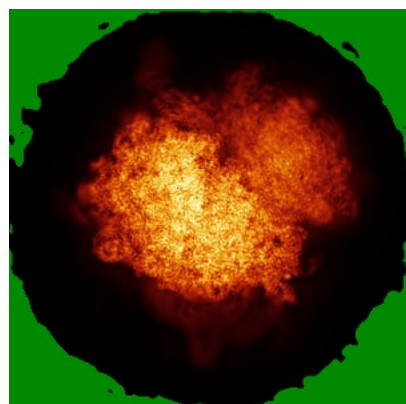


Z Index: 179

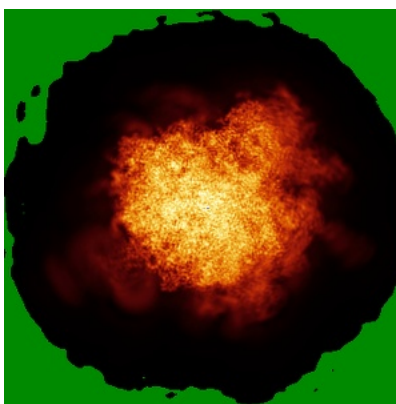
The images above show the largest variance slices of the map in three orthogonal directions.

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

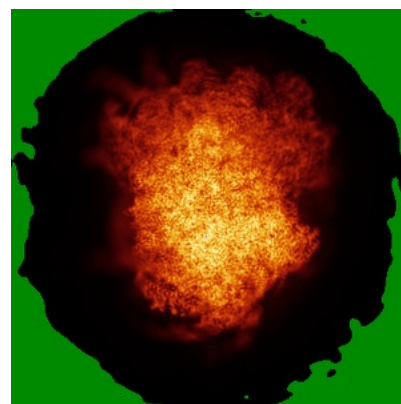
6.4.1 Primary map



X

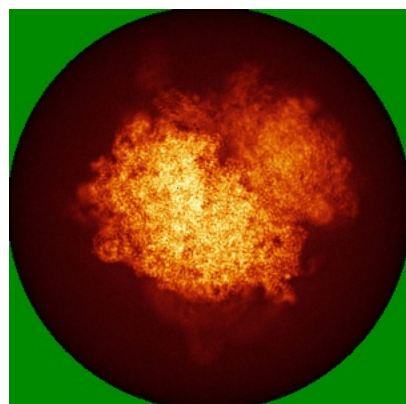


Y

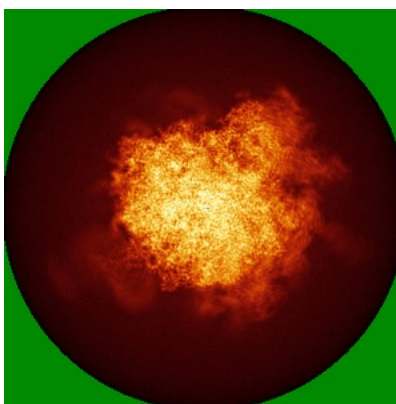


Z

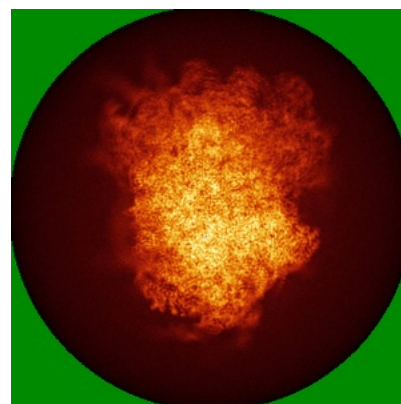
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01527. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

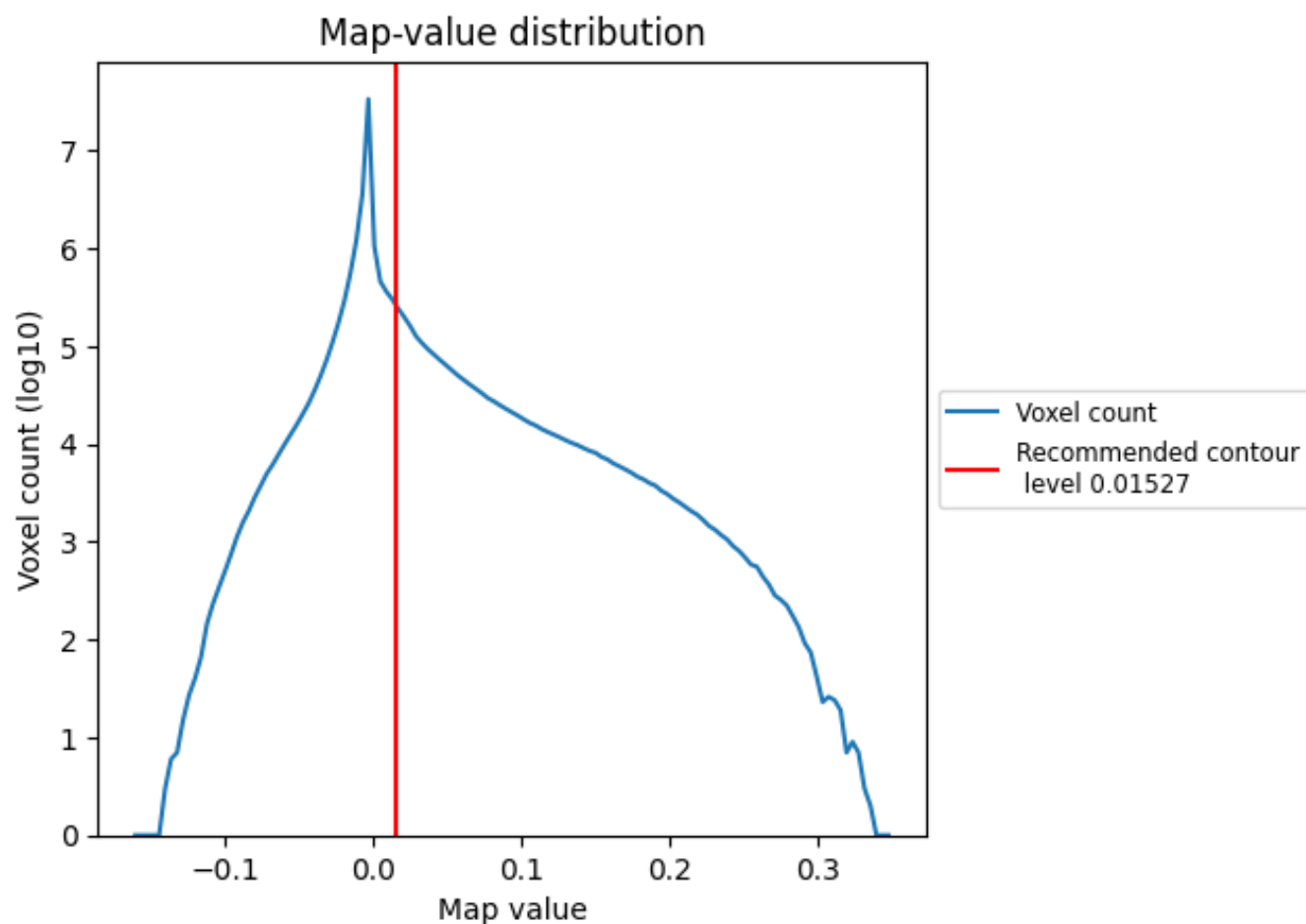
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

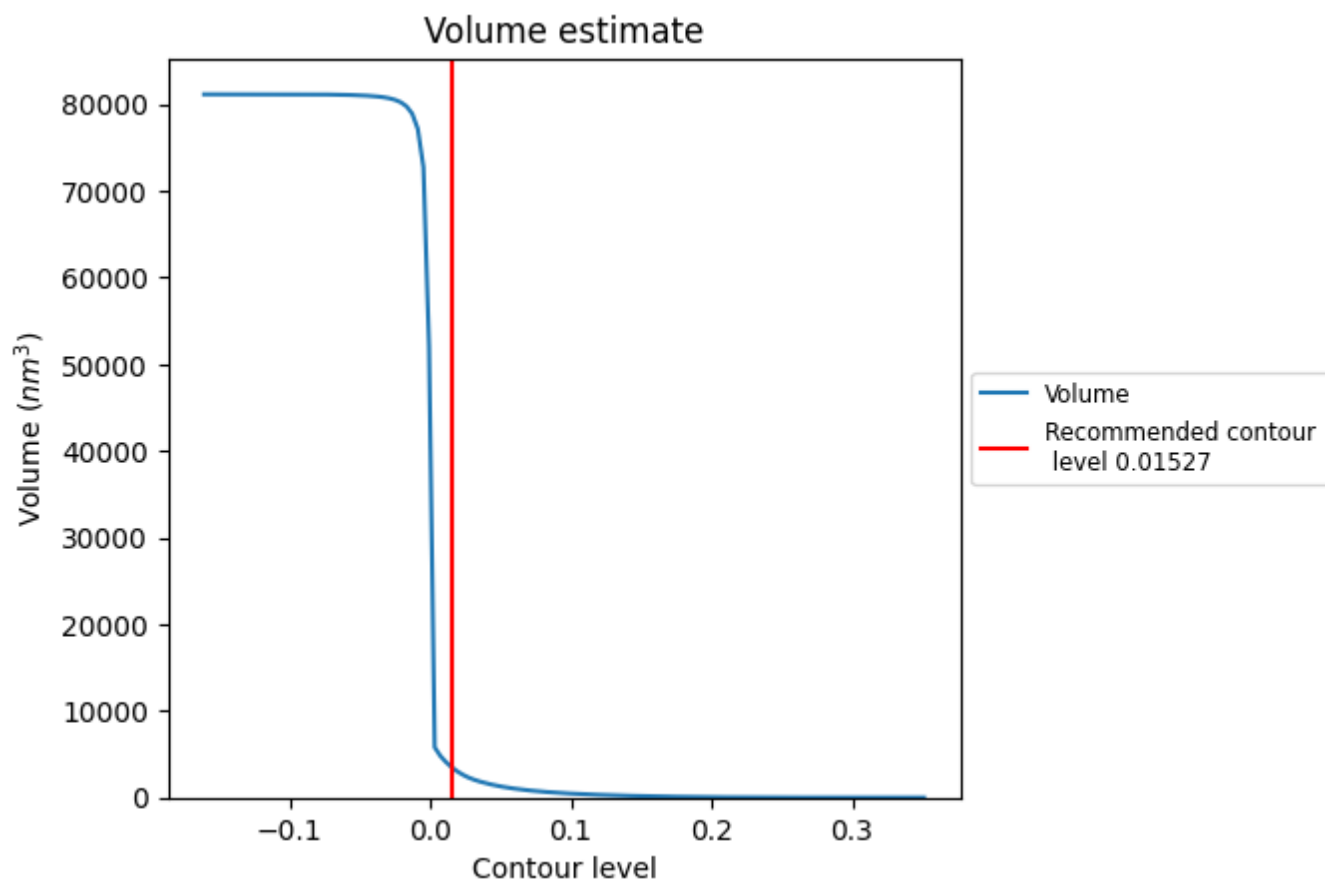
This section contains the results of statistical analysis of the map.

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.

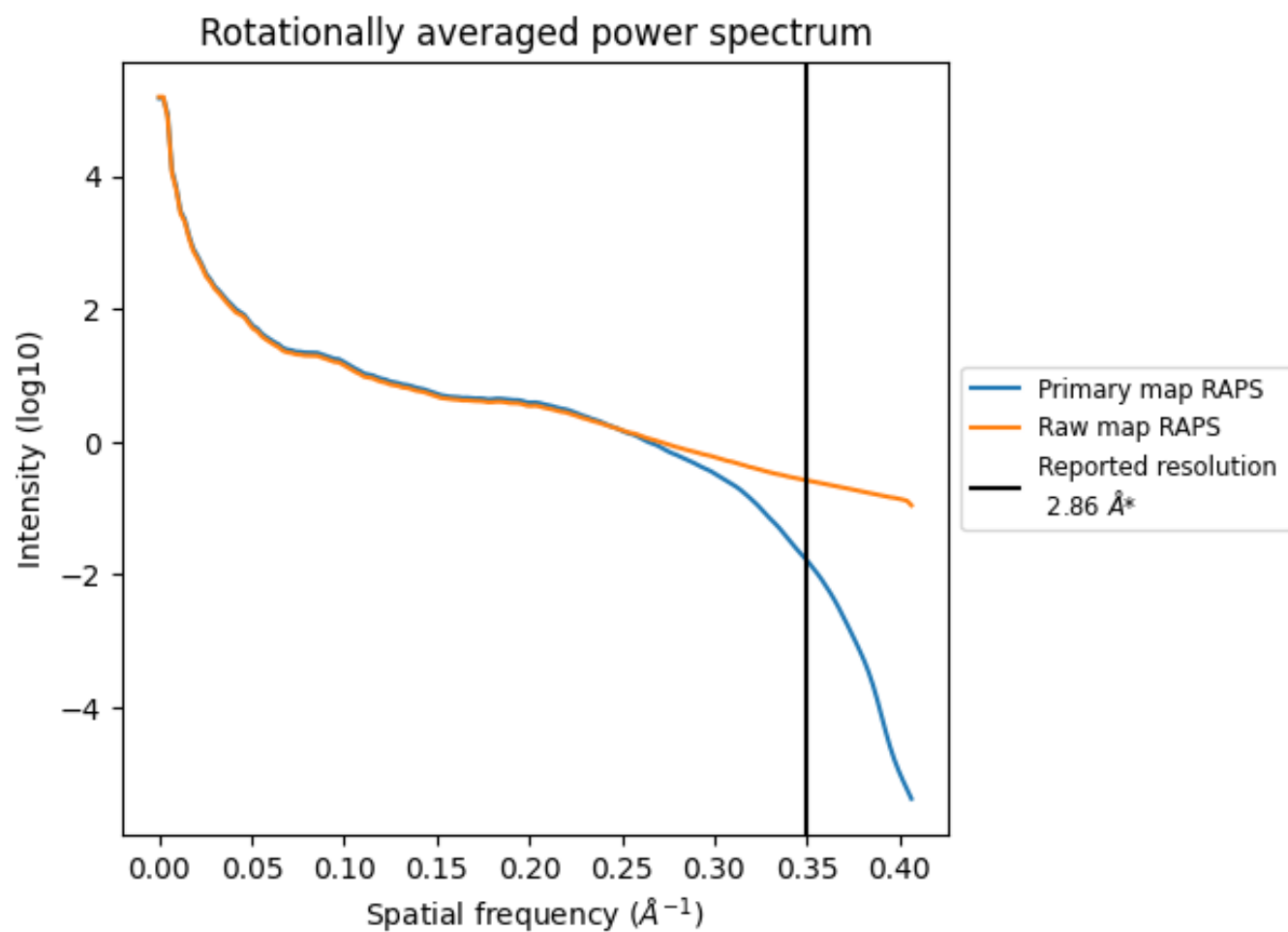
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3499 nm³; this corresponds to an approximate mass of 3161 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

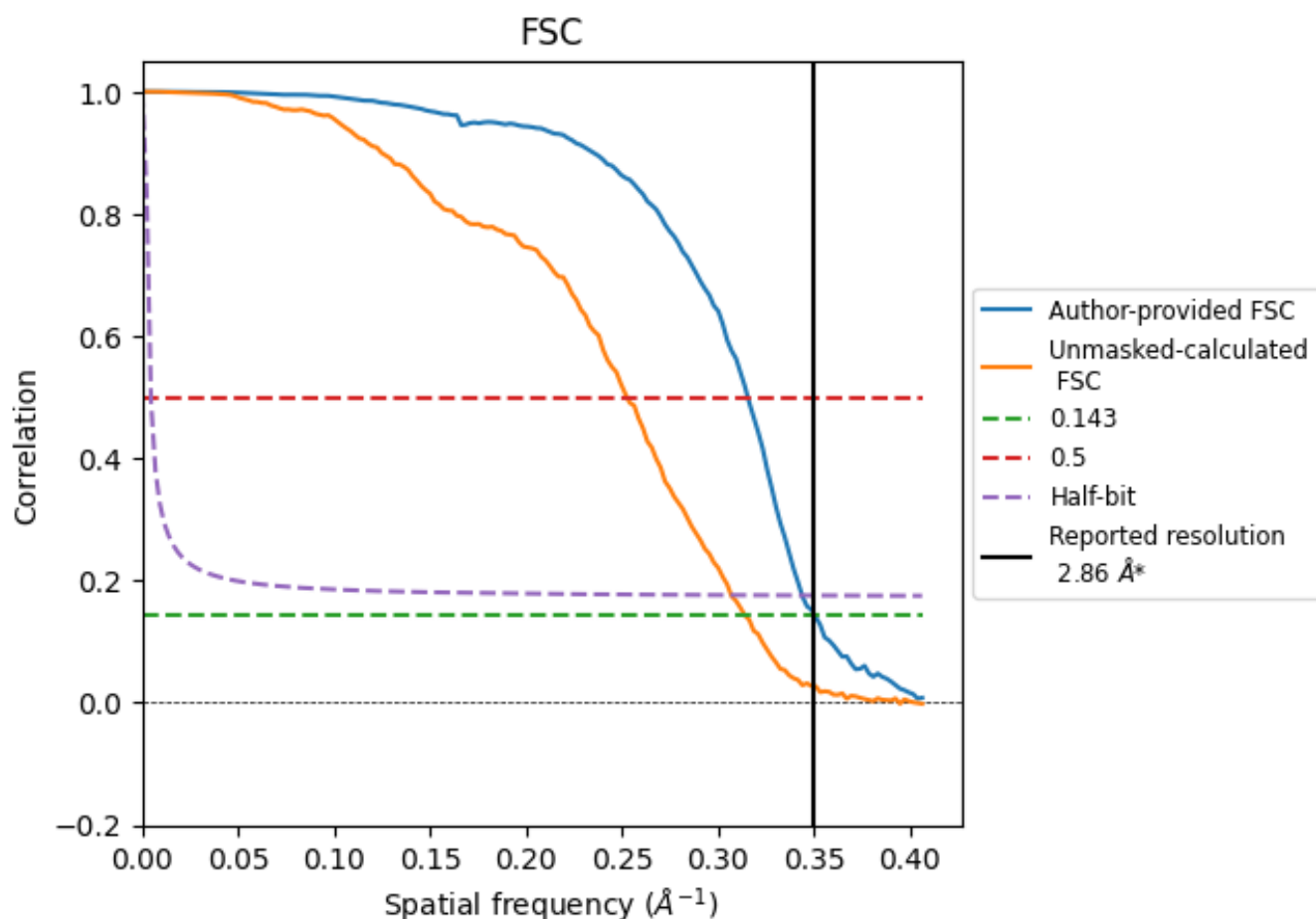


*Reported resolution corresponds to spatial frequency of 0.350 $\text{\AA}^{-1}$

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 0.350 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

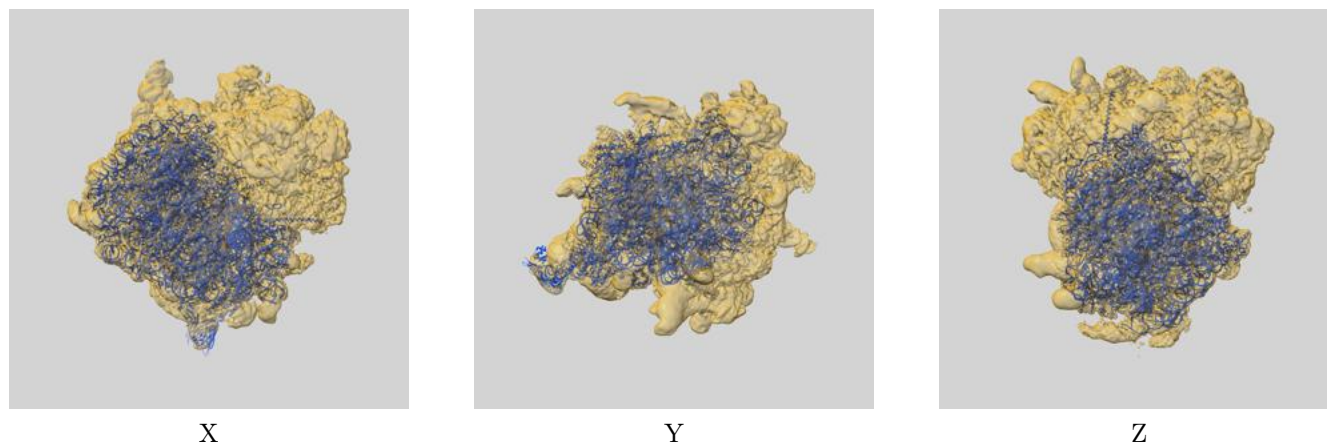
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	2.85	3.17	2.91
Unmasked-calculated*	3.18	3.96	3.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.18 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

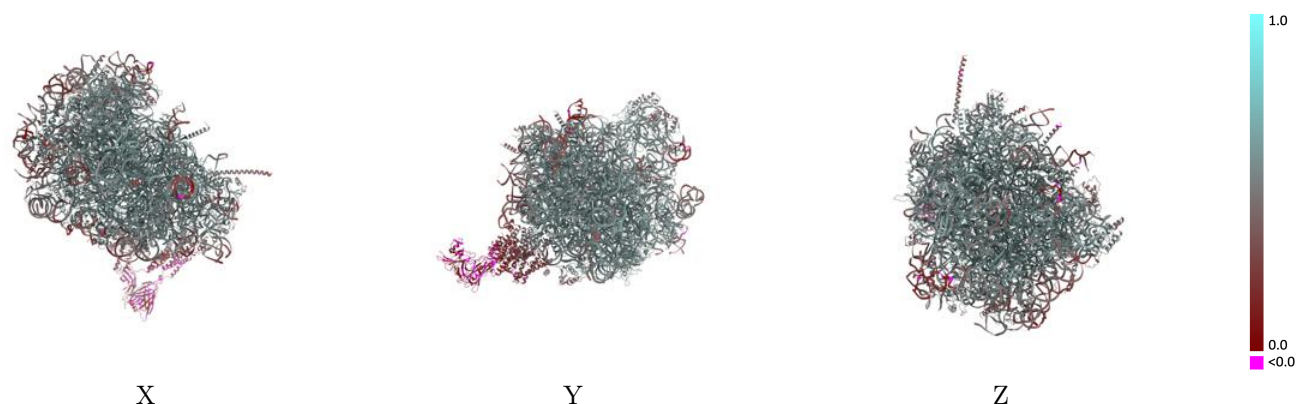
This section contains information regarding the fit between EMDB map EMD-15860 and PDB model 8B5L. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.01527 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](#)

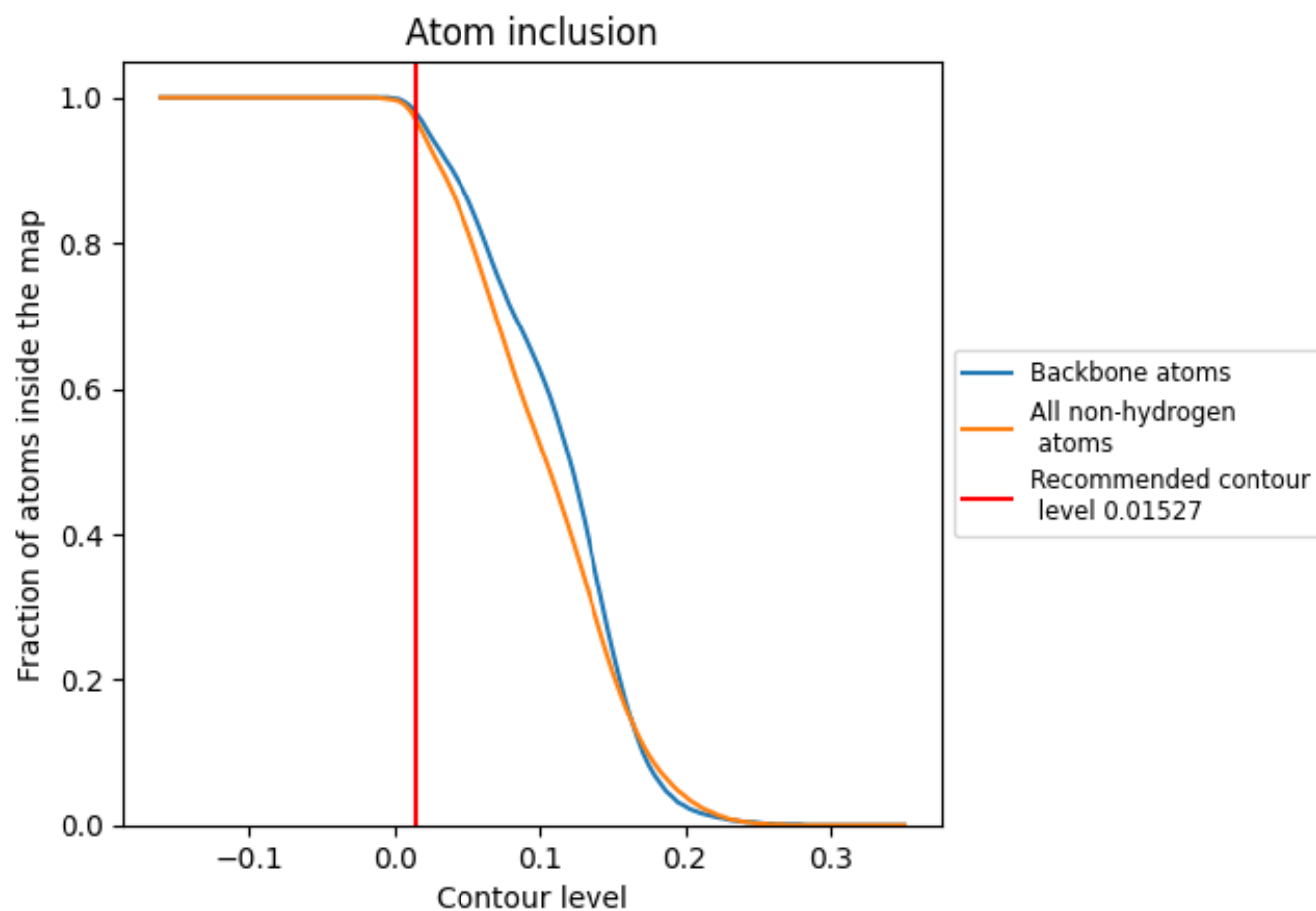


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01527) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.5050
5	 0.9940	 0.5160
7	 0.9990	 0.5490
8	 0.9950	 0.5370
A	 0.9780	 0.5760
B	 0.9850	 0.5590
C	 0.9800	 0.5560
D	 0.9860	 0.5150
E	 0.9840	 0.5230
F	 0.9710	 0.5520
G	 0.9720	 0.4900
H	 0.9820	 0.5390
I	 0.9750	 0.5550
J	 0.9730	 0.4730
K	 0.4630	 0.0490
L	 0.9550	 0.5200
M	 0.9870	 0.5320
N	 0.9860	 0.5850
O	 0.9870	 0.5570
P	 0.9760	 0.5630
Q	 0.9710	 0.5660
R	 0.9600	 0.5060
S	 0.9820	 0.5610
T	 0.9720	 0.5440
U	 0.9720	 0.4550
V	 0.9790	 0.5710
W	 0.9760	 0.5550
X	 0.9510	 0.5350
Y	 0.9730	 0.5310
Z	 0.9850	 0.5230
a	 0.9750	 0.5690
b	 0.9460	 0.4790
c	 0.9560	 0.5170
d	 0.9670	 0.5430
e	 0.9760	 0.5790



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Chain	Atom inclusion	Q-score
f	 0.9790	 0.5840
g	 0.9600	 0.5530
h	 0.9630	 0.5290
i	 0.9720	 0.5190
j	 0.9820	 0.5800
k	 0.9460	 0.4820
l	 0.9630	 0.5570
m	 0.9690	 0.5630
n	 0.9130	 0.5070
o	 0.9800	 0.5620
p	 0.9620	 0.5610
q	 0.5000	 0.0890
r	 0.9860	 0.5540
s	 0.8720	 0.2790
t	 0.7410	 0.2090
u	 0.8960	 0.3230
v	 0.4590	 0.0720