



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 07:19 am BST

PDB ID : 7OW7 / pdb_00007ow7
EMDB ID : EMD-13094
Title : EIF6-bound large subunit of the human ribosome
Authors : Faille, A.; Warren, A.J.
Deposited on : 2021-06-16
Resolution : 2.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
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

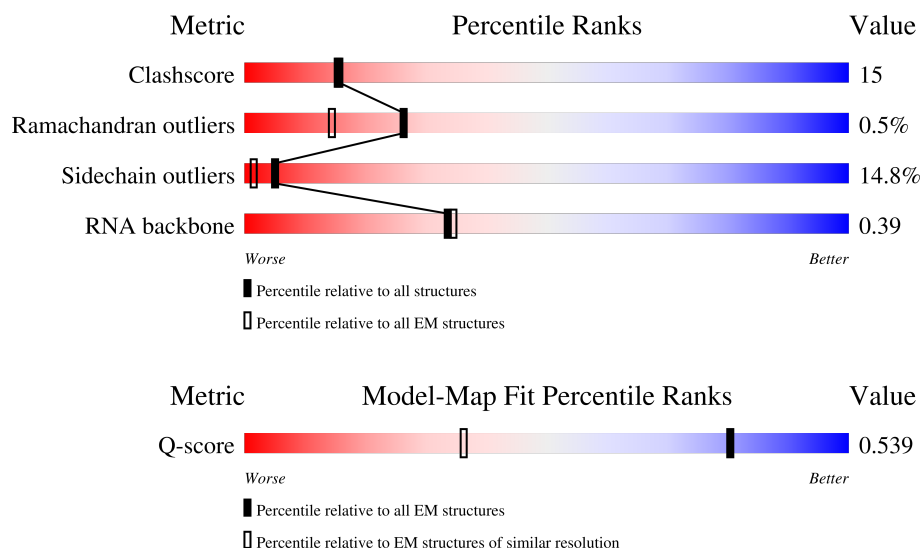
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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.



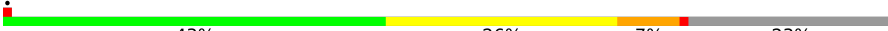
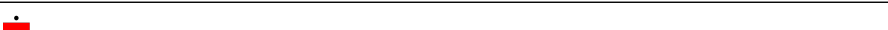
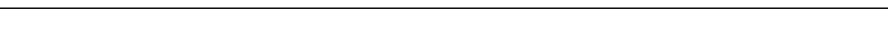
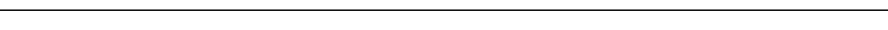
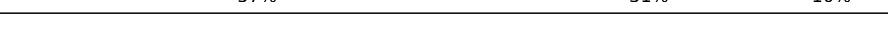
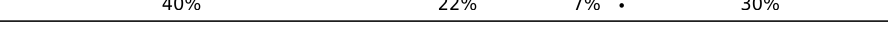
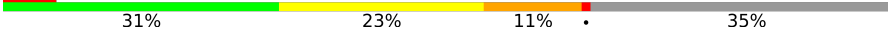
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	A	5070	
2	B	121	
3	C	157	

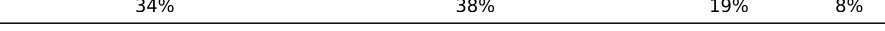
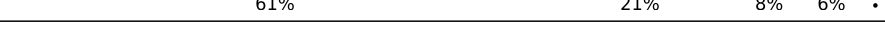
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Mol	Chain	Length	Quality of chain
4	D	257	
5	E	430	
6	F	427	
7	G	297	
8	H	288	
9	m	248	
10	n	266	
11	o	190	
12	p	214	
13	q	178	
14	r	211	
15	s	220	
16	t	204	
17	I	203	
18	J	184	
19	K	188	
20	L	196	
21	M	176	
22	N	160	
23	R	156	
24	S	145	
25	T	136	
26	U	148	
27	V	159	
28	W	115	

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Mol	Chain	Length	Quality of chain
29	X	125	
30	Y	135	
31	Z	110	
32	a	117	
33	b	123	
34	c	105	
35	d	97	
36	e	70	
37	f	157	
38	i	106	
39	j	92	
40	k	137	
41	P	245	
42	Q	140	
43	u	157	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	OMG	A	4228	-	-	X	-
48	BR	G	301	-	-	X	-

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 137413 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3303	Total	C	N	O	P	1	0
			70929	31625	12982	23019	3303		

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

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

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	148	Total	C	N	O	P	0	0
			3153	1408	564	1034	147		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	246	Total	C	N	O	S	0	0
			1887	1183	387	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L3 isoform a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	395	Total	C	N	O	S	1	0
			3194	2034	600	545	15		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	359	Total	C	N	O	S	0	0
			2855	1797	571	474	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	293	Total	C	N	O	S	0	0
			2376	1505	432	425	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	221	Total	C	N	O	S	0	0
			1767	1138	335	290	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	40	ARG	GLY	conflict	UNP Q02878
H	41	ASN	LYS	conflict	UNP Q02878

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	n	223	Total	C	N	O	S	0	0
			1809	1153	349	303	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	p	158	Total	C	N	O	S	0	0
			1283	819	238	216	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	49	CYS	GLY	conflict	UNP Q96L21

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	q	170	Total	C	N	O	S	0	0
			1358	858	253	241	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	r	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	t	203	Total	C	N	O	S	2	0
			1720	1086	361	269	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	137	Total	C	N	O	S	0	0
			1137	716	235	178	8		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called 60S ribosomal protein L26.

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

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called 60S ribosomal protein L27a.

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

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	104	Total	C	N	O	S	0	0
			837	518	185	130	4		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	100	Total	C	N	O	S	0	0
			772	490	136	139	7		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	106	Total	C	N	O	S	0	0
			868	551	170	145	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

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

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	109	Total	C	N	O	S	1	0
			879	557	174	144	4		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	112	Total	C	N	O	S	0	0
			888	555	183	144	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

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

- Molecule 34 is a protein called 60S ribosomal protein L36.

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

- Molecule 35 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	86	Total	C	N	O	S	1	0
			713	442	155	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	29	Total	C	N	O	S	0	0
			249	163	47	38	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	16	PRO	ARG	conflict	UNP P63173
e	23	ILE	VAL	conflict	UNP P63173

- Molecule 37 is a protein called 60S ribosomal protein L39.

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

- Molecule 38 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	97	Total	C	N	O	S	0	0
			794	498	161	129	6		

- Molecule 39 is a protein called 60S ribosomal protein L37a.

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

- Molecule 40 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	124	Total	C	N	O	S	0	0
			992	615	206	167	4		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	225	Total	C	N	O	S	0	0
			1712	1065	295	340	12		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	134	Total	C	N	O	S	0	0
			993	625	187	176	5		

- Molecule 43 is a protein called 60S ribosomal protein L24.

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

- Molecule 44 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
44	A	209	Total	Mg	0
			209	209	
44	B	3	Total	Mg	0
			3	3	
44	C	6	Total	Mg	0
			6	6	
44	J	1	Total	Mg	0
			1	1	
44	L	2	Total	Mg	0
			2	2	
44	Q	2	Total	Mg	0
			2	2	

- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
45	A	1	Total 1	Zn 1	0
45	a	1	Total 1	Zn 1	0
45	d	1	Total 1	Zn 1	0
45	i	1	Total 1	Zn 1	0
45	j	1	Total 1	Zn 1	0

- Molecule 46 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
46	A	139	Total 139	K 139	0
46	B	1	Total 1	K 1	0
46	D	3	Total 3	K 3	0
46	o	1	Total 1	K 1	0
46	p	1	Total 1	K 1	0
46	t	1	Total 1	K 1	0
46	J	1	Total 1	K 1	0
46	N	1	Total 1	K 1	0
46	V	1	Total 1	K 1	0
46	Y	1	Total 1	K 1	0
46	Z	1	Total 1	K 1	0
46	f	1	Total 1	K 1	0
46	i	1	Total 1	K 1	0

- Molecule 47 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
47	A	3	Total 3	Na 3	0
47	t	1	Total 1	Na 1	0

- Molecule 48 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		AltConf
48	G	1	Total 1	Br 1	0

- Molecule 49 is water.

Mol	Chain	Residues	Atoms		AltConf
49	A	6577	Total 6577	O 6577	0
49	B	132	Total 132	O 132	0
49	C	280	Total 280	O 280	0
49	D	109	Total 109	O 109	0
49	E	139	Total 139	O 139	0
49	F	182	Total 182	O 182	0
49	G	34	Total 34	O 34	0
49	H	36	Total 36	O 36	0
49	m	101	Total 101	O 101	0
49	n	35	Total 35	O 35	0
49	o	11	Total 11	O 11	0
49	p	12	Total 12	O 12	0
49	q	5	Total 5	O 5	0
49	r	84	Total 84	O 84	0
49	s	14	Total 14	O 14	0

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Mol	Chain	Residues	Atoms		AltConf
49	t	153	Total 153	O 153	0
49	I	87	Total 87	O 87	0
49	J	66	Total 66	O 66	0
49	K	130	Total 130	O 130	0
49	L	37	Total 37	O 37	0
49	M	53	Total 53	O 53	0
49	N	71	Total 71	O 71	0
49	R	29	Total 29	O 29	0
49	S	40	Total 40	O 40	0
49	T	6	Total 6	O 6	0
49	U	80	Total 80	O 80	0
49	V	27	Total 27	O 27	0
49	W	6	Total 6	O 6	0
49	X	24	Total 24	O 24	0
49	Y	96	Total 96	O 96	0
49	Z	58	Total 58	O 58	0
49	a	52	Total 52	O 52	0
49	b	38	Total 38	O 38	0
49	c	15	Total 15	O 15	0
49	d	56	Total 56	O 56	0
49	e	1	Total 1	O 1	0

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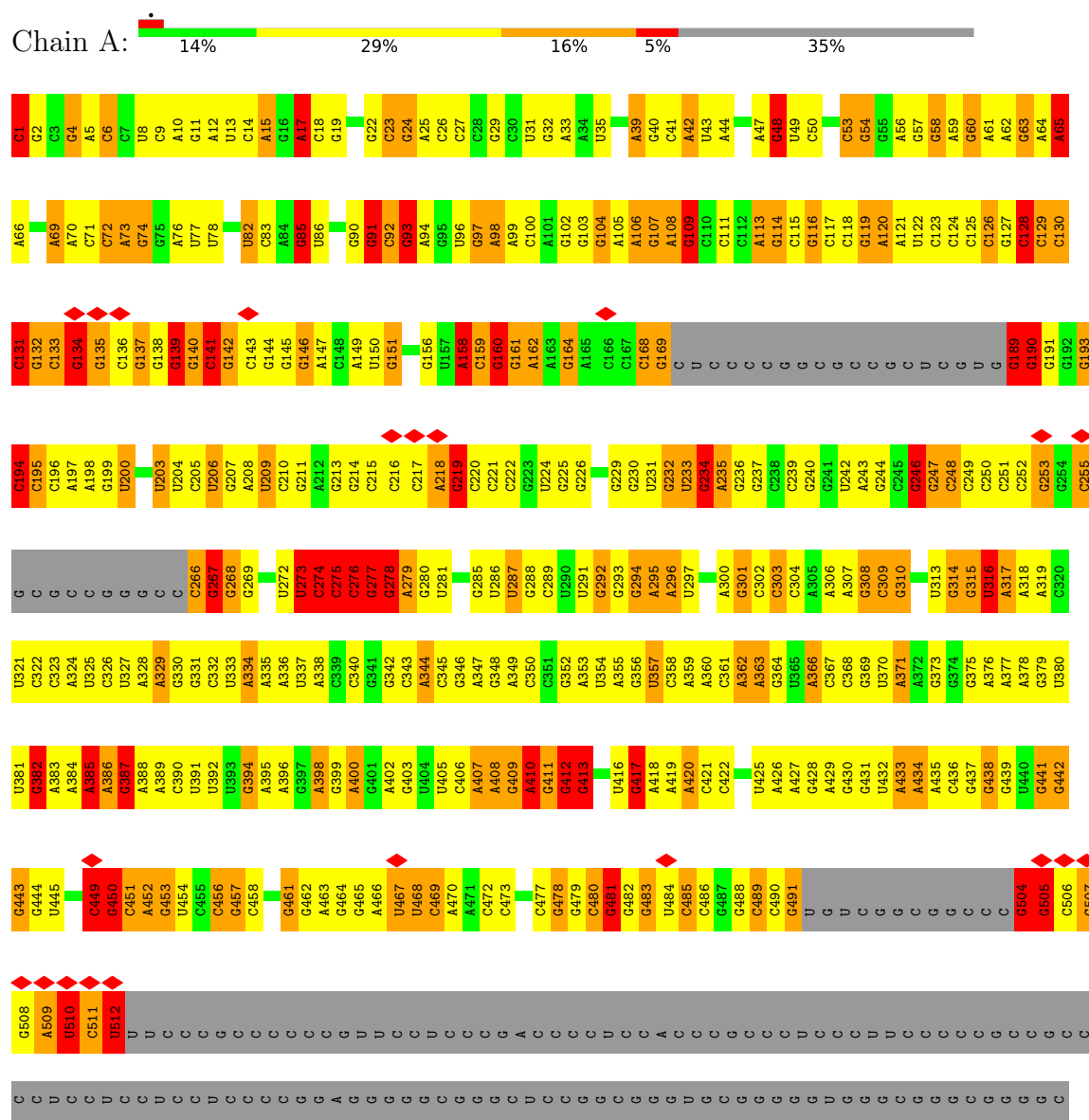
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Mol	Chain	Residues	Atoms		AltConf
49	f	12	Total 12	O 12	0
49	i	35	Total 35	O 35	0
49	j	24	Total 24	O 24	0
49	k	59	Total 59	O 59	0
49	P	1	Total 1	O 1	0
49	Q	31	Total 31	O 31	0
49	u	6	Total 6	O 6	0

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: 28S rRNA

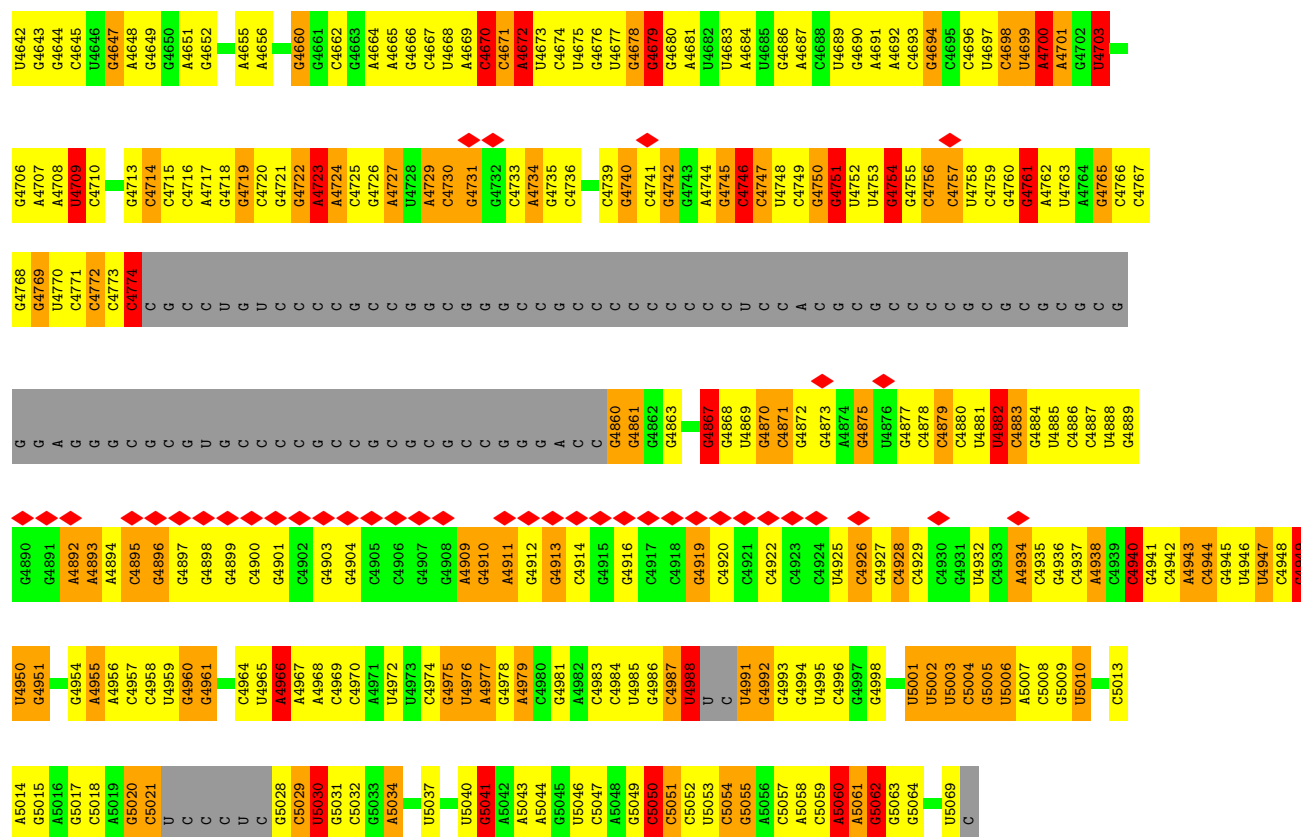




C2458	A2396	G2326	G2259	G	C	G	C2079	G1951	G1884	G1823	A	C	A	G1634	A1634	A1572
G2459	G2397	G2327	C2260	U	C	U	G2080	G1952	G1885	G1824	C	C	G	C1635	C1635	U1572
A2460	G2400	G2328	G2261	C	U	U	U2080	U1953	G1886	A1825	A	G	A	U1636	U1636	G1573
C2462	A2401	U2329	G2262	U	C	U	U2081	U1954	G1887	G1826	C	A	A	G1637	G1637	G1574
G2463	C2463	G2330	C2263	C	A	C	C2083	G1955	G1890	C1827	A	A	A	A1638	A1638	A1575
C2464	A2404	G2331	C2264	C	C	C	C2084	G1956	G1891	G1828	C	C	C	C1640	C1640	G1576
C2465	G2405	A2332	C2265	C	U	U	G2085	U1959	A1891					G1641	G1641	G1577
C2466	G2406	C2333	C2266	C	U	U	G2086	A1892	A1892					G1642	G1642	U1578
U2467	G2407	G2334	C2267	A	C	C	C2087	G1960	C1893	G1831	A	G	A	A1643	A1643	
U2468	U2408	G2335	A2088	C	C	C	A2088	A1961	C1894	G1832	U	U	U	A1644	A1644	U1582
C2469	U2409	G2336	C2089	G	G	G	C2089	A1962	G1895	G1833	C	C	C	C1645	C1645	
C2470	C2410	C2337	U2090	C	A	A	U2090	C1963	A1896	G1835	U	U	U	G1646	G1646	C1586
G2471	C2411	G2338	G2273	C	C	C	G	A1964	A1897	G1836	A	A	A	U1647	U1647	
A2472	A2412	C2339	C2274	U	U	U	G	C	C1898	A1837				G1648	G1648	G1587
A2473	U2413	G2340	G2275	C	G	G	G	A	G1899	A1838	C	C	C	U1649	U1649	U1588
G2474	U2413	A2341	C2276	C	C	C	A	A	C1900	G1839	C	C	C	G1650	G1650	C1589
G2475	G2414	G2342	C2277	U	C	C	G	G	C1901	G1840	G	G	G	A1651	A1651	G1590
G2476	G2415	G2343	C2278	C	C	C	A	A	G1902	G1841	U	U	U	G1652	G1652	U1591
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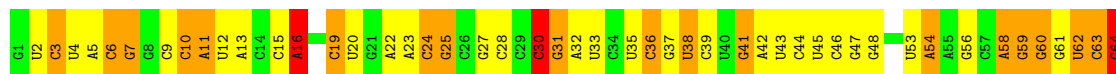


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• Molecule 2: 5S rRNA

Chain B: 29% 41% 26%



• Molecule 3: 5.8S ribosomal RNA

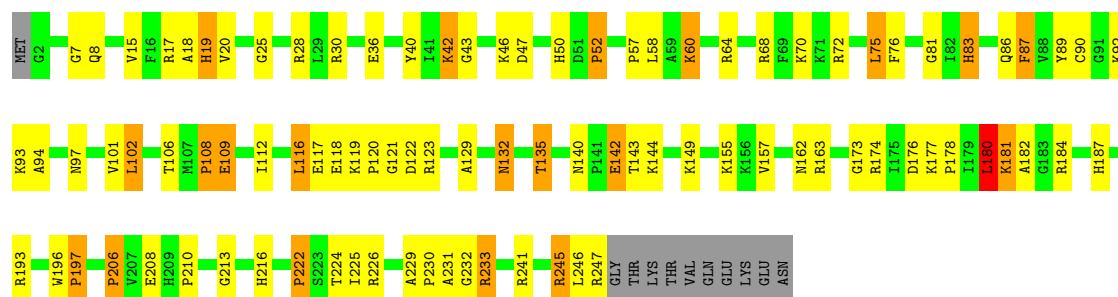
Chain C: 26% 38% 24% 6% 6%



• Molecule 4: 60S ribosomal protein L8

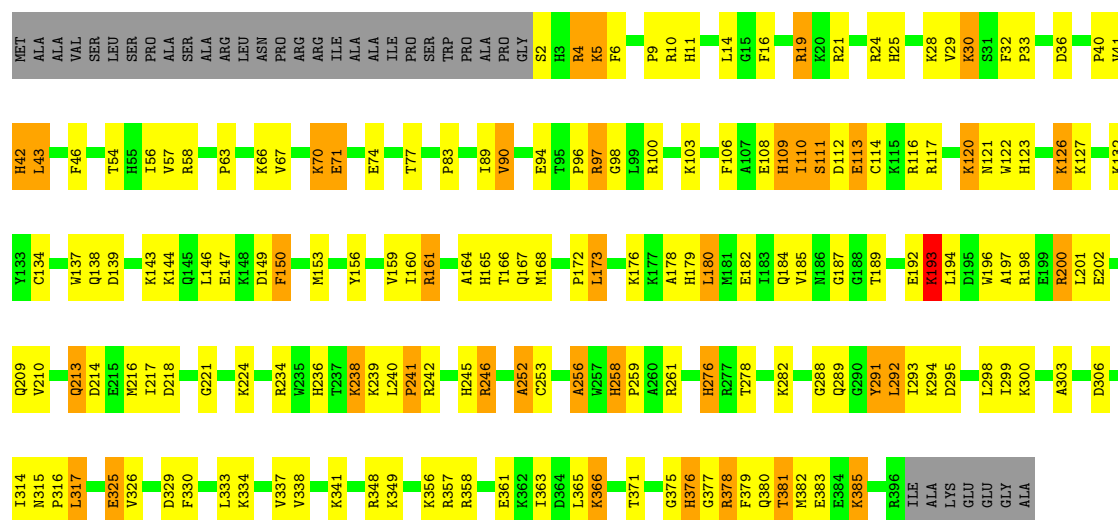


Chain D: 



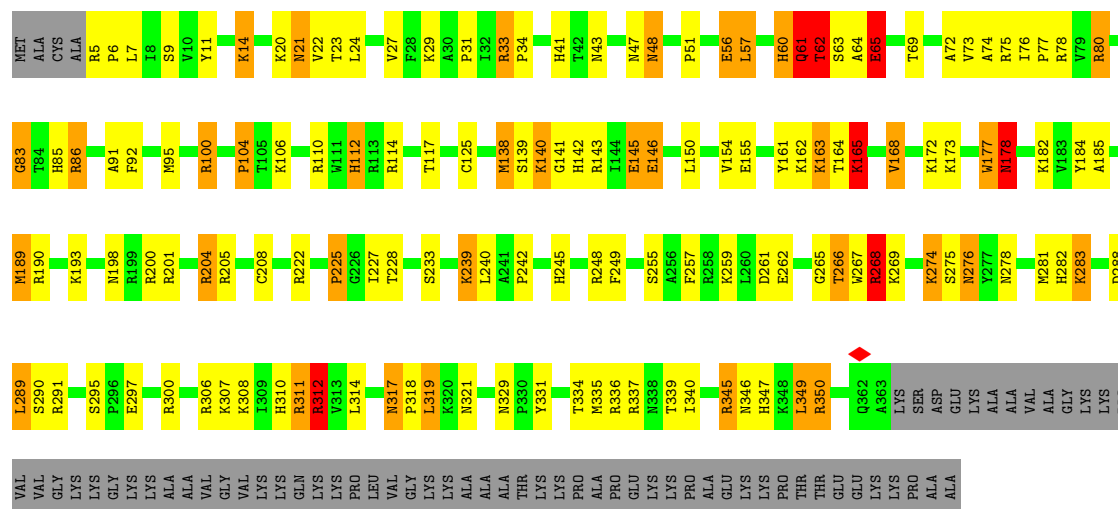
• Molecule 5: 60S ribosomal protein L3 isoform a

Chain E: 

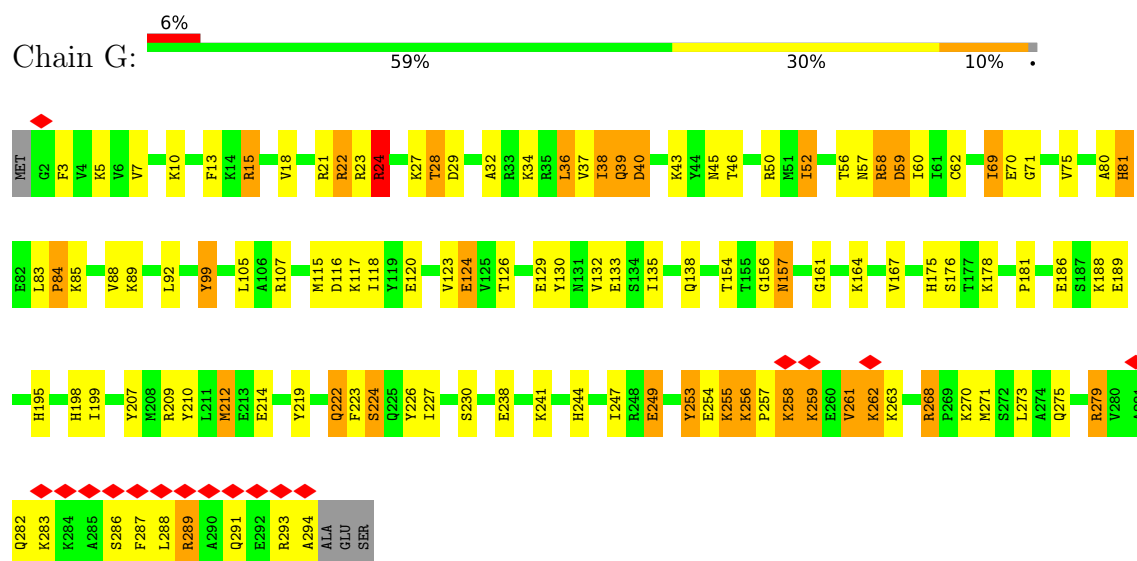


• Molecule 6: 60S ribosomal protein L4

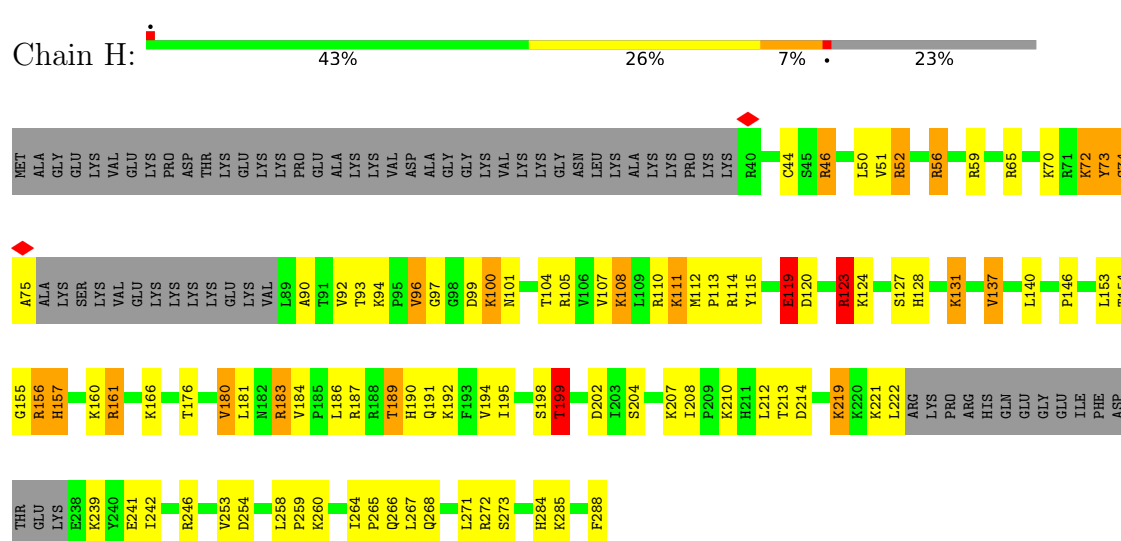
Chain F: 



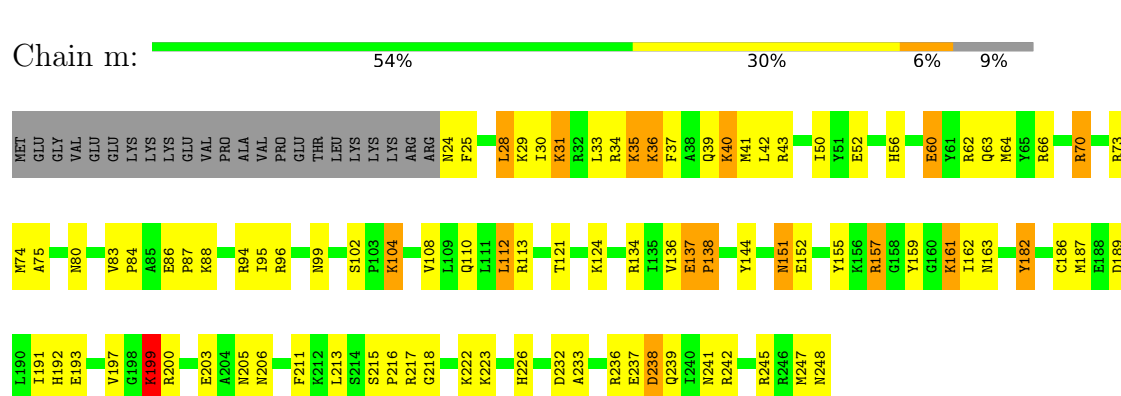
- Molecule 7: 60S ribosomal protein L5



- Molecule 8: 60S ribosomal protein L6

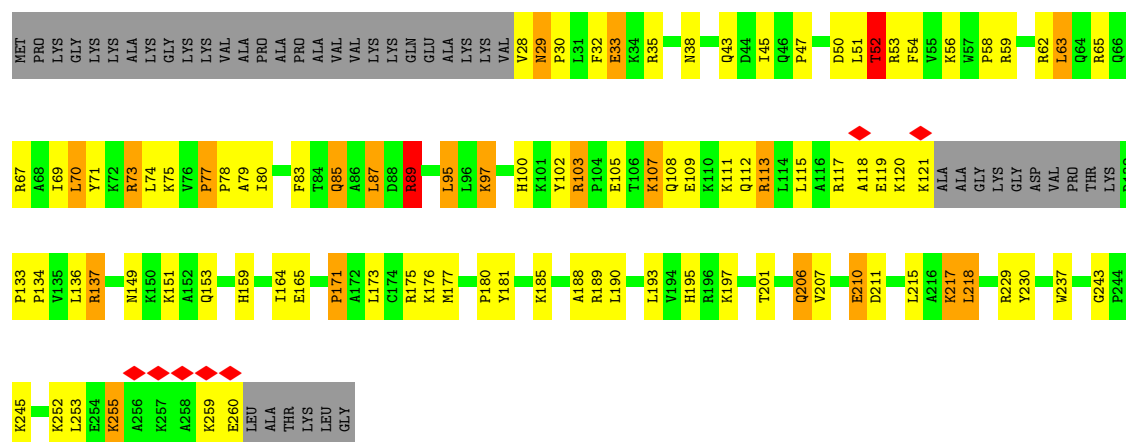


- Molecule 9: 60S ribosomal protein L7



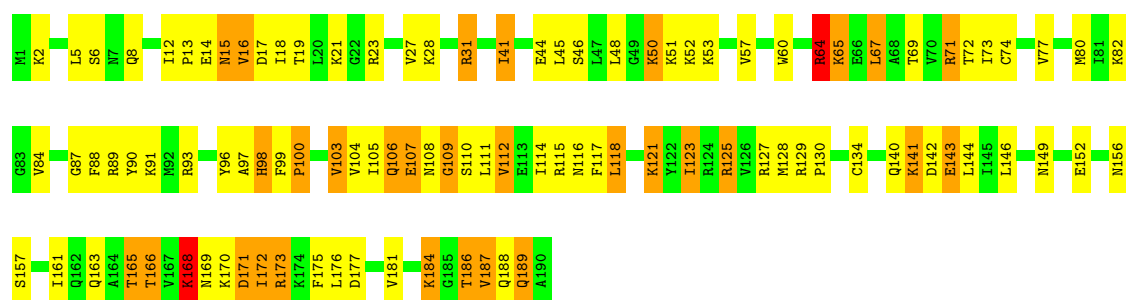
- Molecule 10: 60S ribosomal protein L7a

Chain n: 



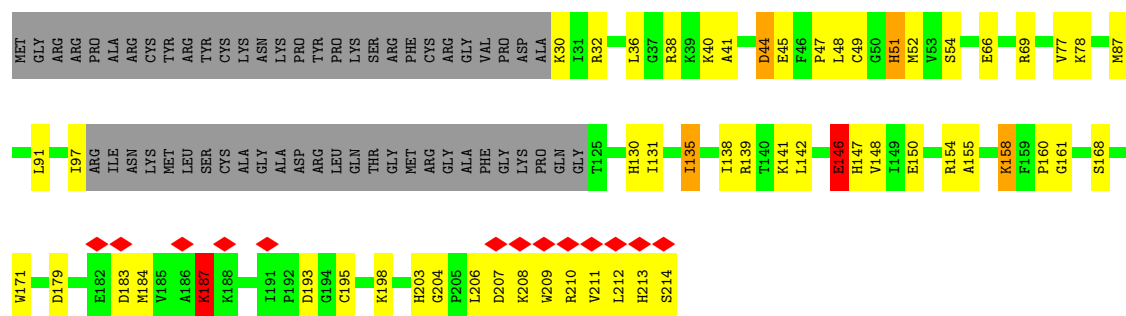
- Molecule 11: 60S ribosomal protein L9

Chain o: 



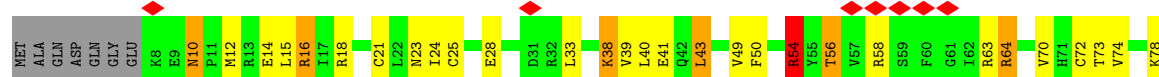
- Molecule 12: 60S ribosomal protein L10-like

Chain p: 



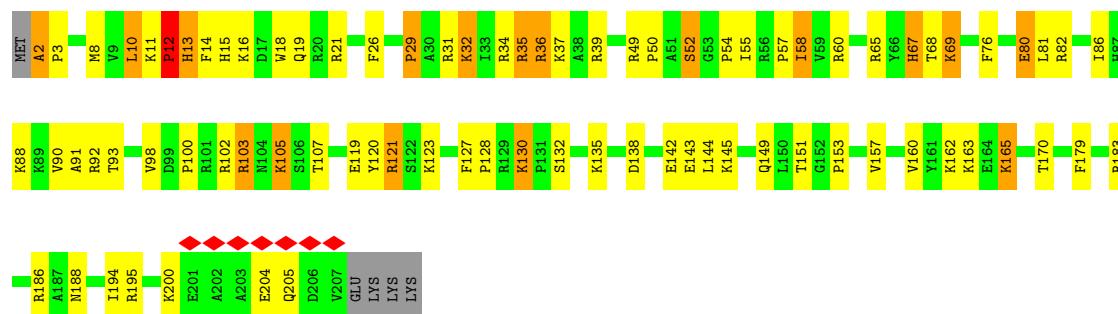
- Molecule 13: 60S ribosomal protein L11

Chain q: 

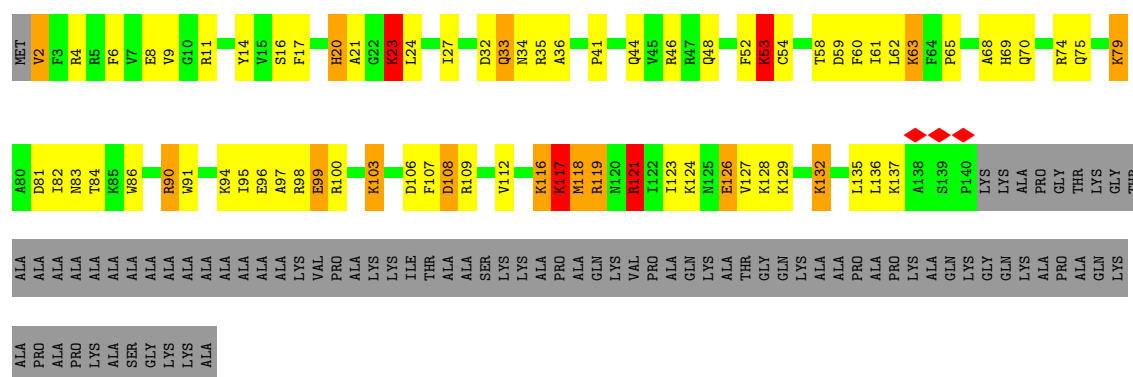
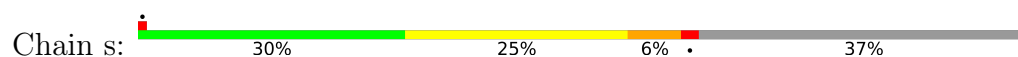




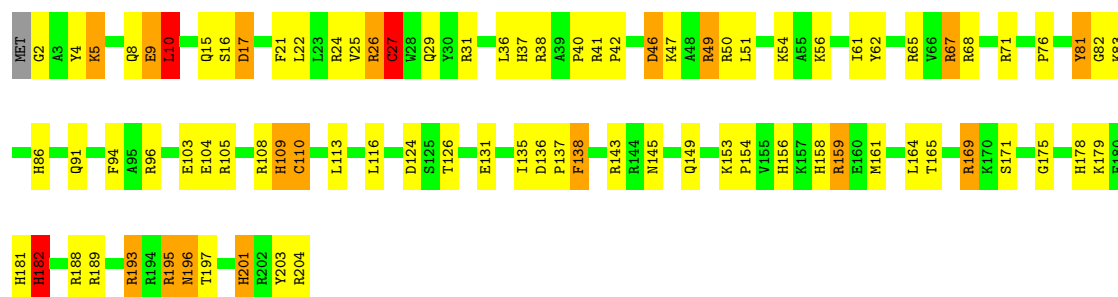
• Molecule 14: 60S ribosomal protein L13



• Molecule 15: 60S ribosomal protein L14

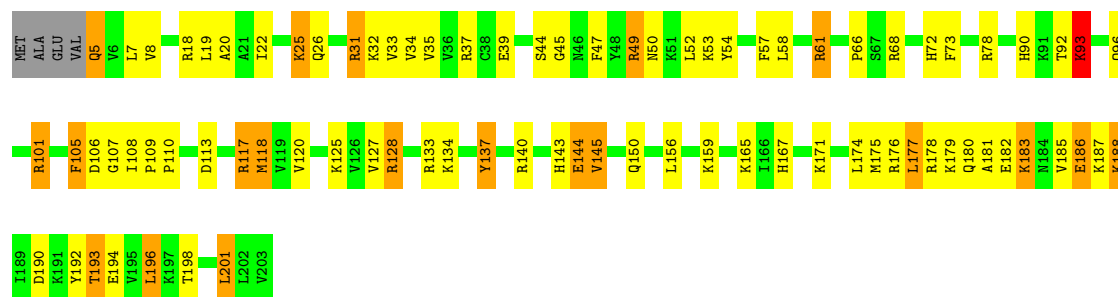


• Molecule 16: 60S ribosomal protein L15



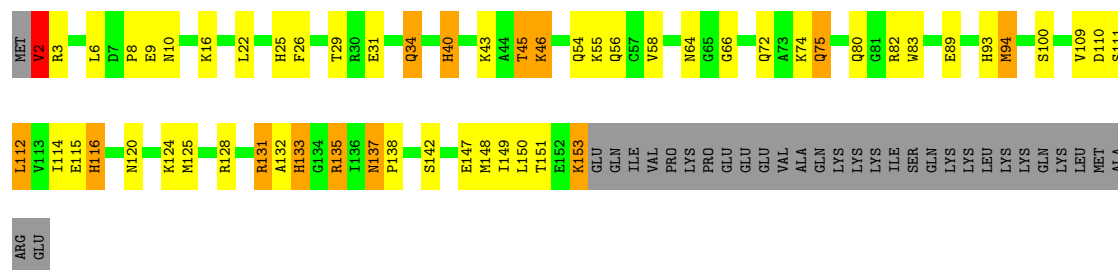
• Molecule 17: 60S ribosomal protein L13a





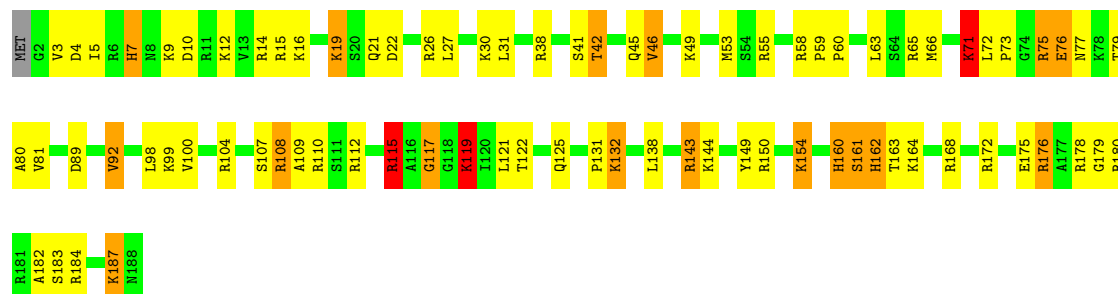
- Molecule 18: 60S ribosomal protein L17

Chain J: 52% 23% 7% • 17%



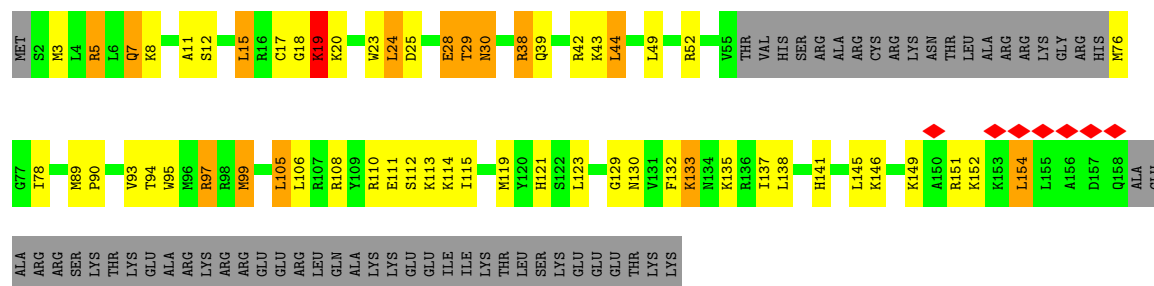
- Molecule 19: 60S ribosomal protein L18

Chain K: 56% 32% 9% ••



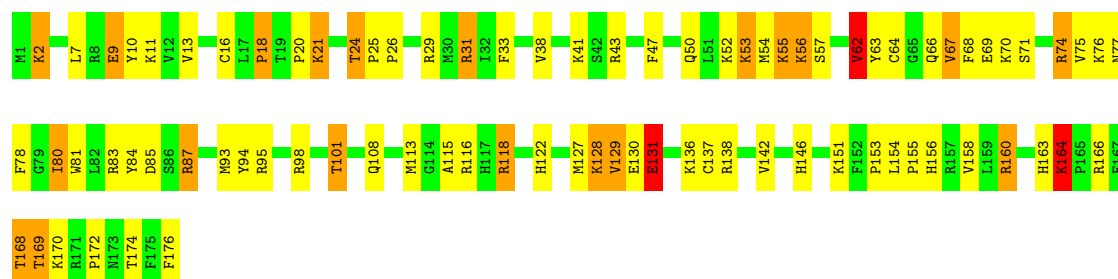
- Molecule 20: 60S ribosomal protein L19

Chain L: 40% 22% 7% • 30%



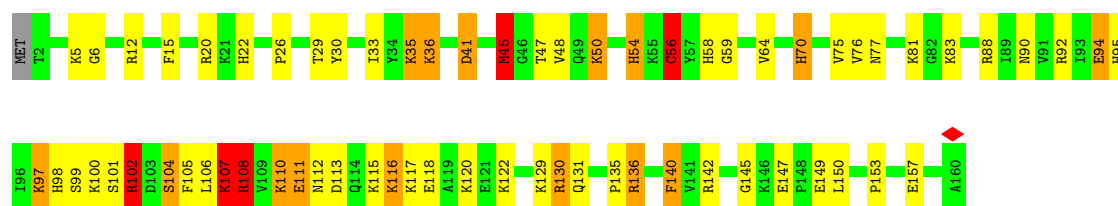
- Molecule 21: 60S ribosomal protein L18a

Chain M: 

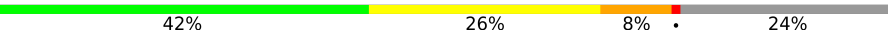


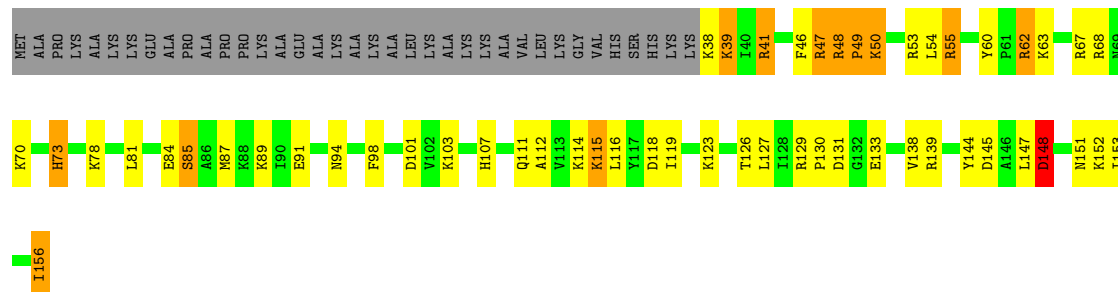
- Molecule 22: 60S ribosomal protein L21

Chain N: 



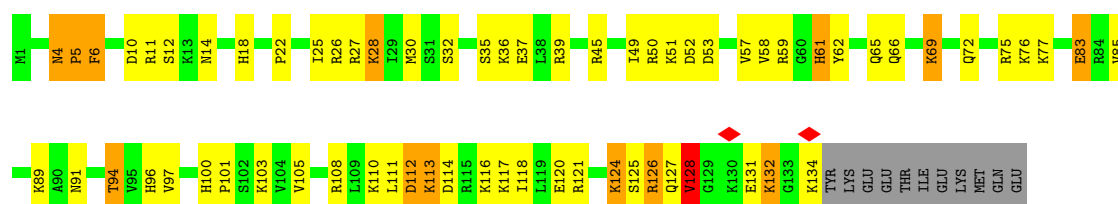
- Molecule 23: 60S ribosomal protein L23a

Chain R: 



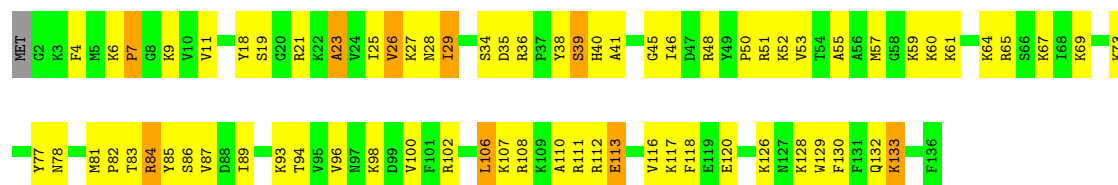
- Molecule 24: 60S ribosomal protein L26

Chain S: 



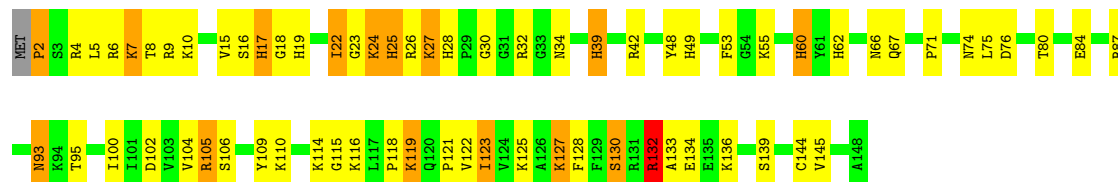
- Molecule 25: 60S ribosomal protein L27

Chain T: 



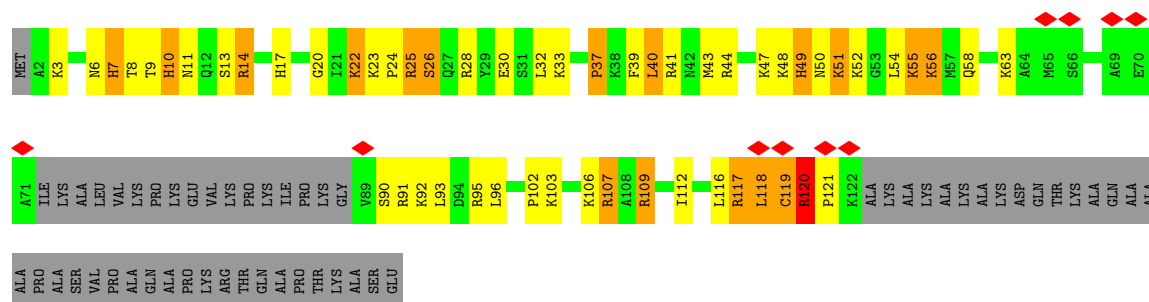
- Molecule 26: 60S ribosomal protein L27a

Chain U: 53% 35% 10% ..



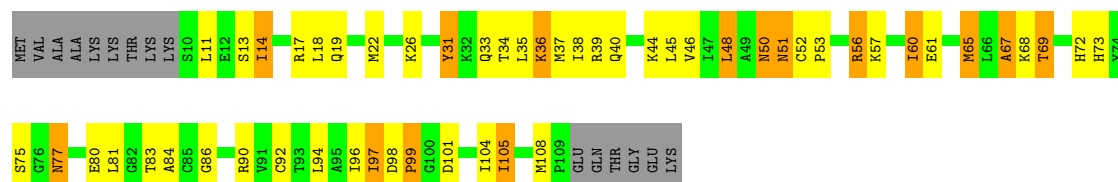
- Molecule 27: 60S ribosomal protein L29

Chain V: 6% 31% 23% 11% 35%



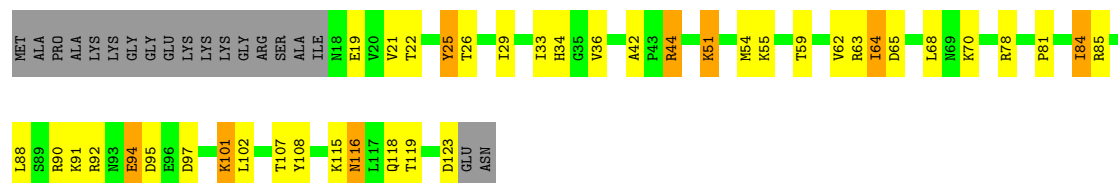
- Molecule 28: 60S ribosomal protein L30

Chain W: 41% 33% 13% 13%



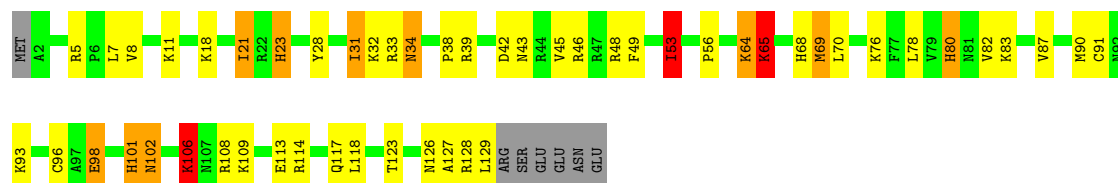
- Molecule 29: 60S ribosomal protein L31

Chain X: 52% 26% 6% 15%



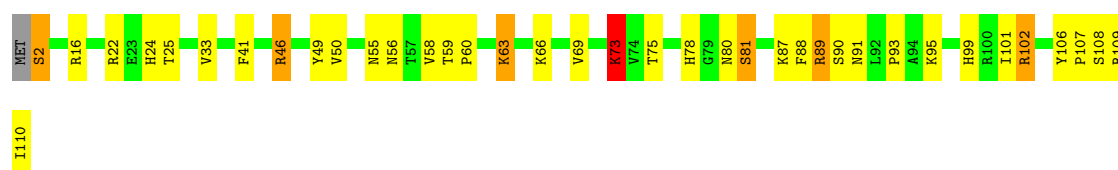
- Molecule 30: 60S ribosomal protein L32

Chain Y:  56% 29% 7% 5%



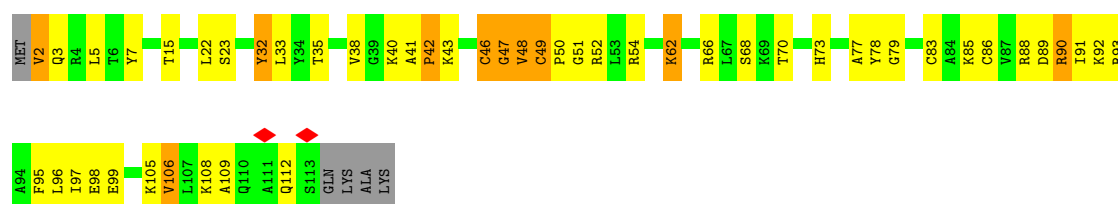
- Molecule 31: 60S ribosomal protein L35a

Chain Z:  65% 28% 5%



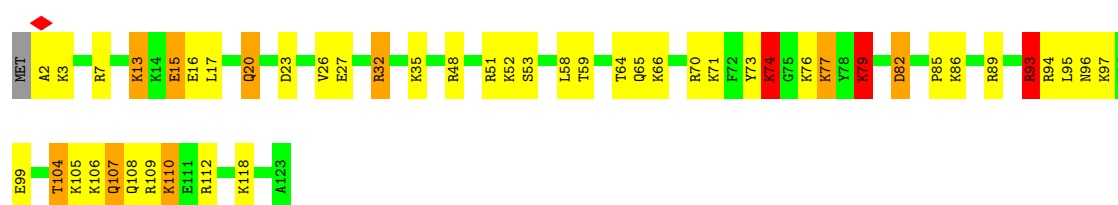
- Molecule 32: 60S ribosomal protein L34

Chain a:  53% 34% 9%



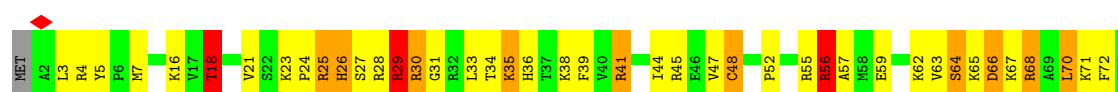
- Molecule 33: 60S ribosomal protein L35

Chain b:  60% 29% 7%



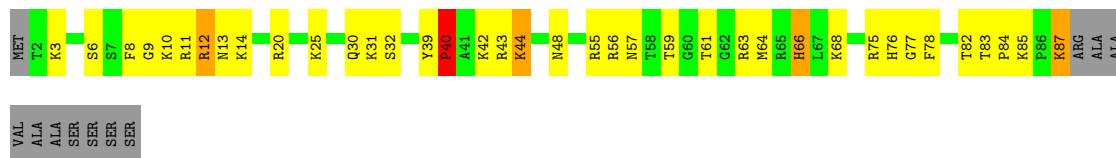
- Molecule 34: 60S ribosomal protein L36

Chain c:  47% 33% 13%





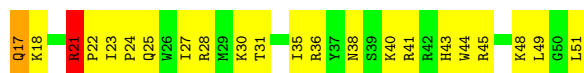
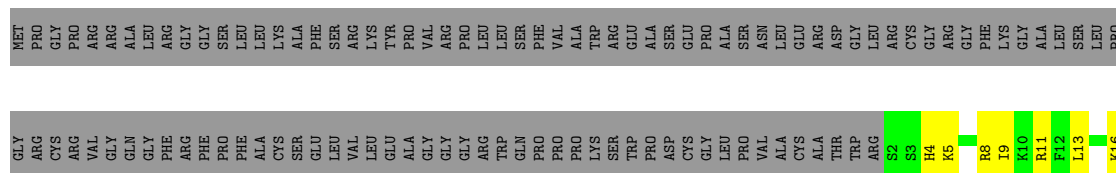
• Molecule 35: 60S ribosomal protein L37



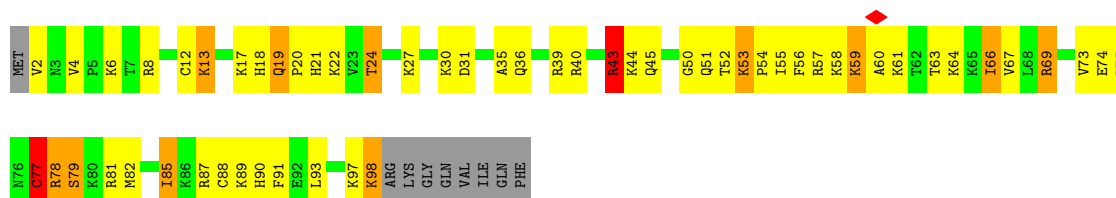
• Molecule 36: 60S ribosomal protein L38



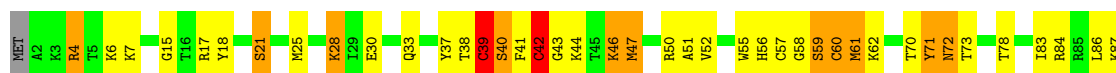
• Molecule 37: 60S ribosomal protein L39



• Molecule 38: 60S ribosomal protein L36a



• Molecule 39: 60S ribosomal protein L37a





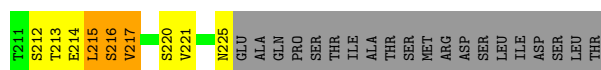
- Molecule 40: 60S ribosomal protein L28

Chain k: 53% 29% 7% 9%



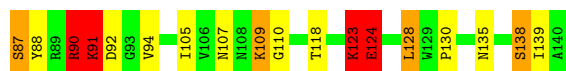
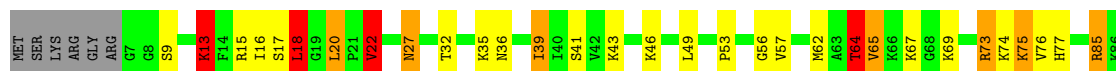
- Molecule 41: Eukaryotic translation initiation factor 6

Chain P: 34% 38% 19% 8%



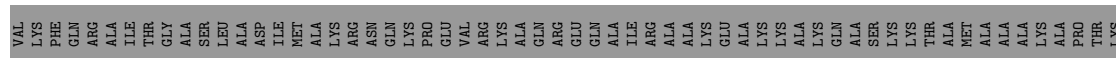
- Molecule 42: 60S ribosomal protein L23

Chain Q: 61% 21% 8% 6%



- Molecule 43: 60S ribosomal protein L24

Chain u: 19% 17% 61%



ALA
ALA
PRO
LYS
GLN
LYS
ILE
VAL
LYS
PRO
VAL
LYS
VAL
SER
ALA
PRO
ARG
VAL
GLY
GLY
LYS
ARG

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30000	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.235	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 6MZ, UR3, 1MA, K, MG, OMG, OMC, OMU, NA, 5MC, A2M, PSU, BR

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	A	0.96	106/76620 (0.1%)	1.62	2585/119500 (2.2%)
2	B	0.81	3/2858 (0.1%)	1.43	78/4455 (1.8%)
3	C	0.98	5/3450 (0.1%)	1.71	130/5372 (2.4%)
4	D	1.07	3/1925 (0.2%)	2.07	65/2581 (2.5%)
5	E	1.01	7/3265 (0.2%)	1.93	106/4369 (2.4%)
6	F	1.09	9/2909 (0.3%)	2.13	121/3908 (3.1%)
7	G	0.68	1/2422 (0.0%)	1.70	42/3244 (1.3%)
8	H	0.74	0/1801	1.73	43/2418 (1.8%)
9	m	1.05	2/1905 (0.1%)	1.93	48/2539 (1.9%)
10	n	0.74	1/1840 (0.1%)	1.76	39/2476 (1.6%)
11	o	0.60	0/1537	1.50	9/2066 (0.4%)
12	p	0.59	0/1312	1.32	8/1754 (0.5%)
13	q	0.57	0/1381	1.33	6/1848 (0.3%)
14	r	0.96	4/1695 (0.2%)	1.86	42/2270 (1.9%)
15	s	0.75	1/1161 (0.1%)	1.75	31/1554 (2.0%)
16	t	1.26	7/1766 (0.4%)	2.07	68/2366 (2.9%)
17	I	1.03	7/1666 (0.4%)	1.98	60/2228 (2.7%)
18	J	1.16	4/1259 (0.3%)	1.96	33/1689 (2.0%)
19	K	1.10	2/1537 (0.1%)	2.15	70/2052 (3.4%)
20	L	0.84	1/1150 (0.1%)	1.72	13/1523 (0.9%)
21	M	0.92	3/1501 (0.2%)	1.99	59/2013 (2.9%)
22	N	0.97	5/1326 (0.4%)	2.00	48/1770 (2.7%)
23	R	0.86	0/993	1.93	27/1334 (2.0%)
24	S	1.08	5/1132 (0.4%)	2.11	34/1504 (2.3%)
25	T	0.64	0/1130	1.59	14/1507 (0.9%)
26	U	1.21	5/1191 (0.4%)	2.13	54/1591 (3.4%)
27	V	0.86	3/850 (0.4%)	1.98	29/1123 (2.6%)
28	W	0.72	0/783	1.70	15/1052 (1.4%)
29	X	0.91	1/883 (0.1%)	1.82	15/1190 (1.3%)
30	Y	1.16	5/1071 (0.5%)	1.97	21/1429 (1.5%)
31	Z	1.08	2/901 (0.2%)	2.03	29/1206 (2.4%)
32	a	0.99	1/898 (0.1%)	2.00	27/1197 (2.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.83	1/1023 (0.1%)	1.86	21/1351 (1.6%)
34	c	0.87	1/843 (0.1%)	1.83	22/1115 (2.0%)
35	d	1.37	3/732 (0.4%)	2.11	28/968 (2.9%)
36	e	0.54	0/251	1.27	0/330
37	f	0.91	2/454 (0.4%)	1.81	7/599 (1.2%)
38	i	0.76	1/807 (0.1%)	1.83	20/1065 (1.9%)
39	j	1.05	1/718 (0.1%)	2.21	34/953 (3.6%)
40	k	1.12	3/1007 (0.3%)	1.91	24/1351 (1.8%)
41	P	0.56	0/1736	1.36	10/2362 (0.4%)
42	Q	1.11	1/1007 (0.1%)	2.13	39/1350 (2.9%)
43	u	0.93	2/532 (0.4%)	1.64	6/708 (0.8%)
All	All	0.95	208/135228 (0.2%)	1.72	4180/199280 (2.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	59
3	C	0	2
8	H	0	1
21	M	0	1
33	b	0	1
34	c	0	2
43	u	0	1
All	All	0	67

The worst 5 of 208 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4273	A	O3'-P	15.19	1.83	1.61
32	a	2	VAL	N-CA	15.05	1.74	1.46
16	t	109	HIS	CE1-NE2	12.37	1.45	1.32
35	d	66	HIS	CE1-NE2	12.34	1.44	1.32
5	E	179	HIS	CE1-NE2	11.91	1.44	1.32

The worst 5 of 4180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	277	G	C2'-C3'-O3'	-19.75	84.08	113.70
1	A	2652	G	C4'-C3'-O3'	-19.08	84.38	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4722	G	C2'-C3'-O3'	-18.83	85.45	113.70
1	A	209	U	C4'-C3'-O3'	-18.80	84.81	113.00
1	A	4273	A	C3'-C2'-O2'	18.46	138.39	110.70

There are no chirality outliers.

5 of 67 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	275	C	Sidechain
1	A	276	C	Sidechain
1	A	292	G	Sidechain
1	A	91	G	Sidechain
1	A	93	G	Sidechain

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	A	70929	0	35891	1648	0
2	B	2558	0	1295	70	0
3	C	3153	0	1604	77	0
4	D	1887	0	1983	55	0
5	E	3194	0	3336	107	0
6	F	2855	0	3021	91	0
7	G	2376	0	2406	116	0
8	H	1767	0	1913	78	0
9	m	1870	0	1996	48	0
10	n	1809	0	1941	53	0
11	o	1518	0	1601	71	0
12	p	1283	0	1309	40	0
13	q	1358	0	1388	47	0
14	r	1664	0	1773	66	0
15	s	1138	0	1204	83	0
16	t	1720	0	1764	57	0
17	I	1634	0	1779	44	0
18	J	1233	0	1263	32	0
19	K	1513	0	1628	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	L	1137	0	1251	50	0
21	M	1461	0	1500	52	0
22	N	1298	0	1366	31	0
23	R	976	0	1053	42	0
24	S	1115	0	1205	65	0
25	T	1107	0	1182	37	0
26	U	1162	0	1213	46	0
27	V	837	0	895	62	0
28	W	772	0	808	30	0
29	X	868	0	913	19	0
30	Y	1053	0	1146	45	0
31	Z	879	0	916	19	0
32	a	888	0	979	34	0
33	b	1015	0	1148	30	0
34	c	832	0	917	56	0
35	d	713	0	746	24	0
36	e	249	0	285	14	0
37	f	444	0	482	27	0
38	i	794	0	856	61	0
39	j	708	0	756	54	0
40	k	992	0	1052	25	0
41	P	1712	0	1689	87	0
42	Q	993	0	1050	24	0
43	u	519	0	533	24	0
44	A	209	0	0	1	0
44	B	3	0	0	0	0
44	C	6	0	0	0	0
44	J	1	0	0	0	0
44	L	2	0	0	0	0
44	Q	2	0	0	0	0
45	A	1	0	0	0	0
45	a	1	0	0	0	0
45	d	1	0	0	0	0
45	i	1	0	0	0	0
45	j	1	0	0	0	0
46	A	139	0	0	1	0
46	B	1	0	0	0	0
46	D	3	0	0	0	0
46	J	1	0	0	0	0
46	N	1	0	0	0	0
46	V	1	0	0	0	0
46	Y	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	Z	1	0	0	0	0
46	f	1	0	0	0	0
46	i	1	0	0	0	0
46	o	1	0	0	0	0
46	p	1	0	0	0	0
46	t	1	0	0	0	0
47	A	3	0	0	0	0
47	t	1	0	0	0	0
48	G	1	0	0	3	0
49	A	6577	0	0	540	0
49	B	132	0	0	20	0
49	C	280	0	0	26	0
49	D	109	0	0	14	0
49	E	139	0	0	23	0
49	F	182	0	0	32	0
49	G	34	0	0	4	0
49	H	36	0	0	4	0
49	I	87	0	0	6	0
49	J	66	0	0	8	0
49	K	130	0	0	16	0
49	L	37	0	0	5	0
49	M	53	0	0	11	0
49	N	71	0	0	10	0
49	P	1	0	0	0	0
49	Q	31	0	0	2	0
49	R	29	0	0	5	0
49	S	40	0	0	4	0
49	T	6	0	0	1	0
49	U	80	0	0	19	0
49	V	27	0	0	2	0
49	W	6	0	0	2	0
49	X	24	0	0	0	0
49	Y	96	0	0	11	0
49	Z	58	0	0	5	0
49	a	52	0	0	7	0
49	b	38	0	0	3	0
49	c	15	0	0	4	0
49	d	56	0	0	5	0
49	e	1	0	0	0	0
49	f	12	0	0	1	0
49	i	35	0	0	11	0
49	j	24	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	k	59	0	0	3	0
49	m	101	0	0	8	0
49	n	35	0	0	2	0
49	o	11	0	0	3	0
49	p	12	0	0	1	0
49	q	5	0	0	0	0
49	r	84	0	0	22	0
49	s	14	0	0	7	0
49	t	153	0	0	19	0
49	u	6	0	0	5	0
All	All	137413	0	93036	3182	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 15.

The worst 5 of 3182 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)
1:A:247:G:C4'	24:S:128:VAL:HG11	1.30	1.60
1:A:247:G:H4'	24:S:128:VAL:CG1	1.14	1.55
32:a:2:VAL:N	32:a:2:VAL:CA	1.74	1.47
1:A:4373:G:N7	38:i:61:LYS:HE3	1.10	1.41
1:A:4337:C:N3	38:i:61:LYS:HE2	1.33	1.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	D	244/257 (95%)	234 (96%)	9 (4%)	1 (0%)	30 43
5	E	394/430 (92%)	373 (95%)	20 (5%)	1 (0%)	36 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	357/427 (84%)	341 (96%)	16 (4%)	0	100	100
7	G	291/297 (98%)	280 (96%)	10 (3%)	1 (0%)	36	50
8	H	215/288 (75%)	202 (94%)	13 (6%)	0	100	100
9	m	223/248 (90%)	214 (96%)	9 (4%)	0	100	100
10	n	219/266 (82%)	202 (92%)	15 (7%)	2 (1%)	14	22
11	o	188/190 (99%)	169 (90%)	12 (6%)	7 (4%)	2	2
12	p	154/214 (72%)	146 (95%)	8 (5%)	0	100	100
13	q	168/178 (94%)	157 (94%)	10 (6%)	1 (1%)	21	32
14	r	204/211 (97%)	195 (96%)	9 (4%)	0	100	100
15	s	137/220 (62%)	128 (93%)	9 (7%)	0	100	100
16	t	203/204 (100%)	196 (97%)	7 (3%)	0	100	100
17	I	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
18	J	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
19	K	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
20	L	133/196 (68%)	130 (98%)	1 (1%)	2 (2%)	8	12
21	M	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
22	N	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	21	32
23	R	117/156 (75%)	116 (99%)	1 (1%)	0	100	100
24	S	132/145 (91%)	124 (94%)	7 (5%)	1 (1%)	16	25
25	T	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	U	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	18	28
27	V	100/159 (63%)	91 (91%)	9 (9%)	0	100	100
28	W	98/115 (85%)	91 (93%)	7 (7%)	0	100	100
29	X	104/125 (83%)	100 (96%)	4 (4%)	0	100	100
30	Y	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
31	Z	108/110 (98%)	108 (100%)	0	0	100	100
32	a	110/117 (94%)	105 (96%)	5 (4%)	0	100	100
33	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	c	100/105 (95%)	93 (93%)	4 (4%)	3 (3%)	3	3
35	d	85/97 (88%)	82 (96%)	3 (4%)	0	100	100
36	e	25/70 (36%)	24 (96%)	1 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	f	48/157 (31%)	45 (94%)	3 (6%)	0	100	100
38	i	95/106 (90%)	87 (92%)	6 (6%)	2 (2%)	5	7
39	j	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	11	18
40	k	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
41	P	223/245 (91%)	173 (78%)	44 (20%)	6 (3%)	4	4
42	Q	132/140 (94%)	122 (92%)	7 (5%)	3 (2%)	5	6
43	u	60/157 (38%)	56 (93%)	3 (5%)	1 (2%)	7	10
All	All	6265/7312 (86%)	5923 (94%)	308 (5%)	34 (0%)	26	37

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	o	98	HIS
11	o	187	VAL
11	o	188	GLN
38	i	79	SER
39	j	39	CYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	189/199 (95%)	176 (93%)	13 (7%)	14	24
5	E	345/368 (94%)	310 (90%)	35 (10%)	7	11
6	F	297/348 (85%)	268 (90%)	29 (10%)	7	12
7	G	245/250 (98%)	203 (83%)	42 (17%)	2	2
8	H	193/253 (76%)	162 (84%)	31 (16%)	2	3
9	m	194/215 (90%)	176 (91%)	18 (9%)	8	14
10	n	193/223 (86%)	157 (81%)	36 (19%)	1	2
11	o	169/169 (100%)	125 (74%)	44 (26%)	0	0
12	p	138/182 (76%)	120 (87%)	18 (13%)	4	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	q	142/149 (95%)	106 (75%)	36 (25%)	0	1
14	r	172/177 (97%)	148 (86%)	24 (14%)	3	4
15	s	118/161 (73%)	97 (82%)	21 (18%)	2	2
16	t	173/172 (101%)	166 (96%)	7 (4%)	28	47
17	I	171/174 (98%)	151 (88%)	20 (12%)	5	7
18	J	133/163 (82%)	120 (90%)	13 (10%)	7	12
19	K	164/165 (99%)	152 (93%)	12 (7%)	13	22
20	L	121/175 (69%)	99 (82%)	22 (18%)	2	2
21	M	157/157 (100%)	139 (88%)	18 (12%)	5	8
22	N	139/140 (99%)	116 (84%)	23 (16%)	2	3
23	R	107/133 (80%)	91 (85%)	16 (15%)	3	3
24	S	124/135 (92%)	104 (84%)	20 (16%)	2	3
25	T	117/118 (99%)	91 (78%)	26 (22%)	1	1
26	U	120/121 (99%)	114 (95%)	6 (5%)	22	38
27	V	83/126 (66%)	60 (72%)	23 (28%)	0	0
28	W	84/97 (87%)	63 (75%)	21 (25%)	0	1
29	X	93/110 (84%)	82 (88%)	11 (12%)	5	7
30	Y	114/121 (94%)	104 (91%)	10 (9%)	9	15
31	Z	89/89 (100%)	84 (94%)	5 (6%)	19	33
32	a	96/100 (96%)	85 (88%)	11 (12%)	5	8
33	b	109/110 (99%)	93 (85%)	16 (15%)	3	4
34	c	86/89 (97%)	66 (77%)	20 (23%)	1	1
35	d	74/80 (92%)	70 (95%)	4 (5%)	20	35
36	e	29/65 (45%)	24 (83%)	5 (17%)	2	2
37	f	47/130 (36%)	41 (87%)	6 (13%)	4	6
38	i	86/94 (92%)	77 (90%)	9 (10%)	6	10
39	j	74/75 (99%)	62 (84%)	12 (16%)	2	3
40	k	107/121 (88%)	97 (91%)	10 (9%)	8	14
41	P	195/213 (92%)	122 (63%)	73 (37%)	0	0
42	Q	102/107 (95%)	76 (74%)	26 (26%)	0	0
43	u	54/126 (43%)	40 (74%)	14 (26%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5443/6200 (88%)	4637 (85%)	806 (15%)	5 4

5 of 806 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	R	39	LYS
28	W	108	MET
43	u	44	ARG
23	R	152	LYS
23	R	38	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 162 such sidechains are listed below:

Mol	Chain	Res	Type
26	U	39	HIS
38	i	51	GLN
27	V	10	HIS
30	Y	101	HIS
40	k	100	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3282/5070 (64%)	742 (22%)	151 (4%)
2	B	119/121 (98%)	19 (15%)	6 (5%)
3	C	145/157 (92%)	21 (14%)	4 (2%)
All	All	3546/5348 (66%)	782 (22%)	161 (4%)

5 of 782 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	4	G
1	A	15	A
1	A	17	A
1	A	18	C

5 of 161 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	4228	OMG
1	A	4910	G
1	A	4265	U
1	A	4449	A
1	A	5061	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

117 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	$\# Z > 2$
1	PSU	A	4493	1,46	18,21,22	1.30	2 (11%)	22,30,33	7.39	13 (59%)
3	OMG	C	75	3	23,26,27	1.27	2 (8%)	33,38,41	2.30	12 (36%)
1	OMU	A	4498	1,46	19,22,23	1.35	3 (15%)	26,31,34	2.60	9 (34%)
1	OMC	A	2365	1,44	19,22,23	1.46	4 (21%)	26,31,34	2.49	10 (38%)
1	OMG	A	4370	1,44	23,26,27	1.53	6 (26%)	33,38,41	3.36	11 (33%)
1	OMG	A	4623	1	23,26,27	2.23	7 (30%)	33,38,41	2.54	11 (33%)
1	OMU	A	2837	1	19,22,23	2.33	6 (31%)	26,31,34	3.98	11 (42%)
1	A2M	A	1871	1,46,44	22,25,26	2.03	6 (27%)	31,36,39	2.59	13 (41%)
1	PSU	A	2632	1	18,21,22	1.72	3 (16%)	22,30,33	2.03	7 (31%)
1	PSU	A	4500	1,46	18,21,22	1.75	5 (27%)	22,30,33	4.02	9 (40%)
1	OMC	A	3887	1	19,22,23	1.18	1 (5%)	26,31,34	3.82	13 (50%)
1	PSU	A	4353	1,46	18,21,22	2.53	7 (38%)	22,30,33	4.81	14 (63%)
1	OMG	A	2424	1	23,26,27	1.91	6 (26%)	33,38,41	3.62	18 (54%)
1	OMU	A	3925	1	19,22,23	1.74	5 (26%)	26,31,34	3.99	13 (50%)
1	A2M	A	4523	1,44	22,25,26	1.89	5 (22%)	31,36,39	3.53	16 (51%)
1	OMG	A	4196	1,44	23,26,27	1.45	3 (13%)	33,38,41	2.62	13 (39%)
1	PSU	A	4579	1	18,21,22	1.70	4 (22%)	22,30,33	3.51	11 (50%)
1	OMG	A	1625	1,46	23,26,27	1.81	8 (34%)	33,38,41	3.71	17 (51%)
1	PSU	A	3844	1	18,21,22	2.32	5 (27%)	22,30,33	4.20	13 (59%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A	3851	1	18,21,22	1.64	4 (22%)	22,30,33	4.68	16 (72%)
1	PSU	A	3729	1	18,21,22	1.85	5 (27%)	22,30,33	2.96	9 (40%)
1	PSU	A	4972	1,46	18,21,22	2.31	6 (33%)	22,30,33	4.72	14 (63%)
1	PSU	A	3884	1,46	18,21,22	2.87	10 (55%)	22,30,33	4.09	14 (63%)
1	A2M	A	4571	1	22,25,26	1.83	7 (31%)	31,36,39	3.19	16 (51%)
1	PSU	A	4552	1	18,21,22	1.83	7 (38%)	22,30,33	4.53	14 (63%)
1	OMG	A	4392	1	23,26,27	1.89	8 (34%)	33,38,41	3.26	12 (36%)
1	PSU	A	1683	1,46	18,21,22	2.86	10 (55%)	22,30,33	4.18	13 (59%)
1	OMG	A	3899	1	23,26,27	2.25	10 (43%)	33,38,41	2.56	10 (30%)
1	OMC	A	4456	1	19,22,23	1.74	5 (26%)	26,31,34	2.64	14 (53%)
1	OMG	A	4494	1	23,26,27	2.18	10 (43%)	33,38,41	3.08	14 (42%)
1	PSU	A	5001	1,46	18,21,22	1.69	5 (27%)	22,30,33	3.58	12 (54%)
1	A2M	A	2401	1	22,25,26	1.48	5 (22%)	31,36,39	3.03	18 (58%)
1	PSU	A	4293	1	18,21,22	1.53	4 (22%)	22,30,33	3.96	12 (54%)
1	6MZ	A	4220	1	22,25,26	1.53	5 (22%)	30,36,39	2.71	10 (33%)
1	OMU	A	4620	1	19,22,23	2.06	6 (31%)	26,31,34	4.12	14 (53%)
1	PSU	A	3695	1,46	18,21,22	1.88	5 (27%)	22,30,33	2.50	7 (31%)
1	A2M	A	3825	1	22,25,26	1.81	6 (27%)	31,36,39	3.20	16 (51%)
1	1MA	A	1322	1,44	21,25,26	2.27	8 (38%)	31,37,40	2.74	11 (35%)
1	OMU	A	4227	1	19,22,23	1.76	5 (26%)	26,31,34	5.63	16 (61%)
1	A2M	A	3785	1	22,25,26	1.41	4 (18%)	31,36,39	3.13	17 (54%)
1	OMG	A	1522	1	23,26,27	2.18	5 (21%)	33,38,41	3.18	17 (51%)
1	OMG	A	2364	1	23,26,27	1.95	8 (34%)	33,38,41	3.11	21 (63%)
1	OMU	A	4306	1	19,22,23	2.46	6 (31%)	26,31,34	3.34	13 (50%)
1	A2M	A	3867	1	22,25,26	2.17	7 (31%)	31,36,39	2.06	10 (32%)
1	PSU	A	1792	1,46	18,21,22	1.36	1 (5%)	22,30,33	2.27	7 (31%)
1	OMG	A	2876	1	23,26,27	1.79	3 (13%)	33,38,41	2.53	8 (24%)
1	A2M	A	1524	1	22,25,26	2.29	10 (45%)	31,36,39	2.52	9 (29%)
1	A2M	A	2787	1,46,44	22,25,26	1.67	5 (22%)	31,36,39	3.16	15 (48%)
1	PSU	A	4403	1,46	18,21,22	2.32	6 (33%)	22,30,33	3.73	10 (45%)
1	PSU	A	4296	1	18,21,22	1.80	5 (27%)	22,30,33	3.04	13 (59%)
1	OMC	A	2422	1,44	19,22,23	2.58	6 (31%)	26,31,34	9.61	12 (46%)
1	OMC	A	1340	1	19,22,23	1.45	5 (26%)	26,31,34	2.73	12 (46%)
1	OMG	A	4228	1	23,26,27	2.41	10 (43%)	33,38,41	4.77	26 (78%)
1	OMG	A	4637	1,46	23,26,27	1.68	4 (17%)	33,38,41	2.78	12 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A	4361	1,46	18,21,22	1.69	5 (27%)	22,30,33	3.92	9 (40%)
1	PSU	A	1582	1	18,21,22	1.92	3 (16%)	22,30,33	4.03	15 (68%)
1	OMG	A	3627	1	23,26,27	1.65	6 (26%)	33,38,41	2.86	15 (45%)
1	PSU	A	5010	1	18,21,22	1.49	2 (11%)	22,30,33	2.12	5 (22%)
1	PSU	A	4673	1,46	18,21,22	2.18	5 (27%)	22,30,33	4.58	13 (59%)
1	A2M	A	3724	1	22,25,26	1.47	3 (13%)	31,36,39	2.70	11 (35%)
1	PSU	A	1781	1	18,21,22	2.03	3 (16%)	22,30,33	2.83	6 (27%)
1	PSU	A	4423	1	18,21,22	1.61	2 (11%)	22,30,33	2.00	5 (22%)
1	A2M	A	1326	1	22,25,26	2.14	5 (22%)	31,36,39	3.26	13 (41%)
1	PSU	A	1677	1,46	18,21,22	3.32	11 (61%)	22,30,33	3.93	10 (45%)
1	PSU	A	1782	1	18,21,22	2.55	4 (22%)	22,30,33	3.13	9 (40%)
1	OMG	A	4499	1	23,26,27	1.41	5 (21%)	33,38,41	2.39	11 (33%)
1	UR3	A	4530	1	19,22,23	2.00	5 (26%)	26,32,35	2.91	14 (53%)
1	OMG	A	3744	1	23,26,27	1.55	6 (26%)	33,38,41	3.04	19 (57%)
1	PSU	A	3637	1,46	18,21,22	2.21	7 (38%)	22,30,33	4.12	12 (54%)
1	A2M	A	2815	1	22,25,26	1.91	5 (22%)	31,36,39	2.57	11 (35%)
1	A2M	A	1534	1,44	22,25,26	2.61	9 (40%)	31,36,39	2.65	15 (48%)
1	OMC	A	3808	1,46	19,22,23	1.24	1 (5%)	26,31,34	1.91	7 (26%)
1	5MC	A	3782	1,44	18,22,23	1.67	4 (22%)	26,32,35	1.79	4 (15%)
1	OMG	A	3792	1	23,26,27	1.59	5 (21%)	33,38,41	2.33	12 (36%)
1	OMU	A	2415	1	19,22,23	1.63	5 (26%)	26,31,34	5.14	12 (46%)
1	PSU	A	4471	1	18,21,22	1.42	5 (27%)	22,30,33	3.37	9 (40%)
1	PSU	A	4576	1	18,21,22	1.61	5 (27%)	22,30,33	3.23	12 (54%)
1	PSU	A	2839	1	18,21,22	1.77	4 (22%)	22,30,33	3.73	15 (68%)
1	OMG	A	1316	1,46	23,26,27	2.50	9 (39%)	33,38,41	2.91	15 (45%)
1	OMC	A	2861	1	19,22,23	1.53	4 (21%)	26,31,34	1.07	3 (11%)
1	A2M	A	3830	1	22,25,26	2.06	6 (27%)	31,36,39	2.96	12 (38%)
1	OMU	A	3818	1,46	19,22,23	1.93	6 (31%)	26,31,34	3.62	11 (42%)
1	OMC	A	3841	1	19,22,23	2.07	6 (31%)	26,31,34	1.96	7 (26%)
1	PSU	A	3715	1	18,21,22	1.94	4 (22%)	22,30,33	1.86	7 (31%)
1	PSU	A	3920	1,44	18,21,22	2.52	9 (50%)	22,30,33	4.23	13 (59%)
1	PSU	A	4299	1	18,21,22	2.27	6 (33%)	22,30,33	4.39	10 (45%)
3	PSU	C	69	3	18,21,22	2.05	4 (22%)	22,30,33	2.92	9 (40%)
1	PSU	A	4689	1	18,21,22	1.86	5 (27%)	22,30,33	3.06	11 (50%)
1	OMC	A	3869	1	19,22,23	2.00	6 (31%)	26,31,34	2.63	8 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	C	55	3	18,21,22	1.41	3 (16%)	22,30,33	3.59	10 (45%)
1	PSU	A	4312	1	18,21,22	1.79	6 (33%)	22,30,33	3.63	12 (54%)
1	OMC	A	2824	1	19,22,23	1.51	5 (26%)	26,31,34	2.81	13 (50%)
1	PSU	A	4457	1	18,21,22	2.02	6 (33%)	22,30,33	3.47	9 (40%)
1	PSU	A	4628	1	18,21,22	2.41	6 (33%)	22,30,33	4.28	14 (63%)
1	PSU	A	4532	1,46	18,21,22	2.86	9 (50%)	22,30,33	4.16	17 (77%)
1	PSU	A	4521	1,46,44	18,21,22	2.44	8 (44%)	22,30,33	4.68	13 (59%)
1	PSU	A	3853	1,44	18,21,22	2.65	10 (55%)	22,30,33	5.12	11 (50%)
1	A2M	A	4590	1	22,25,26	2.24	8 (36%)	31,36,39	2.60	16 (51%)
1	OMC	A	4536	1	19,22,23	2.11	9 (47%)	26,31,34	2.51	12 (46%)
1	PSU	A	4420	1	18,21,22	1.62	2 (11%)	22,30,33	2.13	6 (27%)
1	PSU	A	1862	1	18,21,22	1.70	3 (16%)	22,30,33	3.15	11 (50%)
1	OMC	A	2804	1	19,22,23	1.54	3 (15%)	26,31,34	1.91	9 (34%)
1	OMG	A	4618	1,46	23,26,27	1.89	4 (17%)	33,38,41	2.92	17 (51%)
1	A2M	A	400	1	22,25,26	1.98	6 (27%)	31,36,39	2.67	14 (45%)
1	A2M	A	3718	1	22,25,26	1.82	5 (22%)	31,36,39	2.21	13 (41%)
1	PSU	A	2508	1	18,21,22	1.97	7 (38%)	22,30,33	3.11	10 (45%)
1	PSU	A	4442	1	18,21,22	1.85	3 (16%)	22,30,33	4.30	9 (40%)
1	PSU	A	1860	1	18,21,22	1.88	3 (16%)	22,30,33	3.07	4 (18%)
1	PSU	A	1744	1,46	18,21,22	1.78	2 (11%)	22,30,33	2.71	8 (36%)
1	OMC	A	3701	1,46	19,22,23	1.49	3 (15%)	26,31,34	2.25	9 (34%)
1	A2M	A	398	1	22,25,26	1.94	3 (13%)	31,36,39	3.51	15 (48%)
1	PSU	A	4431	1,46	18,21,22	1.26	2 (11%)	22,30,33	2.49	6 (27%)
1	A2M	A	2363	1,44	22,25,26	1.84	6 (27%)	31,36,39	3.24	17 (54%)
1	5MC	A	4447	1,46	18,22,23	1.88	2 (11%)	26,32,35	3.20	14 (53%)
1	PSU	A	3639	1	18,21,22	2.56	6 (33%)	22,30,33	4.59	12 (54%)
1	OMC	A	2351	1,44	19,22,23	2.43	9 (47%)	26,31,34	2.55	13 (50%)
1	PSU	A	1536	1	18,21,22	2.70	8 (44%)	22,30,33	4.92	13 (59%)

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
1	PSU	A	4493	1,46	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMG	C	75	3	-	1/9/27/28	0/3/3/3
1	OMU	A	4498	1,46	-	0/9/27/28	0/2/2/2
1	OMC	A	2365	1,44	-	2/9/27/28	0/2/2/2
1	OMG	A	4370	1,44	-	2/9/27/28	0/3/3/3
1	OMG	A	4623	1	-	0/9/27/28	0/3/3/3
1	OMU	A	2837	1	-	0/9/27/28	0/2/2/2
1	A2M	A	1871	1,46,44	-	0/9/27/28	0/3/3/3
1	PSU	A	2632	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4500	1,46	-	3/7/25/26	0/2/2/2
1	OMC	A	3887	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4353	1,46	-	0/7/25/26	0/2/2/2
1	OMG	A	2424	1	-	2/9/27/28	0/3/3/3
1	OMU	A	3925	1	-	0/9/27/28	0/2/2/2
1	A2M	A	4523	1,44	-	0/9/27/28	0/3/3/3
1	OMG	A	4196	1,44	-	1/9/27/28	0/3/3/3
1	PSU	A	4579	1	-	0/7/25/26	0/2/2/2
1	OMG	A	1625	1,46	-	1/9/27/28	0/3/3/3
1	PSU	A	3844	1	-	1/7/25/26	0/2/2/2
1	PSU	A	3851	1	-	1/7/25/26	0/2/2/2
1	PSU	A	3729	1	-	1/7/25/26	0/2/2/2
1	PSU	A	4972	1,46	-	2/7/25/26	0/2/2/2
1	PSU	A	3884	1,46	-	0/7/25/26	0/2/2/2
1	A2M	A	4571	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4552	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4392	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1683	1,46	-	0/7/25/26	0/2/2/2
1	OMG	A	3899	1	-	0/9/27/28	0/3/3/3
1	OMC	A	4456	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4494	1	-	0/9/27/28	0/3/3/3
1	PSU	A	5001	1,46	-	1/7/25/26	0/2/2/2
1	A2M	A	2401	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4293	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	4220	1	-	0/9/27/28	0/3/3/3
1	OMU	A	4620	1	-	0/9/27/28	0/2/2/2
1	PSU	A	3695	1,46	-	0/7/25/26	0/2/2/2
1	A2M	A	3825	1	-	1/9/27/28	0/3/3/3
1	1MA	A	1322	1,44	-	1/7/25/26	0/3/3/3
1	OMU	A	4227	1	-	2/9/27/28	0/2/2/2
1	A2M	A	3785	1	-	2/9/27/28	0/3/3/3
1	OMG	A	1522	1	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	A	2364	1	-	2/9/27/28	0/3/3/3
1	OMU	A	4306	1	-	0/9/27/28	0/2/2/2
1	A2M	A	3867	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1792	1,46	-	2/7/25/26	0/2/2/2
1	OMG	A	2876	1	-	0/9/27/28	0/3/3/3
1	A2M	A	1524	1	-	3/9/27/28	0/3/3/3
1	A2M	A	2787	1,46,44	-	3/9/27/28	0/3/3/3
1	PSU	A	4403	1,46	-	0/7/25/26	0/2/2/2
1	PSU	A	4296	1	-	1/7/25/26	0/2/2/2
1	OMC	A	2422	1,44	-	1/9/27/28	0/2/2/2
1	OMC	A	1340	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4228	1	-	1/9/27/28	0/3/3/3
1	OMG	A	4637	1,46	-	0/9/27/28	0/3/3/3
1	PSU	A	4361	1,46	-	0/7/25/26	0/2/2/2
1	PSU	A	1582	1	-	1/7/25/26	0/2/2/2
1	OMG	A	3627	1	-	0/9/27/28	0/3/3/3
1	PSU	A	5010	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4673	1,46	-	0/7/25/26	0/2/2/2
1	A2M	A	3724	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1781	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4423	1	-	0/7/25/26	0/2/2/2
1	A2M	A	1326	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1677	1,46	-	1/7/25/26	0/2/2/2
1	PSU	A	1782	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4499	1	-	0/9/27/28	0/3/3/3
1	UR3	A	4530	1	-	1/7/25/26	0/2/2/2
1	OMG	A	3744	1	-	0/9/27/28	0/3/3/3
1	PSU	A	3637	1,46	-	0/7/25/26	0/2/2/2
1	A2M	A	2815	1	-	3/9/27/28	0/3/3/3
1	A2M	A	1534	1,44	-	2/9/27/28	0/3/3/3
1	OMC	A	3808	1,46	-	1/9/27/28	0/2/2/2
1	5MC	A	3782	1,44	-	0/7/25/26	0/2/2/2
1	OMG	A	3792	1	-	0/9/27/28	0/3/3/3
1	OMU	A	2415	1	-	1/9/27/28	0/2/2/2
1	PSU	A	4471	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4576	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2839	1	-	2/7/25/26	0/2/2/2
1	OMG	A	1316	1,46	-	0/9/27/28	0/3/3/3
1	OMC	A	2861	1	-	0/9/27/28	0/2/2/2
1	A2M	A	3830	1	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	A	3818	1,46	-	1/9/27/28	0/2/2/2
1	OMC	A	3841	1	-	0/9/27/28	0/2/2/2
1	PSU	A	3715	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3920	1,44	-	0/7/25/26	0/2/2/2
1	PSU	A	4299	1	-	0/7/25/26	0/2/2/2
3	PSU	C	69	3	-	0/7/25/26	0/2/2/2
1	PSU	A	4689	1	-	1/7/25/26	0/2/2/2
1	OMC	A	3869	1	-	1/9/27/28	0/2/2/2
3	PSU	C	55	3	-	0/7/25/26	0/2/2/2
1	PSU	A	4312	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2824	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4457	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4628	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4532	1,46	-	0/7/25/26	0/2/2/2
1	PSU	A	4521	1,46,44	-	0/7/25/26	0/2/2/2
1	PSU	A	3853	1,44	-	0/7/25/26	0/2/2/2
1	A2M	A	4590	1	-	1/9/27/28	0/3/3/3
1	OMC	A	4536	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4420	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1862	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2804	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4618	1,46	-	0/9/27/28	0/3/3/3
1	A2M	A	400	1	-	1/9/27/28	0/3/3/3
1	A2M	A	3718	1	-	1/9/27/28	0/3/3/3
1	PSU	A	2508	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4442	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1860	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1744	1,46	-	0/7/25/26	0/2/2/2
1	OMC	A	3701	1,46	-	5/9/27/28	0/2/2/2
1	A2M	A	398	1	-	1/9/27/28	0/3/3/3
1	PSU	A	4431	1,46	-	0/7/25/26	0/2/2/2
1	A2M	A	2363	1,44	-	0/9/27/28	0/3/3/3
1	5MC	A	4447	1,46	-	4/7/25/26	0/2/2/2
1	PSU	A	3639	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2351	1,44	-	2/9/27/28	0/2/2/2
1	PSU	A	1536	1	-	0/7/25/26	0/2/2/2

The worst 5 of 631 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1782	PSU	C6-C5	8.00	1.44	1.35
1	A	1677	PSU	C2'-C1'	-7.78	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2422	OMC	C5-C4	7.46	1.60	1.42
1	A	4623	OMG	C6-N1	-7.14	1.25	1.38
1	A	4353	PSU	C2-N3	-6.82	1.25	1.37

The worst 5 of 1395 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2422	OMC	N4-C4-N3	-27.53	69.65	117.97
1	A	2422	OMC	C4-N3-C2	-23.05	83.03	120.25
1	A	4493	PSU	C4-N3-C2	-19.76	97.87	126.34
1	A	2422	OMC	C5-C4-N4	18.62	149.88	120.57
1	A	4493	PSU	N1-C2-N3	16.91	134.29	115.13

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	400	A2M	C1'-C2'-O2'-CM'
1	A	1582	PSU	C3'-C4'-C5'-O5'
1	A	1625	OMG	C3'-C2'-O2'-CM2
1	A	2415	OMU	C1'-C2'-O2'-CM2
1	A	2424	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

52 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	75	OMG	3	0
1	A	4498	OMU	1	0
1	A	4370	OMG	2	0
1	A	1871	A2M	3	0
1	A	2632	PSU	1	0
1	A	3887	OMC	1	0
1	A	3925	OMU	2	0
1	A	4196	OMG	1	0
1	A	4579	PSU	1	0
1	A	3851	PSU	1	0
1	A	4571	A2M	2	0
1	A	4392	OMG	2	0
1	A	4494	OMG	1	0
1	A	5001	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	2401	A2M	1	0
1	A	1322	1MA	1	0
1	A	4227	OMU	4	0
1	A	3785	A2M	1	0
1	A	3867	A2M	2	0
1	A	2876	OMG	1	0
1	A	1524	A2M	1	0
1	A	2787	A2M	3	0
1	A	4403	PSU	1	0
1	A	2422	OMC	1	0
1	A	1340	OMC	1	0
1	A	4228	OMG	14	0
1	A	4637	OMG	1	0
1	A	3627	OMG	1	0
1	A	5010	PSU	1	0
1	A	1781	PSU	1	0
1	A	4423	PSU	1	0
1	A	1677	PSU	1	0
1	A	1782	PSU	1	0
1	A	4530	UR3	2	0
1	A	2815	A2M	1	0
1	A	1534	A2M	3	0
1	A	2415	OMU	1	0
1	A	2839	PSU	1	0
1	A	2861	OMC	2	0
1	A	3830	A2M	1	0
1	A	3818	OMU	1	0
1	A	4532	PSU	1	0
1	A	4521	PSU	1	0
1	A	4590	A2M	3	0
1	A	4420	PSU	1	0
1	A	1862	PSU	2	0
1	A	400	A2M	1	0
1	A	3718	A2M	2	0
1	A	1860	PSU	5	0
1	A	398	A2M	2	0
1	A	4431	PSU	2	0
1	A	2351	OMC	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 386 ligands modelled in this entry, 386 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	4273:A	O3'	4274:A	P	1.83
1	A	3823:G	O3'	3824:A	P	1.77

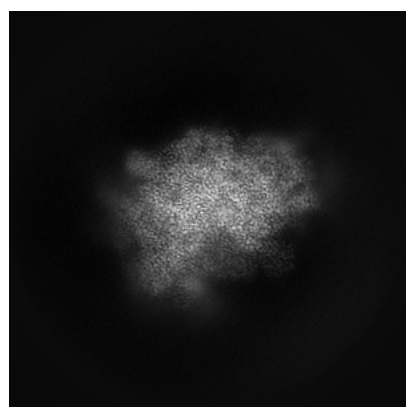
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13094. These allow visual inspection of the internal detail of the map and identification of artifacts.

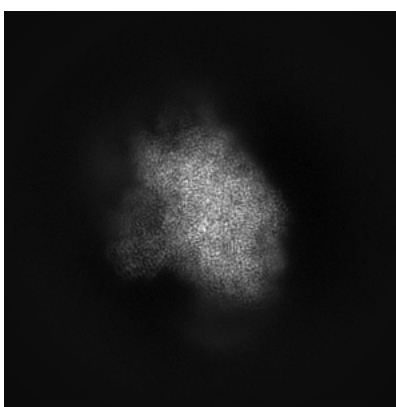
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

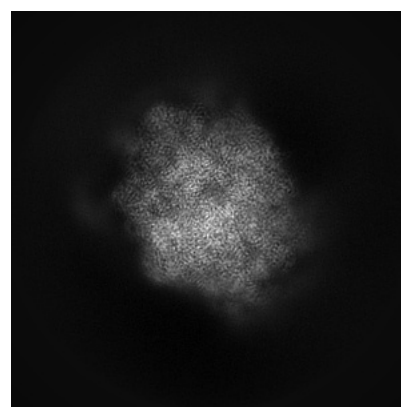
6.1.1 Primary map



X



Y

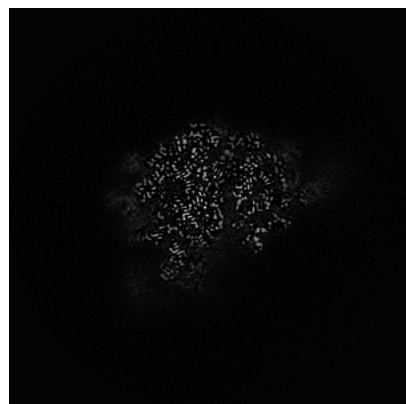


Z

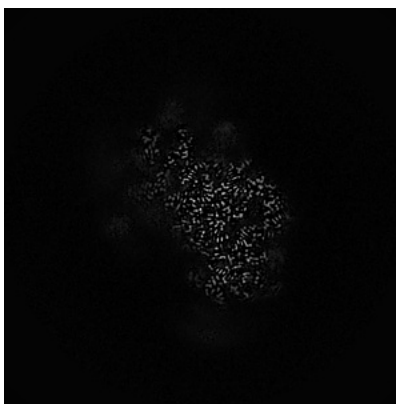
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

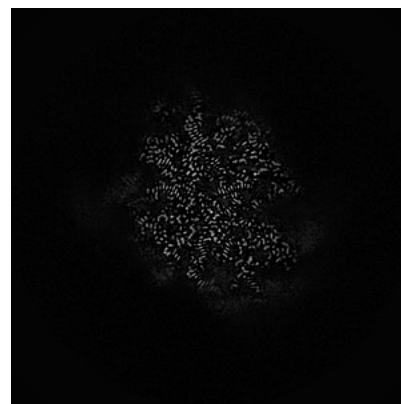
6.2.1 Primary map



X Index: 256



Y Index: 256

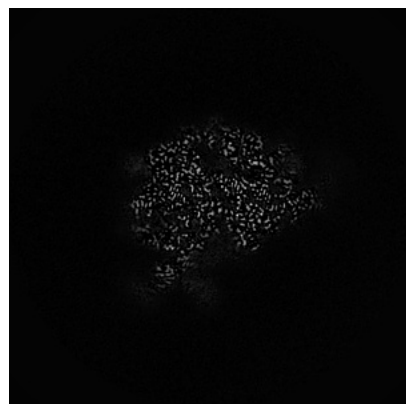


Z Index: 256

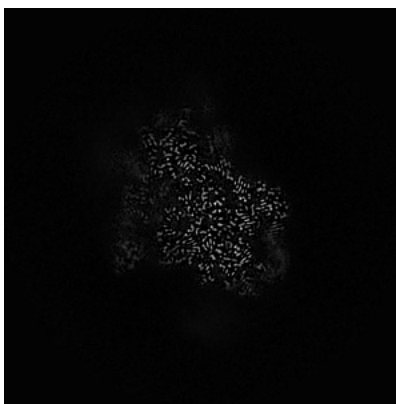
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

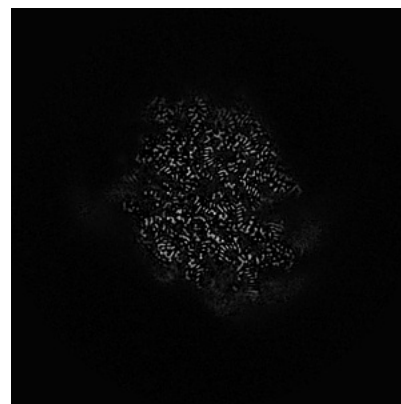
6.3.1 Primary map



X Index: 239



Y Index: 238

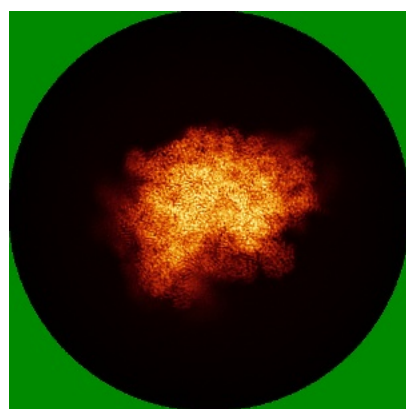


Z Index: 261

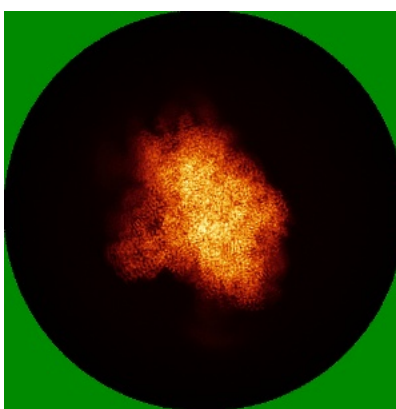
The images above show the largest variance slices of the map in three orthogonal directions.

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

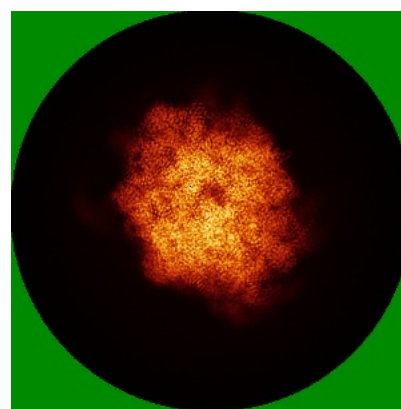
6.4.1 Primary map



X



Y

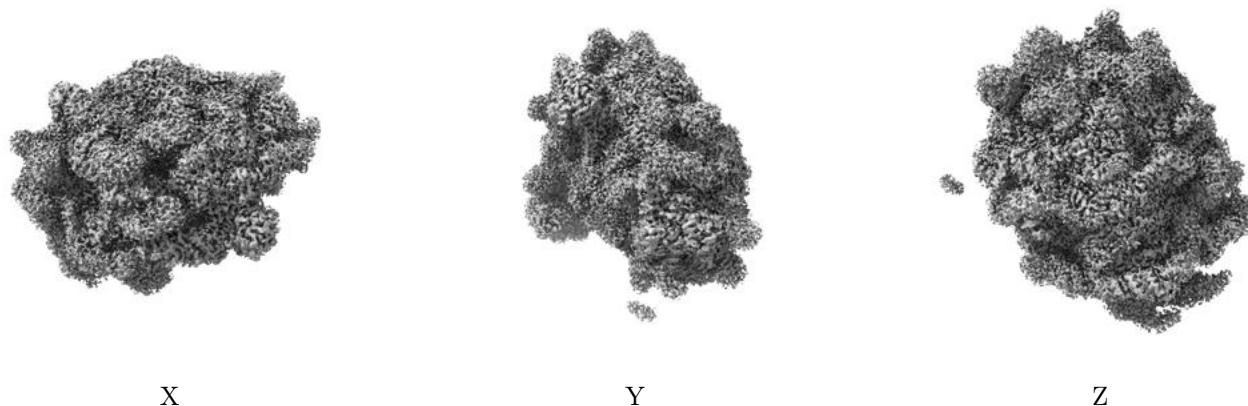


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

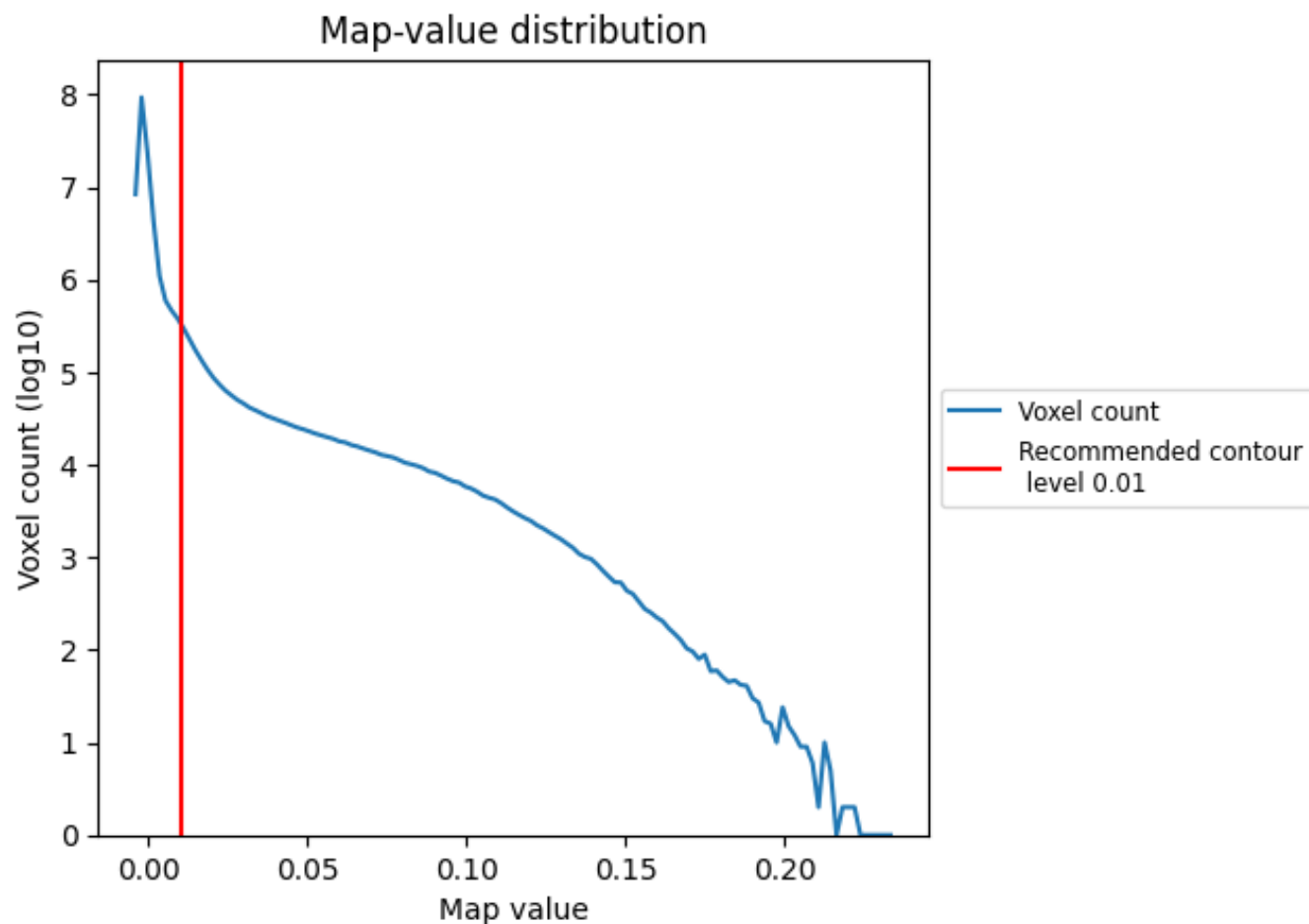
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

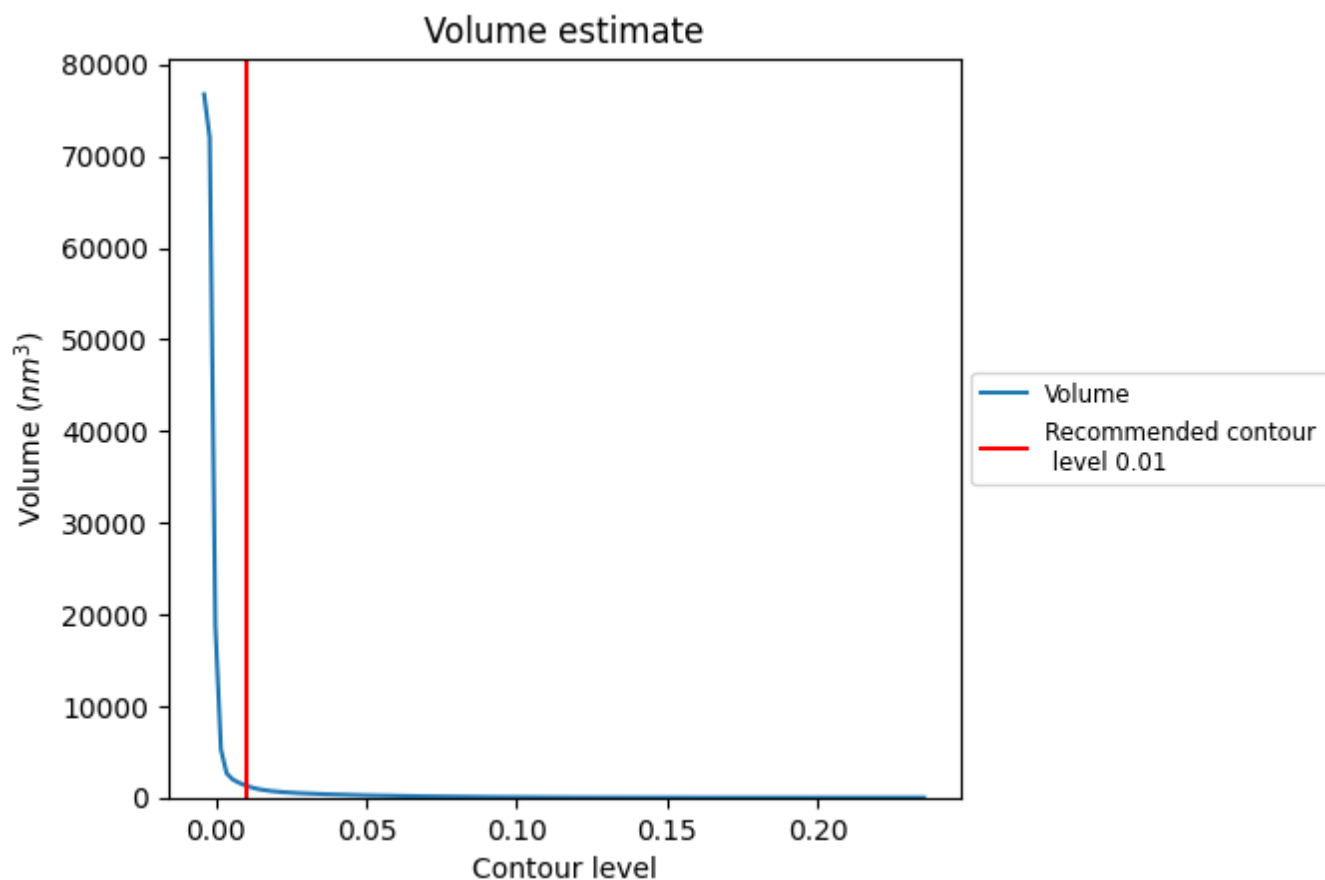
This section contains the results of statistical analysis of the map.

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.

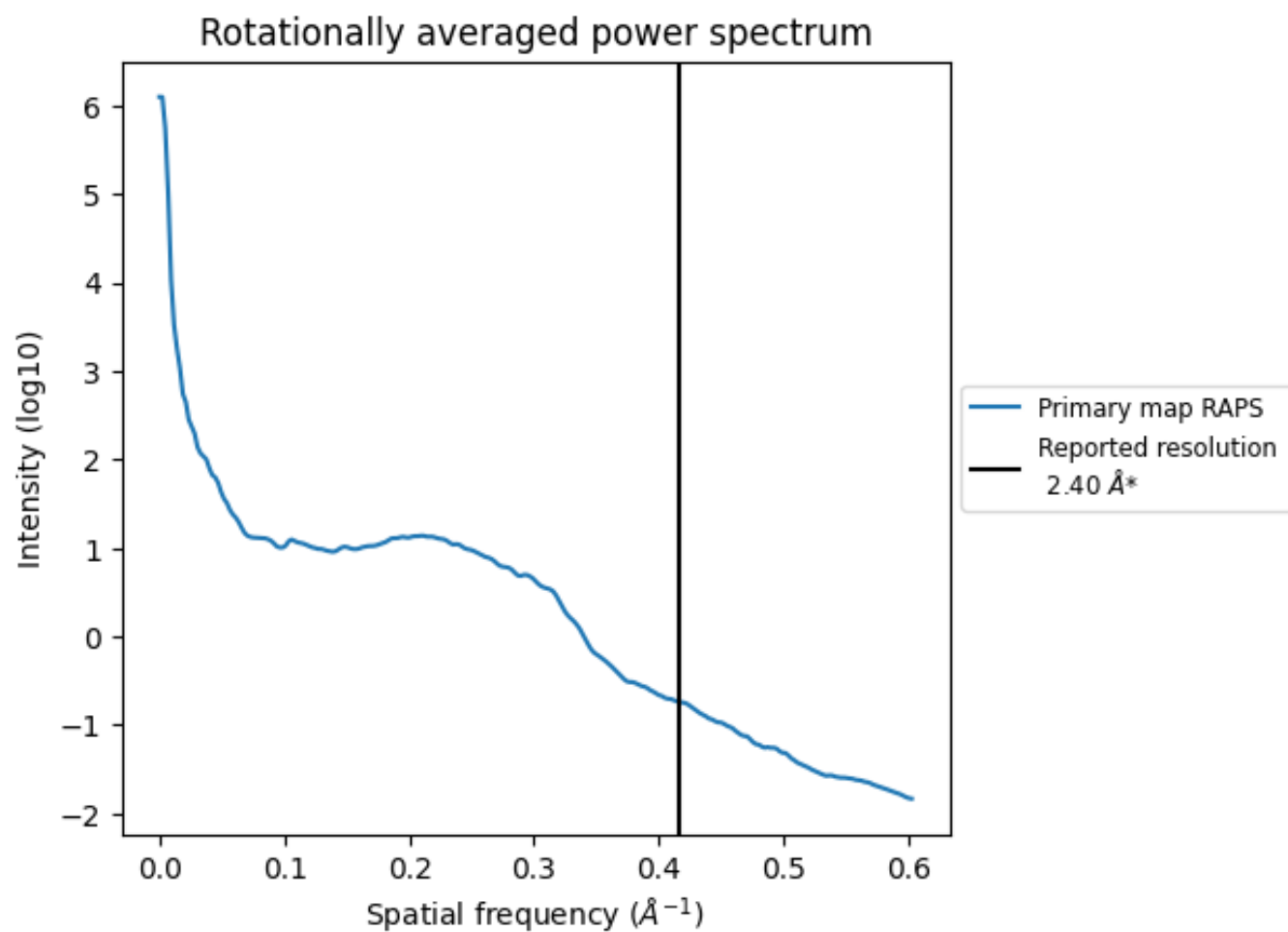
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1295 nm³; this corresponds to an approximate mass of 1170 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 ⓘ

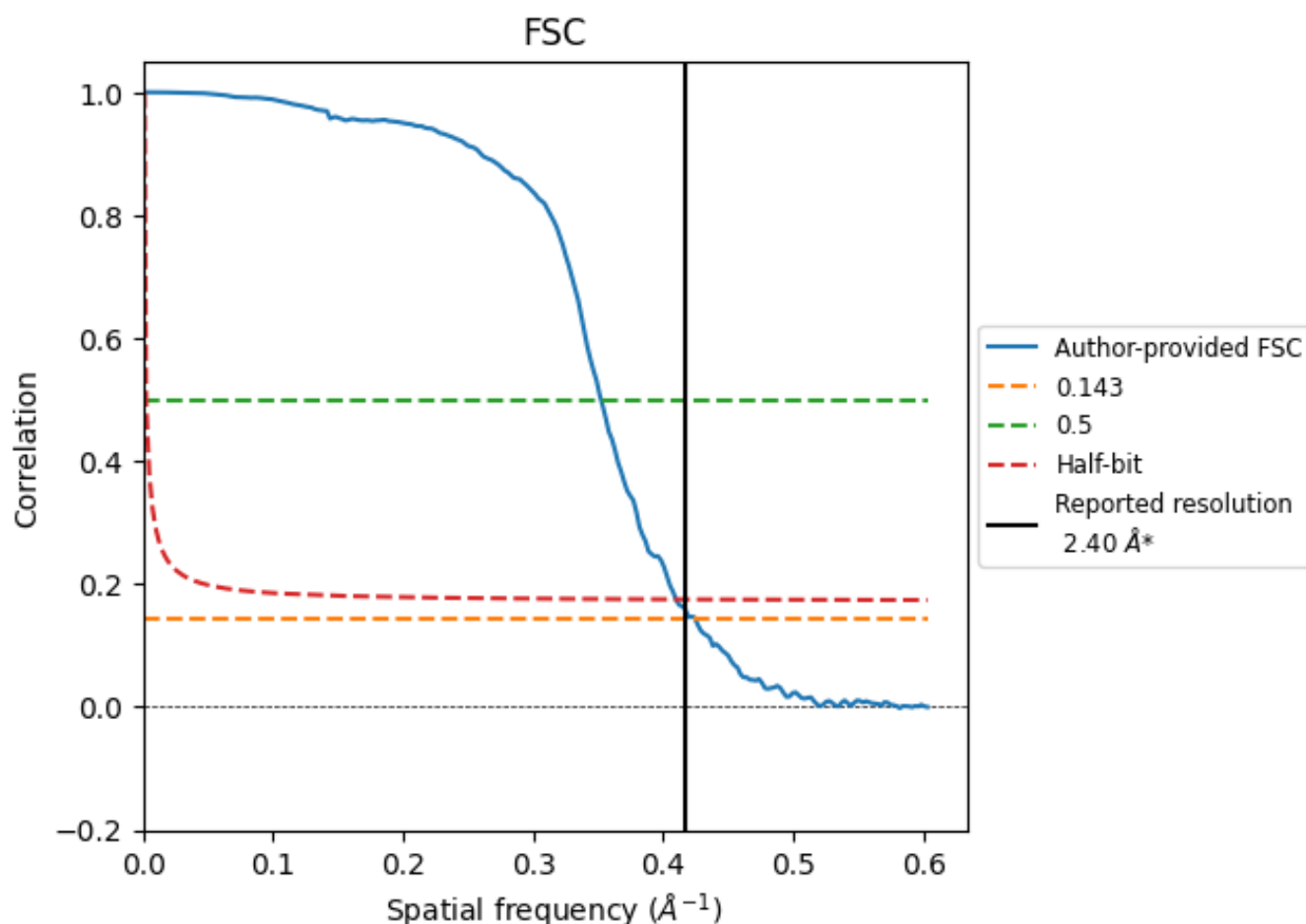


*Reported resolution corresponds to spatial frequency of 0.417 $\text{\AA}^{-1}$

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 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

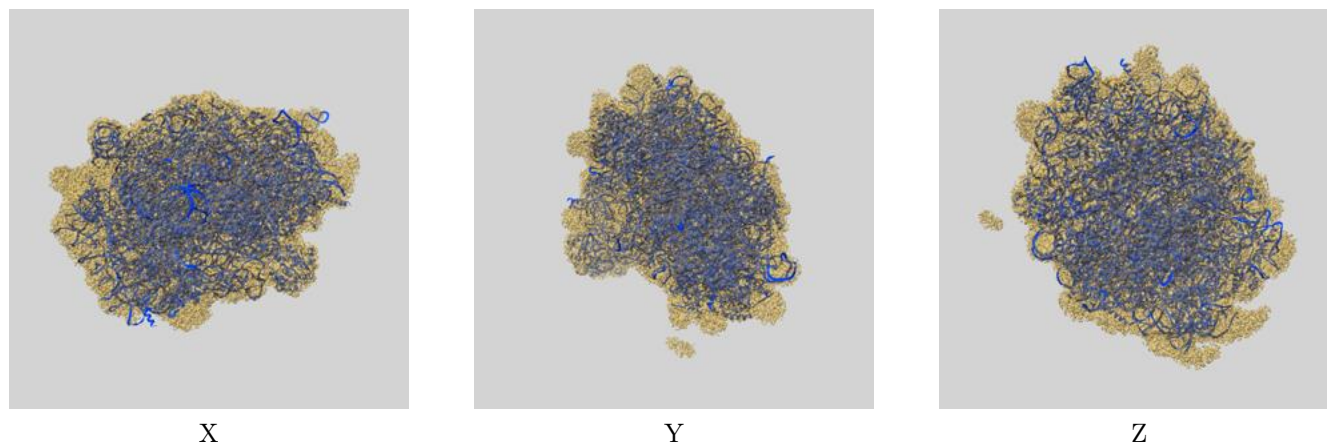
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.36	2.84	2.44
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

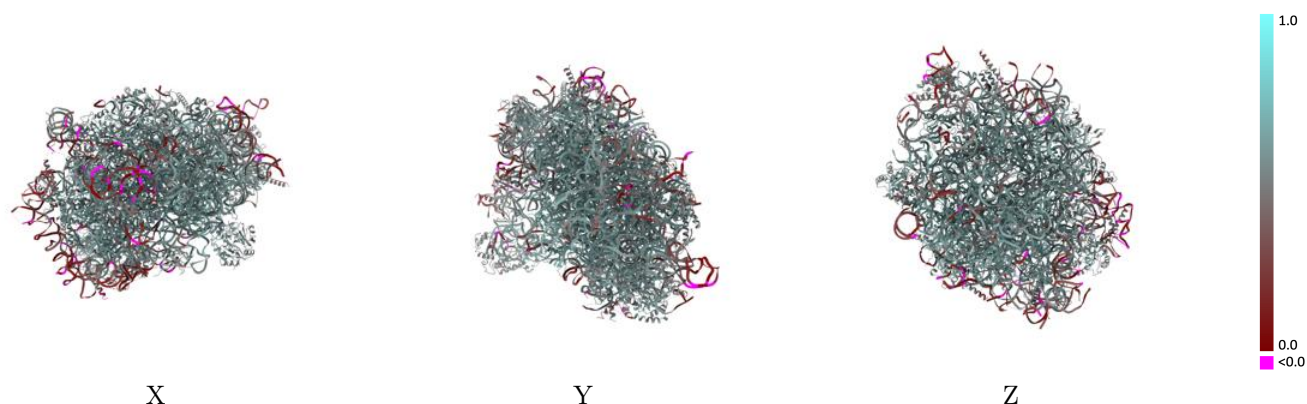
This section contains information regarding the fit between EMDB map EMD-13094 and PDB model 7OW7. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



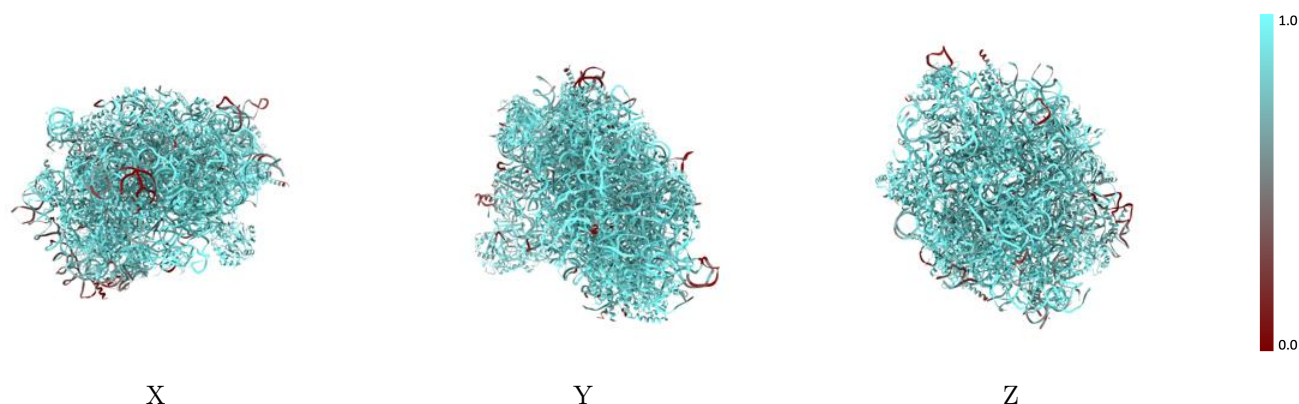
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



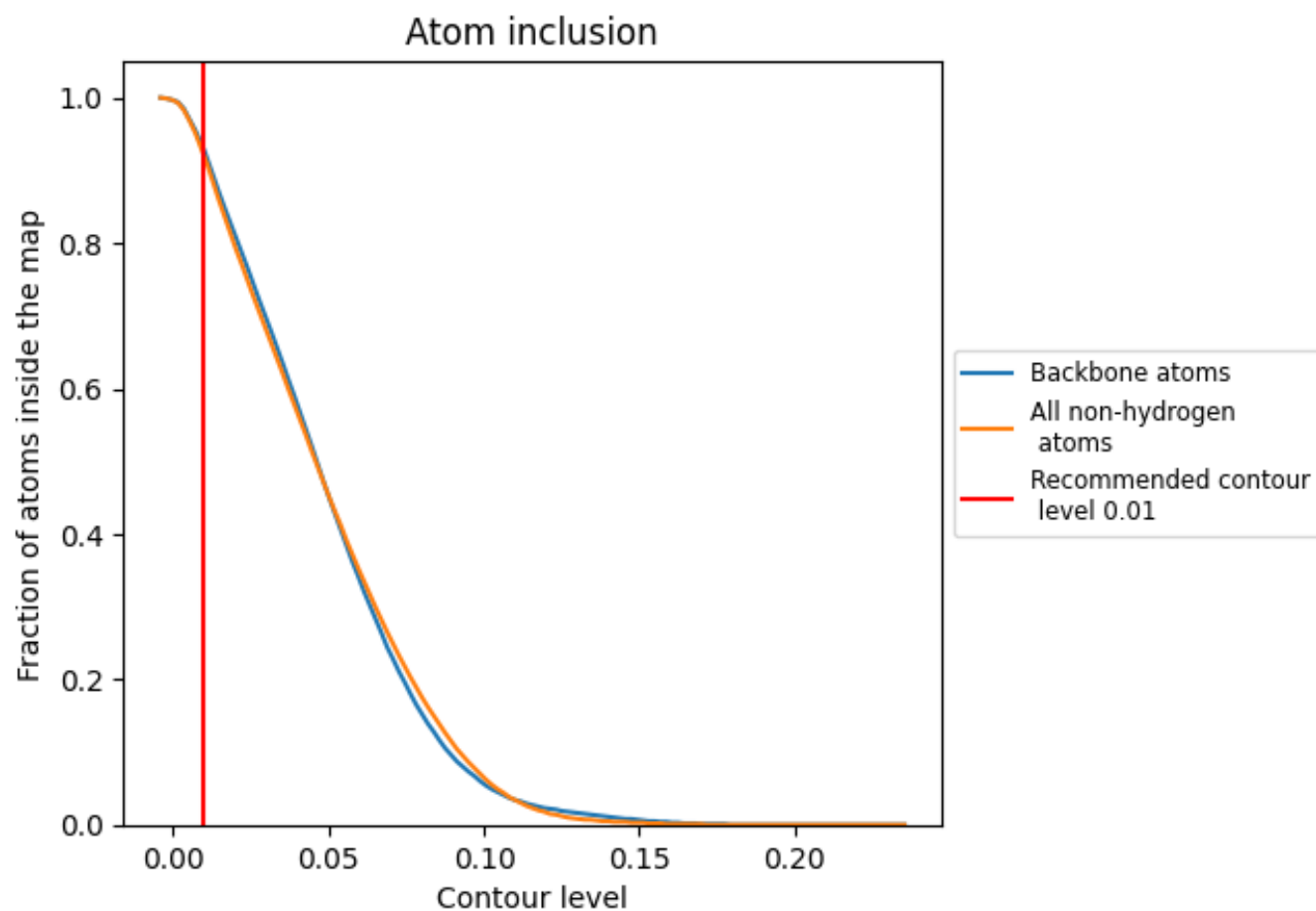
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.5390
A	 0.9100	 0.5170
B	 0.9820	 0.5800
C	 0.9720	 0.5680
D	 0.9800	 0.6120
E	 0.9510	 0.5750
F	 0.9700	 0.6060
G	 0.8790	 0.5420
H	 0.9240	 0.5500
I	 0.9510	 0.5810
J	 0.9710	 0.5870
K	 0.9790	 0.6260
L	 0.8900	 0.5270
M	 0.9660	 0.5890
N	 0.9530	 0.5920
P	 0.8820	 0.5290
Q	 0.9610	 0.5910
R	 0.9480	 0.5570
S	 0.9240	 0.5500
T	 0.8980	 0.5210
U	 0.9720	 0.6220
V	 0.8640	 0.5150
W	 0.9100	 0.5350
X	 0.9350	 0.5560
Y	 0.9750	 0.6060
Z	 0.9820	 0.6150
a	 0.9150	 0.5470
b	 0.9180	 0.5540
c	 0.8900	 0.5400
d	 0.9750	 0.6080
e	 0.7390	 0.4490
f	 0.9460	 0.5630
i	 0.9300	 0.5710
j	 0.9330	 0.5590
k	 0.9710	 0.6020



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Chain	Atom inclusion	Q-score
m	 0.9660	 0.6060
n	 0.9040	 0.5520
o	 0.9030	 0.5300
p	 0.7930	 0.4490
q	 0.8100	 0.4810
r	 0.9200	 0.5760
s	 0.9150	 0.5410
t	 0.9880	 0.6240
u	 0.9220	 0.5420