



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:29 PM UTC

PDB ID : 5UYP / pdb_00005uyp
EMDB ID : EMD-8619
Title : 70S ribosome bound with near-cognate ternary complex base-paired to A site codon, open 30S (Structure II-nc)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.90 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:

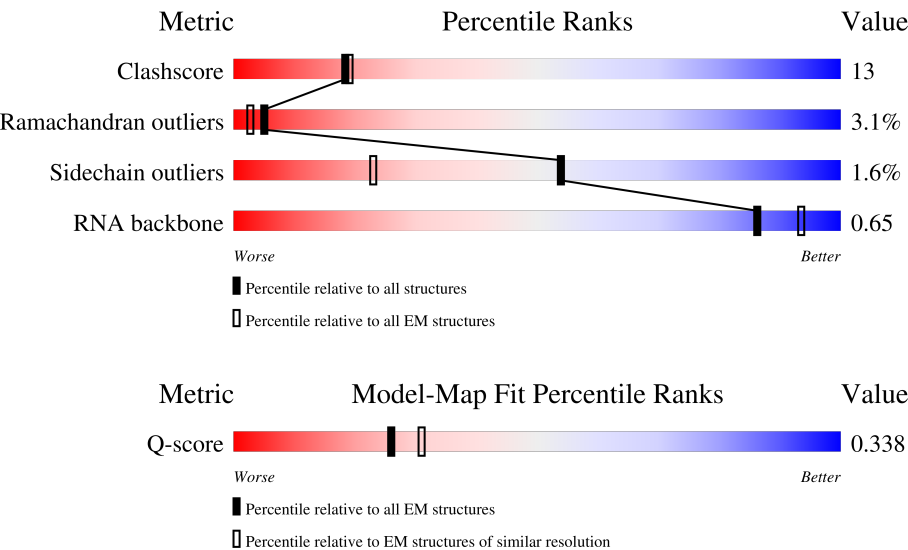
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.90 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.



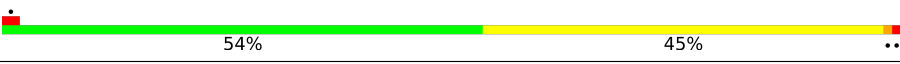
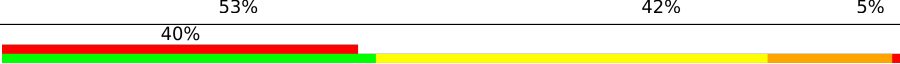
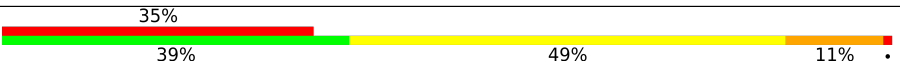
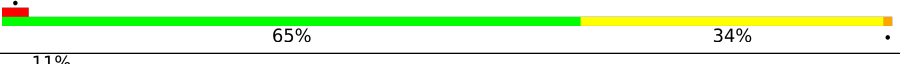
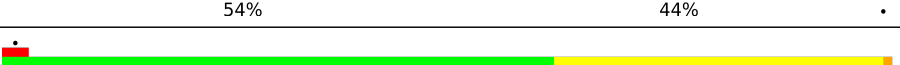
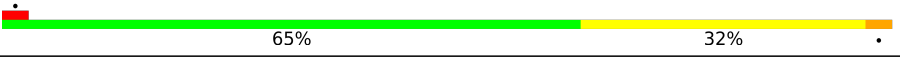
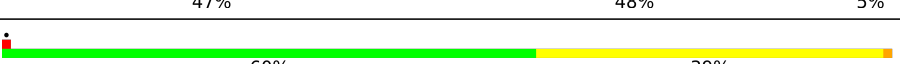
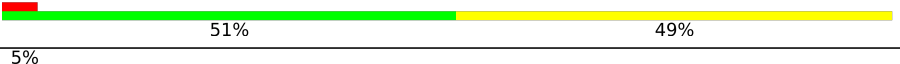
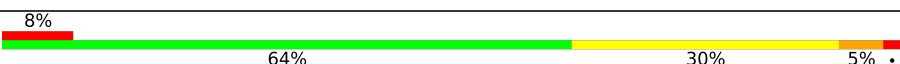
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	04	271	56% 41%
2	05	209	63% 36%
3	06	201	5% 65% 32%

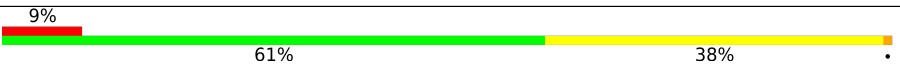
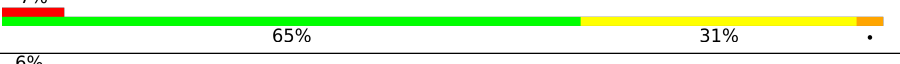
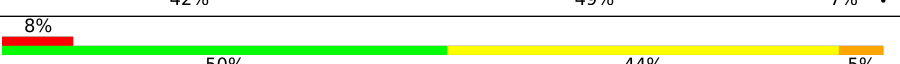
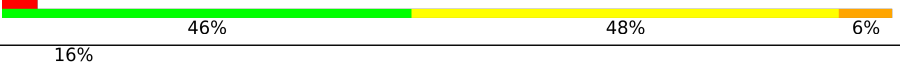
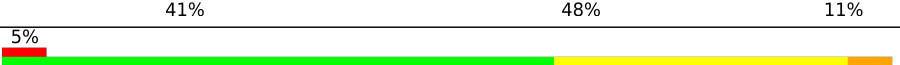
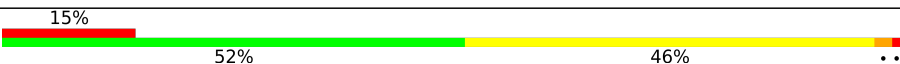
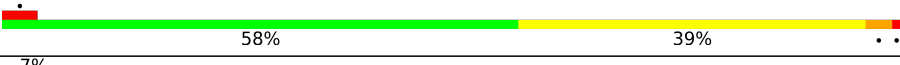
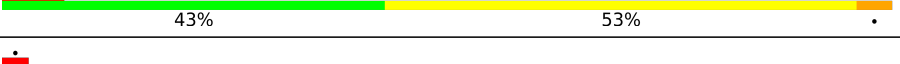
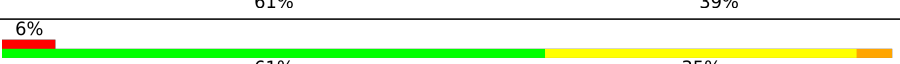
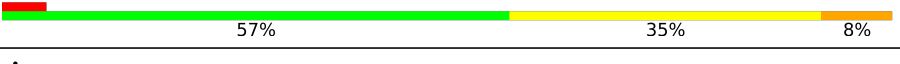
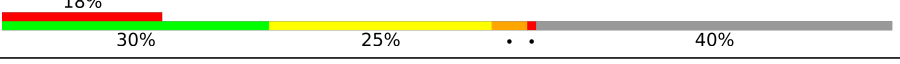
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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	19	
58	Y	76	
59	Z	392	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 153780 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	22	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	19	Total	C	N	O	P	0	0
			417	188	89	122	18		

- Molecule 58 is a RNA chain called tRNA^{Lys}.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Y	76	Total	C	N	O	P	S	0	0
			1618	723	282	536	76	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	34	U8U	-	insertion	GB 558570689

- Molecule 59 is a protein called Elongation factor Tu 2.

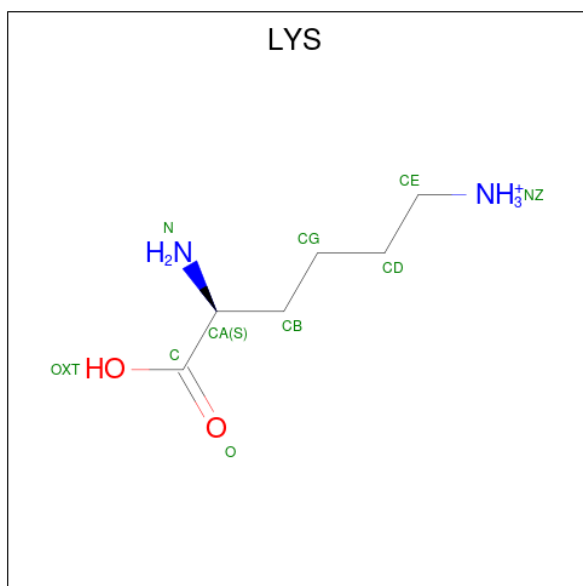
Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



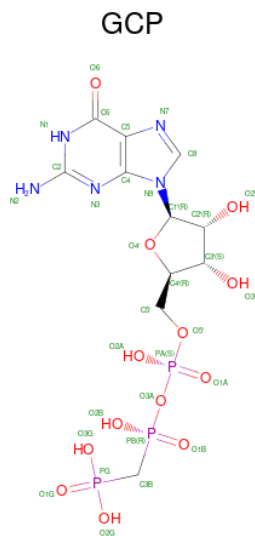
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	W	1	10	6	1	2	1	0

- Molecule 61 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
61	Y	1	9	6	2	1	0

- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

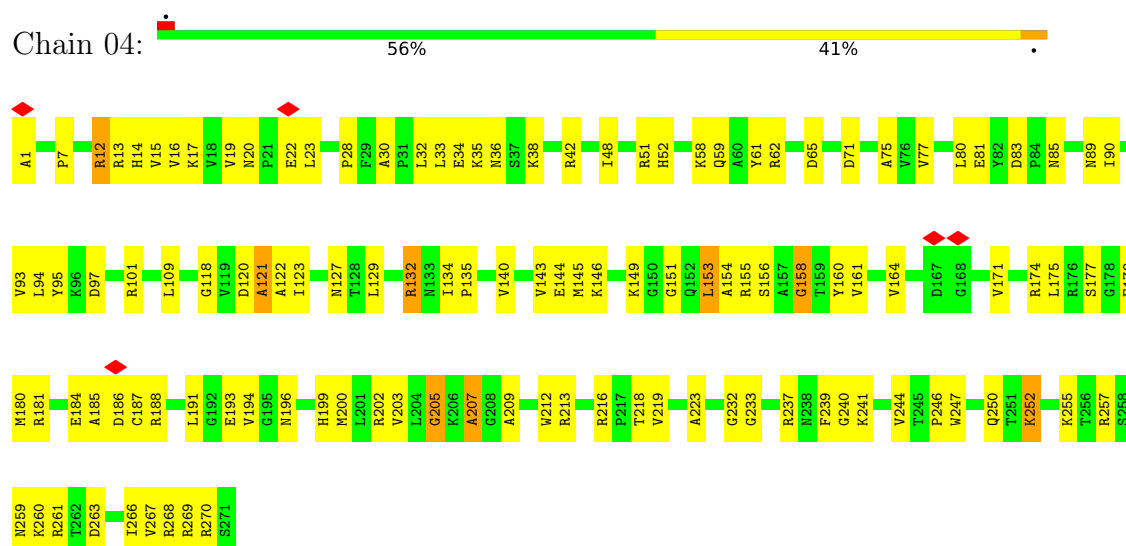


Mol	Chain	Residues	Atoms					AltConf
62	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

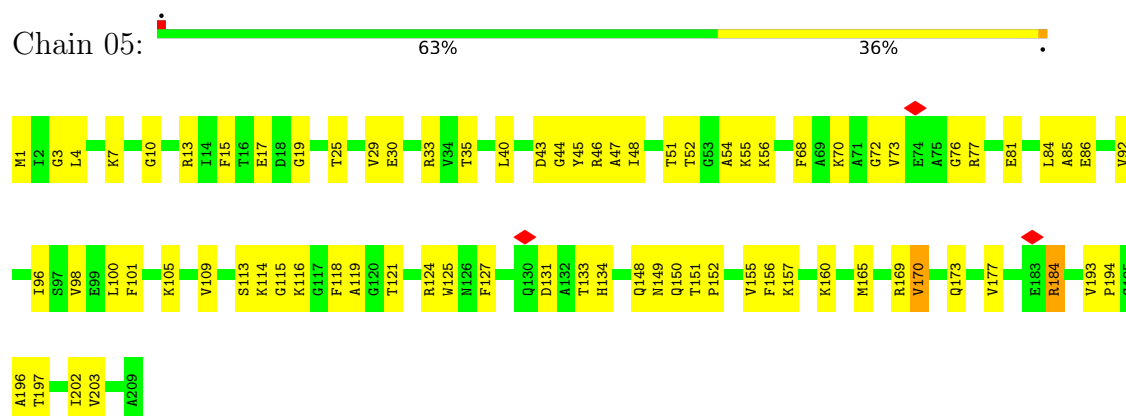
3 Residue-property plots

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: 50S ribosomal protein L2

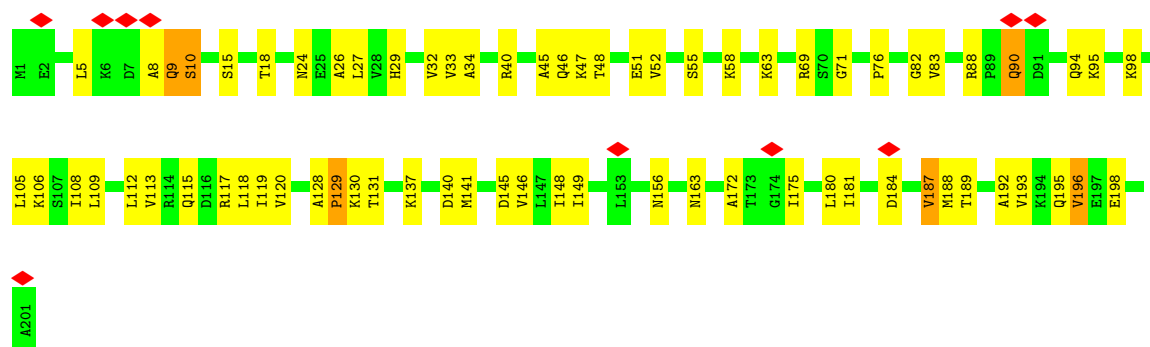


• Molecule 2: 50S ribosomal protein L3



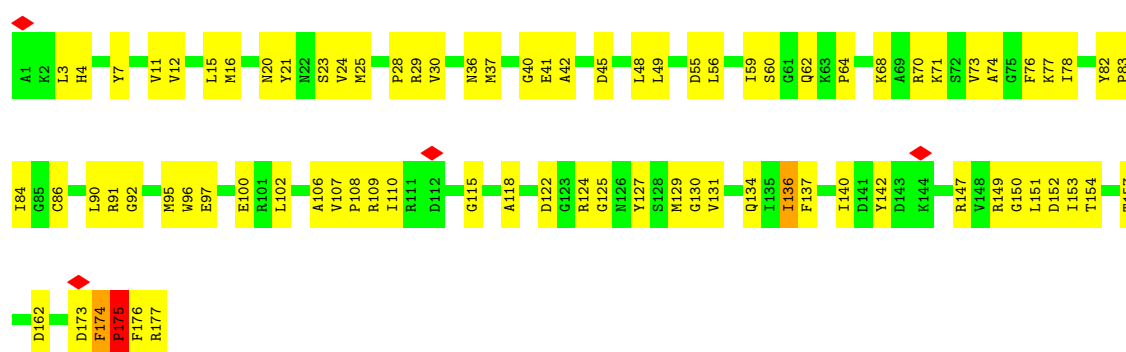
• Molecule 3: 50S ribosomal protein L4





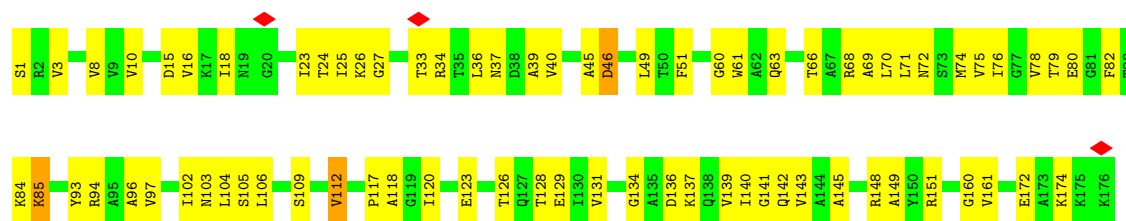
• Molecule 4: 50S ribosomal protein L5

Chain 07: 54% 45% ..



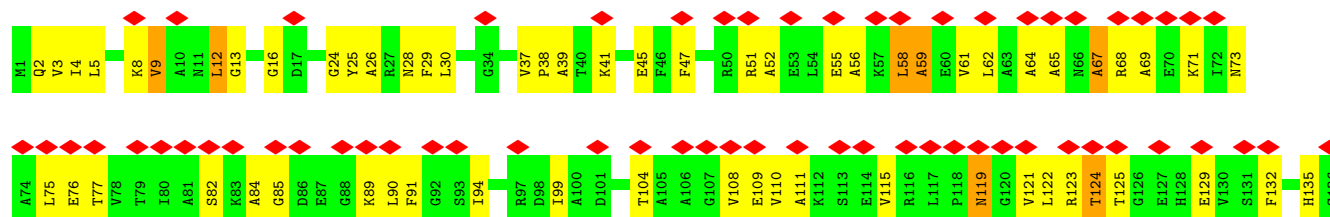
• Molecule 5: 50S ribosomal protein L6

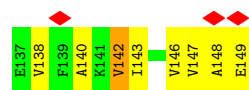
Chain 08: 57% 41% .



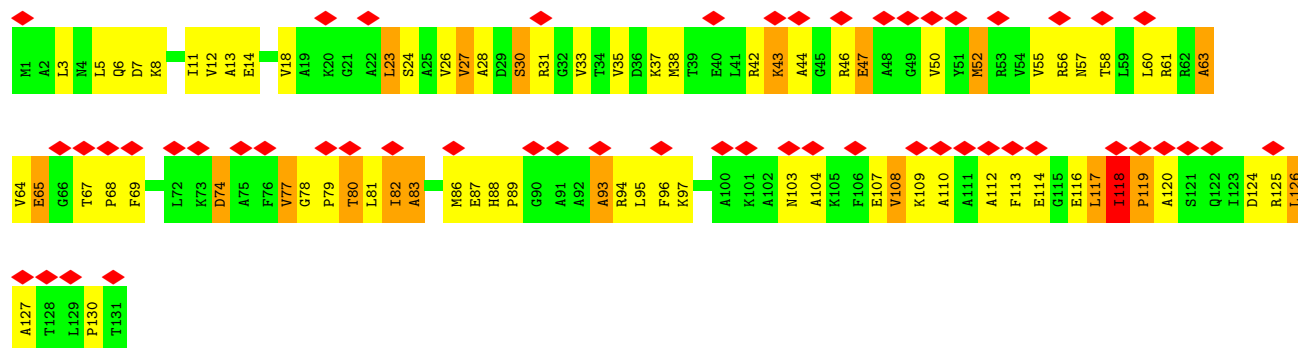
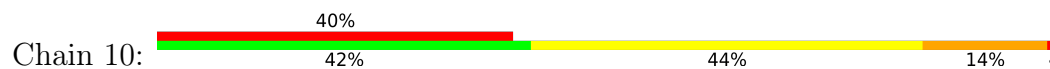
• Molecule 6: 50S ribosomal protein L9

Chain 09: 44% 53% 42% 5%

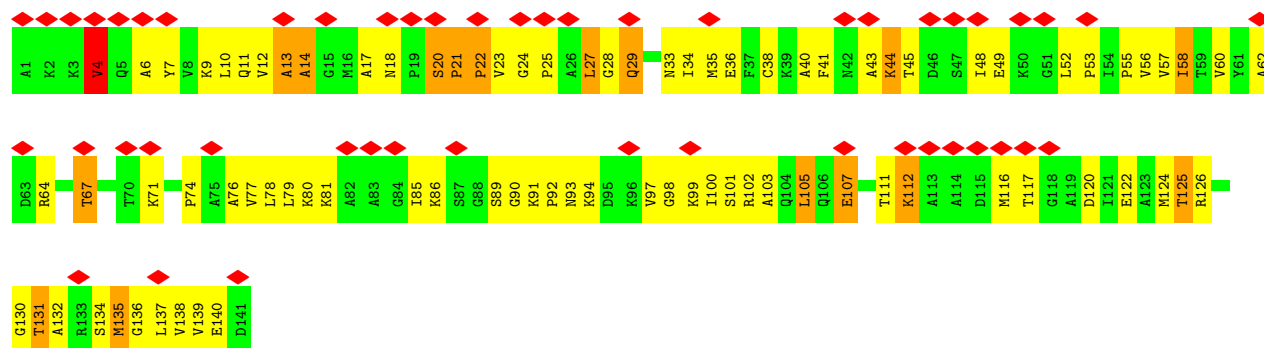




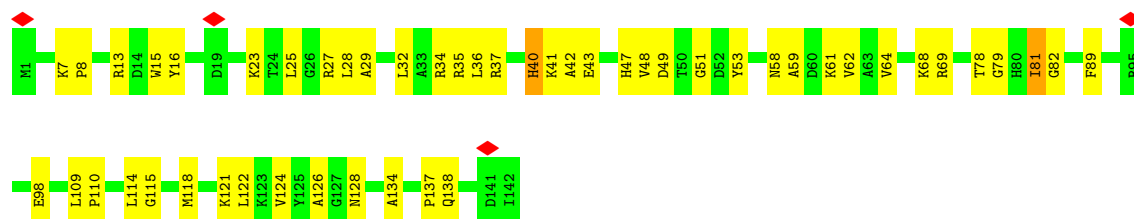
• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11

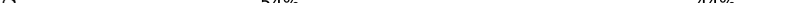


• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14



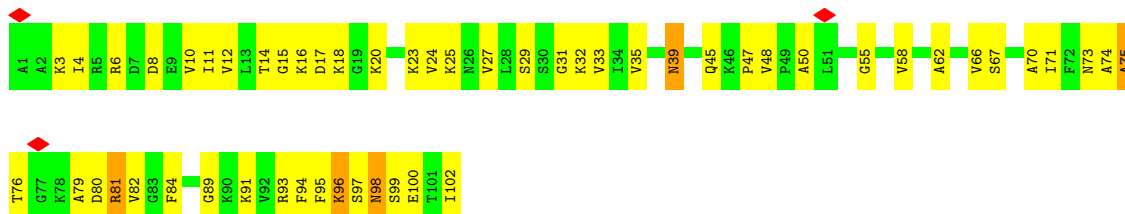
- Chain 18:  54% 44%





- Molecule 20: 50S ribosomal protein L24

Chain 23: 47% 48% 5%



- Molecule 21: 50S ribosomal protein L25

Chain 24: 60% 39% .



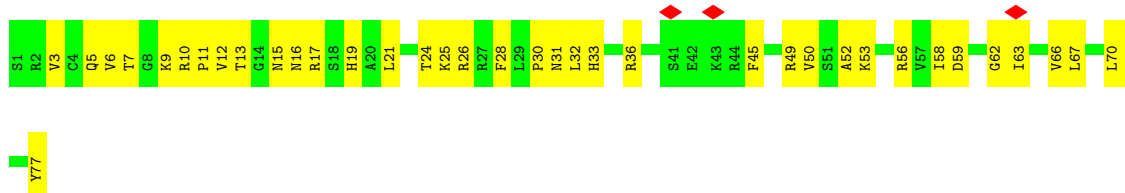
- Molecule 22: 50S ribosomal protein L27

Chain 25: 5% 65% 33% .



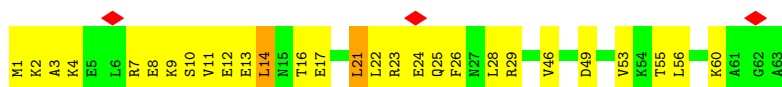
- Molecule 23: 50S ribosomal protein L28

Chain 26: 51% 49%

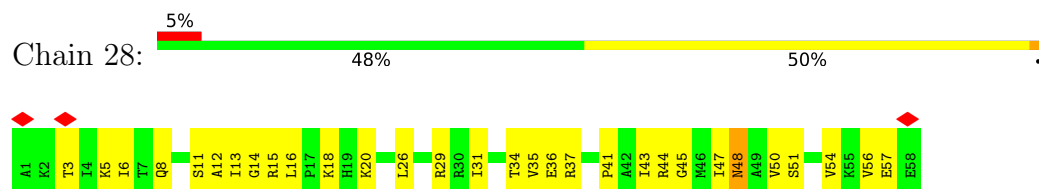


- Molecule 24: 50S ribosomal protein L29

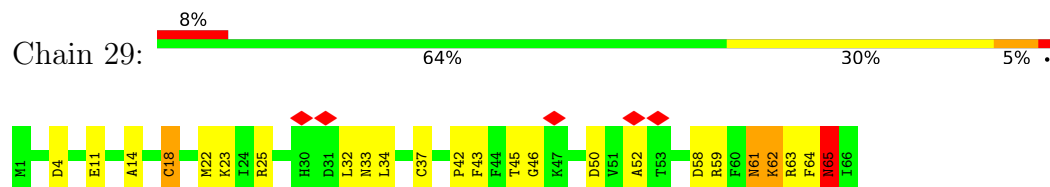
Chain 27: 5% 56% 41% .



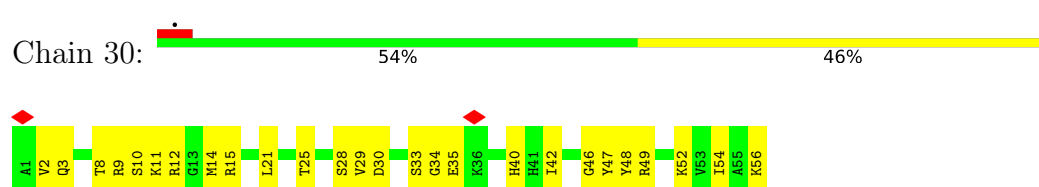
- Molecule 25: 50S ribosomal protein L30



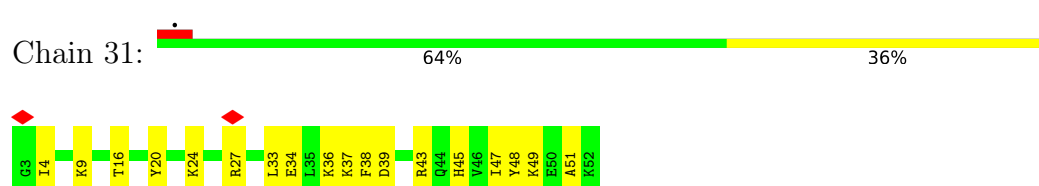
- Molecule 26: 50S ribosomal protein L31



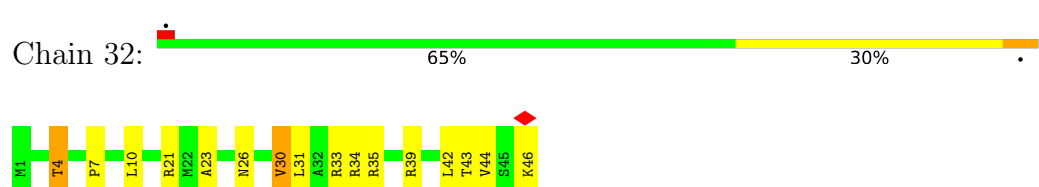
- Molecule 27: 50S ribosomal protein L32



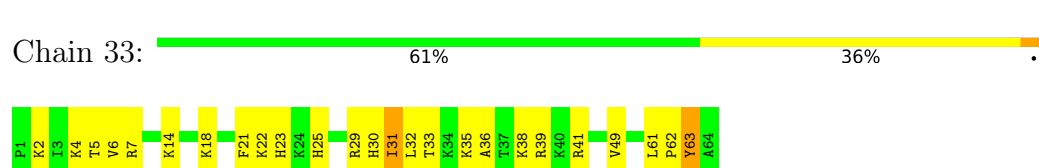
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35

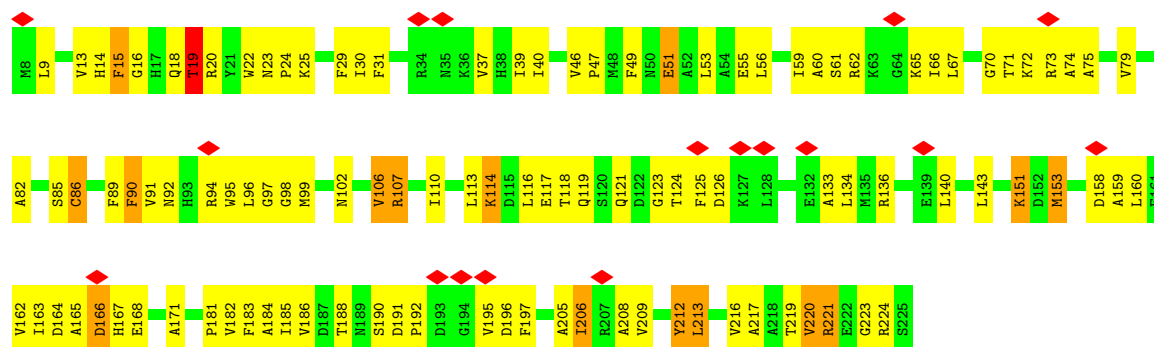


- Molecule 31: 50S ribosomal protein L36

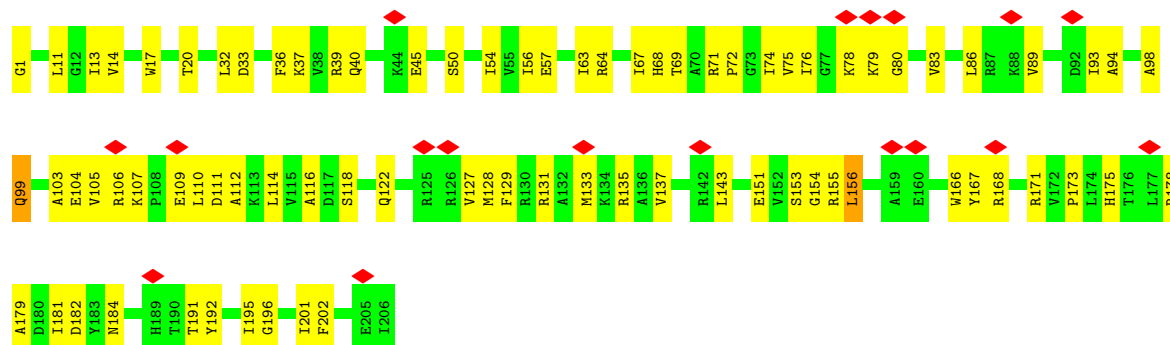




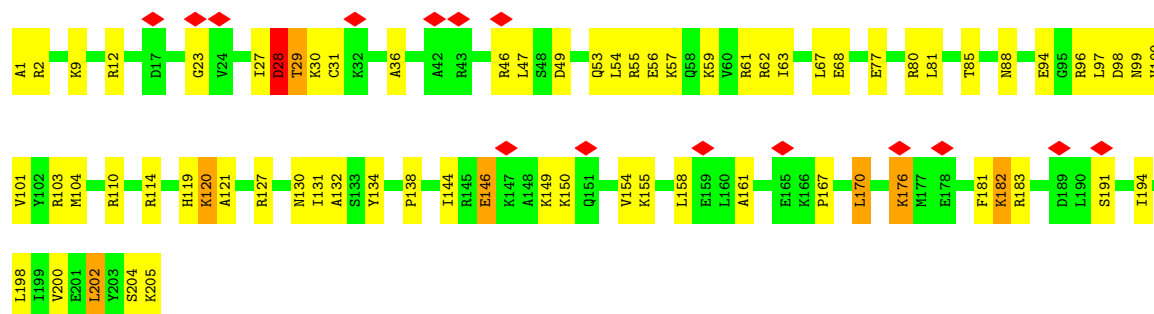
• Molecule 32: 30S ribosomal protein S2



• Molecule 33: 30S ribosomal protein S3

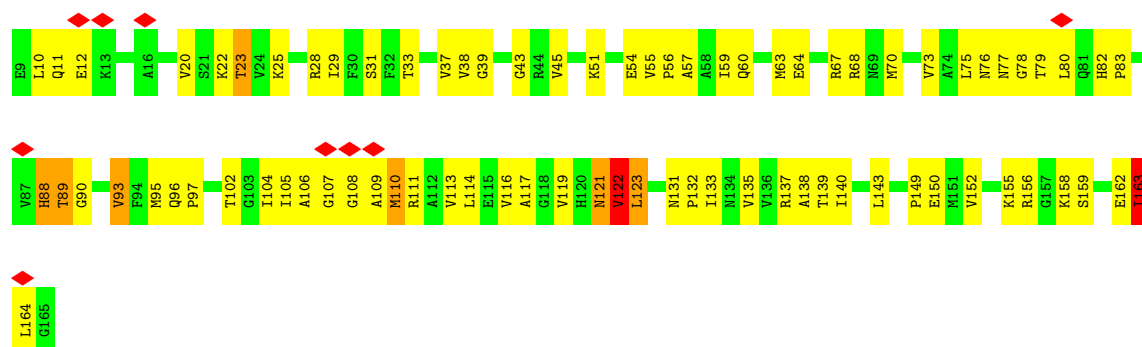


• Molecule 34: 30S ribosomal protein S4



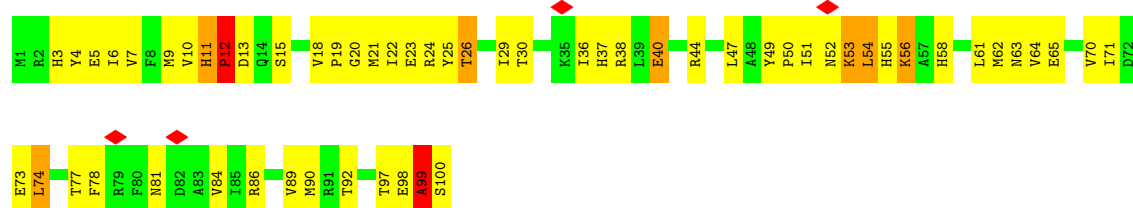
• Molecule 35: 30S ribosomal protein S5





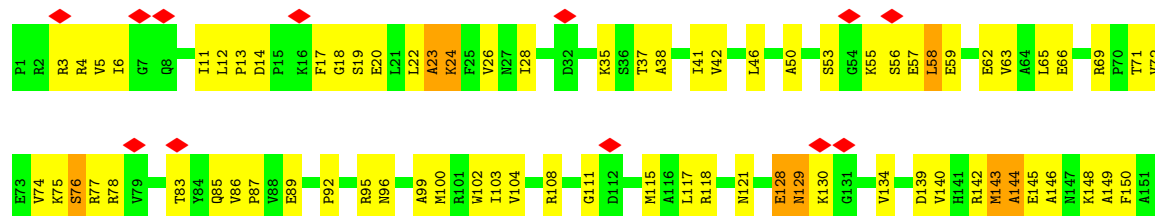
- Molecule 36: 30S ribosomal protein S6

Chain F: 42% 49% 7%



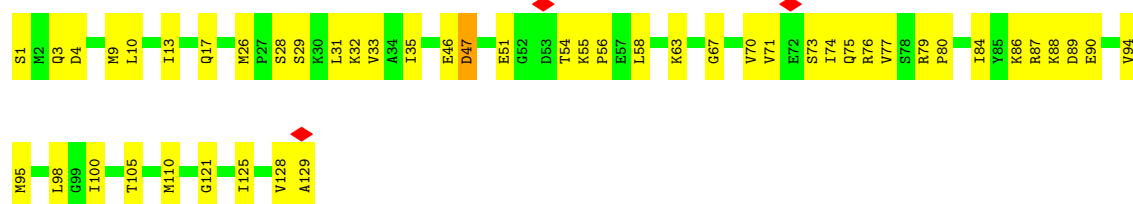
- Molecule 37: 30S ribosomal protein S7

Chain G: 8% 50% 44% 5%



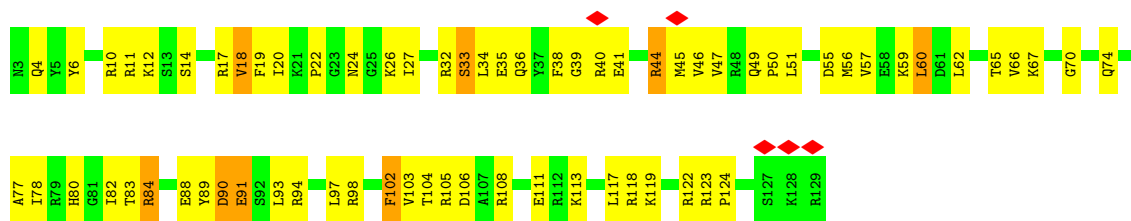
- Molecule 38: 30S ribosomal protein S8

Chain H: 63% 36%

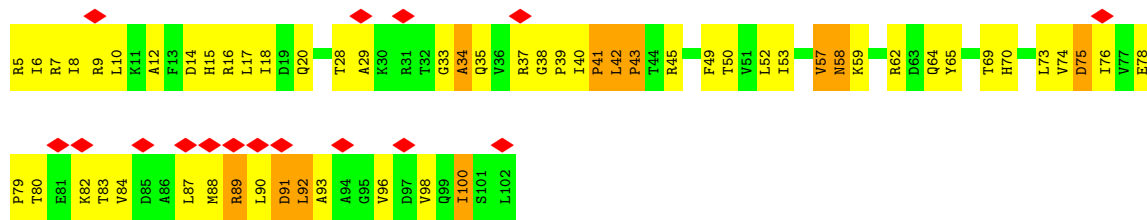


- Molecule 39: 30S ribosomal protein S9

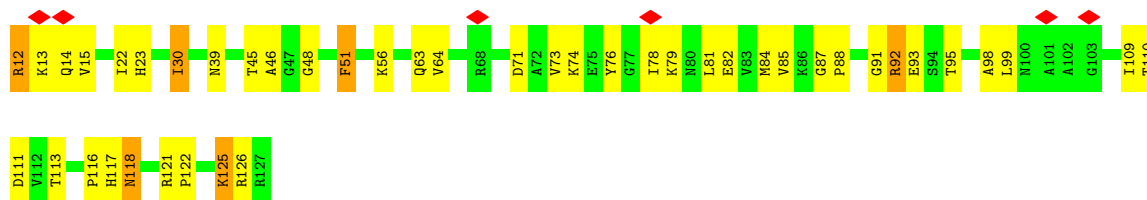
Chain I: 46% 48% 6%



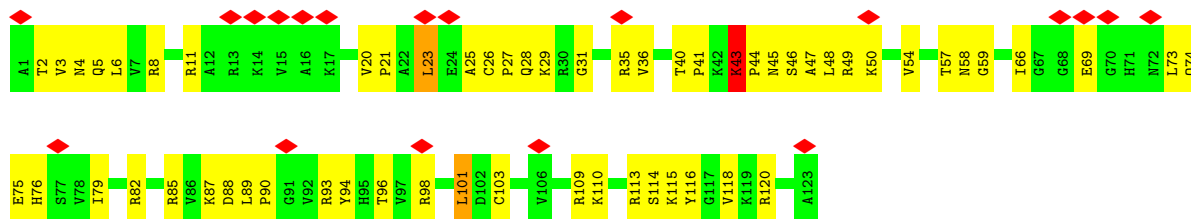
• Molecule 40: 30S ribosomal protein S10



• Molecule 41: 30S ribosomal protein S11

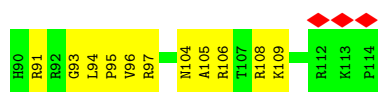


• Molecule 42: 30S ribosomal protein S12

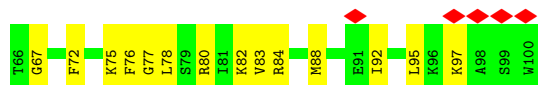
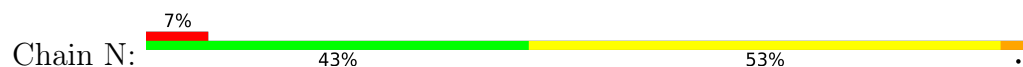


• Molecule 43: 30S ribosomal protein S13

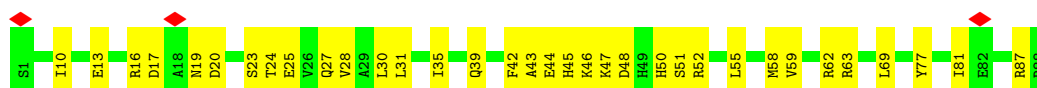




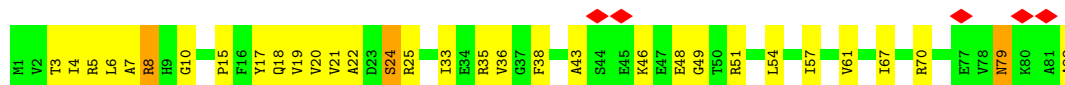
- Molecule 44: 30S ribosomal protein S14



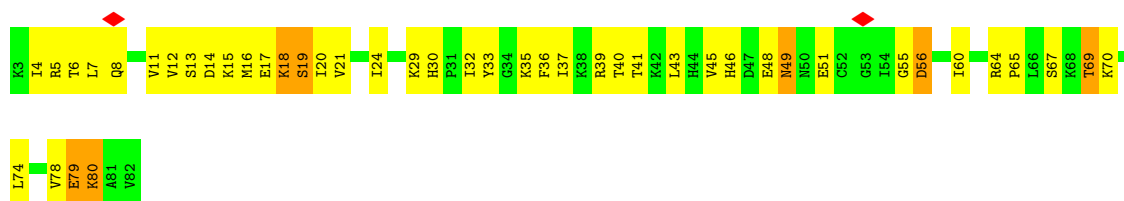
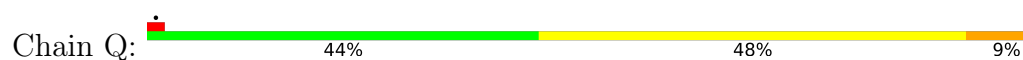
- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

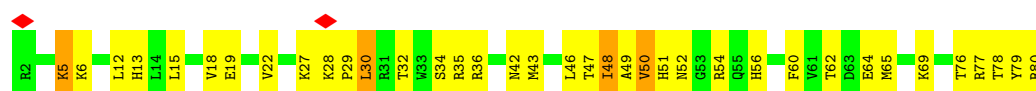


- Molecule 48: 30S ribosomal protein S18



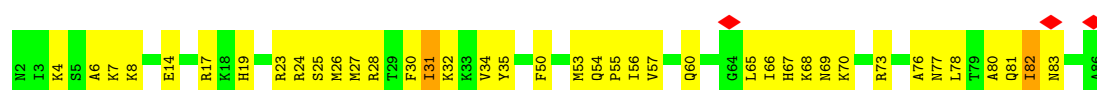
- Molecule 49: 30S ribosomal protein S19

Chain S: 

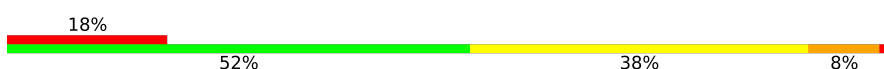


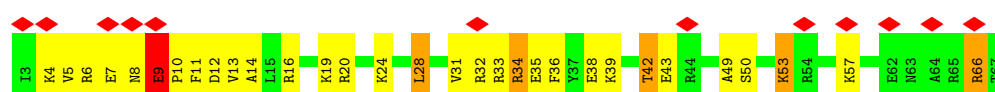
- Molecule 50: 30S ribosomal protein S20

Chain T: 

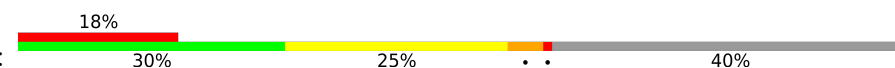


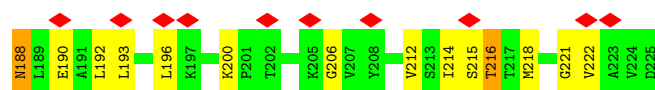
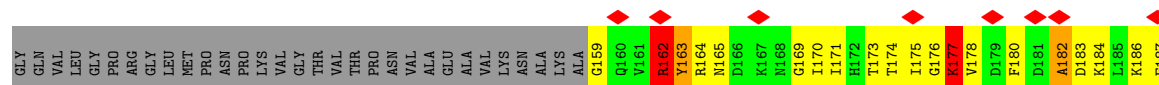
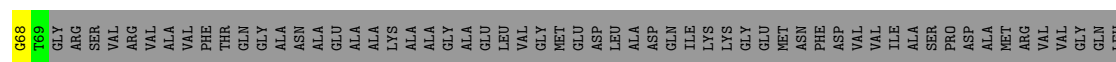
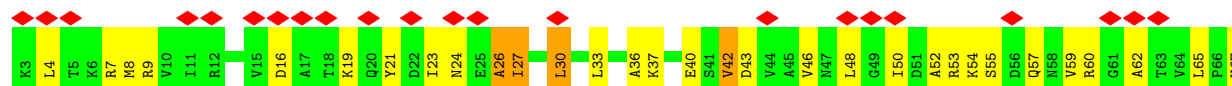
- Molecule 51: 30S ribosomal protein S21

Chain U: 



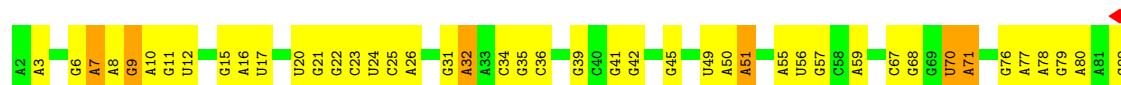
- Molecule 52: 50S ribosomal protein L1

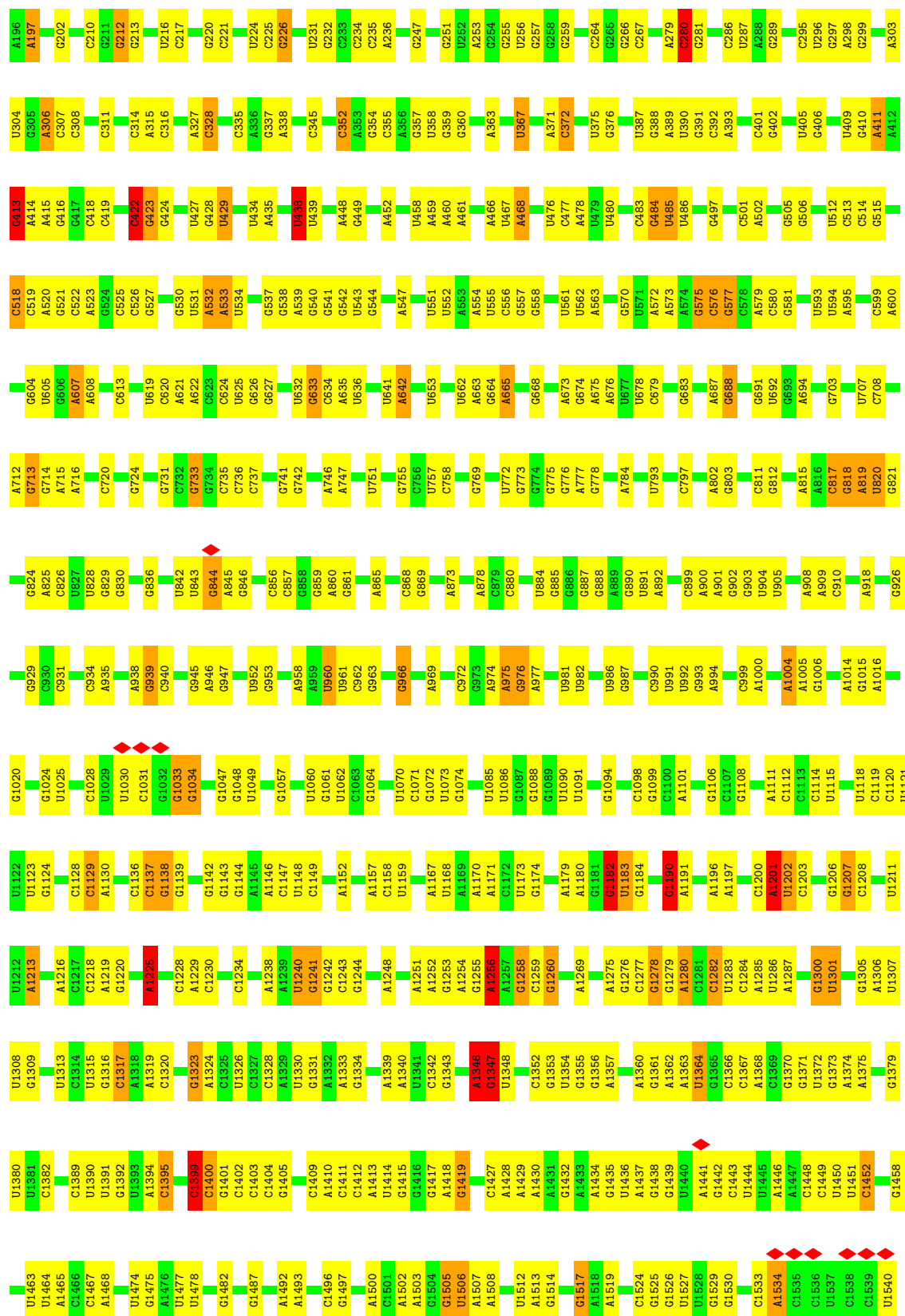
Chain 03: 



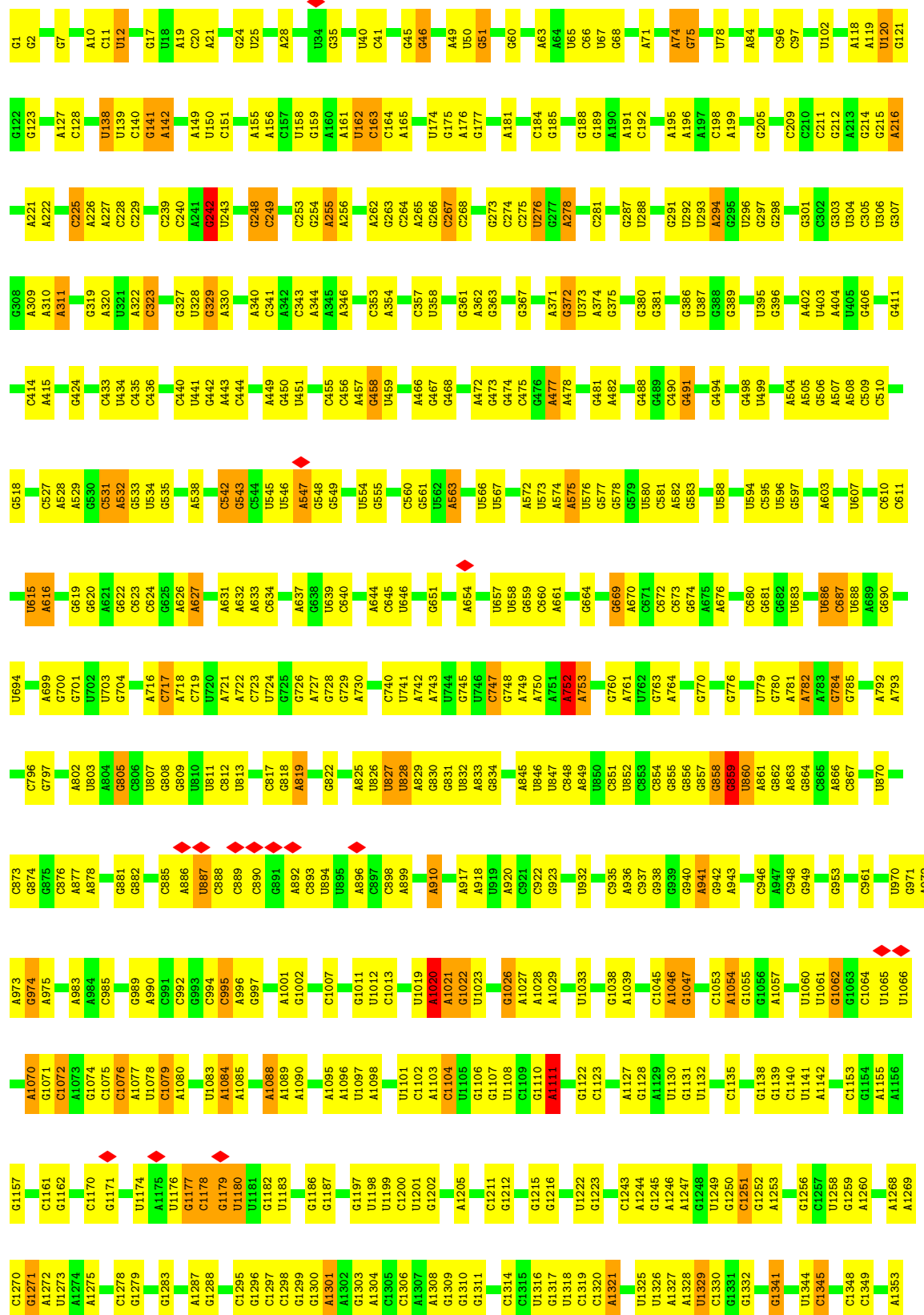
- Molecule 53: 16S ribosomal RNA

Chain A: 





Chain 01:  54% 40% 5%

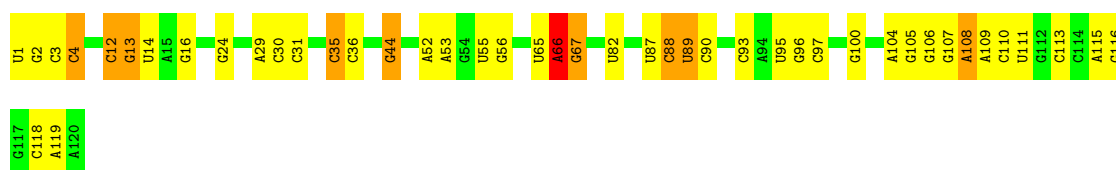


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U2554	A2450	A2287	C2206	G2140	G2057	G1972	U1859	U1758	G1653	C1536	C1445	C1356
U2555	C2452	A2288	C2207	G2141	A2058	U1978	G1860	U1759	G1654	G1540	C1446	C1357
C2556	C2452	U2291	C2208	G2142	A2059	U1979	G1861	C1760	U1657	U1550	G1447	G1358
C2557	C2462	U2292	U2210	C2143	A2060	G1980	A1871	C1761	C1658	C1550	G1448	A1359
C2558	C2463	A2211	A2211	G2144	G2061	U1991	A1872	C1764	U1662	A1551	C1451	G1360
C2567	C2467	A2212	A2212	C2145	A2062	U1991	G1872	U1765	U1662	C1452	G1452	C1363
C2573	A2468	A2297	C2213	C2146	C2065	U1993	A1877	G1766	A1664	U1554	A1453	G1364
C2574	C2373	C2214	C2214	A2147	G2066	C1994	G1878	A1773	A1665	G1555	C1454	A1365
A2577	U2473	C2215	C2216	U2148	G2067	C1997	G1885	C1774	G1666	U1560	C1461	A1366
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U2581	A2478	C2312	C2312	U2151	A2070	C1999	C1893	A1784	A1670	U1563	G1464	C1370
U2582	U2479	U2314	U2314	G2152	A2071	C1999	C1893	A1784	A1670	U1563	G1464	C1370
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A2587	U2321	A2157	A2157	A2157	A2080	G2010	A1901	G1797	U1680	A1569	C1376	C1376
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A2588	U2322	C2160	C2160	U2160	G2093	G2012	G1906	U1797	U1680	A1571	U1474	U1378
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C2420	U2334	U2257	U2257	A2176	G2111	U2028	A1936	A1603	A1501	A1419	A1419	A1419
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C2422	A2336	C2259	C2259	U2182	G2113	A2031	A1938	A1608	A1505	G1424	G1424	G1424
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C2430	G2345	U2265	U2265	U2188	A2119	A2037	U1943	A1625	A1513	G1432	G1432	G1432
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A2435	C2350	A2274	A2274	G2193	G2124	A2042	G1966	A1638	A1526	U1438	U1438	U1438
C2440	G2351	U2277	U2277	U2194	G2125	C2043	C1967	A1640	A1527	U1440	U1440	U1440
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C2442	G2357	U2281	U2281	U2196	G2127	C2045	A1969	A1642	A1533	C1646	C1646	C1646
C2443	A2358	C2282	C2282	U2200	G2128	G2046	A1969	A1643	A1534	A1534	A1534	A1534
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C2447	C2283	C2283	C2283	U2203	U2132	A2052	A1969	A1647	A1538	A1538	A1538	A1538
C2448	C2283	C2283	C2283	U2203	U2133	A2052	A1969	A1648	A1539	A1539	A1539	A1539
C2449	C2283	C2283	C2283	U2203	U2134	A2052	A1969	A1649	A1540	A1540	A1540	A1540
C2450	C2283	C2283	C2283	U2203	U2135	A2052	A1969	A1650	A1541	A1541	A1541	A1541
C2451	C2283	C2283	C2283	U2203	U2136	A2052	A1969	A1651	A1542	A1542	A1542	A1542
C2452	C2283	C2283	C2283	U2203	U2137	A2052	A1969	A1652	A1543	A1543	A1543	A1543
C2453	C2283	C2283	C2283	U2203	U2138	A2052	A1969	A1653	A1544	A1544	A1544	A1544
C2454	C2283	C2283	C2283	U2203	U2139	A2052	A1969	A1654	A1545	A1545	A1545	A1545
C2455	C2283	C2283	C2283	U2203	U2140	A2052	A1969	A1655	A1546	A1546	A1546	A1546
C2456	C2283	C2283	C2283	U2203	U2141	A2052	A1969	A1656	A1547	A1547	A1547	A1547
C2457	C2283	C2283	C2283	U2203	U2142	A2052	A1969	A1657	A1548	A1548	A1548	A1548
C2458	C2283	C2283	C2283	U2203	U2143	A2052	A1969	A1658	A1549	A1549	A1549	A1549
C2459	C2283	C2283	C2283	U2203	U2144	A2052	A1969	A1659	A1550	A1550	A1550	A1550
C2460	C2283	C2283	C2283	U2203	U2145	A2052	A1969	A1660	A1551	A1551	A1551	A1551
C2461	C2283	C2283	C2283	U2203	U2146	A2052	A1969	A1661	A1552	A1552	A1552	A1552
C2462	C2283	C2283	C2283	U2203	U2147	A2052	A1969	A1662	A1553	A1553	A1553	A1553
C2463	C2283	C2283	C2283	U2203	U2148	A2052	A1969	A1663	A1554	A1554	A1554	A1554
C2464	C2283	C2283	C2283	U2203	U2149	A2052	A1969	A1664	A1555	A1555	A1555	A1555
C2465	C2283	C2283	C2283	U2203	U2150	A2052	A1969	A1665	A1556	A1556	A1556	A1556
C2466	C2283	C2283	C2283	U2203	U2151	A2052	A1969	A1666	A1557	A1557	A1557	A1557
C2467	C2283	C2283	C2283	U2203	U2152	A2052	A1969	A1667	A1558	A1558	A1558	A1558
C2468	C2283	C2283	C2283	U2203	U2153	A2052	A1969	A1668	A1559	A1559	A1559	A1559
C2469	C2283	C2283	C2283	U2203	U2154	A2052	A1969	A1669	A1560	A1560	A1560	A1560
C2470	C2283	C2283	C2283	U2203	U2155	A2052	A1969	A1670	A1561	A1561	A1561	A1561
C2471	C2283	C2283	C2283	U2203	U2156	A2052	A1969	A1671	A1562	A1562	A1562	A1562
C2472	C2283	C2283	C2283	U2203	U2157	A2052	A1969	A1672	A1563	A1563	A1563	A1563
C2473	C2283	C2283	C2283	U2203	U2158	A2052	A1969	A1673	A1564	A1564	A1564	A1564
C2474	C2283	C2283	C2283	U2203	U2159	A2052	A1969	A1674	A1565	A1565	A1565	A1565
C2475	C2283	C2283	C2283	U2203	U2160	A2052	A1969	A1675	A1566	A1566	A1566	A1566
C2476	C2283	C2283	C2283	U2203	U2161	A2052	A1969	A1676	A1567	A1567	A1567	A1567
C2477	C2283	C2283	C2283	U2203	U2162	A2052	A1969	A1677	A1568	A1568	A1568	A1568
C2478	C2283	C2283	C2283	U2203	U2163	A2052	A1969	A1678	A1569	A1569	A1569	A1569
C2479	C2283	C2283	C2283	U2203	U2164	A2052	A1969	A1679	A1570	A1570	A1570	A1570
C2480	C2283	C2283	C2283	U2203	U2165	A2052	A1969	A1680	A1571	A1571	A1571	A1571
C2481	C2283	C2283	C2283	U2203	U2166	A2052	A1969	A1681	A1572	A1572	A1572	A1572
C2482	C2283	C2283	C2283	U2203	U2167	A2052	A1969	A1682	A1573	A1573	A1573	A1573
C2483	C2283	C2283	C2283	U2203	U2168	A2052	A1969	A1683	A1574	A1574	A1574	A1574
C2484	C2283	C2283	C2283	U2203	U2169	A2052	A1969	A1684	A1575	A1575	A1575	A1575
C2485	C2283	C2283	C2283	U2203	U2170	A2052	A1969	A1685	A1576	A1576	A1576	A1576
C2486	C2283	C2283	C2283	U2203	U2171	A2052	A1969	A1686	A1577	A1577	A1577	A1577
C2487	C2283	C2283	C2283	U2203	U2172	A2052	A1969	A1687	A1578	A1578	A1578	A1578
C2488	C2283	C2283	C2283	U2203	U2173	A2052	A1969	A1688	A1579	A1579	A1579	A1579
C2489	C2283	C2283	C2283	U2203	U2174	A2052	A1969	A1689	A1580	A1580	A1580	A1580
C2490	C2283	C2283	C2283	U2203	U2175	A2052	A1969	A1690	A1581	A1581	A1581	A1581
C2491	C2283	C2283	C2283	U2203	U2176	A2052	A1969	A1691	A1582	A1582	A1582	A1582
C2492	C2283	C2283	C2283	U2203	U2177	A2052	A1969	A1692	A1583	A1583	A1583	A158



• Molecule 55: 5S ribosomal RNA

Chain 02: 62% 29% 8%



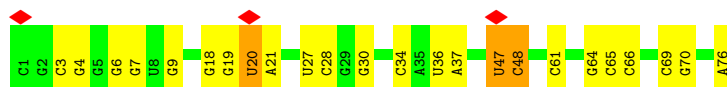
• Molecule 56: tRNAfMet

Chain X: 8% 58% 36% 5%



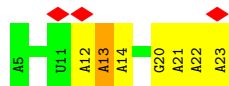
• Molecule 56: tRNAfMet

Chain W: 69% 27% 5%



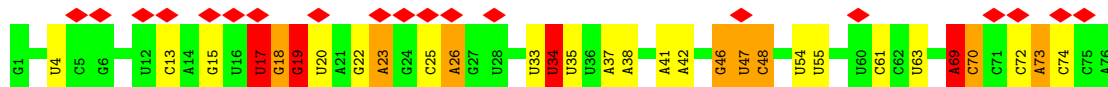
• Molecule 57: mRNA

Chain V: 16% 63% 32% 5%

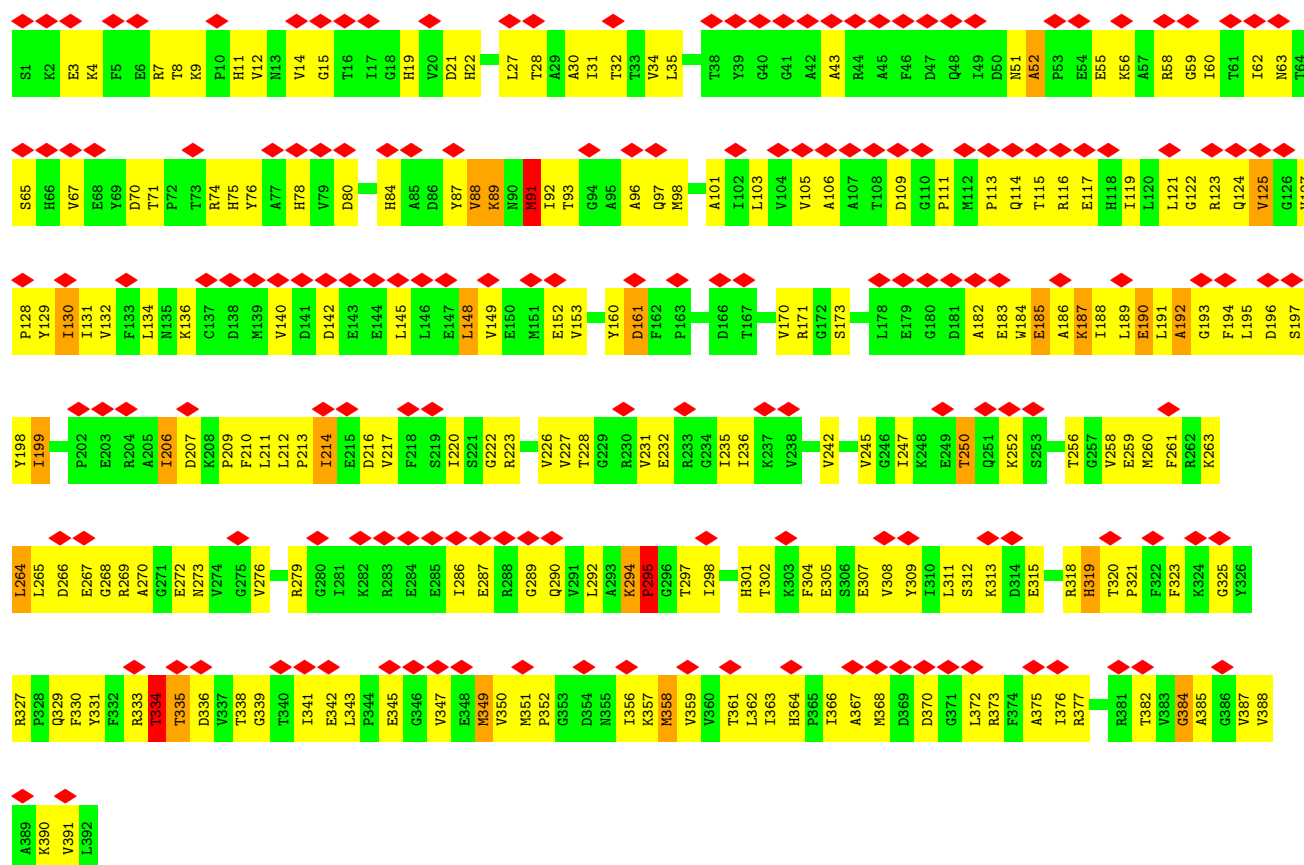
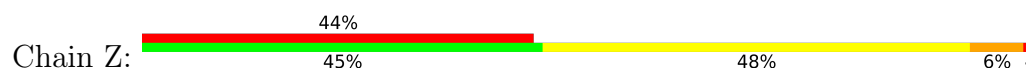


• Molecule 58: tRNALys

Chain Y: 25% 61% 24% 11% 5%



• Molecule 59: Elongation factor Tu 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	6910	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	13.270	Depositor
Minimum map value	-6.345	Depositor
Average map value	-0.332	Depositor
Map value standard deviation	1.036	Depositor
Recommended contour level	2.78	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: U8U, GCP, FME

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	04	0.36	0/2122	0.91	8/2852 (0.3%)
2	05	0.37	0/1586	0.87	3/2134 (0.1%)
3	06	0.36	0/1571	0.96	9/2113 (0.4%)
4	07	0.39	0/1435	0.97	6/1926 (0.3%)
5	08	0.40	0/1343	0.97	7/1816 (0.4%)
6	09	0.43	0/1122	1.06	7/1515 (0.5%)
7	10	0.49	0/1002	1.20	14/1350 (1.0%)
8	11	0.49	0/1046	1.18	19/1410 (1.3%)
9	12	0.38	0/1152	0.93	2/1551 (0.1%)
10	13	0.36	0/948	0.89	0/1268
11	14	0.39	0/1054	1.05	6/1403 (0.4%)
12	15	0.36	0/1093	0.91	0/1460
13	16	0.38	0/974	0.95	6/1301 (0.5%)
14	17	0.36	0/902	0.94	5/1209 (0.4%)
15	18	0.35	0/929	0.91	3/1242 (0.2%)
16	19	0.36	0/960	0.98	2/1278 (0.2%)
17	20	0.37	0/829	0.92	4/1107 (0.4%)
18	21	0.36	0/864	0.95	3/1156 (0.3%)
19	22	0.37	0/745	0.91	2/994 (0.2%)
20	23	0.38	0/788	0.98	6/1051 (0.6%)
21	24	0.36	0/766	0.93	3/1025 (0.3%)
22	25	0.35	0/582	0.86	1/769 (0.1%)
23	26	0.33	0/635	0.88	0/848
24	27	0.34	0/510	1.03	5/677 (0.7%)
25	28	0.37	0/453	0.90	1/605 (0.2%)
26	29	0.39	0/532	1.08	7/709 (1.0%)
27	30	0.36	0/450	0.85	1/599 (0.2%)
28	31	0.40	0/417	0.80	0/554
29	32	0.38	0/380	1.09	3/498 (0.6%)
30	33	0.33	0/513	0.90	1/676 (0.1%)
31	34	0.38	0/303	0.99	3/397 (0.8%)
32	B	0.40	0/1736	1.05	13/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.39	0/1652	0.91	6/2225 (0.3%)
34	D	0.38	0/1665	0.96	7/2227 (0.3%)
35	E	0.42	0/1170	1.03	9/1573 (0.6%)
36	F	0.41	0/836	1.01	7/1128 (0.6%)
37	G	0.38	0/1196	0.98	5/1602 (0.3%)
38	H	0.37	0/989	0.96	1/1326 (0.1%)
39	I	0.38	0/1034	1.03	8/1375 (0.6%)
40	J	0.43	0/797	0.96	0/1077
41	K	0.40	0/886	0.97	3/1195 (0.3%)
42	L	0.39	0/969	1.02	4/1300 (0.3%)
43	M	0.39	0/893	0.99	4/1193 (0.3%)
44	N	0.36	0/817	0.91	3/1088 (0.3%)
45	O	0.34	0/722	0.94	5/964 (0.5%)
46	P	0.38	0/659	0.89	0/884
47	Q	0.40	0/658	1.03	5/881 (0.6%)
48	R	0.40	0/545	0.89	2/731 (0.3%)
49	S	0.40	0/653	0.99	2/877 (0.2%)
50	T	0.36	0/671	1.07	5/888 (0.6%)
51	U	0.46	0/551	1.07	3/728 (0.4%)
52	03	0.54	0/1034	1.08	9/1387 (0.6%)
53	A	0.48	0/36963	0.56	18/57662 (0.0%)
54	01	0.47	0/69796	0.56	20/108888 (0.0%)
55	02	0.50	0/2872	0.56	3/4479 (0.1%)
56	W	0.50	0/1832	0.54	0/2855
56	X	0.52	0/1832	0.58	1/2855 (0.0%)
57	V	0.48	0/471	0.54	0/735
58	Y	0.53	0/1780	0.65	3/2767 (0.1%)
59	Z	0.50	0/3085	1.12	32/4173 (0.8%)
All	All	0.45	0/166770	0.70	315/248894 (0.1%)

There are no bond length outliers.

The worst 5 of 315 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	11	94	LYS	N-CA-C	-10.35	100.72	113.97
7	10	127	ALA	N-CA-C	-10.25	100.45	113.16
7	10	65	GLU	N-CA-C	-9.91	100.68	113.17
32	B	85	SER	N-CA-C	-9.61	100.97	112.89
39	I	89	TYR	N-CA-C	-9.45	98.74	110.65

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	04	2083	0	2157	91	0
2	05	1565	0	1616	56	0
3	06	1552	0	1619	48	0
4	07	1411	0	1447	61	0
5	08	1323	0	1374	55	0
6	09	1111	0	1148	54	0
7	10	989	0	1025	63	0
8	11	1032	0	1088	74	0
9	12	1129	0	1162	46	0
10	13	939	0	1012	40	0
11	14	1045	0	1117	48	0
12	15	1074	0	1157	45	0
13	16	961	0	1000	38	0
14	17	892	0	923	35	0
15	18	917	0	965	43	0
16	19	947	0	1022	34	0
17	20	816	0	839	38	0
18	21	857	0	922	37	0
19	22	739	0	807	28	0
20	23	780	0	834	41	0
21	24	753	0	780	27	0
22	25	575	0	592	25	0
23	26	625	0	655	31	0
24	27	509	0	543	23	0
25	28	449	0	491	22	0
26	29	523	0	524	11	0
27	30	444	0	461	25	0
28	31	410	0	440	16	0
29	32	377	0	418	15	0
30	33	504	0	574	19	0
31	34	302	0	343	9	0
32	B	1705	0	1732	79	0
33	C	1625	0	1699	60	0
34	D	1643	0	1710	56	0
35	E	1157	0	1199	53	0
36	F	818	0	808	47	0
37	G	1182	0	1240	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	H	979	0	1034	40	0
39	I	1022	0	1070	56	0
40	J	787	0	828	52	0
41	K	870	0	878	35	0
42	L	955	0	1019	49	0
43	M	884	0	944	42	0
44	N	805	0	847	46	0
45	O	714	0	737	20	0
46	P	649	0	666	33	0
47	Q	649	0	691	33	0
48	R	536	0	552	19	0
49	S	638	0	665	33	0
50	T	665	0	714	32	0
51	U	545	0	579	28	0
52	03	1027	0	1092	62	0
53	A	33012	0	16618	489	0
54	01	62317	0	31346	912	0
55	02	2568	0	1303	42	0
56	W	1640	0	836	14	0
56	X	1640	0	837	20	0
57	V	417	0	209	6	0
58	Y	1618	0	820	23	0
59	Z	3029	0	3043	178	0
60	W	10	0	10	0	0
61	Y	9	0	12	4	0
62	Z	32	0	14	3	0
All	All	153780	0	104807	3389	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 13.

The worst 5 of 3389 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)
54:01:45:G:H5''	54:01:46:G:H5'	1.35	1.07
54:01:1645:G:H5''	54:01:1646:C:H5'	1.42	1.00
7:10:118:ILE:HG23	7:10:119:PRO:HD3	1.43	0.99
4:07:15:LEU:HD13	4:07:28:PRO:HD2	1.41	0.98
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.44	0.96

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	04	269/271 (99%)	227 (84%)	35 (13%)	7 (3%)	4	28
2	05	207/209 (99%)	171 (83%)	31 (15%)	5 (2%)	4	29
3	06	199/201 (99%)	172 (86%)	24 (12%)	3 (2%)	8	37
4	07	175/177 (99%)	150 (86%)	22 (13%)	3 (2%)	7	35
5	08	174/176 (99%)	151 (87%)	20 (12%)	3 (2%)	7	35
6	09	147/149 (99%)	119 (81%)	26 (18%)	2 (1%)	9	38
7	10	129/131 (98%)	82 (64%)	37 (29%)	10 (8%)	1	12
8	11	139/141 (99%)	109 (78%)	24 (17%)	6 (4%)	2	20
9	12	140/142 (99%)	123 (88%)	15 (11%)	2 (1%)	9	38
10	13	120/122 (98%)	94 (78%)	18 (15%)	8 (7%)	1	14
11	14	141/143 (99%)	110 (78%)	24 (17%)	7 (5%)	1	18
12	15	134/136 (98%)	112 (84%)	19 (14%)	3 (2%)	5	31
13	16	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	50
14	17	114/116 (98%)	98 (86%)	13 (11%)	3 (3%)	4	28
15	18	112/114 (98%)	91 (81%)	21 (19%)	0	100	100
16	19	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
17	20	101/103 (98%)	83 (82%)	17 (17%)	1 (1%)	12	45
18	21	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	6	33
19	22	91/93 (98%)	64 (70%)	24 (26%)	3 (3%)	3	24
20	23	100/102 (98%)	78 (78%)	18 (18%)	4 (4%)	2	21
21	24	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
22	25	73/75 (97%)	62 (85%)	9 (12%)	2 (3%)	4	28
23	26	75/77 (97%)	70 (93%)	4 (5%)	1 (1%)	9	40
24	27	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	28	56/58 (97%)	51 (91%)	4 (7%)	1 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	29	64/66 (97%)	50 (78%)	11 (17%)	3 (5%)	2	19
27	30	54/56 (96%)	47 (87%)	6 (11%)	1 (2%)	6	33
28	31	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	32	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
30	33	62/64 (97%)	49 (79%)	10 (16%)	3 (5%)	2	18
31	34	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	27
32	B	216/218 (99%)	177 (82%)	30 (14%)	9 (4%)	2	20
33	C	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
34	D	203/205 (99%)	169 (83%)	26 (13%)	8 (4%)	2	21
35	E	155/157 (99%)	118 (76%)	27 (17%)	10 (6%)	1	15
36	F	98/100 (98%)	75 (76%)	17 (17%)	6 (6%)	1	15
37	G	149/151 (99%)	124 (83%)	20 (13%)	5 (3%)	3	24
38	H	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	36
39	I	125/127 (98%)	92 (74%)	29 (23%)	4 (3%)	3	25
40	J	96/98 (98%)	74 (77%)	11 (12%)	11 (12%)	0	5
41	K	114/116 (98%)	89 (78%)	20 (18%)	5 (4%)	2	20
42	L	121/123 (98%)	94 (78%)	19 (16%)	8 (7%)	1	14
43	M	112/114 (98%)	91 (81%)	17 (15%)	4 (4%)	2	23
44	N	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	6	32
45	O	86/88 (98%)	71 (83%)	13 (15%)	2 (2%)	5	30
46	P	80/82 (98%)	64 (80%)	13 (16%)	3 (4%)	2	21
47	Q	78/80 (98%)	57 (73%)	15 (19%)	6 (8%)	1	12
48	R	63/65 (97%)	50 (79%)	8 (13%)	5 (8%)	1	11
49	S	77/79 (98%)	62 (80%)	12 (16%)	3 (4%)	2	21
50	T	83/85 (98%)	79 (95%)	2 (2%)	2 (2%)	4	29
51	U	63/65 (97%)	39 (62%)	19 (30%)	5 (8%)	1	11
52	03	130/223 (58%)	112 (86%)	15 (12%)	3 (2%)	5	30
59	Z	390/392 (100%)	330 (85%)	53 (14%)	7 (2%)	6	34
All	All	6366/6563 (97%)	5260 (83%)	911 (14%)	195 (3%)	5	25

5 of 195 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	04	121	ALA
1	04	233	GLY
2	05	170	VAL
3	06	83	VAL
4	07	175	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	04	216/216 (100%)	214 (99%)	2 (1%)	70	75
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	163 (99%)	2 (1%)	63	72
4	07	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	08	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	09	114/114 (100%)	112 (98%)	2 (2%)	51	67
7	10	100/100 (100%)	95 (95%)	5 (5%)	22	47
8	11	109/109 (100%)	106 (97%)	3 (3%)	38	59
9	12	116/116 (100%)	116 (100%)	0	100	100
10	13	103/103 (100%)	101 (98%)	2 (2%)	50	66
11	14	102/102 (100%)	101 (99%)	1 (1%)	68	75
12	15	109/109 (100%)	108 (99%)	1 (1%)	70	75
13	16	100/100 (100%)	100 (100%)	0	100	100
14	17	86/86 (100%)	84 (98%)	2 (2%)	44	63
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	87 (98%)	2 (2%)	45	64
17	20	84/84 (100%)	84 (100%)	0	100	100
18	21	93/93 (100%)	91 (98%)	2 (2%)	45	64
19	22	80/80 (100%)	78 (98%)	2 (2%)	42	62
20	23	83/83 (100%)	81 (98%)	2 (2%)	43	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	55 (100%)	0	100	100
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	58 (98%)	1 (2%)	53	68
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	50 (98%)	1 (2%)	48	65
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	180/180 (100%)	173 (96%)	7 (4%)	28	52
33	C	170/170 (100%)	169 (99%)	1 (1%)	78	80
34	D	172/172 (100%)	168 (98%)	4 (2%)	44	63
35	E	119/119 (100%)	116 (98%)	3 (2%)	42	62
36	F	87/87 (100%)	86 (99%)	1 (1%)	65	74
37	G	124/124 (100%)	121 (98%)	3 (2%)	43	63
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	103 (98%)	2 (2%)	50	66
40	J	86/86 (100%)	84 (98%)	2 (2%)	44	63
41	K	89/89 (100%)	86 (97%)	3 (3%)	32	55
42	L	103/103 (100%)	102 (99%)	1 (1%)	68	75
43	M	92/92 (100%)	90 (98%)	2 (2%)	45	64
44	N	83/83 (100%)	83 (100%)	0	100	100
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	65 (100%)	0	100	100
47	Q	74/74 (100%)	72 (97%)	2 (3%)	39	60
48	R	56/56 (100%)	53 (95%)	3 (5%)	20	46
49	S	70/70 (100%)	70 (100%)	0	100	100
50	T	65/65 (100%)	65 (100%)	0	100	100
51	U	55/55 (100%)	53 (96%)	2 (4%)	31	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	03	110/174 (63%)	106 (96%)	4 (4%)	31	54
59	Z	324/325 (100%)	315 (97%)	9 (3%)	38	59
All	All	5285/5350 (99%)	5203 (98%)	82 (2%)	54	69

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

Mol	Chain	Res	Type
41	K	30	ILE
52	03	177	LYS
42	L	2	THR
48	R	21	ASP
59	Z	125	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
46	P	79	ASN
49	S	52	ASN
15	18	65	ASN
15	18	55	HIS
50	T	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	161 (10%)	7 (0%)
54	01	2902/2903 (99%)	353 (12%)	13 (0%)
55	02	119/120 (99%)	10 (8%)	2 (1%)
56	W	76/77 (98%)	8 (10%)	0
56	X	76/77 (98%)	12 (15%)	1 (1%)
57	V	18/19 (94%)	3 (16%)	0
58	Y	75/76 (98%)	17 (22%)	3 (4%)
All	All	4804/4811 (99%)	564 (11%)	26 (0%)

5 of 564 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	7	A

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Mol	Chain	Res	Type
53	A	9	G
53	A	22	G
53	A	32	A

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	01	1940	U
54	01	2326	C
58	Y	19	G
54	01	2296	U
54	01	2391	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
58	U8U	Y	34	58	20,24,25	1.34	2 (10%)	22,34,37	1.16	2 (9%)

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
58	U8U	Y	34	58	-	4/10/28/29	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	Y	34	U8U	C6-N1	4.21	1.45	1.38
58	Y	34	U8U	C4-C5	2.06	1.50	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Y	34	U8U	C5-C6-N1	2.63	126.48	122.94
58	Y	34	U8U	C1'-N1-C6	-2.21	117.52	121.15

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	Y	34	U8U	N-C-C5-C4
58	Y	34	U8U	C5-C-N-CA
58	Y	34	U8U	N-C-C5-C6
58	Y	34	U8U	C2'-C1'-N1-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Y	34	U8U	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands 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
61	LYS	Y	101	58	7,8,9	0.71	0	3,8,10	0.17	0
60	FME	W	101	-	8,9,10	0.79	0	8,9,11	1.14	1 (12%)
62	GCP	Z	401	-	32,34,34	1.95	5 (15%)	49,54,54	2.59	14 (28%)

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
61	LYS	Y	101	58	-	3/6/7/9	-
60	FME	W	101	-	-	4/7/9/11	-
62	GCP	Z	401	-	-	8/19/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Z	401	GCP	PA-O3A	-6.87	1.52	1.59
62	Z	401	GCP	PB-O3A	-4.96	1.52	1.58
62	Z	401	GCP	C1'-N9	3.10	1.56	1.47
62	Z	401	GCP	O4'-C1'	2.41	1.47	1.42
62	Z	401	GCP	PB-O2B	-2.03	1.51	1.56

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Z	401	GCP	C1'-N9-C4	8.52	151.65	126.49
62	Z	401	GCP	C1'-N9-C8	-8.14	103.61	126.73
62	Z	401	GCP	O1G-PG-C3B	-7.55	94.92	111.37
62	Z	401	GCP	O5'-PA-O1A	-3.94	93.31	108.94
62	Z	401	GCP	O2B-PB-O1B	3.84	122.45	109.95

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	W	101	FME	O1-CN-N-CA
60	W	101	FME	C-CA-CB-CG
60	W	101	FME	O-C-CA-CB
61	Y	101	LYS	N-CA-CB-CG
61	Y	101	LYS	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 7 short contacts:

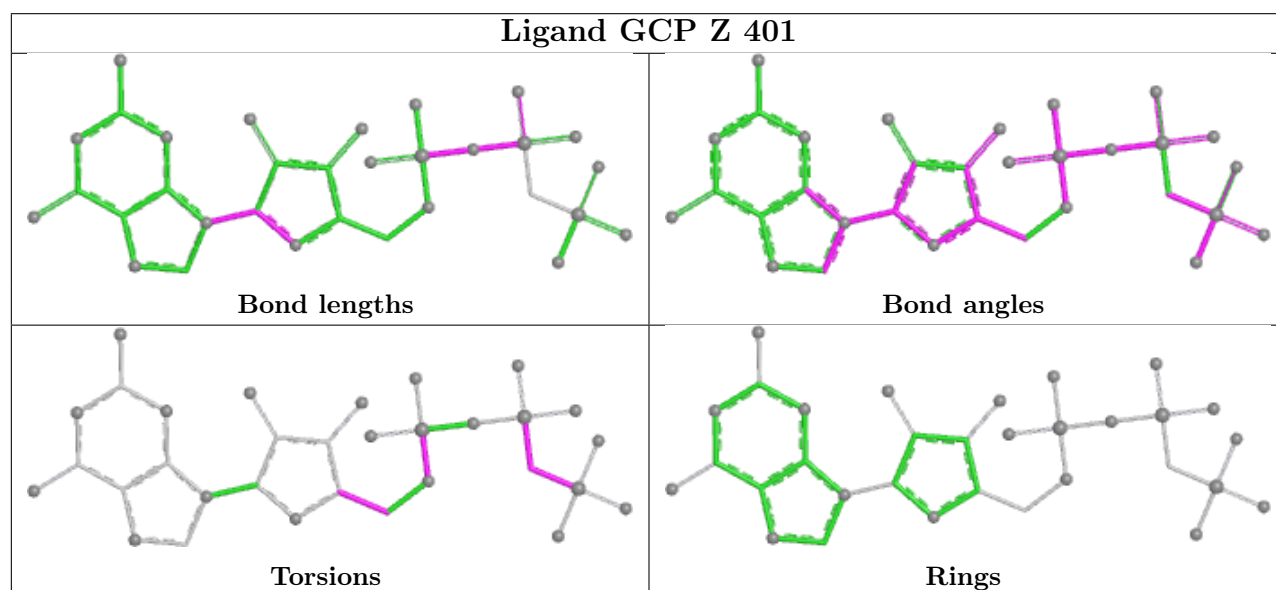
Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	Y	101	LYS	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	Z	401	GCP	3	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

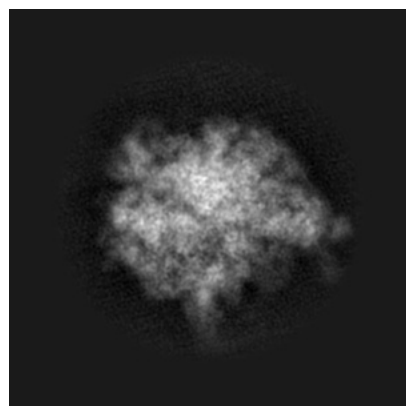
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8619. These allow visual inspection of the internal detail of the map and identification of artifacts.

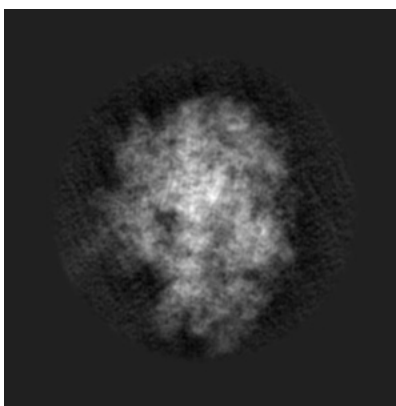
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

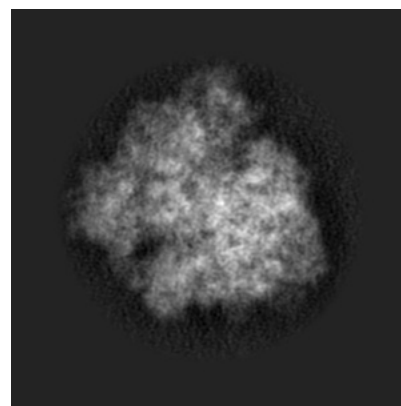
6.1.1 Primary map



X

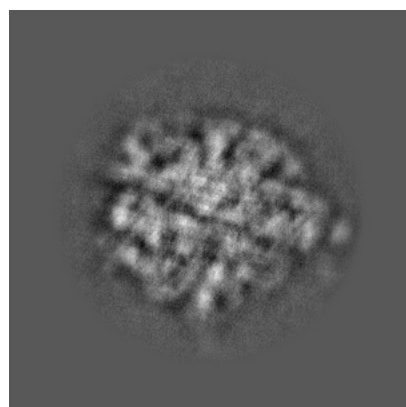


Y

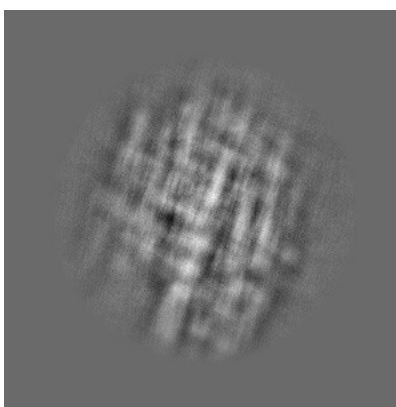


Z

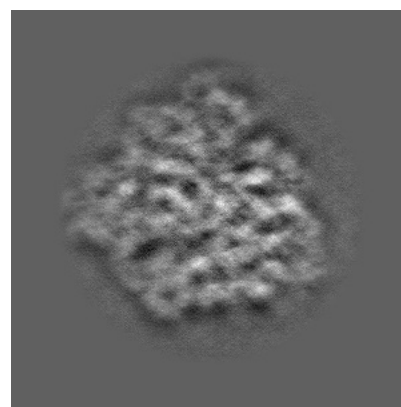
6.1.2 Raw map



X



Y

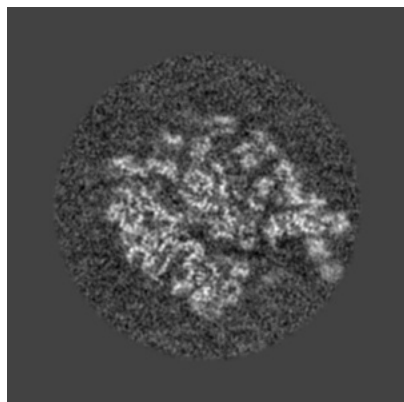


Z

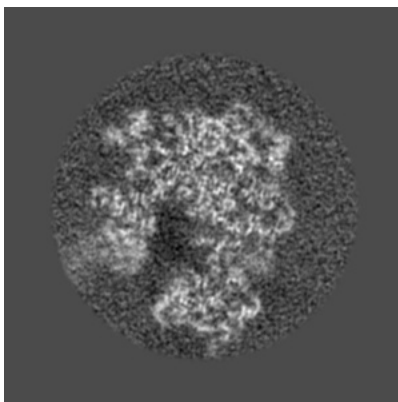
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

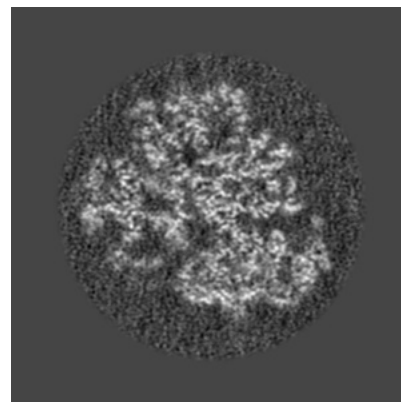
6.2.1 Primary map



X Index: 240

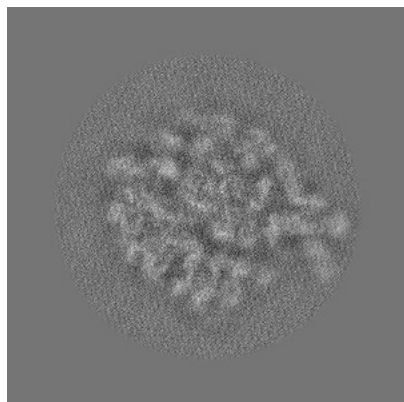


Y Index: 240

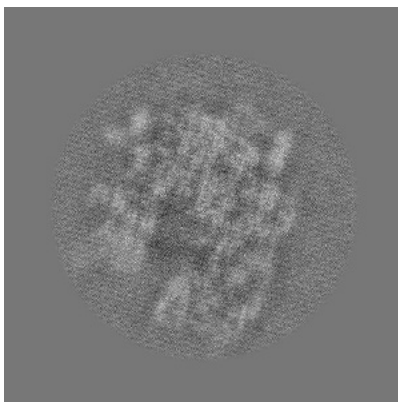


Z Index: 240

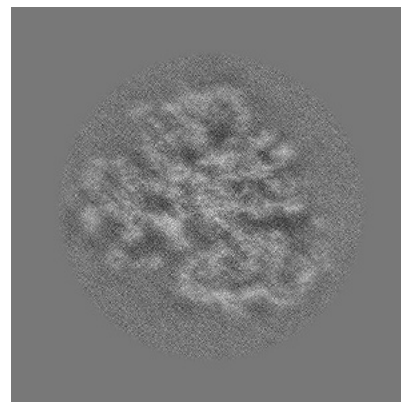
6.2.2 Raw map



X Index: 240



Y Index: 240

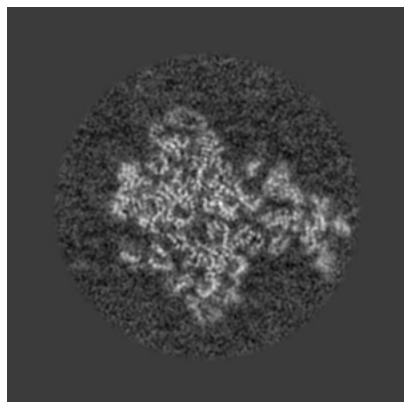


Z Index: 240

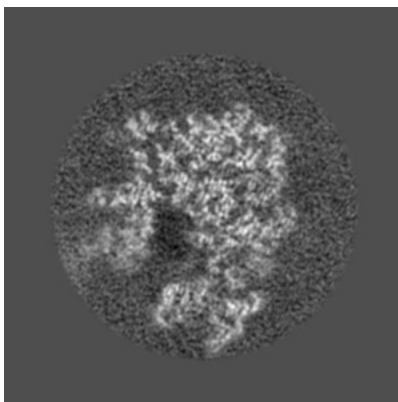
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

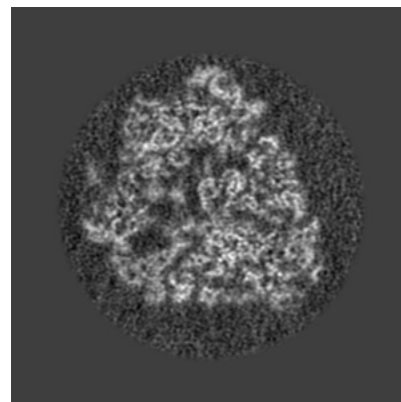
6.3.1 Primary map



X Index: 252

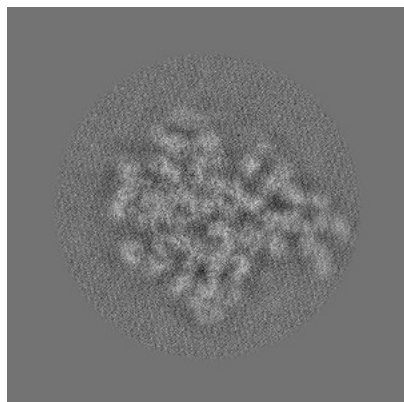


Y Index: 245

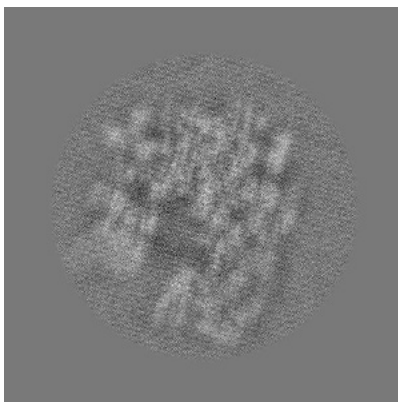


Z Index: 225

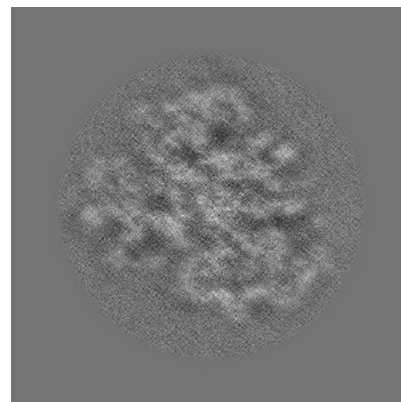
6.3.2 Raw map



X Index: 250



Y Index: 237

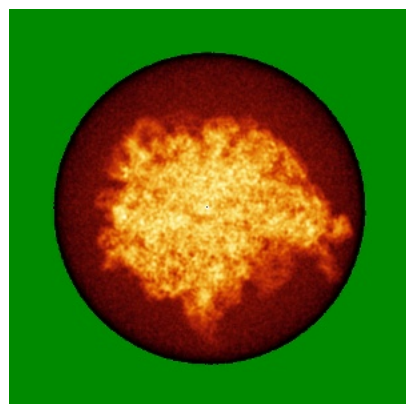


Z Index: 242

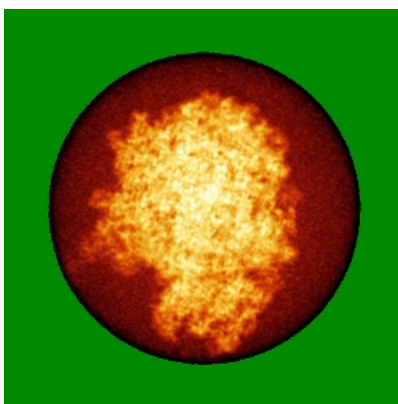
The images above show the largest variance slices of the map in three orthogonal directions.

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

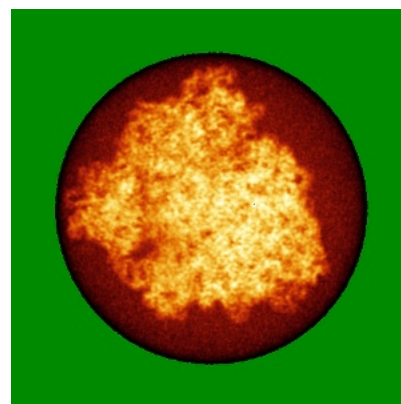
6.4.1 Primary map



X

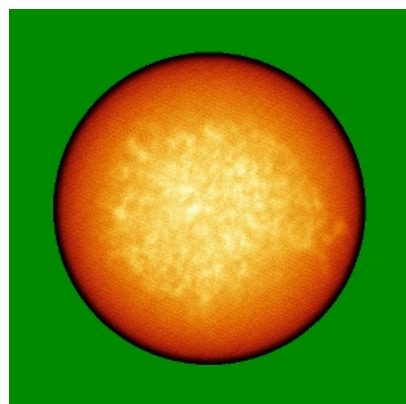


Y

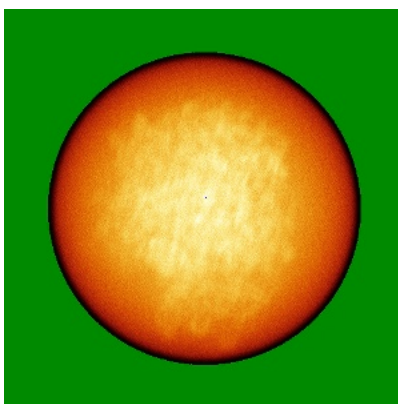


Z

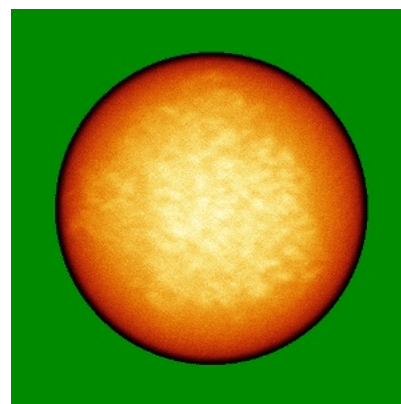
6.4.2 Raw map



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.

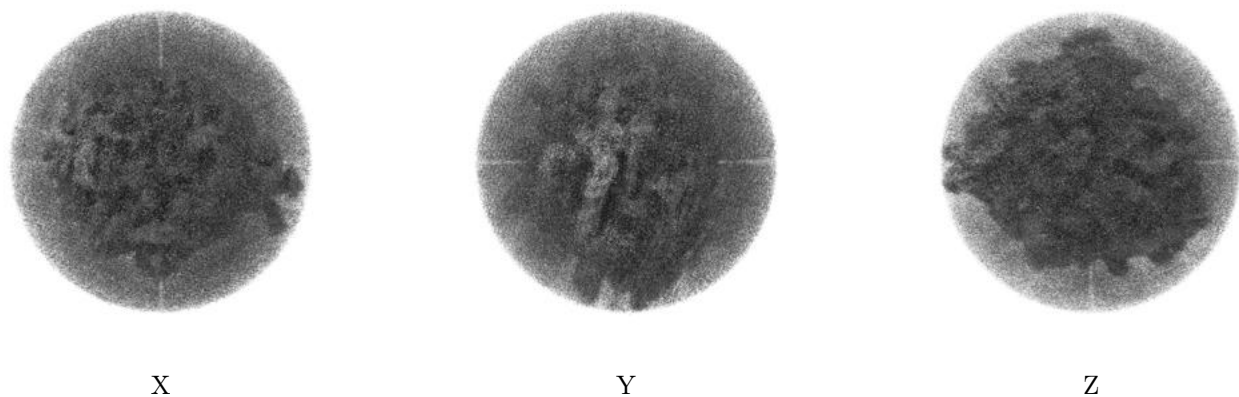
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.78. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

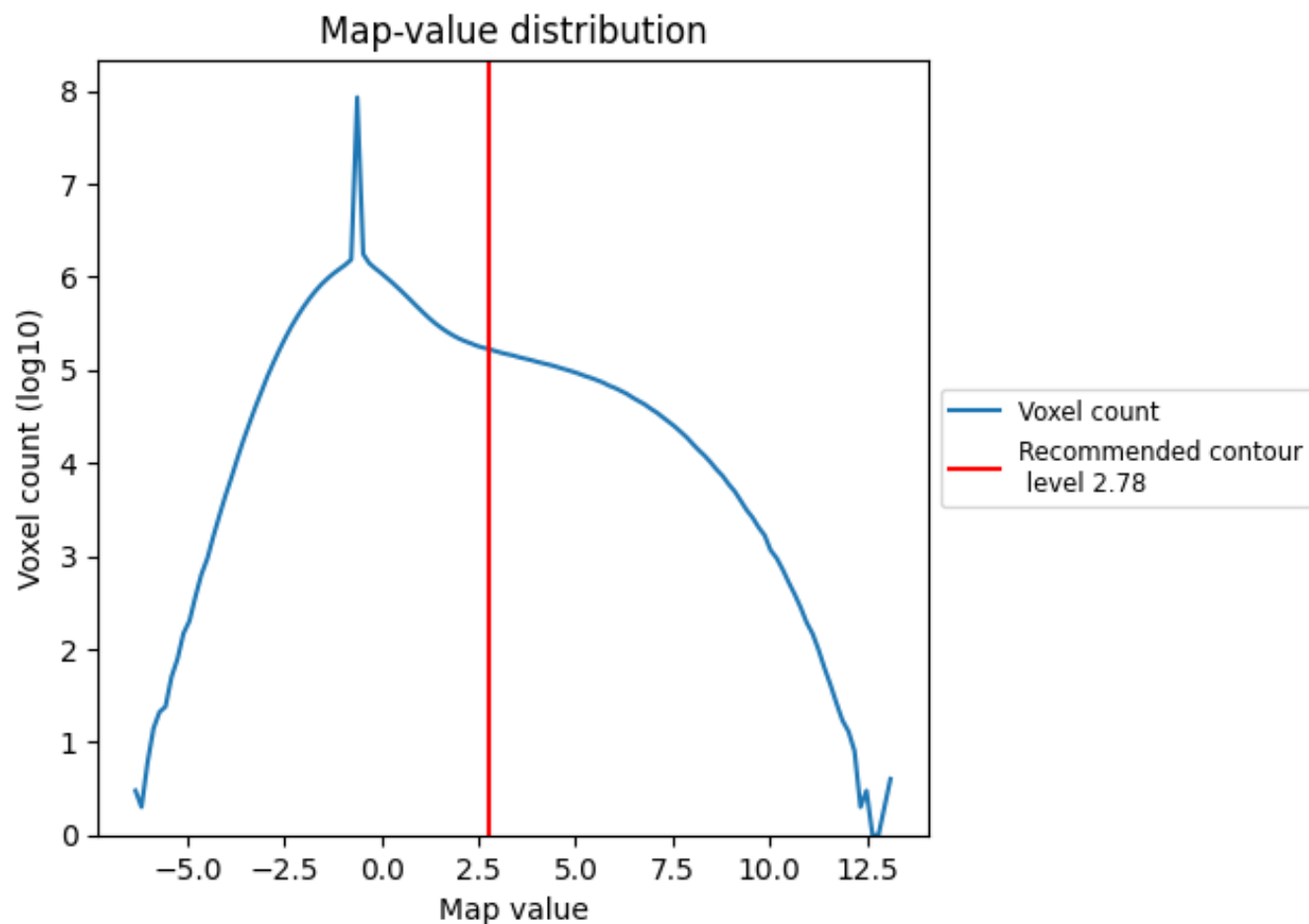
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

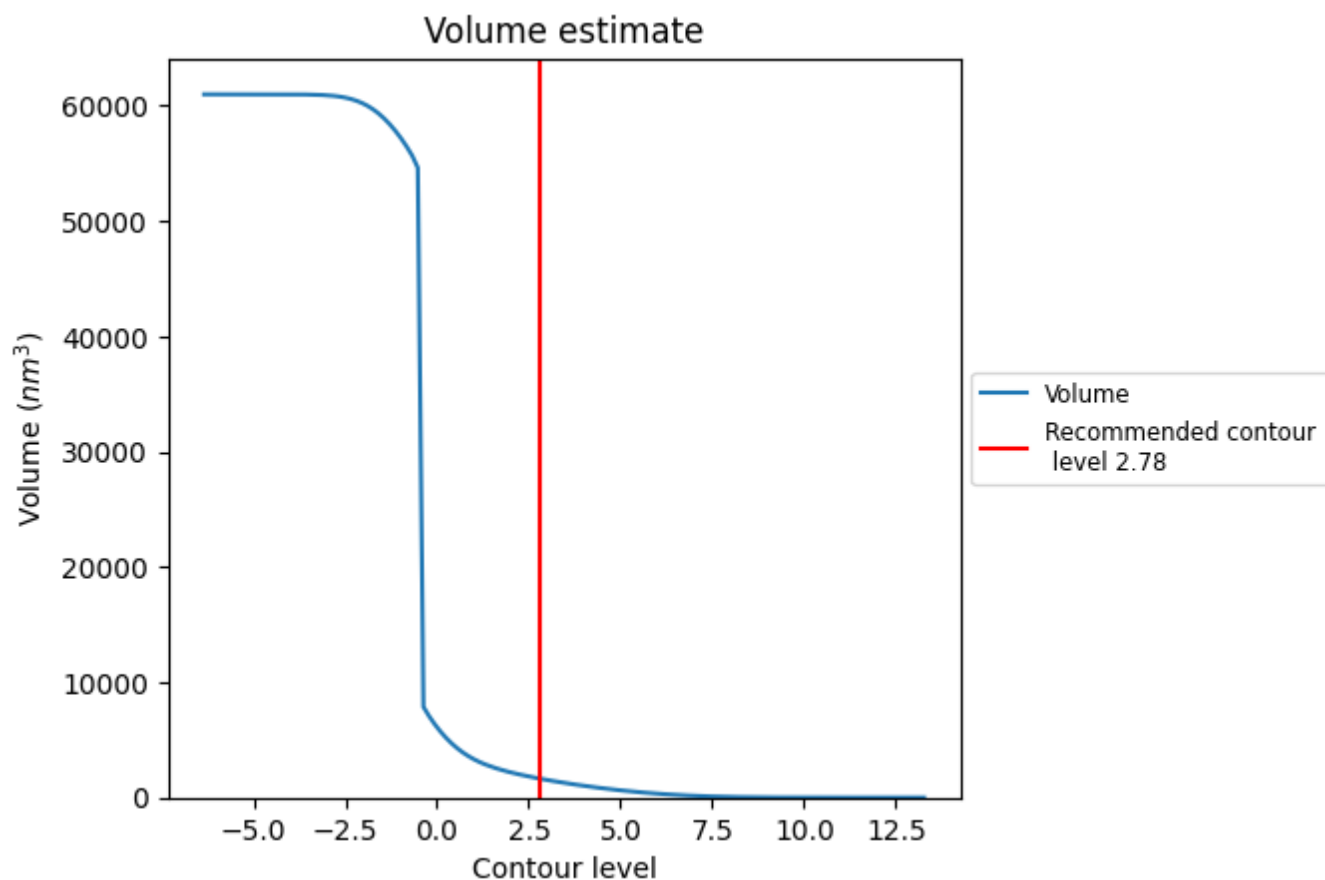
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

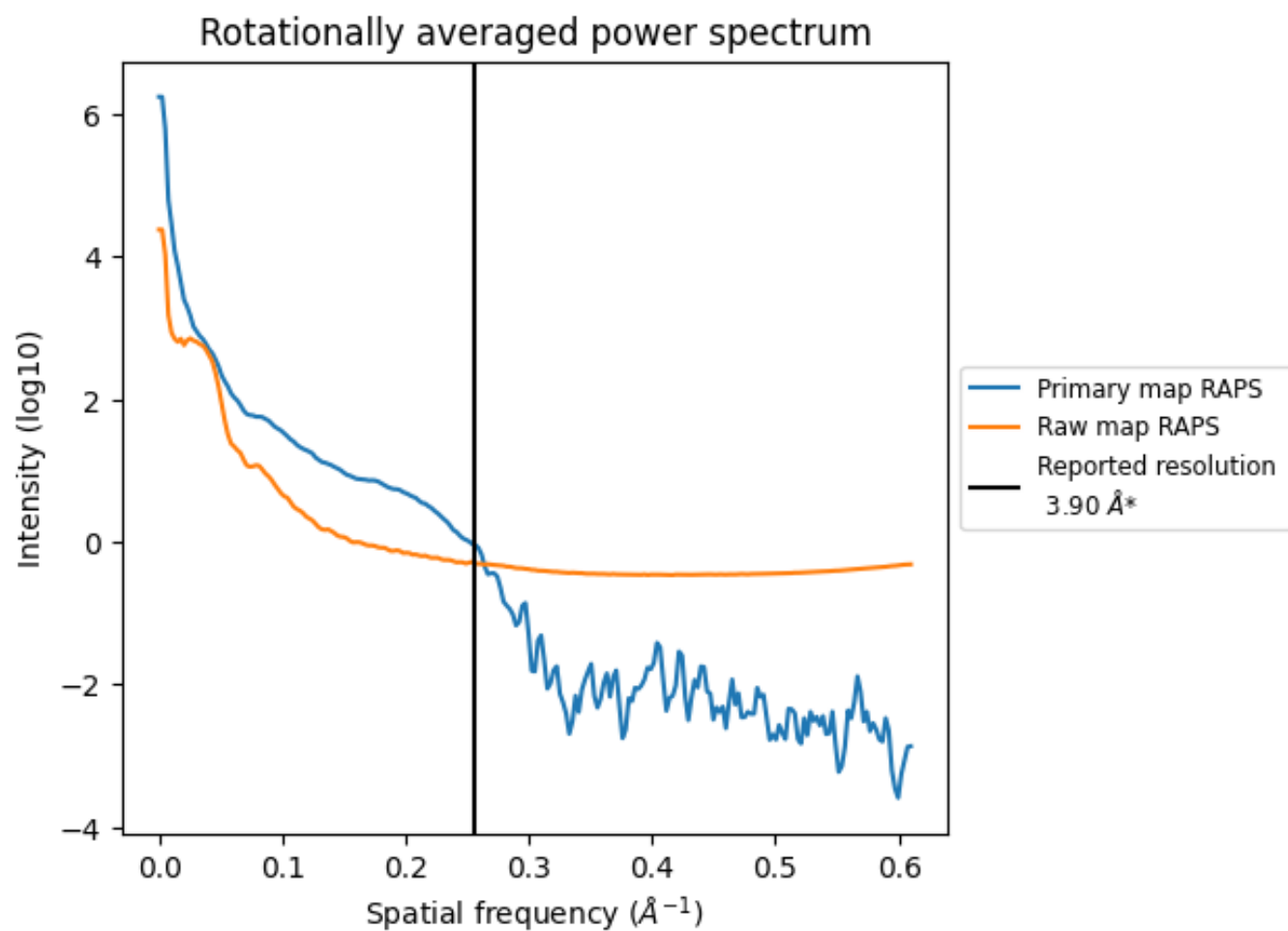
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1654 nm³; this corresponds to an approximate mass of 1494 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 ⓘ

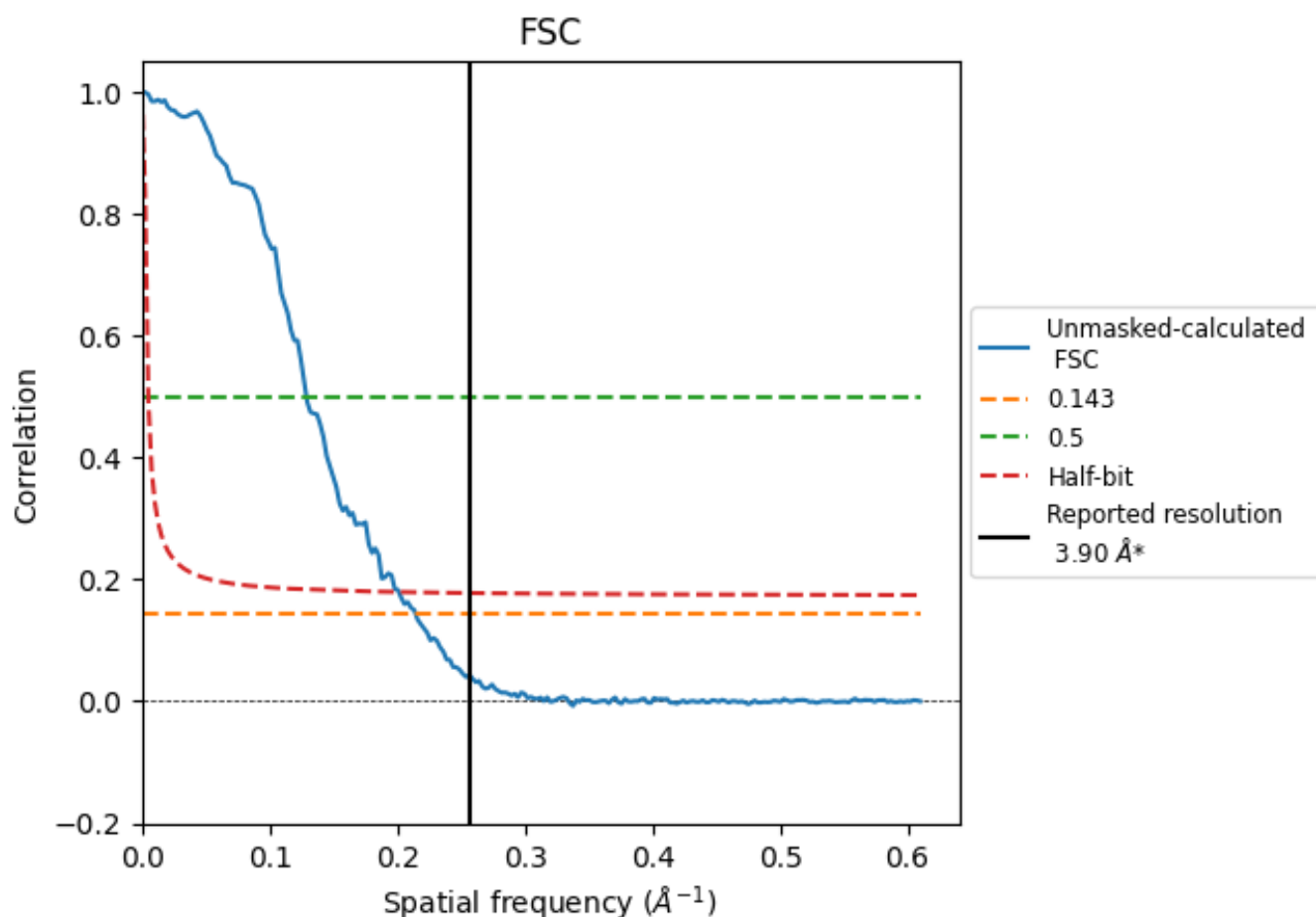


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

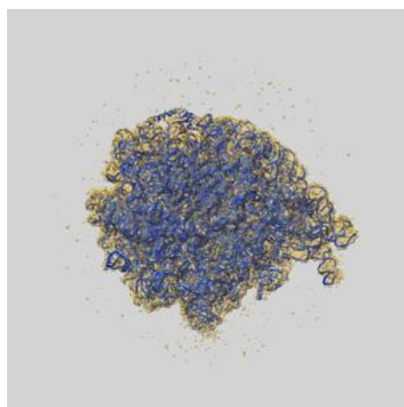
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.66	7.76	4.97

*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 4.66 differs from the reported value 3.9 by more than 10 %

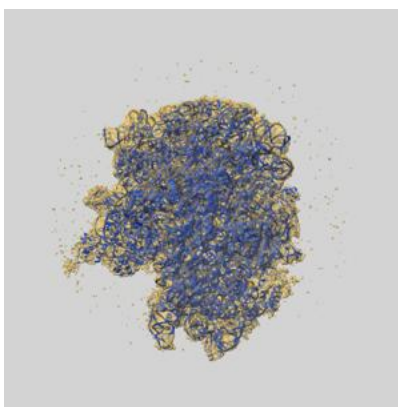
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8619 and PDB model 5UYP. Per-residue inclusion information can be found in section 3 on page 17.

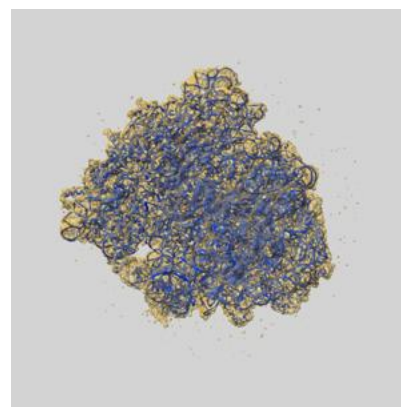
9.1 Map-model overlay [i](#)



X



Y



Z

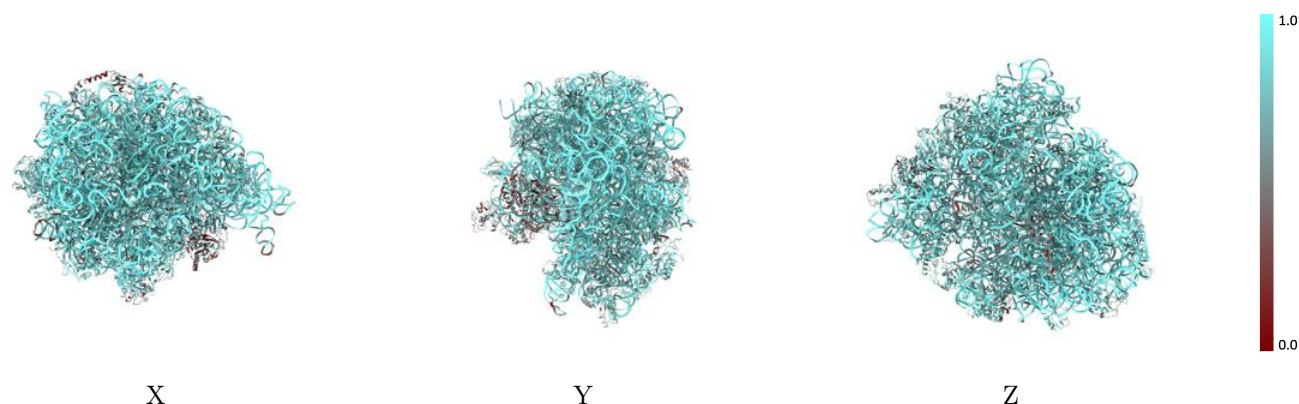
The images above show the 3D surface view of the map at the recommended contour level 2.78 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



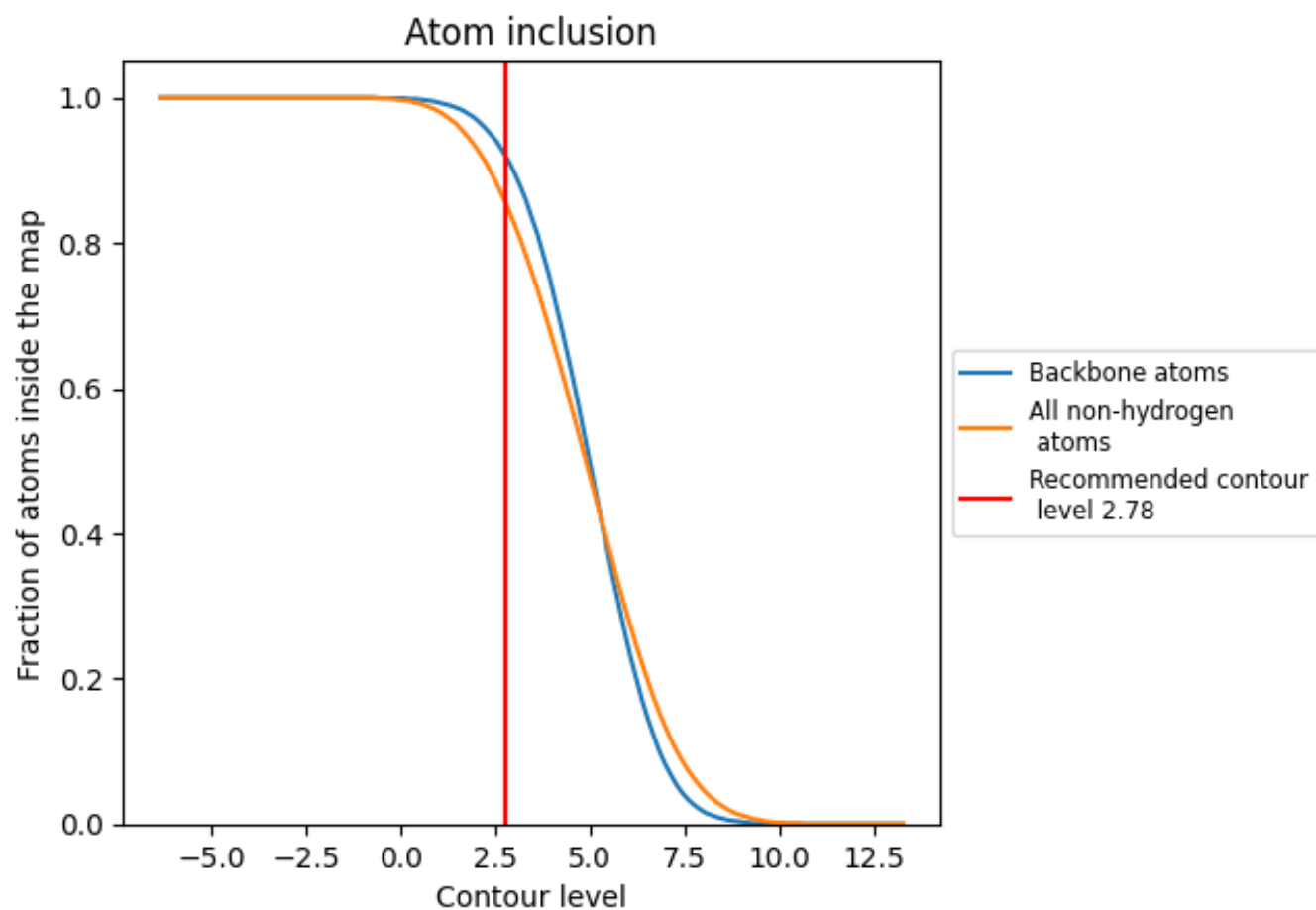
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.78).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (2.78) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8540	 0.3380
01	 0.9360	 0.3520
02	 0.9460	 0.3400
03	 0.5680	 0.2060
04	 0.7850	 0.3870
05	 0.7590	 0.3810
06	 0.7420	 0.3480
07	 0.7700	 0.3230
08	 0.7750	 0.3350
09	 0.4580	 0.2710
10	 0.4770	 0.1730
11	 0.5530	 0.1990
12	 0.7660	 0.3710
13	 0.6660	 0.3750
14	 0.8070	 0.3590
15	 0.7030	 0.3730
16	 0.7930	 0.3510
17	 0.8120	 0.3460
18	 0.7080	 0.3650
19	 0.7830	 0.3500
20	 0.7540	 0.3540
21	 0.7290	 0.3450
22	 0.8020	 0.3590
23	 0.7750	 0.3140
24	 0.7740	 0.3580
25	 0.7510	 0.3800
26	 0.7520	 0.3600
27	 0.7490	 0.2860
28	 0.7870	 0.3610
29	 0.7500	 0.3190
30	 0.7620	 0.3640
31	 0.7840	 0.3330
32	 0.8140	 0.3800
33	 0.8230	 0.3910
34	 0.8190	 0.3770



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Chain	Atom inclusion	Q-score
A	 0.9280	 0.3450
B	 0.7020	 0.3070
C	 0.6690	 0.3510
D	 0.7200	 0.3200
E	 0.7210	 0.3510
F	 0.7450	 0.3290
G	 0.7100	 0.3090
H	 0.7590	 0.3480
I	 0.7730	 0.3170
J	 0.6340	 0.3060
K	 0.7660	 0.3610
L	 0.6830	 0.3740
M	 0.7170	 0.3070
N	 0.7470	 0.3210
O	 0.7700	 0.3340
P	 0.8200	 0.3540
Q	 0.7850	 0.3370
R	 0.7630	 0.3440
S	 0.7720	 0.3420
T	 0.7650	 0.3150
U	 0.6040	 0.2860
V	 0.6830	 0.2740
W	 0.8660	 0.3150
X	 0.6800	 0.1870
Y	 0.6270	 0.1960
Z	 0.4480	 0.2260