



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 10:55 am GMT

PDB ID : 7QG8
EMDB ID : EMD-13952
Title : Structure of the collided E. coli disome - VemP-stalled 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-07
Resolution : 3.97 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:

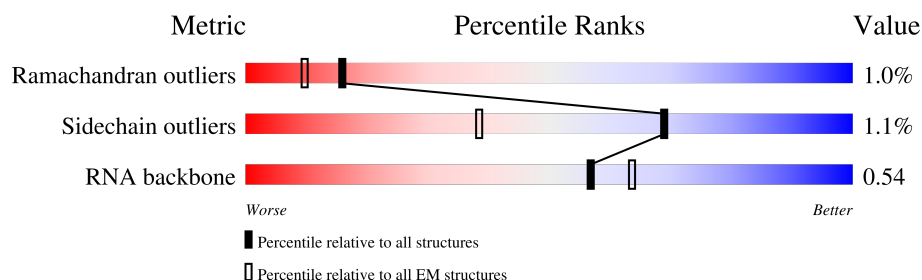
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.97 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	73	
2	s	179	
3	M	75	
4	O	120	
5	P	273	
6	Q	209	
7	R	201	
8	S	179	






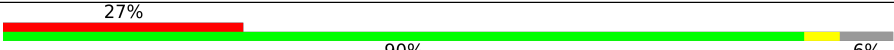
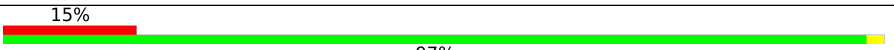
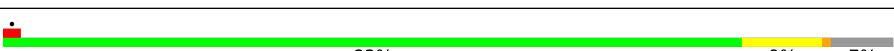
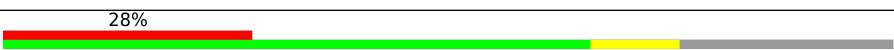

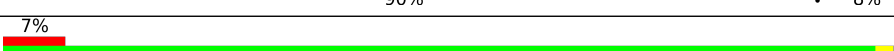
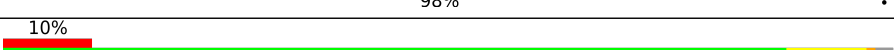
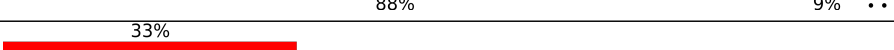
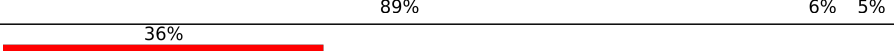
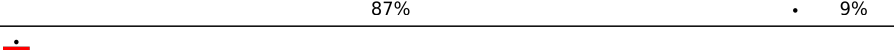
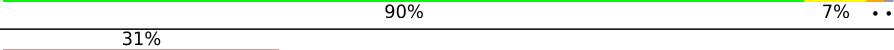
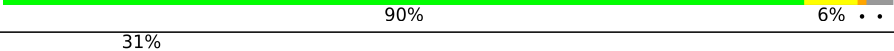

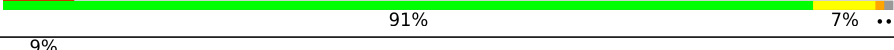
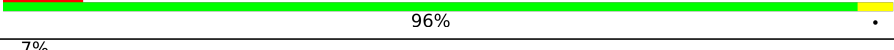
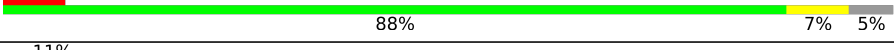
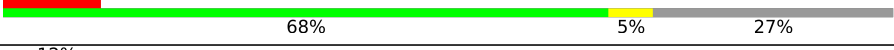
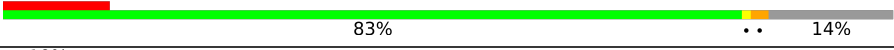
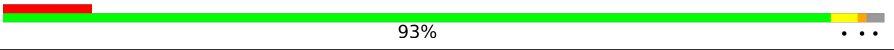
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Mol	Chain	Length	Quality of chain
9	T	177	
10	U	149	
11	V	142	
12	W	142	
13	X	123	
14	Y	144	
15	Z	136	
16	a	127	
17	b	117	
18	c	115	
19	d	118	
20	e	103	
21	f	110	
22	g	100	
23	h	104	
24	i	94	
25	j	85	
26	k	78	
27	l	63	
28	m	59	
29	n	57	
30	o	55	
31	p	46	
32	q	65	
33	r	55	

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Mol	Chain	Length	Quality of chain
34	N	2903	
35	L	70	
36	C	223	
37	0	1539	
38	1	239	
39	2	218	
40	3	206	
41	4	162	
42	5	131	
43	6	156	
44	7	130	
45	8	130	
46	9	103	
47	D	129	
48	E	124	
49	F	118	
50	G	101	
51	H	89	
52	I	82	
53	J	84	
54	K	75	
55	t	92	
56	u	87	
57	v	88	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 147108 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 A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	73	Total	C	N	O	P	0	0
			1561	695	279	514	73		

- Molecule 2 is a protein called VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s	37	Total	C	N	O	S	0	0
			316	198	58	58	2		

- Molecule 3 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	75	Total	C	N	O	P	0	0
			1594	711	281	527	75		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	X	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	a	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	123	ALA	GLU	variant	UNP P0AG44

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	c	114	Total	C	N	O	S	0	0
			915	573	179	162	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	e	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	g	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	98	SER	GLY	variant	UNP P0ADZ0

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	75	Total	C	N	O	S	0	0
			568	353	113	101	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	3	UNK	HIS	variant	UNP P0A7L8

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	k	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	l	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	o	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	p	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	q	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	r	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 34 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	2897	Total	C	N	O	P	1	0
			62215	27754	11448	20115	2898		

- Molecule 35 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	55	Total	C	N	O	S	0	0
			419	258	76	79	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	68	SER	GLY	variant	UNP P0A7M9

- Molecule 36 is a protein called 50S ribosomal protein L1.

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

- Molecule 37 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	0	1532	Total	C	N	O	P	0	0
			32873	14661	6031	10649	1532		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	3	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	4	MET	ILE	variant	UNP P0A7W1

- Molecule 42 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	101	SER	PRO	variant	UNP P02358

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	6	144	Total	C	N	O	S	0	0
			1129	705	213	207	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	78	HIS	ARG	variant	UNP P02359

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	8	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	3	ASP	GLU	variant	UNP P0A7X3

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	D	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	5	ALA	PRO	variant	UNP P0A7R9

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	E	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	F	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	VAL	MET	variant	UNP P0A7S9

- Molecule 50 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	G	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	40	ALA	ASP	variant	UNP P0AG59

- Molecule 51 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	H	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	I	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	J	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	2	ALA	THR	variant	UNP P0AG63

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	K	55	Total	C	N	O	0	0
			455	288	86	81		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	15	THR	ALA	variant	UNP P0A7T7
K	19	VAL	GLN	variant	UNP P0A7T7

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	t	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	82	TYR	GLY	variant	UNP P0A7U3
t	83	TYR	HIS	variant	UNP P0A7U3

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	u	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	1	LEU	MET	variant	UNP P0A7U7

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	51	Total	C	N	O	S	0	0
			421	263	86	71	1		

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

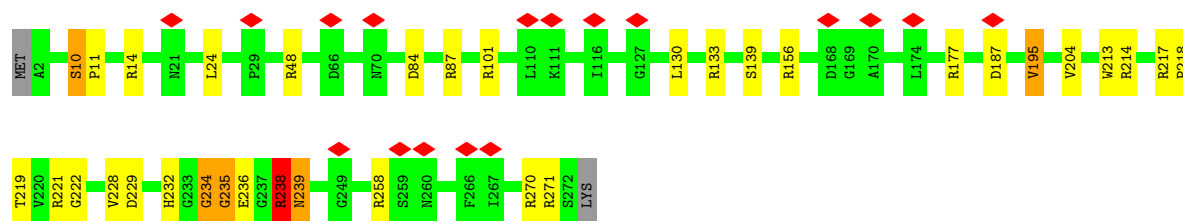
Mol	Chain	Residues	Atoms		AltConf
58	A	2	Total	Mg	0
			2	2	

- Molecule 59 is POTASSIUM ION (three-letter code: K) (formula: K).

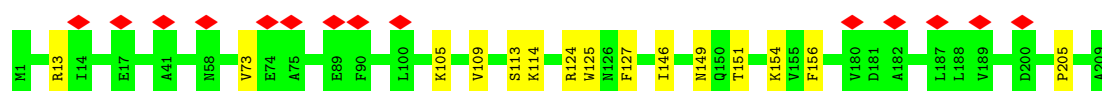
Mol	Chain	Residues	Atoms		AltConf
59	A	1	Total	K	0
			1	1	

- Molecule 60 is water.

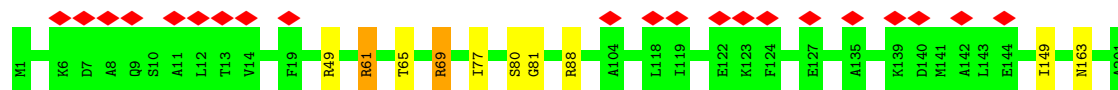
Mol	Chain	Residues	Atoms		AltConf
60	A	9	Total	O	0
			9	9	



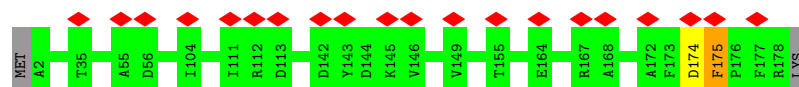
• Molecule 6: 50S ribosomal protein L3



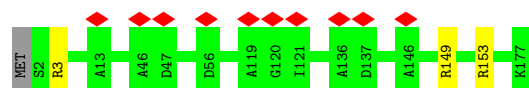
• Molecule 7: 50S ribosomal protein L4



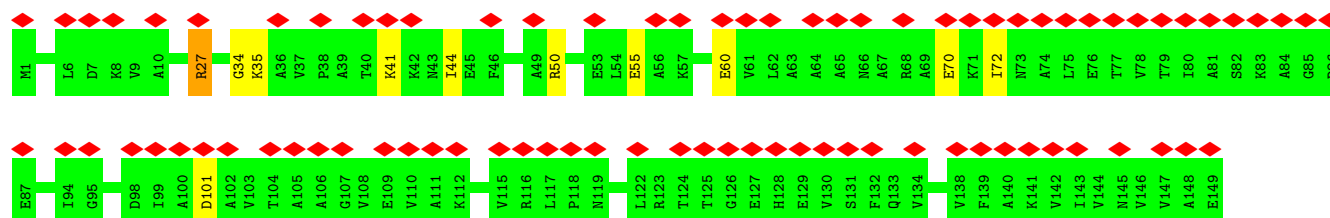
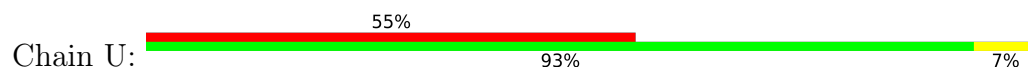
• Molecule 8: 50S ribosomal protein L5



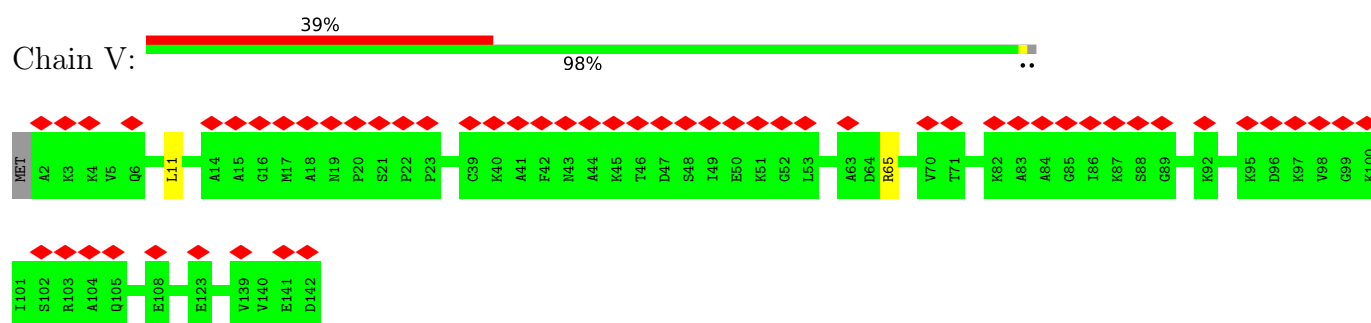
• Molecule 9: 50S ribosomal protein L6



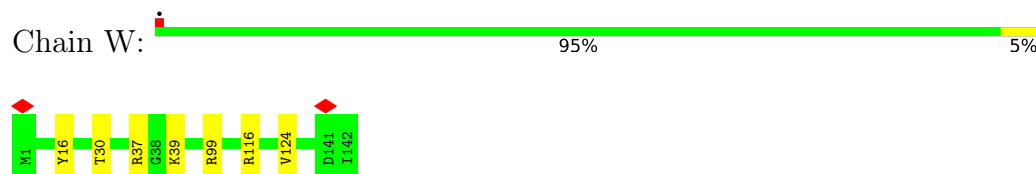
• Molecule 10: 50S ribosomal protein L9



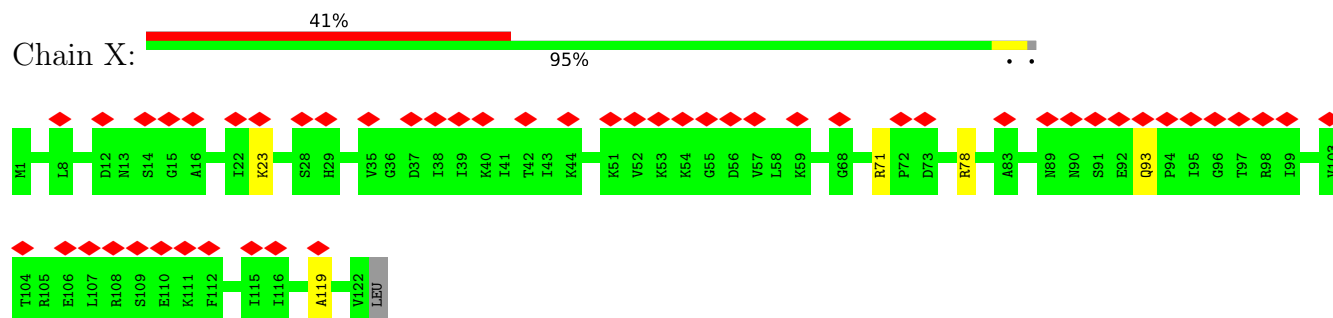
• Molecule 11: 50S ribosomal protein L11



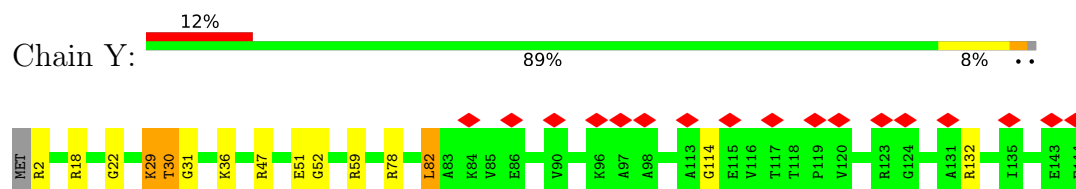
- Molecule 12: 50S ribosomal protein L13



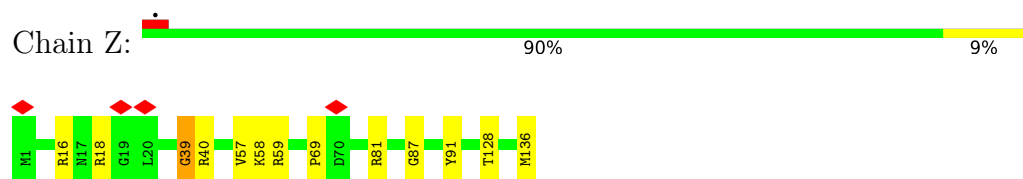
- Molecule 13: 50S ribosomal protein L14



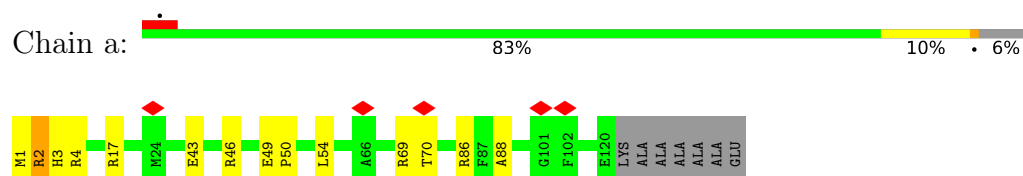
- Molecule 14: 50S ribosomal protein L15



- Molecule 15: 50S ribosomal protein L16



- Molecule 16: 50S ribosomal protein L17




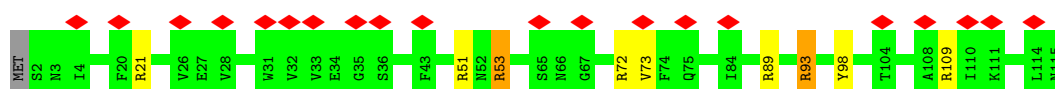
- Molecule 17: 50S ribosomal protein L18

Chain b:  94% 5%




- Molecule 18: 50S ribosomal protein L19

Chain c:  17% 91% 6%




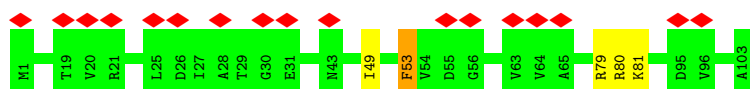
- Molecule 19: 50S ribosomal protein L20

Chain d:  88% 10%



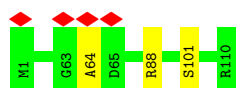
- Molecule 20: 50S ribosomal protein L21

Chain e:  17% 95%




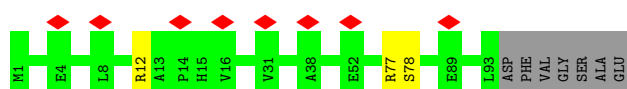
- Molecule 21: 50S ribosomal protein L22

Chain f:  97%



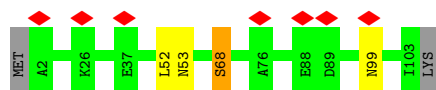
- Molecule 22: 50S ribosomal protein L23

Chain g:  8% 90% 7%

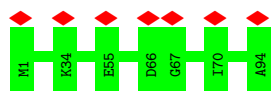


- Molecule 23: 50S ribosomal protein L24

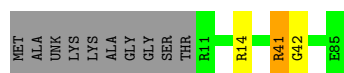
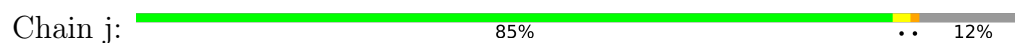
Chain h:  7% 94%



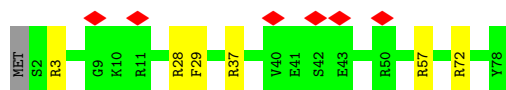
- Molecule 24: 50S ribosomal protein L25



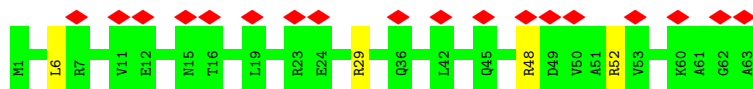
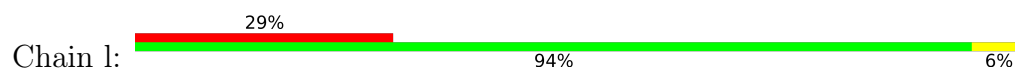
- Molecule 25: 50S ribosomal protein L27



- Molecule 26: 50S ribosomal protein L28



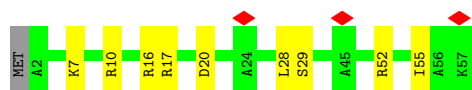
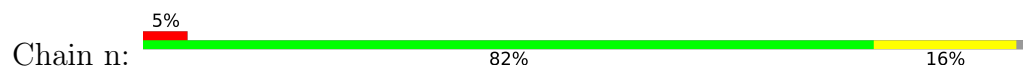
- Molecule 27: 50S ribosomal protein L29



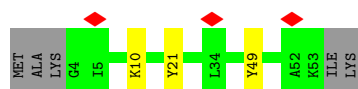
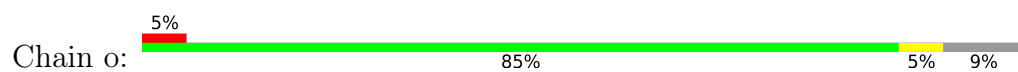
- Molecule 28: 50S ribosomal protein L30



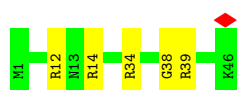
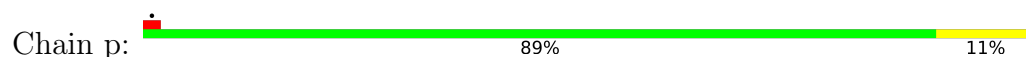
- Molecule 29: 50S ribosomal protein L32



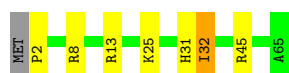
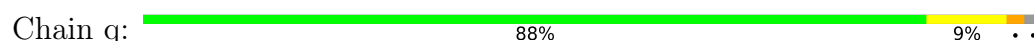
- Molecule 30: 50S ribosomal protein L33



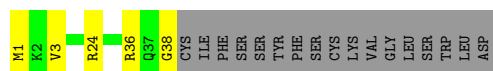
- Molecule 31: 50S ribosomal protein L34



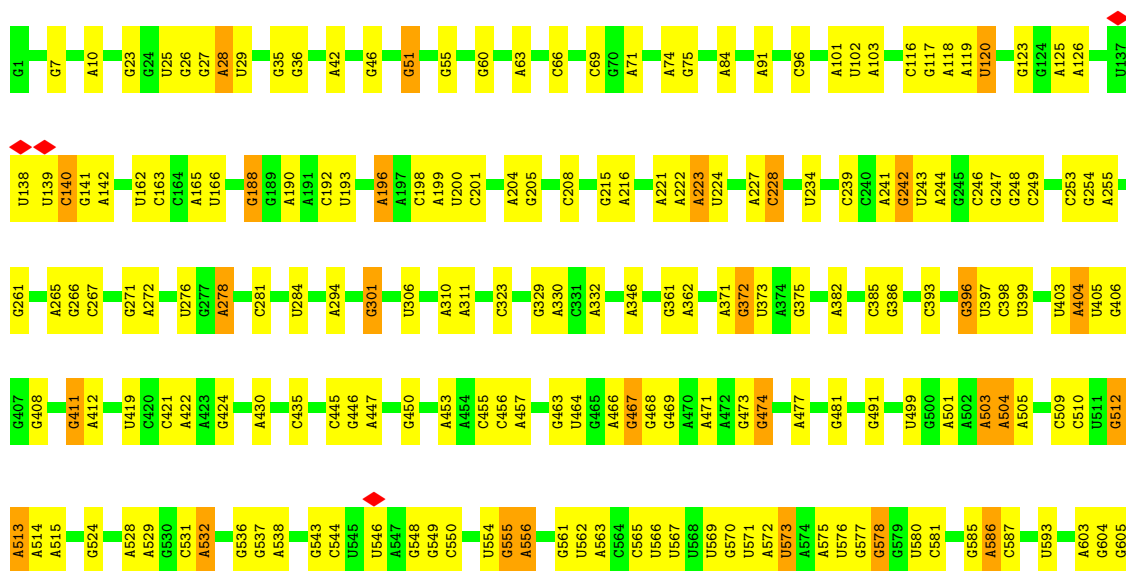
- Molecule 32: 50S ribosomal protein L35



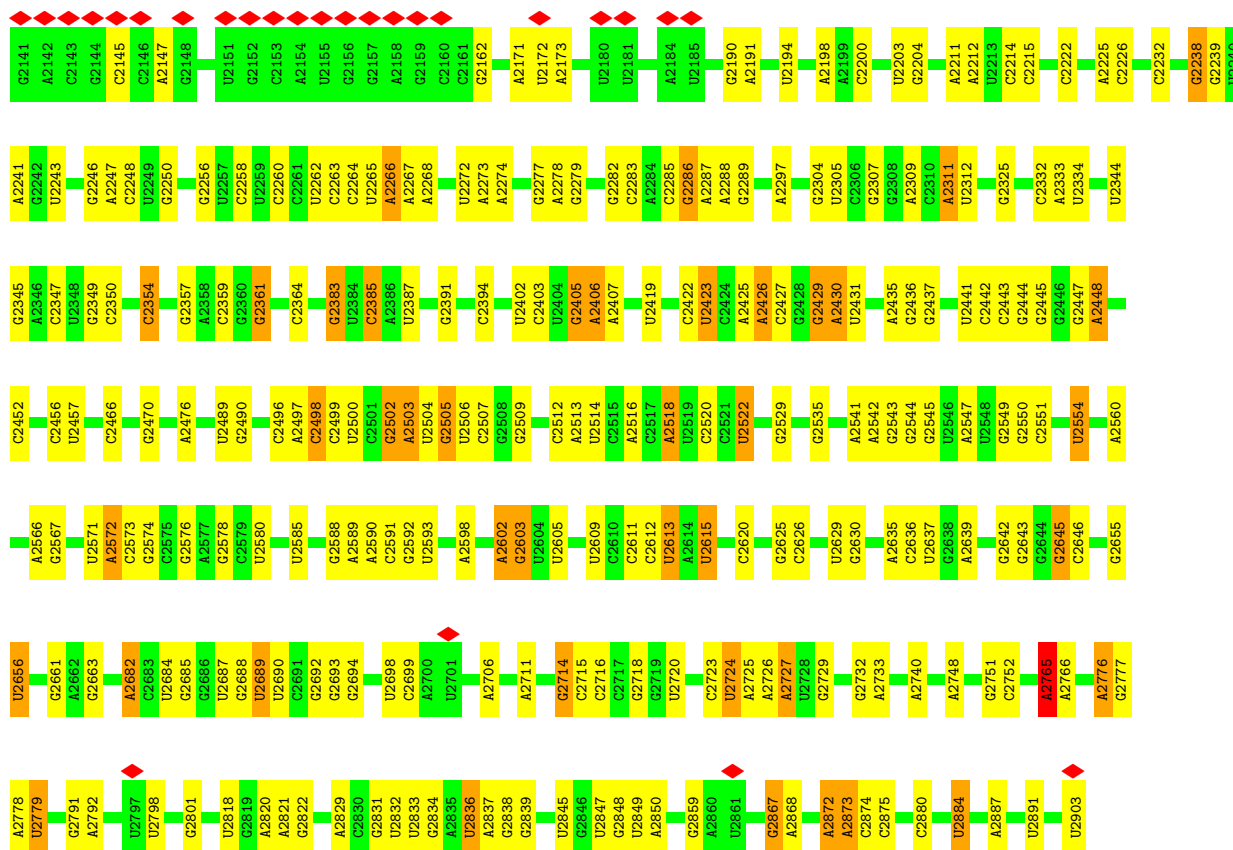
- Molecule 33: 50S ribosomal protein L36



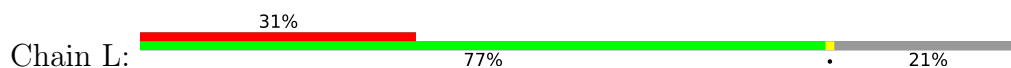
- Molecule 34: 23S rRNA



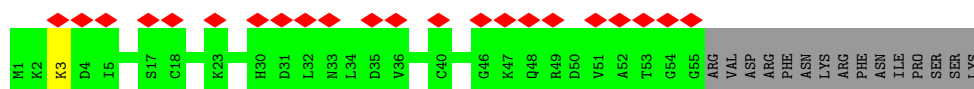
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C1967	G1968	A1969	U1970	U1971	G1972	G1973	A1977	C1985	C1990	U1991	U1992	U1993	C1994	U1995	C1996	C1997	A1998	C2003	G2004	A2005	U2007	U2011	U2012	A2013	G2014	A2015	U2016	U2017	U2018	A2019	A2020	C2021	C2022	U2023	G2024	C2025	U2028	A2031	G2032	A2033	G2035	U2036	A2037	C2043	C2044	C2045	G2046																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
U1834	G1835	C1836	C1837	C1843	C1844	G1857	U1864	U1865	G1869	C1870	A1900	A1901	U1994	U1995	C1996	C1997	A1998	C2003	G2004	A2005	U2007	U2011	U2012	A2013	G2014	A2015	U2016	U2017	U2018	A2019	A2020	C2021	C2022	U2023	G2024	C2025	U2028	A2031	G2032	A2033	G2035	U2036	A2037	C2043	C2044	C2045	G2046																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
C1764	G1770	C1771	A1772	A1773	C1774	U1777	U1778	U1779	A1780	U1781	U1782	A1783	A1784	A1785	A1786	A1787	C1788	A1789	C1790	C1793	A1794	C1795	U1796	U1797	U1798	G1799	C1800	A1801	A1802	A1805	U1808	A1809	A1810	G1811	U1812	G1813	G1814	A1815	C1816	G1817	C1822	G1823	G1824	U1825	G1826	U1827	C2036	U1828	A1829	C1830	G1831	C1832	C1833																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
U1650	G1651	A1652	C1658	U1662	G1663	A1664	U1665	G1666	G1667	A1668	A1669	C1670	U1671	A1672	G1673	G1674	C1675	A1676	A1677	A1678	A1679	U1680	G1681	U1688	G1695	A1696	G1697	C1708	U1713	U1714	G1715	G1723	C1728	U1729	C1730	G1733	G1734	G1738	U1742	U1743	U1751	G1756	A1757	U1758	A1759	C1760																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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G1110	A1111	G1112	U1119	G1122	U1130	G1131	U1132	A1133	A1134	G1135	G1136	U1141	A1142	A1143	C1145	C1152	A1153	G1154	A1155	A1156	G1168	G1171	C1172	U1173	U1174	G1175	G1179	U1180	G1186	G1187	U1188	A1189	G1190	G1191	G1195	C1196	U1203	A1204	A1205	G1206	G1210	C1211	G1212																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
U1004	C1005	A1006	C1007	A1008	A1009	A1010	G1011	U1012	C1013	U1019	A1020	A1021	G1022	U1023	G1024	A1029	C1030	G1031	A1032	U1033	A1046	G1047	A1057	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	A1077	U1082	U1083	A1088	A1089	A1090	U1094	A1095	A1096	U1097	C1100	C1104																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
G696	G697	C698	A699	G704	C717	G725	G726	A727	G728	G729	A730	G733	G738	A739	C740	A741	A742	G745	U746	U747	G748	A752	G760	A761	A764	C765	G771	C772	U773	G774	G775	G776	G777	G780	A781	A782	A783	G784	G785	C786	C787	U790	C791	A792	C795	C796																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
A800	G801	A802	U803	A804	G805	C806	G809	U810	U811	C812	U813	G818	A819	A820	A821	U824	A825	U826	U827	U828	A829	G830	U831	U832	U839	C840	A845	G846	C847	U850	G858	G859	U860	A866	G869	U870	U871	A878	C885	A	U	C	C	A892	A896																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
C897	G907	A910	G914	C915	A919	U919	G923	A927	U932	G940	A941	A942	A943	A944	A945	U946	A947	C948	G953	G954	U955	A960	C961	G962	U963	G966	U967	A973	G974	A975	G976	G977	G978	A981	G982	A983	A984	C985	G989	A990	C995	A996	G997																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
U869	G870	A871	A872	A873	G874	G875	C876	C877	U878	A879	A880	A881	U882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967	A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000	A1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	A1011	A1012	A1013	A1014	A1015	A1016	A1017	A1018	A1019	A1020	A1021	A1022	A1023	A1024	A1025	A1026	A1027	A1028	A1029	A1030	A1031	A1032	A1033	A1034	A1035	A1036	A1037	A1038	A1039	A1040	A1041	A1042	A1043	A1044	A1045	A1046	A1047	A1048	A1049	A1050	A1051	A1052	A1053	A1054	A1055	A1056	A1057	A1058	A1059	A1060	A1061	A1062	A1063	A1064	A1065	A1066	A1067	A1068	A1069	A1070	A1071	A1072	A1073	A1074	A1075	A1076	A1077	A1078	A1079	A1080	A1081	A1082	A1083	A1084	A1085	A1086	A1087	A1088	A1089	A1090	A1091	A1092	A1093	A1094	A1095	A1096	A1097	A1098	A1099	A1100	A1101	A1102	A1103	A1104	A1105	A1106	A1107	A1108	A1109	A1110	A1111	A1112	A1113	A1114	A1115	A1116	A1117	A1118	A1119	A1120	A1121	A1122	A1123	A1124	A1125	A1126	A1127	A1128	A1129	A1130	A1131	A1132	A1133	A1134	A1135	A1136	A1137	A1138	A1139	A1140	A1141	A1142	A1143	A1144	A1145	A1146	A1147	A1148	A1149	A1150	A1151	A1152	A1153	A1154	A1155	A1156	A1157	A1158	A1159	A1160	A1161	A1162	A1163	A1164	A1165	A1166	A1167	A1168	A1169	A1170	A1171	A1172	A1173	A1174	A1175	A1176	A1177	A1178	A1179	A1180	A1181	A1182	A1183	A1184	A1185	A1186	A1187	A1188	A1189	A1190	A1191	A1192	A1193	A1194	A1195	A1196	A1197	A1198	A1199	A1200	A1201	A1202	A1203	A1204	A1205	A1206	A1207	A1208	A1209	A1210	A1211	A1212	A1213	A1214	A1215	A1216	A1217	A1218	A1219	A1220	A1221	A1222	A1223	A1224	A1225	A1226	A1227	A1228	A1229	A1230	A1231	A1232	A1233	A1234	A1235	A1236	A1237	A1238	A1239	A1240	A1241	A1242	A1243	A1244	A1245	A1246	A1247	A1248	A1249	A1250	A1251	A1252	A1253	A1254	A1255	A1256	A1257	A1258	A1259	A1260	A1261	A1262	A1263	A1264	A1265	A1266	A1267	A1268	A1269	A1270	A1271	A1272	A1273	A1274	A1275	A1276	A1277	A1278	A1279	A1280	A1281	A1282	A1283	A1284	A1285	A1286	A1287	A1288	A1289	A1290	A1291	A1292	A1293	A1294	A1295	A1296	A1297	A1298	A1299	A1300	A1301	A1302	A1303	A1304	A1305	A1306	A1307	A1308	A1309	A1310	A1311	A1312	A1313	A1314	A1315	A1316	A1317	A1318	A1319	A1320	A1321	A1322	A1323	A1324	A1325	A1326	A1327	A1328	A1329	A1330	A1331	A1332	A1333	A1334	A1335	A1336	A1337	A1338	A1339	A1340	A1341	A1342	A1343	A1344	A1345	A1346	A1347	A1348	A1349	A1350	A1351	A1352	A1353	A1354	A1355	A1356	A1357	A1358	A1359	A1360	A1361	A1362	A1363	A1364	A1365	A1366	A1367	A1368	A1369	A1370	A1371	A1372	A1373	A1374	A1375	A1376	A1377	A1378	A1379	A1380	A1381	A1382	A1383	A1384	A1385	A1386	A1387	A1388	A1389	A1390	A1391	A1392	A1393	A1394	A1395	A1396	A1397	A1398	A1399	A1400	A1401	A1402	A1403	A1404	A1405	A1406	A1407	A1408	A1409	A1410	A1411	A1412	A1413	A1414	A1415	A1416	A1417	A1418	A1419	A1420	A1421	A1422	A1423	A1424	A1425	A1426	A1427	A1428	A1429	A1430	A1431	A1432	A1433	A1434	A1435	A1436	A1437	A1438	A1439	A1440	A1441	A1442	A1443	A1444	A1445	A1446	A1447	A1448	A1449	A1450	A1451	A1452	A1453	A1454	A1455	A1456	A1457	A1458	A1459	A1460	A1461	A1462	A1463	A1464	A1465	A1466	A1467	A1468	A1469	A1470	A1471	A1472	A1473	A1474	A1475	A1476	A1477	A1478	A1479	A1480	A1481	A1482	A1483	A1484	A1485	A1486	A1487	A1488	A1489	A1490	A1491	A1492	A1493	A1494	A1495	A1496	A1497	A1498	A1499	A1500	A1501	A1502	A1503	A1504	A1505	A1506	A1507	A1508	A1509	A1510	A1511	A1512	A1513	A1514	A1515	A1516	A1517	A1518	A1519	A1520	A1521	A1522	A1523	A1524	A1525	A1526	A1527	A1528	A1529	A1530	A1531	A1532	A1533	A1534	A1535	A1536	A1537	A1538	A1539	A1540	A1541	A1542	A1543	A1544	A1545	A1546	A1547	A1548	A1549	A1550	A1551	A1552	A1553	A1554	A1555	A1556	A1557	A1558	A1559	A1560	A1561	A1562	A1563	A1564	A1565	A1566	A1567	A1568	A1569	A1570	A1571	A1572	A1573	A1574	A1575	A1576	A1577	A1578	A1579	A1580	A1581	A1582	A1583	A1584	A1585	A1586	A1587	A1588	A1589	A1590	A1591	A1592	A1593	A1594	A1595	A1596	A1597	A1598	A1599	A1600	A1601	A1602	A1603	A1604	A1605	A1606	A1607	A1608	A1609	A1610	A1611	A1612	A1613	A1614	A1615	A1616	A1617	A1618	A1619	A1620	A1621	A1622	A1623	A1624	A1625	A1626	A1627	A1628	A1629	A1630	A1631	A1632	A1633	A1634	A1635	A1636	A1637	A1638	A1639	A1640	A1641	A1642	A1643	A1644	A1645	A1646	A1647	A1648	A1649	A1650	A1651	A1652	A1653	A1654	A1655	A1656	A1657	A1658	A1659	A1660	A1661	A1662	A1663	A1664	A1665	A1666	A1667	A1668	A1669	A1670	A1671	A1672	A1673	A1674	A1



• Molecule 35: 50S ribosomal protein L31



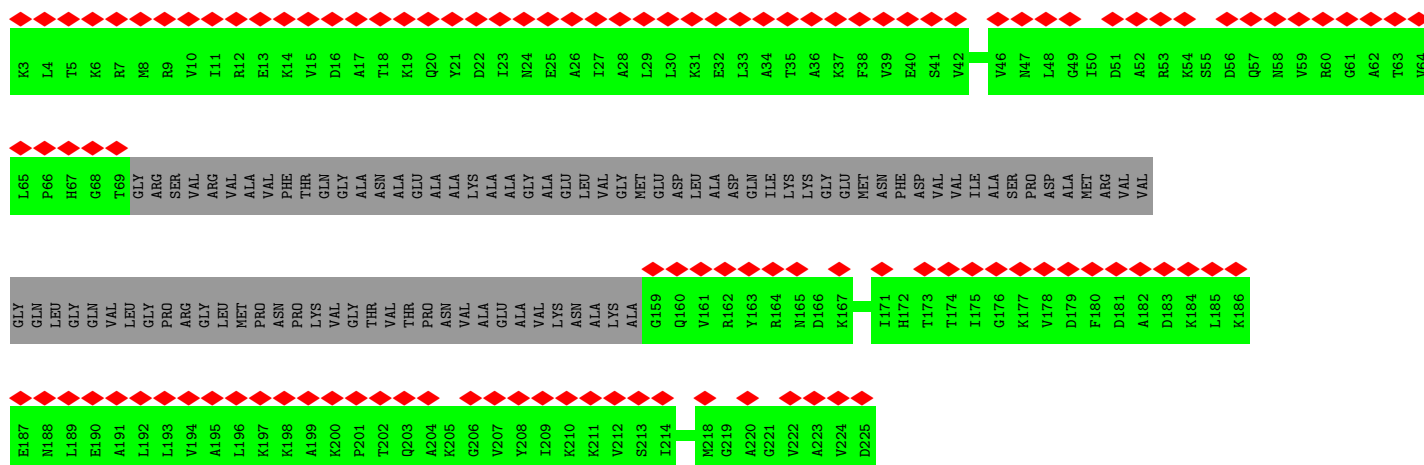
Chain L:



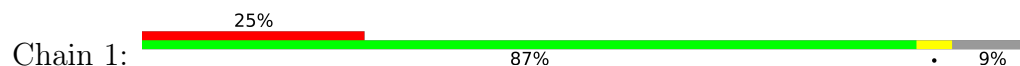
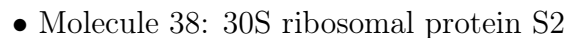
• Molecule 36: 50S ribosomal protein L1

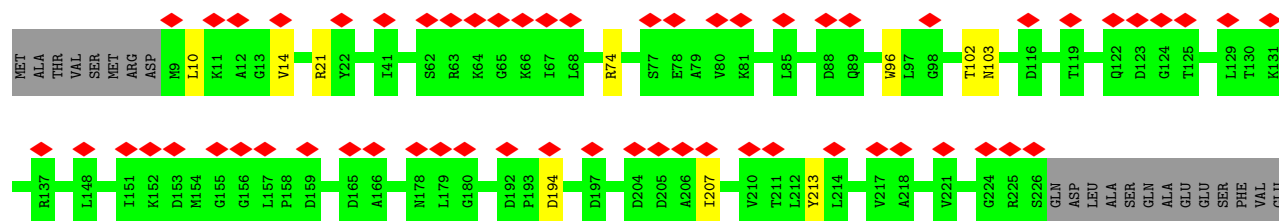


Chain C:

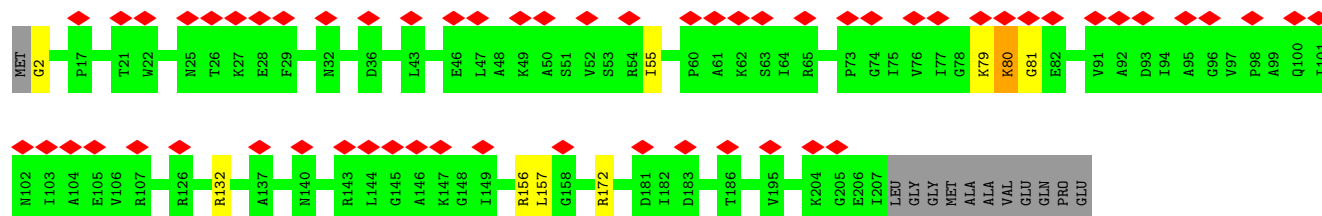
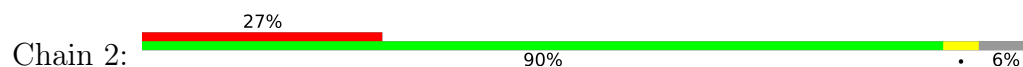


Chain 0: 72% 25% .

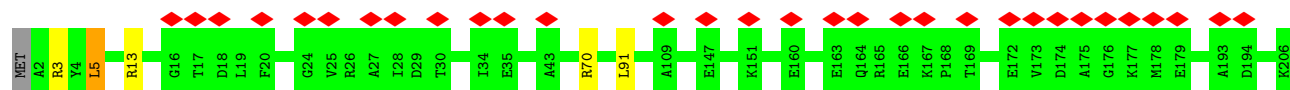




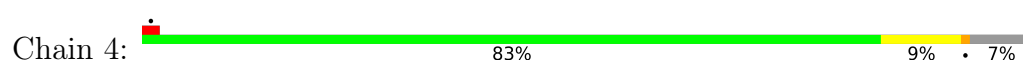
- Molecule 39: 30S ribosomal protein S3



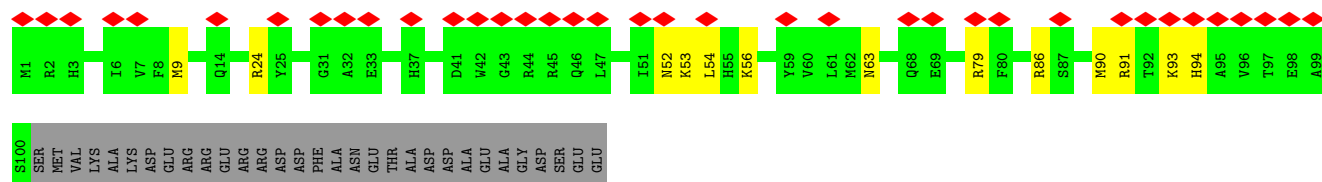
- Molecule 40: 30S ribosomal protein S4



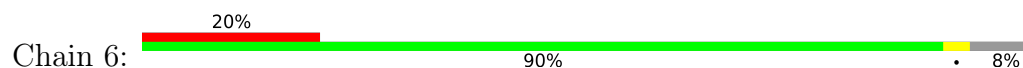
- Molecule 41: 30S ribosomal protein S5

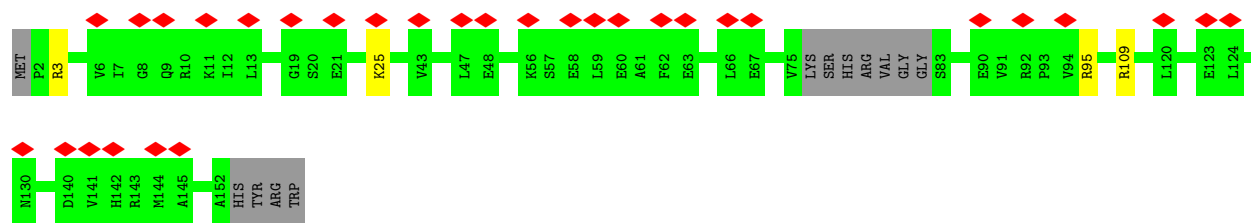


- Molecule 42: 30S ribosomal protein S6, non-modified isoform

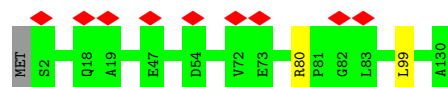


- Molecule 43: 30S ribosomal protein S7

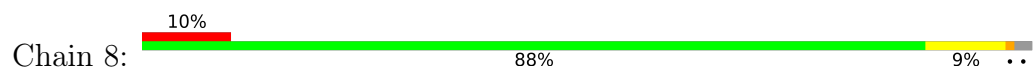




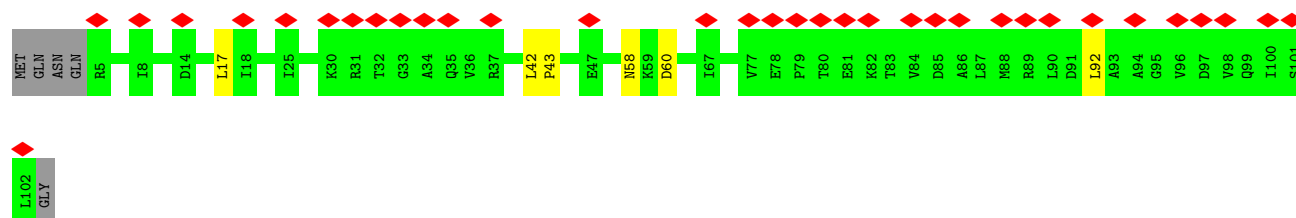
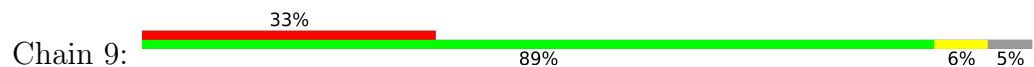
- Molecule 44: 30S ribosomal protein S8



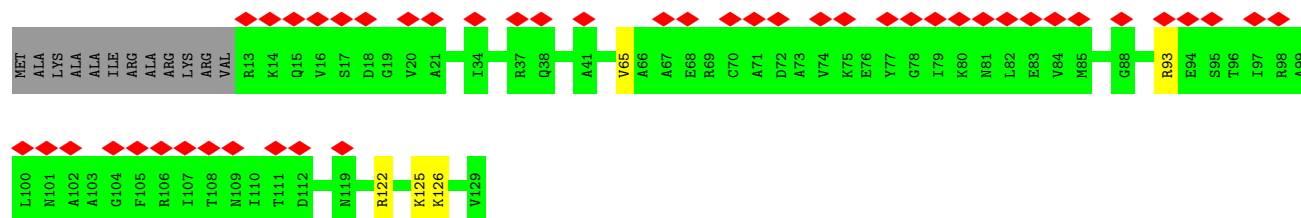
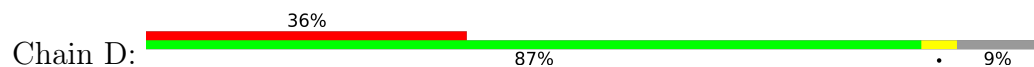
- Molecule 45: 30S ribosomal protein S9



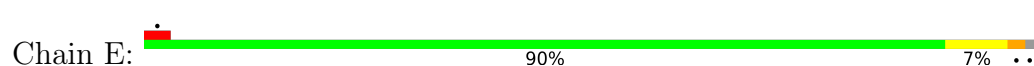
- Molecule 46: 30S ribosomal protein S10

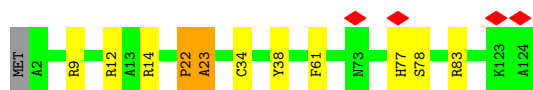


- Molecule 47: 30S ribosomal protein S11

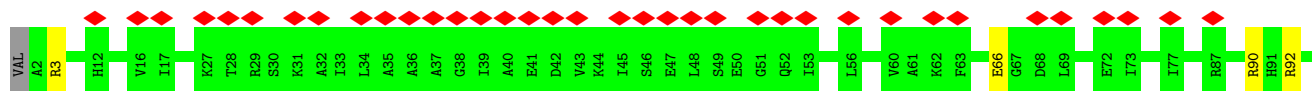
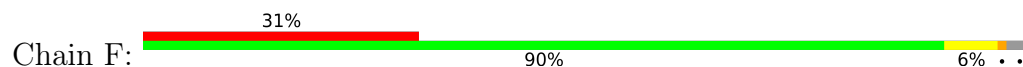


- Molecule 48: 30S ribosomal protein S12

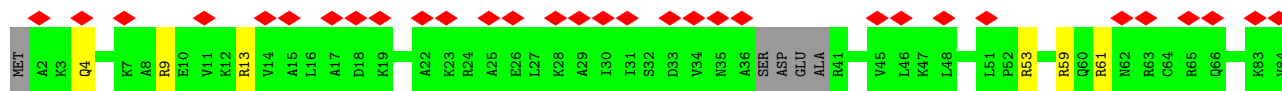
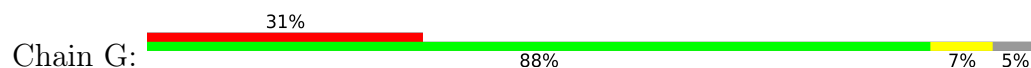




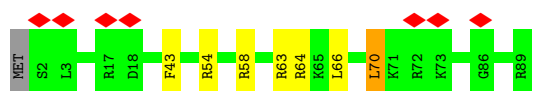
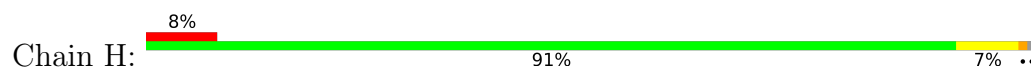
- Molecule 49: 30S ribosomal protein S13



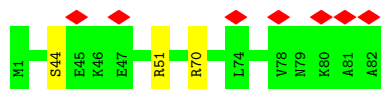
- Molecule 50: 30S ribosomal protein S14



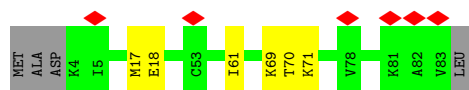
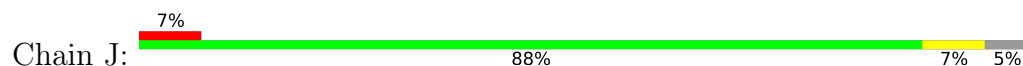
- Molecule 51: 30S ribosomal protein S15



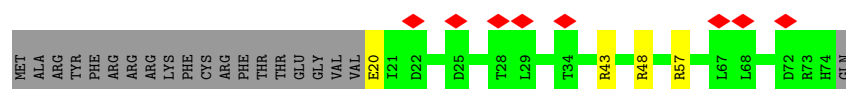
- Molecule 52: 30S ribosomal protein S16



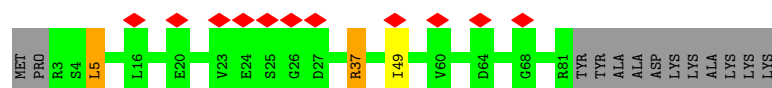
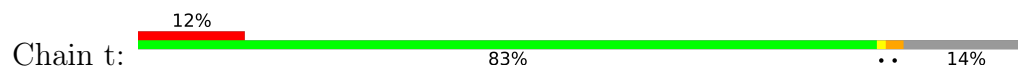
- Molecule 53: 30S ribosomal protein S17



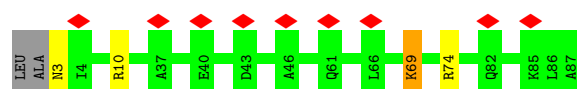
- Molecule 54: 30S ribosomal protein S18



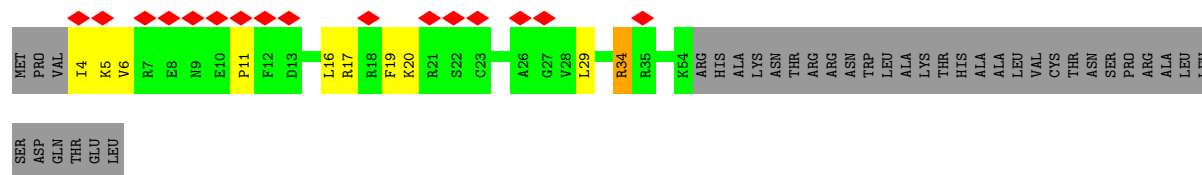
- Molecule 55: 30S ribosomal protein S19



- Molecule 56: 30S ribosomal protein S20



- Molecule 57: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75081	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)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.540	Depositor
Minimum map value	-0.736	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.148	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	654.0, 654.0, 654.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.66	1/1744 (0.1%)	0.86	0/2716
2	s	0.90	1/326 (0.3%)	0.80	1/441 (0.2%)
3	M	0.63	3/1779 (0.2%)	0.83	2/2768 (0.1%)
4	O	0.79	1/2828 (0.0%)	0.88	7/4410 (0.2%)
5	P	1.41	22/2121 (1.0%)	1.32	27/2852 (0.9%)
6	Q	1.18	3/1585 (0.2%)	1.13	8/2134 (0.4%)
7	R	0.97	3/1571 (0.2%)	1.02	9/2113 (0.4%)
8	S	0.67	0/1434	0.85	0/1926
9	T	0.67	0/1342	0.83	4/1816 (0.2%)
10	U	0.51	0/1122	0.78	1/1515 (0.1%)
11	V	0.53	0/1045	0.66	0/1410
12	W	1.10	3/1151 (0.3%)	1.10	7/1551 (0.5%)
13	X	1.15	0/947	1.19	4/1268 (0.3%)
14	Y	1.30	3/1053 (0.3%)	1.38	12/1403 (0.9%)
15	Z	1.13	2/1092 (0.2%)	1.19	6/1460 (0.4%)
16	a	1.28	3/973 (0.3%)	1.29	10/1301 (0.8%)
17	b	0.84	2/901 (0.2%)	1.08	8/1209 (0.7%)
18	c	1.09	3/927 (0.3%)	1.19	8/1240 (0.6%)
19	d	1.32	4/959 (0.4%)	1.37	15/1278 (1.2%)
20	e	1.08	1/828 (0.1%)	1.08	3/1107 (0.3%)
21	f	1.02	1/864 (0.1%)	1.09	1/1156 (0.1%)
22	g	0.91	0/744	1.01	1/994 (0.1%)
23	h	0.82	1/787 (0.1%)	0.89	0/1051
24	i	0.78	0/765	0.87	0/1025
25	j	1.21	2/575 (0.3%)	1.29	5/762 (0.7%)
26	k	1.09	1/634 (0.2%)	1.15	6/848 (0.7%)
27	l	0.71	0/509	1.04	4/677 (0.6%)
28	m	0.86	0/452	1.08	2/605 (0.3%)
29	n	1.16	2/449 (0.4%)	1.42	7/599 (1.2%)
30	o	1.31	7/416 (1.7%)	0.96	1/554 (0.2%)
31	p	1.38	3/379 (0.8%)	1.76	6/498 (1.2%)
32	q	1.15	0/512	1.26	6/676 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	r	1.16	1/302 (0.3%)	1.35	5/397 (1.3%)
34	N	1.24	514/69681 (0.7%)	1.04	349/108706 (0.3%)
35	L	0.61	0/426	0.78	0/570
36	C	0.28	0/1034	0.51	0/1387
37	0	0.97	134/36809 (0.4%)	0.93	106/57423 (0.2%)
38	1	0.82	2/1735 (0.1%)	0.94	4/2338 (0.2%)
39	2	0.85	1/1651 (0.1%)	0.95	4/2225 (0.2%)
40	3	0.76	0/1664	0.98	6/2227 (0.3%)
41	4	1.12	1/1118 (0.1%)	1.21	7/1504 (0.5%)
42	5	0.90	1/835 (0.1%)	1.03	4/1128 (0.4%)
43	6	0.66	0/1142	0.95	6/1532 (0.4%)
44	7	0.88	0/988	0.99	2/1326 (0.2%)
45	8	0.86	0/1033	1.13	7/1375 (0.5%)
46	9	0.74	0/796	1.01	2/1077 (0.2%)
47	D	0.86	1/892 (0.1%)	1.03	3/1205 (0.2%)
48	E	1.09	3/968 (0.3%)	1.22	7/1300 (0.5%)
49	F	0.85	1/892 (0.1%)	1.12	9/1193 (0.8%)
50	G	0.86	0/784	1.14	7/1043 (0.7%)
51	H	0.94	0/717	1.13	8/959 (0.8%)
52	I	0.94	0/658	1.16	3/884 (0.3%)
53	J	0.82	0/657	1.02	0/881
54	K	0.98	1/462 (0.2%)	1.10	2/621 (0.3%)
55	t	0.81	0/652	1.05	3/877 (0.3%)
56	u	0.89	0/670	1.06	3/888 (0.3%)
57	v	0.99	1/426 (0.2%)	1.15	2/565 (0.4%)
All	All	1.09	733/159806 (0.5%)	1.02	720/238994 (0.3%)

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
5	P	0	3
6	Q	0	1
8	S	0	2
10	U	0	1
11	V	0	1
14	Y	0	2
15	Z	0	2
23	h	0	1
32	q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	6
37	0	0	5
38	1	0	3
39	2	0	2
41	4	0	5
42	5	0	2
45	8	0	4
47	D	0	1
48	E	0	2
53	J	0	2
55	t	0	1
56	u	0	1
57	v	0	1
All	All	0	49

The worst 5 of 733 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	2873	A	C6-N1	-20.40	1.21	1.35
34	N	2765	A	C6-N1	-18.58	1.22	1.35
34	N	2502	G	P-OP2	16.61	1.77	1.49
34	N	503	A	C6-N1	-15.24	1.24	1.35
34	N	1156	A	P-OP2	15.21	1.74	1.49

The worst 5 of 720 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	N	2506[A]	U	OP1-P-O3'	17.17	142.97	105.20
34	N	2506[B]	U	OP1-P-O3'	17.17	142.97	105.20
31	p	39	ARG	NE-CZ-NH1	16.09	128.35	120.30
31	p	39	ARG	NE-CZ-NH2	-14.86	112.87	120.30
3	M	73	C	O3'-P-O5'	14.33	131.23	104.00

There are no chirality outliers.

5 of 49 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	P	195	VAL	Peptide
5	P	234	GLY	Peptide
5	P	238	ARG	Peptide
6	Q	151	THR	Peptide

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Mol	Chain	Res	Type	Group
8	S	174	ASP	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	s	35/179 (20%)	32 (91%)	3 (9%)	0	100	100
5	P	269/273 (98%)	247 (92%)	18 (7%)	4 (2%)	8	39
6	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	25	61
7	R	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	22	58
9	T	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
10	U	147/149 (99%)	125 (85%)	19 (13%)	3 (2%)	6	33
11	V	139/142 (98%)	112 (81%)	27 (19%)	0	100	100
12	W	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
13	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	7	36
14	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	4	27
15	Z	134/136 (98%)	119 (89%)	10 (8%)	5 (4%)	2	23
16	a	118/127 (93%)	102 (86%)	14 (12%)	2 (2%)	7	36
17	b	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
18	c	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
19	d	115/118 (98%)	115 (100%)	0	0	100	100
20	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	13	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	14	49
22	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	5	31
23	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	6	33
24	i	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
25	j	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
26	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	10	41
27	l	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
28	m	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
29	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	34
30	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
31	p	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
32	q	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	8	37
33	r	36/55 (66%)	35 (97%)	1 (3%)	0	100	100
35	L	53/70 (76%)	45 (85%)	7 (13%)	1 (2%)	6	34
36	C	130/223 (58%)	123 (95%)	7 (5%)	0	100	100
38	1	216/239 (90%)	187 (87%)	28 (13%)	1 (0%)	25	61
39	2	204/218 (94%)	186 (91%)	16 (8%)	2 (1%)	13	46
40	3	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
41	4	148/162 (91%)	116 (78%)	30 (20%)	2 (1%)	9	39
42	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1	15
43	6	140/156 (90%)	130 (93%)	10 (7%)	0	100	100
44	7	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	8	37
46	9	96/103 (93%)	84 (88%)	9 (9%)	3 (3%)	3	26
47	D	115/129 (89%)	102 (89%)	13 (11%)	0	100	100
48	E	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	7	36
49	F	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	14	49
50	G	92/101 (91%)	77 (84%)	14 (15%)	1 (1%)	12	44
51	H	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
52	I	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	10	41
53	J	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	K	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	6	34
55	t	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
56	u	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	11	42
57	v	49/88 (56%)	41 (84%)	7 (14%)	1 (2%)	6	33
All	All	5826/6442 (90%)	5264 (90%)	503 (9%)	59 (1%)	16	46

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	P	239	ASN
10	U	72	ILE
14	Y	36	LYS
15	Z	58	LYS
20	e	53	PHE

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	
2	s	34/158 (22%)	34 (100%)	0	100	100
5	P	216/218 (99%)	215 (100%)	1 (0%)	86	90
6	Q	164/164 (100%)	161 (98%)	3 (2%)	54	71
7	R	165/165 (100%)	161 (98%)	4 (2%)	44	63
8	S	148/150 (99%)	148 (100%)	0	100	100
9	T	137/138 (99%)	137 (100%)	0	100	100
10	U	114/114 (100%)	107 (94%)	7 (6%)	15	39
11	V	109/110 (99%)	108 (99%)	1 (1%)	75	83
12	W	116/116 (100%)	116 (100%)	0	100	100
13	X	103/104 (99%)	103 (100%)	0	100	100
14	Y	102/103 (99%)	102 (100%)	0	100	100
15	Z	109/109 (100%)	108 (99%)	1 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	a	100/102 (98%)	97 (97%)	3 (3%)	36	57
17	b	86/87 (99%)	86 (100%)	0	100	100
18	c	98/100 (98%)	95 (97%)	3 (3%)	35	56
19	d	89/90 (99%)	88 (99%)	1 (1%)	70	80
20	e	84/84 (100%)	82 (98%)	2 (2%)	44	63
21	f	93/93 (100%)	93 (100%)	0	100	100
22	g	80/85 (94%)	80 (100%)	0	100	100
23	h	83/85 (98%)	82 (99%)	1 (1%)	67	79
24	i	78/78 (100%)	78 (100%)	0	100	100
25	j	56/62 (90%)	55 (98%)	1 (2%)	54	71
26	k	67/68 (98%)	67 (100%)	0	100	100
27	l	55/55 (100%)	55 (100%)	0	100	100
28	m	48/49 (98%)	48 (100%)	0	100	100
29	n	47/48 (98%)	46 (98%)	1 (2%)	48	66
30	o	45/49 (92%)	45 (100%)	0	100	100
31	p	38/38 (100%)	38 (100%)	0	100	100
32	q	51/52 (98%)	49 (96%)	2 (4%)	27	50
33	r	34/50 (68%)	34 (100%)	0	100	100
35	L	48/63 (76%)	48 (100%)	0	100	100
36	C	110/174 (63%)	110 (100%)	0	100	100
38	1	180/198 (91%)	179 (99%)	1 (1%)	84	88
39	2	170/178 (96%)	169 (99%)	1 (1%)	84	88
40	3	172/173 (99%)	171 (99%)	1 (1%)	84	88
41	4	113/123 (92%)	110 (97%)	3 (3%)	40	60
42	5	87/112 (78%)	86 (99%)	1 (1%)	70	80
43	6	119/129 (92%)	118 (99%)	1 (1%)	79	84
44	7	104/105 (99%)	104 (100%)	0	100	100
45	8	105/107 (98%)	104 (99%)	1 (1%)	73	81
46	9	86/90 (96%)	85 (99%)	1 (1%)	67	79
47	D	90/98 (92%)	89 (99%)	1 (1%)	70	80
48	E	103/104 (99%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	F	92/96 (96%)	91 (99%)	1 (1%)	70	80
50	G	79/83 (95%)	79 (100%)	0	100	100
51	H	75/77 (97%)	74 (99%)	1 (1%)	65	77
52	I	65/65 (100%)	65 (100%)	0	100	100
53	J	74/77 (96%)	73 (99%)	1 (1%)	62	76
54	K	48/66 (73%)	48 (100%)	0	100	100
55	t	70/80 (88%)	68 (97%)	2 (3%)	37	58
56	u	65/66 (98%)	65 (100%)	0	100	100
57	v	43/76 (57%)	35 (81%)	8 (19%)	1	9
All	All	4847/5264 (92%)	4792 (99%)	55 (1%)	69	80

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	n	28	LEU
41	4	115	LEU
57	v	29	LEU
57	v	6	VAL
32	q	2	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
36	C	172	HIS
45	8	32	GLN
38	1	177	ASN
42	5	11	HIS
49	F	8	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	72/73 (98%)	19 (26%)	8 (11%)
3	M	74/75 (98%)	11 (14%)	0
34	N	2894/2903 (99%)	519 (17%)	34 (1%)
37	0	1531/1539 (99%)	275 (17%)	22 (1%)
4	O	117/120 (97%)	21 (17%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4688/4710 (99%)	845 (18%)	65 (1%)

5 of 845 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	C
1	A	14	A
1	A	16	U
1	A	17	C
1	A	18	G

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
37	0	1190	G
37	0	1300	G
34	N	784	G
34	N	774	G
37	0	1345	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

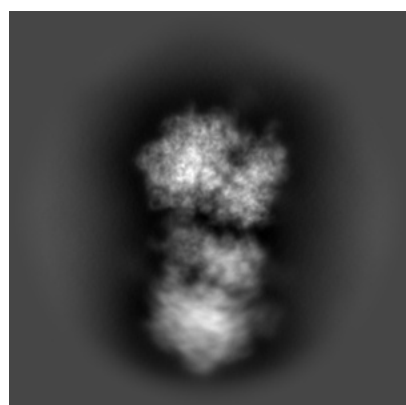
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13952. These allow visual inspection of the internal detail of the map and identification of artifacts.

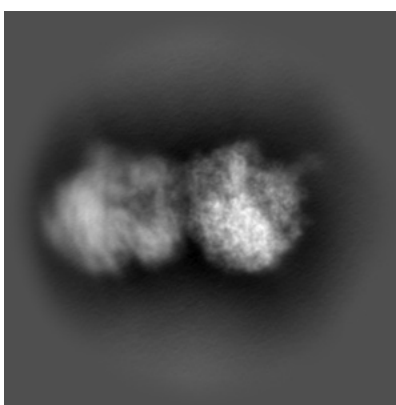
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

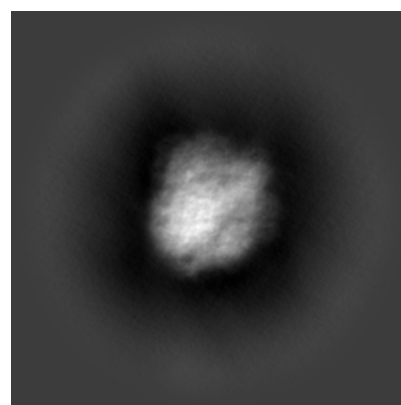
6.1.1 Primary map



X



Y

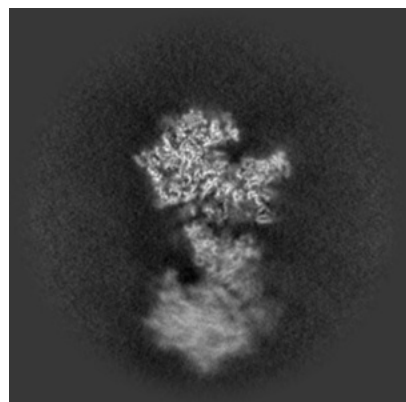


Z

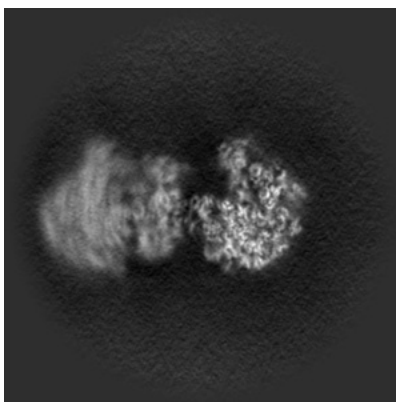
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

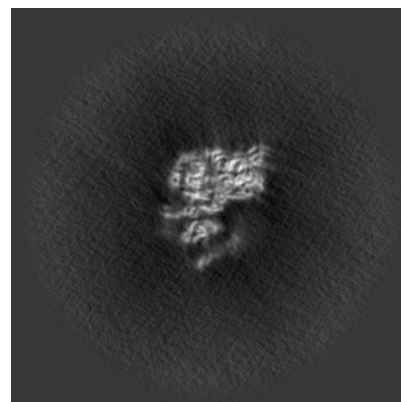
6.2.1 Primary map



X Index: 300



Y Index: 300

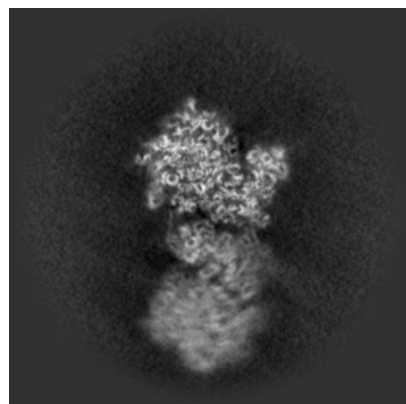


Z Index: 300

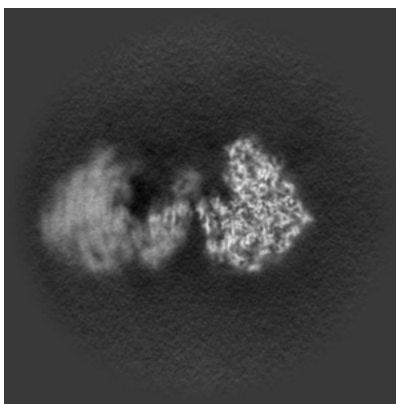
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

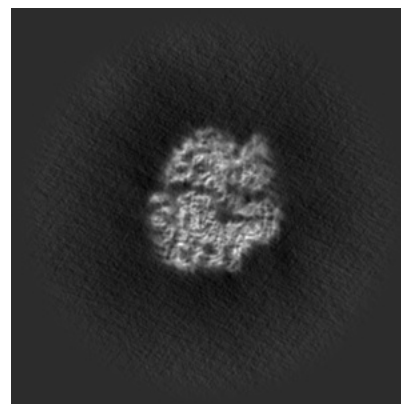
6.3.1 Primary map



X Index: 282



Y Index: 275

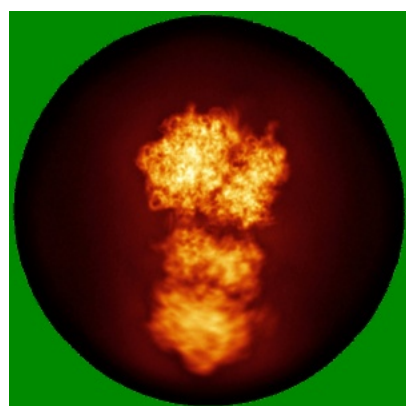


Z Index: 348

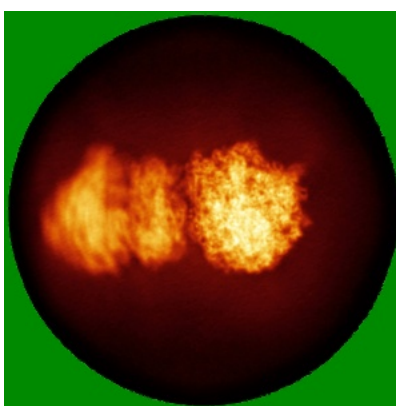
The images above show the largest variance slices of the map in three orthogonal directions.

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

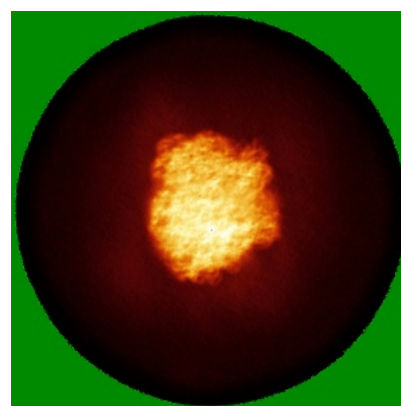
6.4.1 Primary map



X



Y



Z

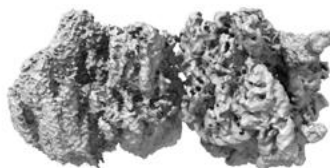
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

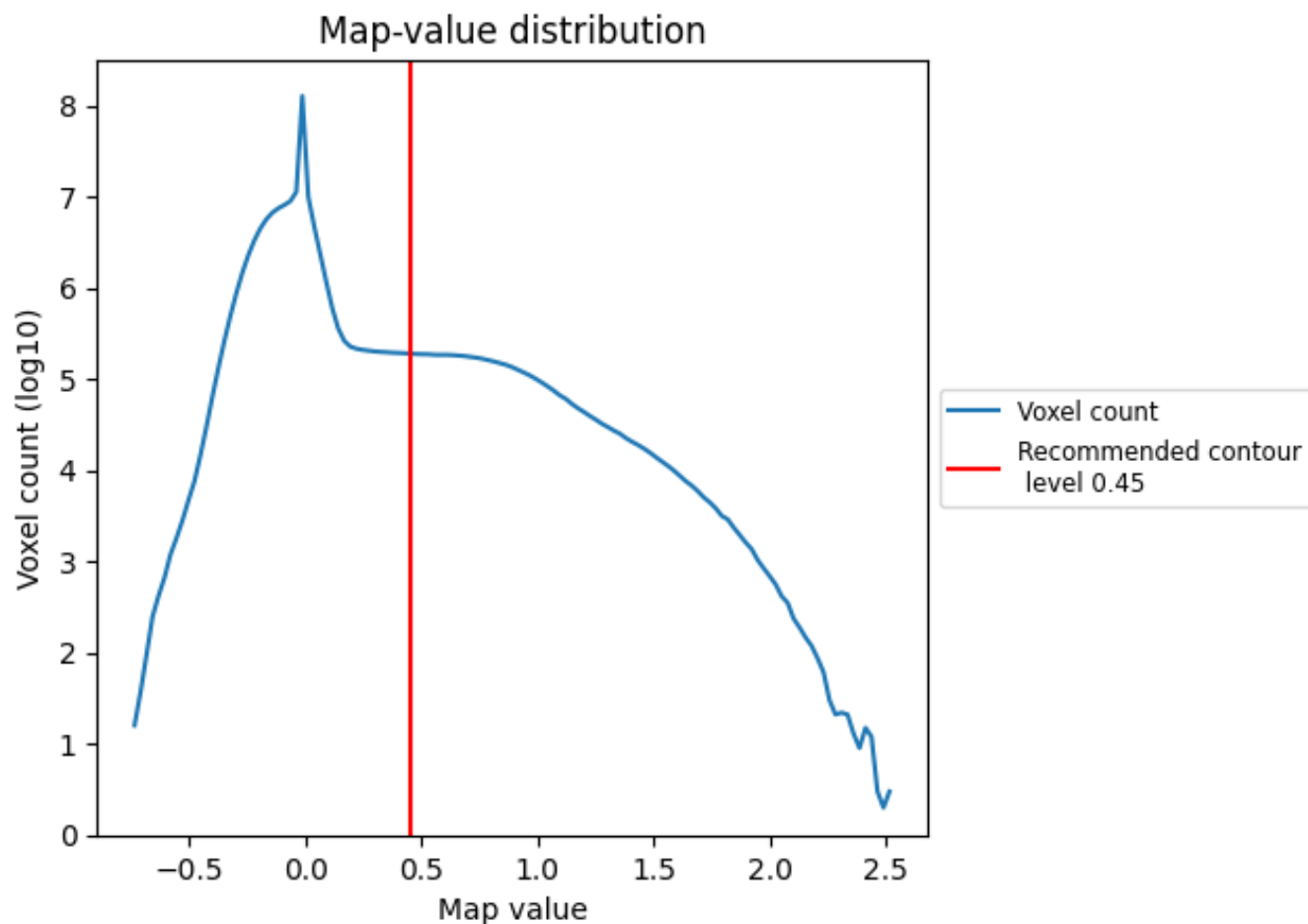
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

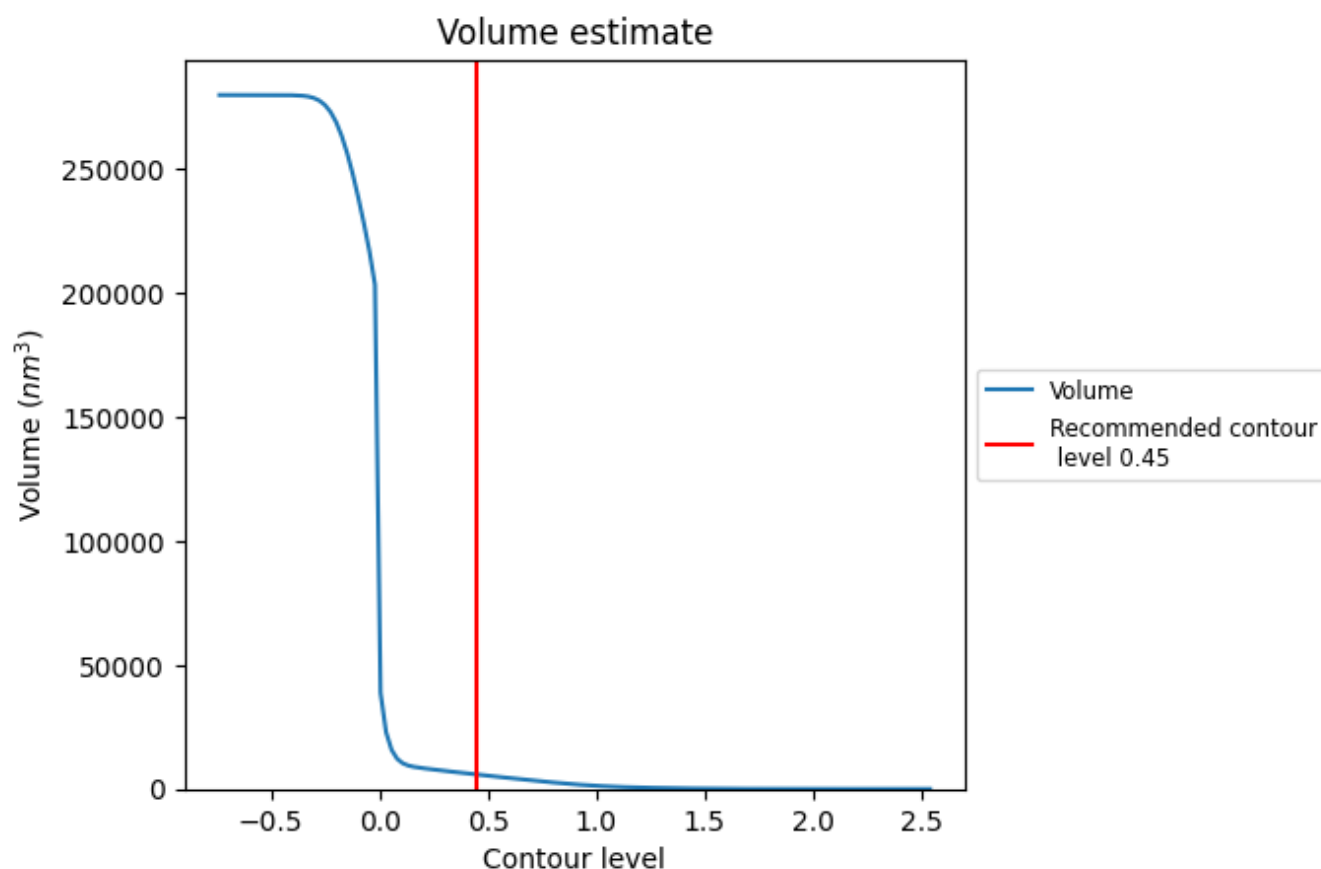
This section contains the results of statistical analysis of the map.

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.

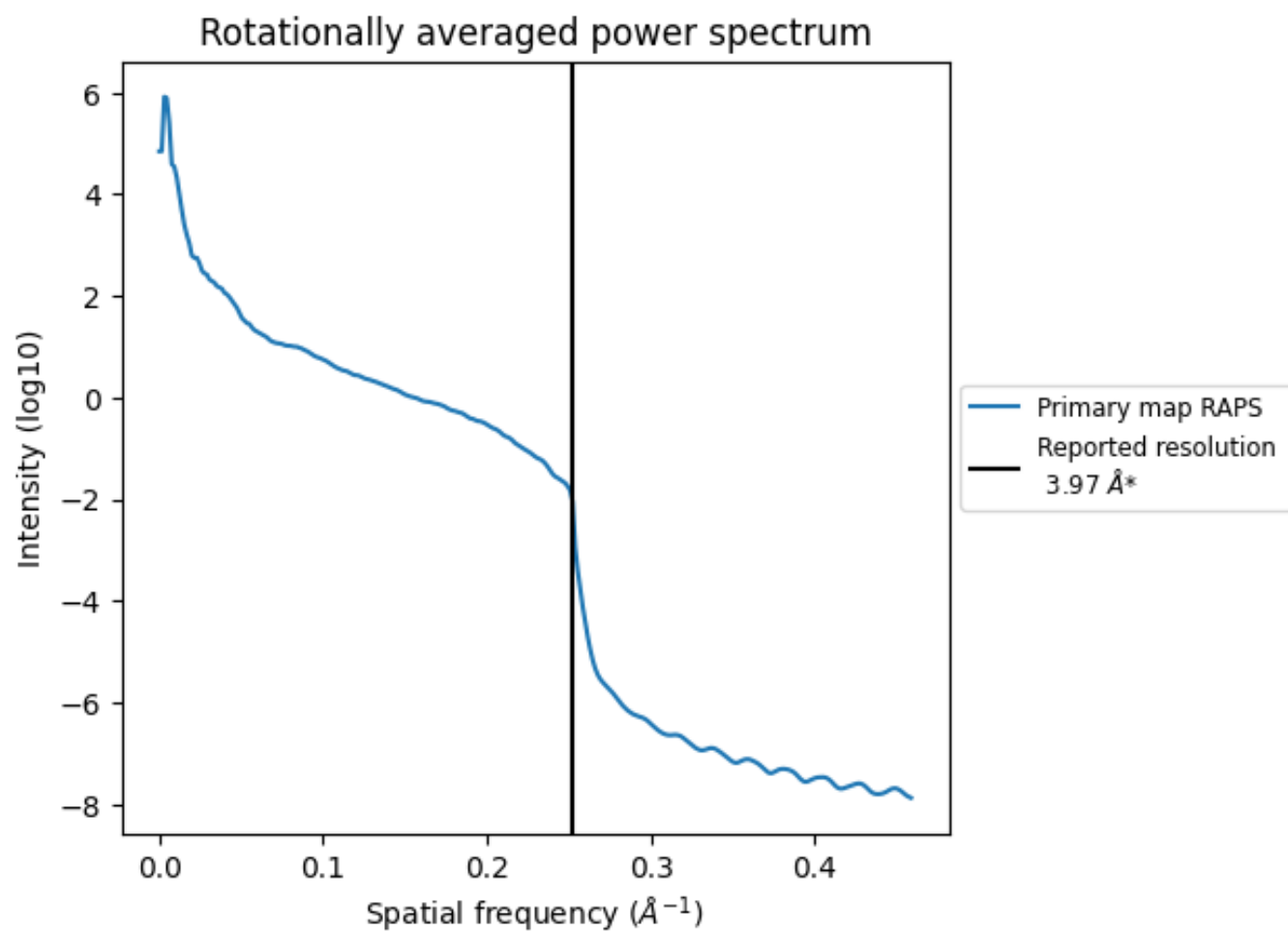
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5826 nm^3 ; this corresponds to an approximate mass of 5263 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 0.252 Å⁻¹

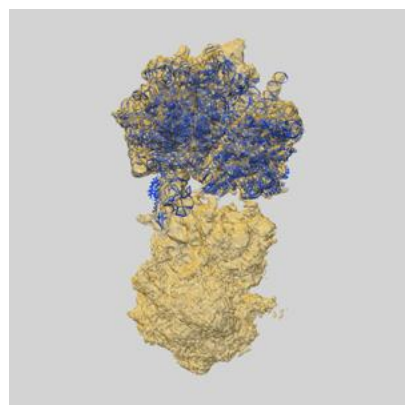
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

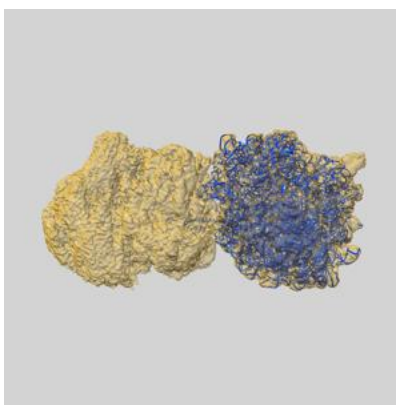
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13952 and PDB model 7QG8. Per-residue inclusion information can be found in section [3](#) on page [16](#).

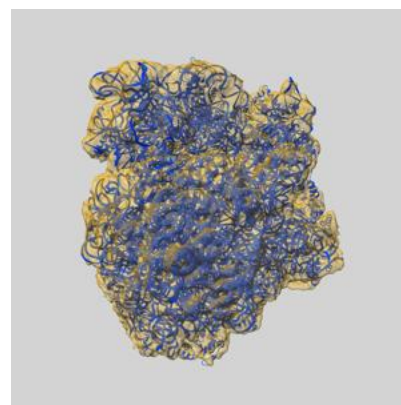
9.1 Map-model overlay [i](#)



X



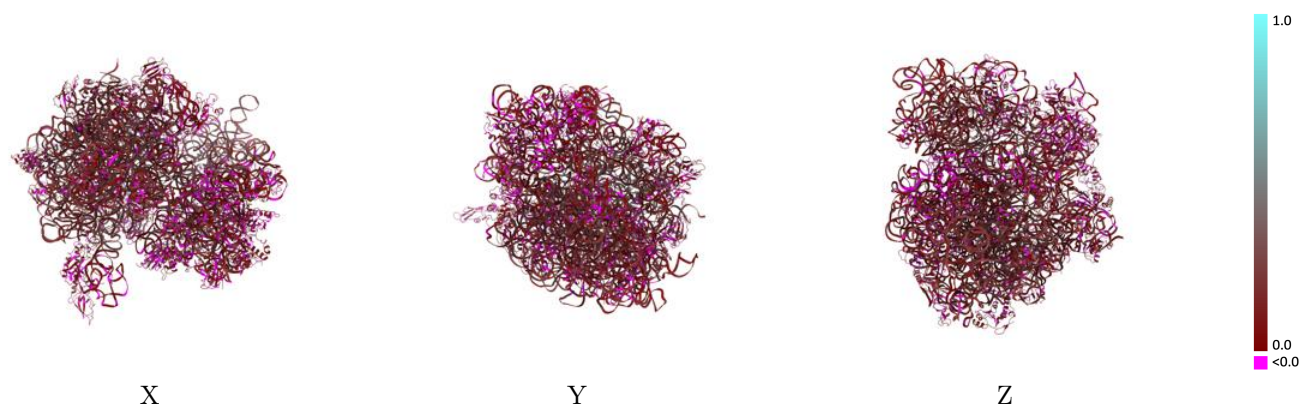
Y



Z

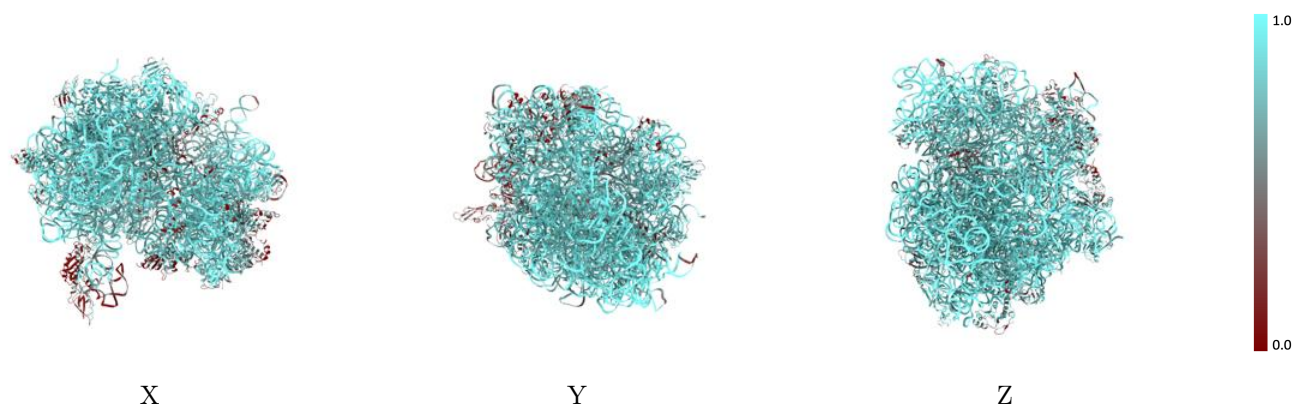
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



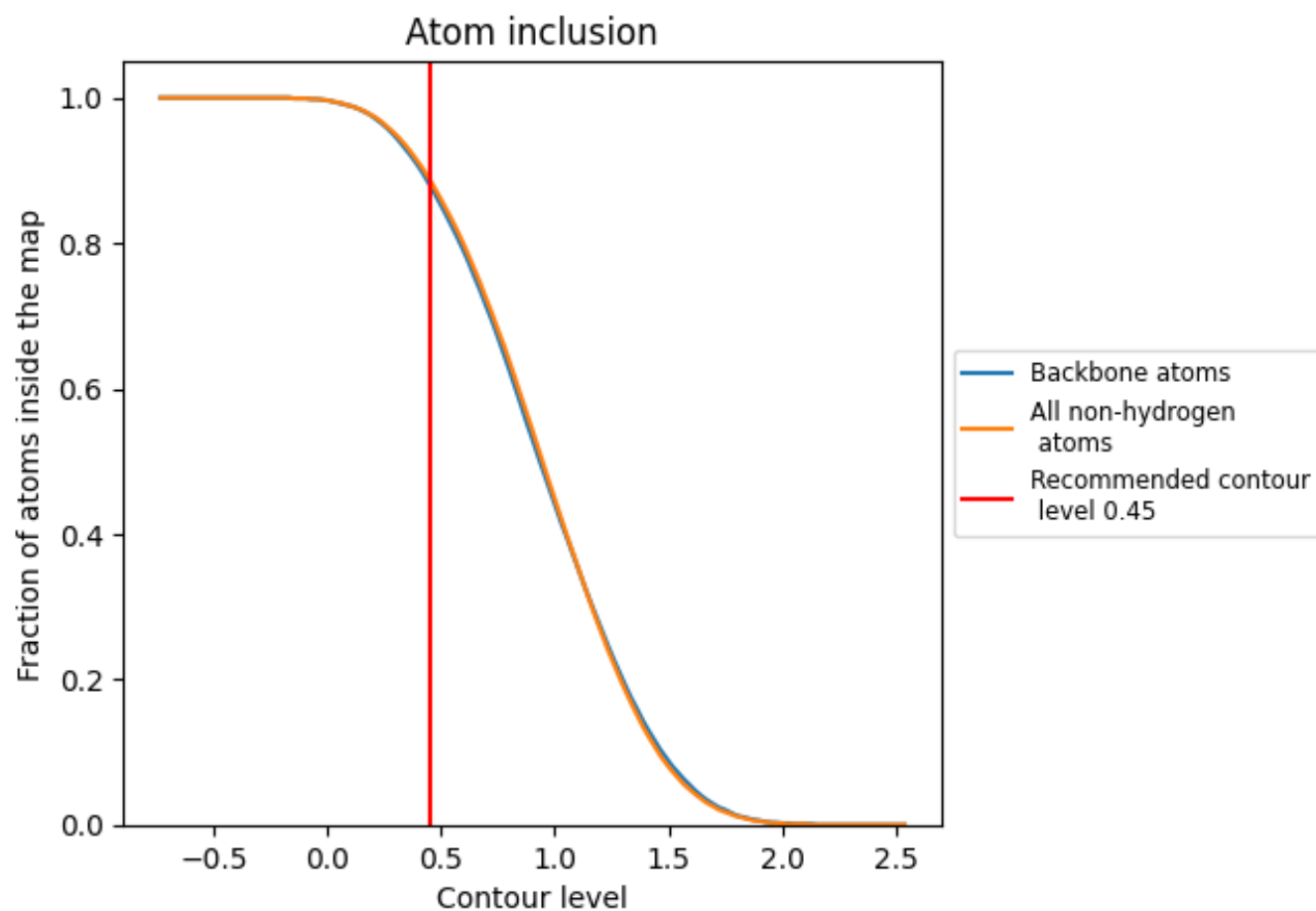
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8870	 0.1450
0	 0.9490	 0.1580
1	 0.5930	 0.1110
2	 0.6140	 0.0610
3	 0.7810	 0.1020
4	 0.9050	 0.1390
5	 0.5230	 0.1150
6	 0.6800	 0.0780
7	 0.8020	 0.1190
8	 0.8100	 0.0840
9	 0.5700	 0.0820
A	 0.7540	 0.1560
C	 0.0970	 0.0690
D	 0.5490	 0.0490
E	 0.8960	 0.0910
F	 0.6170	 0.0710
G	 0.6480	 0.0470
H	 0.8100	 0.1300
I	 0.8750	 0.1250
J	 0.8260	 0.0380
K	 0.6810	 0.1310
L	 0.5070	 0.1250
M	 0.9150	 0.1840
N	 0.9560	 0.1680
O	 0.9550	 0.1550
P	 0.8630	 0.0740
Q	 0.8170	 0.0790
R	 0.7890	 0.1310
S	 0.7900	 0.0960
T	 0.8470	 0.1070
U	 0.3990	 0.1080
V	 0.5640	 0.0520
W	 0.9230	 0.1590
X	 0.5170	 0.0200
Y	 0.8110	 0.1500



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Chain	Atom inclusion	Q-score
Z	 0.8730	 0.1730
a	 0.9130	 0.0930
b	 0.8500	 0.1160
c	 0.7270	 0.0160
d	 0.9130	 0.1470
e	 0.7430	 0.1710
f	 0.8900	 0.1250
g	 0.7700	 0.0810
h	 0.8570	 0.1110
i	 0.8560	 0.1420
j	 0.9820	 0.1180
k	 0.7880	 0.1460
l	 0.6030	 0.1020
m	 0.8900	 0.1580
n	 0.8500	 0.0900
o	 0.8700	 0.1480
p	 0.9660	 0.1100
q	 0.9740	 0.1670
r	 0.9490	 0.1150
s	 0.9480	 0.1080
t	 0.7970	 0.0600
u	 0.7810	 0.1080
v	 0.5870	 0.1390