



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:34 AM UTC

PDB ID : 5UQ8 / pdb_00005uq8
EMDB ID : EMD-8597
Title : 70S ribosome complex with dnaX mRNA stem-loop and E-site tRNA ("out" conformation)
Authors : Zhang, Y.; Hong, S.; Skiniotis, G.; Dunham, C.M.
Deposited on : 2017-02-07
Resolution : 3.20 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:

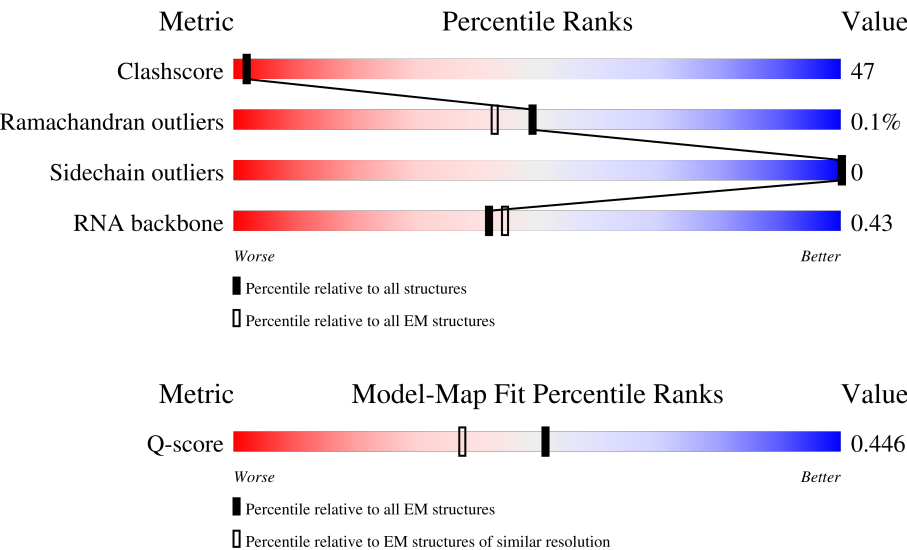
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.20 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	15020 (2.70 - 3.70)

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	2915	9% 9% 69% 20% .
2	B	120	5% 7% 78% 16%
3	D	275	10% 35% 65%

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Mol	Chain	Length	Quality of chain
4	E	204	
5	F	203	
6	G	181	
7	H	173	
8	I	146	
9	N	140	
10	O	122	
11	P	149	
12	Q	141	
13	R	118	
14	S	110	
15	T	131	
16	U	116	
17	V	101	
18	W	112	
19	X	95	
20	Y	107	
21	Z	187	
22	0	77	
23	1	97	
24	2	70	
25	3	59	
26	4	69	
27	5	59	
28	6	53	

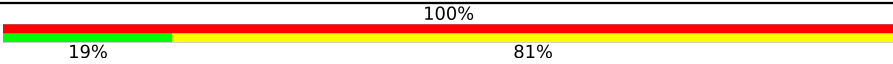
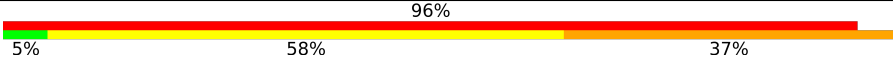
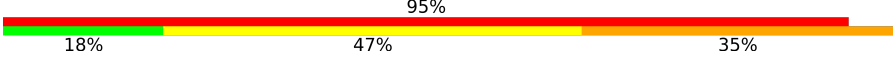
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Mol	Chain	Length	Quality of chain
29	7	48	
30	8	64	
31	9	37	
32	a	1521	
33	b	231	
34	c	206	
35	d	208	
36	e	148	
37	f	100	
38	g	155	
39	h	137	
40	i	126	
41	j	96	
42	k	114	
43	l	122	
44	m	114	
45	n	60	
46	o	88	
47	p	82	
48	q	99	
49	r	68	
50	s	83	
51	t	98	
52	u	23	
53	y	77	

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Mol	Chain	Length	Quality of chain
54	C	226	
55	z	76	
56	x	55	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148590 atoms, of which 4 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2867	Total	C	N	O	P	0	0
			61758	27491	11552	19850	2865		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2573	1146	476	832	119		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	275	Total	C	N	O	S	0	0
			2136	1349	423	361	3		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	204	Total	C	N	O	S	0	0
			1559	985	298	270	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	203	Total	C	N	O	S	0	1
			1580	1007	297	274	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	181	Total	C	N	O	S	0	0
			1424	912	259	249	4		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	173	Total	C	N	O	S	0	0
			1324	842	247	234	1		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	146	Total	C	N	O	S	0	0
			1076	687	186	202	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	140	Total	C	N	O	S	0	0
			1117	719	207	187	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	149	Total	C	N	O	S	0	0
			1135	706	230	196	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	118	Total	C	N	O	S	0	0
			968	604	203	160	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	S	110	Total	C	N	O		
			870	549	173	148	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	T	131	Total	C	N	O	S	
			1083	675	224	183	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	U	116	Total	C	N	O	S	
			959	608	201	149	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	V	101	Total	C	N	O	S	
			771	495	140	135	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	W	112	Total	C	N	O	S	
			886	557	174	153	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	95	Total	C	N	O	S	
			750	488	135	126	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Y	107	Total	C	N	O	S	
			810	519	153	132	6	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	187	Total	C	N	O	S	0	0
			1459	932	257	268	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	77	Total	C	N	O	S	0	0
			608	375	129	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	97	Total	C	N	O	S	0	0
			759	478	149	131	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	70	Total	C	N	O	S	0	0
			592	368	119	103	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	3	59	Total	C	N	O	0	0
			464	296	90	78		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	69	Total	C	N	O	S	0	0
			536	342	98	91	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	59	Total	C	N	O	S	0	0
			455	285	89	76	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	53	Total	C	N	O	S	0	0
			449	279	91	75	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	48	Total	C	N	O	S	0	0
			418	257	104	55	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	64	Total	C	N	O	S	0	0
			517	331	102	82	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1513	Total	C	N	O	P	0	0
			32532	14488	6021	10510	1513		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1542	G	-	insertion	GB 55771382
a	1543	C	-	insertion	GB 55771382
a	1544	U	-	insertion	GB 55771382

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	231	Total	C	N	O	S	0	0
			1825	1167	326	327	5		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	206	Total	C	N	O	S	0	0
			1542	968	300	273	1		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	208	Total	C	N	O	S	0	0
			1668	1047	330	284	7		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	148	Total	C	N	O	S	0	0
			1133	716	214	199	4		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	100	Total	C	N	O	S	0	0
			816	516	146	151	3		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	155	Total	C	N	O	S	0	0
			1229	766	241	216	6		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	137	Total	C	N	O	S	0	0
			1088	689	206	191	2		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	126	Total	C	N	O		0	0
			966	613	186	167			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	j	96	Total	C	N	O	0	0
			710	442	137	131		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	114	Total	C	N	O	S	0	0
			833	519	156	155	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	122	Total	C	N	O	S	0	0
			932	586	185	159	2		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	114	Total	C	N	O	S	0	0
			895	550	186	157	2		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	88	Total	C	N	O	S	0	0
			728	456	144	126	2		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	82	Total	C	N	O	S	0	0
			677	430	133	113	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	68	Total	C	N	O		0	0
			555	355	108	92			

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	83	Total	C	N	O	S	0	0
			645	410	118	115	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	98	Total	C	N	O	S	0	0
			733	451	154	126	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
52	u	23	Total	C	N	O		0
			199	122	48	29		0

- Molecule 53 is a RNA chain called P-site tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	77	Total	C	N	O	P	0	0
			1640	732	298	534	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	17B	C	U	conflict	GB 1126835761

- Molecule 54 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	C	225	Total	C	N	O	S	0	0
			1718	1085	315	316	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	MET	deletion	UNP Q5SLP7

- Molecule 55 is a RNA chain called E-site tRNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

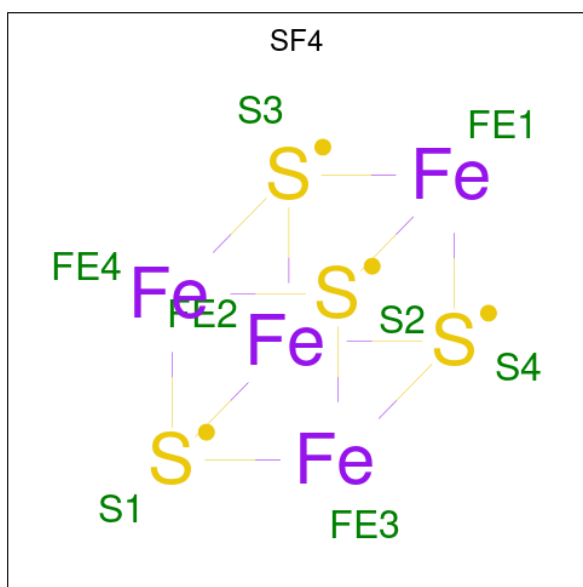
- Molecule 56 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	55	Total	C	H	N	O	P	
			1180	527	4	219	376	54	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Y	1	Total	Zn	0
			1	1	
57	4	1	Total	Zn	0
			1	1	
57	5	1	Total	Zn	0
			1	1	
57	6	1	Total	Zn	0
			1	1	
57	9	1	Total	Zn	0
			1	1	
57	n	1	Total	Zn	0
			1	1	

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

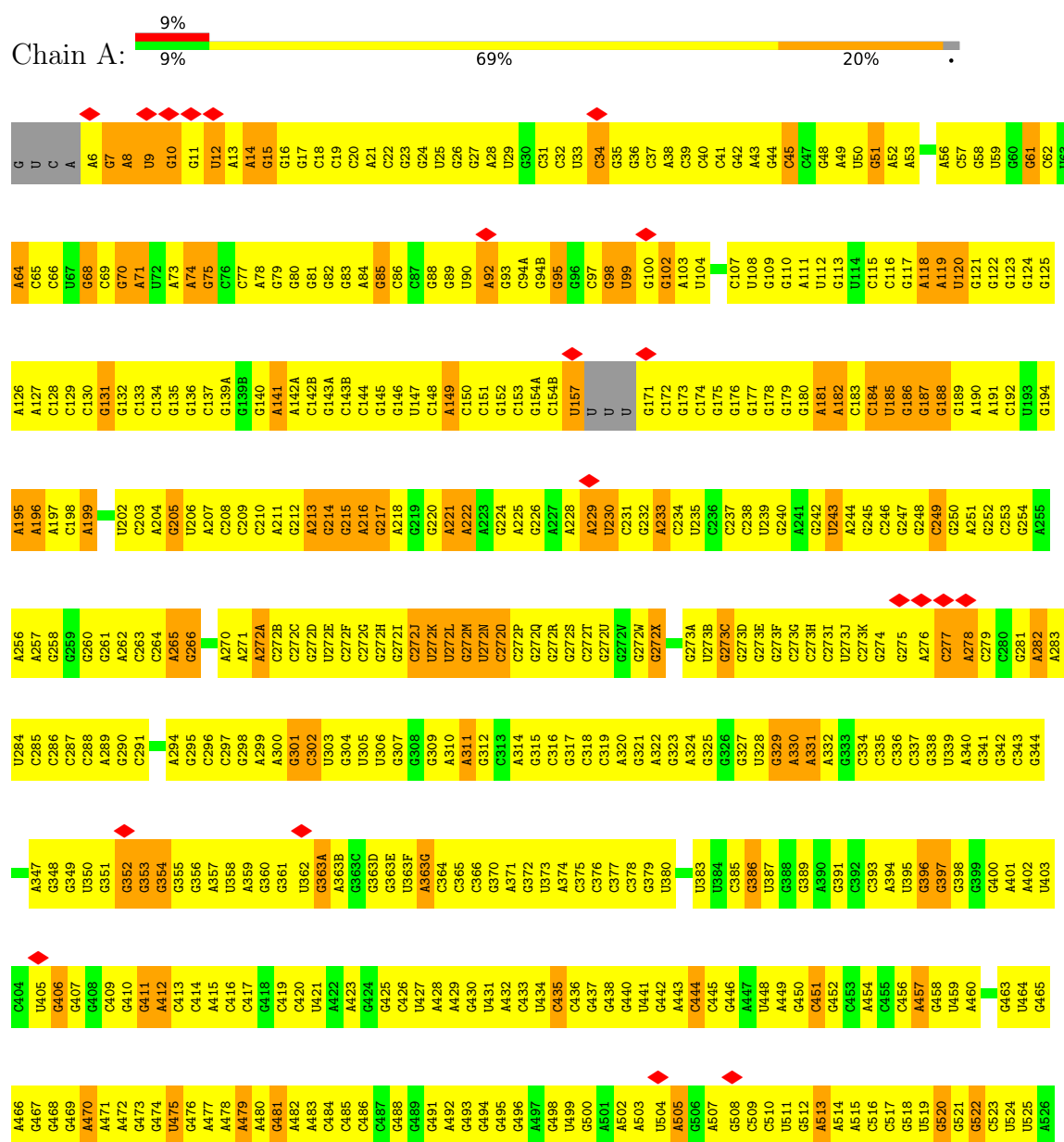


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
58	d	1	8	4	4	0

3 Residue-property plots

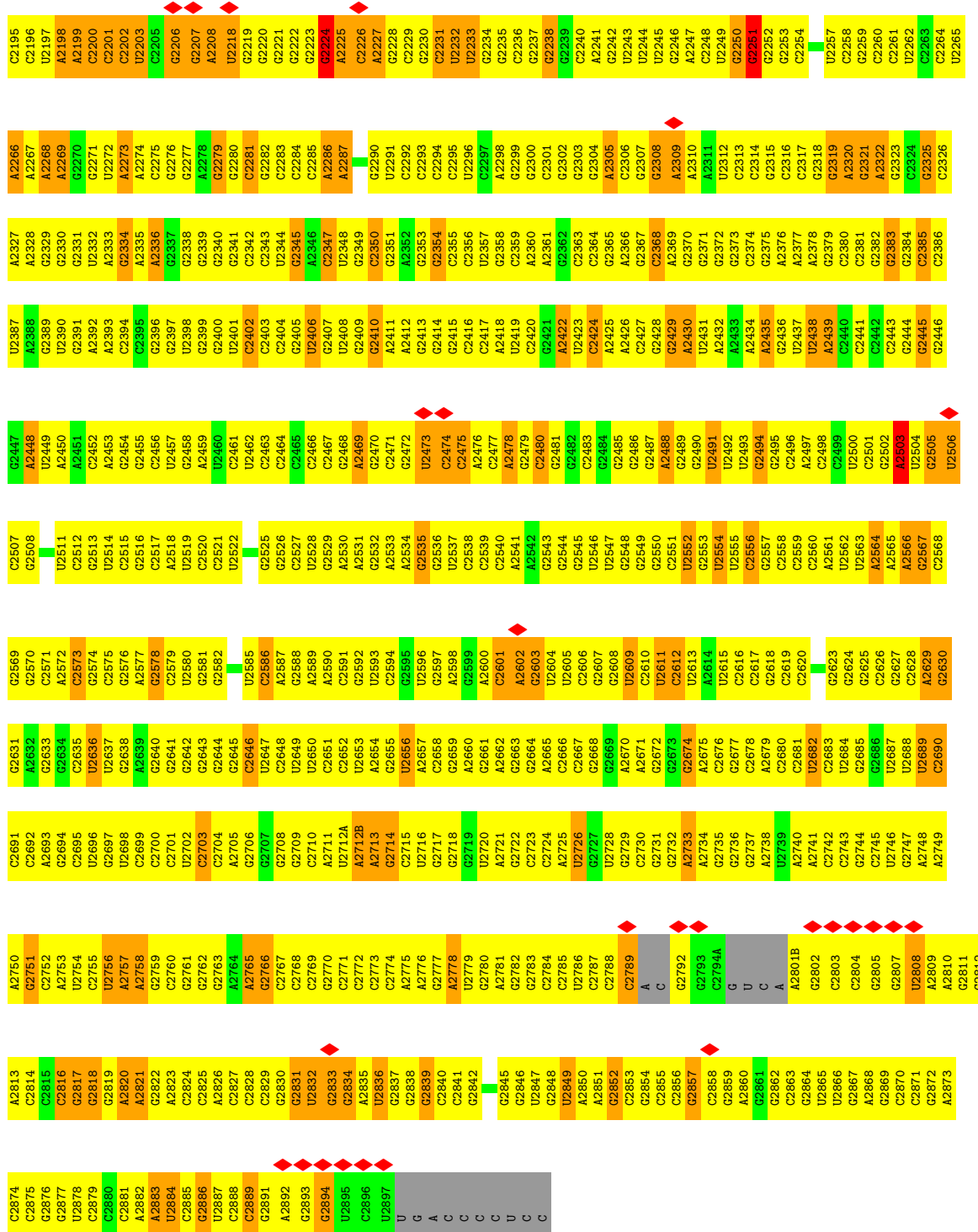
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S rRNA



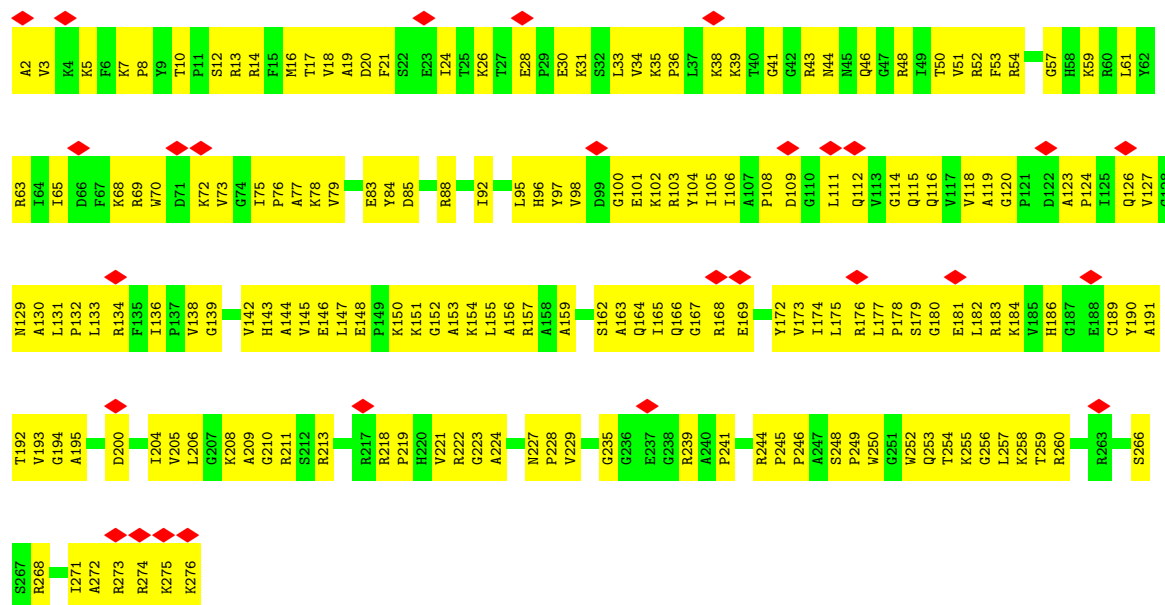


A2135	U2075	A2014	A1952	G1888	G1817	G1753	G1675	A1545	A1486	G1423	C1363
C2136	U2076	A2015	A1953	A1889	U1818	C1754	A1676	C1546	G1487	G1424	G1364
C2137	A2077	U2016	G1954	A1819	A1819	A1755	A1677	C1547	G1488	G1425	A1365
C2138	C2077	U2017	U1955	G1891	G1820	G1756	G1678	C1548	G1489	G1426	A1366
C2139	U2079	A2018	U1956	A1821	A1821	U1757	U1679	C1549	A1490	A1427	A1367
C2140	G2080	A2019	C1957	G1822	G1822	G1758	U1680	C1550	G1491	C1428	G1368
C2141	C2081	A2020	C1958	G1823	G1823	A1759	G1681	C1551	G1492	G1429	G1369
C2142	A2082	G2021	G1959	G1824	G1824	A1760	C1684	G1552	A1493	G1430	C1370
C2143	C2083	U2022	A1960	A1825	A1825	C1761	A1618	C1557	A1494	U1431	G1371
U2144	C2084	G2023	C1961	G1902	C1885	A1762	C1685	C1558	A1495	U1372	U1372
C2145	C2085	G2024	A1901	C1826	C1826	G1763	C1686	G1559	A1496	U1373	A1373
C2146	U2086	C2025	U1963	G1903	C1827	G1764	C1687	G1560	U1497	A1434	G1374
C2147	G2087	G2026	G1964	G1904	A1828	C1765	U1688	G1561	C1498	G1435	C1375
C2148	G2088	G2027	C1965	C1905	C1830	U1766	A1869	G1562	C1499	G1436	C1376
C2149	U2089	U2028	G1966	G1906	G1831	C1767	A1690	A1563	G1500	C1437	G1377
C2150	G2090	G2029	C1967	G1907	C1832	U1768	C1691	G1564	C1501	U1438	A1378
C2151	U2091	A2030	G1968	U1833	U1833	G1769	U1692	C1565	C1502	G1440	A1379
C2152	G2092	A2031	A1969	U1834	G1835	A1772	C1694	A1566	U1503	G1441	G1380
C2153	C2093	G2032	C1970	G1835	G1836	C1773	G1695	A1567	C1504	G1442	G1381
C2154	G2094	A2033	A1971	C1837	C1837	C1774	G1696	G1568	C1505	G1443	G1382
C2155	U2095	U2034	A1972	C1838	C1838	A1777	G1697	A1569	C1506	A1444	C1383
C2156	G2096	A2035	A1913	A1913	U1777	U1778	A1698	A1570	A1507	G1445A	A1384
C2157	C2097	G2036	C1914	C1914	U1779	U1779	G1699	A1571	A1508	C1445B	G1385
C2158	U2098	G2037	U1915	U1915	A1780	A1780	A1701	A1572	C1509A	C1446	C1386
C2159	G2099	U2038	A1916	A1916	C1842	C1842	G1702	G1573	A1509B	G1447	C1387
C2160	C2100	C2040	U1917	U1917	G1843	G1843	U1700	C1574	G1509C	G1448	G1388
C2161	U2101	U2041	A1918	A1918	G1844	G1844	G1701	U1575	A1510	U1449	U1390
C2162	G2102	A2042	C1979	C1979	G1845	G1845	G1702	U1576	G1511	G1450A	U1391
C2163	U2103	C2043	A1981	A1981	A1847	A1847	G1703	C1577	C1512	C1450B	A1392
C2164	C2104	C2044	G1921	G1921	A1848	A1848	G1704	U1578	U1513	C1451	A1393
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C2166	U2106	U2046	A1923	A1923	G1850	G1850	G1645	A1580	G1515	U1453	A1395
C2167	G2107	G2047	C1924	C1924	U1851	A1789	G1646	C1581	U1516	G1455	U1396
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C2170	C2110	A2051	G1927	G1927	G1854	G1792	G1713	C1584	G1519	G1461	G1400
C2171	G2111	G2052	A1928	A1928	G1855	C1793	G1714	A1586	G1520	C1462	G1401
C2172	C2112	G2053	G1929	G1929	G1856	U1794	G1715	A1587	U1523	G1403	C1402
C2173	U2113	C2054	U1930	U1930	G1857	G1795	G1716	C1588	G1524	G1465	C1404
C2174	C2114	A2055	U1931	U1931	G1858	U1796	G1717	C1589	G1525	G1466	U1405
C2175	G2115	G2056	A1932	A1932	A1859	C1797	U1720	U1590	G1526	C1467	U1406
C2176	U2116	U2057	G1933	G1933	G1860	U1798	G1721	C1591	A1528A	C1468	C1407
C2177	C2117	A2060	C1934	C1934	G1861	G1799	A1722	C1592	G1529	A1470	C1408
C2178	U2118	G2061	G1935	G1935	G1862	C1800	G1739	G1593	C1530	A1471	C1409
C2179	C2119	C2062	A1936	A1936	G1863	A1801	U1740	A1596	C1531	A1472	G1410
C2180	G2120	G2063	U1937	U1937	G1864	A1802	G1741	A1597	C1532	C1473	C1411
C2181	U2121	A2064	A1938	A1938	C1865	C1804	G1742	C1598	G1533	C1474	A1412
C2182	C2122	C2065	U1939	U1939	A1876	U1805	C1743	C1600	U	G1475	G1413
C2183	G2123	G2066	U1940	U1940	A1877	C1806	C1744	C1601	A	C1476	G1414
C2184	U2124	U2067	C1941	C1941	G1878	G1807	C1745A	G1602	G1536	A1477	U1415
C2185	C2125	C2068	C1942	C1942	C1879	U1808	C1745B	U1603	G1537	G1478	C1416
C2186	U2126	G2069	U1943	U1943	C1880	A1809	G1746	C1604	G1538	G1479	G1417
C2187	G2127	C2070	U1944	U1944	C1881	A1810	G1747A	G1605	G1539	U1480	G1418
C2188	U2128	C2071	G1945	G1945	C1882	G1747B	G1747B	G1606	U1540	G1482	U1420
C2189	C2129	A2071	C1947	C1947	G1883	A1749	C1674	G1607	A1542	G1484	G1422
C2190	G2130	G2072	G1948	G1948	A1884	G1750	G1751	A1608	A1543	A1544	
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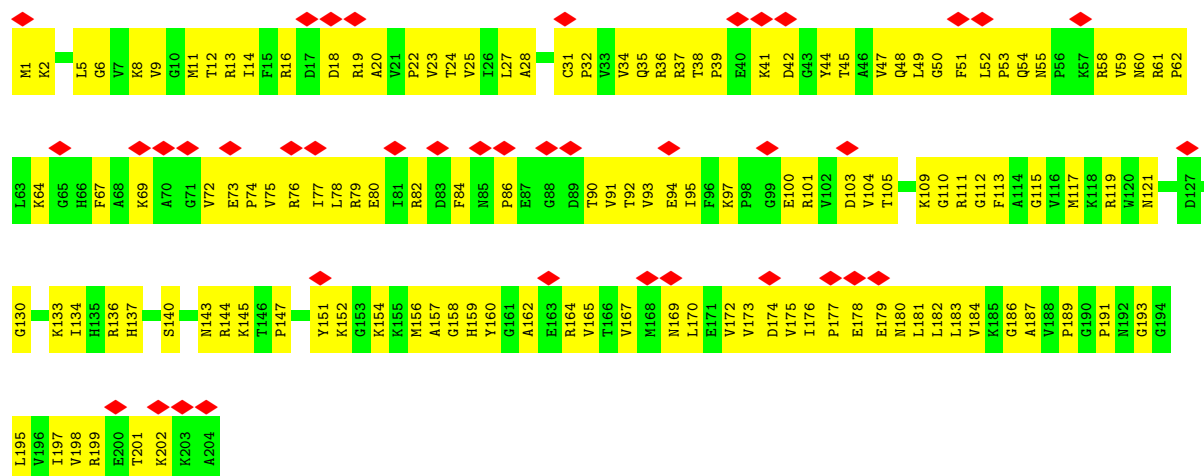




• Molecule 3: 50S ribosomal protein L2

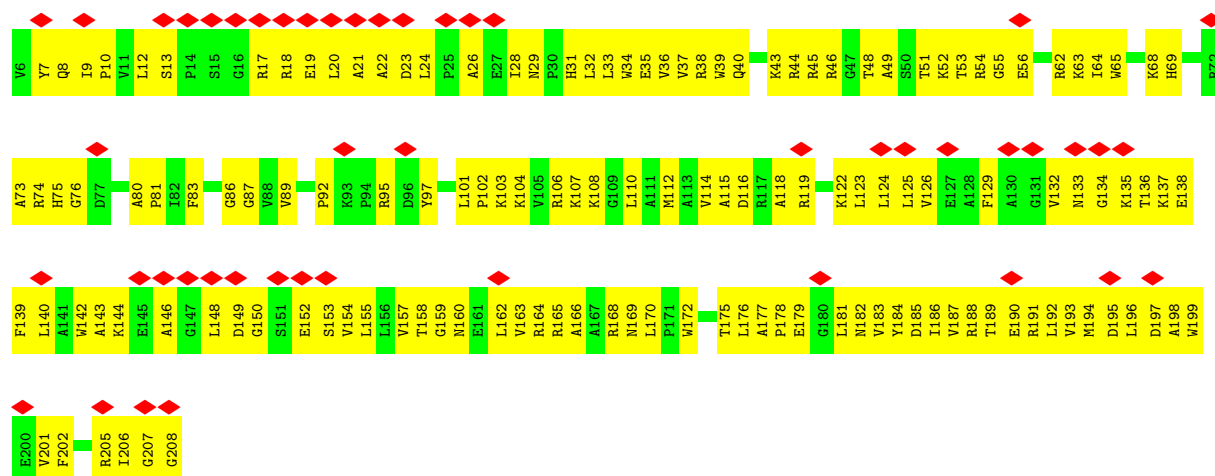


• Molecule 4: 50S ribosomal protein L3

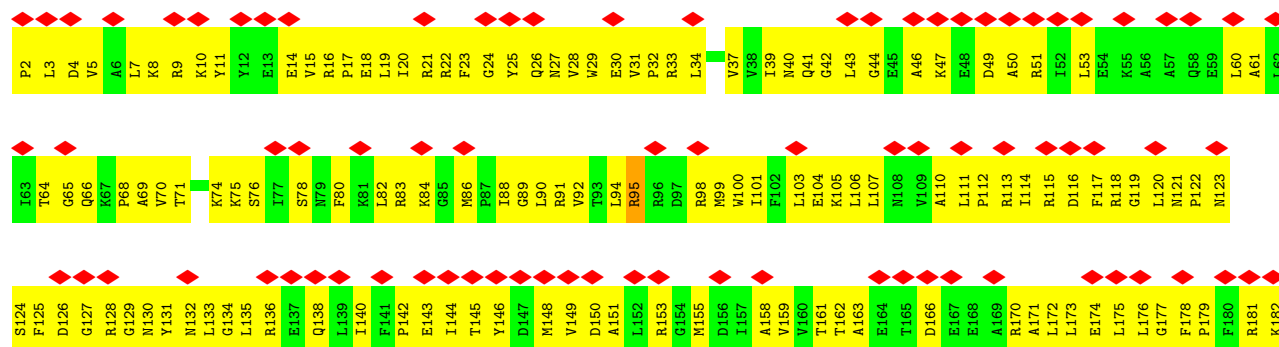


• Molecule 5: 50S ribosomal protein L4

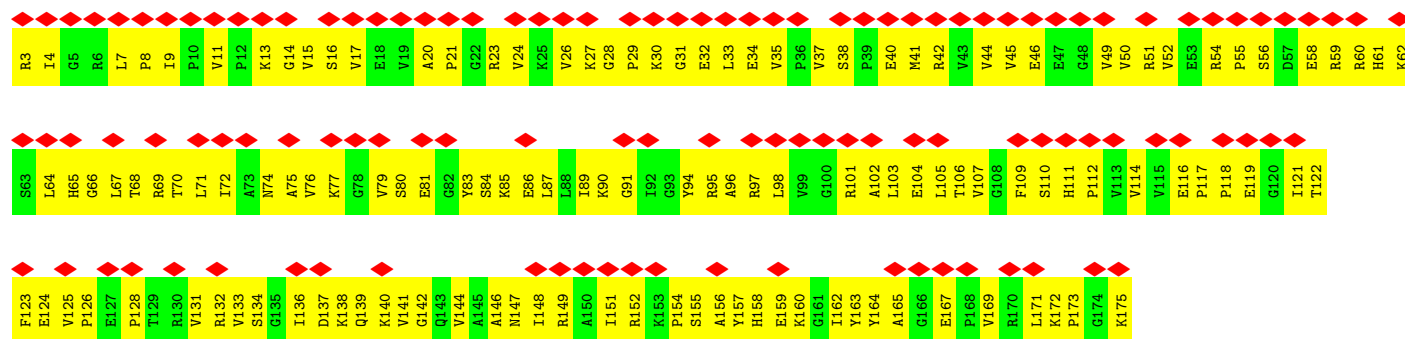


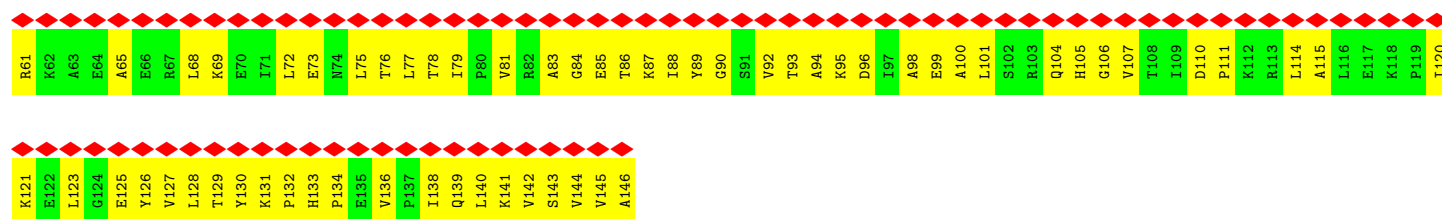


• Molecule 6: 50S ribosomal protein L5

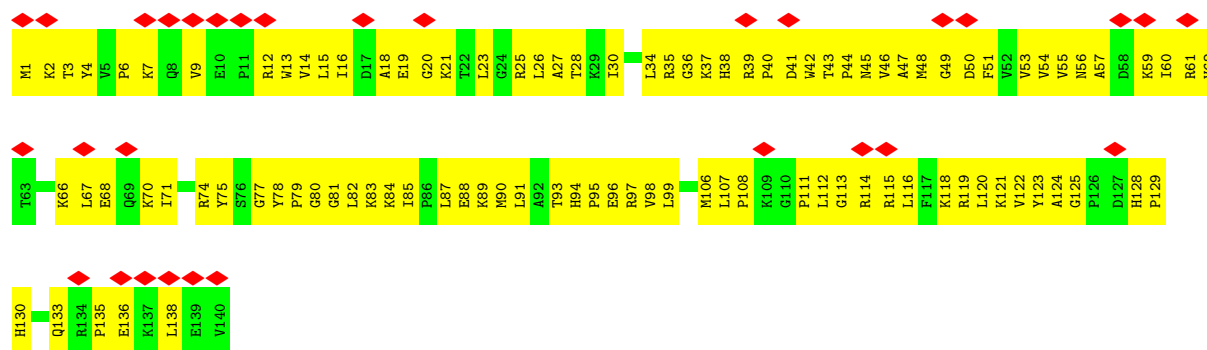


• Molecule 7: 50S ribosomal protein L6

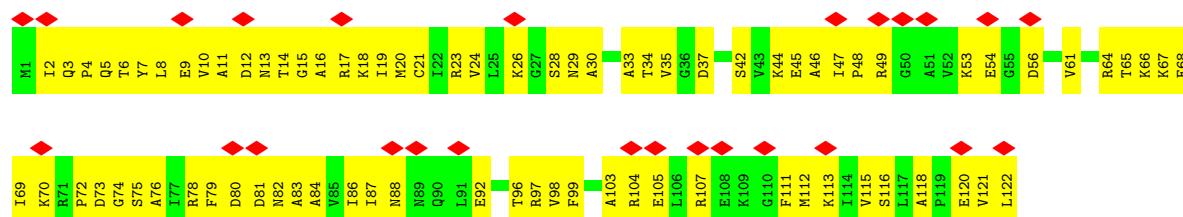




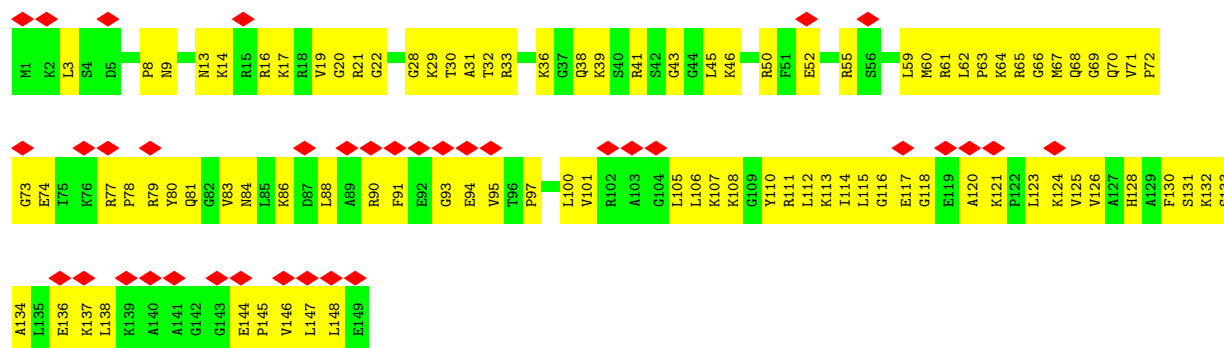
• Molecule 9: 50S ribosomal protein L13



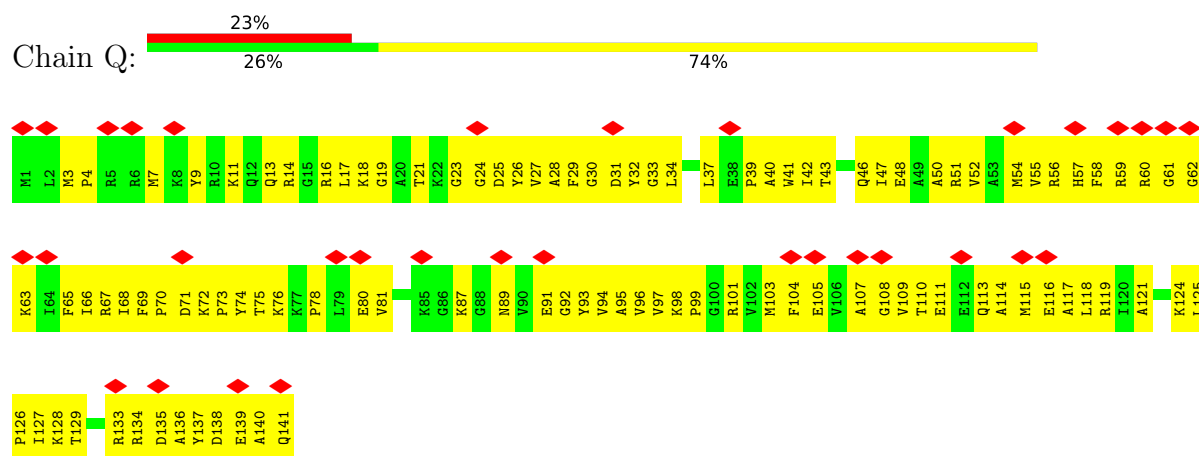
• Molecule 10: 50S ribosomal protein L14



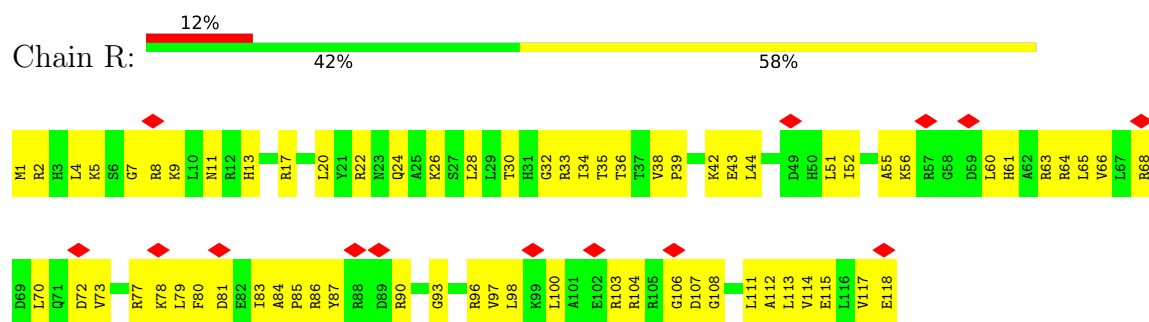
• Molecule 11: 50S ribosomal protein L15



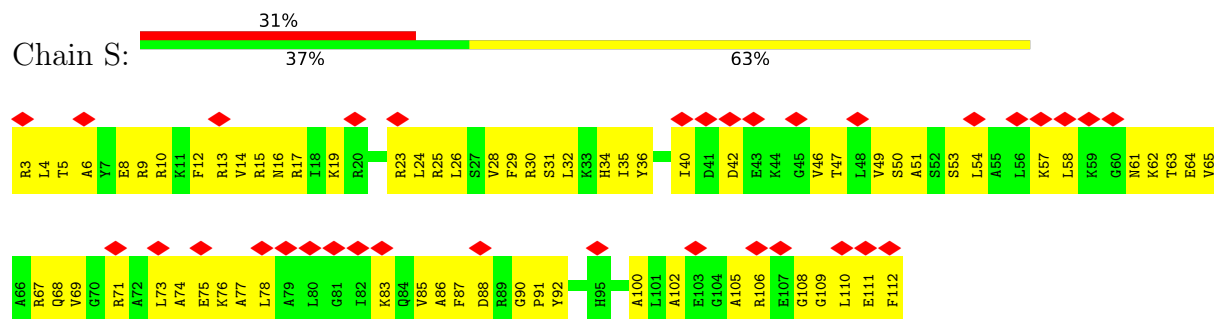
• Molecule 12: 50S ribosomal protein L16



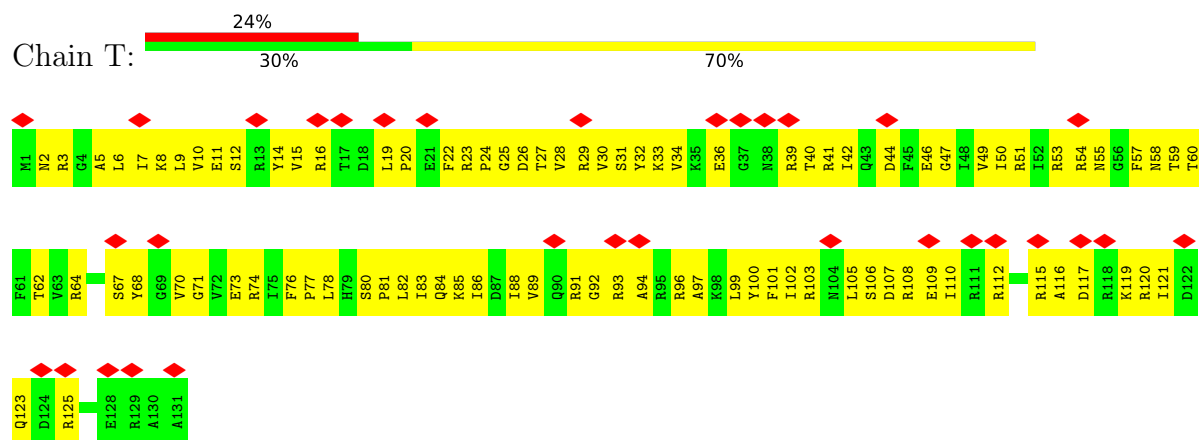
- Molecule 13: 50S ribosomal protein L17



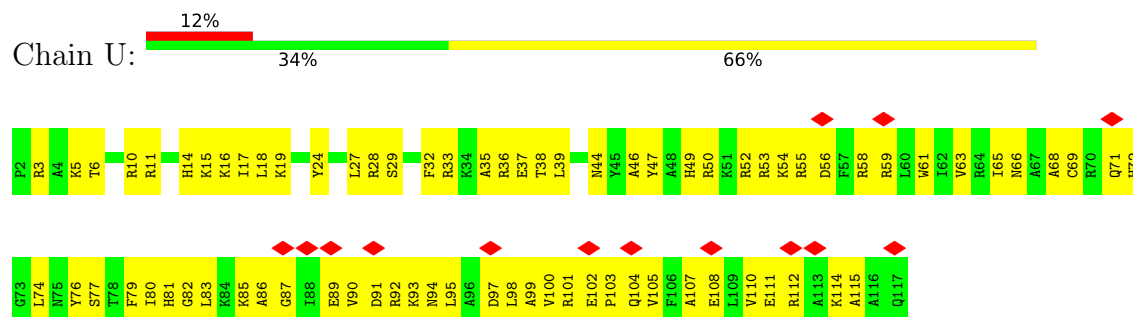
- Molecule 14: 50S ribosomal protein L18



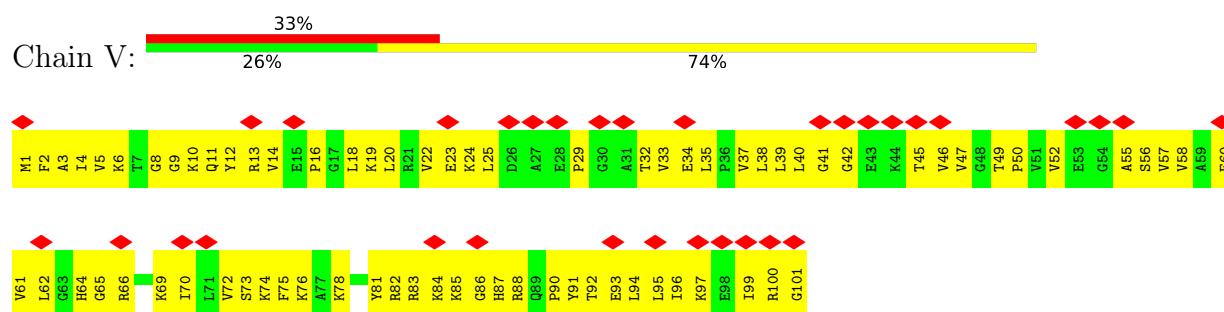
- Molecule 15: 50S ribosomal protein L19



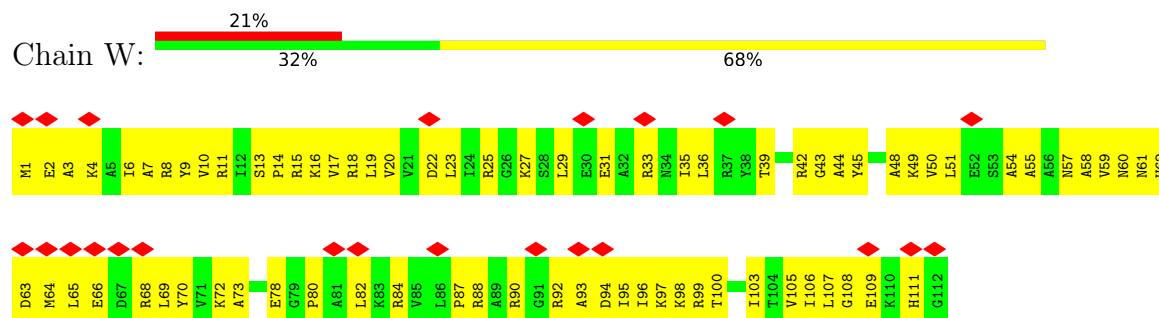
- Molecule 16: 50S ribosomal protein L20



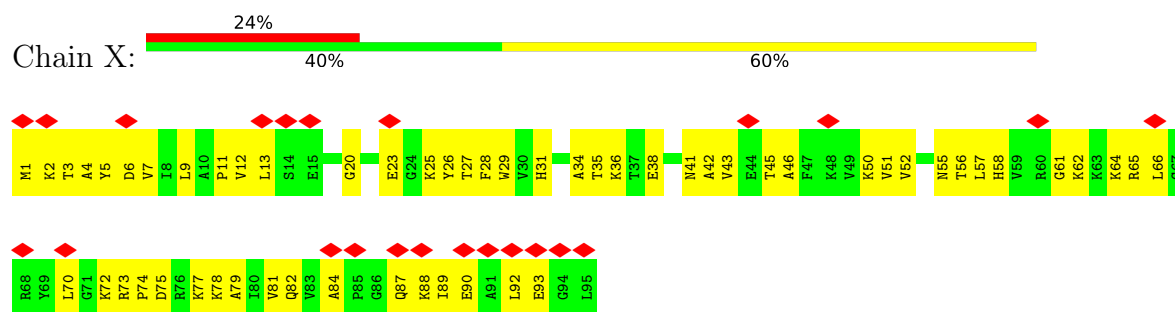
- Molecule 17: 50S ribosomal protein L21



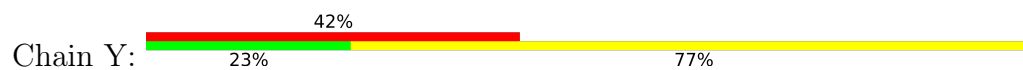
- Molecule 18: 50S ribosomal protein L22

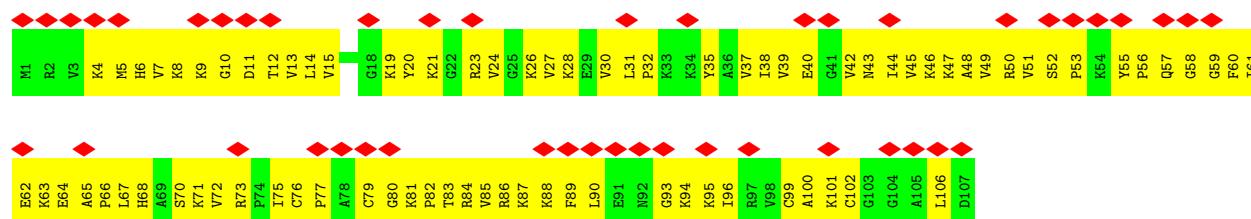


- Molecule 19: 50S ribosomal protein L23

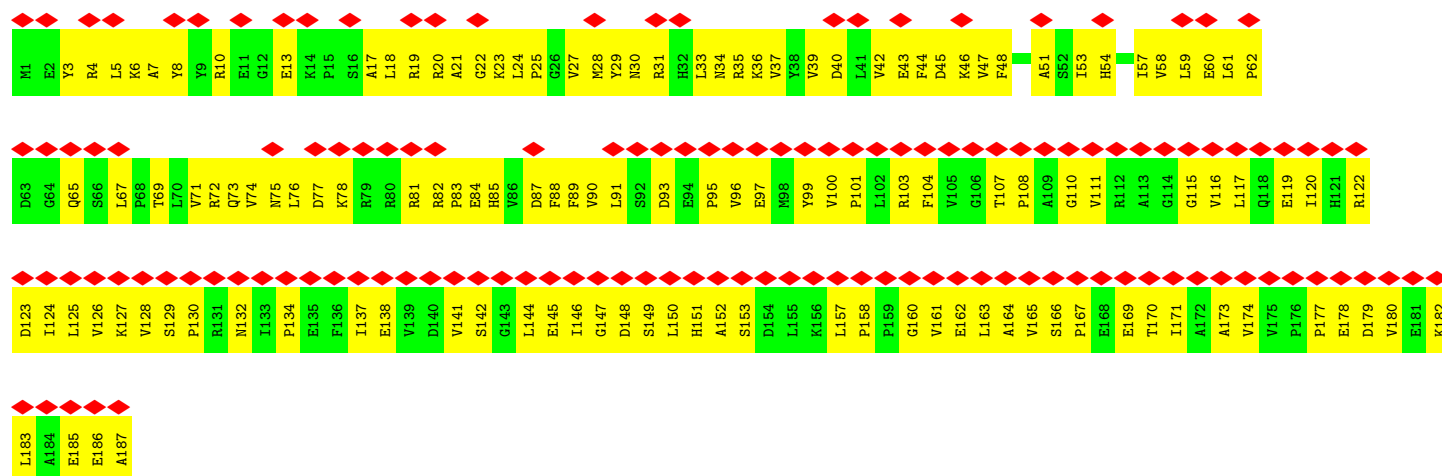
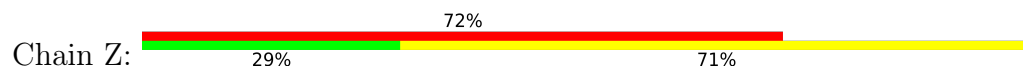


- Molecule 20: 50S ribosomal protein L24

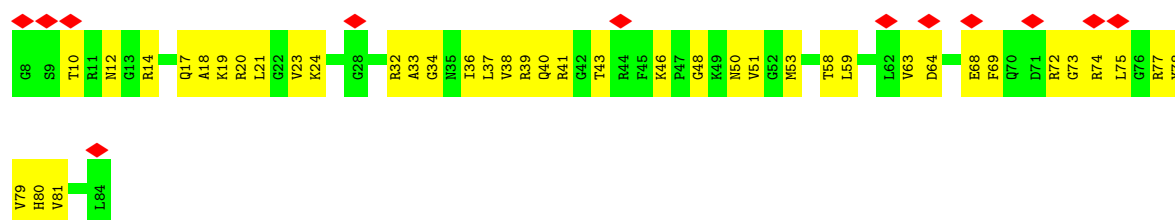




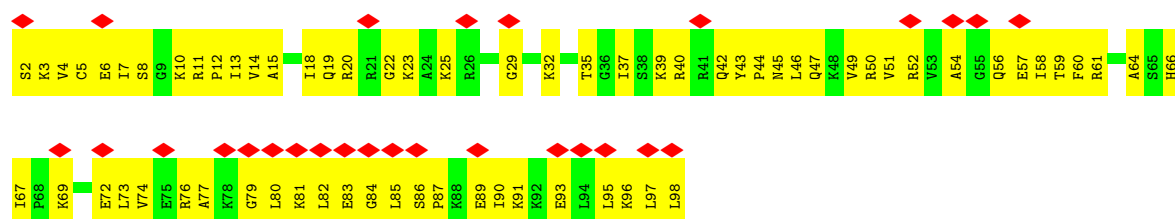
• Molecule 21: 50S ribosomal protein L25



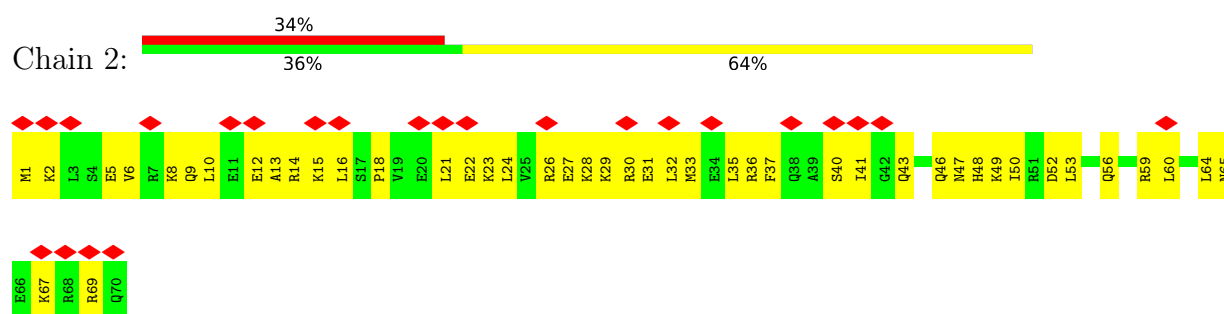
• Molecule 22: 50S ribosomal protein L27



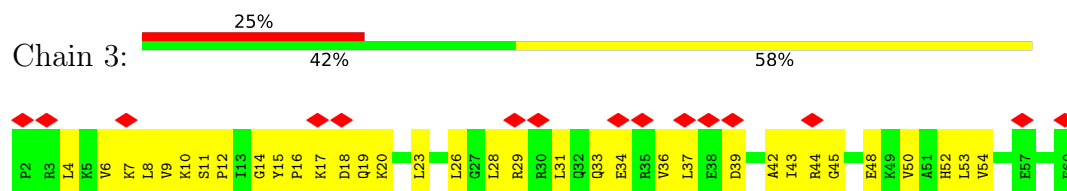
• Molecule 23: 50S ribosomal protein L28



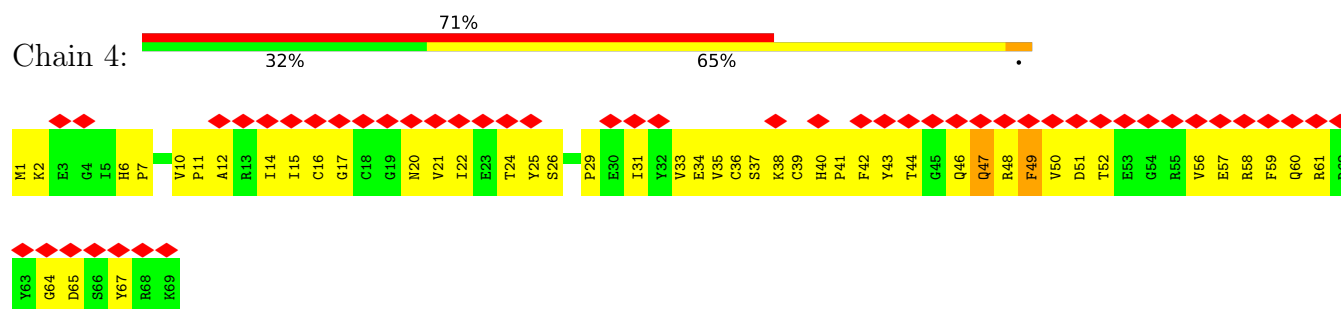
• Molecule 24: 50S ribosomal protein L29



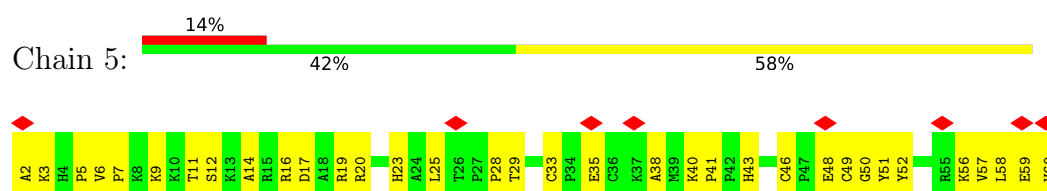
- Molecule 25: 50S ribosomal protein L30



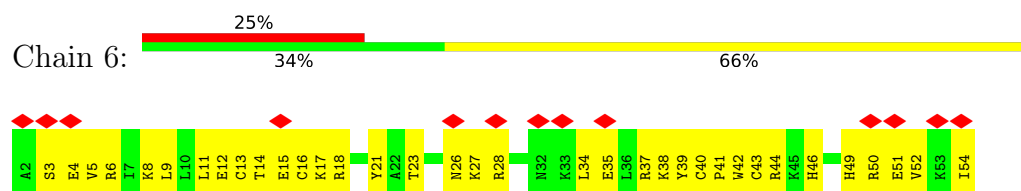
- Molecule 26: 50S ribosomal protein L31



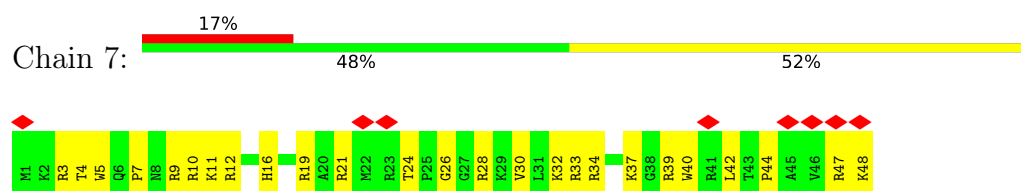
- Molecule 27: 50S ribosomal protein L32



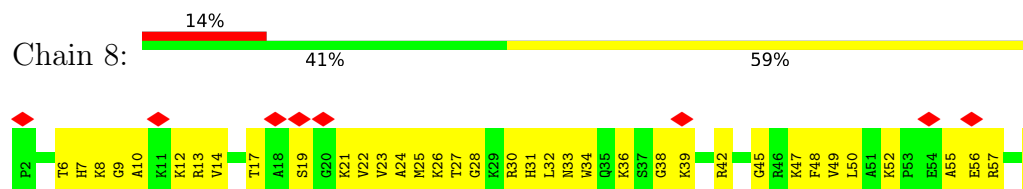
- Molecule 28: 50S ribosomal protein L33



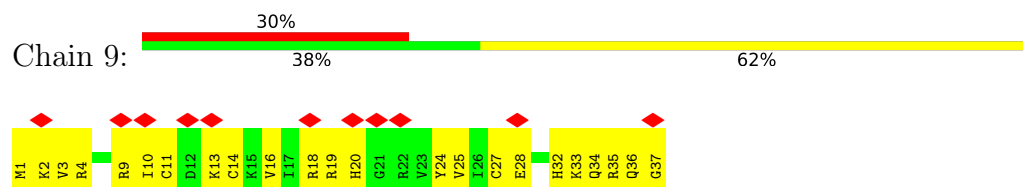
- Molecule 29: 50S ribosomal protein L34



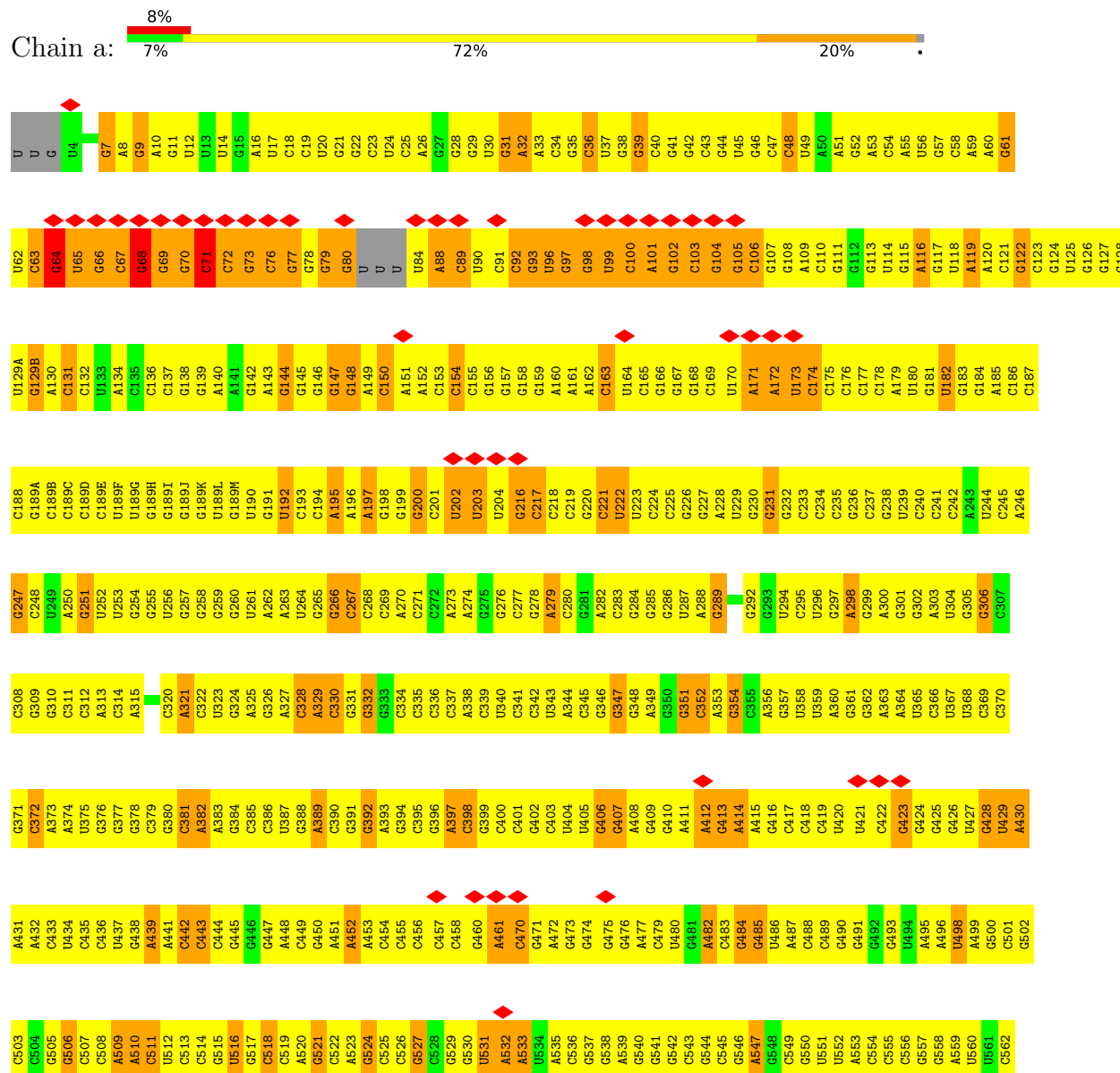
- Molecule 30: 50S ribosomal protein L35



- Molecule 31: 50S ribosomal protein L36

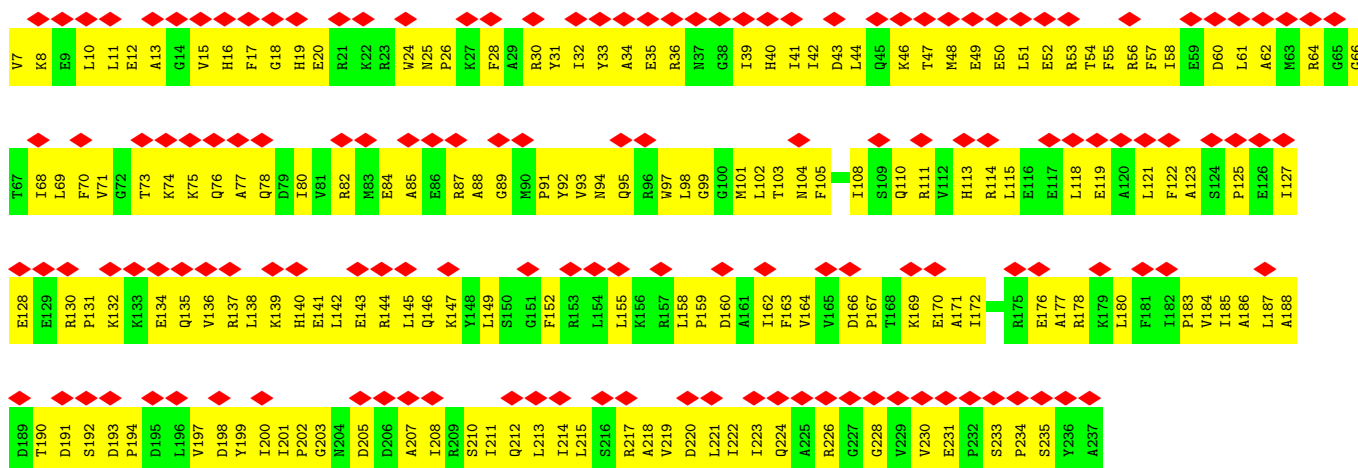


- Molecule 32: 16S rRNA

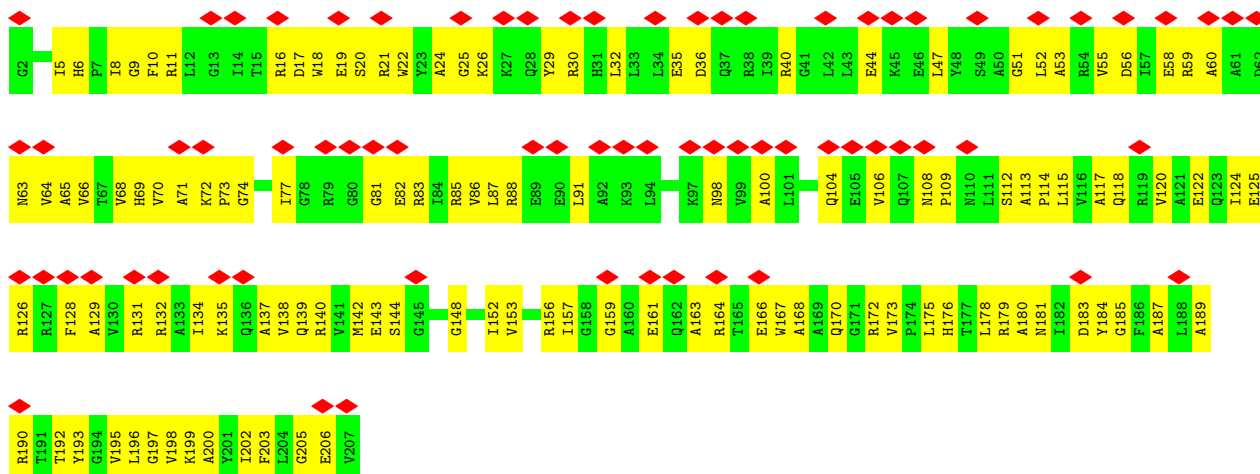
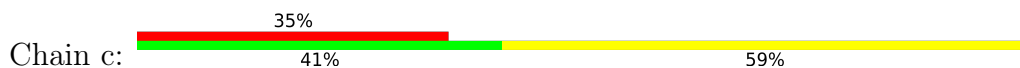


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- Molecule 33: 30S ribosomal protein S2

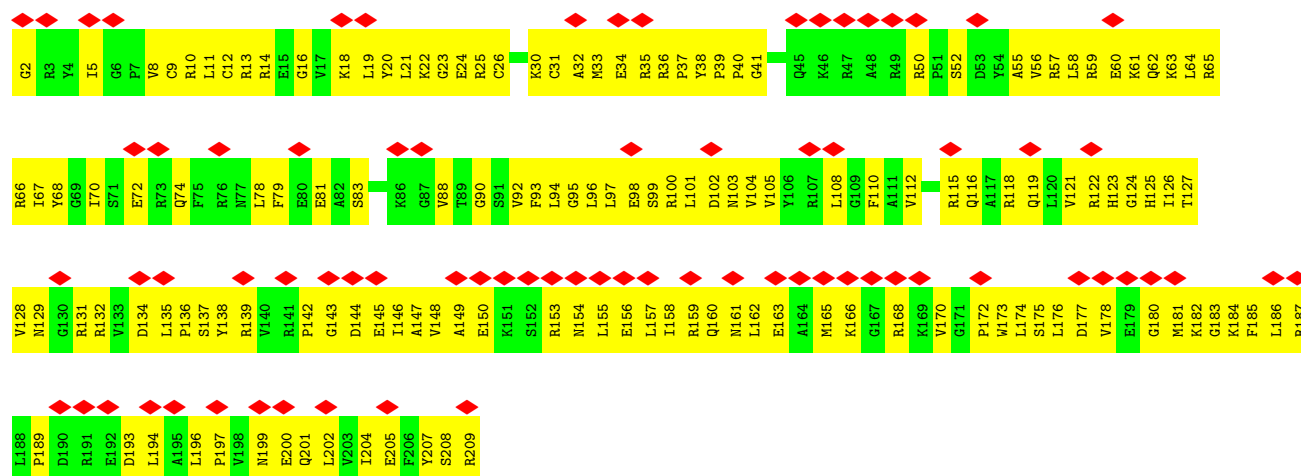


- Molecule 34: 30S ribosomal protein S3

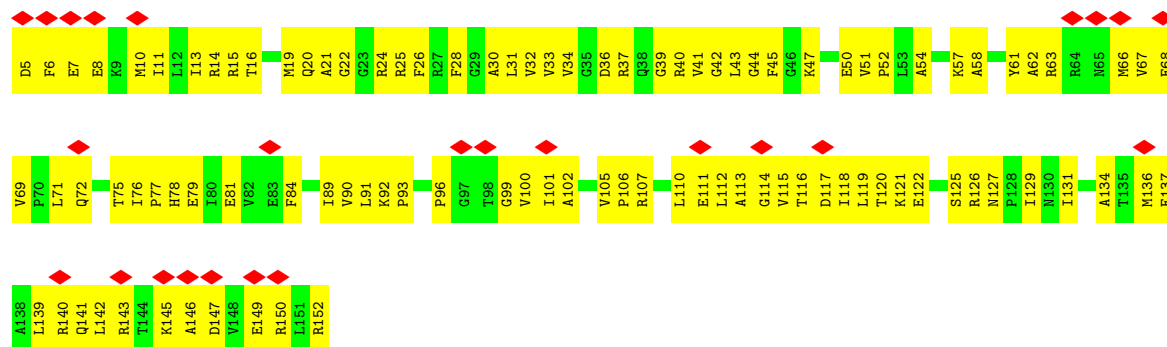


- Molecule 35: 30S ribosomal protein S4

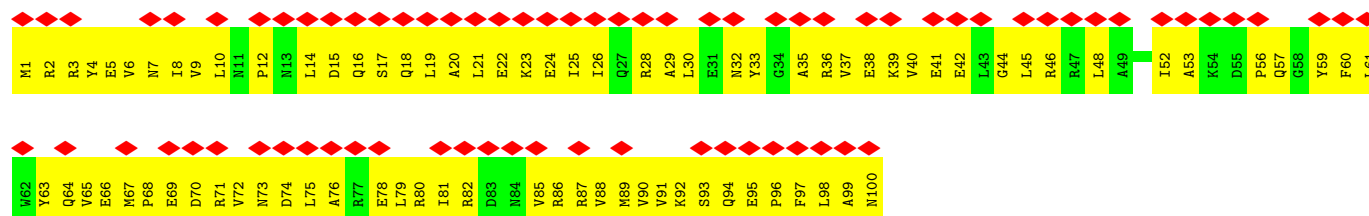
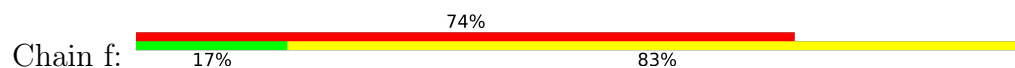




- Molecule 36: 30S ribosomal protein S5

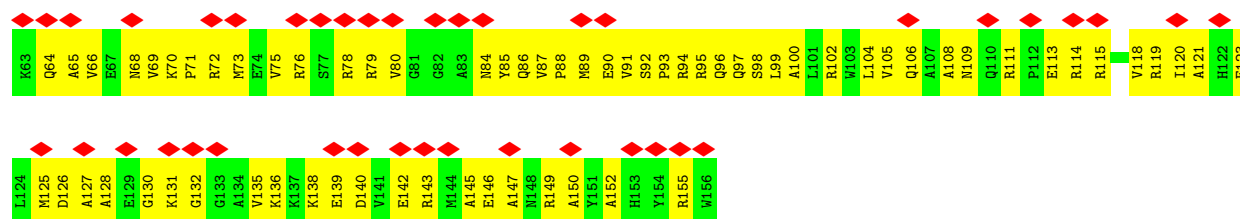


- Molecule 37: 30S ribosomal protein S6

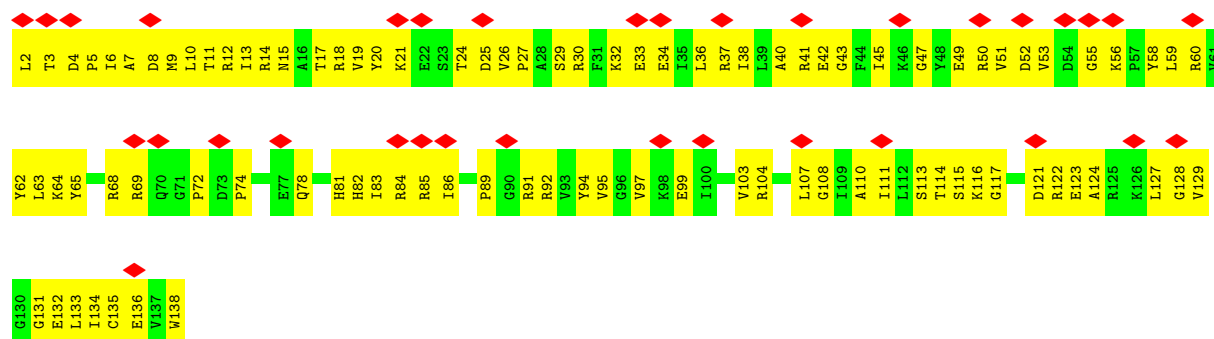


- Molecule 38: 30S ribosomal protein S7

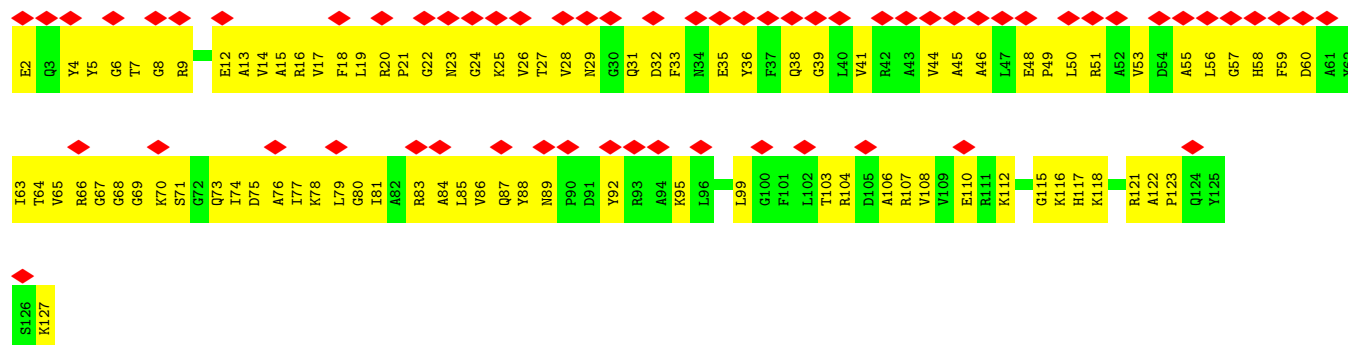




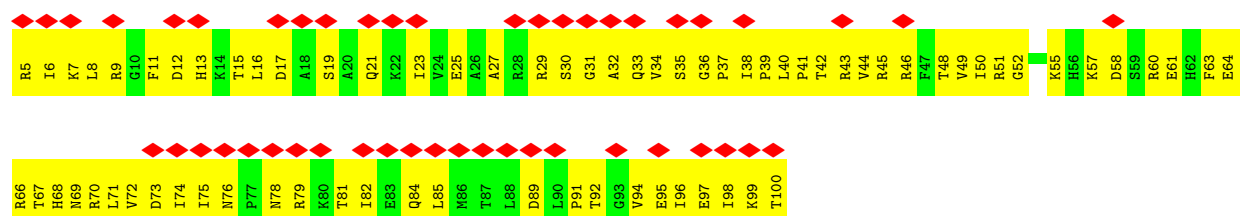
• Molecule 39: 30S ribosomal protein S8



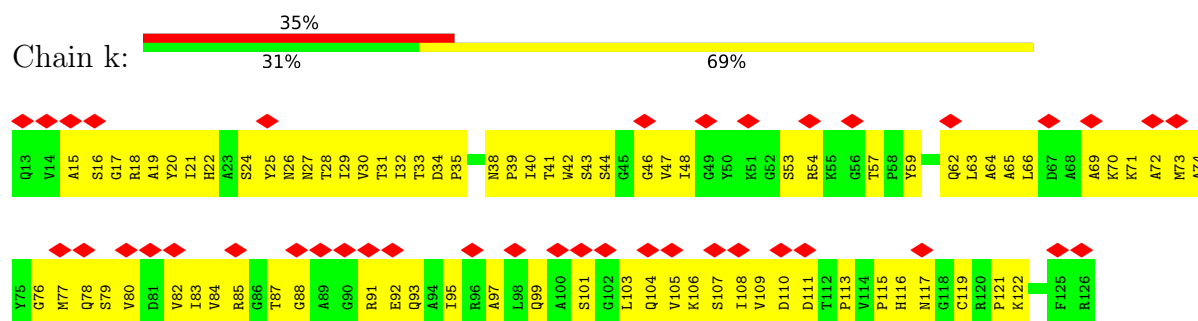
• Molecule 40: 30S ribosomal protein S9



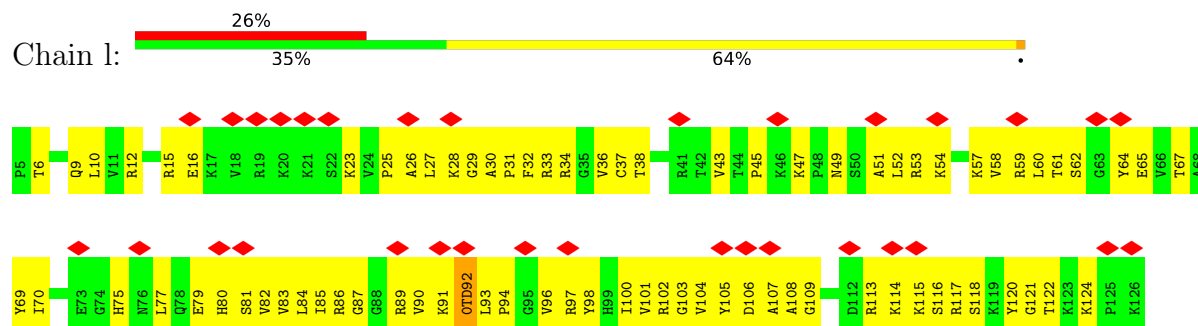
• Molecule 41: 30S ribosomal protein S10



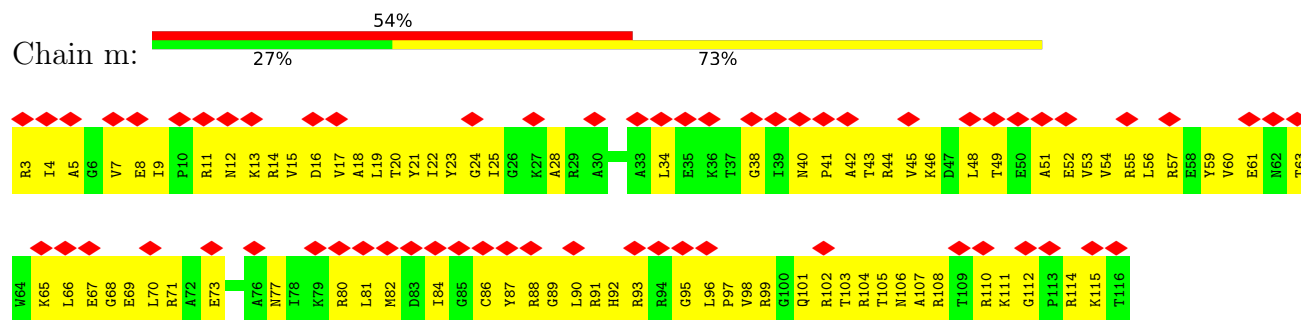
• Molecule 42: 30S ribosomal protein S11



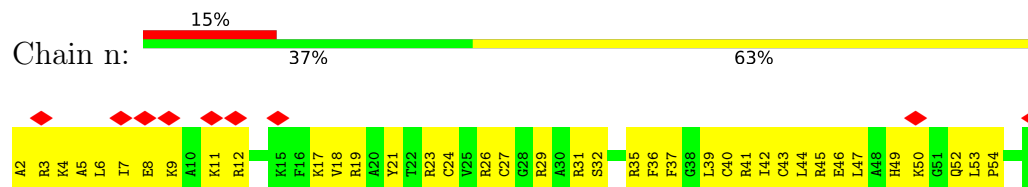
- Molecule 43: 30S ribosomal protein S12



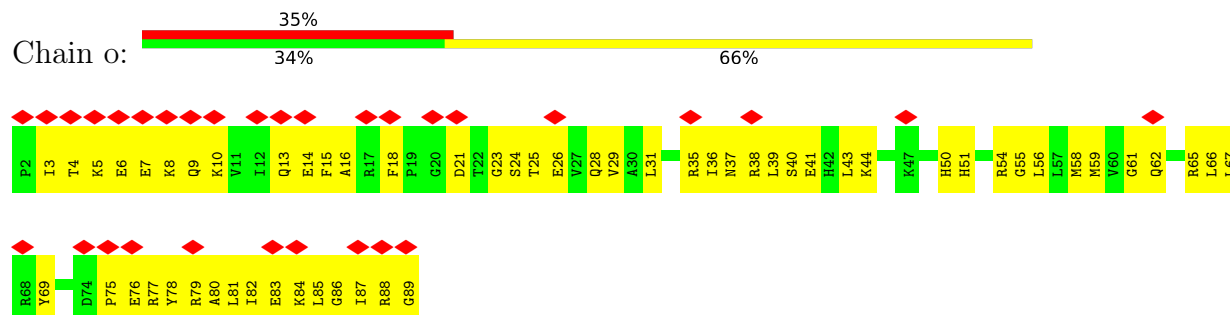
- Molecule 44: 30S ribosomal protein S13



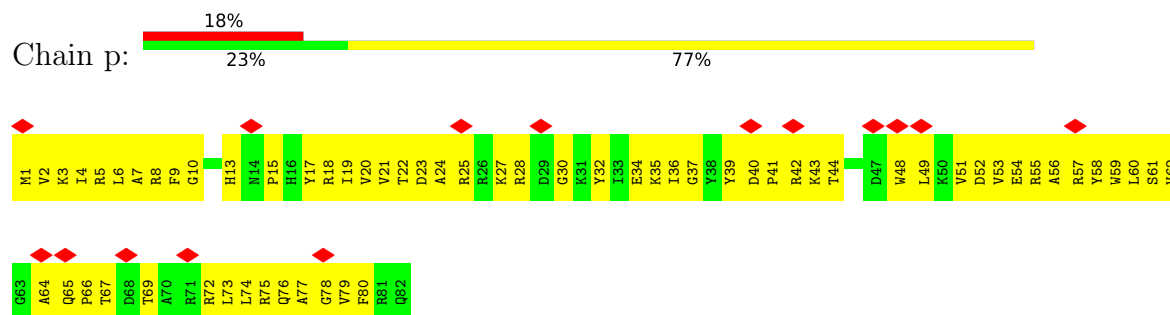
- Molecule 45: 30S ribosomal protein S14 type Z



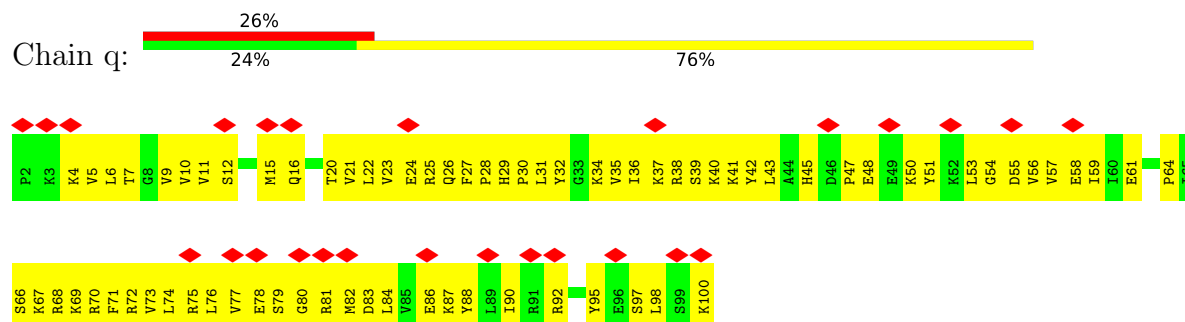
- Molecule 46: 30S ribosomal protein S15



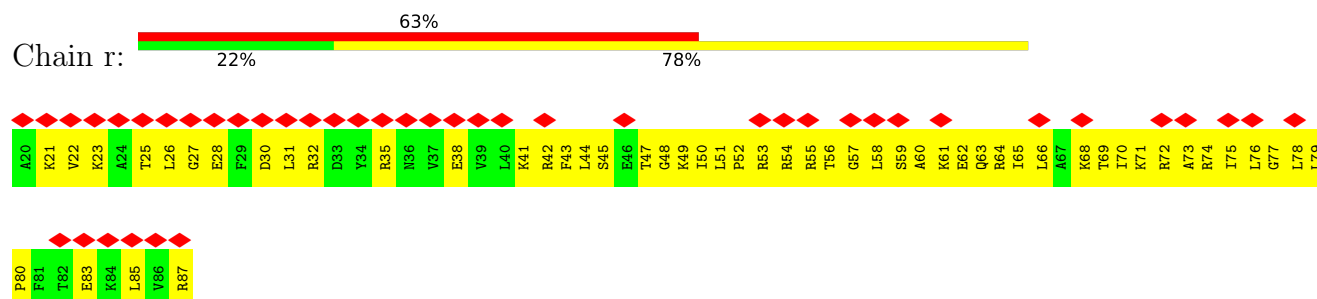
- Molecule 47: 30S ribosomal protein S16



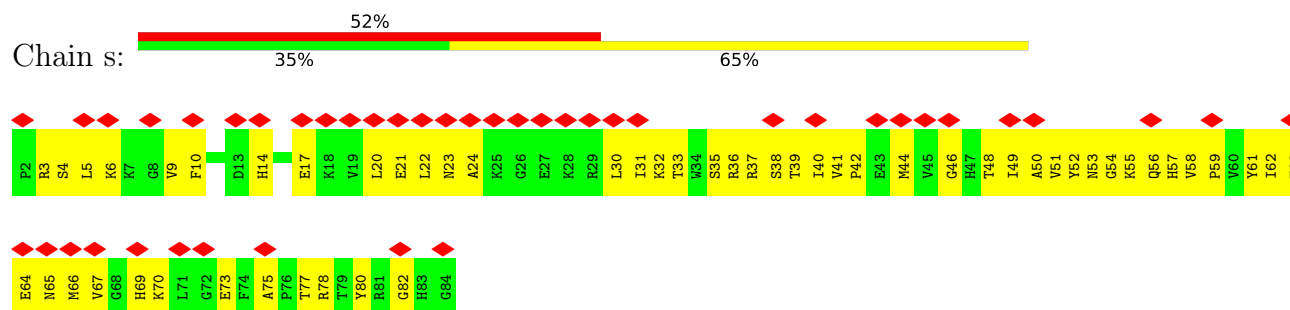
- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

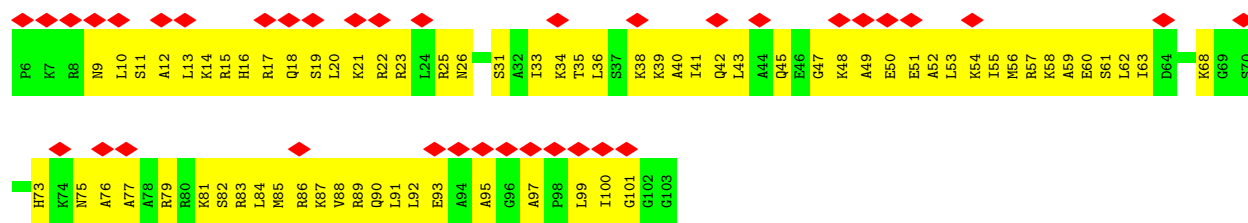


- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20

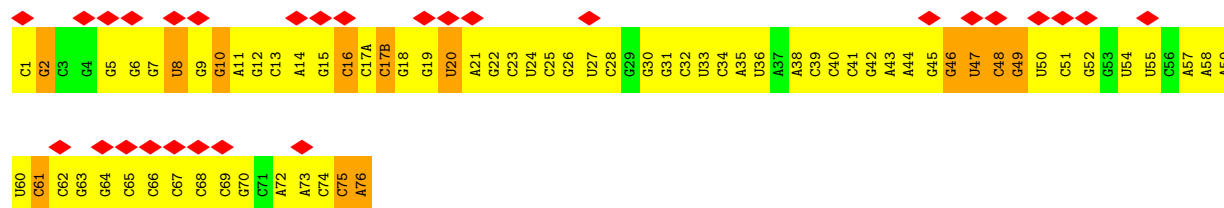
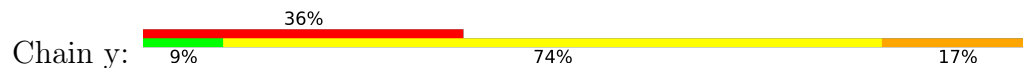




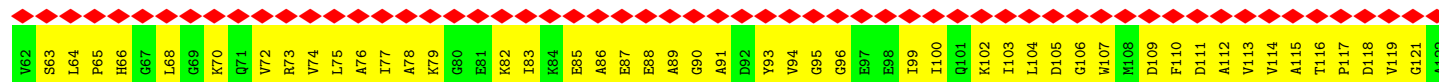
• Molecule 52: 30S ribosomal protein Thx



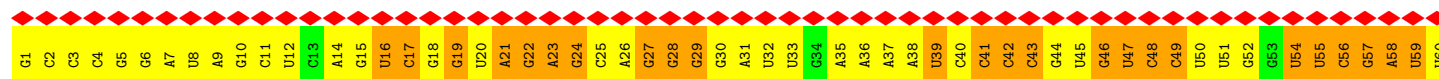
• Molecule 53: P-site tRNA fMet

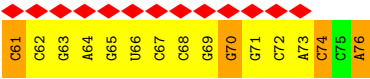


• Molecule 54: 50S ribosomal protein L1

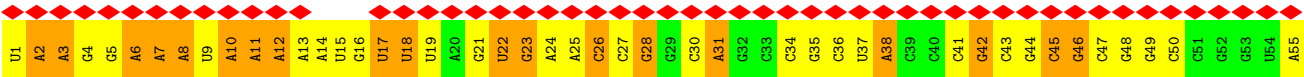
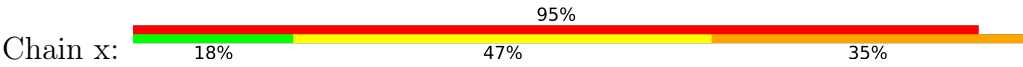


• Molecule 55: E-site tRNA Phe





● Molecule 56: messenger RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36361	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.150	Depositor
Minimum map value	-0.080	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, UR3, 2MG, OMG, PSU, ZN, MA6, 2MA, 7MG, 5MU, 5MC, 4OC, 2MU, M2G, 0TD

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	0.40	0/68899	0.36	4/107536 (0.0%)
2	B	0.35	0/2878	0.31	0/4490
3	D	0.38	0/2186	0.46	0/2944
4	E	0.37	0/1592	0.50	0/2149
5	F	0.34	0/1615	0.43	0/2188
6	G	0.29	0/1449	0.45	0/1957
7	H	0.27	0/1347	0.44	0/1817
8	I	0.18	0/1091	0.39	0/1490
9	N	0.35	0/1144	0.44	0/1543
10	O	0.37	0/943	0.42	0/1269
11	P	0.34	0/1152	0.46	0/1533
12	Q	0.37	0/1143	0.44	0/1527
13	R	0.35	0/982	0.52	0/1312
14	S	0.31	0/880	0.44	0/1172
15	T	0.36	0/1097	0.49	0/1468
16	U	0.35	0/977	0.45	0/1301
17	V	0.33	0/782	0.46	0/1049
18	W	0.37	0/897	0.45	0/1205
19	X	0.34	0/764	0.41	0/1025
20	Y	0.28	0/823	0.41	0/1100
21	Z	0.25	0/1491	0.44	0/2029
22	0	0.36	0/616	0.48	0/821
23	1	0.35	0/766	0.46	0/1018
24	2	0.32	0/594	0.47	0/785
25	3	0.33	0/469	0.44	0/630
26	4	0.27	0/549	0.62	0/741
27	5	0.33	0/469	0.42	0/635
28	6	0.38	0/456	0.50	0/608
29	7	0.38	0/426	0.51	0/561
30	8	0.35	0/525	0.45	0/691
31	9	0.33	0/310	0.52	0/407
32	a	0.64	7/36109 (0.0%)	0.38	2/56341 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.27	0/1860	0.42	0/2518
34	c	0.32	0/1566	0.40	0/2119
35	d	0.29	0/1698	0.42	0/2277
36	e	0.36	0/1149	0.46	0/1548
37	f	0.27	0/829	0.39	0/1123
38	g	0.29	0/1248	0.40	0/1676
39	h	0.34	0/1108	0.44	0/1494
40	i	0.29	0/985	0.46	1/1329 (0.1%)
41	j	0.29	0/723	0.42	0/984
42	k	0.29	0/848	0.40	0/1149
43	l	0.32	0/937	0.46	0/1260
44	m	0.30	0/905	0.48	0/1217
45	n	0.33	0/501	0.45	0/664
46	o	0.32	0/739	0.43	0/985
47	p	0.33	0/693	0.45	0/935
48	q	0.36	0/836	0.44	0/1117
49	r	0.28	0/560	0.43	0/746
50	s	0.27	0/660	0.40	0/893
51	t	0.31	0/736	0.51	0/976
52	u	0.33	0/203	0.52	0/266
53	y	0.30	0/1832	0.34	0/2855
54	C	0.15	0/1748	0.42	0/2354
55	z	0.21	0/1809	0.33	0/2819
56	x	0.18	0/1315	0.34	0/2046
All	All	0.44	7/160909 (0.0%)	0.39	7/240692 (0.0%)

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
6	G	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	71	C	C2-N3	41.51	2.18	1.35
32	a	71	C	N1-C2	41.29	2.22	1.40
32	a	71	C	N3-C4	40.36	2.14	1.33
32	a	71	C	N1-C6	39.59	2.16	1.37
32	a	71	C	C4-C5	37.79	2.18	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2224	G	OP1-P-O3'	-10.30	77.11	108.00
1	A	2883	A	OP2-P-O3'	-8.84	81.48	108.00
1	A	2883	A	OP1-P-O3'	-8.51	82.47	108.00
1	A	2224	G	OP2-P-O3'	-7.57	85.30	108.00
40	i	44	VAL	N-CA-C	-6.52	107.51	113.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	G	95	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	61758	0	31153	3990	0
2	B	2573	0	1306	177	0
3	D	2136	0	2218	231	0
4	E	1559	0	1618	181	0
5	F	1580	0	1619	199	0
6	G	1424	0	1441	193	0
7	H	1324	0	1399	206	0
8	I	1076	0	1094	141	0
9	N	1117	0	1184	121	0
10	O	933	0	996	99	0
11	P	1135	0	1212	150	0
12	Q	1122	0	1179	154	0
13	R	968	0	1033	83	0
14	S	870	0	923	93	0
15	T	1083	0	1136	126	0
16	U	959	0	1019	97	0
17	V	771	0	830	102	0
18	W	886	0	940	84	0
19	X	750	0	814	68	0
20	Y	810	0	887	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Z	1459	0	1457	192	0
22	0	608	0	622	52	0
23	1	759	0	837	87	0
24	2	592	0	654	49	0
25	3	464	0	514	45	0
26	4	536	0	514	95	0
27	5	455	0	465	46	0
28	6	449	0	469	43	0
29	7	418	0	467	39	0
30	8	517	0	582	59	0
31	9	307	0	335	24	0
32	a	32532	0	16451	2589	0
33	b	1825	0	1828	234	0
34	c	1542	0	1517	149	0
35	d	1668	0	1707	234	0
36	e	1133	0	1191	142	0
37	f	816	0	808	139	0
38	g	1229	0	1238	125	0
39	h	1088	0	1126	113	0
40	i	966	0	953	121	0
41	j	710	0	661	98	0
42	k	833	0	836	111	0
43	l	932	0	981	123	0
44	m	895	0	920	144	0
45	n	492	0	529	66	0
46	o	728	0	760	71	0
47	p	677	0	686	93	0
48	q	823	0	891	92	0
49	r	555	0	618	83	0
50	s	645	0	635	80	0
51	t	733	0	795	116	0
52	u	199	0	208	22	0
53	y	1640	0	838	122	0
54	C	1718	0	1767	363	0
55	z	1619	0	822	134	0
56	x	1176	4	596	56	0
57	4	1	0	0	0	0
57	5	1	0	0	0	0
57	6	1	0	0	0	0
57	9	1	0	0	0	0
57	Y	1	0	0	0	0
57	n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	d	8	0	0	1	0
All	All	148586	4	100279	11478	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 47.

The worst 5 of 11478 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)
32:a:64:G:C3'	32:a:64:G:O3'	1.65	1.44
32:a:71:C:C5	32:a:71:C:C6	2.09	1.38
32:a:71:C:C5	32:a:71:C:C4	2.18	1.29
7:H:16:SER:O	7:H:26:VAL:HA	1.36	1.22
32:a:71:C:C4	32:a:71:C:N3	2.14	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	273/275 (99%)	245 (90%)	28 (10%)	0	100	100
4	E	202/204 (99%)	188 (93%)	14 (7%)	0	100	100
5	F	201/203 (99%)	193 (96%)	7 (4%)	1 (0%)	24	59
6	G	179/181 (99%)	160 (89%)	19 (11%)	0	100	100
7	H	166/173 (96%)	152 (92%)	14 (8%)	0	100	100
8	I	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
9	N	138/140 (99%)	127 (92%)	11 (8%)	0	100	100
10	O	120/122 (98%)	112 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	P	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
12	Q	139/141 (99%)	128 (92%)	11 (8%)	0	100	100
13	R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
15	T	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
16	U	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
17	V	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
18	W	110/112 (98%)	97 (88%)	13 (12%)	0	100	100
19	X	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
20	Y	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
21	Z	185/187 (99%)	161 (87%)	24 (13%)	0	100	100
22	0	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
23	1	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
24	2	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
25	3	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
26	4	67/69 (97%)	55 (82%)	10 (15%)	2 (3%)	3	23
27	5	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
28	6	51/53 (96%)	46 (90%)	5 (10%)	0	100	100
29	7	46/48 (96%)	46 (100%)	0	0	100	100
30	8	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
31	9	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
33	b	229/231 (99%)	209 (91%)	20 (9%)	0	100	100
34	c	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
35	d	206/208 (99%)	201 (98%)	5 (2%)	0	100	100
36	e	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
37	f	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
38	g	153/155 (99%)	145 (95%)	8 (5%)	0	100	100
39	h	135/137 (98%)	123 (91%)	12 (9%)	0	100	100
40	i	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
41	j	94/96 (98%)	82 (87%)	11 (12%)	1 (1%)	11	43
42	k	112/114 (98%)	107 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	l	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
44	m	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
45	n	58/60 (97%)	57 (98%)	1 (2%)	0	100	100
46	o	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
47	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
48	q	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
49	r	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
50	s	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
51	t	96/98 (98%)	84 (88%)	12 (12%)	0	100	100
52	u	21/23 (91%)	21 (100%)	0	0	100	100
54	C	221/226 (98%)	199 (90%)	22 (10%)	0	100	100
All	All	5919/6028 (98%)	5464 (92%)	451 (8%)	4 (0%)	49	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	4	49	PHE
26	4	47	GLN
41	j	55	LYS
5	F	207	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	215/217 (99%)	215 (100%)	0	100	100
4	E	164/165 (99%)	164 (100%)	0	100	100
5	F	159/161 (99%)	159 (100%)	0	100	100
6	G	142/155 (92%)	142 (100%)	0	100	100
7	H	143/144 (99%)	143 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	I	108/122 (88%)	108 (100%)	0	100	100
9	N	118/119 (99%)	118 (100%)	0	100	100
10	O	100/100 (100%)	100 (100%)	0	100	100
11	P	115/116 (99%)	115 (100%)	0	100	100
12	Q	111/111 (100%)	111 (100%)	0	100	100
13	R	101/101 (100%)	101 (100%)	0	100	100
14	S	85/87 (98%)	85 (100%)	0	100	100
15	T	113/115 (98%)	113 (100%)	0	100	100
16	U	93/93 (100%)	93 (100%)	0	100	100
17	V	80/82 (98%)	80 (100%)	0	100	100
18	W	90/91 (99%)	90 (100%)	0	100	100
19	X	77/77 (100%)	77 (100%)	0	100	100
20	Y	86/88 (98%)	86 (100%)	0	100	100
21	Z	156/164 (95%)	156 (100%)	0	100	100
22	0	61/62 (98%)	61 (100%)	0	100	100
23	1	81/82 (99%)	81 (100%)	0	100	100
24	2	66/66 (100%)	66 (100%)	0	100	100
25	3	50/51 (98%)	50 (100%)	0	100	100
26	4	54/62 (87%)	54 (100%)	0	100	100
27	5	50/51 (98%)	50 (100%)	0	100	100
28	6	50/51 (98%)	50 (100%)	0	100	100
29	7	41/41 (100%)	41 (100%)	0	100	100
30	8	54/54 (100%)	54 (100%)	0	100	100
31	9	34/34 (100%)	34 (100%)	0	100	100
33	b	187/199 (94%)	187 (100%)	0	100	100
34	c	140/160 (88%)	140 (100%)	0	100	100
35	d	172/180 (96%)	172 (100%)	0	100	100
36	e	114/114 (100%)	114 (100%)	0	100	100
37	f	85/90 (94%)	85 (100%)	0	100	100
38	g	119/126 (94%)	119 (100%)	0	100	100
39	h	114/118 (97%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	i	88/97 (91%)	88 (100%)	0	100	100
41	j	68/86 (79%)	68 (100%)	0	100	100
42	k	83/86 (96%)	83 (100%)	0	100	100
43	l	96/102 (94%)	96 (100%)	0	100	100
44	m	87/93 (94%)	87 (100%)	0	100	100
45	n	49/49 (100%)	49 (100%)	0	100	100
46	o	78/79 (99%)	78 (100%)	0	100	100
47	p	68/71 (96%)	68 (100%)	0	100	100
48	q	94/94 (100%)	94 (100%)	0	100	100
49	r	59/59 (100%)	59 (100%)	0	100	100
50	s	67/72 (93%)	67 (100%)	0	100	100
51	t	70/76 (92%)	70 (100%)	0	100	100
52	u	18/18 (100%)	18 (100%)	0	100	100
54	C	177/178 (99%)	177 (100%)	0	100	100
All	All	4830/5009 (96%)	4830 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
47	p	65	GLN
50	s	69	HIS
20	Y	43	ASN
19	X	82	GLN
50	s	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2857/2915 (98%)	634 (22%)	46 (1%)
2	B	119/120 (99%)	23 (19%)	0
32	a	1509/1521 (99%)	331 (21%)	0
53	y	76/77 (98%)	13 (17%)	0
55	z	75/76 (98%)	29 (38%)	0
56	x	54/55 (98%)	24 (44%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4690/4764 (98%)	1054 (22%)	46 (0%)

5 of 1054 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	10	G
1	A	12	U
1	A	14	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1491	G
1	A	2172	U
1	A	1493	C
1	A	2126	A
1	A	2321	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	5MC	a	967	32	19,22,23	1.44	3 (15%)	26,32,35	1.14	2 (7%)
1	5MC	A	1942	1	19,22,23	1.41	3 (15%)	26,32,35	1.17	2 (7%)
32	M2G	a	966	32	24,27,28	1.30	5 (20%)	33,40,43	1.87	6 (18%)
32	2MG	a	1207	32	23,26,27	1.27	4 (17%)	33,38,41	2.23	10 (30%)
43	0TD	l	92	43	8,9,10	2.21	1 (12%)	6,11,13	1.20	0
32	PSU	a	516	32	18,21,22	1.45	5 (27%)	21,30,33	2.19	5 (23%)
32	MA6	a	1519	32	23,26,27	1.41	5 (21%)	33,38,41	2.48	14 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	A	2251	1,53	23,26,27	1.25	4 (17%)	32,38,41	2.00	6 (18%)
32	4OC	a	1402	32	20,23,24	0.77	1 (5%)	25,32,35	0.93	0
32	5MC	a	1400	32	19,22,23	1.44	3 (15%)	26,32,35	1.20	2 (7%)
1	PSU	A	2605	1	18,21,22	1.45	4 (22%)	21,30,33	2.25	4 (19%)
32	5MC	a	1407	32	19,22,23	1.47	3 (15%)	26,32,35	1.26	2 (7%)
1	5MU	A	1939	1	19,22,23	1.37	3 (15%)	27,32,35	2.35	6 (22%)
1	2MA	A	2503	1	22,25,26	1.46	5 (22%)	32,37,40	2.26	7 (21%)
1	2MU	A	2552	1	19,22,24	1.37	4 (21%)	25,31,36	2.22	6 (24%)
1	5MU	A	1915	1	19,22,23	1.42	5 (26%)	27,32,35	2.44	9 (33%)
1	4OC	A	1920	1	19,22,24	0.81	1 (5%)	25,31,35	0.85	0
1	5MC	A	1962	1	19,22,23	1.42	3 (15%)	26,32,35	1.25	2 (7%)
1	PSU	A	1911	1	18,21,22	1.40	3 (16%)	21,30,33	2.19	4 (19%)
32	UR3	a	1498	32	19,22,23	0.94	2 (10%)	26,32,35	1.76	3 (11%)
32	7MG	a	527	32	23,26,27	1.35	4 (17%)	27,39,42	2.71	7 (25%)
32	5MC	a	1404	32	19,22,23	1.51	3 (15%)	26,32,35	1.25	3 (11%)
32	MA6	a	1518	32	23,26,27	1.41	5 (21%)	33,38,41	2.41	14 (42%)
1	PSU	A	1917	1	18,21,22	1.39	3 (16%)	21,30,33	2.11	5 (23%)

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
32	5MC	a	967	32	-	0/7/25/26	0/2/2/2
1	5MC	A	1942	1	-	0/7/25/26	0/2/2/2
32	M2G	a	966	32	-	0/11/29/30	0/3/3/3
32	2MG	a	1207	32	-	0/9/27/28	0/3/3/3
43	0TD	l	92	43	-	4/7/12/14	-
32	PSU	a	516	32	-	0/7/25/26	0/2/2/2
32	MA6	a	1519	32	-	4/11/29/30	0/3/3/3
1	OMG	A	2251	1,53	-	2/9/27/28	0/3/3/3
32	4OC	a	1402	32	-	0/9/29/30	0/2/2/2
32	5MC	a	1400	32	-	2/7/25/26	0/2/2/2
1	PSU	A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	a	1407	32	-	0/7/25/26	0/2/2/2
1	5MU	A	1939	1	-	0/7/25/26	0/2/2/2
1	2MA	A	2503	1	-	1/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MU	A	2552	1	-	0/9/27/28	0/2/2/2
1	5MU	A	1915	1	-	2/7/25/26	0/2/2/2
1	4OC	A	1920	1	-	0/9/27/30	0/2/2/2
1	5MC	A	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1911	1	-	0/7/25/26	0/2/2/2
32	UR3	a	1498	32	-	0/7/25/26	0/2/2/2
32	7MG	a	527	32	-	3/7/37/38	0/3/3/3
32	5MC	a	1404	32	-	1/7/25/26	0/2/2/2
32	MA6	a	1518	32	-	1/11/29/30	0/3/3/3
1	PSU	A	1917	1	-	0/7/25/26	0/2/2/2

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	1404	5MC	C5-C4	5.05	1.47	1.44
32	a	1407	5MC	C5-C4	5.03	1.47	1.44
43	l	92	0TD	CB-CA	-4.99	1.53	1.54
1	A	1942	5MC	C5-C4	4.86	1.47	1.44
32	a	967	5MC	C5-C4	4.86	1.47	1.44

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	527	7MG	N9-C4-N3	9.30	139.09	125.46
1	A	2503	2MA	C5-C4-N3	-8.18	118.57	127.18
32	a	1498	UR3	C4-N3-C2	-7.06	118.90	124.58
1	A	2605	PSU	N1-C2-N3	6.90	122.45	115.17
32	a	516	PSU	N1-C2-N3	6.80	122.34	115.17

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1915	5MU	O4'-C1'-N1-C2
1	A	1915	5MU	O4'-C1'-N1-C6
32	a	527	7MG	C3'-C4'-C5'-O5'
32	a	1519	MA6	O4'-C4'-C5'-O5'
43	l	92	0TD	O-C-CA-CB

There are no ring outliers.

22 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	a	967	5MC	4	0
1	A	1942	5MC	2	0
32	a	966	M2G	4	0
32	a	1207	2MG	2	0
43	l	92	0TD	1	0
32	a	516	PSU	4	0
32	a	1519	MA6	4	0
1	A	2251	OMG	4	0
32	a	1402	4OC	5	0
32	a	1400	5MC	2	0
32	a	1407	5MC	3	0
1	A	1939	5MU	1	0
1	A	2503	2MA	3	0
1	A	2552	2MU	2	0
1	A	1915	5MU	1	0
1	A	1920	4OC	4	0
1	A	1962	5MC	3	0
1	A	1911	PSU	1	0
32	a	1498	UR3	4	0
32	a	1404	5MC	2	0
32	a	1518	MA6	7	0
1	A	1917	PSU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	SF4	d	301	35	0,12,12	-	-	-		

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	SF4	d	301	35	-	-	0/6/5/5

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	d	301	SF4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	a	4
7	H	3
1	A	2

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1000:U	O3'	1001(A):A	P	4.17
1	a	1029:C	O3'	1030(A):C	P	4.08
1	A	2103:C	O3'	2104:G	P	3.60
1	A	2180:U	O3'	2181:G	P	3.49
1	H	3:ARG	C	4:ILE	N	3.23

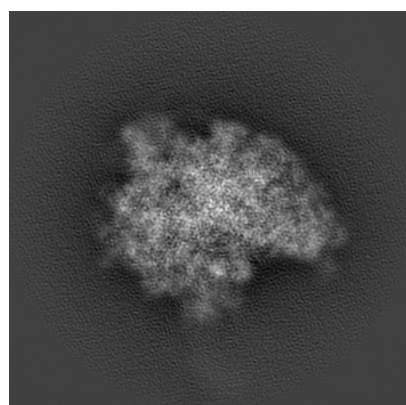
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8597. These allow visual inspection of the internal detail of the map and identification of artifacts.

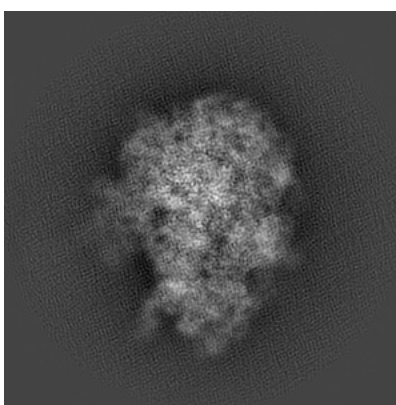
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

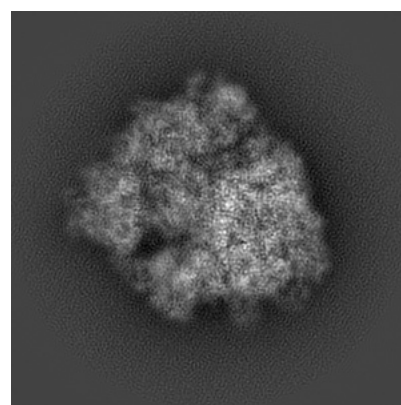
6.1.1 Primary map



X



Y

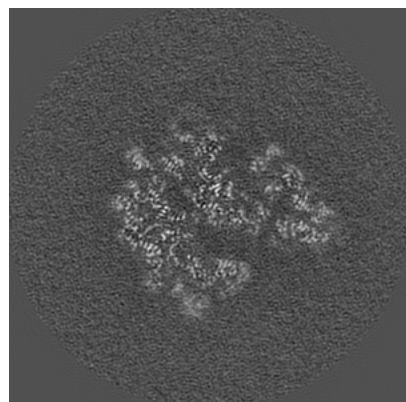


Z

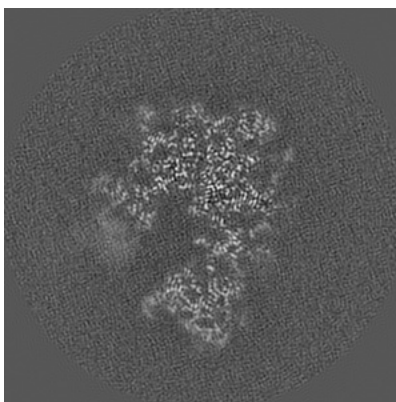
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

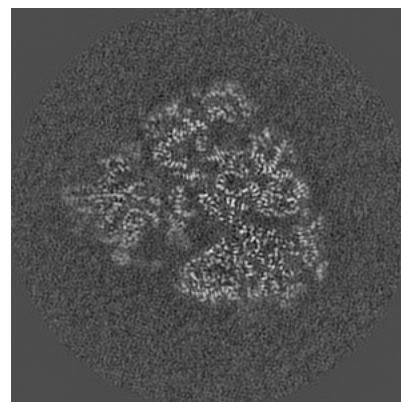
6.2.1 Primary map



X Index: 192



Y Index: 192

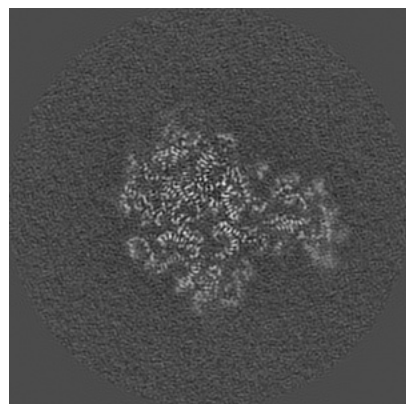


Z Index: 192

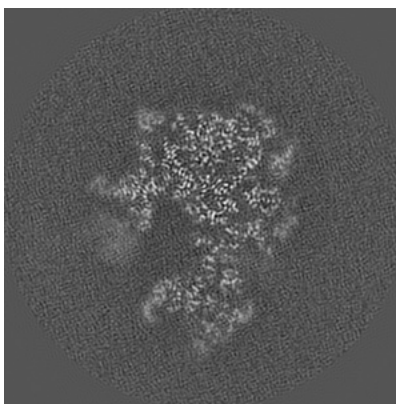
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

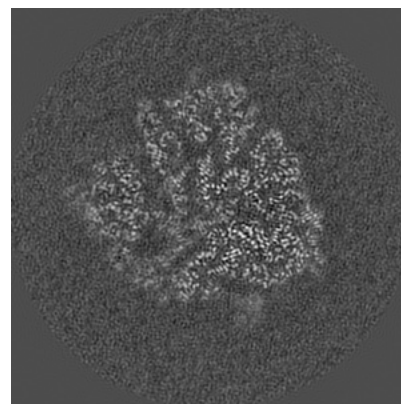
6.3.1 Primary map



X Index: 203



Y Index: 197

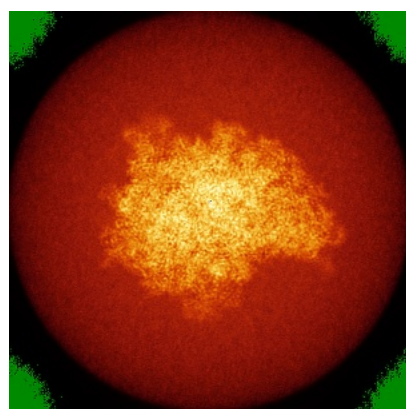


Z Index: 184

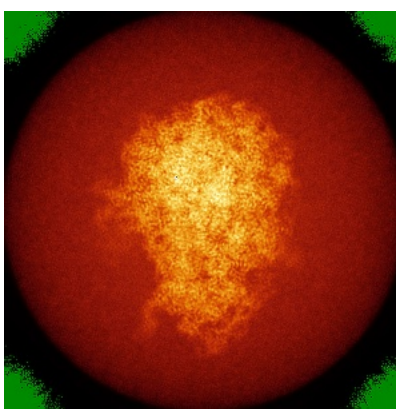
The images above show the largest variance slices of the map in three orthogonal directions.

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

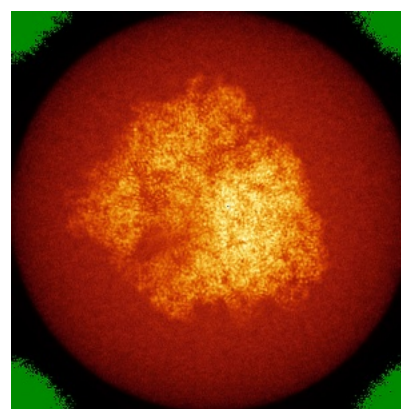
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

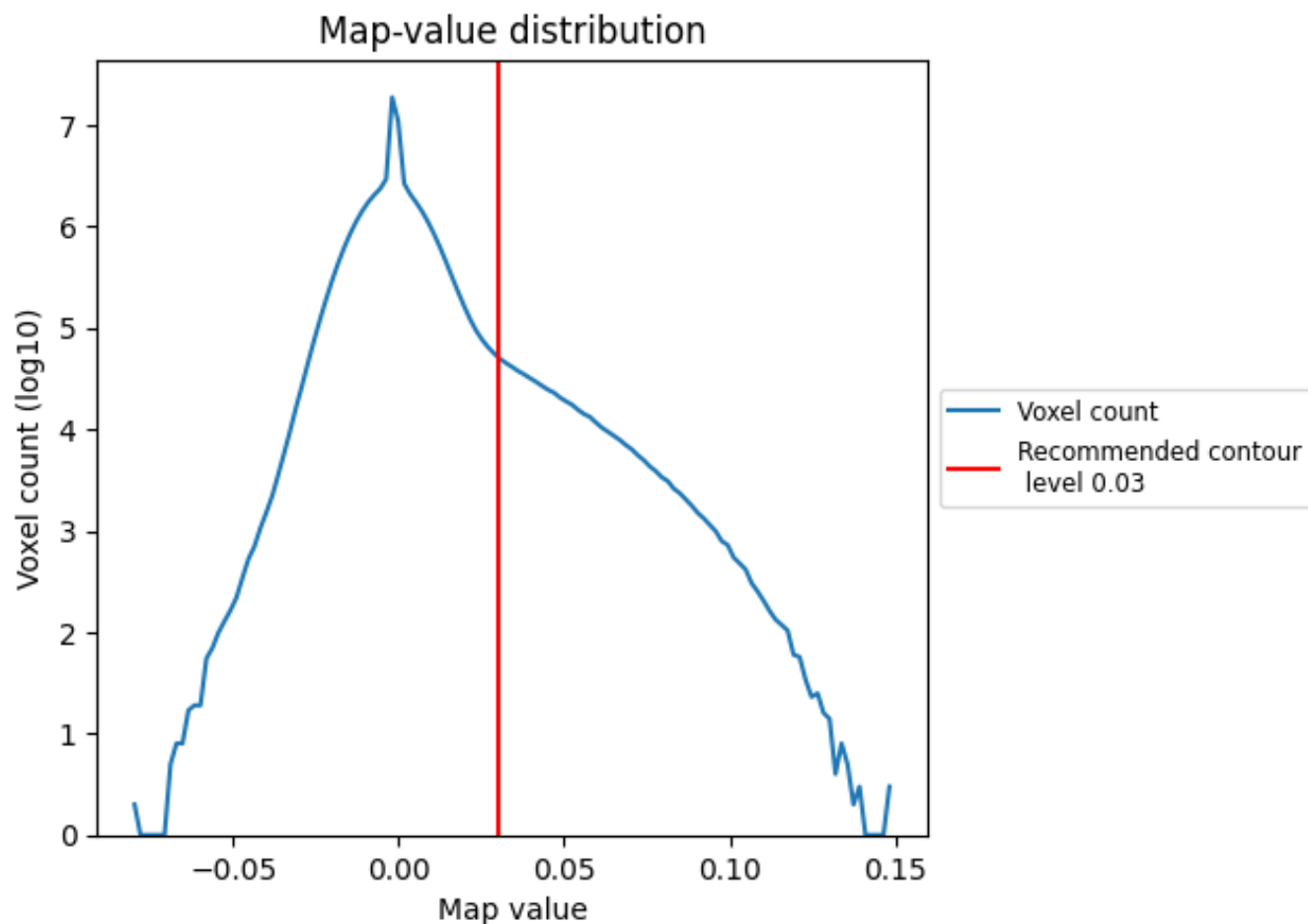
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

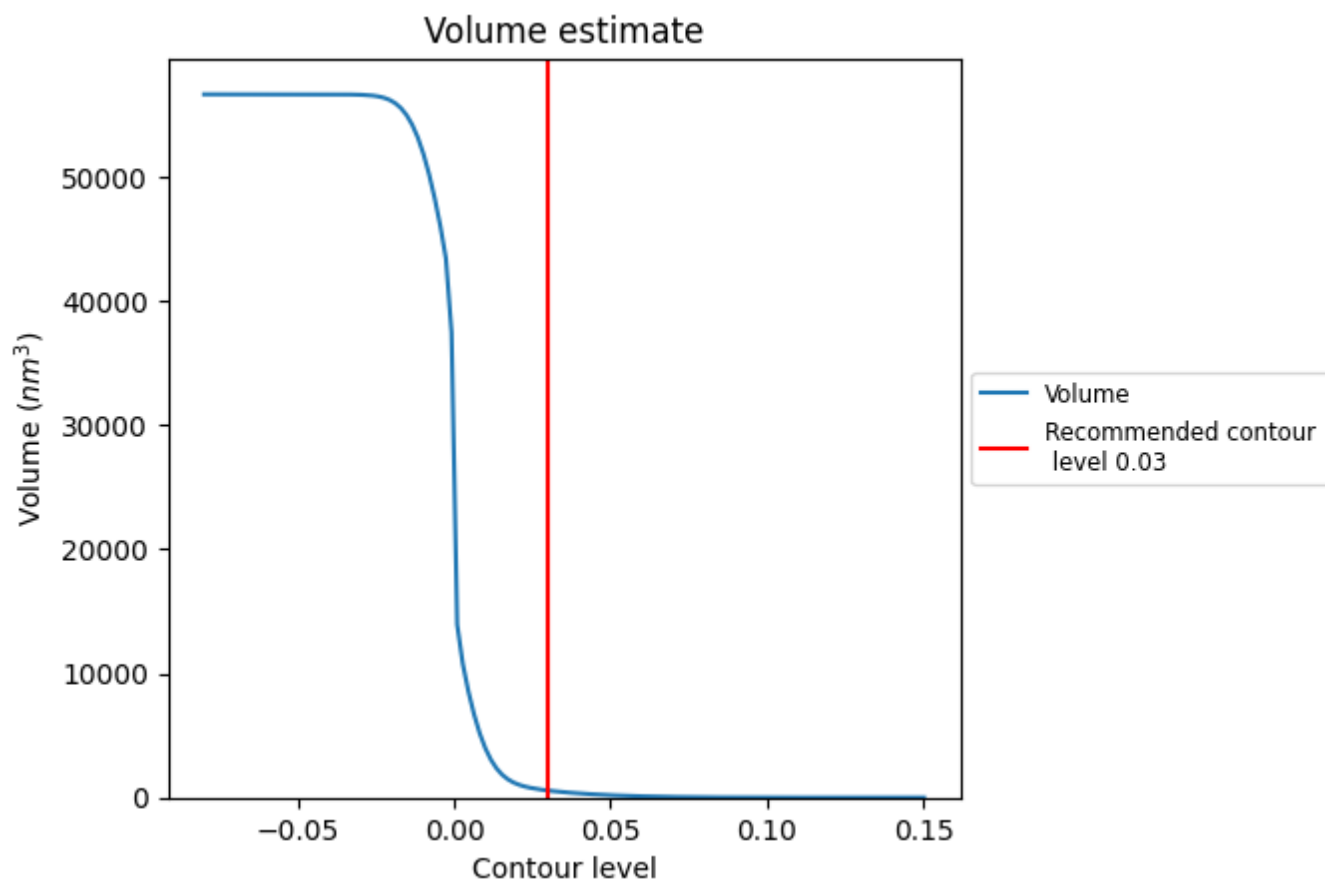
This section contains the results of statistical analysis of the map.

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.

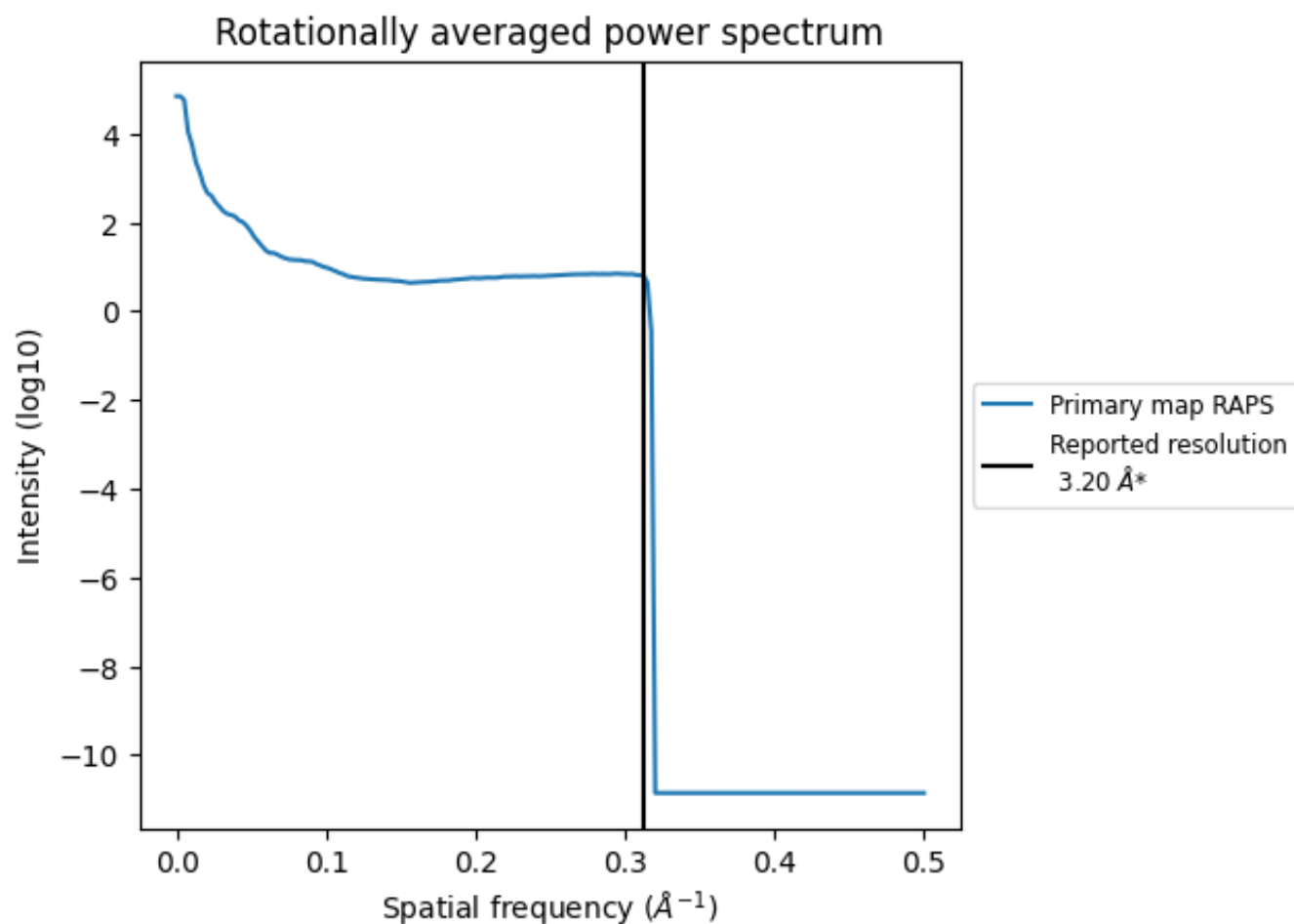
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm³; this corresponds to an approximate mass of 513 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 0.312 $\text{\AA}^{-1}$

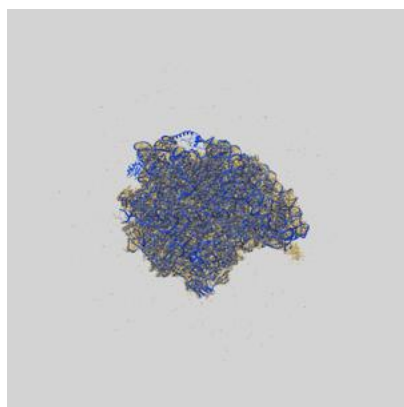
8 Fourier-Shell correlation

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

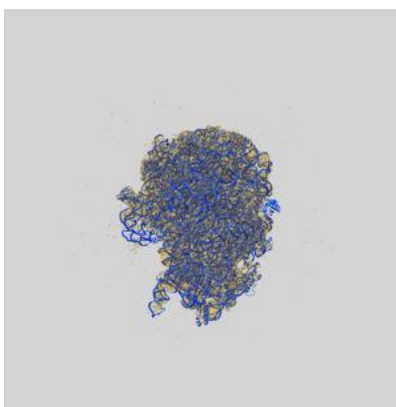
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8597 and PDB model 5UQ8. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

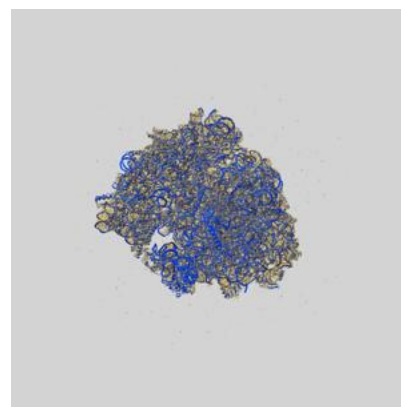
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

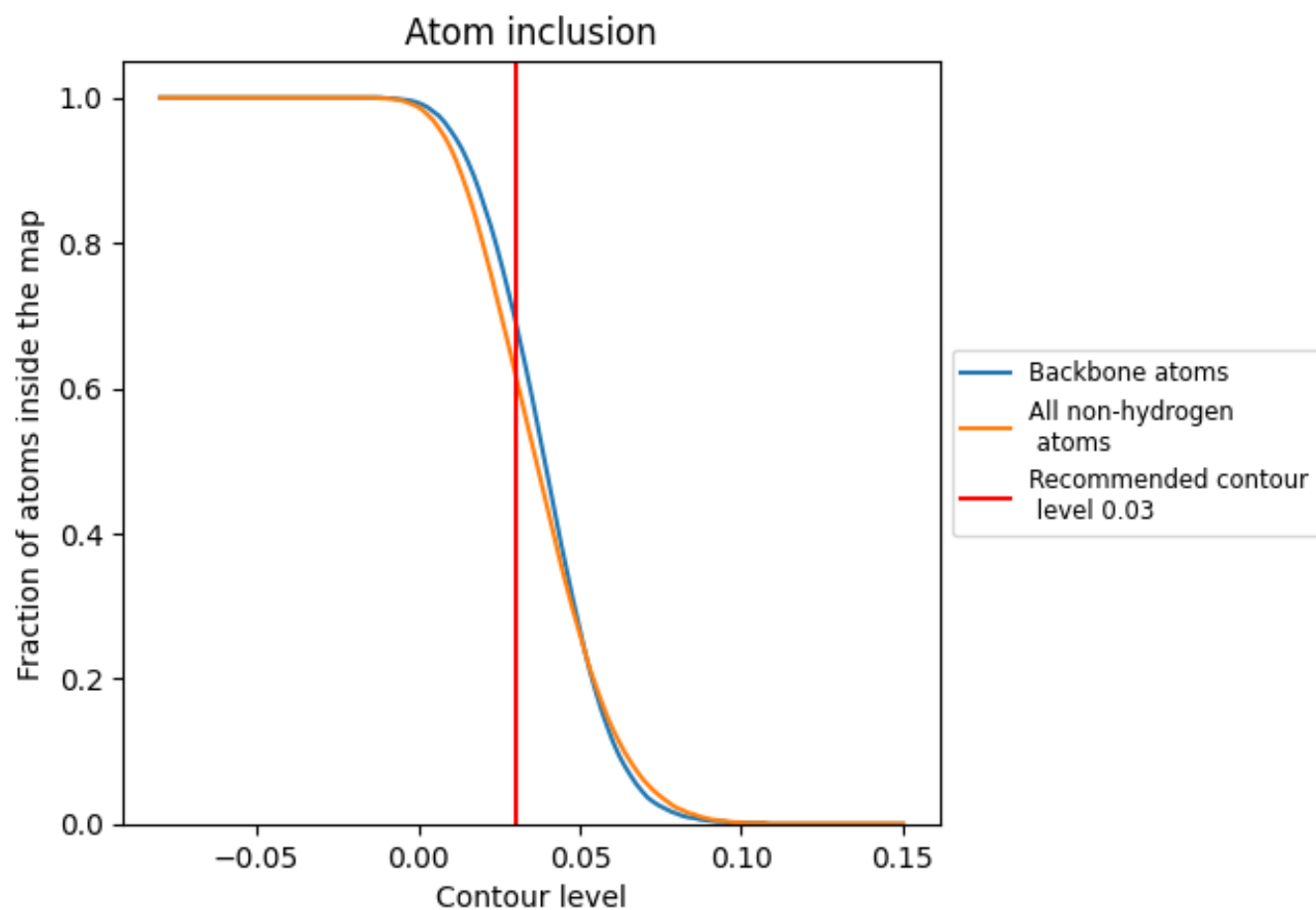


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6210	 0.4460
0	 0.6220	 0.5150
1	 0.4800	 0.4560
2	 0.4580	 0.4020
3	 0.5340	 0.4700
4	 0.2580	 0.2770
5	 0.6240	 0.4980
6	 0.6010	 0.4790
7	 0.6310	 0.5220
8	 0.5980	 0.5070
9	 0.5630	 0.4940
A	 0.7190	 0.4760
B	 0.6900	 0.4450
C	 0.0040	 0.1160
D	 0.6390	 0.5080
E	 0.5950	 0.4920
F	 0.5630	 0.4650
G	 0.4270	 0.3970
H	 0.3290	 0.3420
I	 0.0860	 0.2550
N	 0.5440	 0.4750
O	 0.5470	 0.4920
P	 0.5390	 0.4670
Q	 0.5380	 0.4550
R	 0.6130	 0.4880
S	 0.5100	 0.4270
T	 0.5540	 0.4570
U	 0.6370	 0.4910
V	 0.5000	 0.4490
W	 0.5840	 0.4930
X	 0.5290	 0.4570
Y	 0.4260	 0.4240
Z	 0.2590	 0.3350
a	 0.6970	 0.4530
b	 0.3650	 0.3780



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Chain	Atom inclusion	Q-score
c	 0.4980	 0.4410
d	 0.4770	 0.4090
e	 0.5410	 0.4680
f	 0.3390	 0.3510
g	 0.4250	 0.3840
h	 0.5610	 0.4710
i	 0.4220	 0.3910
j	 0.4030	 0.3890
k	 0.4760	 0.4330
l	 0.5440	 0.4880
m	 0.4260	 0.3980
n	 0.5790	 0.4760
o	 0.4890	 0.4180
p	 0.5700	 0.4630
q	 0.5150	 0.4750
r	 0.3600	 0.3650
s	 0.4030	 0.3860
t	 0.4630	 0.3910
u	 0.4890	 0.4420
x	 0.0590	 0.1030
y	 0.4630	 0.4070
z	 0.0920	 0.1510