



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:48 AM UTC

PDB ID : 8QPP / pdb_00008qpp
EMDB ID : EMD-18558
Title : Bacillus subtilis MutS2-collided disome complex (stalled 70S)
Authors : Park, E.; Mackens-Kiani, T.; Berhane, R.; Esser, H.; Erdenebat, C.; Burroughs, A.M.; Berninghausen, O.; Aravind, L.; Beckmann, R.; Green, R.; Buskirk, A.R.
Deposited on : 2023-10-02
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

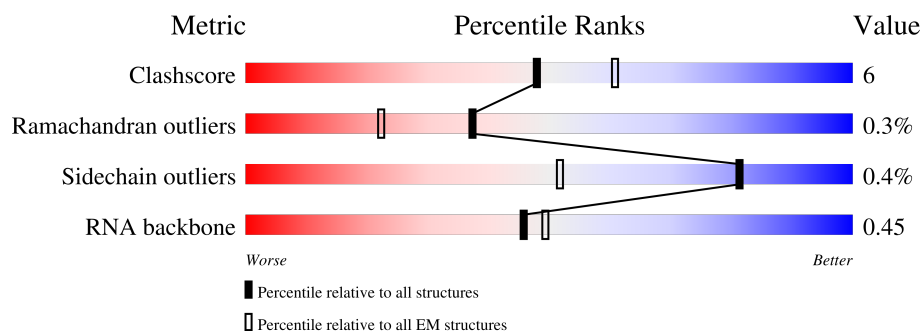
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	59	
2	1	48	
3	2	44	
4	3	66	
5	4	37	
6	6	64	
7	B	246	

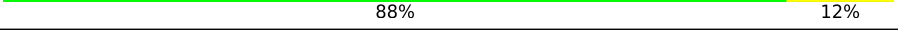
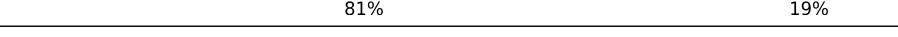
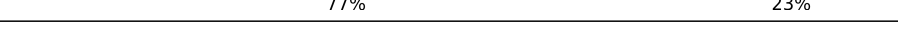
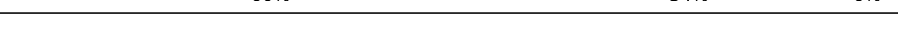
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Mol	Chain	Length	Quality of chain
8	C	218	
9	D	200	
10	E	166	
11	F	95	
12	G	156	
13	H	132	
14	I	130	
15	J	102	
16	K	131	
17	L	138	
18	M	121	
19	N	61	
20	O	89	
21	P	90	
22	Q	87	
23	R	79	
24	S	92	
25	T	88	
26	U	77	
27	V	33	
28	W	785	
29	Y	112	
30	Z	275	
31	a	207	
32	b	205	

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Mol	Chain	Length	Quality of chain
33	c	178	
34	d	175	
35	e	142	
36	f	122	
37	i	146	
38	j	138	
39	k	119	
40	l	120	
41	m	115	
42	n	117	
43	o	101	
44	r	109	
45	s	93	
46	t	101	
47	u	82	
48	v	58	
49	w	65	
50	x	58	
51	9	149	
52	X	2928	
53	A	1533	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 237112 atoms, of which 94493 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	54	Total	C	H	N	O	S	0	0
			872	262	446	86	71	7		

- Molecule 2 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	48	Total	C	H	N	O	S	0	0
			815	244	413	80	74	4		

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	44	Total	C	H	N	O	S	0	0
			778	222	410	89	55	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	64	Total	C	H	N	O	S	0	0
			1075	321	563	107	82	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	48	SER	ALA	conflict	UNP A0A063XFQ7

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	37	Total	C	H	N	O	S	0	0
			639	186	342	60	46	5		

- Molecule 6 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	6	63	Total	C	H	N	O	S	0	0
			990	312	491	91	91	5		

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	218	Total	C	H	N	O	S	0	0
			3588	1119	1831	309	323	6		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C	206	Total	C	H	N	O	S	0	0
			3278	1011	1659	304	301	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	195	Total	C	H	N	O	S	0	0
			3174	991	1605	291	285	2		

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	164	Total	C	H	N	O	S	0	0
			2520	767	1301	225	225	2		

- Molecule 11 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	92	Total	C	H	N	O	S	0	0
			1502	476	747	132	146	1		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	149	Total	C	H	N	O	S	0	0
			2417	740	1236	220	215	6		

- Molecule 13 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	H	131	Total	C	H	N	O	S	0	0
			2133	655	1096	191	188	3		

- Molecule 14 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	I	125	Total	C	H	N	O	S	0	0
			1972	599	1006	191	175	1		

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	J	95	Total	C	H	N	O	S	0	0
			1557	479	796	139	141	2		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	K	114	Total	C	H	N	O	S	0	0
			1694	516	855	164	157	2		

- Molecule 17 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	L	136	Total	C	H	N	O	S	0	0
			2164	653	1112	211	186	2		

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	M	108	Total	C	H	N	O		0	0
			1794	534	926	176	158			

- Molecule 19 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	N	60	Total	C	H	N	O	S	0	0
			1030	317	532	98	78	5		

- Molecule 20 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	O	85	Total	C	H	N	O	S	0	0
			1446	436	736	144	129	1		

- Molecule 21 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	P	88	Total	C	H	N	O	S	0	0
			1417	441	722	128	124	2		

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	Q	84	Total	C	H	N	O	S	0	0
			1420	435	729	128	126	2		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	R	64	Total	C	H	N	O	S	0	0
			1074	332	556	96	88	2		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	S	78	Total	C	H	N	O	S	0	0
			1283	409	650	112	110	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	T	83	Total	C	H	N	O	S	0	0
			1334	390	697	130	116	1		

- Molecule 26 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
26	U	77	Total	C	H	N	O	P	0	0
			2474	731	831	290	545	77		

- Molecule 27 is a RNA chain called mRNA (33-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
27	V	33	Total	C	H	N	O	P	0	0
			1063	315	359	130	226	33		

- Molecule 28 is a protein called Endonuclease MutS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	W	86	Total	C	H	N	O		0	0
			1335	411	673	124	127			

- Molecule 29 is a RNA chain called 5S rRNA (112-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Y	112	Total	C	H	N	O	P	0	0
			3605	1068	1213	435	778	111		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Z	272	Total	C	H	N	O	S	0	0
			4254	1296	2171	408	373	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	206	Total	C	H	N	O	S	0	0
			3209	985	1640	289	290	5		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	205	Total	C	H	N	O	S	0	0
			3211	980	1649	289	291	2		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	176	Total	C	H	N	O	S	0	0
			2835	882	1449	241	256	7		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	175	Total	C	H	N	O	S	0	0
			2734	835	1391	248	258	2		

- Molecule 35 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	142	Total	C	H	N	O	S	0	0
			2289	710	1165	206	203	5		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	122	Total	C	H	N	O	S	0	0
			1898	571	977	173	173	4		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	i	146	Total	C	H	N	O	S	0	0
			2214	671	1132	207	202	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	j	135	Total	C	H	N	O	S	0	0
			2221	690	1145	205	176	5		

- Molecule 39 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	k	119	Total	C	H	N	O	S	0	0
			1940	583	986	186	181	4		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	l	120	Total	C	H	N	O	S	0	0
			1860	564	947	176	172	1		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	m	115	Total	C	H	N	O	S	0	0
			1965	600	1020	185	159	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	n	117	Total	C	H	N	O	S	0	0
			1948	591	1007	189	157	4		

- Molecule 43 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	o	101	Total	C	H	N	O		0	0
			1616	501	829	139	147			

- Molecule 44 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	r	109	Total	C	H	N	O	S	0	0
			1745	525	902	164	151	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	s	90	Total	C	H	N	O	S	0	0
			1496	452	771	134	136	3		

- Molecule 46 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	t	101	Total	C	H	N	O	S	0	0
			1584	478	821	142	139	4		

- Molecule 47 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	u	82	Total	C	H	N	O		0	0
			1278	390	647	123	118			

- Molecule 48 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	v	58	Total	C	H	N	O	S	0	0
			935	275	490	92	76	2		

- Molecule 49 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	w	65	Total	C	H	N	O	S	0	0
			1099	328	568	102	99	2		

- Molecule 50 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	x	58	Total	C	H	N	O	S	0	0
			950	281	494	89	85	1		

- Molecule 51 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	9	149	Total	C	N	O	0	0
			733	435	149	149		

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	X	2887	Total	C	H	N	O	P	0	0
			93205	27661	31200	11460	19998	2886		

- Molecule 53 is a RNA chain called 16S rRNA (1533-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
53	A	1533	Total	C	H	N	O	P	0	0
			49450	14667	16559	6034	10657	1533		

3 Residue-property plots [i](#)

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. 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 50S ribosomal protein L32

Chain 0:  73% 19% 8%

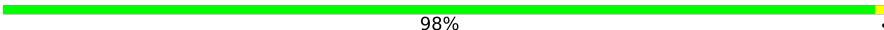


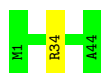
- Molecule 2: Large ribosomal subunit protein bL33

Chain 1:  71% 29%



- Molecule 3: Large ribosomal subunit protein bL34

Chain 2:  98%



- Molecule 4: Large ribosomal subunit protein bL35

Chain 3:  77% 20%



- Molecule 5: 50S ribosomal protein L36

Chain 4:  54% 46%



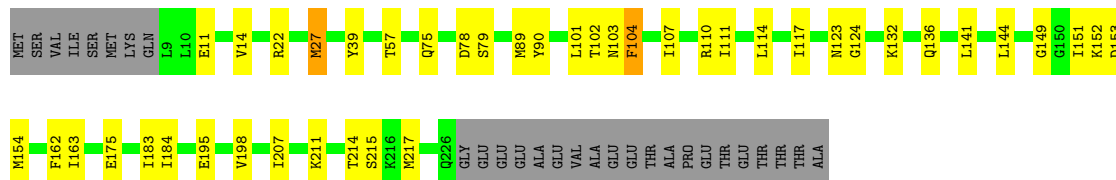
- Molecule 6: Large ribosomal subunit protein bL31

Chain 6:  83% 14%



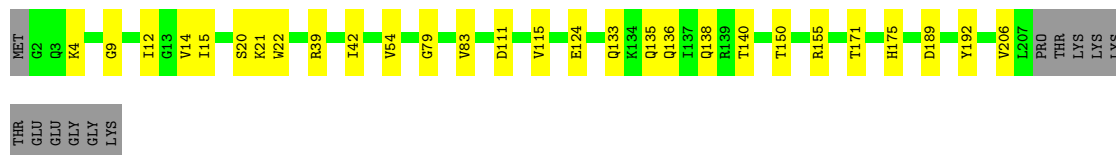
• Molecule 7: 30S ribosomal protein S2

Chain B: 71% 17% 11%



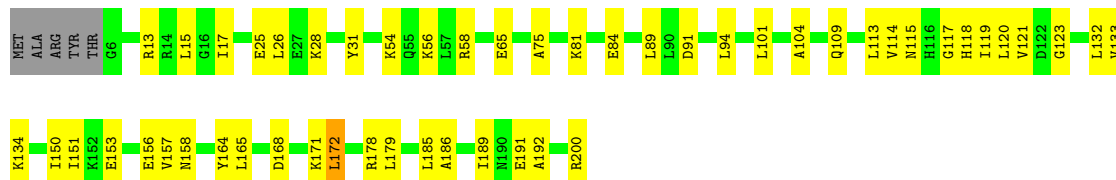
• Molecule 8: 30S ribosomal protein S3

Chain C: 82% 13% 6%



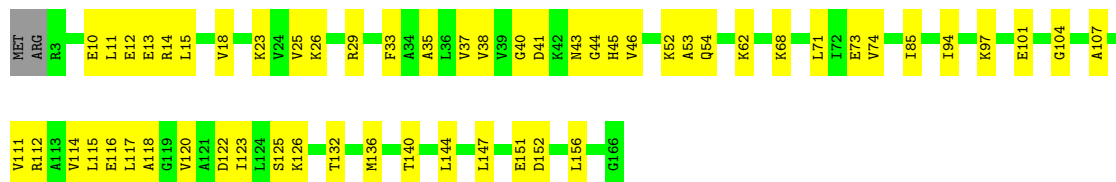
• Molecule 9: 30S ribosomal protein S4

Chain D: 72% 25% 3%



• Molecule 10: 30S ribosomal protein S5

Chain E: 66% 33% 1%

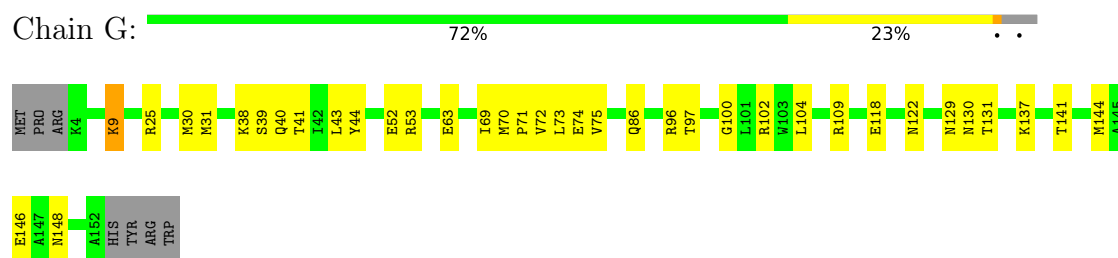


• Molecule 11: 30S ribosomal protein S6

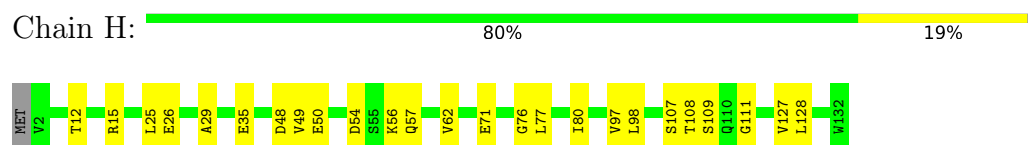
Chain F: 69% 27% 4%



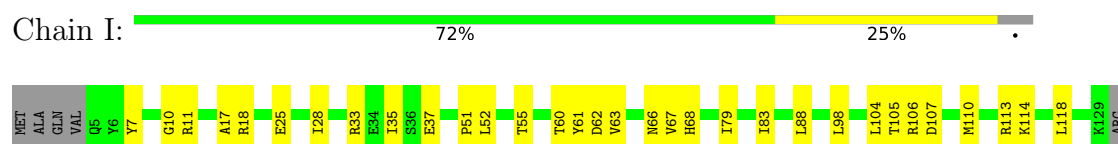
- Molecule 12: 30S ribosomal protein S7



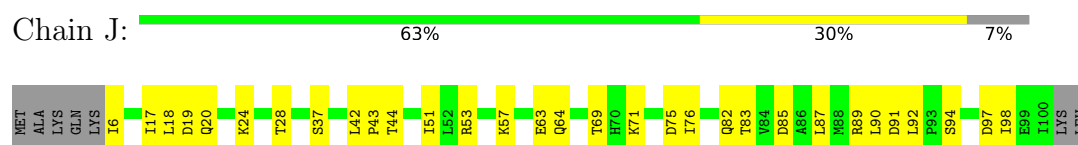
- Molecule 13: 30S ribosomal protein S8



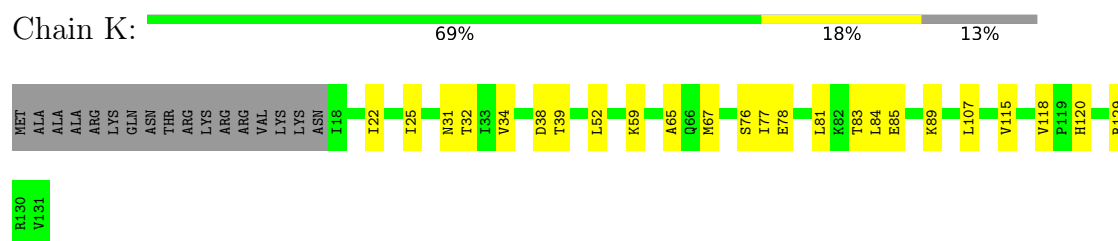
- Molecule 14: 30S ribosomal protein S9



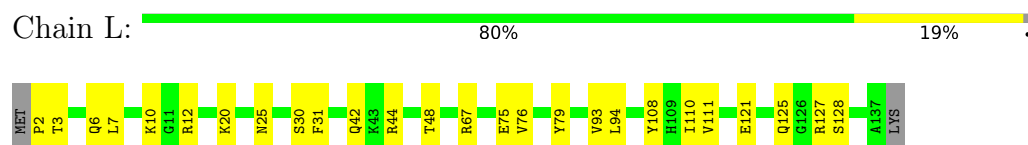
- Molecule 15: 30S ribosomal protein S10



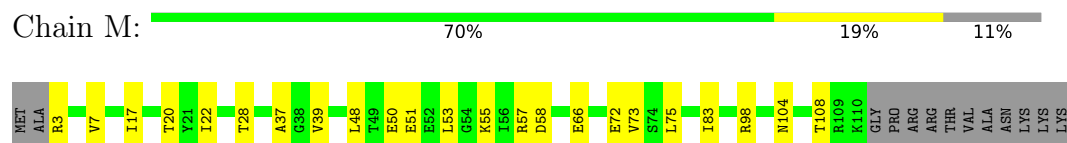
- Molecule 16: 30S ribosomal protein S11



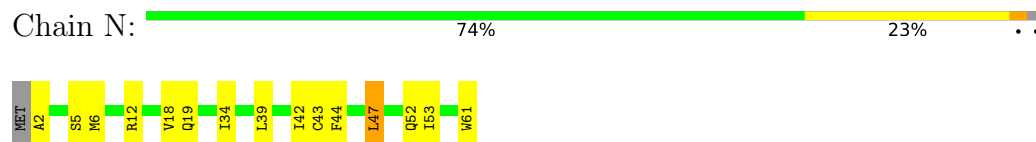
- Molecule 17: 30S ribosomal protein S12



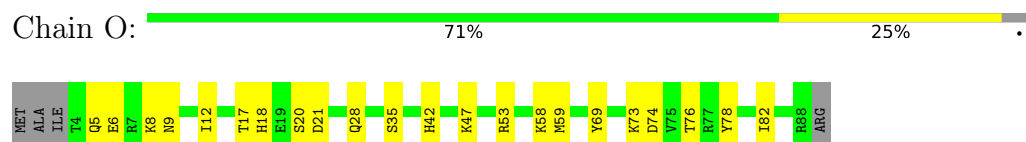
- Molecule 18: 30S ribosomal protein S13



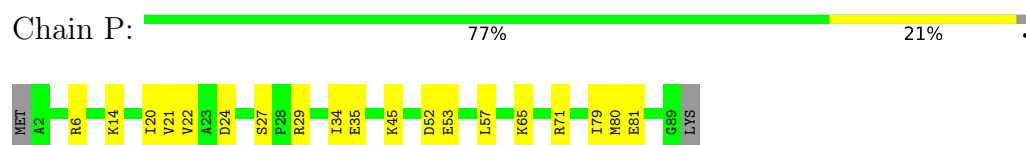
- Molecule 19: 30S ribosomal protein S14 type Z



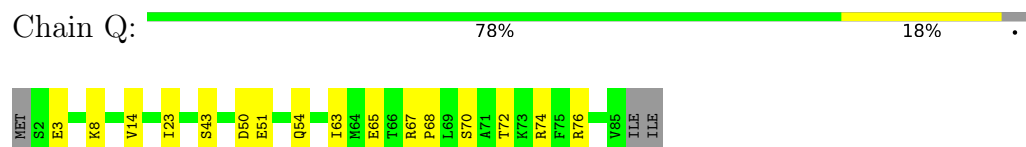
- Molecule 20: 30S ribosomal protein S15



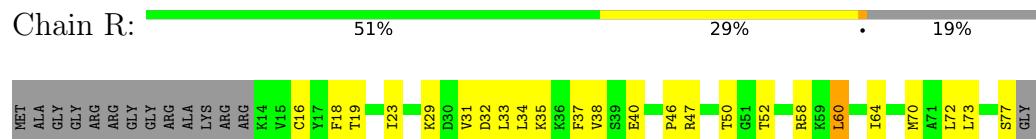
- Molecule 21: 30S ribosomal protein S16



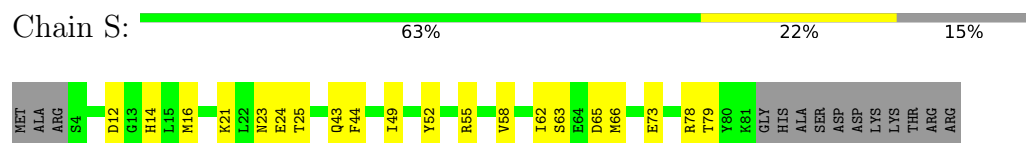
- Molecule 22: 30S ribosomal protein S17



- Molecule 23: 30S ribosomal protein S18

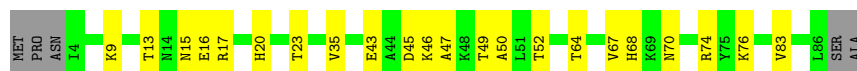


- Molecule 24: 30S ribosomal protein S19



- Molecule 25: 30S ribosomal protein S20

Chain T:  69% 25% 6%

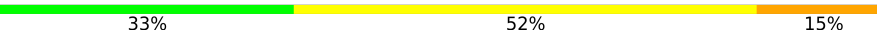


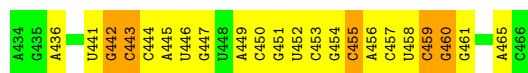
• Molecule 26: tRNA (77-MER)

Chain U:  64% 27% 9%



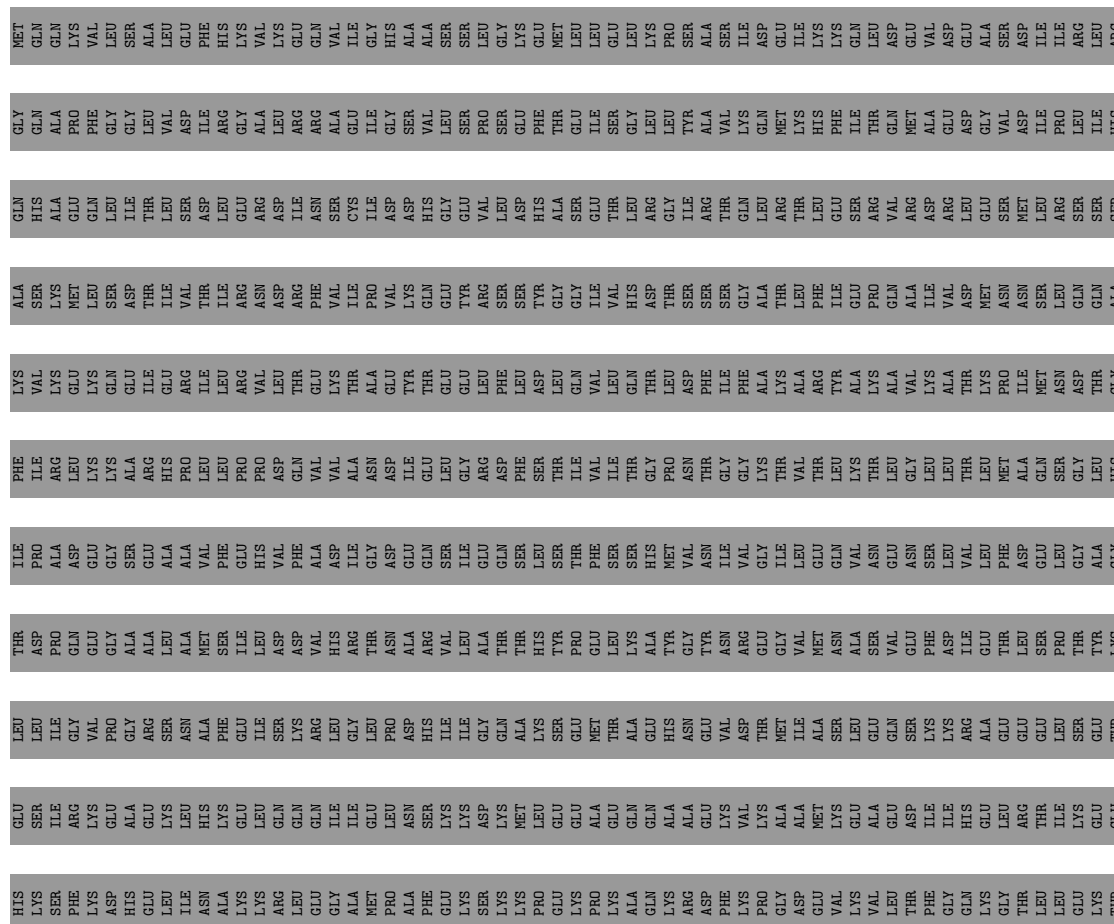
• Molecule 27: mRNA (33-MER)

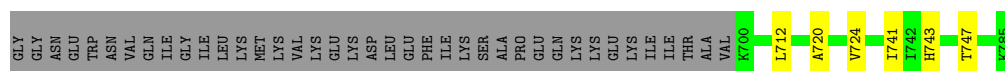
Chain V:  33% 52% 15%



• Molecule 28: Endonuclease MutS2

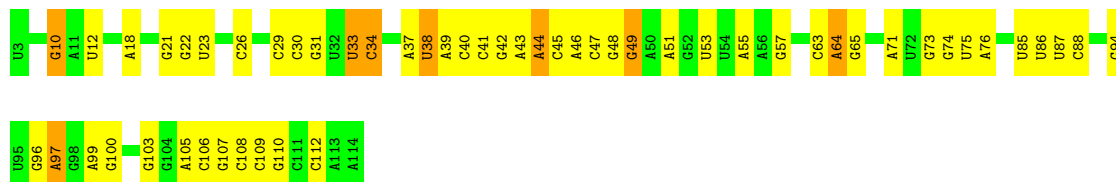
Chain W:  10% 89%





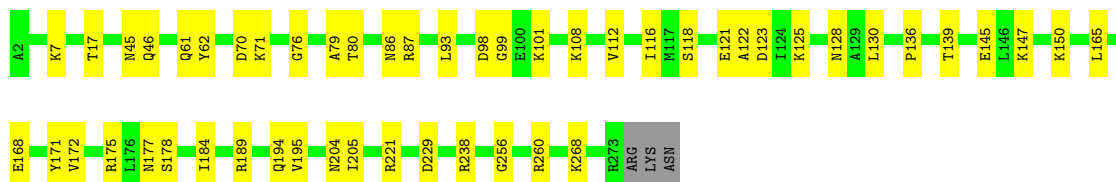
- Molecule 29: 5S rRNA (112-MER)

Chain Y: 52% 41% 7%



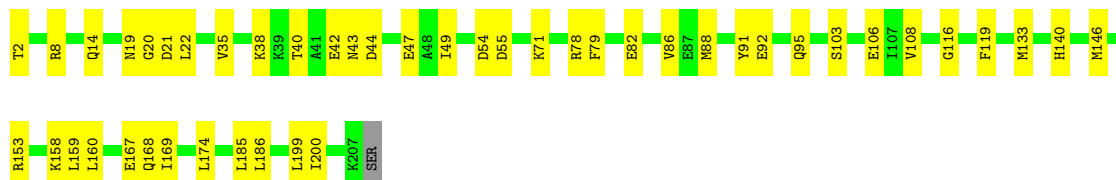
- Molecule 30: Large ribosomal subunit protein uL2

Chain Z: 80% 19%



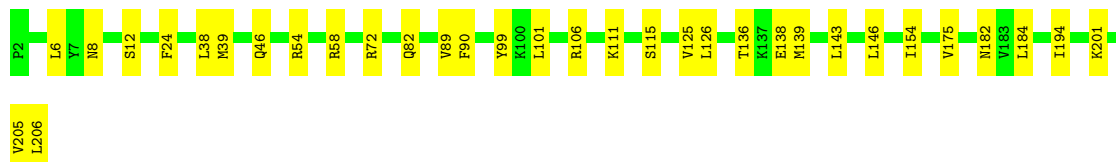
- Molecule 31: Large ribosomal subunit protein uL3

Chain a: 77% 22%



- Molecule 32: Large ribosomal subunit protein uL4

Chain b: 84% 16%



- Molecule 33: Large ribosomal subunit protein uL5

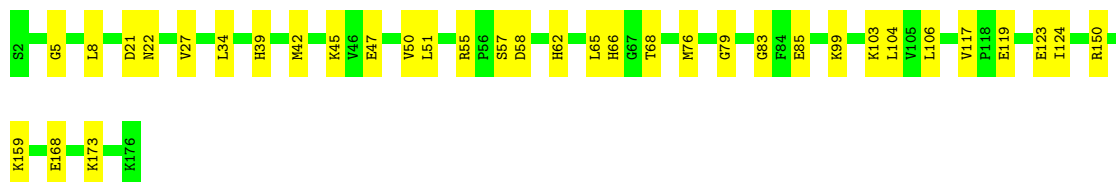
Chain c: 70% 26%





- Molecule 34: Large ribosomal subunit protein uL6

Chain d: 80% 20%



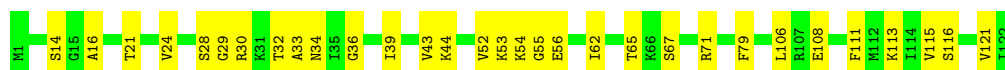
- Molecule 35: Large ribosomal subunit protein uL13

Chain e: 75% 24%



- Molecule 36: 50S ribosomal protein L14

Chain f: 75% 25%



- Molecule 37: 50S ribosomal protein L15

Chain i: 90% 10%



- Molecule 38: Large ribosomal subunit protein uL16

Chain j: 78% 20%

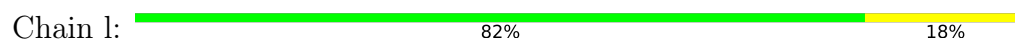


- Molecule 39: Large ribosomal subunit protein bL17

Chain k: 87% 13%



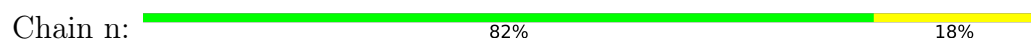
- Molecule 40: 50S ribosomal protein L18



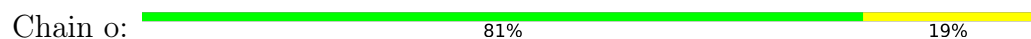
- Molecule 41: 50S ribosomal protein L19



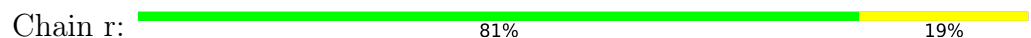
- Molecule 42: Large ribosomal subunit protein bL20



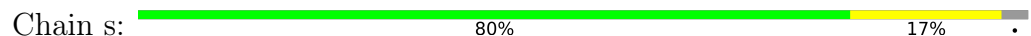
- Molecule 43: Large ribosomal subunit protein bL21



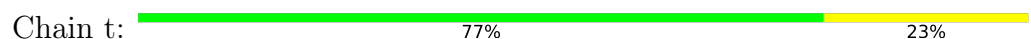
- Molecule 44: Large ribosomal subunit protein uL22

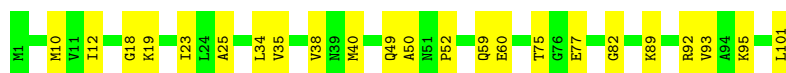


- Molecule 45: Large ribosomal subunit protein uL23

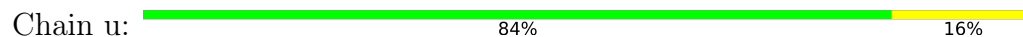


- Molecule 46: Large ribosomal subunit protein uL24

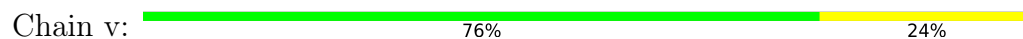




- Molecule 47: Large ribosomal subunit protein bL27



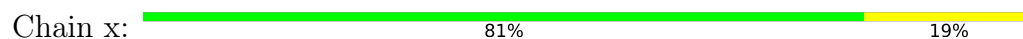
- Molecule 48: Large ribosomal subunit protein bL28



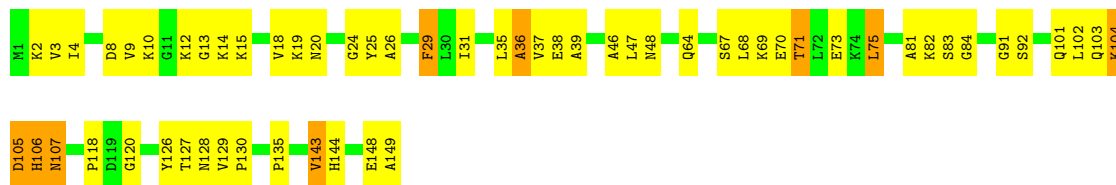
- Molecule 49: Large ribosomal subunit protein uL29



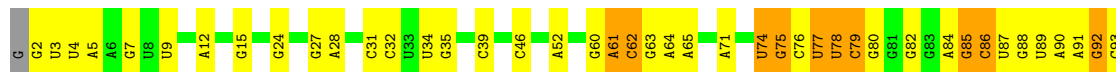
- Molecule 50: Large ribosomal subunit protein uL30



- Molecule 51: 50S ribosomal protein L9



- Molecule 52: 23S ribosomal RNA



G1742	A1743	G1744	A1745	G1757	U1758	U1759	A1760	G1761	U1764	G1765	C1766	A1767	U1774	G1775	A1776	G1779	G1792	G1793	A1797	A1802	U1808	C1811	A1812	A1813	A1820	G1828	C1829	G1830	A1831	A1832	G1836	U1837	A1838	A1839	A1845	G1846	U1847	A1848	U1856	G1857	A1858	C1872	U1877														
A	G1589	A1592	C1598	U1599	G1600	U1601	U1602	C1514	A1617	A1618	U1626	G1630	A1631	G1632	G1633	C1645	A1653	G1657	A1658	A1659	C1683	C1694	A1695	G1696	A1697	A1698	A1699	U1704	G1710	G1711	G1712	A1713	G1715	U1716	G1717	G1718	G1719	G	A1727	G1732	U1733	A1734	U1738	U1739	C1741												
U1136	G1137	C1138	G1139	U1140	A1141	A1142	U1143	A1144	G1145	C1146	U1147	C1148	U1151	U1154	C1155	G1156	A1157	G1158	U1159	G1160	A1161	G1166	G1171	A1172	U1176	G1177	A1178	A1179	C1180	C1181	G1182	G1183	G1184	C1186	U1187	A1188	A1201	U1215	C1216	U	U	C	G1220	G1227	G1236	C1241	C1248										
C1256	A1260	G1263	G1264	A1265	G1266	A1277	G1278	U1283	A1284	G1285	G1290	A1291	G1292	A1293	U1294	U1295	G1296	C1297	G1306	G1311	A1312	G1315	G1322	A1325	A1339	A1340	G1184	C1353	G1359	C1364	U1368	C1369	G1370	G1371	U1379	U1380	A1388	C1389	G1390	U1391	A1392	A1398															
C1402	G1403	A1404	A1405	A1406	G1410	U1417	U1418	A1423	A1424	C1425	A1426	G1427	U1433	A1434	U1435	U1436	C1437	A1442	C1449	C1450	U1451	C1452	A1453	C1454	G1455	A1456	U1457	U1458	U1459	G1460	A1461	G1462	A1465	U1466	G1467	G1471	G1472	A1473	C1474	A1477	A1480	A1483	U1484	A1485	U1489	A1490											
A1499	U1500	U1501	G1502	U1505	U1506	U1507	C1508	C1514	C1515	A1516	G1525	C1527	U1528	G1529	A1536	G1537	G1538	C1539	A1540	A1541	A1542	U1543	C1544	C1545	G1546	C1552	A1553	U	A1555	G1563	G1566	U1567	G1568	A1569	U1570	G1571	G1574	G1577	A	A	A	A	U														
G1845	G1846	U1847	A1848	U1856	G1857	A1858	C1872	U1877	A219	A220	G221	A224	A225	A226	G227	C228	A229	A230	A231	U232	G233	C234	U238	A244	G245	A246	A247	G251	C252	G253	C256	G257	A258	U266	C267	A268	A275	C276	A279	G282	G283	C284	U285	U286	G287	C288	C289	U290	C291	U292	U293	G294	G295	G296	G297	U298	A302
U398	C399	U	C	U	C	U	C	U	C	U	A	C	A	U	U	A	C	A	A	A	G	G328	A329	A330	C331	G332	U336	A337	G338	A342	A346	G347	G348	A353	A354	C451	G452	G453	G458	A459	G471	A475	A476	U481	C482	C483	G489	A490	A491	A494	U495						
U498	C502	G503	A504	G510	U511	G512	A513	G528	C529	G540	G541	G542	A548	A549	G550	A551	G552	A553	U554	C555	C556	C563	G564	U567	C573	A574	A575	G576	U577	A578	G579	A584	U590	A591	A592	A593	C594	G595	G599	U606	G607	G617	A618	A619	U620												
G621	A630	G631	U632	A646	A647	G648	G649	G657	A658	A659	G660	A661	A673	C674	G675	G682	A683	G684	G688	U691	G697	C698	A699	U700	G701	A702	U704	A717	G718	C719	C720	A729	U733	A740	A753	U761	A762	A763	C764	A765	A774	C777															
A790	U794	G795	U801	G804	G822	G823	G824	G825	U826	A829	A830	U831	G832	U837	A840	G852	C859	A866	A867	A868	C872	U873	U874	U875	U882	A904	G905	G906	G911	C912	A913	A917	G928	G929	C930	C933	U934	A935	C936																		
G939	U940	G941	U942	A943	A957	A958	C959	G963	A964	G973	C980	A987	G988	U1091	C990	A991	G992	A999	G1002	A1005	A1006	G1007	G1012	G1018	A1019	A1020	A1029	C1030	C1031	G1035	A1036	G1043	C1044	U1045	A1046	C1052	C1053	U1057	U1058	A1059	U1064	A1065															
G1068	U1069	G1070	U1071	A1072	A1073	A1074	G1076	U1079	G1080	U1081	G1085	U1086	U1087	U1090	U1091	A1092	G1093	A1100	G1101	A1103	U1104	G1105	U1106	U1107	G1108	C1109	U1110	U1111	U1112	A1113	G1114	A1115	G1117	C1118	A1119	G1120	C1121	A1123	C1124	C1125	A1126	U1127	U1128	U1129	A1130	U1131	A1132	G1133	A1134	G1135							
U1136	G1137	C1138	G1139	U1140	A1141	A1142	U1143	A1144	U1145	C1146	U1147	C1148	U1151	U1154	C1155	G1156	A1157	G1158	U1159	G1160	A1161	G1166	U1176	G1177	A1178	A1179	C1180	C1181	G1182	G1183	G1184	C1186	U1187	A1188	A1201	U1215	C1216	U	U	C	G1220	G1227	G1236	C1241	C1248												
C1256	A1260	G1263	G1264	A1265	G1266	A1277	G1278	U1283	A1284	G1285	G1290	A1291	G1292	A1293	U1294	U1295	G1296	C1297	G1306	G1311	A1312	G1315	G1322	A1325	A1339	A1340	G1184	C1353	G1359	C1364	U1368	C1369	G1370	G1371	U1379	U1380	A1388	C1389	G1390	U1391	A1392	A1398															
C1402	G1403	A1404	A1405	A1406	G1410	U1417	U1418	A1423	A1424	C1425	A1426	G1427	U1433	A1434	U1435	U1436	C1437	A1442	C1449	C1450	U1451	C1452	A1453	C1454	G1455	A1456	U1457	U1458	U1459	G1460	A1461	G1462	A1465	U1466	G1467	G1471	G1472	A1473	C1474	A1477	A1480	A1483	U1484	A1485	U1489	A1490											
A1499	U1500	U1501	G1502	U1505	U1506	U1507	C1508	C1514	C1515	A1516	G1525	C1527	U1528	G1529	A1536	G1537	G1538	C1539	A1540	A1541	A1542	U1543	C1544	C1545	G1546	C1552	A1553	U	A1555	G1563	G1566	U1567	G1568	A1569	U1570	G1571	G1574	G1577	A	A	A	A	U														

G1507	G1387	A1294	A1200	G1087	A1004	A899	A768	A649	A506	U429
U1508	G1388	C1295	C1201	U1088	G1005	G900	A769	A650	C510	C430
A1513	G1396	A1296	A1205	G1089	A1006	G908	G774	A651	G510	G431
G1514	U1306	U1206	A1206	G1091	U1012	G908	G778	G655	A518	G432
G1515	C1307	A1210	A1210	U1092	G1013	A911	A786	A659	A519	A433
U1516	A1308	U1211	U1211	U1093	A1014	G916	A790	G660	U434	U435
A1517	G1309	C1212	C1212	G1094	C1015	G916	A790	U662	C520	C436
A1523	U1310	U1213	A1213	U1096	U1018	A924	A796	G666	U437	U438
G1526	U1311	G1215	U1214	U1095	C1019	A924	A796	C531	G530	A439
A1529	G1314	C1216	C1216	U1104	U1021	A929	U797	G673	A440	A440
G1539	A1315	C1217	C1217	U1105	A1022	G936	U798	A674	U443	U443
G1540	U1316	C1218	C1218	C1106	G1023	G937	A799	U540	C944	C944
	C1317	C1219	C1219	A1111	A1024	G937	A801	A541	U445	U445
	G1318	U1220	U1220	G1113	G1025	G943	U802	U547	C446	C446
	U1324	U1221	U1221	G1114	A1028	C944	A803		U447	U447
	G1325	A1222	A1222	G1118	G1029	A945	G804	A556	G455	G455
	A1328	U1223	U1223	C1119	G1030	G949	C805	G566	A456	A456
	C1329	C1226	C1226	G1127	A1031	G949	G812	G567	A457	A457
	U1330	C1227	C1227	U1134	G1033	G954	G821	A568	C461	C461
	C1331	G1231	G1231	U1135	C1035	G955	U822	U571	A462	A462
		C1232	C1232	U1136	C1036	A959	A823	A572	A463	A463
		U1233	U1233	G1137	U1039	U960	A824	U573	G464	G464
		A1234	A1234	U1145	U1040	G961	C826	U574	U465	U465
		C1235	C1235	C1146	C1041	U967	A703		C468	C468
		A1236	A1236	A1147	G1042	A968	A704	U580	C472	C472
				G1148	G1043	A969	U716	A581	A473	A473
				U1152	G1046	U970	A837	G585	U476	U476
				G1153	C1047	U971	G720	C587	A477	A477
				C1154	A1048	G973	G841	U588	G478	G478
				A1155	G1053	A974	G845	C481	C481	C481
				C1156	A1054	A975	G848	G482	G482	G482
				G1165	C1055	G976	G849	G483	U484	U484
				U1168	A1056	C977	U850	A485	A485	A485
				G1169	G1057	A979	U851	C486	C486	C486
				A1176	U1058	G981	U852	U603	U603	U603
				C1177	G1060	A985	C853	A604	A604	A604
				A1178	U1062	G986	G854	A605	A605	A605
				U1179	G1063	A987	C856	U628	U628	U628
				A1180	C1064	A987	U861	C629	C629	C629
				G1186	A1065	A993	A874	A630	A630	A630
				U1187	U1066	C994	A875	A631	A631	A631
				G1188	G1067	G995	A882	G641	G641	G641
				A1189	U1068	A996	A886	U642	U642	U642
				U1190	G1078	U999	C889	C643	C643	C643
				G1193	U1083	C1000				
					U1084	U1001				
					G1084	U1002				
						G1003				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11740	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 ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0	0.21	0/433	0.51	0/574
2	1	0.22	0/407	0.51	0/540
3	2	0.18	0/371	0.45	0/483
4	3	0.18	0/519	0.44	0/680
5	4	0.21	0/300	0.54	0/393
6	6	0.20	0/509	0.49	0/678
7	B	0.25	0/1782	0.62	2/2392 (0.1%)
8	C	0.21	0/1641	0.50	0/2208
9	D	0.23	0/1599	0.56	0/2147
10	E	0.21	0/1231	0.51	0/1655
11	F	0.27	0/766	0.59	0/1031
12	G	0.29	0/1196	0.79	0/1604
13	H	0.24	0/1049	0.61	0/1407
14	I	0.25	0/979	0.57	0/1315
15	J	0.26	0/773	0.59	0/1044
16	K	0.24	0/853	0.56	0/1153
17	L	0.21	0/1069	0.52	0/1435
18	M	0.22	0/873	0.58	0/1166
19	N	0.24	0/508	0.63	0/672
20	O	0.24	0/718	0.57	0/960
21	P	0.25	0/708	0.57	0/950
22	Q	0.21	0/699	0.52	0/933
23	R	0.24	0/526	0.60	0/705
24	S	0.22	0/649	0.54	0/872
25	T	0.23	0/639	0.53	0/852
26	U	0.14	0/1834	0.29	0/2858
27	V	0.13	0/787	0.32	0/1224
28	W	0.15	0/670	0.29	0/894
29	Y	0.17	0/2675	0.35	0/4170
30	Z	0.20	0/2120	0.49	0/2845
31	a	0.19	0/1591	0.47	0/2132
32	b	0.21	0/1581	0.52	0/2132
33	c	0.33	0/1405	0.59	2/1887 (0.1%)
34	d	0.21	0/1361	0.48	0/1832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.21	0/1147	0.50	1/1542 (0.1%)
36	f	0.23	0/928	0.60	0/1245
37	i	0.21	0/1094	0.45	0/1457
38	j	0.23	0/1099	0.53	0/1468
39	k	0.21	0/961	0.54	0/1284
40	l	0.19	0/922	0.51	0/1236
41	m	0.20	0/958	0.52	0/1279
42	n	0.22	0/953	0.52	0/1266
43	o	0.22	0/798	0.53	0/1070
44	r	0.22	0/852	0.58	0/1146
45	s	0.23	0/731	0.55	0/974
46	t	0.25	0/773	0.64	1/1032 (0.1%)
47	u	0.20	0/639	0.45	0/847
48	v	0.22	0/449	0.52	0/596
49	w	0.25	0/532	0.66	0/707
50	x	0.20	0/458	0.51	0/613
51	9	0.77	1/732 (0.1%)	1.24	7/1016 (0.7%)
52	X	0.18	0/69451	0.33	3/108344 (0.0%)
53	A	0.16	0/36826	0.31	0/57450
All	All	0.19	1/155124 (0.0%)	0.40	16/232395 (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
33	c	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	9	104	LYS	N-CA	6.41	1.54	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	X	138	U	OP1-P-O3'	-27.15	26.55	108.00
51	9	69	LYS	N-CA-C	-11.56	98.76	111.36
46	t	52	PRO	CA-N-CD	-9.96	98.06	112.00
51	9	120	GLY	N-CA-C	-7.92	102.40	112.54
33	c	45	GLN	N-CA-C	-6.91	104.84	113.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	c	43	ALA	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	446	445	8	0
2	1	402	413	413	10	0
3	2	368	410	410	1	0
4	3	512	563	561	10	0
5	4	297	342	342	13	0
6	6	499	491	491	7	0
7	B	1757	1831	1830	36	0
8	C	1619	1659	1658	17	0
9	D	1569	1605	1604	38	0
10	E	1219	1301	1300	44	0
11	F	755	747	746	20	0
12	G	1181	1236	1235	28	0
13	H	1037	1096	1095	20	0
14	I	966	1006	1005	30	0
15	J	761	796	795	21	0
16	K	839	855	854	21	0
17	L	1052	1112	1112	22	0
18	M	868	926	925	19	0
19	N	498	532	531	16	0
20	O	710	736	735	14	0
21	P	695	722	721	15	0
22	Q	691	729	728	12	0
23	R	518	556	555	18	0
24	S	633	650	649	16	0
25	T	637	697	696	16	0
26	U	1643	831	831	9	0
27	V	704	359	359	5	0
28	W	662	673	672	4	0
29	Y	2392	1213	1213	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Z	2083	2171	2168	38	0
31	a	1569	1640	1637	32	0
32	b	1562	1649	1647	23	0
33	c	1386	1449	1446	35	0
34	d	1343	1391	1388	25	0
35	e	1124	1165	1162	31	0
36	f	921	977	977	21	0
37	i	1082	1132	1132	10	0
38	j	1076	1145	1145	27	0
39	k	954	986	983	12	0
40	l	913	947	947	16	0
41	m	945	1020	1020	11	0
42	n	941	1007	1005	14	0
43	o	787	829	826	13	0
44	r	843	902	899	17	0
45	s	725	771	770	14	0
46	t	763	821	821	15	0
47	u	631	647	644	11	0
48	v	445	490	487	11	0
49	w	531	568	568	19	0
50	x	456	494	491	8	0
51	9	733	0	348	48	0
52	X	62005	31200	31207	371	0
53	A	32891	16559	16559	234	0
All	All	142619	94493	94788	1357	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 6.

The worst 5 of 1357 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)
51:9:3:VAL:HA	51:9:38:GLU:CA	1.75	1.16
51:9:3:VAL:CA	51:9:38:GLU:HA	1.83	1.09
51:9:3:VAL:HA	51:9:38:GLU:HA	1.05	1.04
51:9:2:LYS:HA	51:9:20:ASN:HA	1.39	1.03
19:N:47:LEU:HD13	19:N:53:ILE:HD11	1.41	1.02

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
2	1	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
3	2	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
4	3	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	61/64 (95%)	52 (85%)	9 (15%)	0	100	100
7	B	216/246 (88%)	199 (92%)	17 (8%)	0	100	100
8	C	204/218 (94%)	189 (93%)	15 (7%)	0	100	100
9	D	193/200 (96%)	171 (89%)	22 (11%)	0	100	100
10	E	162/166 (98%)	148 (91%)	14 (9%)	0	100	100
11	F	90/95 (95%)	84 (93%)	6 (7%)	0	100	100
12	G	147/156 (94%)	126 (86%)	21 (14%)	0	100	100
13	H	129/132 (98%)	119 (92%)	10 (8%)	0	100	100
14	I	123/130 (95%)	113 (92%)	10 (8%)	0	100	100
15	J	93/102 (91%)	87 (94%)	6 (6%)	0	100	100
16	K	112/131 (86%)	107 (96%)	5 (4%)	0	100	100
17	L	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
18	M	106/121 (88%)	95 (90%)	11 (10%)	0	100	100
19	N	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
20	O	83/89 (93%)	75 (90%)	8 (10%)	0	100	100
21	P	86/90 (96%)	80 (93%)	6 (7%)	0	100	100
22	Q	82/87 (94%)	79 (96%)	3 (4%)	0	100	100
23	R	62/79 (78%)	57 (92%)	5 (8%)	0	100	100
24	S	76/92 (83%)	67 (88%)	9 (12%)	0	100	100
25	T	81/88 (92%)	78 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	W	84/785 (11%)	78 (93%)	6 (7%)	0	100	100
30	Z	270/275 (98%)	253 (94%)	17 (6%)	0	100	100
31	a	204/207 (99%)	190 (93%)	14 (7%)	0	100	100
32	b	203/205 (99%)	186 (92%)	17 (8%)	0	100	100
33	c	174/178 (98%)	160 (92%)	13 (8%)	1 (1%)	21	50
34	d	173/175 (99%)	154 (89%)	19 (11%)	0	100	100
35	e	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
36	f	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
37	i	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
38	j	133/138 (96%)	123 (92%)	10 (8%)	0	100	100
39	k	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
40	l	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
41	m	113/115 (98%)	106 (94%)	7 (6%)	0	100	100
42	n	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
43	o	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
44	r	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
45	s	88/93 (95%)	81 (92%)	7 (8%)	0	100	100
46	t	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
47	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
48	v	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
49	w	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
50	x	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
51	9	147/149 (99%)	107 (73%)	27 (18%)	13 (9%)	0	3
All	All	5438/6399 (85%)	4977 (92%)	447 (8%)	14 (0%)	37	65

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
51	9	37	VAL
51	9	107	ASN
51	9	130	PRO
51	9	135	PRO
51	9	104	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	48/53 (91%)	48 (100%)	0	100	100
2	1	46/46 (100%)	45 (98%)	1 (2%)	45	63
3	2	39/39 (100%)	39 (100%)	0	100	100
4	3	54/57 (95%)	54 (100%)	0	100	100
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	53/53 (100%)	52 (98%)	1 (2%)	50	66
7	B	189/212 (89%)	189 (100%)	0	100	100
8	C	168/178 (94%)	167 (99%)	1 (1%)	78	80
9	D	169/173 (98%)	167 (99%)	2 (1%)	63	72
10	E	128/130 (98%)	128 (100%)	0	100	100
11	F	81/84 (96%)	80 (99%)	1 (1%)	63	72
12	G	125/132 (95%)	124 (99%)	1 (1%)	73	77
13	H	111/112 (99%)	109 (98%)	2 (2%)	51	67
14	I	98/102 (96%)	98 (100%)	0	100	100
15	J	86/92 (94%)	84 (98%)	2 (2%)	44	63
16	K	86/100 (86%)	86 (100%)	0	100	100
17	L	114/116 (98%)	114 (100%)	0	100	100
18	M	94/104 (90%)	94 (100%)	0	100	100
19	N	53/54 (98%)	52 (98%)	1 (2%)	50	66
20	O	80/83 (96%)	80 (100%)	0	100	100
21	P	74/76 (97%)	74 (100%)	0	100	100
22	Q	77/80 (96%)	77 (100%)	0	100	100
23	R	56/64 (88%)	55 (98%)	1 (2%)	51	67
24	S	70/81 (86%)	70 (100%)	0	100	100
25	T	66/70 (94%)	65 (98%)	1 (2%)	57	69
28	W	69/673 (10%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Z	220/223 (99%)	220 (100%)	0	100	100
31	a	167/168 (99%)	167 (100%)	0	100	100
32	b	169/169 (100%)	168 (99%)	1 (1%)	78	80
33	c	151/153 (99%)	148 (98%)	3 (2%)	48	65
34	d	148/148 (100%)	148 (100%)	0	100	100
35	e	120/120 (100%)	120 (100%)	0	100	100
36	f	101/101 (100%)	101 (100%)	0	100	100
37	i	110/110 (100%)	110 (100%)	0	100	100
38	j	109/111 (98%)	108 (99%)	1 (1%)	70	76
39	k	99/99 (100%)	99 (100%)	0	100	100
40	l	93/93 (100%)	93 (100%)	0	100	100
41	m	100/100 (100%)	100 (100%)	0	100	100
42	n	96/96 (100%)	96 (100%)	0	100	100
43	o	83/83 (100%)	83 (100%)	0	100	100
44	r	90/90 (100%)	90 (100%)	0	100	100
45	s	81/84 (96%)	81 (100%)	0	100	100
46	t	85/85 (100%)	84 (99%)	1 (1%)	63	72
47	u	64/64 (100%)	64 (100%)	0	100	100
48	v	47/47 (100%)	47 (100%)	0	100	100
49	w	56/56 (100%)	56 (100%)	0	100	100
50	x	52/52 (100%)	52 (100%)	0	100	100
All	All	4510/5251 (86%)	4490 (100%)	20 (0%)	81	83

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	b	184	LEU
33	c	101	ASP
46	t	75	THR
38	j	68	ILE
12	G	9	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
31	a	50	GLN
35	e	78	HIS
42	n	101	ASN
35	e	8	ASN
35	e	80	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	U	76/77 (98%)	21 (27%)	0
27	V	32/33 (96%)	21 (65%)	0
29	Y	111/112 (99%)	35 (31%)	3 (2%)
52	X	2881/2928 (98%)	685 (23%)	36 (1%)
53	A	1532/1533 (99%)	384 (25%)	20 (1%)
All	All	4632/4683 (98%)	1146 (24%)	59 (1%)

5 of 1146 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	U	2	G
26	U	6	G
26	U	8	U
26	U	16	U
26	U	17	U

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	X	2192	U
53	A	1369	A
52	X	2469	C
53	A	1316	U
53	A	1022	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

This section contains visualisations of the EMDB entry EMD-18558. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.