



# wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 11:37 PM EDT

PDB ID : 7UPH / pdb\_00007uph  
EMDB ID : EMD-26666  
Title : Structure of a ribosome with tethered subunits  
Authors : Kim, D.S.; Watkins, A.; Bidstrup, E.; Lee, J.; Topkar, V.V.; Kofman, C.;  
Schwarz, K.J.; Liu, Y.; Pintilie, G.; Roney, E.; Das, R.; Jewett, M.C.  
Deposited on : 2022-04-15  
Resolution : 4.18 Å(reported)  
Based on initial model : 4YBB

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

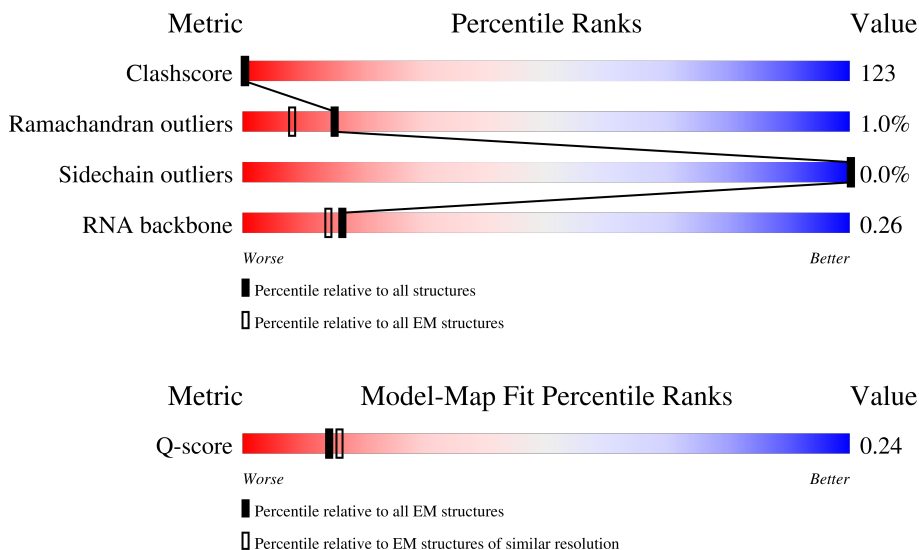
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 4.18 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	5389 ( 3.68 - 4.68 )

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  $\geq 3$ , 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	100	
2	B	88	
3	C	82	

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Mol	Chain	Length	Quality of chain
4	D	80	44% 16% 79% 5%
5	E	55	40% 13% 85%
6	F	79	76% 33% 66%
7	G	85	67% 25% 74%
8	H	56	75% 23% 77%
9	I	4438	63% 34%
10	J	118	53% 47%
11	K	271	18% 79%
12	L	209	13% 83%
13	M	201	16% 83%
14	N	177	5% 12% 87%
15	O	176	6% 13% 86%
16	R	142	14% 83%
17	S	122	12% 83% 5%
18	T	144	26% 73%
19	U	136	12% 85%
20	V	120	10% 89%
21	W	224	87% 25% 75%
22	X	206	53% 26% 73%
23	Y	205	41% 25% 75%
24	Z	150	14% 11% 87%
25	a	100	58% 20% 78%
26	b	151	63% 25% 75%
27	c	129	28% 20% 79%
28	d	127	17% 20% 79%

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Mol	Chain	Length	Quality of chain
29	e	98	48% 22% 76%
30	f	117	42% 10% 89%
31	g	123	13% 15% 84%
32	h	114	37% 19% 80%
33	i	56	29% 68%
34	j	50	6% 8% 90%
35	k	46	41% 57%
36	l	64	16% 84%
37	m	38	97%
38	n	116	9% 91%
39	o	114	7% 16% 82%
40	p	117	17% 83%
41	q	103	12% 88%
42	r	110	16% 83%
43	s	93	10% 88%
44	t	102	5% 93%
45	u	94	10% 89%
46	v	75	5% 95%
47	w	77	21% 78%
48	x	62	11% 87%
49	y	58	9% 90%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
31	D2T	g	88	-	-	X	-
9	1MG	I	2245	-	-	X	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
9	PSU	I	2449	-	-	X	-
9	3TD	I	3409	-	-	X	-
9	PSU	I	3411	-	-	X	-
9	PSU	I	3951	-	-	X	-
9	OMC	I	3992	-	-	X	-
9	5MC	I	966	-	-	X	-

## 2 Entry composition [i](#)

There are 49 unique types of molecules in this entry. The entry contains 141080 atoms, of which 625 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 30S ribosomal protein S14.

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

- Molecule 2 is a protein called 30S ribosomal protein S15.

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

- Molecule 3 is a protein called 30S ribosomal protein S16.

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

- Molecule 4 is a protein called 30S ribosomal protein S17.

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

- Molecule 5 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	55	456	288	86	82	0	0

- Molecule 6 is a protein called 30S ribosomal protein S19.

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

- Molecule 7 is a protein called 30S ribosomal protein S20.

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

- Molecule 8 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	56	465	290	96	78	1	0	0

- Molecule 9 is a RNA chain called Tethered rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
9	I	4438	95909	42519	625	17511	30816	4438	0	0

- Molecule 10 is a RNA chain called 5S rRNA.

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

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

- Molecule 16 is a protein called 50S ribosomal protein L13.

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

- Molecule 17 is a protein called 50S ribosomal protein L14.

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

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

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

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 22 is a protein called 30S ribosomal protein S3.

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

- Molecule 23 is a protein called 30S ribosomal protein S4.

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

- Molecule 24 is a protein called 30S ribosomal protein S5.

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

- Molecule 25 is a protein called 30S ribosomal protein S6.

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

- Molecule 26 is a protein called 30S ribosomal protein S7.

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

- Molecule 27 is a protein called 30S ribosomal protein S8.

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

- Molecule 28 is a protein called 30S ribosomal protein S9.

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

- Molecule 29 is a protein called 30S ribosomal protein S10.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 31 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 32 is a protein called 30S ribosomal protein S13.

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

- Molecule 33 is a protein called 50S ribosomal protein L32.

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

- Molecule 34 is a protein called 50S ribosomal protein L33.

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

- Molecule 35 is a protein called 50S ribosomal protein L34.

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

- Molecule 36 is a protein called 50S ribosomal protein L35.

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

- Molecule 37 is a protein called 50S ribosomal protein L36.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L25.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

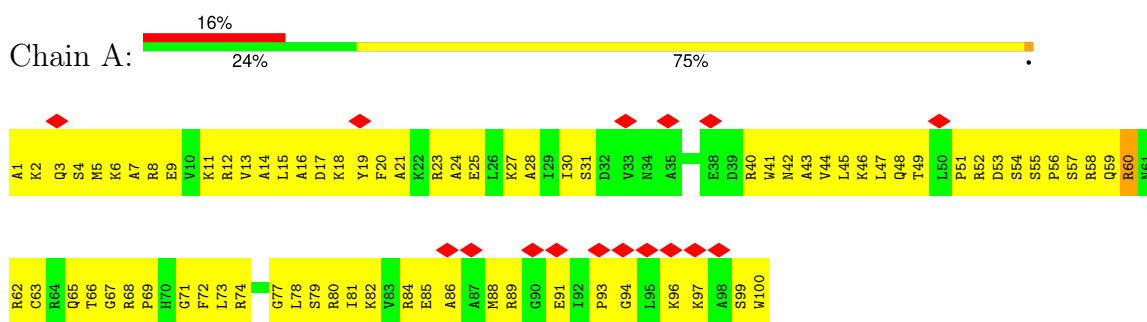
- Molecule 49 is a protein called 50S ribosomal protein L30.

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

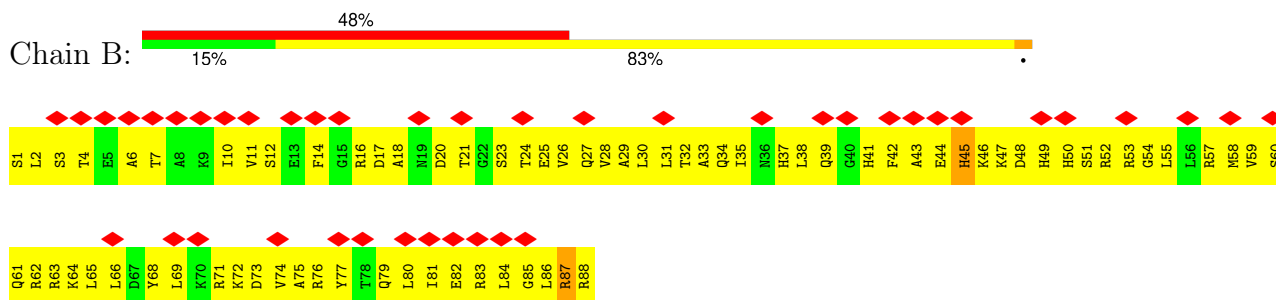
### 3 Residue-property plots

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.

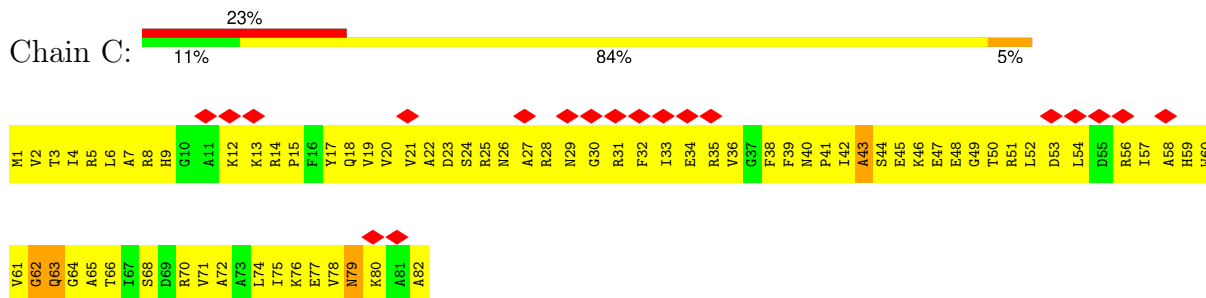
- Molecule 1: 30S ribosomal protein S14



- Molecule 2: 30S ribosomal protein S15

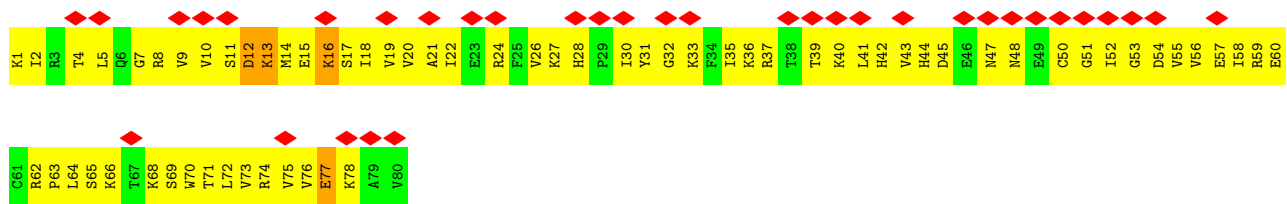


- Molecule 3: 30S ribosomal protein S16



- Molecule 4: 30S ribosomal protein S17

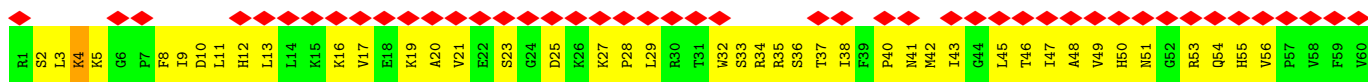
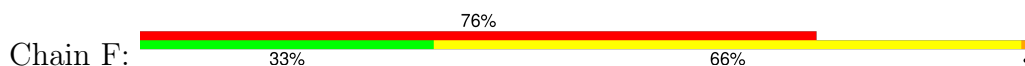




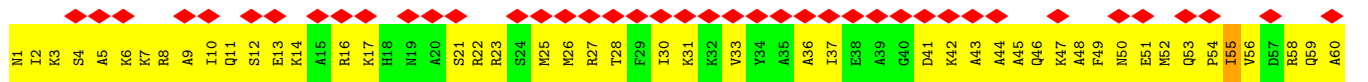
• Molecule 5: 30S ribosomal protein S18



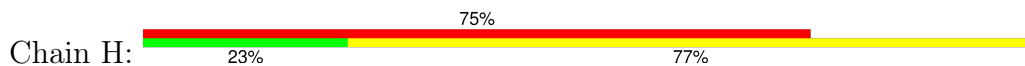
• Molecule 6: 30S ribosomal protein S19



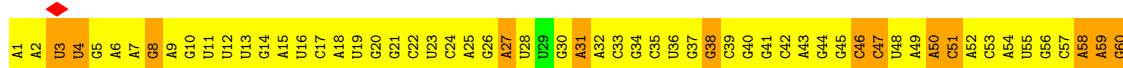
• Molecule 7: 30S ribosomal protein S20



• Molecule 8: 30S ribosomal protein S21



• Molecule 9: Tethered rRNA





A1690	A1691	A1692	A1693	A1694	A1695	A1696	A1697	A1698	A1699	A1700	A1701	A1702	A1703	A1704	A1705	A1706	A1707	A1708	A1709	A1710	A1711	A1712	A1713	A1714	A1715	A1716	A1717	A1718	A1719	A1720	A1721	A1722	A1723	A1724	A1725	A1726	A1727	A1728	A1729	A1730	A1731	A1732	A1733	A1734	A1735	A1736	A1737	A1738	A1739	A1800	A1801	A1802	A1803	A1804	A1805	A1806	A1807	A1808	A1809	
C1629	C1630	A1631	A1632	A1633	A1634	A1635	A1636	A1637	A1638	A1639	A1640	A1641	A1642	A1643	A1644	A1645	A1646	A1647	A1648	A1649	A1650	A1651	A1652	A1653	A1654	A1655	A1656	A1657	A1658	A1659	A1660	A1661	A1662	A1663	A1664	A1665	A1666	A1667	A1668	A1669	A1670	A1671	A1672	A1673	A1674	A1675	A1676	A1677	A1678	A1679	A1680	A1681	A1682	A1683	A1684	A1685	A1686	A1687	A1688	A1689
G1509	A1510	A1511	A1512	A1513	A1514	A1515	A1516	A1517	A1518	A1519	A1520	A1521	A1522	A1523	A1524	A1525	A1526	A1527	A1528	A1529	A1530	A1531	A1532	A1533	A1534	A1535	A1536	A1537	A1538	A1539	A1540	A1541	A1542	A1543	A1544	A1545	A1546	A1547	A1548	A1549	A1550	A1551	A1552	A1553	A1554	A1555	A1556	A1557	A1558	A1559	A1560	A1561	A1562	A1563	A1564	A1565	A1566	A1567	A1568	
C1448	A1449	A1450	A1451	A1452	A1453	A1454	A1455	A1456	A1457	A1458	A1459	A1460	A1461	A1462	A1463	A1464	A1465	A1466	A1467	A1468	A1469	A1470	A1471	A1472	A1473	A1474	A1475	A1476	A1477	A1478	A1479	A1480	A1481	A1482	A1483	A1484	A1485	A1486	A1487	A1488	A1489	A1490	A1491	A1492	A1493	A1494	A1495	A1496	A1497	A1498	A1499	A1500	A1501	A1502	A1503	A1504	A1505	A1506	A1507	A1508
A1328	A1329	A1330	A1331	A1332	A1333	A1334	A1335	A1336	A1337	A1338	A1339	A1340	A1341	A1342	A1343	A1344	A1345	A1346	A1347	A1348	A1349	A1350	A1351	A1352	A1353	A1354	A1355	A1356	A1357	A1358	A1359	A1360	A1361	A1362	A1363	A1364	A1365	A1366	A1367	A1368	A1369	A1370	A1371	A1372	A1373	A1374	A1375	A1376	A1377	A1378	A1379	A1380	A1381	A1382	A1383	A1384	A1385	A1386	A1387	
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A3926	A3927	A3928	A3929	A3930	A3931	A3932	A3933	A3934	A3935	A3936	A3937	A3938	A3939	A3940	A3941	A3942	A3943	A3944	A3945	A3946	A3947	A3948	A3949	A3950	A3951	A3952	A3953	A3954	A3955	A3956	A3957	A3958	A3959	A3960	A3961	A3962	A3963	A3964	A3965	A3966	A3967	A3968	A3969	A3970	A3971	A3972	A3973	A3974	A3975	A3976	A3977	A3978	A3979	A3980											
G3981	G3982	G3983	G3984	G3985	G3986	G3987	G3988	G3989	G3990	G3991	G3992	G3993	G3994	G3995	G3996	G3997	G3998	G3999	G4000	G4001	G4002	G4003	G4004	G4005	G4006	G4007	G4008	G4009	G4010	G4011	G4012	G4013	G4014	G4015	G4016	G4017	G4018	G4019	G4020	G4021	G4022	G4023	G4024	G4025	G4026	G4027	G4028	G4029	G4030	G4031	G4032	G4033	G4034	G4035	G4036	G4037	G4038	G4039	G4040						
A4041	A4042	A4043	A4044	A4045	A4046	A4047	A4048	A4049	A4050	A4051	A4052	A4053	A4054	A4055	A4056	A4057	A4058	A4059	A4060	A4061	A4062	A4063	A4064	A4065	A4066	A4067	A4068	A4069	A4070	A4071	A4072	A4073	A4074	A4075	A4076	A4077	A4078	A4079	A4080	A4081	A4082	A4083	A4084	A4085	A4086	A4087	A4088	A4089	A4090	A4091	A4092	A4093	A4094	A4095	A4096	A4097	A4098	A4099	A4100						
G4101	G4102	G4103	G4104	G4105	G4106	G4107	G4108	G4109	G4110	G4111	G4112	G4113	G4114	G4115	G4116	G4117	G4118	G4119	G4120	G4121	G4122	G4123	G4124	G4125	G4126	G4127	G4128	G4129	G4130	G4131	G4132	G4133	G4134	G4135	G4136	G4137	G4138	G4139	G4140	G4141	G4142	G4143	G4144	G4145	G4146	G4147	G4148	G4149	G4150	G4151	G4152	G4153	G4154	G4155	G4156	G4157	G4158	G4159	G4160						
A4161	A4162	A4163	A4164	A4165	A4166	A4167	A4168	A4169	A4170	A4171	A4172	A4173	A4174	A4175	A4176	A4177	A4178	A4179	A4180	A4181	A4182	A4183	A4184	A4185	A4186	A4187	A4188	A4189	A4190	A4191	A4192	A4193	A4194	A4195	A4196	A4197	A4198	A4199	A4200	A4201	A4202	A4203	A4204	A4205	A4206	A4207	A4208	A4209	A4210	A4211	A4212	A4213	A4214	A4215	A4216	A4217	A4218	A4219	A4220						
A4221	A4222	A4223	A4224	A4225	A4226	A4227	A4228	A4229	A4230	A4231	A4232	A4233	A4234	A4235	A4236	A4237	A4238	A4239	A4240	A4241	A4242	A4243	A4244	A4245	A4246	A4247	A4248	A4249	A4250	A4251	A4252	A4253	A4254	A4255	A4256	A4257	A4258	A4259	A4260	A4261	A4262	A4263	A4264	A4265	A4266	A4267	A4268	A4269	A4270	A4271	A4272	A4273	A4274	A4275	A4276	A4277	A4278	A4279	A4280						
C4281	C4282	C4283	C4284	C4285	C4286	C4287	C4288	C4289	C4290	C4291	C4292	C4293	C4294	C4295	C4296	C4297	C4298	C4299	C4300	C4301	C4302	C4303	C4304	C4305	C4306	C4307	C4308	C4309	C4310	C4311	C4312	C4313	C4314	C4315	C4316	C4317	C4318	C4319	C4320	C4321	C4322	C4323	C4324	C4325	C4326	C4327	C4328	C4329	C4330	C4331	C4332	C4333	C4334	C4335	C4336	C4337	C4338	C4339	C4340						
U4341	U4342	U4343	U4344	U4345	U4346	U4347	U4348	U4349	U4350	U4351	U4352	U4353	U4354	U4355	U4356	U4357	U4358	U4359	U4360	U4361	U4362	U4363	U4364	U4365	U4366	U4367	U4368	U4369	U4370	U4371	U4372	U4373	U4374	U4375	U4376	U4377	U4378	U4379	U4380	U4381	U4382	U4383	U4384	U4385	U4386	U4387	U4388	U4389	U4390	U4391	U4392	U4393	U4394	U4395	U4396	U4397	U4398	U4399	U4400						
G4401	G4402	G4403	G4404	G4405	G4406	G4407	G4408	G4409	G4410	G4411	G4412	G4413	G4414	G4415	G4416	G4417	G4418	G4419	G4420	G4421	G4422	G4423	G4424	G4425	G4426	G4427	G4428	G4429	G4430	G4431	G4432	G4433	G4434	G4435	G4436	G4437	G4438	G4439	G4440	G4441	G4442	G4443	G4444	G4445	G4446	G4447	G4448	G4449	G4450	G4451	G4452	G4453	G4454	G4455	G4456	G4457	G4458	G4459	G4460						

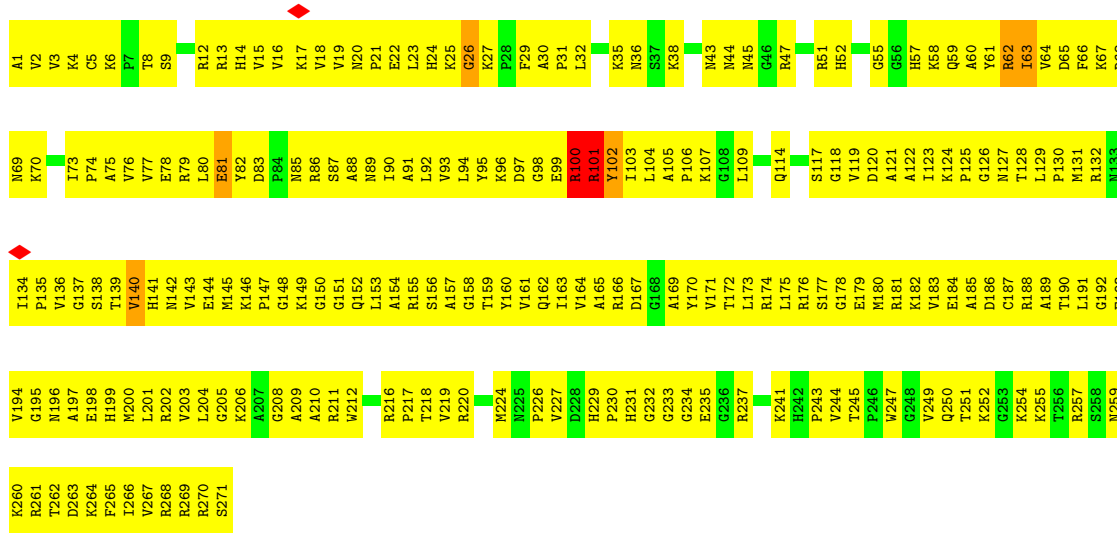
• Molecule 10: 5S rRNA



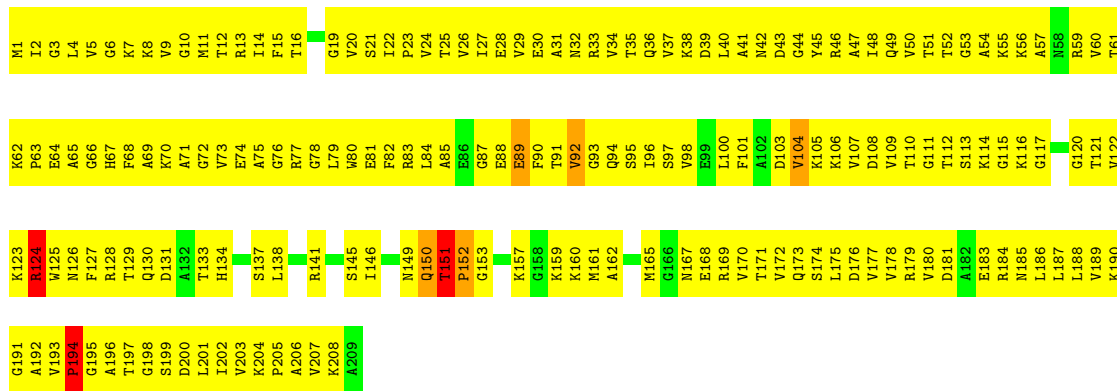
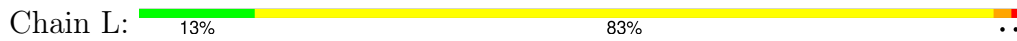
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

• Molecule 11: 50S ribosomal protein L2

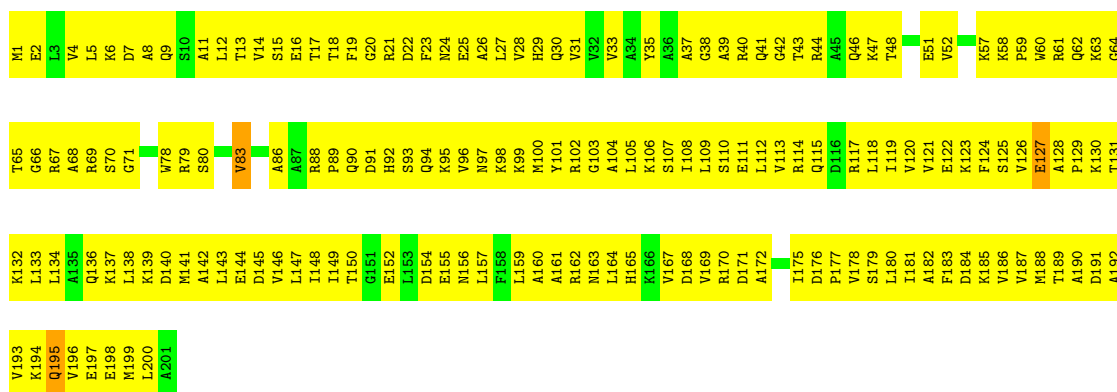




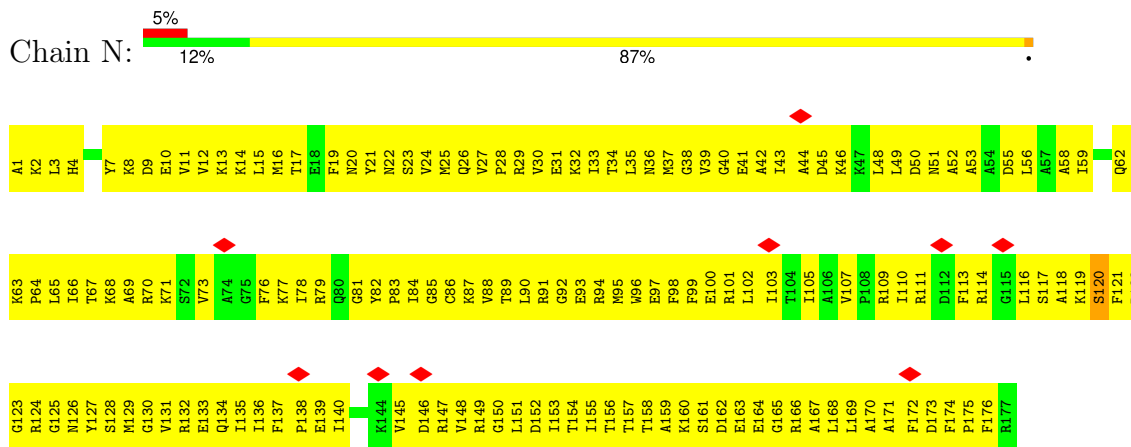
• Molecule 12: 50S ribosomal protein L3



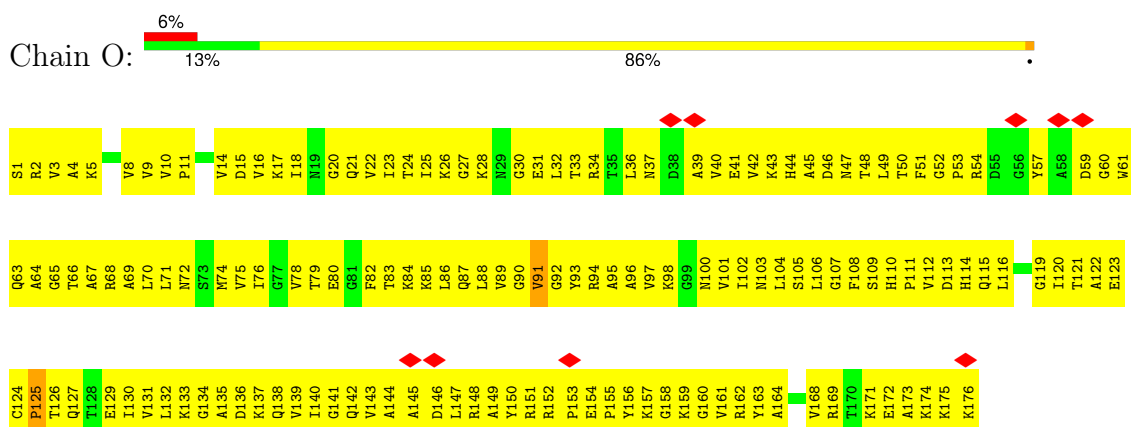
• Molecule 13: 50S ribosomal protein L4



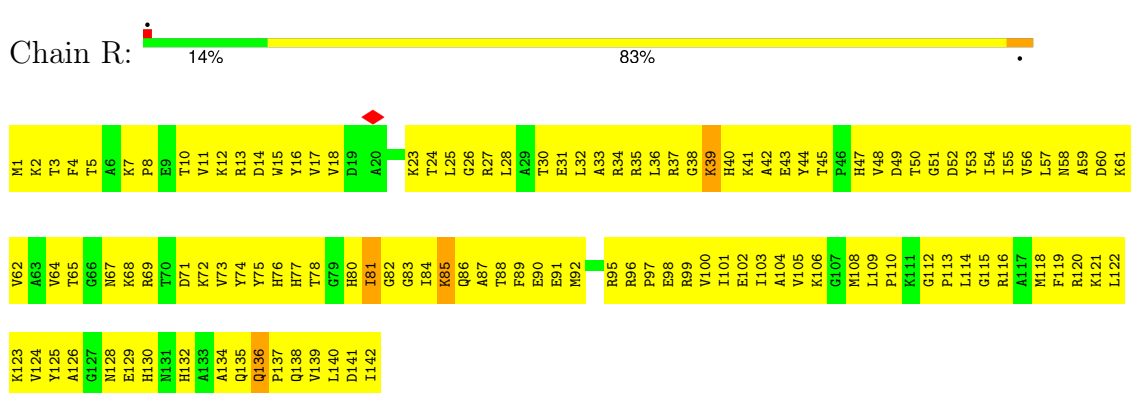
• Molecule 14: 50S ribosomal protein L5



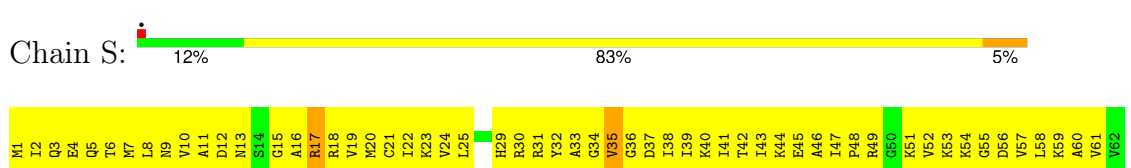
• Molecule 15: 50S ribosomal protein L6

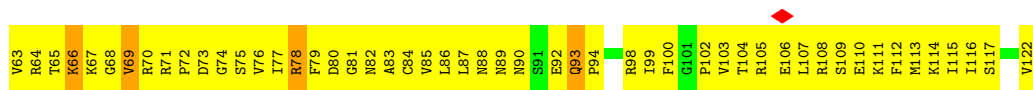


• Molecule 16: 50S ribosomal protein L13

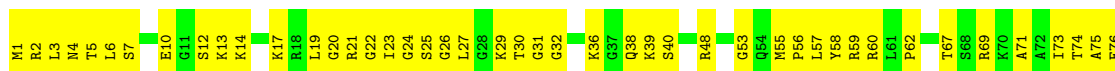
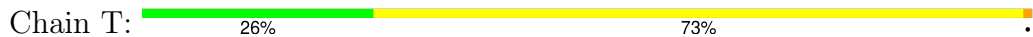


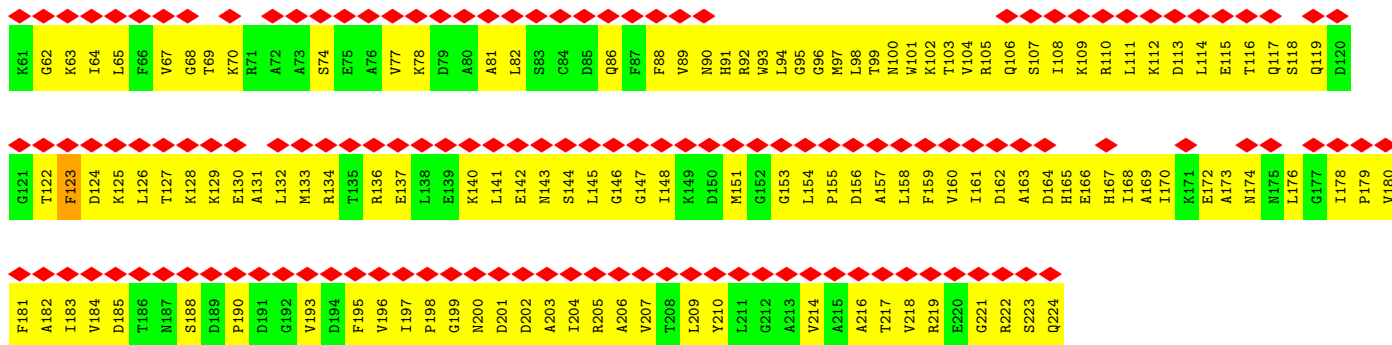
• Molecule 17: 50S ribosomal protein L14





• Molecule 18: 50S ribosomal protein L15

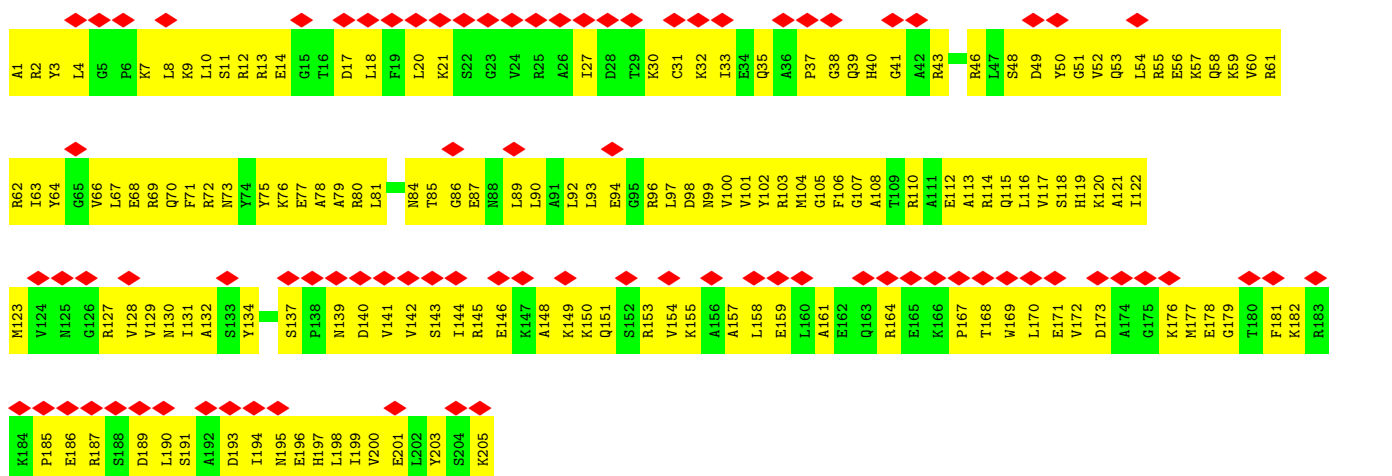




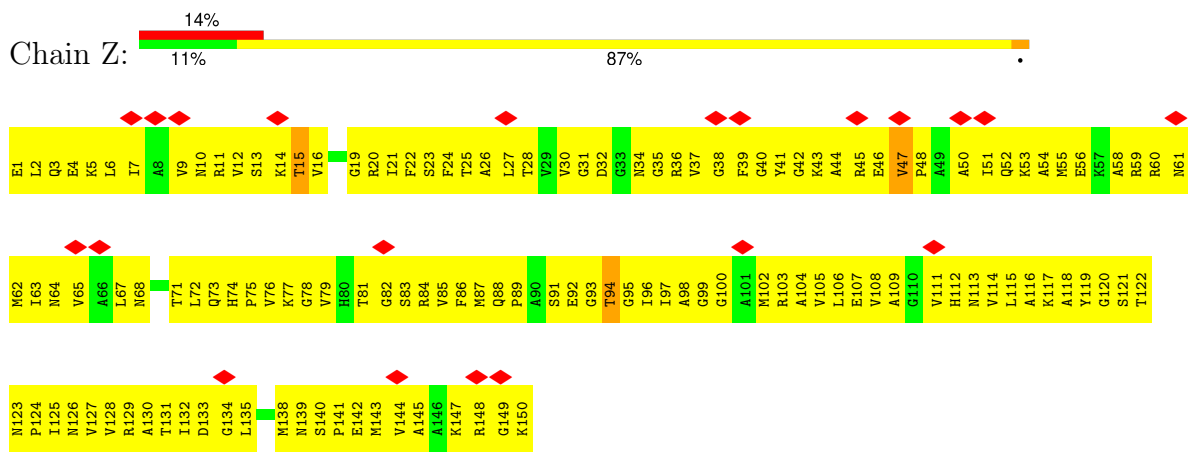
• Molecule 22: 30S ribosomal protein S3



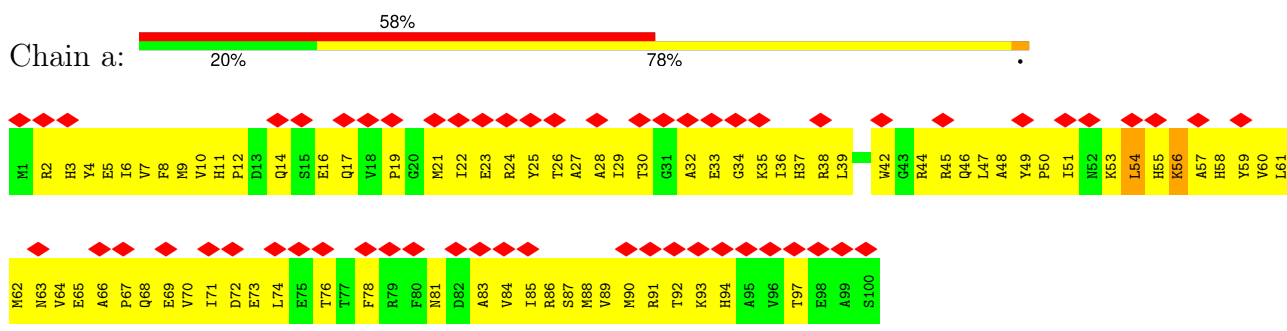
• Molecule 23: 30S ribosomal protein S4



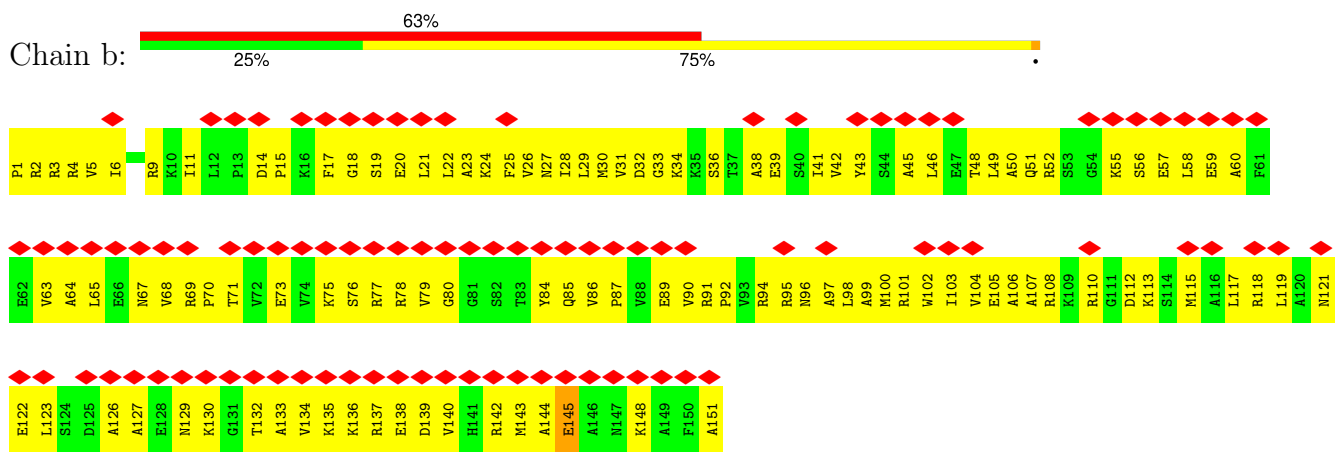
• Molecule 24: 30S ribosomal protein S5



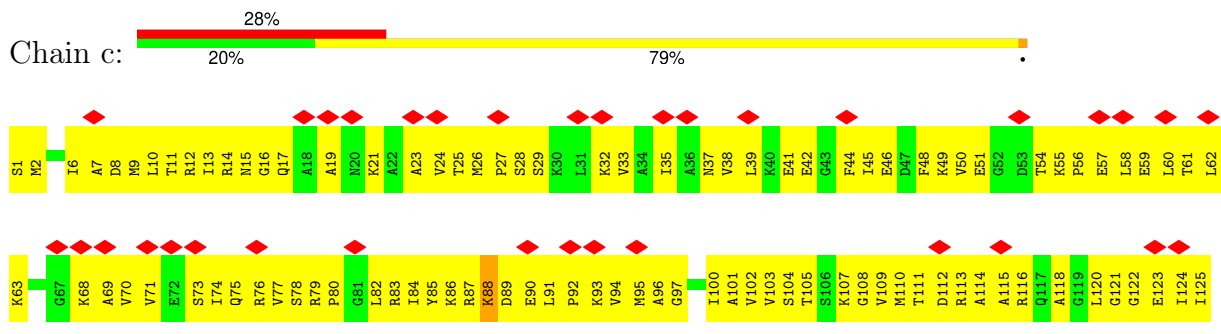
• Molecule 25: 30S ribosomal protein S6



• Molecule 26: 30S ribosomal protein S7

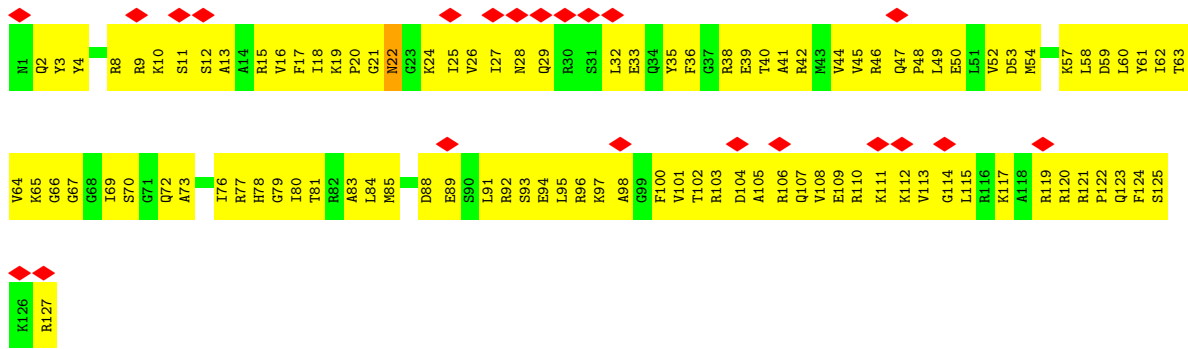


• Molecule 27: 30S ribosomal protein S8



C126  
Y127  
V128  
A129

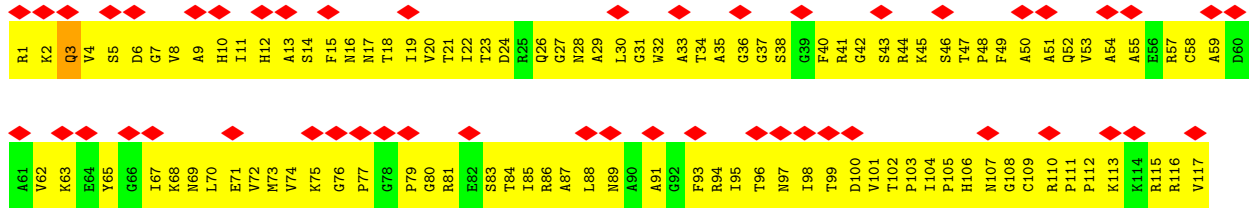
• Molecule 28: 30S ribosomal protein S9



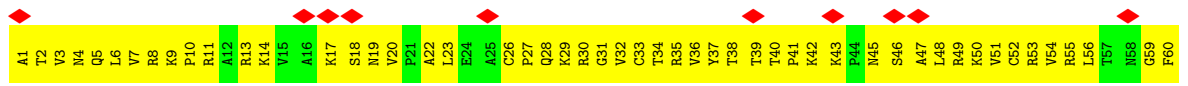
• Molecule 29: 30S ribosomal protein S10

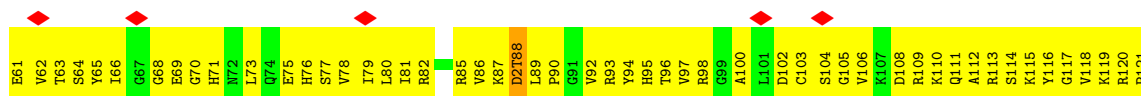


• Molecule 30: 30S ribosomal protein S11

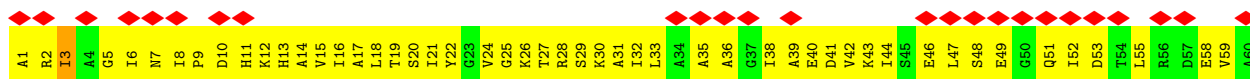


• Molecule 31: 30S ribosomal protein S12

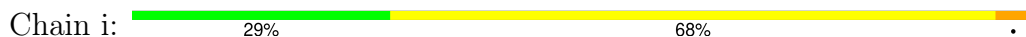




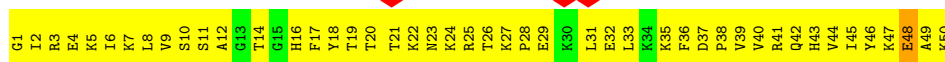
• Molecule 32: 30S ribosomal protein S13



• Molecule 33: 50S ribosomal protein L32



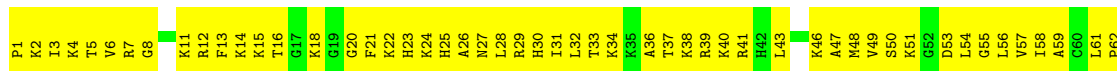
• Molecule 34: 50S ribosomal protein L33



• Molecule 35: 50S ribosomal protein L34



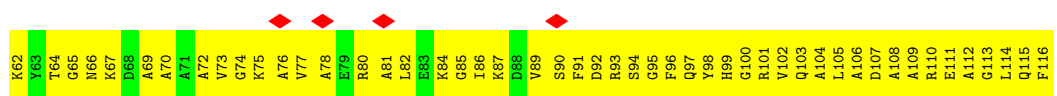
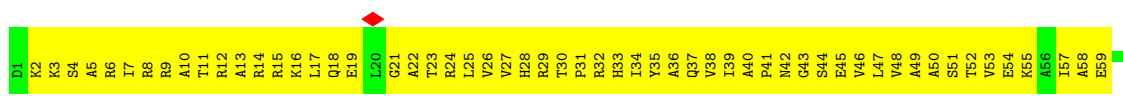
• Molecule 36: 50S ribosomal protein L35



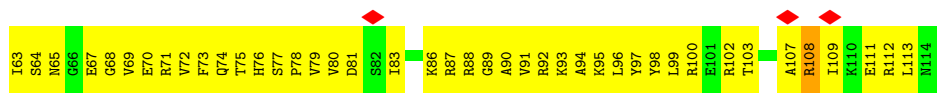
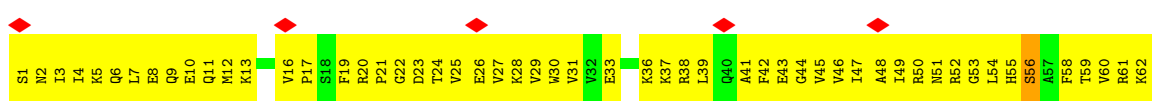
• Molecule 37: 50S ribosomal protein L36



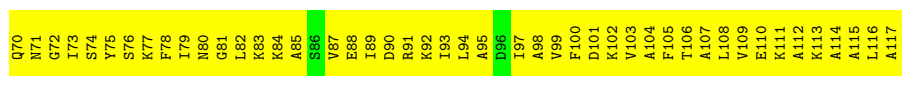
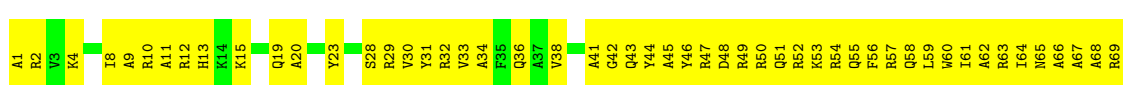
• Molecule 38: 50S ribosomal protein L18



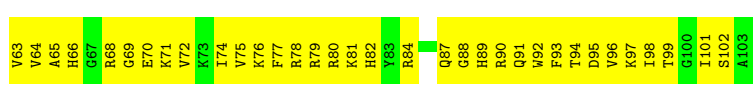
• Molecule 39: 50S ribosomal protein L19



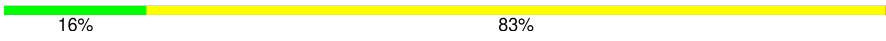
• Molecule 40: 50S ribosomal protein L20

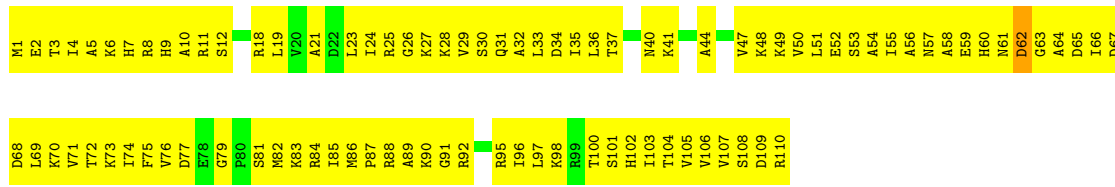


• Molecule 41: 50S ribosomal protein L21



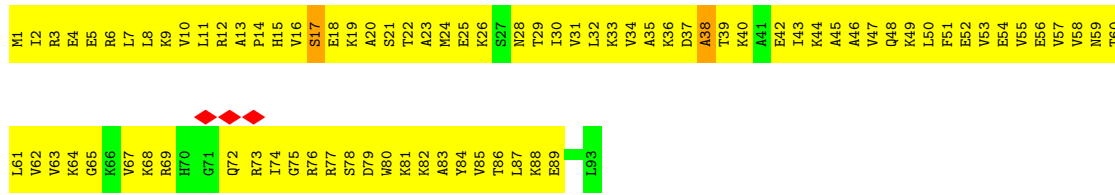
• Molecule 42: 50S ribosomal protein L22

Chain r:  16% 83%



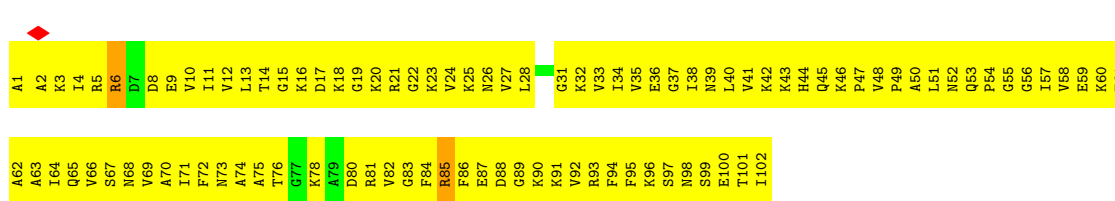
• Molecule 43: 50S ribosomal protein L23

Chain s:  10% 88%

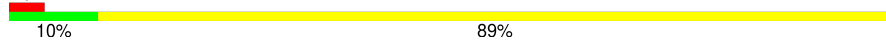


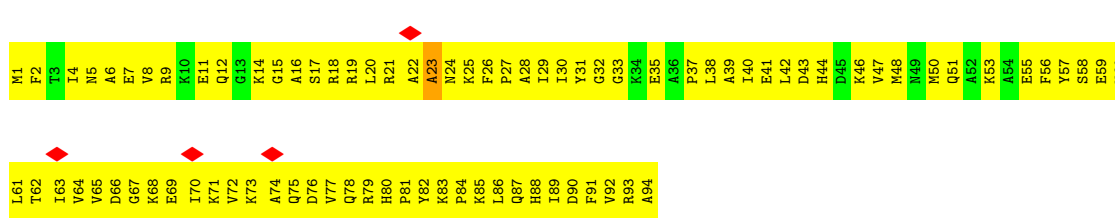
• Molecule 44: 50S ribosomal protein L24

Chain t:  5% 93%

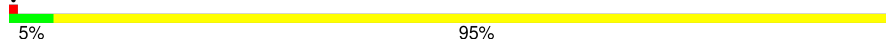


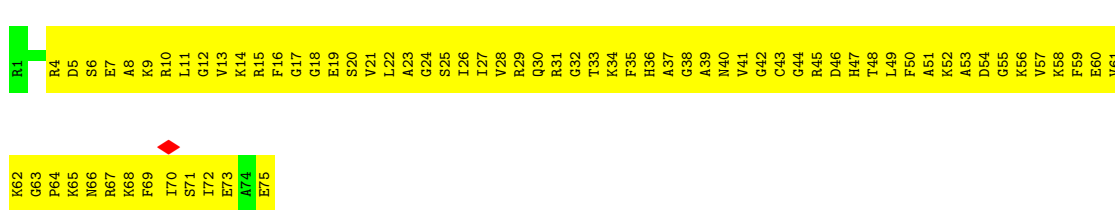
• Molecule 45: 50S ribosomal protein L25

Chain u:  10% 89%



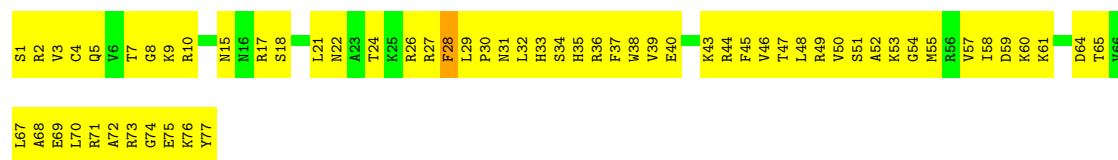
• Molecule 46: 50S ribosomal protein L27

Chain v:  5% 95%



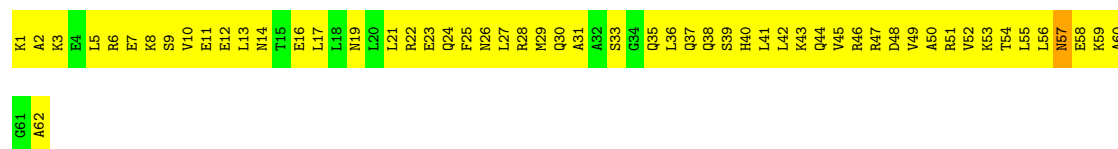
- Molecule 47: 50S ribosomal protein L28

Chain w:  21% 78%



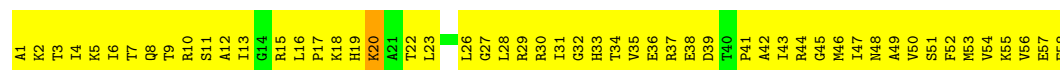
- Molecule 48: 50S ribosomal protein L29

Chain x:  11% 87%



- Molecule 49: 50S ribosomal protein L30

Chain y:  9% 90%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34852	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.073	Depositor
Minimum map value	-0.210	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	430.0, 430.0, 430.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.86, 0.86, 0.86	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 4OC, UR3, 2MA, 2MG, D2T, 5MU, 3TD, G7M, OMU, 1MG, 6MZ, OMC, 4D4, PSU, OMG, MA6

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	0.24	0/817	0.46	0/1088
2	B	0.20	0/722	0.51	0/964
3	C	0.81	2/659 (0.3%)	1.06	3/884 (0.3%)
4	D	0.28	0/658	0.64	0/881
5	E	0.18	0/463	0.56	0/621
6	F	0.16	0/653	0.43	0/877
7	G	0.20	0/671	0.52	1/888 (0.1%)
8	H	0.16	0/472	0.72	2/627 (0.3%)
9	I	0.33	6/105898 (0.0%)	0.46	4/165194 (0.0%)
10	J	0.33	0/2828	0.57	0/4410
11	K	0.80	6/2122 (0.3%)	0.99	7/2852 (0.2%)
12	L	0.49	1/1586 (0.1%)	0.84	2/2134 (0.1%)
13	M	0.35	0/1571	0.69	2/2113 (0.1%)
14	N	0.40	0/1435	0.68	1/1926 (0.1%)
15	O	0.34	0/1343	0.70	0/1816
16	R	0.54	1/1152 (0.1%)	0.83	0/1551
17	S	0.60	1/947 (0.1%)	0.93	2/1268 (0.2%)
18	T	0.42	0/1062	0.83	4/1413 (0.3%)
19	U	0.43	0/1081	0.73	2/1443 (0.1%)
20	V	0.39	0/973	0.78	0/1301
21	W	0.14	0/1784	0.40	0/2403
22	X	0.13	0/1652	0.36	0/2225
23	Y	0.13	0/1665	0.32	0/2227
24	Z	0.38	1/1118 (0.1%)	0.63	0/1504
25	a	0.21	0/835	0.50	0/1128
26	b	0.15	0/1196	0.41	0/1602
27	c	0.16	0/989	0.41	0/1326
28	d	0.16	0/1034	0.42	0/1375
29	e	0.19	0/797	0.50	0/1077
30	f	0.19	0/893	0.55	0/1205
31	g	0.18	0/960	0.41	0/1286

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	h	0.17	0/893	0.43	0/1193
33	i	0.33	0/450	0.57	0/599
34	j	0.26	0/416	0.59	0/554
35	k	0.36	0/380	0.66	0/498
36	l	0.36	0/513	0.66	0/676
37	m	0.32	0/303	0.67	0/397
38	n	0.30	0/902	0.68	0/1209
39	o	0.42	0/929	0.75	0/1242
40	p	0.40	0/960	0.71	0/1278
41	q	0.36	0/829	0.67	0/1107
42	r	0.35	0/864	0.57	0/1156
43	s	0.46	0/745	0.75	1/994 (0.1%)
44	t	0.38	0/788	0.84	0/1051
45	u	0.33	0/766	0.71	0/1025
46	v	0.38	0/576	0.74	0/762
47	w	0.37	0/635	0.70	2/848 (0.2%)
48	x	0.50	0/502	0.82	0/667
49	y	0.34	0/453	0.76	0/605
All	All	0.35	18/151940 (0.0%)	0.52	33/227470 (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
1	A	0	1
4	D	0	2
11	K	0	5
12	L	0	3
16	R	0	1
20	V	0	1
39	o	0	1
44	t	0	1
All	All	0	15

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	226	G	C2-N3	23.37	1.79	1.32
9	I	226	G	N3-C4	23.05	1.81	1.35
11	K	26	GLY	C-N	20.00	1.59	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	226	G	N1-C2	17.98	1.73	1.37
9	I	226	G	C6-N1	17.44	1.74	1.39

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	62	GLY	CA-C-N	18.33	149.36	122.41
3	C	62	GLY	C-N-CA	18.33	149.36	122.41
8	H	8	ASN	CA-C-N	-10.05	106.15	121.83
8	H	8	ASN	C-N-CA	-10.05	106.15	121.83
11	K	26	GLY	N-CA-C	9.88	120.76	111.67

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	60	ARG	Sidechain
4	D	12	ASP	Peptide
4	D	13	LYS	Peptide
11	K	63	ILE	Mainchain
11	K	81	GLU	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	805	0	847	335	0
2	B	714	0	737	214	0
3	C	649	0	665	246	0
4	D	649	0	694	312	0
5	E	456	0	481	191	0
6	F	638	0	668	84	0
7	G	665	0	717	142	0
8	H	465	0	493	199	0
9	I	95284	625	47973	16244	0
10	J	2529	0	1281	760	0
11	K	2083	0	2157	881	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1565	0	1616	851	0
13	M	1552	0	1619	578	0
14	N	1411	0	1447	634	0
15	O	1323	0	1374	662	0
16	R	1129	0	1162	429	0
17	S	938	0	1012	464	0
18	T	1053	0	1129	357	0
19	U	1075	0	1155	384	0
20	V	960	0	1000	411	0
21	W	1753	0	1783	395	0
22	X	1625	0	1699	298	0
23	Y	1643	0	1710	323	0
24	Z	1105	0	1151	267	0
25	a	817	0	808	243	0
26	b	1182	0	1240	240	0
27	c	979	0	1034	211	0
28	d	1022	0	1073	240	0
29	e	787	0	831	217	0
30	f	877	0	890	394	0
31	g	957	0	1020	239	0
32	h	884	0	944	237	0
33	i	444	0	461	85	0
34	j	409	0	443	206	0
35	k	377	0	418	51	0
36	l	504	0	574	127	0
37	m	302	0	343	210	0
38	n	892	0	926	383	0
39	o	917	0	965	513	0
40	p	947	0	1022	367	0
41	q	816	0	839	337	0
42	r	857	0	922	195	0
43	s	739	0	807	336	0
44	t	780	0	834	454	0
45	u	753	0	780	382	0
46	v	569	0	584	356	0
47	w	625	0	655	200	0
48	x	501	0	534	226	0
49	y	449	0	491	231	0
All	All	140455	625	94008	28535	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 123.

The worst 5 of 28535 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)
3:C:63:GLN:N	9:I:226:G:C4	1.68	1.57
9:I:226:G:N1	9:I:226:G:C6	1.74	1.56
9:I:226:G:N1	9:I:226:G:C2	1.73	1.54
10:J:76:U:C2	10:J:98:A:N7	1.82	1.47
9:I:226:G:C4	9:I:226:G:N3	1.81	1.44

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	
1	A	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
2	B	86/88 (98%)	78 (91%)	6 (7%)	2 (2%)	5	29
3	C	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	27
4	D	78/80 (98%)	66 (85%)	10 (13%)	2 (3%)	4	26
5	E	53/55 (96%)	47 (89%)	5 (9%)	1 (2%)	6	33
6	F	77/79 (98%)	74 (96%)	2 (3%)	1 (1%)	9	41
7	G	83/85 (98%)	77 (93%)	6 (7%)	0	100	100
8	H	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
11	K	269/271 (99%)	216 (80%)	52 (19%)	1 (0%)	30	66
12	L	207/209 (99%)	171 (83%)	30 (14%)	6 (3%)	3	24
13	M	199/201 (99%)	172 (86%)	25 (13%)	2 (1%)	12	47
14	N	175/177 (99%)	147 (84%)	27 (15%)	1 (1%)	21	58
15	O	174/176 (99%)	133 (76%)	38 (22%)	3 (2%)	7	35
16	R	140/142 (99%)	113 (81%)	24 (17%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S	120/122 (98%)	97 (81%)	20 (17%)	3 (2%)	4	27
18	T	142/144 (99%)	118 (83%)	23 (16%)	1 (1%)	18	55
19	U	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
20	V	118/120 (98%)	100 (85%)	18 (15%)	0	100	100
21	W	222/224 (99%)	211 (95%)	10 (4%)	1 (0%)	24	62
22	X	204/206 (99%)	190 (93%)	12 (6%)	2 (1%)	12	47
23	Y	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
24	Z	148/150 (99%)	127 (86%)	19 (13%)	2 (1%)	9	39
25	a	98/100 (98%)	85 (87%)	11 (11%)	2 (2%)	6	32
26	b	149/151 (99%)	143 (96%)	5 (3%)	1 (1%)	18	55
27	c	127/129 (98%)	116 (91%)	10 (8%)	1 (1%)	16	52
28	d	125/127 (98%)	118 (94%)	6 (5%)	1 (1%)	16	52
29	e	96/98 (98%)	81 (84%)	13 (14%)	2 (2%)	5	30
30	f	115/117 (98%)	94 (82%)	20 (17%)	1 (1%)	14	49
31	g	120/123 (98%)	107 (89%)	13 (11%)	0	100	100
32	h	112/114 (98%)	105 (94%)	6 (5%)	1 (1%)	14	49
33	i	54/56 (96%)	45 (83%)	7 (13%)	2 (4%)	2	20
34	j	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	30
35	k	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	29
36	l	62/64 (97%)	53 (86%)	9 (14%)	0	100	100
37	m	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
38	n	114/116 (98%)	96 (84%)	18 (16%)	0	100	100
39	o	112/114 (98%)	93 (83%)	18 (16%)	1 (1%)	14	49
40	p	115/117 (98%)	97 (84%)	18 (16%)	0	100	100
41	q	101/103 (98%)	79 (78%)	22 (22%)	0	100	100
42	r	108/110 (98%)	94 (87%)	13 (12%)	1 (1%)	14	49
43	s	91/93 (98%)	71 (78%)	19 (21%)	1 (1%)	11	45
44	t	100/102 (98%)	72 (72%)	27 (27%)	1 (1%)	12	47
45	u	92/94 (98%)	80 (87%)	11 (12%)	1 (1%)	11	45
46	v	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
47	w	75/77 (97%)	63 (84%)	12 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	x	60/62 (97%)	49 (82%)	10 (17%)	1 (2%)	7	35
49	y	56/58 (97%)	46 (82%)	9 (16%)	1 (2%)	6	34
All	All	5346/5442 (98%)	4625 (86%)	668 (12%)	53 (1%)	15	47

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	43	ALA
11	K	101	ARG
12	L	104	VAL
15	O	91	VAL
16	R	81	ILE

### 5.3.2 Protein sidechains [i](#)

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	A	83/83 (100%)	83 (100%)	0	100	100
2	B	76/76 (100%)	76 (100%)	0	100	100
3	C	65/65 (100%)	65 (100%)	0	100	100
4	D	74/74 (100%)	74 (100%)	0	100	100
5	E	48/48 (100%)	48 (100%)	0	100	100
6	F	70/70 (100%)	70 (100%)	0	100	100
7	G	65/65 (100%)	65 (100%)	0	100	100
8	H	48/48 (100%)	48 (100%)	0	100	100
11	K	216/216 (100%)	216 (100%)	0	100	100
12	L	164/164 (100%)	164 (100%)	0	100	100
13	M	165/165 (100%)	165 (100%)	0	100	100
14	N	148/148 (100%)	148 (100%)	0	100	100
15	O	137/137 (100%)	137 (100%)	0	100	100
16	R	116/116 (100%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	S	103/103 (100%)	103 (100%)	0	100	100
18	T	103/103 (100%)	103 (100%)	0	100	100
19	U	108/108 (100%)	107 (99%)	1 (1%)	70	75
20	V	100/100 (100%)	100 (100%)	0	100	100
21	W	186/186 (100%)	186 (100%)	0	100	100
22	X	170/170 (100%)	170 (100%)	0	100	100
23	Y	172/172 (100%)	172 (100%)	0	100	100
24	Z	113/113 (100%)	113 (100%)	0	100	100
25	a	87/87 (100%)	87 (100%)	0	100	100
26	b	124/124 (100%)	124 (100%)	0	100	100
27	c	104/104 (100%)	104 (100%)	0	100	100
28	d	105/105 (100%)	105 (100%)	0	100	100
29	e	86/86 (100%)	86 (100%)	0	100	100
30	f	90/90 (100%)	90 (100%)	0	100	100
31	g	102/102 (100%)	102 (100%)	0	100	100
32	h	92/92 (100%)	92 (100%)	0	100	100
33	i	47/47 (100%)	47 (100%)	0	100	100
34	j	45/45 (100%)	45 (100%)	0	100	100
35	k	38/38 (100%)	38 (100%)	0	100	100
36	l	51/51 (100%)	51 (100%)	0	100	100
37	m	34/34 (100%)	34 (100%)	0	100	100
38	n	86/86 (100%)	86 (100%)	0	100	100
39	o	99/99 (100%)	99 (100%)	0	100	100
40	p	89/89 (100%)	89 (100%)	0	100	100
41	q	84/84 (100%)	84 (100%)	0	100	100
42	r	93/93 (100%)	93 (100%)	0	100	100
43	s	80/80 (100%)	80 (100%)	0	100	100
44	t	83/83 (100%)	83 (100%)	0	100	100
45	u	78/78 (100%)	78 (100%)	0	100	100
46	v	56/57 (98%)	56 (100%)	0	100	100
47	w	67/67 (100%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	x	54/54 (100%)	54 (100%)	0	100	100
49	y	48/48 (100%)	48 (100%)	0	100	100
All	All	4452/4453 (100%)	4451 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	U	13	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
32	h	90	HIS
44	t	44	HIS
33	i	41	HIS
40	p	58	GLN
45	u	78	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	J	117/118 (99%)	54 (46%)	2 (1%)
9	I	4435/4438 (99%)	1494 (33%)	119 (2%)
All	All	4552/4556 (99%)	1548 (34%)	121 (2%)

5 of 1548 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	I	3	U
9	I	4	U
9	I	8	G
9	I	27	A
9	I	31	A

5 of 121 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	I	2363	A
9	I	4174	U

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Mol	Chain	Res	Type
9	I	2832	G
9	I	4096	A
9	I	4325	G

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

35 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
9	PSU	I	3411	9	18,21,22	4.61	8 (44%)	21,30,33	1.94	6 (28%)
9	2MG	I	4420	9	23,26,27	2.98	9 (39%)	33,38,41	2.18	10 (30%)
9	2MG	I	3329	9	23,26,27	2.94	9 (39%)	33,38,41	2.27	9 (27%)
9	5MC	I	1406	9	19,22,23	3.99	9 (47%)	26,32,35	1.00	1 (3%)
9	MA6	I	4422	9	23,26,27	1.35	4 (17%)	33,38,41	4.72	13 (39%)
9	PSU	I	3951	9	18,21,22	4.33	8 (44%)	21,30,33	2.54	7 (33%)
9	6MZ	I	3524	9	22,25,26	2.51	5 (22%)	29,36,39	2.45	12 (41%)
9	5MC	I	966	9	19,22,23	4.12	9 (47%)	26,32,35	1.02	1 (3%)
19	4D4	U	81	19	9,11,12	2.74	3 (33%)	7,13,15	0.82	0
9	2MG	I	965	9	23,26,27	3.01	9 (39%)	33,38,41	2.15	10 (30%)
9	PSU	I	4099	9	18,21,22	4.39	9 (50%)	21,30,33	2.07	7 (33%)
9	2MG	I	1206	9	23,26,27	3.01	8 (34%)	33,38,41	2.16	10 (30%)
31	D2T	g	88	31	8,9,10	2.93	1 (12%)	6,11,13	2.42	2 (33%)
9	2MA	I	3997	9	22,25,26	3.78	7 (31%)	32,37,40	3.23	11 (34%)
9	3TD	I	3409	9	19,22,23	4.14	6 (31%)	23,32,35	1.74	3 (13%)
9	4OC	I	1401	9	20,23,24	3.16	8 (40%)	25,32,35	0.84	0
9	MA6	I	4423	9	23,26,27	1.35	4 (17%)	33,38,41	4.77	13 (39%)
9	PSU	I	3998	9	18,21,22	4.50	9 (50%)	21,30,33	2.19	5 (23%)
9	G7M	I	3563	9	23,26,27	2.78	8 (34%)	34,39,42	1.89	8 (23%)
9	OMC	I	3992	9	19,22,23	3.34	8 (42%)	25,31,34	0.81	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	5MC	I	3456	9	19,22,23	3.89	9 (47%)	26,32,35	1.11	1 (3%)
9	6MZ	I	3112	9	22,25,26	2.59	4 (18%)	29,36,39	2.30	9 (31%)
9	PSU	I	3405	9	18,21,22	4.57	8 (44%)	21,30,33	2.12	5 (23%)
9	PSU	I	2246	9	18,21,22	4.61	8 (44%)	21,30,33	2.51	6 (28%)
9	PSU	I	2449	9	18,21,22	4.36	8 (44%)	21,30,33	2.23	5 (23%)
9	PSU	I	515	9	18,21,22	4.58	8 (44%)	21,30,33	2.18	6 (28%)
9	2MG	I	3939	9	23,26,27	2.81	9 (39%)	33,38,41	2.35	9 (27%)
9	OMG	I	3745	9	23,26,27	2.58	9 (39%)	32,38,41	1.97	9 (28%)
9	1MG	I	2245	9	23,26,27	2.77	8 (34%)	33,39,42	1.53	5 (15%)
9	5MU	I	3433	9	19,22,23	4.60	6 (31%)	27,32,35	3.84	10 (37%)
9	G7M	I	526	9	23,26,27	2.85	9 (39%)	34,39,42	1.74	8 (23%)
9	5MU	I	2247	9	19,22,23	4.64	6 (31%)	27,32,35	3.79	10 (37%)
9	OMU	I	4046	9	19,22,23	2.86	6 (31%)	25,31,34	1.83	4 (16%)
9	UR3	I	4402	9	19,22,23	2.86	8 (42%)	26,32,35	1.61	4 (15%)
9	PSU	I	4074	9	18,21,22	4.37	9 (50%)	21,30,33	2.18	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
9	PSU	I	3411	9	-	1/7/25/26	0/2/2/2
9	2MG	I	4420	9	-	1/9/27/28	0/3/3/3
9	2MG	I	3329	9	-	1/9/27/28	0/3/3/3
9	5MC	I	1406	9	-	4/7/25/26	0/2/2/2
9	MA6	I	4422	9	-	4/11/29/30	0/3/3/3
9	PSU	I	3951	9	-	2/7/25/26	0/2/2/2
9	6MZ	I	3524	9	-	4/9/27/28	0/3/3/3
9	5MC	I	966	9	-	1/7/25/26	0/2/2/2
19	4D4	U	81	19	-	5/11/12/14	-
9	2MG	I	965	9	-	2/9/27/28	0/3/3/3
9	PSU	I	4099	9	-	5/7/25/26	0/2/2/2
9	2MG	I	1206	9	-	1/9/27/28	0/3/3/3
31	D2T	g	88	31	-	3/7/12/14	-
9	2MA	I	3997	9	-	4/7/25/26	0/3/3/3
9	3TD	I	3409	9	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	4OC	I	1401	9	-	1/9/29/30	0/2/2/2
9	MA6	I	4423	9	-	1/11/29/30	0/3/3/3
9	PSU	I	3998	9	-	2/7/25/26	0/2/2/2
9	G7M	I	3563	9	-	1/7/25/26	0/3/3/3
9	OMC	I	3992	9	-	4/9/27/28	0/2/2/2
9	5MC	I	3456	9	-	4/7/25/26	0/2/2/2
9	6MZ	I	3112	9	-	6/9/27/28	0/3/3/3
9	PSU	I	3405	9	-	0/7/25/26	0/2/2/2
9	PSU	I	2246	9	-	3/7/25/26	0/2/2/2
9	PSU	I	2449	9	-	2/7/25/26	0/2/2/2
9	PSU	I	515	9	-	0/7/25/26	0/2/2/2
9	2MG	I	3939	9	-	2/9/27/28	0/3/3/3
9	OMG	I	3745	9	-	0/9/27/28	0/3/3/3
9	1MG	I	2245	9	-	2/7/25/26	0/3/3/3
9	5MU	I	3433	9	-	1/7/25/26	0/2/2/2
9	G7M	I	526	9	-	3/7/25/26	0/3/3/3
9	5MU	I	2247	9	-	2/7/25/26	0/2/2/2
9	OMU	I	4046	9	-	4/9/27/28	0/2/2/2
9	UR3	I	4402	9	-	4/7/25/26	0/2/2/2
9	PSU	I	4074	9	-	2/7/25/26	0/2/2/2

The worst 5 of 256 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	3409	3TD	C6-C5	12.54	1.49	1.35
9	I	3411	PSU	C6-C5	12.31	1.48	1.35
9	I	2246	PSU	C6-C5	12.21	1.48	1.35
9	I	515	PSU	C6-C5	11.97	1.48	1.35
9	I	3405	PSU	C6-C5	11.97	1.48	1.35

The worst 5 of 224 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	4422	MA6	N1-C6-N6	-17.74	95.25	116.86
9	I	4423	MA6	N1-C6-N6	-17.65	95.36	116.86
9	I	3433	5MU	C5-C4-N3	12.34	126.05	115.32
9	I	4422	MA6	C5-C6-N6	12.20	144.65	125.33
9	I	2247	5MU	C5-C4-N3	12.12	125.86	115.32

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	U	81	4D4	O-C-CA-CB
19	U	81	4D4	N-CA-CB-CG
19	U	81	4D4	NE-CD-CG-CB
31	g	88	D2T	CA-CB-SB-CB1
31	g	88	D2T	CG-CB-SB-CB1

There are no ring outliers.

34 monomers are involved in 182 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	I	3411	PSU	7	0
9	I	4420	2MG	7	0
9	I	3329	2MG	3	0
9	I	1406	5MC	6	0
9	I	4422	MA6	8	0
9	I	3951	PSU	7	0
9	I	3524	6MZ	4	0
9	I	966	5MC	9	0
9	I	965	2MG	1	0
9	I	4099	PSU	6	0
9	I	1206	2MG	5	0
31	g	88	D2T	6	0
9	I	3997	2MA	5	0
9	I	3409	3TD	7	0
9	I	1401	4OC	7	0
9	I	4423	MA6	8	0
9	I	3998	PSU	3	0
9	I	3563	G7M	1	0
9	I	3992	OMC	7	0
9	I	3456	5MC	6	0
9	I	3112	6MZ	5	0
9	I	3405	PSU	6	0
9	I	2246	PSU	3	0
9	I	2449	PSU	9	0
9	I	515	PSU	3	0
9	I	3939	2MG	8	0
9	I	3745	OMG	6	0
9	I	2245	1MG	12	0
9	I	3433	5MU	4	0
9	I	526	G7M	6	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	I	2247	5MU	1	0
9	I	4046	OMU	6	0
9	I	4402	UR3	3	0
9	I	4074	PSU	5	0

## 5.5 Carbohydrates [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	I	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	1500:U	O3'	1501:G	P	17.28
1	I	2385:C	O3'	2386:A	P	15.64

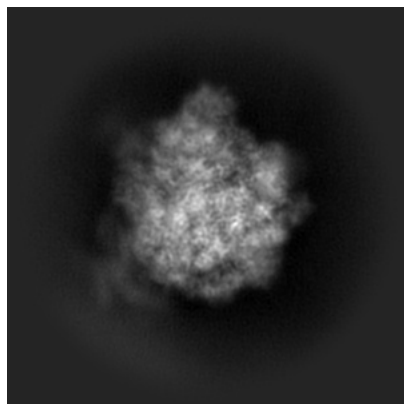
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26666. These allow visual inspection of the internal detail of the map and identification of artifacts.

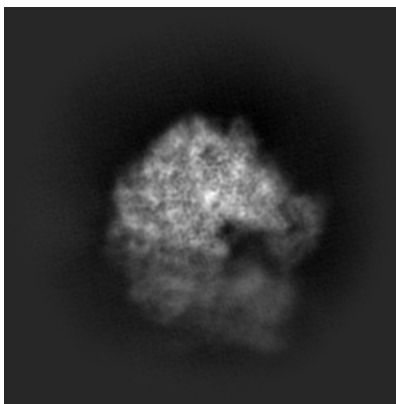
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

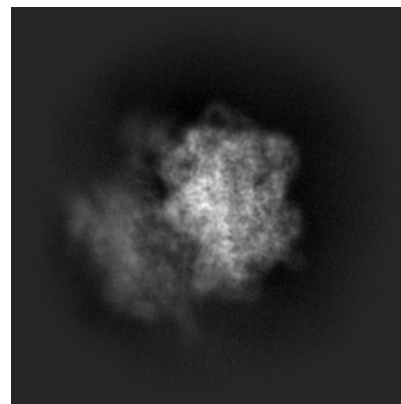
#### 6.1.1 Primary map



X

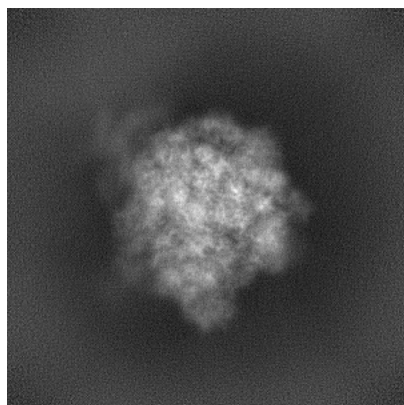


Y

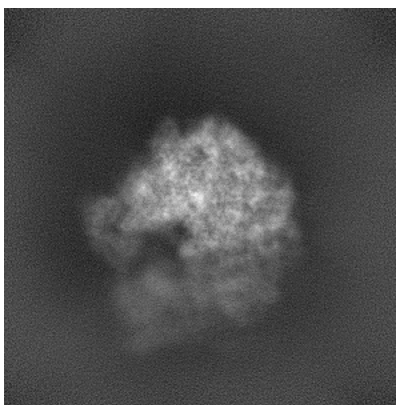


Z

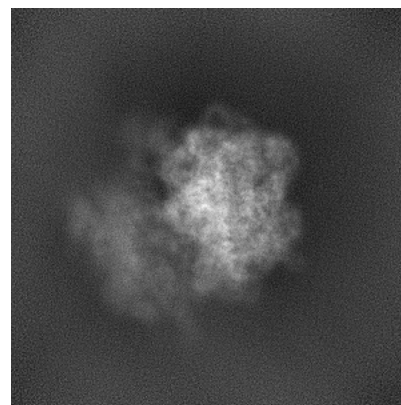
#### 6.1.2 Raw map



X



Y

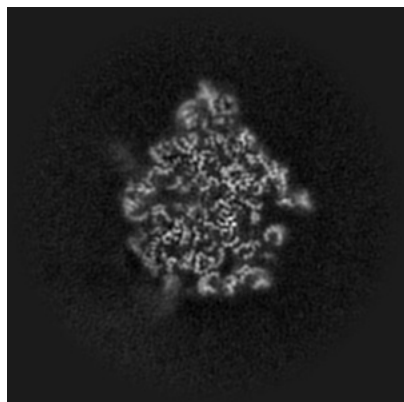


Z

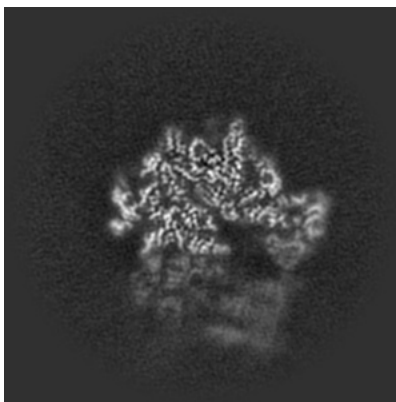
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

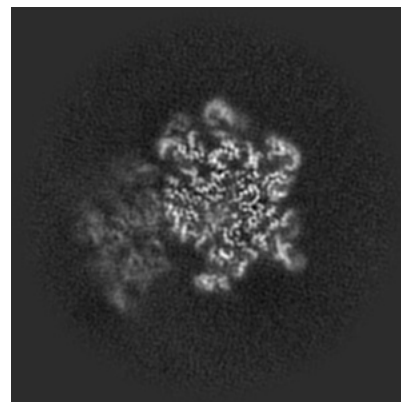
### 6.2.1 Primary map



X Index: 250

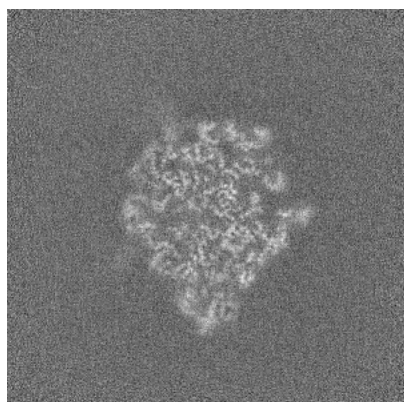


Y Index: 250

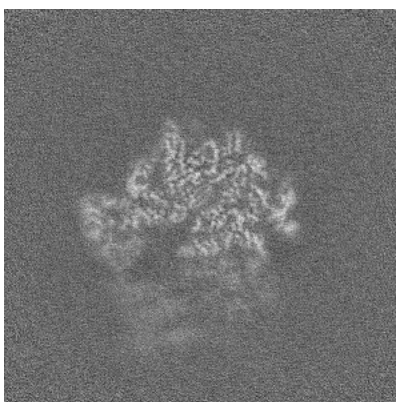


Z Index: 250

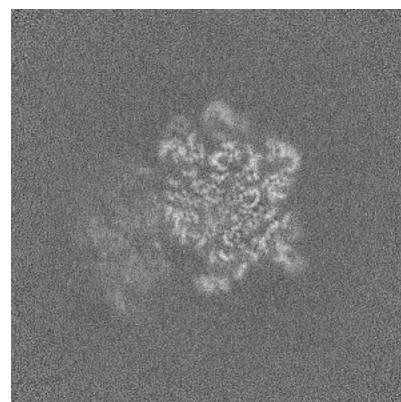
### 6.2.2 Raw map



X Index: 250



Y Index: 250

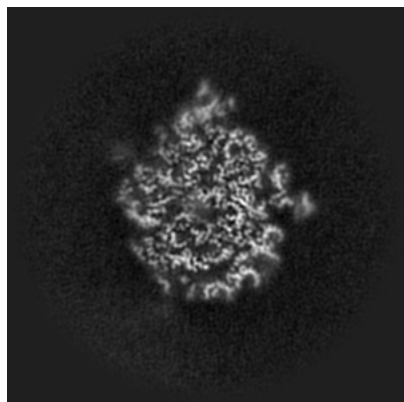


Z Index: 250

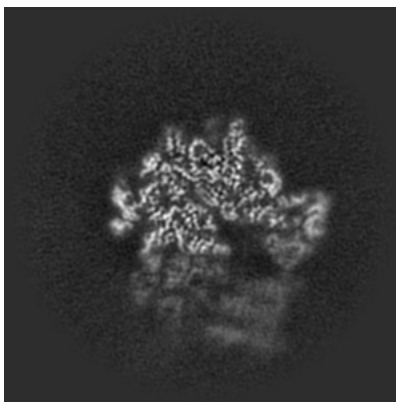
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

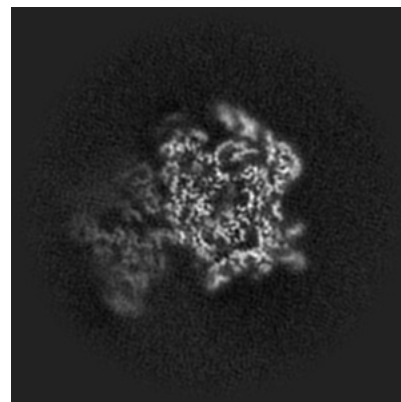
### 6.3.1 Primary map



X Index: 259

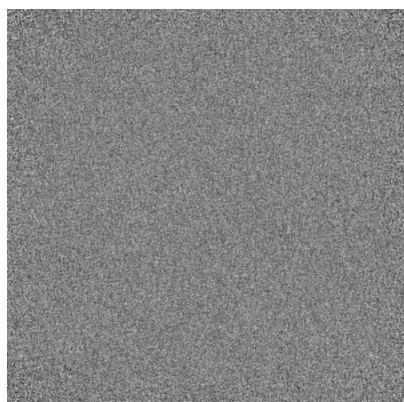


Y Index: 249

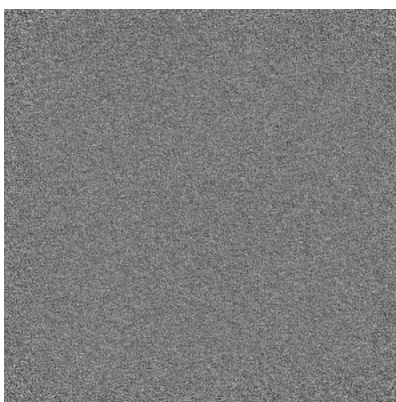


Z Index: 239

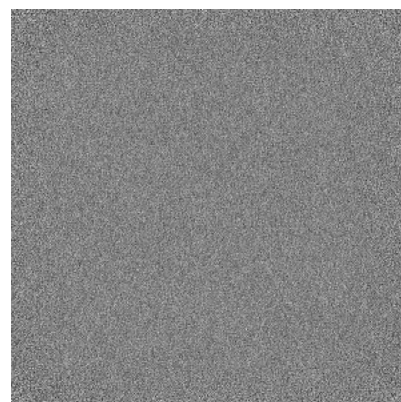
### 6.3.2 Raw map



X Index: 0



Y Index: 0

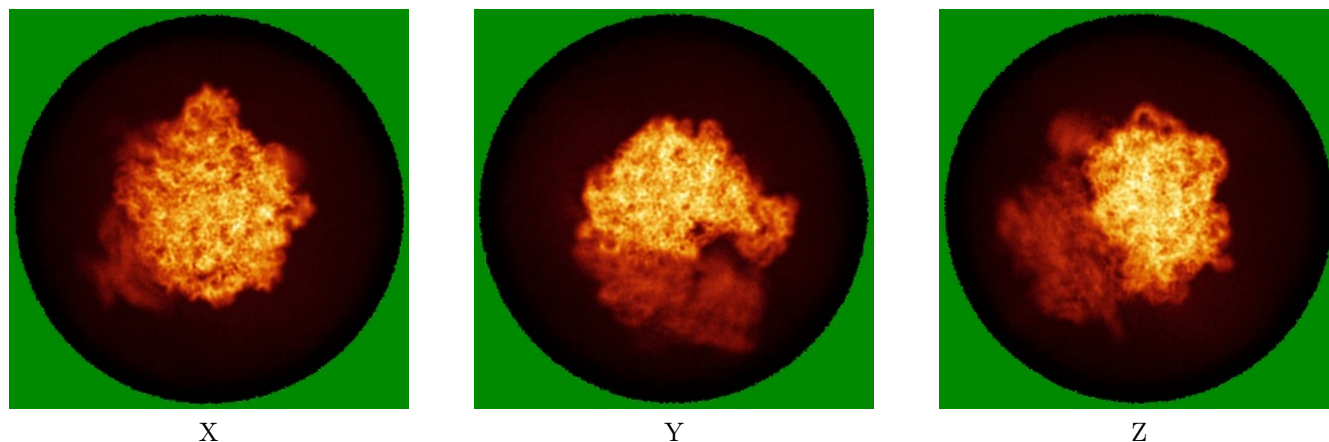


Z Index: 0

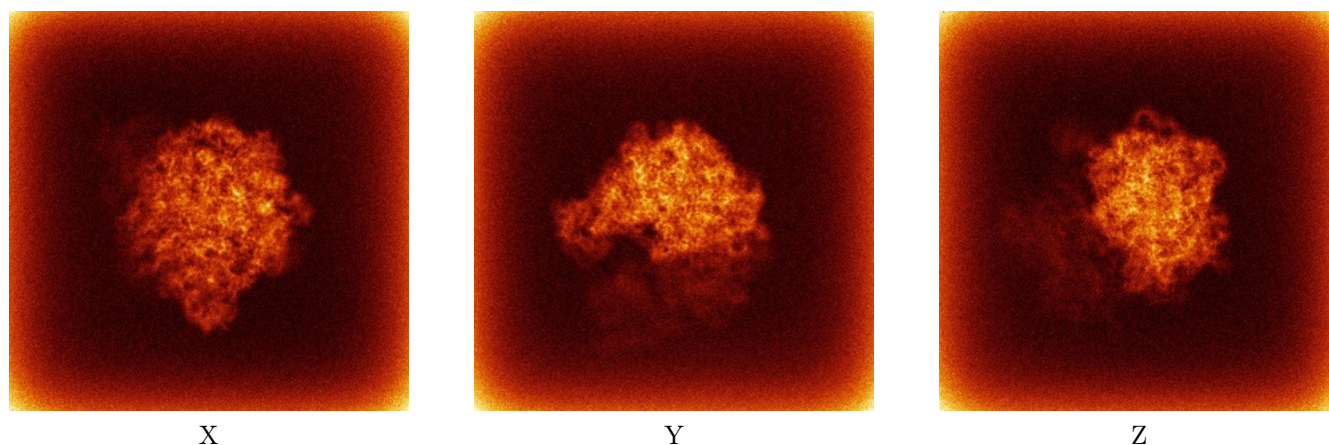
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



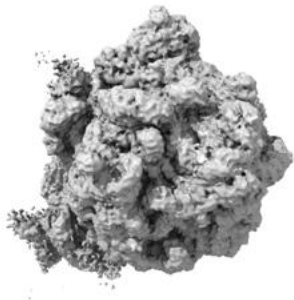
### 6.4.2 Raw map



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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



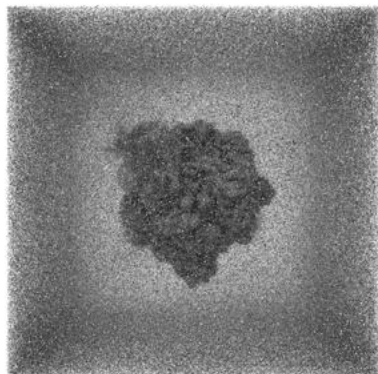
Y



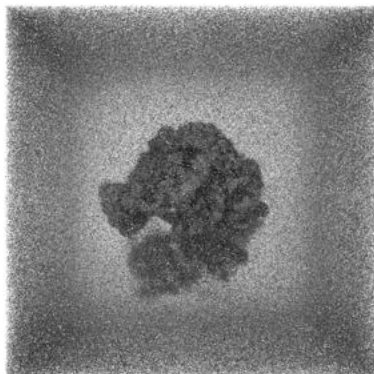
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

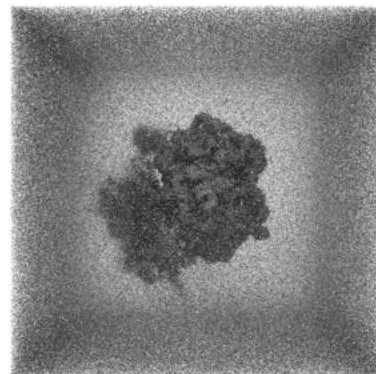
### 6.5.2 Raw map



X



Y



Z

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

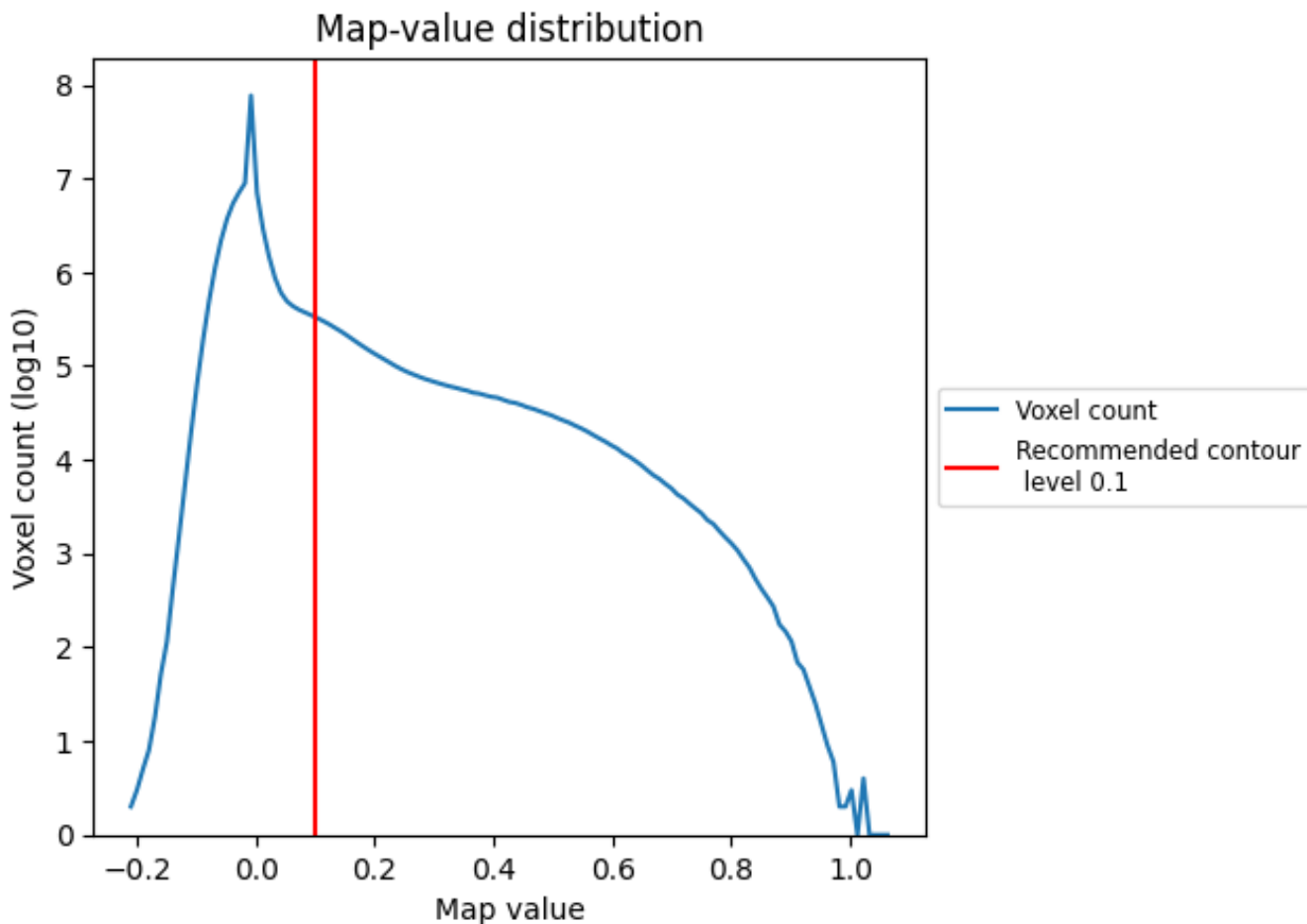
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

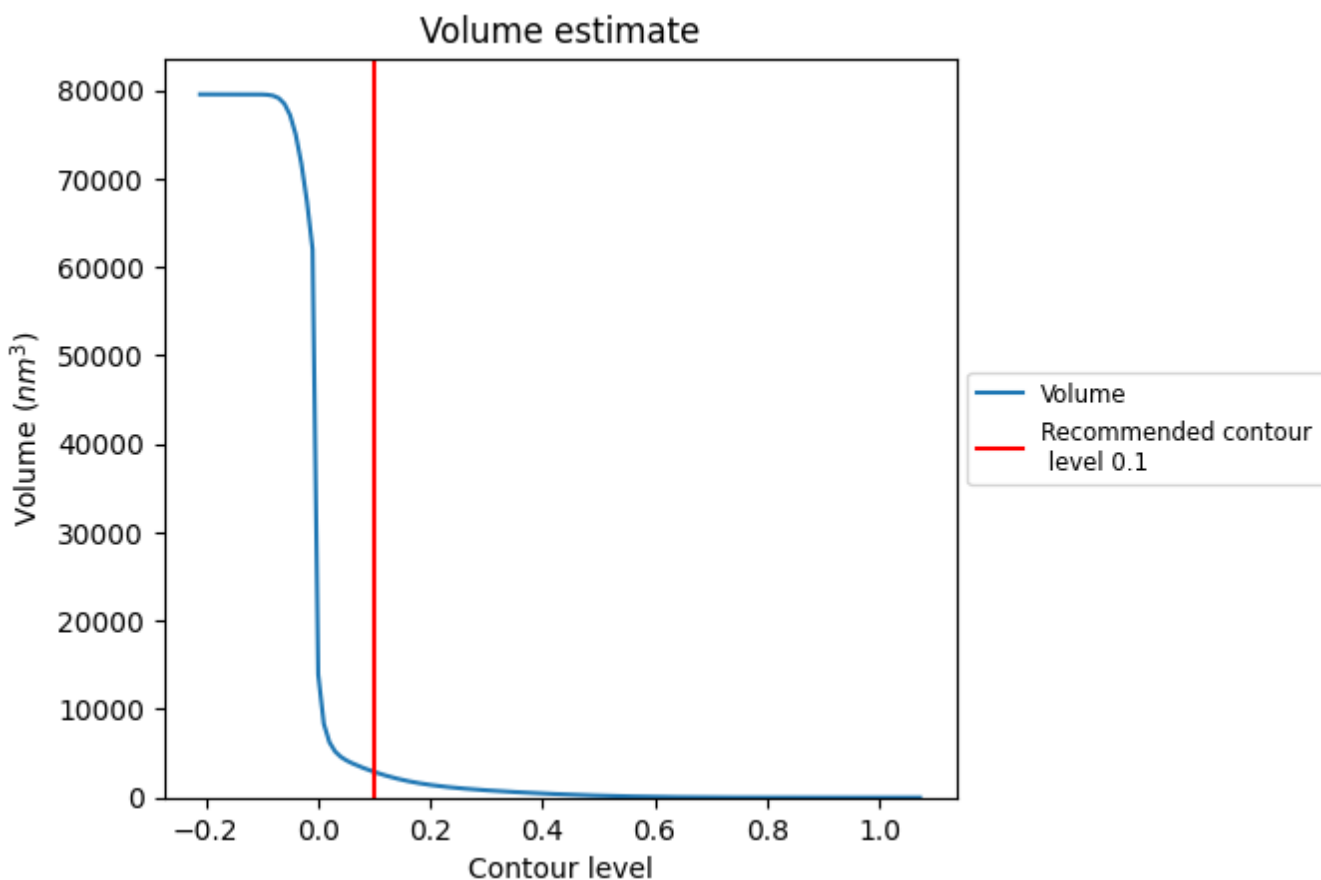
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

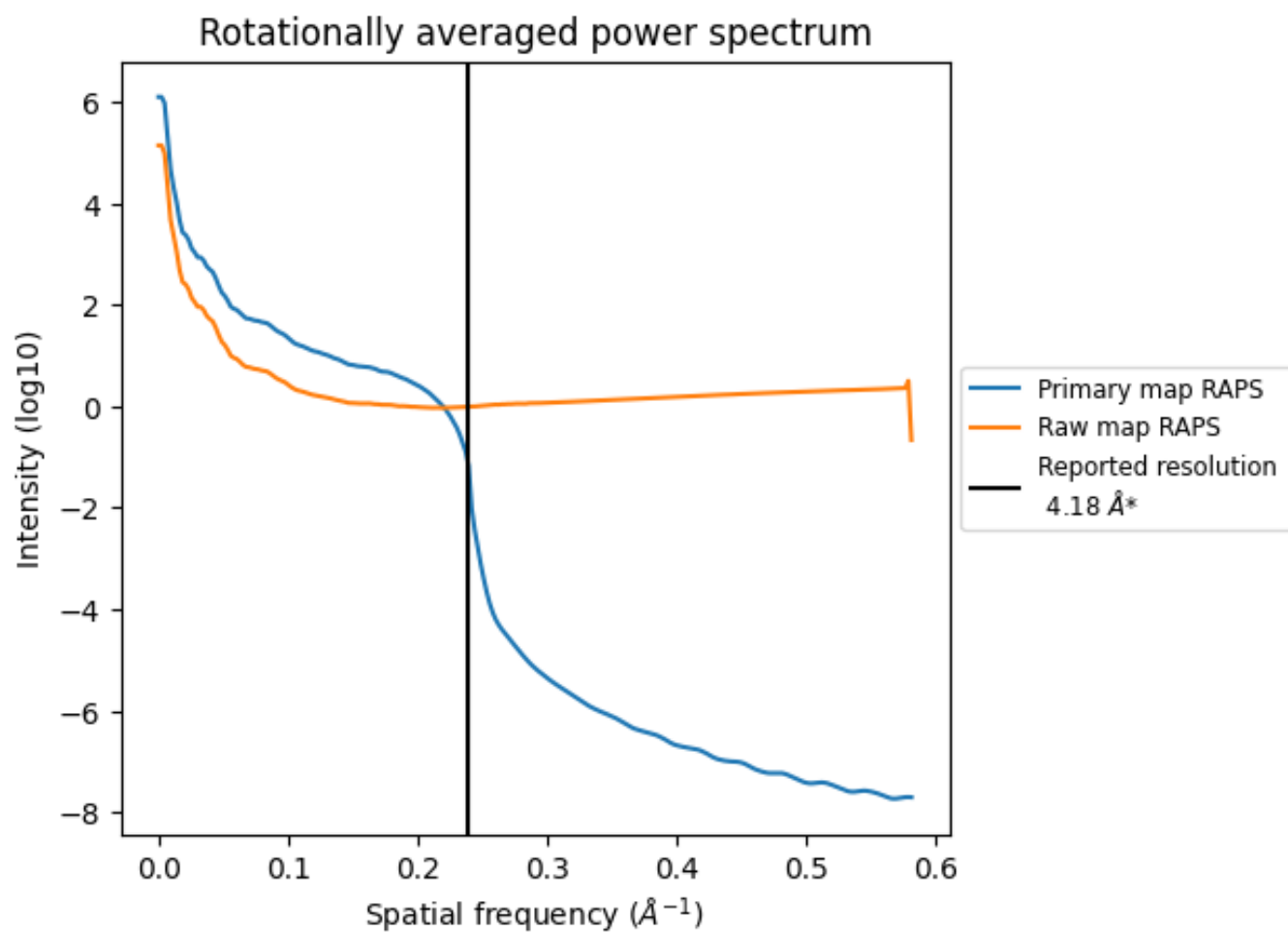
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2909 nm<sup>3</sup>; this corresponds to an approximate mass of 2628 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 i

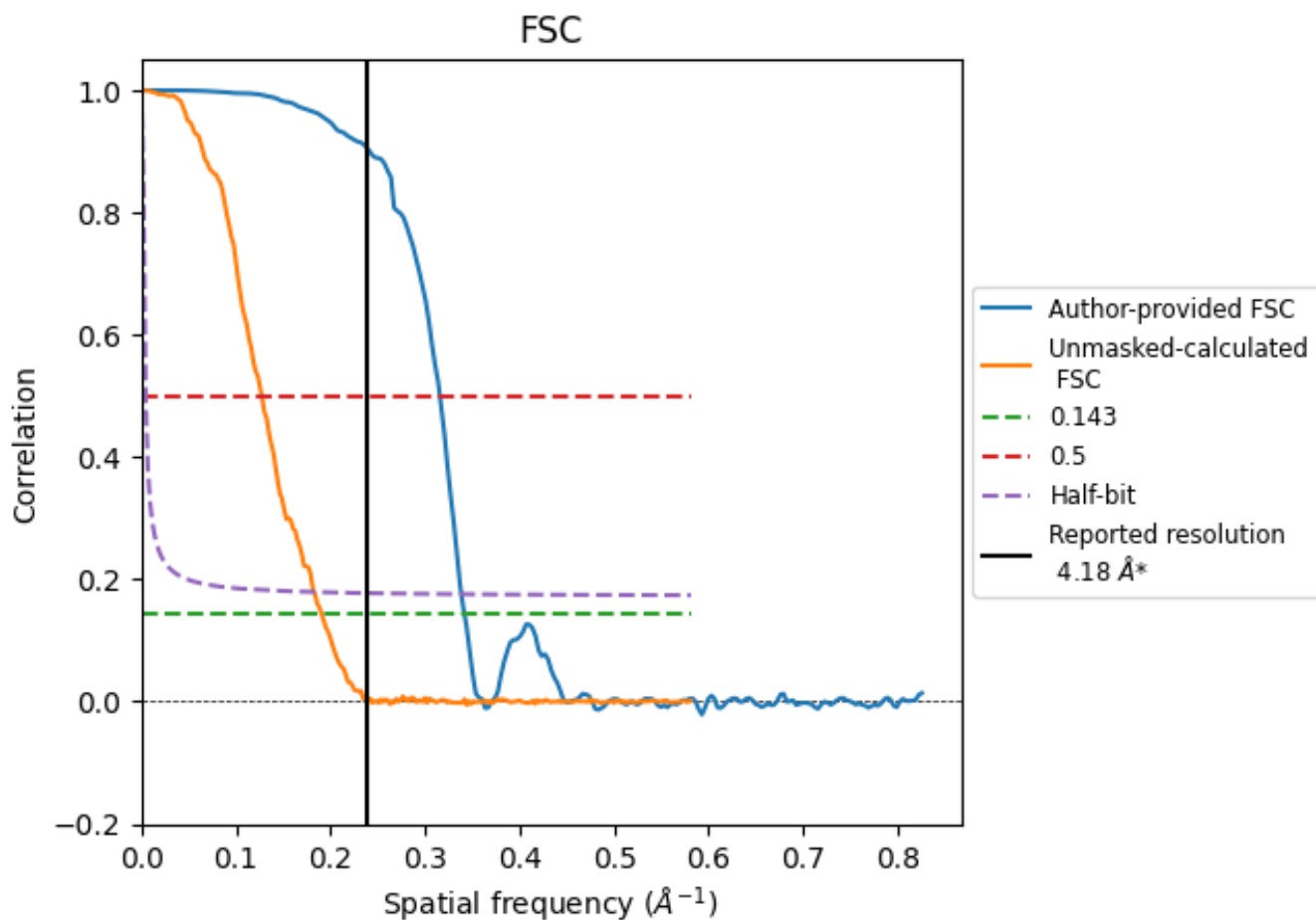


\*Reported resolution corresponds to spatial frequency of 0.239 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.239 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.18	-	-
Author-provided FSC curve	2.93	3.17	2.96
Unmasked-calculated*	5.24	7.85	5.47

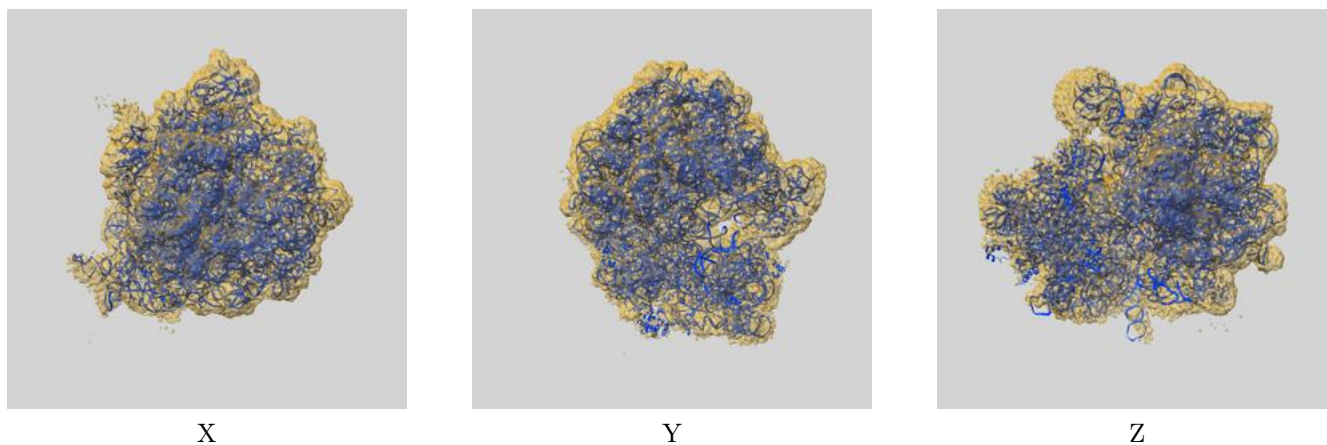
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.93 differs from the reported value 4.18 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.24 differs from the reported value 4.18 by more than 10 %

## 9 Map-model fit [i](#)

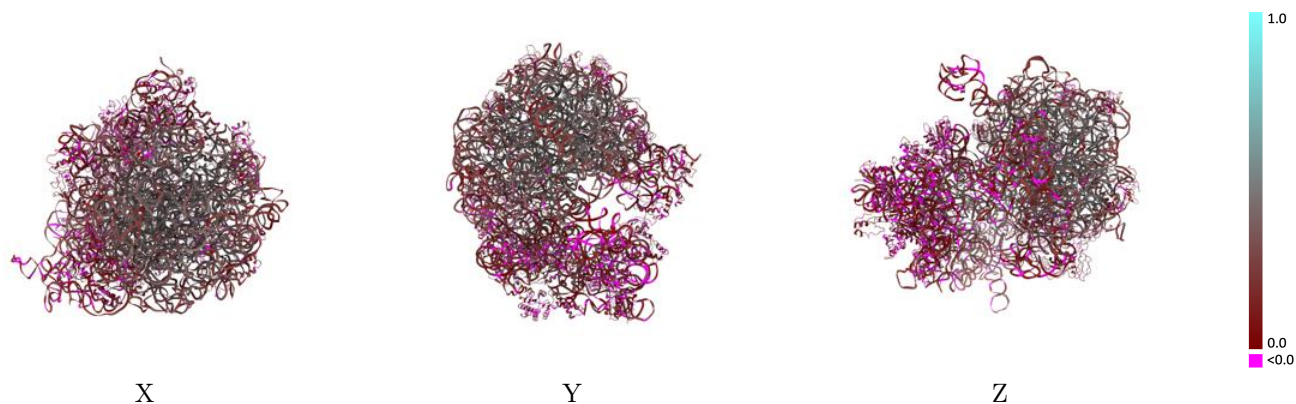
This section contains information regarding the fit between EMDB map EMD-26666 and PDB model 7UPH. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay [i](#)



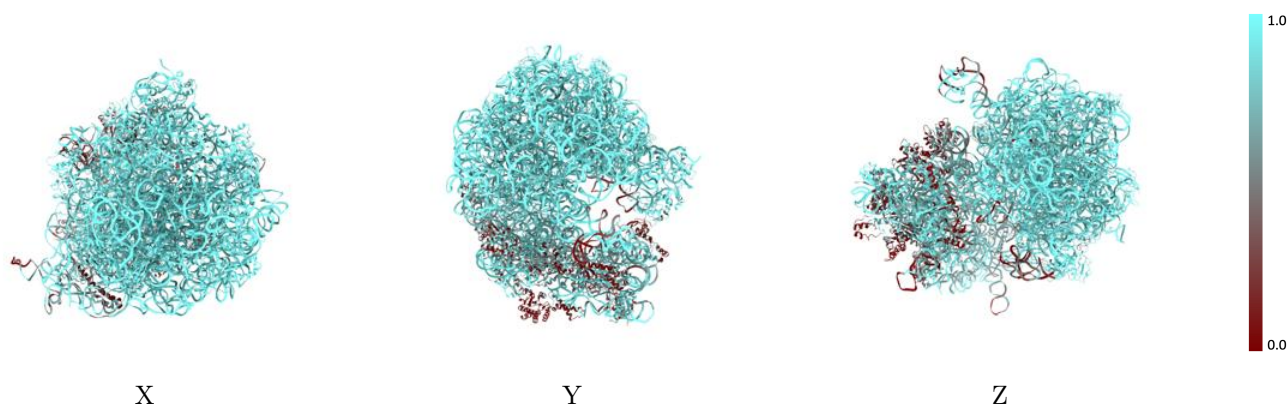
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



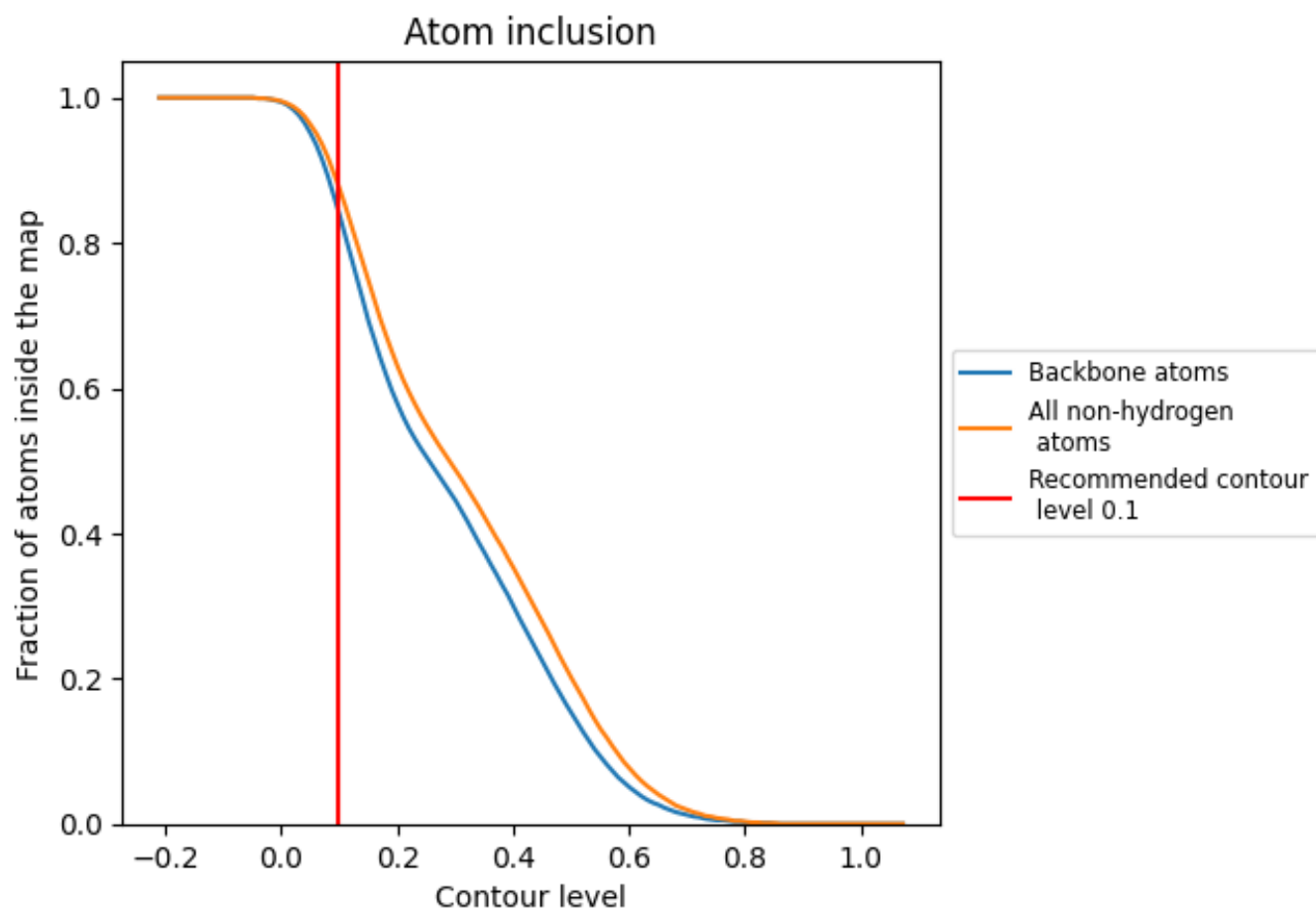
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 88% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.2400
A	 0.7610	 0.0710
B	 0.4930	 0.1220
C	 0.7030	 0.1010
D	 0.4990	 0.1100
E	 0.5420	 0.1030
F	 0.2240	 0.0820
G	 0.2720	 0.0490
H	 0.2070	 0.0660
I	 0.9290	 0.2690
J	 0.9840	 0.1870
K	 0.9670	 0.2620
L	 0.9720	 0.2320
M	 0.9860	 0.2770
N	 0.9030	 0.1100
O	 0.9240	 0.1440
R	 0.9800	 0.2660
S	 0.9100	 0.1770
T	 0.9770	 0.2820
U	 0.9750	 0.2430
V	 0.9650	 0.2620
W	 0.1530	 0.0940
X	 0.4000	 0.0950
Y	 0.4910	 0.0880
Z	 0.7220	 0.1790
a	 0.3730	 0.1020
b	 0.3680	 0.1200
c	 0.6360	 0.1640
d	 0.7370	 0.0920
e	 0.4960	 0.1210
f	 0.4700	 0.0950
g	 0.7480	 0.2300
h	 0.5410	 0.1190
i	 0.9860	 0.3590
j	 0.8650	 0.1050



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Chain	Atom inclusion	Q-score
k	 0.9920	 0.4020
l	 0.9880	 0.3730
m	 0.9110	 0.1150
n	 0.9290	 0.1460
o	 0.8480	 0.1160
p	 0.9780	 0.2860
q	 0.9770	 0.2520
r	 0.9900	 0.3640
s	 0.9500	 0.2180
t	 0.9600	 0.1780
u	 0.9380	 0.1380
v	 0.9300	 0.1640
w	 0.9770	 0.2910
x	 0.9960	 0.2010
y	 0.9950	 0.2680