



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:13 PM UTC

PDB ID : 6R86 / pdb_00006r86
EMDB ID : EMD-4752
Title : Yeast Vms1-60S ribosomal subunit complex (post-state)
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;
Neupert, W.; Beckmann, R.
Deposited on : 2019-03-31
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:

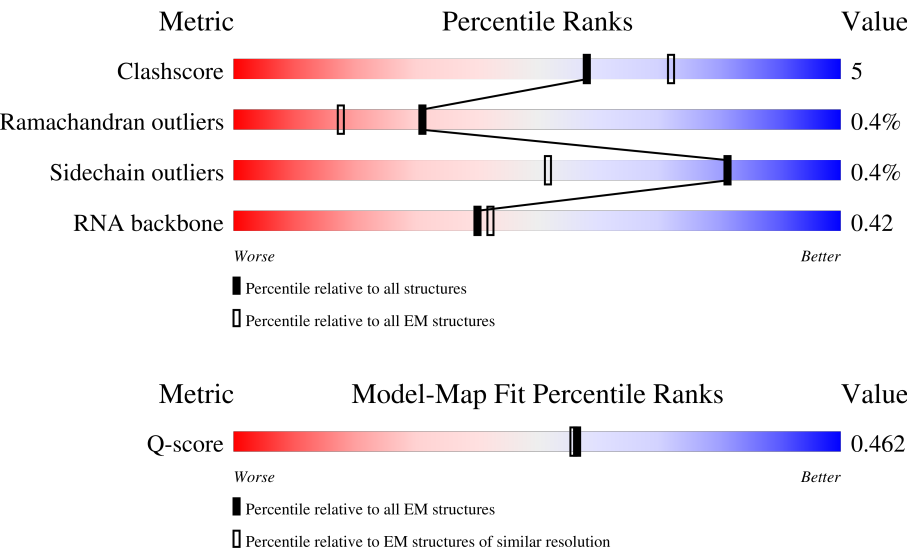
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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.



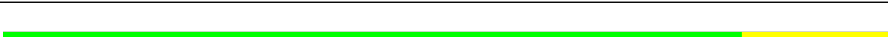
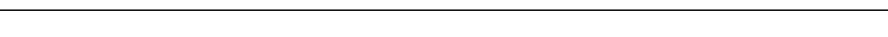
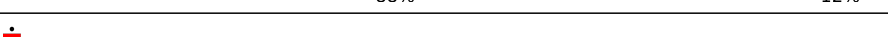
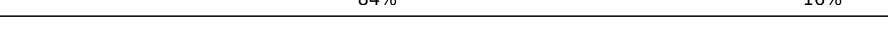
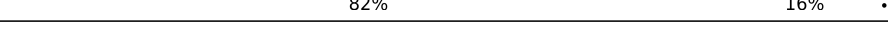
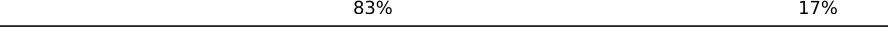
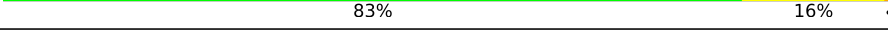
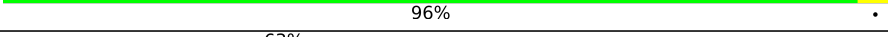
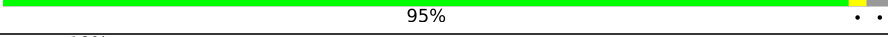
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	R	475	
2	X	224	
3	i	112	

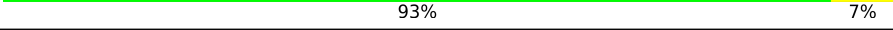
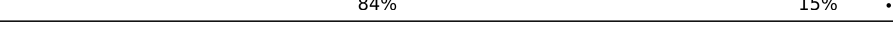
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Mol	Chain	Length	Quality of chain
4	J	222	
5	j	119	
6	K	233	
7	k	99	
8	7	191	
9	l	87	
10	M	169	
11	m	77	
12	N	193	
13	n	50	
14	O	136	
15	o	52	
16	p	203	
17	Q	197	
18	5	183	
19	S	185	
20	s	220	
21	T	152	
22	U	172	
23	V	159	
24	W	100	
25	P	155	
26	r	197	
27	x	136	
28	3	121	

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Mol	Chain	Length	Quality of chain
29	Y	62	
30	4	158	
31	Z	121	
32	a	126	
33	b	135	
34	C	105	
35	c	148	
36	D	91	
37	d	58	
38	E	252	
39	e	97	
40	F	386	
41	f	109	
42	G	361	
43	g	127	
44	H	296	
45	h	106	
46	I	175	
47	L	204	
48	1	3260	

2 Entry composition [i](#)

There are 49 unique types of molecules in this entry. The entry contains 132446 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	356	Total	C	N	O	S	Se	0	0
			2784	1776	495	500	12	1		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 3 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 5 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 6 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 7 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 10 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 13 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	P	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 26 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 28 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 29 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 34 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 36 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	D	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 37 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 38 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 39 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 43 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 44 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 45 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 46 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	I	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 47 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 48 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	3260	Total	C	N	O	P	0	0
			69730	31146	12569	22755	3260		

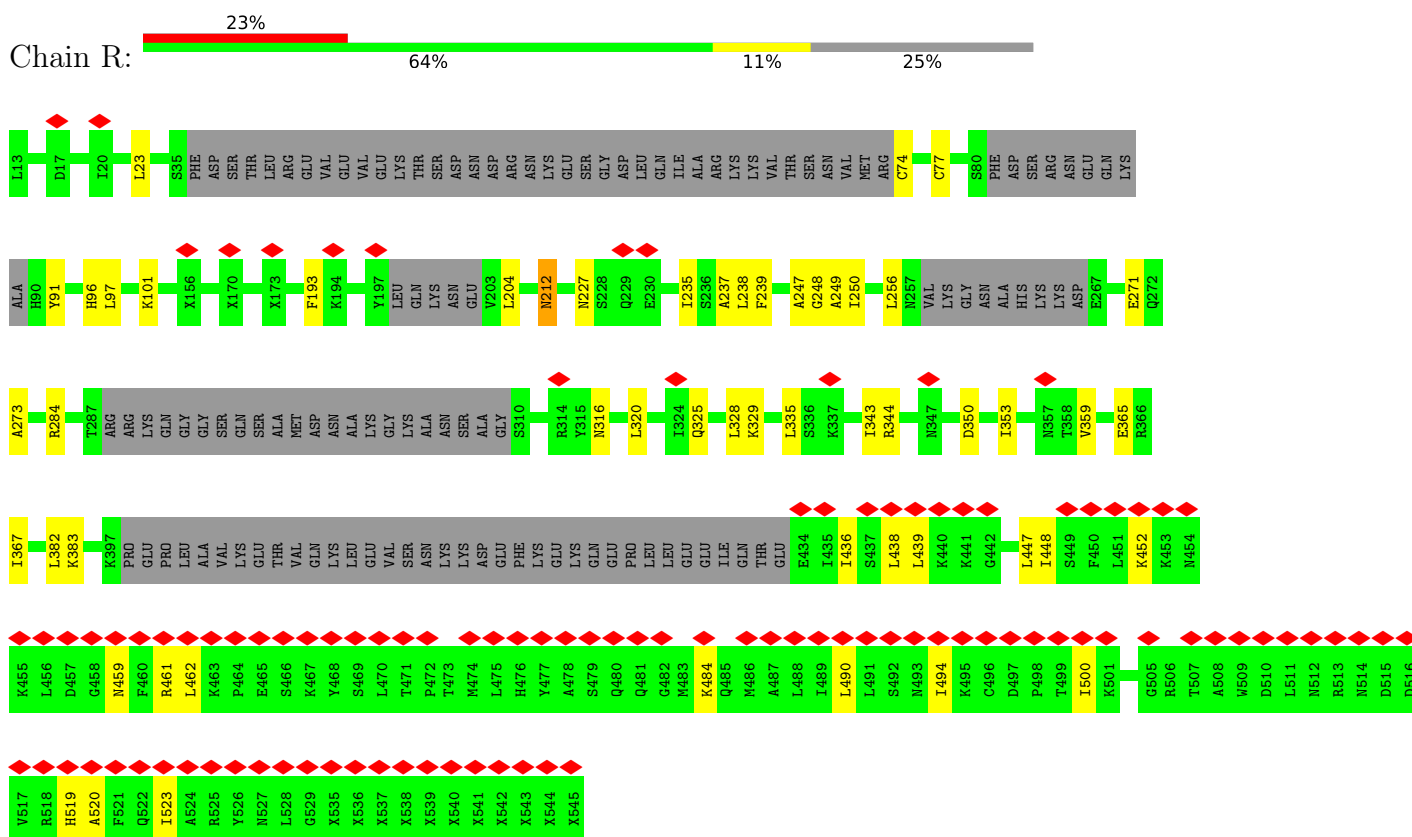
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	R	1	Total 1	Zn 1	0

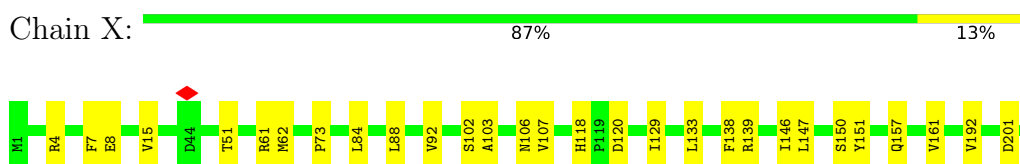
3 Residue-property plots

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.

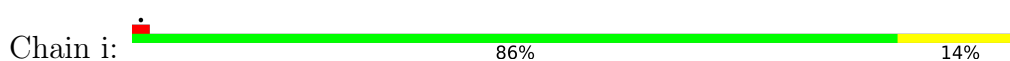
- Molecule 1: Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1



- Molecule 2: Eukaryotic translation initiation factor 6

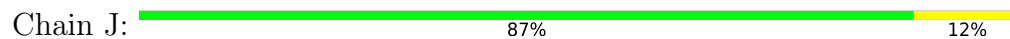


- Molecule 3: 60S ribosomal protein L34-A

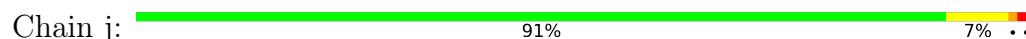




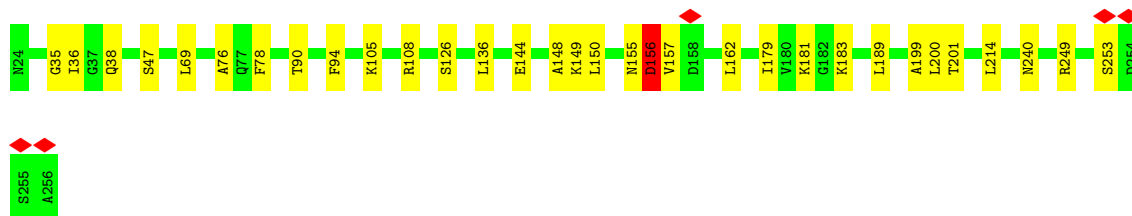
- Molecule 4: 60S ribosomal protein L7-A



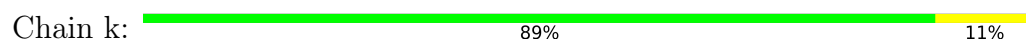
- Molecule 5: 60S ribosomal protein L35-A



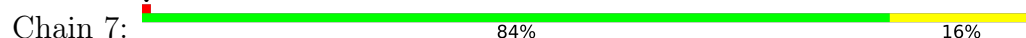
- Molecule 6: 60S ribosomal protein L8-A



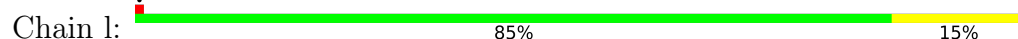
- Molecule 7: 60S ribosomal protein L36-A



- Molecule 8: 60S ribosomal protein L9-A

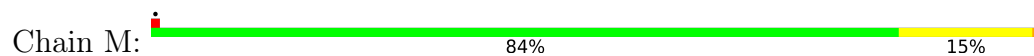


- Molecule 9: 60S ribosomal protein L37-A

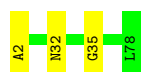




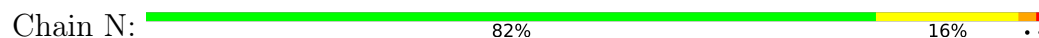
- Molecule 10: 60S ribosomal protein L11-B



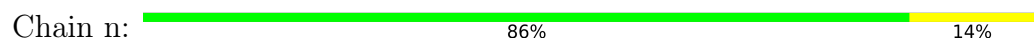
- Molecule 11: 60S ribosomal protein L38



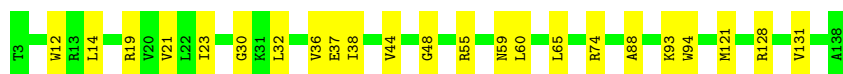
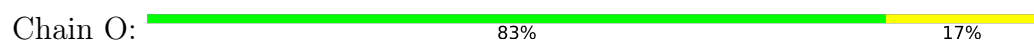
- Molecule 12: 60S ribosomal protein L13-A



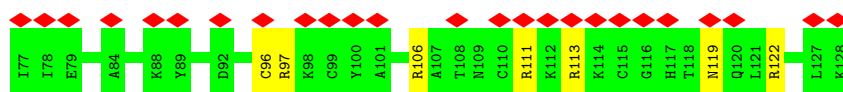
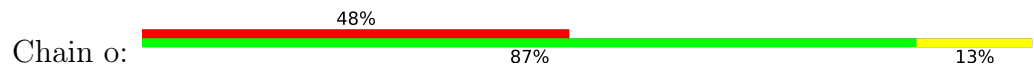
- Molecule 13: 60S ribosomal protein L39



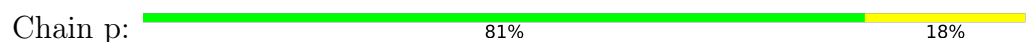
- Molecule 14: 60S ribosomal protein L14-A



- Molecule 15: Ubiquitin-60S ribosomal protein L40



- Molecule 16: 60S ribosomal protein L15-A





- Molecule 17: 60S ribosomal protein L16-A

Chain Q: 88% 12% .



- Molecule 18: 60S ribosomal protein L17-A

Chain 5: 84% 16% .



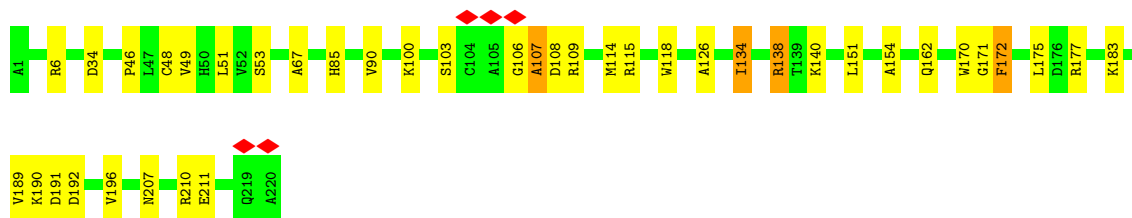
- Molecule 19: 60S ribosomal protein L18-A

Chain S: 87% 13%



- Molecule 20: 60S ribosomal protein L10

Chain s: 82% 16% .



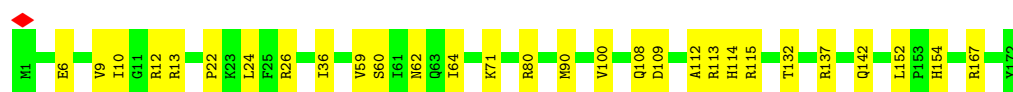
- Molecule 21: 60S ribosomal protein L19-A

Chain T: 89% 11%



- Molecule 22: 60S ribosomal protein L20-A

Chain U: 83% 17%



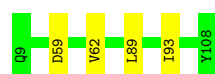
- Molecule 23: 60S ribosomal protein L21-A

Chain V: 83% 16%



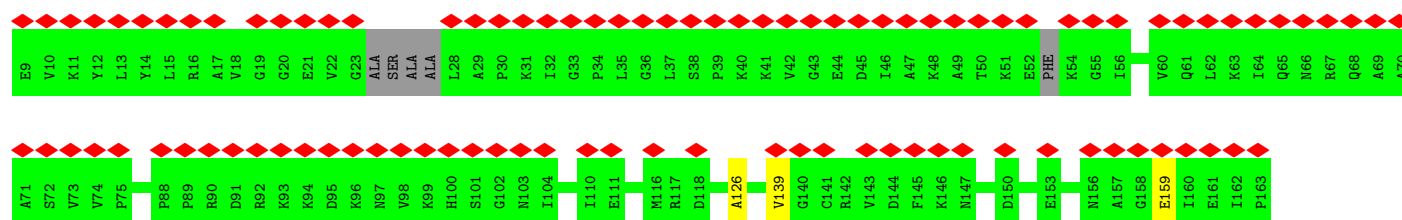
- Molecule 24: 60S ribosomal protein L22-A

Chain W: 96%



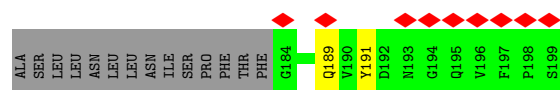
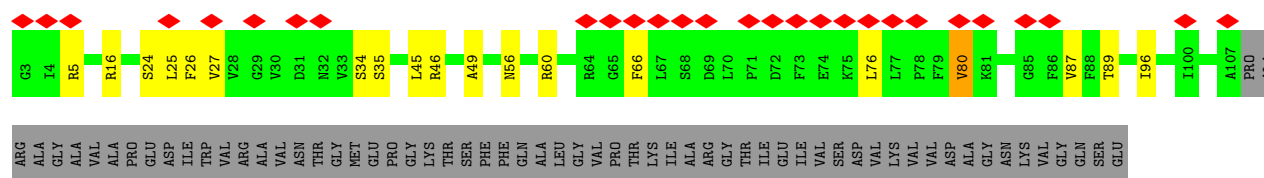
- Molecule 25: 60S ribosomal protein L12-A

Chain P: 63% 95%



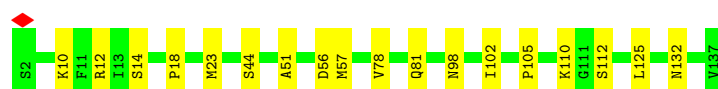
- Molecule 26: 60S acidic ribosomal protein P0

Chain r: 19% 51% 10% 39%

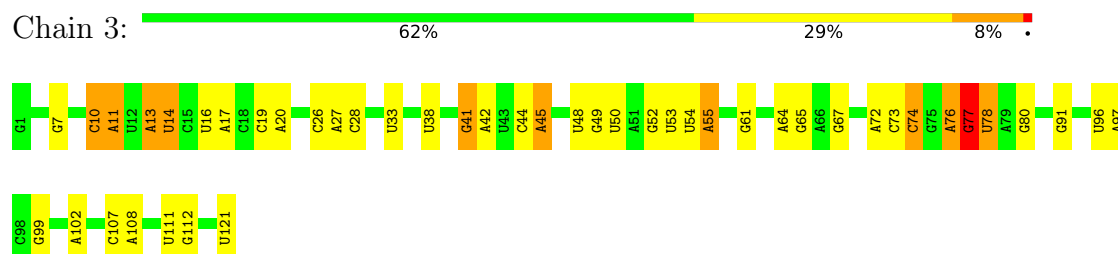


- Molecule 27: 60S ribosomal protein L23-A

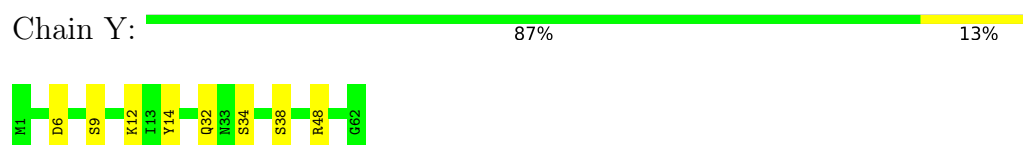
Chain x: 87% 13%



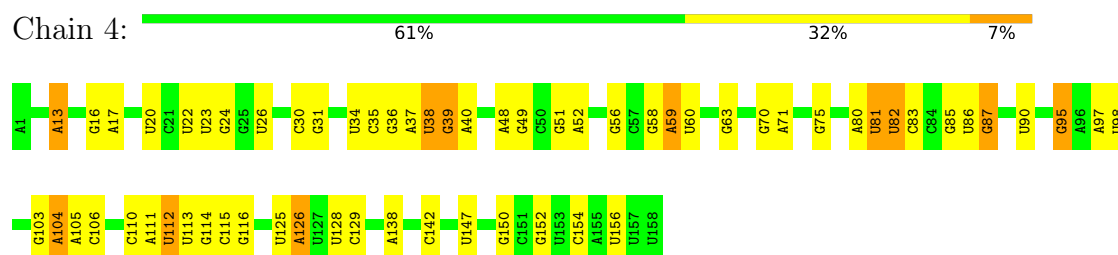
- Molecule 28: 5S ribosomal RNA



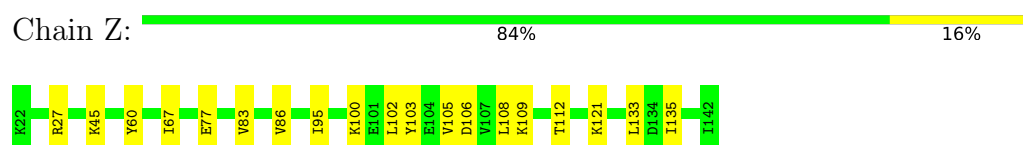
- Molecule 29: 60S ribosomal protein L24-A



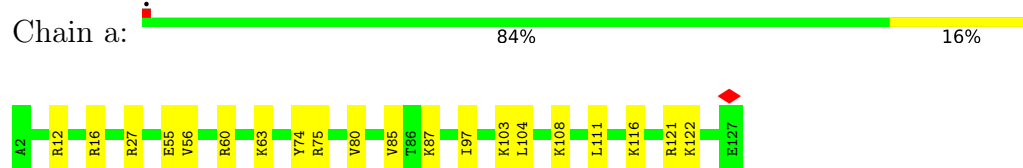
- Molecule 30: 5.8S ribosomal RNA



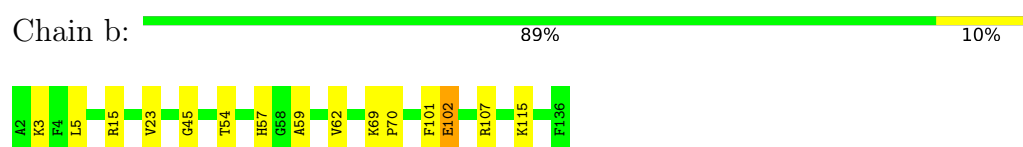
- Molecule 31: 60S ribosomal protein L25



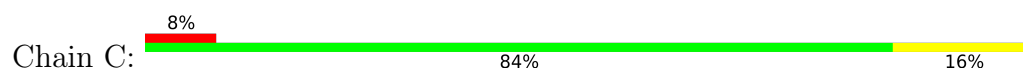
- Molecule 32: 60S ribosomal protein L26-A



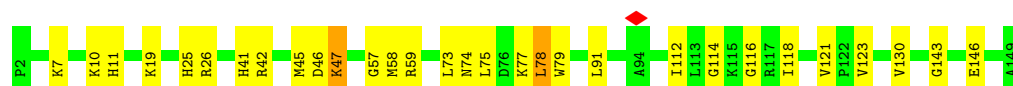
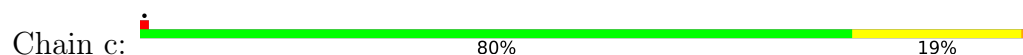
- Molecule 33: 60S ribosomal protein L27-A



- Molecule 34: 60S ribosomal protein L42-A



- Molecule 35: 60S ribosomal protein L28



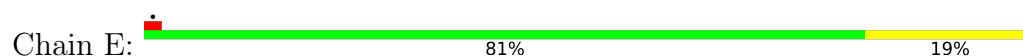
- Molecule 36: 60S ribosomal protein L43-A



- Molecule 37: 60S ribosomal protein L29



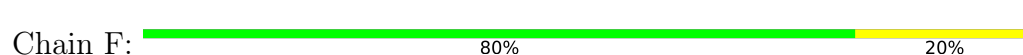
- Molecule 38: 60S ribosomal protein L2-A

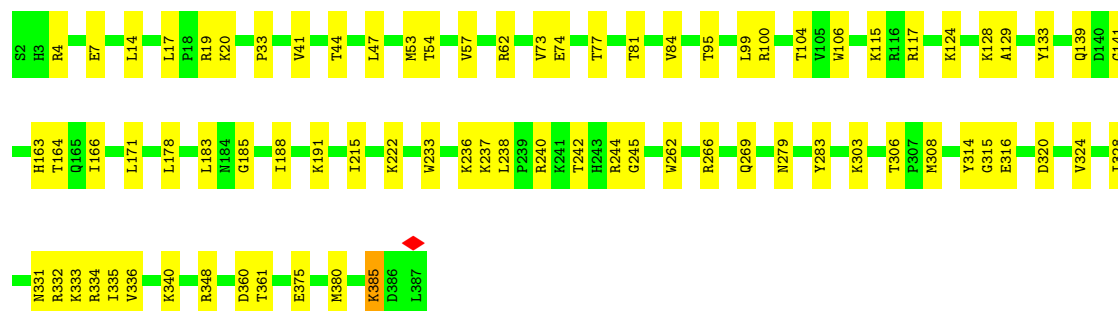


- Molecule 39: 60S ribosomal protein L30

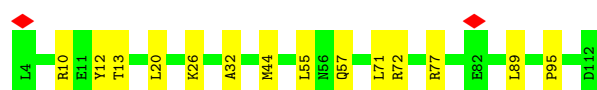
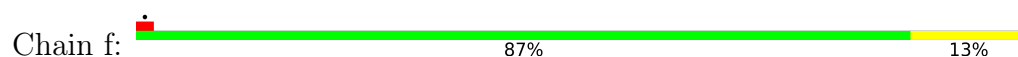


- Molecule 40: 60S ribosomal protein L3

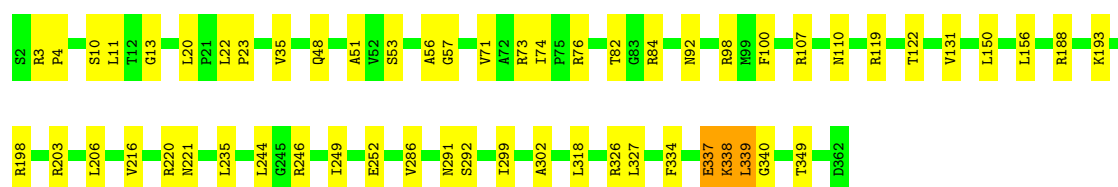
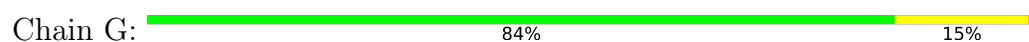




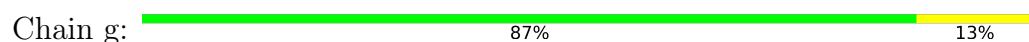
- Molecule 41: 60S ribosomal protein L31-A



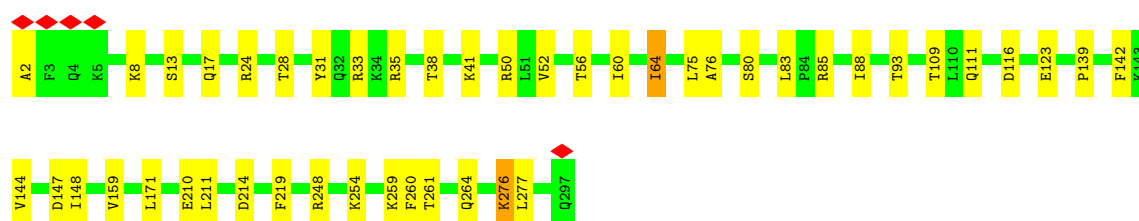
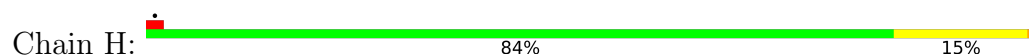
- Molecule 42: 60S ribosomal protein L4-A



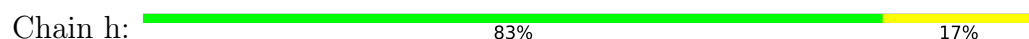
- Molecule 43: 60S ribosomal protein L32

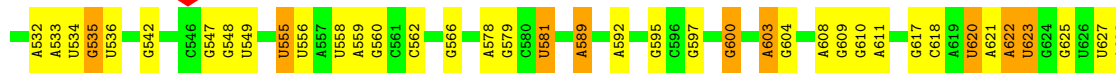


- Molecule 44: 60S ribosomal protein L5



- Molecule 45: 60S ribosomal protein L33-A





A1900	C1793	U1672	C1574	G1487	G1389	G1285	U1211	G1126	G1029	A933	G842	G728	C636
A1901	G1794	G1675	A1575	G1488	A1390	A1286	A1212	G1127	U1032	G937	A843	G737	C637
G1905	U1795	A1676	G1577	A1489	G1392	A1287	G1213	U1128	U1033	C938	U850	A738	C638
G1906	G1796	G1677	C1578	A1490	A1393	C1292	C1219	A1129	G1034	C944	C849	G742	G639
C1907	A1797	A1683	A1580	G1493	A1394	U1293	A1221	G1130	A1035	C949	C851	C743	C641
A1913	G1812	U1687	C1581	U1494	A1399	A1301	G1222	G1134	C1037	C953	C857	C744	A645
G1914	A1813	U1687	C1582	U1495	G1400	A1302	A1223	U1139	U1038	G953	A858	A744	A646
A1915	A1814	U1695	A1583	C1497	A1401	A1303	C1224	U1138	A1039	C959	G859	C753	A647
U1920	A1815	A1696	G1404	A1498	G1404	U1305	G1226	G1139	A1040	C961	G860	C758	C648
G1927	G1817	U1712	A1587	A1503	U1410	G1307	G1230	G1140	U1044	U960	C861	U759	A649
G1928	U1818	G1713	A1588	C1508	G1417	A1308	A1231	A1143	C1045	A962	U865	G760	A655
G1929	U1819	A1714	G1590	C1508	A1418	A1314	C1232	U1144	A1046	G964	G869	G763	A656
A1930	U1820	A1594	A1593	U1511	A1419	G1315	U1235	G1145	A1048	G971	G870	G764	G661
U1931	C1822	U1716	A1595	U1512	C1420	U1316	G1236	A1150	C1049	A972	U871	C765	U664
A1932	G1830	U1717	C1596	U1523	G1421	A1317	G1237	U1151	A1062	A973	U872	C766	A665
G1935	U1831	G1718	C1597	G1523	U1422	U1322	U1241	U1152	A1063	G978	C873	U767	A666
U1938	G1838	U1722	A1605	C1527	A1432	U1329	G1242	A1155	A1064	U979	U879	G770	G674
G1939	A1839	A1723	U1606	G1528	A1433	A1330	U1243	A1156	A1065	U980	C880	U776	C675
C1943	U1840	C1725	A1613	U1533	G1434	U1331	A1244	A1157	A1066	U981	C881	U777	G676
G1953	A1842	U1729	C1615	A1534	A1435	U1336	G1245	A1158	U1071	U982	U882	U777	G677
G1954	C1844	G1730	G1618	G1536	A1436	U1337	U1247	A1159	A1072	U985	U883	G781	G678
U1955	G1845	U1732	A1619	G1543	G1437	A1338	A1248	A1169	A1075	U989	U884	U782	U679
A1956	C1846	G1733	U1620	A1546	A1438	U1339	G1249	G1177	C1076	U990	U885	U783	G680
U1957	A1847	G1733	A1621	G1547	G1439	A1340	G1250	G1178	U1081	G991	C893	U784	U681
G1958	G1848	U1740	U1622	C1548	A1440	U1349	A1251	A1179	U1082	G994	U894	G785	U682
G1959	C1849	A1741	G1623	U1549	G1450	A1351	A1252	A1181	G1083	U995	U895	U786	G683
A1960	G1851	U1742	U1628	C1550	U1455	A1352	C1254	A1182	U1088	A996	G900	G789	G684
G1961	U1852	A1749	U1629	G1551	A1456	U1353	C1255	G1183	U1089	U999	A906	G800	U687
A1962	G1861	A1750	U1630	U1552	G1460	A1355	G1256	A1184	G1090	C1000	G907	A801	A690
G1963	U1862	C1755	C1631	U1553	A1461	U1356	C1257	A1190	A1091	G1001	G908	C804	A691
C1964	A1863	U1763	C1632	U1554	A1462	G1357	U1258	U1191	C1092	G805	G909	G805	A692
C1965	A1864	A1760	G1634	U1555	U1463	A1358	A1259	C1192	U1093	G1005	G910	A806	C896
U1966	G1865	C1761	U1641	A1556	G1464	A1363	A1260	A1193	A1094	A1006	C911	A807	A699
U1967	A1866	C1762	A1642	U1558	A1467	C1364	G1261	G1194	U1095	G1010	G912	A808	
G1968	U1867	U1763	A1642	A1559	A1468	G1365	G1262	A1195	U1096	U1015	A913	U814	A705
G1969	A1868	U1765	U1645	G1560	A1469	A1366	G1263	C1196	G1097	C1016	A914	U814	
U1970	U1871	G1766	G1646	G1561	C1469	G1367	G1264	A1197	A1098	C1017	G916	A817	G708
C1971	A1874	U1769	A1656	C1562	A1474	U1368	G1265	G1198	U1102	C1017	A917	C824	A709
A1972	G1878	G1770	C1657	U1564	A1477	G1374	U1267	A1200	A1103	G1018	A920	U825	A710
G1973	U1879	C1771	G1657	G1565	G1480	A1380	A1270	C1201	G1104	G1019	C923	A830	A711
A1974	U1880	G1775	G1661	U1566	A1481	A1381	A1271	A1202	U1110	G1020	G924	G831	G712
C1975	A1886	U1780	G1662	U1568	A1482	G1382	C1277	A1203	G1115	G1021	A925	G832	G713
G1976	U1887	G1786	G1666	U1569	G1483	C1385	C1278	G1206	G1116	G1024	A929	G833	G714
C1977	A1888	U1786	A1667	U1570	U1484	A1386	C1279	G1207	G1117	G1025	A836	U837	A715
A1978	U1893	G1787	G1668	U1571	U1485	G1387	G1281	U1208	U1122	A1026	U932	G837	A716
G1979	U1894			U1572	G1486	U1388	G1282	U1210		A1027			U719
C1980				G1573						U1028			A720
U2043													
U2044													
G2045													



A3375	
A3376	
G3377	
C3378	
C3379	
U3382	
G3383	
G3386	
G3390	
U3393	
U3396	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	115812	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.812	Depositor
Minimum map value	-0.588	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	R	0.21	0/2631	0.56	0/3532
2	X	0.24	0/1653	0.62	4/2255 (0.2%)
3	i	0.39	0/890	0.76	1/1189 (0.1%)
4	J	0.41	0/1821	0.72	0/2451
5	j	0.32	0/978	0.84	8/1301 (0.6%)
6	K	0.33	0/1836	0.77	4/2481 (0.2%)
7	k	0.35	0/778	0.75	0/1034
8	7	0.28	0/1539	0.62	0/2073
9	l	0.44	0/696	0.79	0/923
10	M	0.26	0/1374	0.72	0/1842
11	m	0.32	0/618	0.64	0/826
12	N	0.42	0/1568	0.84	2/2106 (0.1%)
13	n	0.44	0/443	0.73	0/588
14	O	0.31	0/1068	0.67	0/1438
15	o	0.25	0/423	0.68	0/562
16	p	0.46	0/1757	0.85	3/2354 (0.1%)
17	Q	0.38	0/1585	0.72	0/2128
18	5	0.38	0/1443	0.74	2/1944 (0.1%)
19	S	0.36	0/1465	0.78	1/1965 (0.1%)
20	s	0.32	0/1807	0.80	6/2425 (0.2%)
21	T	0.34	0/1245	0.73	0/1661
22	U	0.37	0/1481	0.74	0/1990
23	V	0.37	0/1300	0.70	2/1743 (0.1%)
24	W	0.27	0/812	0.68	0/1099
25	P	0.25	0/734	0.85	1/1015 (0.1%)
26	r	0.21	0/982	0.65	1/1320 (0.1%)
27	x	0.40	0/1018	0.71	0/1369
28	3	0.29	0/2883	0.46	1/4491 (0.0%)
29	Y	0.32	0/525	0.64	0/696
30	4	0.35	0/3746	0.47	0/5832
31	Z	0.35	0/979	0.66	0/1321
32	a	0.32	0/1004	0.70	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.30	0/1118	0.68	2/1497 (0.1%)
34	C	0.32	0/860	0.74	0/1136
35	c	0.42	0/1204	0.82	1/1612 (0.1%)
36	D	0.39	0/701	0.74	0/934
37	d	0.32	0/473	0.64	0/629
38	E	0.46	0/1948	0.77	0/2617
39	e	0.26	0/751	0.61	0/1008
40	F	0.44	1/3146 (0.0%)	0.73	1/4228 (0.0%)
41	f	0.40	0/890	0.68	0/1196
42	G	0.38	0/2800	0.77	2/3790 (0.1%)
43	g	0.35	0/1041	0.67	1/1394 (0.1%)
44	H	0.31	0/2425	0.70	2/3271 (0.1%)
45	h	0.40	0/868	0.66	0/1168
46	I	0.27	0/1260	0.61	0/1694
47	L	0.25	0/1634	0.74	1/2195 (0.0%)
48	1	0.35	0/78052	0.53	17/121690 (0.0%)
All	All	0.35	1/142253 (0.0%)	0.60	63/209354 (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
2	X	0	1
4	J	0	2
5	j	0	2
6	K	0	3
7	k	0	1
8	7	0	1
10	M	0	1
11	m	0	2
12	N	0	3
14	O	0	1
20	s	0	4
33	b	0	1
35	c	0	3
36	D	0	1
37	d	0	1
38	E	0	1
40	F	0	1
42	G	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	H	0	1
All	All	0	34

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	F	237	LYS	C-N	-8.30	1.17	1.33

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	N	61	PRO	CA-C-N	7.76	136.36	121.54
12	N	61	PRO	C-N-CA	7.76	136.36	121.54
6	K	38	GLN	CA-C-N	6.80	131.44	121.31
6	K	38	GLN	C-N-CA	6.80	131.44	121.31
23	V	133	ALA	CA-C-N	6.78	130.98	120.60

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	J	157	ASN	Peptide
4	J	232	ARG	Peptide
2	X	8	GLU	Peptide
5	j	90	ARG	Peptide
5	j	91	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	R	2784	0	2683	38	0
2	X	1633	0	1596	16	0
3	i	880	0	945	10	0
4	J	1784	0	1862	20	0
5	j	969	0	1078	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	1804	0	1877	20	0
7	k	771	0	849	9	0
8	7	1518	0	1587	17	0
9	l	681	0	687	11	0
10	M	1353	0	1383	15	0
11	m	612	0	682	1	0
12	N	1543	0	1608	24	0
13	n	436	0	475	4	0
14	O	1053	0	1149	17	0
15	o	417	0	459	6	0
16	p	1720	0	1779	28	0
17	Q	1555	0	1659	16	0
18	5	1420	0	1437	18	0
19	S	1441	0	1543	21	0
20	s	1770	0	1808	21	0
21	T	1228	0	1314	14	0
22	U	1445	0	1487	21	0
23	V	1276	0	1323	21	0
24	W	796	0	812	2	0
25	P	737	0	341	1	0
26	r	967	0	991	15	0
27	x	1003	0	1048	13	0
28	3	2579	0	1304	23	0
29	Y	513	0	540	7	0
30	4	3353	0	1695	28	0
31	Z	964	0	1025	11	0
32	a	993	0	1081	12	0
33	b	1092	0	1155	8	0
34	C	847	0	918	12	0
35	c	1173	0	1215	20	0
36	D	694	0	738	8	0
37	d	462	0	491	2	0
38	E	1914	0	1981	35	0
39	e	743	0	797	6	0
40	F	3075	0	3142	56	0
41	f	876	0	912	9	0
42	G	2748	0	2859	37	0
43	g	1020	0	1090	12	0
44	H	2375	0	2325	33	0
45	h	850	0	880	11	0
46	I	1239	0	1326	8	0
47	L	1609	0	1701	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	1	69730	0	35041	530	0
49	R	1	0	0	0	0
All	All	132446	0	96678	1020	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 5.

The worst 5 of 1020 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)
48:1:3231:U:H3	48:1:3256:G:H1	1.13	0.96
48:1:196:G:H21	48:1:219:A:H61	1.08	0.96
48:1:3160:U:H3	48:1:3290:G:H1	1.14	0.92
48:1:196:G:N2	48:1:219:A:H61	1.71	0.89
48:1:1257:C:N4	48:1:1261:G:H22	1.73	0.86

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	R	300/475 (63%)	284 (95%)	16 (5%)	0	100	100
2	X	222/224 (99%)	211 (95%)	11 (5%)	0	100	100
3	i	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
4	J	220/222 (99%)	202 (92%)	16 (7%)	2 (1%)	14	42
5	j	117/119 (98%)	109 (93%)	5 (4%)	3 (3%)	4	21
6	K	231/233 (99%)	215 (93%)	14 (6%)	2 (1%)	14	42
7	k	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
8	7	189/191 (99%)	176 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	l	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
10	M	167/169 (99%)	145 (87%)	22 (13%)	0	100	100
11	m	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
12	N	191/193 (99%)	173 (91%)	14 (7%)	4 (2%)	5	24
13	n	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
14	O	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
15	o	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
16	p	201/203 (99%)	182 (90%)	16 (8%)	3 (2%)	8	30
17	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
18	5	181/183 (99%)	163 (90%)	18 (10%)	0	100	100
19	S	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
20	s	218/220 (99%)	194 (89%)	22 (10%)	2 (1%)	14	42
21	T	150/152 (99%)	141 (94%)	8 (5%)	1 (1%)	18	47
22	U	170/172 (99%)	158 (93%)	11 (6%)	1 (1%)	21	50
23	V	157/159 (99%)	145 (92%)	12 (8%)	0	100	100
24	W	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
25	P	144/155 (93%)	124 (86%)	20 (14%)	0	100	100
26	r	117/197 (59%)	108 (92%)	9 (8%)	0	100	100
27	x	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
29	Y	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
31	Z	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
32	a	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
33	b	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	44
34	C	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
35	c	146/148 (99%)	128 (88%)	16 (11%)	2 (1%)	9	31
36	D	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
37	d	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
38	E	250/252 (99%)	229 (92%)	21 (8%)	0	100	100
39	e	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
40	F	384/386 (100%)	354 (92%)	29 (8%)	1 (0%)	36	65
41	f	107/109 (98%)	96 (90%)	11 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	G	359/361 (99%)	325 (90%)	32 (9%)	2 (1%)	21	50
43	g	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
44	H	294/296 (99%)	274 (93%)	18 (6%)	2 (1%)	18	47
45	h	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
46	I	152/175 (87%)	147 (97%)	5 (3%)	0	100	100
47	L	202/204 (99%)	165 (82%)	37 (18%)	0	100	100
All	All	7086/7457 (95%)	6532 (92%)	528 (8%)	26 (0%)	31	59

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	s	108	ASP
35	c	47	LYS
35	c	78	LEU
42	G	339	LEU
4	J	158	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	R	288/392 (74%)	287 (100%)	1 (0%)	86	84
2	X	177/192 (92%)	177 (100%)	0	100	100
3	i	95/95 (100%)	95 (100%)	0	100	100
4	J	186/186 (100%)	186 (100%)	0	100	100
5	j	104/104 (100%)	103 (99%)	1 (1%)	68	75
6	K	187/191 (98%)	186 (100%)	1 (0%)	81	81
7	k	81/81 (100%)	81 (100%)	0	100	100
8	7	171/171 (100%)	170 (99%)	1 (1%)	78	80
9	l	70/70 (100%)	70 (100%)	0	100	100
10	M	147/147 (100%)	146 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	m	68/68 (100%)	68 (100%)	0	100	100
12	N	154/154 (100%)	151 (98%)	3 (2%)	50	66
13	n	45/45 (100%)	45 (100%)	0	100	100
14	O	107/107 (100%)	107 (100%)	0	100	100
15	o	47/47 (100%)	47 (100%)	0	100	100
16	p	175/175 (100%)	174 (99%)	1 (1%)	78	80
17	Q	160/160 (100%)	159 (99%)	1 (1%)	78	80
18	5	140/145 (97%)	138 (99%)	2 (1%)	59	70
19	S	150/150 (100%)	150 (100%)	0	100	100
20	s	184/186 (99%)	184 (100%)	0	100	100
21	T	126/126 (100%)	126 (100%)	0	100	100
22	U	156/156 (100%)	155 (99%)	1 (1%)	78	80
23	V	136/136 (100%)	134 (98%)	2 (2%)	57	69
24	W	87/87 (100%)	87 (100%)	0	100	100
26	r	105/166 (63%)	105 (100%)	0	100	100
27	x	104/104 (100%)	104 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
31	Z	104/105 (99%)	104 (100%)	0	100	100
32	a	109/109 (100%)	108 (99%)	1 (1%)	70	76
33	b	115/115 (100%)	115 (100%)	0	100	100
34	C	90/90 (100%)	90 (100%)	0	100	100
35	c	118/118 (100%)	117 (99%)	1 (1%)	73	77
36	D	71/71 (100%)	71 (100%)	0	100	100
37	d	46/46 (100%)	46 (100%)	0	100	100
38	E	193/194 (100%)	190 (98%)	3 (2%)	55	68
39	e	81/81 (100%)	81 (100%)	0	100	100
40	F	319/322 (99%)	318 (100%)	1 (0%)	86	84
41	f	92/96 (96%)	92 (100%)	0	100	100
42	G	288/288 (100%)	288 (100%)	0	100	100
43	g	109/109 (100%)	109 (100%)	0	100	100
44	H	244/244 (100%)	243 (100%)	1 (0%)	84	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	h	90/90 (100%)	90 (100%)	0	100	100
46	I	134/152 (88%)	134 (100%)	0	100	100
47	L	185/185 (100%)	184 (100%)	1 (0%)	81	81
All	All	5892/6110 (96%)	5869 (100%)	23 (0%)	81	83

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	V	128	LEU
38	E	101	VAL
35	c	78	LEU
38	E	225	ILE
12	N	85	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
43	g	88	HIS
45	h	42	GLN
47	L	108	ASN
18	5	116	HIS
17	Q	31	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	3	120/121 (99%)	28 (23%)	1 (0%)
30	4	157/158 (99%)	36 (22%)	5 (3%)
48	1	3257/3260 (99%)	908 (27%)	158 (4%)
All	All	3534/3539 (99%)	972 (27%)	164 (4%)

5 of 972 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	3	10	C
28	3	11	A
28	3	13	A
28	3	14	U
28	3	33	U

5 of 164 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	1	2282	U
48	1	2911	A
48	1	2385	G
48	1	2617	U
48	1	3156	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	4
48	1	3

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Mol	Chain	Number of breaks
40	F	1

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	173:UNK	C	188:SER	N	30.28
1	R	105:ARG	C	113:UNK	N	19.44
1	1	1980:C	O3'	2042:G	P	19.07
1	R	529:GLY	C	535:UNK	N	17.02
1	R	123:UNK	C	156:UNK	N	12.97

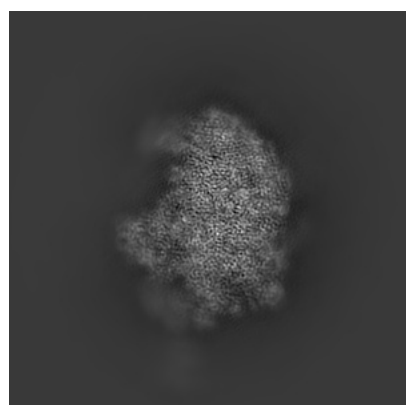
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4752. These allow visual inspection of the internal detail of the map and identification of artifacts.

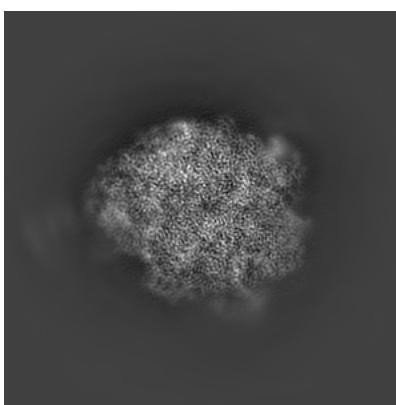
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

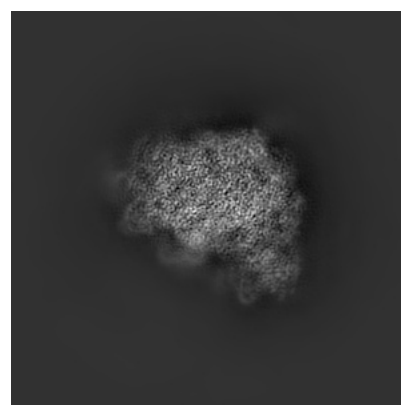
6.1.1 Primary map



X



Y

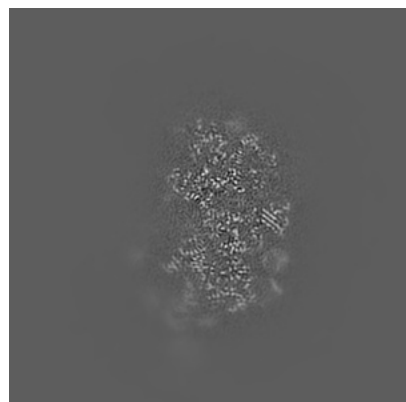


Z

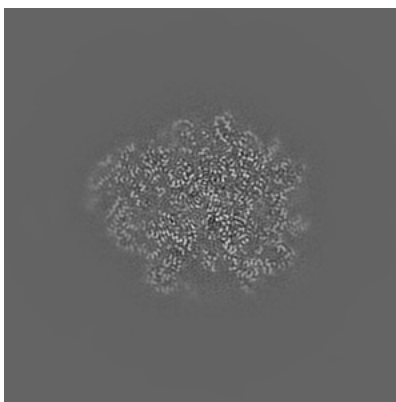
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

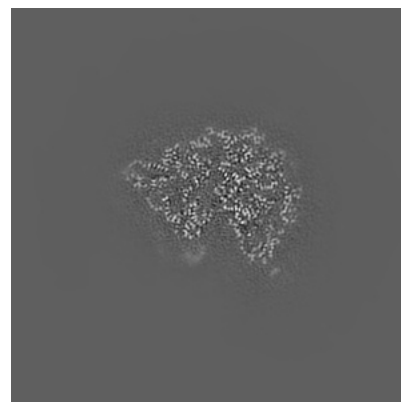
6.2.1 Primary map



X Index: 198



Y Index: 198

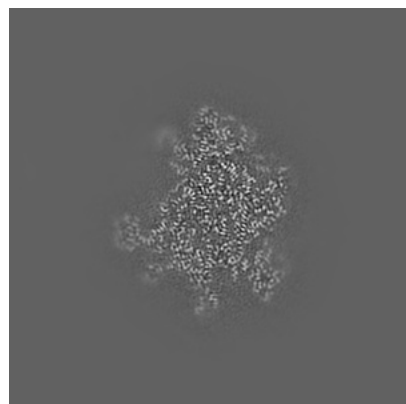


Z Index: 198

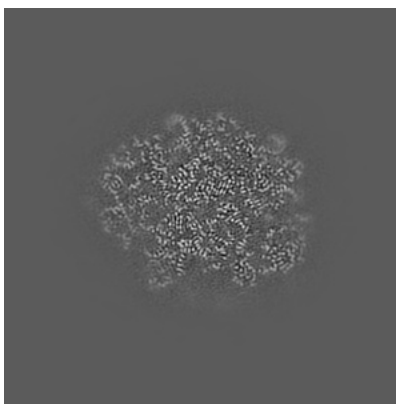
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

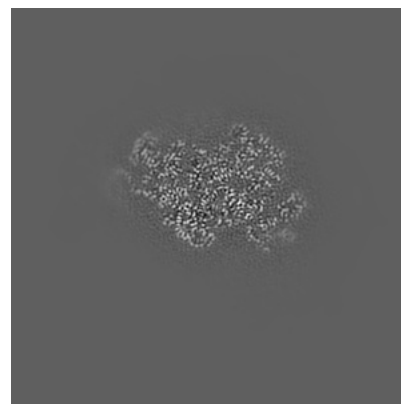
6.3.1 Primary map



X Index: 235



Y Index: 206

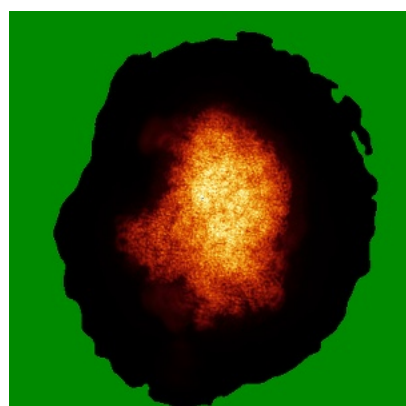


Z Index: 217

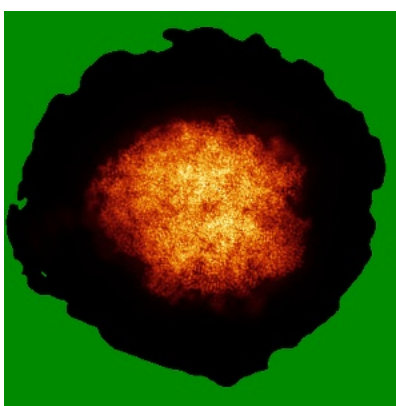
The images above show the largest variance slices of the map in three orthogonal directions.

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

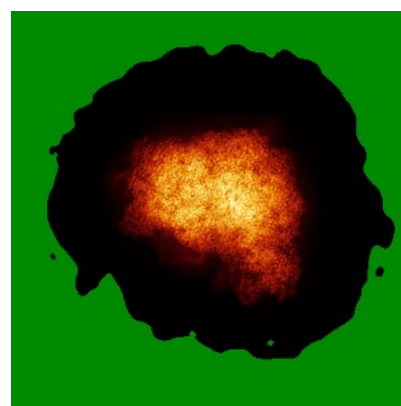
6.4.1 Primary map



X



Y

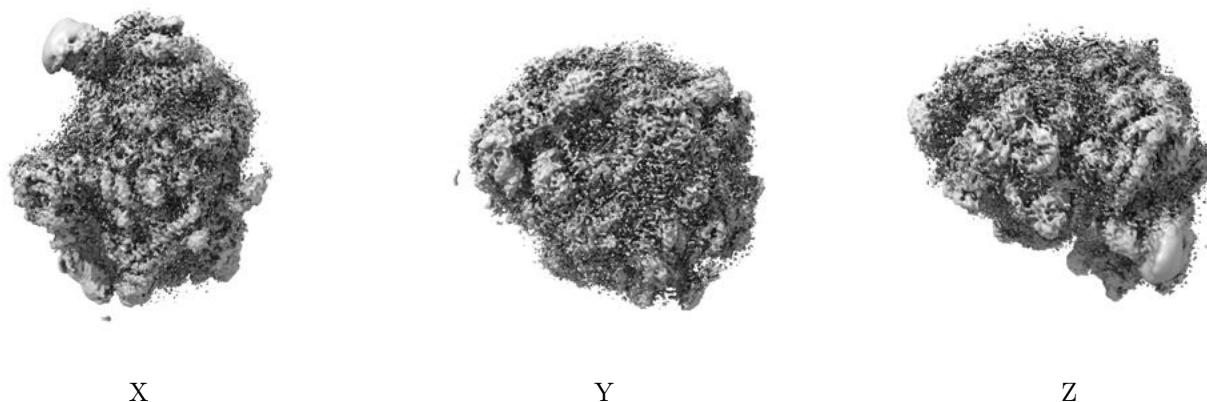


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

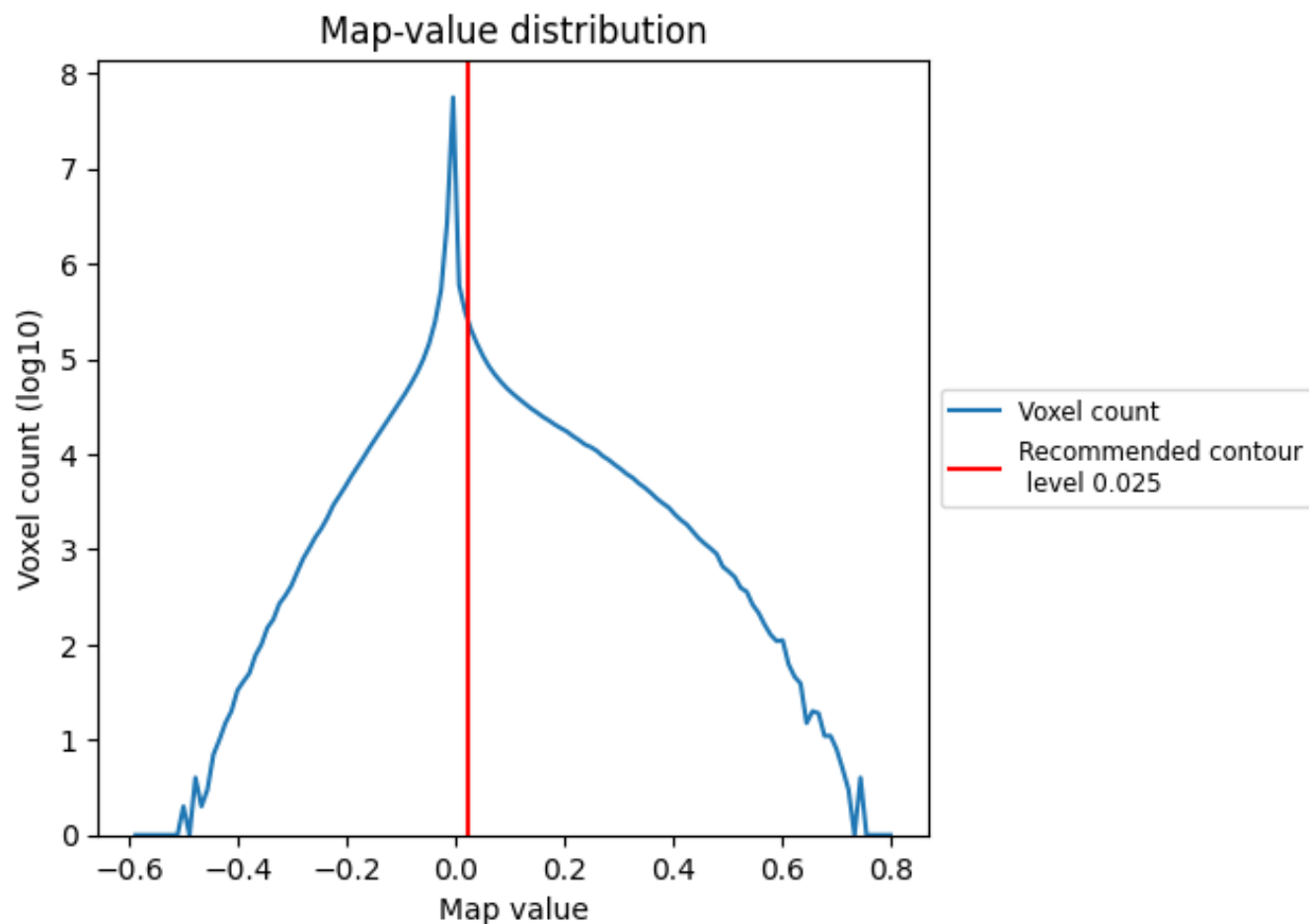
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

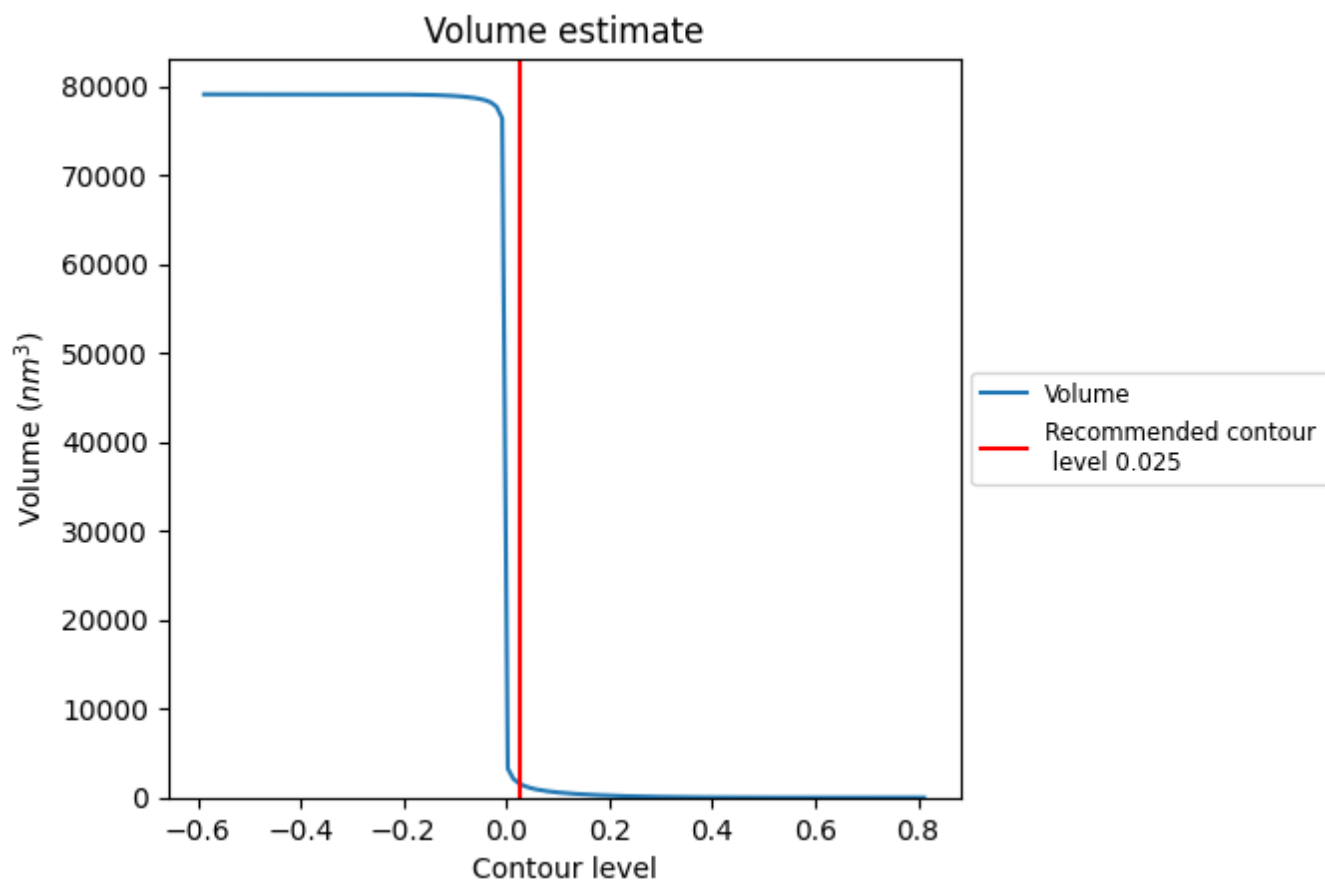
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

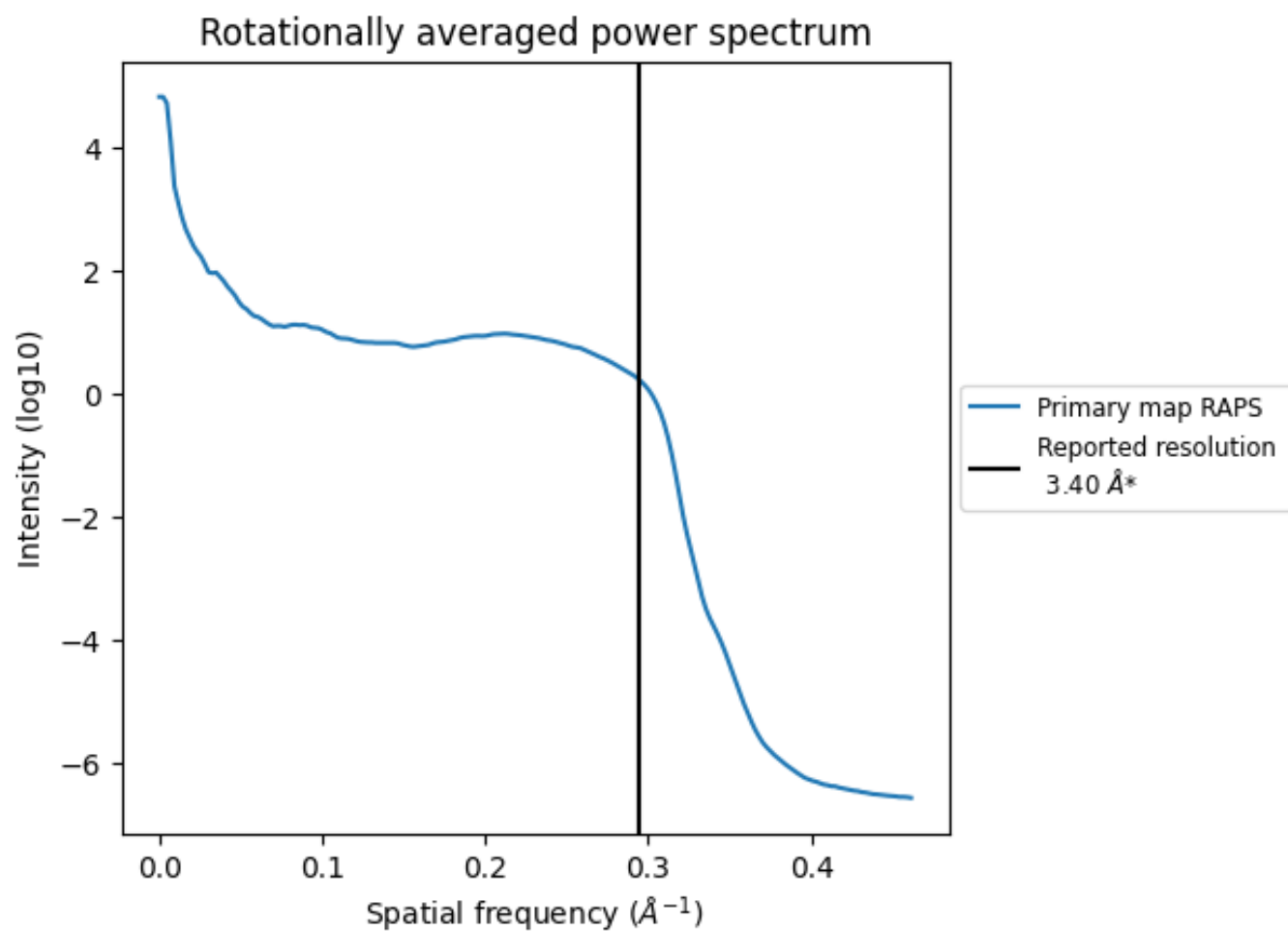
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1583 nm³; this corresponds to an approximate mass of 1430 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

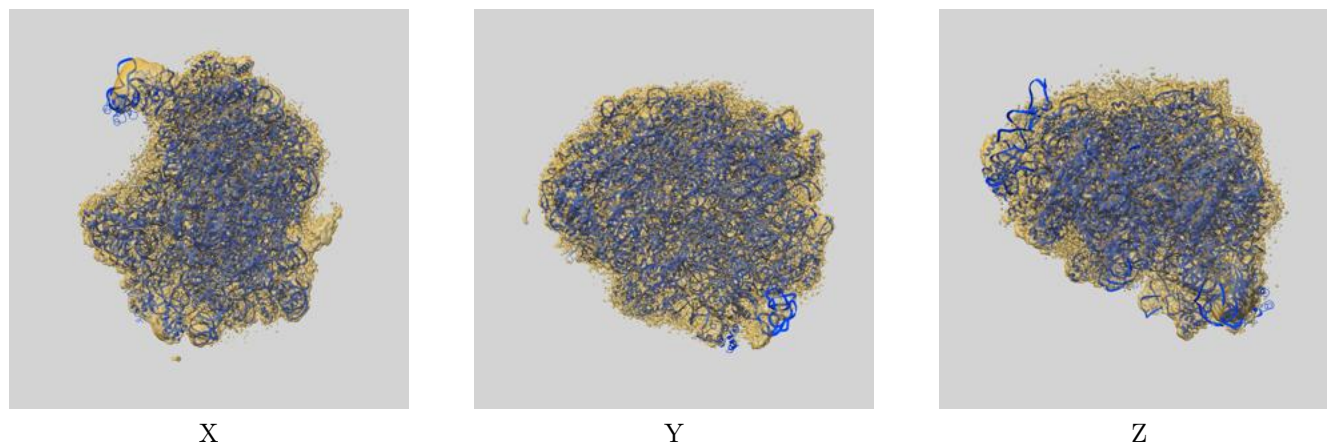
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

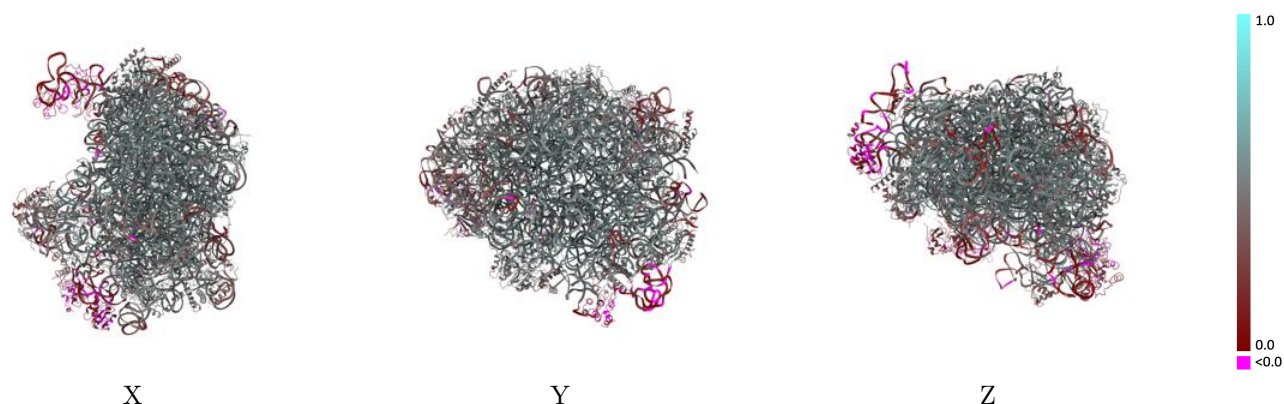
This section contains information regarding the fit between EMDB map EMD-4752 and PDB model 6R86. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



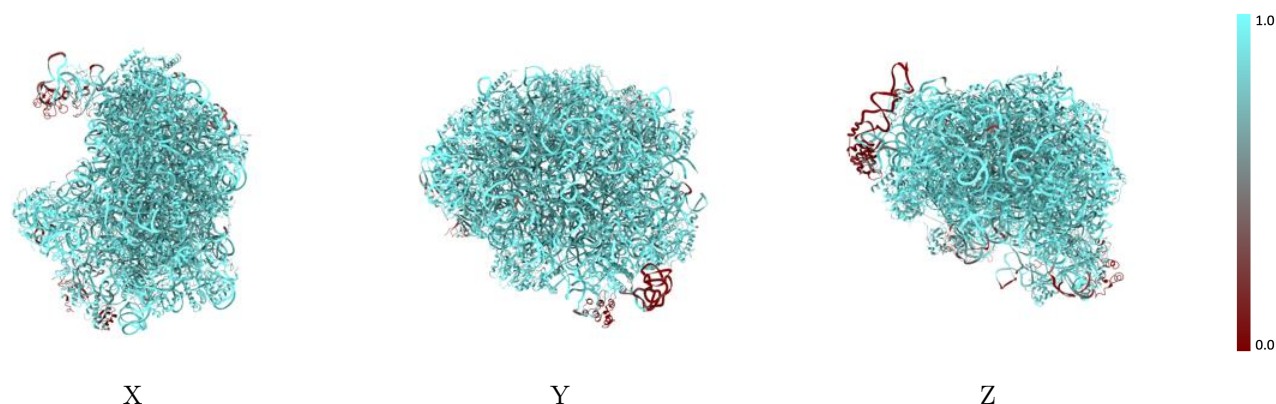
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



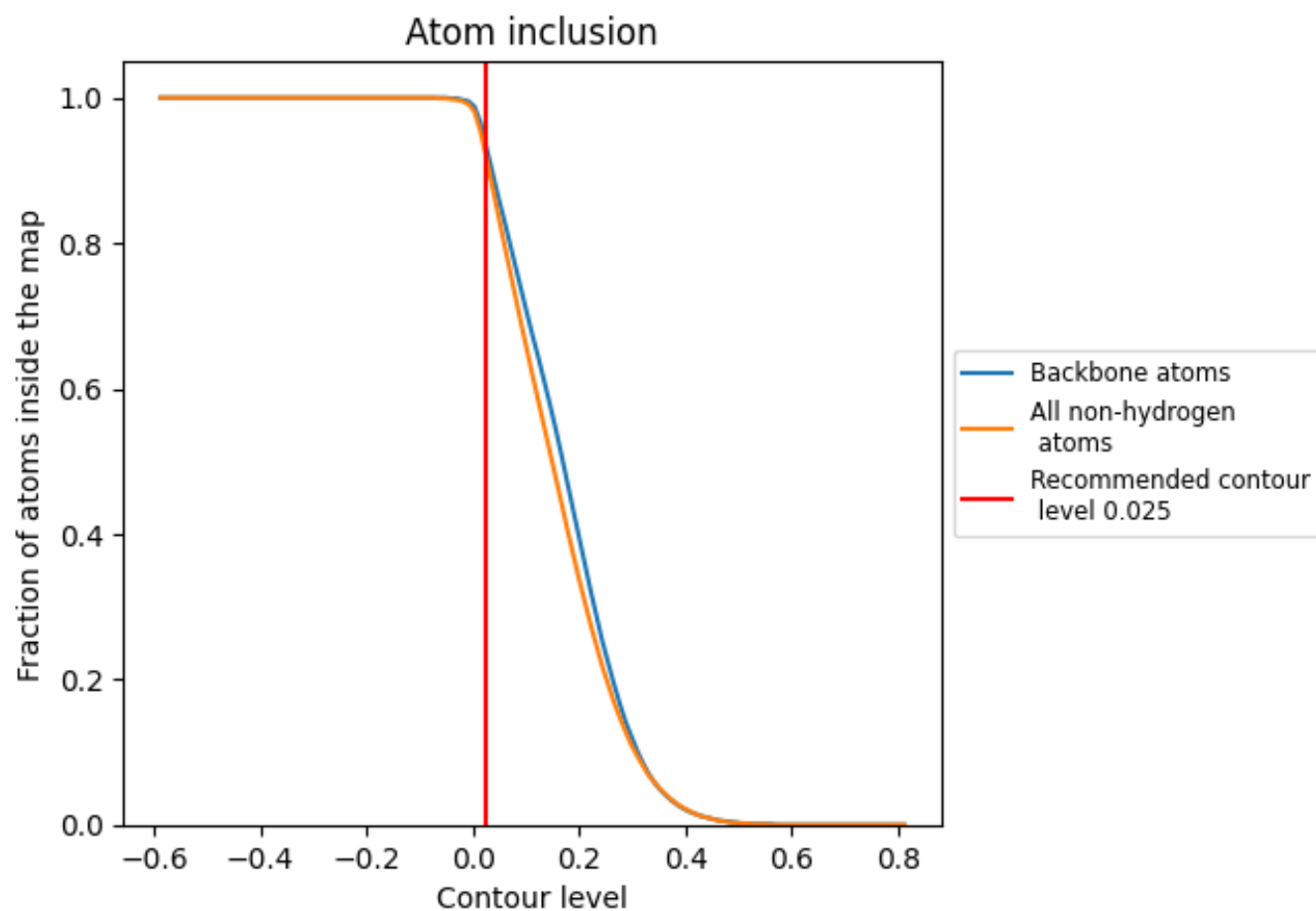
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4620
1	 0.9430	 0.4680
3	 0.9850	 0.4910
4	 0.9750	 0.5130
5	 0.9210	 0.4980
7	 0.9150	 0.4580
C	 0.8560	 0.4840
D	 0.9220	 0.5110
E	 0.9330	 0.5330
F	 0.9440	 0.5170
G	 0.9400	 0.5110
H	 0.9070	 0.4360
I	 0.9110	 0.4590
J	 0.9400	 0.5070
K	 0.9180	 0.4680
L	 0.3870	 0.0560
M	 0.8700	 0.3790
N	 0.9360	 0.5050
O	 0.9230	 0.4740
P	 0.3660	 0.0790
Q	 0.9510	 0.5190
R	 0.6070	 0.1760
S	 0.9340	 0.5090
T	 0.9300	 0.5060
U	 0.9180	 0.4900
V	 0.9430	 0.5100
W	 0.9050	 0.4440
X	 0.9220	 0.4450
Y	 0.9400	 0.5090
Z	 0.9440	 0.5110
a	 0.9250	 0.5030
b	 0.9240	 0.4710
c	 0.9560	 0.5330
d	 0.9180	 0.4880
e	 0.9040	 0.4580



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Chain	Atom inclusion	Q-score
f	 0.9070	 0.4930
g	 0.9440	 0.5280
h	 0.9460	 0.5350
i	 0.9170	 0.5070
j	 0.9240	 0.4930
k	 0.9230	 0.4740
l	 0.9590	 0.5480
m	 0.9100	 0.4610
n	 0.9590	 0.5320
o	 0.4270	 0.1660
p	 0.9570	 0.5540
r	 0.6380	 0.0610
s	 0.8920	 0.4590
x	 0.9410	 0.5320