



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:49 PM UTC

PDB ID : 8BH7 / pdb_00008bh7
EMDB ID : EMD-16049
Title : The complex of immature 30S ribosomal subunit with Ribosome maturation factor P (RimP) from *Staphylococcus aureus*
Authors : Garaeva, N.; Fatkhullin, B.; Jenner, L.; Soufari, H.; Yusupov, M.; Usachev, K.
Deposited on : 2022-10-30
Resolution : 4.23 Å(reported)

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The types of validation reports are described at

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

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

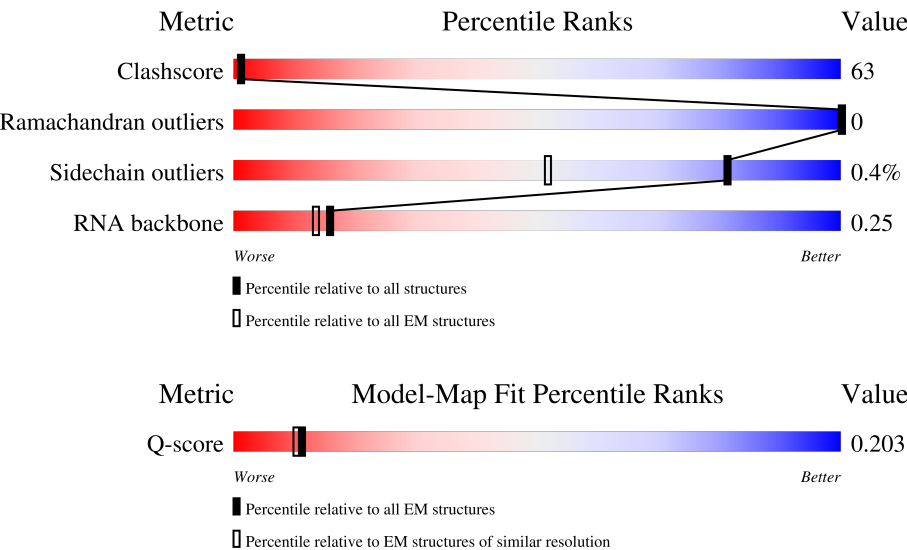
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.23 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.



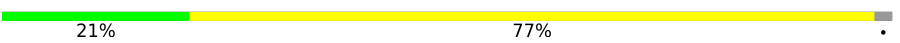
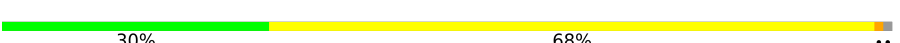
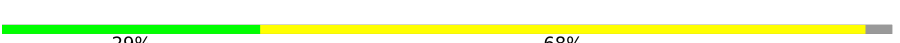
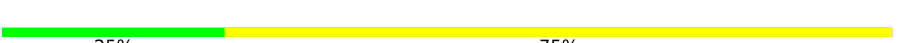
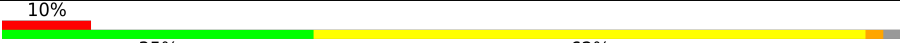
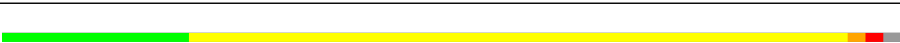
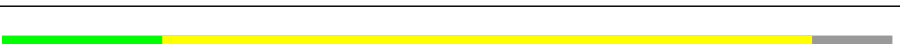
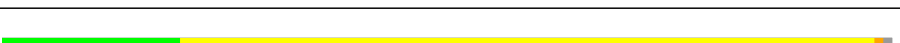
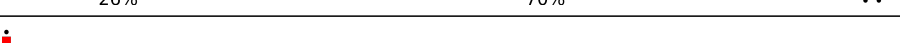
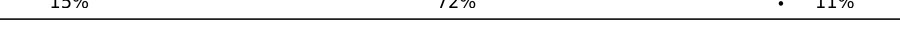
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4685 (3.74 - 4.73)

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

Mol	Chain	Length	Quality of chain
1	a	1547	58% 39%
2	A	156	30% 69%
3	b	255	6% 25% 59% 15%

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Mol	Chain	Length	Quality of chain
4	d	200	
5	c	217	
6	e	166	
7	f	98	
8	g	156	
9	h	132	
10	k	129	
11	l	137	
12	i	132	
13	j	102	
14	m	121	
15	n	61	
16	s	92	
17	o	89	
18	p	91	
19	q	87	
20	r	80	
21	t	83	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 52615 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1541	Total	C	N	O	P	0	0
			33006	14736	6021	10708	1541		

- Molecule 2 is a protein called Ribosome maturation factor RimP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	156	Total	C	N	O	S	0	0
			1242	789	204	243	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q2G2D3
A	2	ALA	-	expression tag	UNP Q2G2D3

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	216	Total	C	N	O	S	0	0
			1725	1098	297	324	6		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	192	Total	C	N	O	S	0	0
			1570	992	294	282	2		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	208	Total	C	N	O	S	0	0
			1638	1032	306	298	2		

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	e	158	Total	C	N	O	S	0	0
			1178	741	216	219	2		

- Molecule 7 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	96	Total	C	N	O	S	0	0
			798	503	139	153	3		

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	g	147	Total	C	N	O	S	0	0
			1189	744	227	214	4		

- Molecule 9 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			869	537	165	164	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	135	Total	C	N	O	S	0	0
			1062	658	218	184	2		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j	102	Total	C	N	O	S	0	0
			813	512	148	150	3		

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	m	119	Total	C	N	O	S	0	0
			945	581	188	175	1		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	60	Total	C	N	O	S	0	0
			502	317	100	80	5		

- Molecule 16 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	84	Total	C	N	O	S	0	0
			677	434	120	121	2		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	q	86	Total	C	N	O	S	0	0
			707	447	126	133	1		

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	71	Total	C	N	O	S	0	0
			589	372	115	99	3		

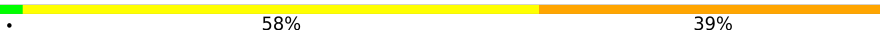
- Molecule 21 is a protein called 30S ribosomal protein S20.

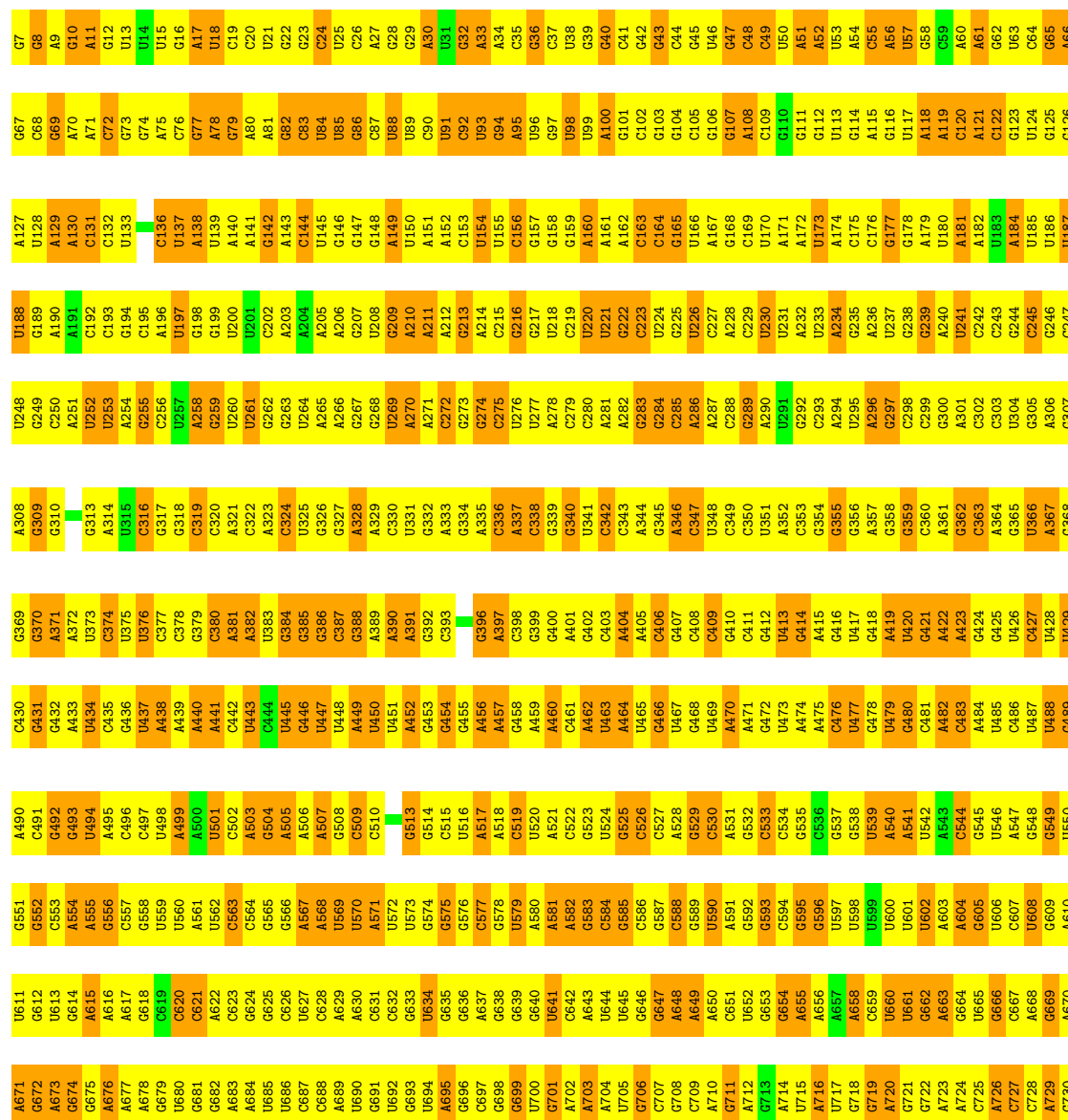
Mol	Chain	Residues	Atoms					AltConf	Trace
21	t	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

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: 16S ribosomal RNA

Chain a: 



U731	C791	U851	A911	U971	G1031	G1091	U1151	C1211	G1271	U1332	U1392	G1452	A1512
G732	A792	C852	A912	C972	C1032	A1092	U1152	A1212	A1272	C1333	C1393	G1453	C1512
C734	G793	C853	G913	G973	U1033	G1093	U1153	C1213	A1273	G1334	C1394	G1454	C1513
A735	G794	C854	U914	A974	U1034	A1094	G1154	C1214	A1274	C1335	C1395	G1455	A1514
G736	A795	C855	U915	A975	U1035	U1095	G1155	U1215		C1336	G1396	G1456	A1515
A737	G796	C856	G916	G976	C1036	U1096	G1156	U1216	G1277	U1337	G1397	A1457	G1516
G738	U797	C857	A917	C977	C1037	U1097	A1157	G1217	C1278	C1338	G1398	A1458	G1517
G739	A798	C858	A918	A978	C1038	U1098	U1158	C1218	G1279	C1339	U1399	A1459	U1518
C740	G799	C859	A919	A979	C1039	U1099	U1159	C1219	A1280	C1340	U1400	G1460	A1519
U741	A800	U860	C920	C980	U1040	G1100	U1160	C1220	G1281	U1341	U1401	U1461	G1520
A742	U801	U861	U921	G981	U1041	G1101	U1161	C1221	G1282	C1342	U1402	C1462	C1521
G743	C802	A862	C922	C982	C1042	U1102	A1162	U1222	U1283	A1343	G1403	U1463	C1522
U744	C803	G863	C923	G983	G1043	U1103	A1163	U1223	C1284	A1344	U1404	U1464	U1524
	C804	U864	A924	A984	G1044	A1104	G1164	A1224	A1285	G1345	A1405	A1465	A1525
	C805	G865	A925	A985	G1045	A1105	U1165	U1225	G1286	C1346	C1406	G1466	U1526
	U806	C866	G927	G987	G1046	U1106	U1166	U1226	G1287	U1347	A1407	G1467	U1527
	G807	U867	C928	A987	G1047	U1107	G1167	A1227	C1288	C1348	C1408	A1468	G1528
	U808	G868	A929	A988	A1048	U1108	A1168	U1228	A1289	G1349	A1409	G1469	G1529
	G809	C869	U929	C989	C1049	C1109	U1169	U1229	A1290	A1350	C1410	C1470	A1530
	A810	U870	U930	C990	A1050	C1110	U1170	U1230	A1291	A1351	C1411	U1471	A1531
	G811	G871	U931	C991	A1051	C1111	G1171	G1231	U1292	U1352	G1412	A1472	G1532
	C752	C872	G932	A992	A1052	C1112	U1172	G1232	C1293	C1353	C1413	G1473	G1533
	U753	U873	A933	A993	G1053	C1113	C1173	G1233	C1294	C1354	C1414	C1474	U1534
	G754	A874	C934	C994	U1054	A1114	G1174	C1234	C1295	C1355	C1415	G1475	G1535
	U755	A875	G935	C995	G1055	C1115	U1175	U1235	C1296	U1356	G1416	G1476	C1536
	A756	C876	G936	A996	A1056	G1116	U1176	A1236	U1297	C1357	U1417	U1477	G1537
	U757	G877	G937	A997	C1057	A1117	G1177	G1237	A1298	G1358	C1418	C1478	G1538
	C758	C878	U938	A998	A1058	U1118	A1178	A1238	A1299	U1359	A1419	G1479	C1539
	U759	A879	U939	A999	G1059	C1119	C1179	C1239	A1300	C1360	C1420	A1480	U1540
	G760	U880	C940	C1000	G1060	G1120	A1180	A1240	G1301	A1361	A1421	A1481	G1541
	A761	U881	C941	U1001	U1061	C1121	A1181	C1241	U1302	C1362	C1422	G1482	G1542
	C762	A882	C942	U1002	G1062	A1122	A1182	G1242	U1303	C1363	C1423	G1483	A1543
	G763	G883	G943	U1003	G1063	C1123	C1183	U1243	U1304	C1364	A1424	U1484	U1544
	U764	C884	C944	U1004	U1064	C1124	G1184	G1244	U1305	U1365	C1425	G1485	C1545
	C765	C885	A945	C1005	G1065	C1125	G1185	C1245	U1306	C1366	G1426	G1486	A1546
	G766	A886	C946	U1006	C1066	C1126	G1186	U1246	C1307	C1367	A1427	G1487	C1547
	U767	G887	A947	U1007	A1067	U1127	A1187	A1247	U1308	C1368	G1428	A1488	C
	G768	U888	C948	U1008	U1068	U1128	G1188	C1248	C1309	U1369	A1429	C1489	U
	U769	C889	G949	C1009	G1069	A1129	U1189	A1249	A1310	C1370	G1430	A1490	C
	G770	A890	C950	U1010	G1070	C1130	A1190	U1250	G1311	C1371	U1431	A1491	C
	U771	G891	G951	U1011	U1071	G1131	A1191	U1251	U1312	C1372	U1432	A1492	U
	C772	C892	G952	U1012	U1072	C1132	G1192	G1252	U1313	C1373	U1433	A1493	U
	G773	C893	U953	G1013	G1073	U1133	G1193	C1253	C1314	A1374	G1434	G1494	U
	A774	U894	G954	U1014	U1074	U1134	U1194	A1254	G1315	U1375	U1435	A1495	
	U775	G895	G955	C1015	C1075	A1135	G1195	C1255	G1316	C1376	A1436	U1496	
	A776	C896	A956	A1016	G1076	U1136	U1196	A1256	U1317	C1377	A1437	U1497	
	G777	G897	G957	U1017	U1077	U1137	G1197	C1257	U1318	C1378	C1438	G1498	
	C778	C898	C958	U1018	C1078	U1138	G1198	U1258	U1319	A1379	A1439	G1499	
	U779	A899	A959	U1019	A1079	G1139	U1199	A1259	G1320	C1380	C1440	G1500	
	G780	U900	U960	C1020	G1080	C1140	U1200	C1260	U1321	G1381	C1441	G1501	
	A781	U901	G961	U1021	C1081	C1141	G1201	A1261	A1322	C1382	G1442	U1502	
	G782	A902	U962	A1022	U1082	A1142	A1202	A1262	G1323	U1383	G1443	G1503	
	U783	C903	G963	C1023	C1083	C1143	C1203	A1263	U1324	C1384	A1444	A1504	
	G784	G904	G964	A1024	G1084	C1144	G1204	G1264	C1325	A1385	A1445	A1505	
	A785	A905	U965	G1025	U1085	U1145	U1205	G1265	U1326	A1386	G1446	G1506	
	U786	G906	U966	A1026	G1086	U1146	C1206	G1266	G1327	U1387	C1447	U1507	
	C787	C907	U967	U1027	U1087	U1147	A1207	C1267	C1328	A1388	G1448	C1508	
	U788	G908	A968	A1028	C1088	U1148	A1208	A1268	A1329	C1389	G1449	G1509	
	A789	C909	U969	G1029	G1089	A1149	A1209	A1269	A1330	U1390	G1450	U1510	
	U790	U850	U970	A1030	U1090	G1150	U1210	C1270	C1331	U1391	U1451	A1511	

● Molecule 2: Ribosome maturation factor RimP

Chain A: 

M67	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20	M21	M22	M23	M24	M25	M26	M27	M28	M29	M30	M31	M32	M33	M34	M35	M36	M37	M38	M39	M40	M41	M42	M43	M44	M45	M46	M47	M48	M49	M50	M51	M52	M53	M54	M55	M56	M57	M58	M59	M60	M61	M62	M63	M64	M65	M66	M67	M68	M69	M70	M71	M72	M73	M74	M75	M76	M77	M78	M79	M80	M81	M82	M83	M84	M85	M86	M87	M88	M89	M90	M91	M92	M93	M94	M95	M96	M97	M98	M99	M100	M101	M102	M103	M104	M105	M106	M107	M108	M109	M110	M111	M112	M113	M114	M115	M116	M117	M118	M119	M120	M121	M122	M123	M124	M125	M126	M127	M128	M129	M130	M131	M132	M133	M134	M135	M136	M137	M138	M139	M140	M141	M142	M143	M144	M145	M146	M147	M148	M149	M150	M151	M152	M153	M154	M155	M156	M157	M158	M159	M160	M161	M162	M163	M164	M165	M166	M167	M168	M169	M170	M171	M172	M173	M174	M175	M176	M177	M178	M179	M180	M181	M182	M183	M184	M185	M186	M187	M188	M189	M190	M191	M192	M193	M194	M195	M196	M197	M198	M199	M200	M201	M202	M203	M204	M205	M206	M207	M208	M209	M210	M211	M212	M213	M214	M215	M216	M217	M218	M219	M220	M221	M222	M223	M224	M225	M226	M227	M228	M229	M230	M231	M232	M233	M234	M235	M236	M237	M238	M239	M240	M241	M242	M243	M244	M245	M246	M247	M248	M249	M250	M251	M252	M253	M254	M255	M256	M257	M258	M259	M260	M261	M262	M263	M264	M265	M266	M267	M268	M269	M270	M271	M272	M273	M274	M275	M276	M277	M278	M279	M280	M281	M282	M283	M284	M285	M286	M287	M288	M289	M290	M291	M292	M293	M294	M295	M296	M297	M298	M299	M300	M301	M302	M303	M304	M305	M306	M307	M308	M309	M310	M311	M312	M313	M314	M315	M316	M317	M318	M319	M320	M321	M322	M323	M324	M325	M326	M327	M328	M329	M330	M331	M332	M333	M334	M335	M336	M337	M338	M339	M340	M341	M342	M343	M344	M345	M346	M347	M348	M349	M350	M351	M352	M353	M354	M355	M356	M357	M358	M359	M360	M361	M362	M363	M364	M365	M366	M367	M368	M369	M370	M371	M372	M373	M374	M375	M376	M377	M378	M379	M380	M381	M382	M383	M384	M385	M386	M387	M388	M389	M390	M391	M392	M393	M394	M395	M396	M397	M398	M399	M400	M401	M402	M403	M404	M405	M406	M407	M408	M409	M410	M411	M412	M413	M414	M415	M416	M417	M418	M419	M420	M421	M422	M423	M424	M425	M426	M427	M428	M429	M430	M431	M432	M433	M434	M435	M436	M437	M438	M439	M440	M441	M442	M443	M444	M445	M446	M447	M448	M449	M450	M451	M452	M453	M454	M455	M456	M457	M458	M459	M460	M461	M462	M463	M464	M465	M466	M467	M468	M469	M470	M471	M472	M473	M474	M475	M476	M477	M478	M479	M480	M481	M482	M483	M484	M485	M486	M487	M488	M489	M490	M491	M492	M493	M494	M495	M496	M497	M498	M499	M500	M501	M502	M503	M504	M505	M506	M507	M508	M509	M510	M511	M512	M513	M514	M515	M516	M517	M518	M519	M520	M521	M522	M523	M524	M525	M526	M527	M528	M529	M530	M531	M532	M533	M534	M535	M536	M537	M538	M539	M540	M541	M542	M543	M544	M545	M546	M547	M548	M549	M550	M551	M552	M553	M554	M555	M556	M557	M558	M559	M560	M561	M562	M563	M564	M565	M566	M567	M568	M569	M570	M571	M572	M573	M574	M575	M576	M577	M578	M579	M580	M581	M582	M583	M584	M585	M586	M587	M588	M589	M590	M591	M592	M593	M594	M595	M596	M597	M598	M599	M600	M601	M602	M603	M604	M605	M606	M607	M608	M609	M610	M611	M612	M613	M614	M615	M616	M617	M618	M619	M620	M621	M622	M623	M624	M625	M626	M627	M628	M629	M630	M631	M632	M633	M634	M635	M636	M637	M638	M639	M640	M641	M642	M643	M644	M645	M646	M647	M648	M649	M650	M651	M652	M653	M654	M655	M656	M657	M658	M659	M660	M661	M662	M663	M664	M665	M666	M667	M668	M669	M670	M671	M672	M673	M674	M675	M676	M677	M678	M679	M680	M681	M682	M683	M684	M685	M686	M687	M688	M689	M690	M691	M692	M693	M694	M695	M696	M697	M698	M699	M700	M701	M702	M703	M704	M705	M706	M707	M708	M709	M710	M711	M712	M713	M714	M715	M716	M717	M718	M719	M720	M721	M722	M723	M724	M725	M726	M727	M728	M729	M730	M731	M732	M733	M734	M735	M736	M737	M738	M739	M740	M741	M742	M743	M744	M745	M746	M747	M748	M749	M750	M751	M752	M753	M754	M755	M756	M757	M758	M759	M760	M761	M762	M763	M764	M765	M766	M767	M768	M769	M770	M771	M772	M773	M774	M775	M776	M777	M778	M779	M780	M781	M782	M783	M784	M785	M786	M787	M788	M789	M790	M791	M792	M793	M794	M795	M796	M797	M798	M799	M800	M801	M802	M803	M804	M805	M806	M807	M808	M809	M810	M811	M812	M813	M814	M815	M816	M817	M818	M819	M820	M821	M822	M823	M824	M825	M826	M827	M828	M829	M830	M831	M832	M833	M834	M835	M836	M837	M838	M839	M840	M841	M842	M843	M844	M845	M846	M847	M848	M849	M850	M851	M852	M853	M854	M855	M856	M857	M858	M859	M860	M861	M862	M863	M864	M865	M866	M867	M868	M869	M870	M871	M872	M873	M874	M875	M876	M877	M878	M879	M880	M881	M882	M883	M884	M885	M886	M887	M888	M889	M890	M891	M892	M893	M894	M895	M896	M897	M898	M899	M900	M901	M902	M903	M904	M905	M906	M907	M908	M909	M910	M911	M912	M913	M914	M915	M916	M917	M918	M919	M920	M921	M922	M923	M924	M925	M926	M927	M928	M929	M930	M931	M932	M933	M934	M935	M936	M937	M938	M939	M940	M941	M942	M943	M944	M945	M946	M947	M948	M949	M950	M951	M952	M953	M954	M955	M956	M957	M958	M959	M960	M961	M962	M963	M964	M965	M966	M967	M968	M969	M970	M971	M972	M973	M974	M975	M976	M977	M978	M979	M980	M981	M982	M983	M984	M985	M986	M987	M988	M989	M990	M991	M992	M993	M994	M995	M996	M997	M998	M999	M1000
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D146
K146
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A148
K149
A150
R151
H152
A153
V154
M155
I156

• Molecule 3: 30S ribosomal protein S2



MET
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Q224
Q225
Q226
S229
ASN
GLU
GLU
VAL
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ALA
GLU
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ASP
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ASP
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THR
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ALA
THR
GLU

• Molecule 4: 30S ribosomal protein S4



MET
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G174
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P180
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R182
S183
E184
E188
E191
Q192
L193
I194

V195
E196
Y197
Y198
S199
R200

• Molecule 5: 30S ribosomal protein S3



MET
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Q4
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K37
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R39
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S52
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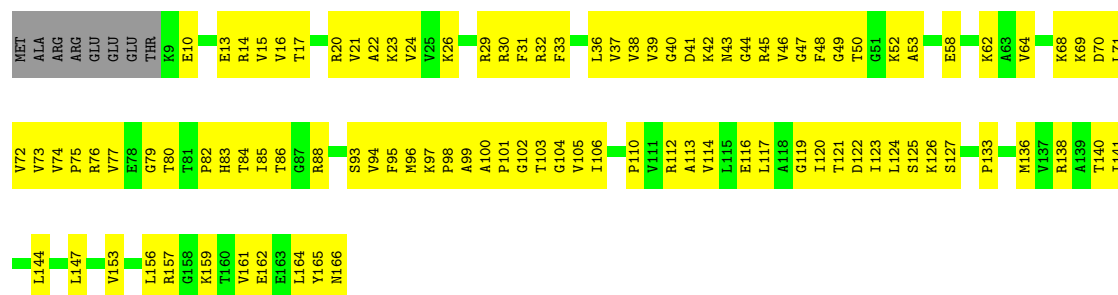
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K134

Q135
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D160
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A162
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Y167
S168
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L177
R178
A179
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I181
D182
Y183
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H185
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Y202
R203
G204



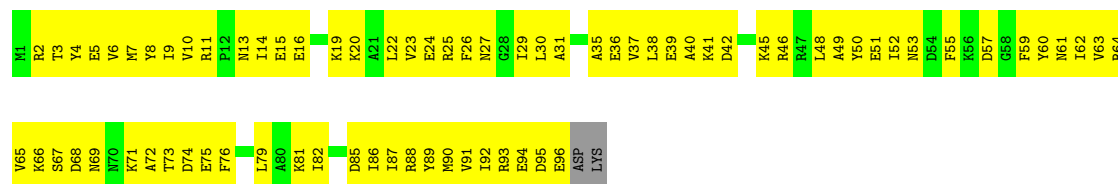
• Molecule 6: 30S ribosomal protein S5

Chain e: 35% 60% 5%



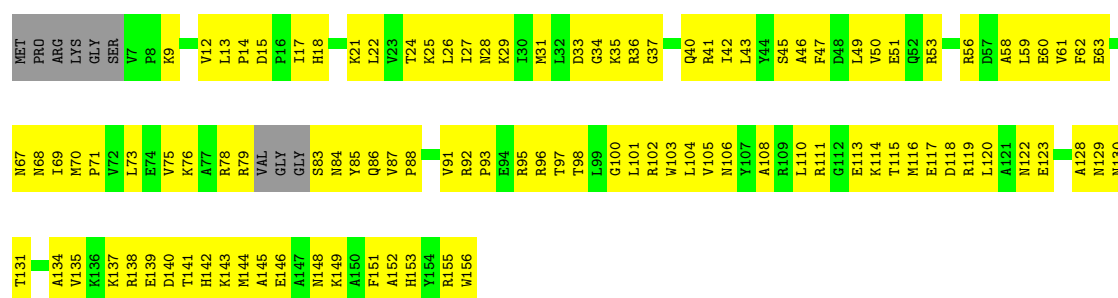
• Molecule 7: 30S ribosomal protein S6

Chain f: 21% 77% .



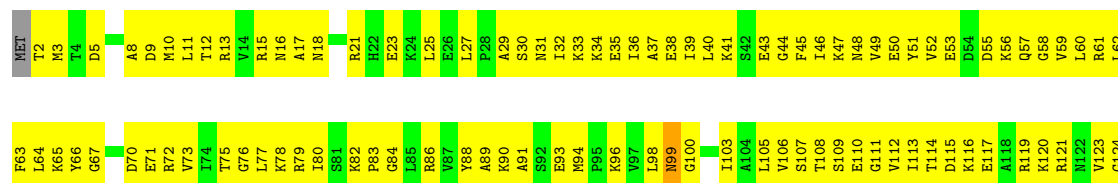
• Molecule 8: 30S ribosomal protein S7

Chain g: 27% 67% 6%



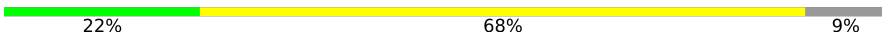
• Molecule 9: 30S ribosomal protein S8

Chain h: 20% 78% ..



G125
E126
I127
I128
A129
Y130
V131
W132

• Molecule 10: 30S ribosomal protein S11

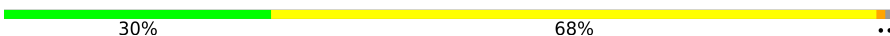
Chain k:  22% 68% 9%

MET
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ARG
LYS
GLN
VAL
SER
ARG
LYS
ARG
R11
V12
K13
K14
N15
I16
E17
N18
G19
V20
A21
H22
I23
R24
S25
T26
F27
N28
N29
T30
I31
V32
T33
I34
T35
F38
G39
N40
A41
L42
S43
V44
S45
S46
A47
G48
A49
L50
G51
F52
K53
G54
S55
K56
K57
S58
T59
P60
F61

A62
A63
Q64
N65
A66
S67
E68
T69
A70
S71
K72
S73
A74
H75
E76
H77
G78
L79
K80
T81
W82
E83
H84
T85
W86
K87
G88
P89
G90
P91
G92
R93
E94
S95
A96
I97
R98
A99
L100
A103
V107
T108
A109
I110
R111
D112
V113
P117
H118
N119
G120
C121
R122
P123
R126
R127

ARG
VAL

• Molecule 11: 30S ribosomal protein S12

Chain l:  30% 68% ..

MET
P2
T3
T4
N5
Q6
N7
L7
F8
R9
K10
P11
R12
K15
P22
A23
L24
H25
K26
G27
F28
N29
S30
K31
K32
K33
K34
F35
G36
D37
L38
N39
S40
P41
Q42
K43
R44
G45
V46
C47
T48
R49
V50
S51
T52
M53
T54
P55
R56
K57
P58
N59
S60
A61
R63
R64
Y65
A66

R67
V68
R69
L70
S71
N72
W73
I74
E75
A78
Y79
T80
P81
G82
T83
G84
H85
N86
L87
Q88
E89
V92
V93
L94
Y95
R96
G97
G98
R99
V100
R101
D102
L103
P104
G105
V106
R107
Y108
H109
I110
V111
R112
G113
A114
D115
D116
T117
S118
G119
R123
R124
R127
S128
L129
G131

T132
K133
K134
P135
K136
ASN

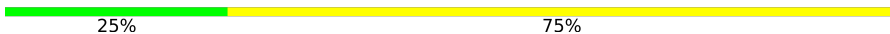
• Molecule 12: 30S ribosomal protein S9

Chain i:  29% 68% .

MET
THR
LEU
ALA
Q5
E6
Y7
Y8
R9
G10
T11
G12
R13
R14
K15
N16
S17
V18
A19
R20
V21
R22
L23
V24
P25
G26
E27
G28
N29
I30
R35
D36
V37
R38
E39
Y40
L41
E44
S45
L46
I47
L48
D49
L50
N51
Q52
P53
F54
D55
V56
T57
E58
T59
K60
G61
N62
Y63
D64

V65
L66
V67
N68
V69
G72
T75
G76
Q77
A78
Q79
A80
I81
R82
H83
G84
I85
A86
R87
A88
L89
L90
Y96
R97
G98
S99
L100
K101
A102
R103
G104
L105
L106
E107
R108
R111
M112
K113
E114
R115
K116
K117
L120
K121
A122
A123
R124
K131
R132

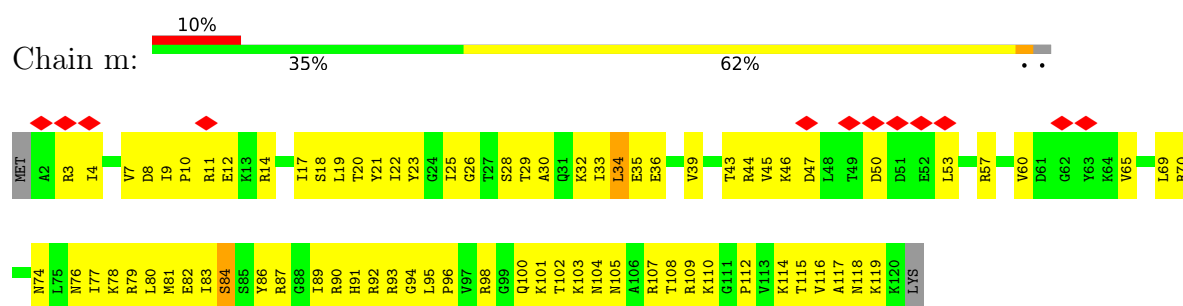
• Molecule 13: 30S ribosomal protein S10

Chain j:  25% 75%

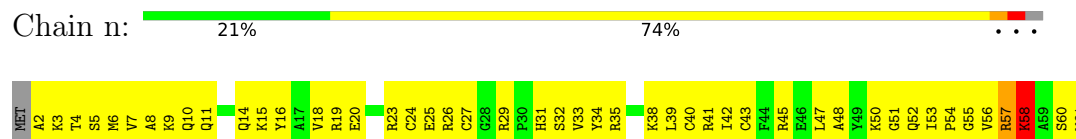
M1
A2
K3
Q4
K5
I6
R7
I8
R9
L10
K11
A12
Y13
D14
H15
R16
V17
I18
D19
Q20
S21
A22
E23
L24
I25
V26
E27
T28
A29
K30
R31
S32
D35
V36
S37
G38
P39
I40
P41
L42
P43
T44
E45
K46
S47
V48
I51
I52
R53
A54
D60
S61
R62
E63
Q64
F65
E66

Q67
R68
T69
H70
K71
R72
L73
I74
D75
I76
V77
N78
P79
T80
P81
K82
T83
V84
D85
A86
L87
M88
S94
D97
I98
E99
I100
K101
L102

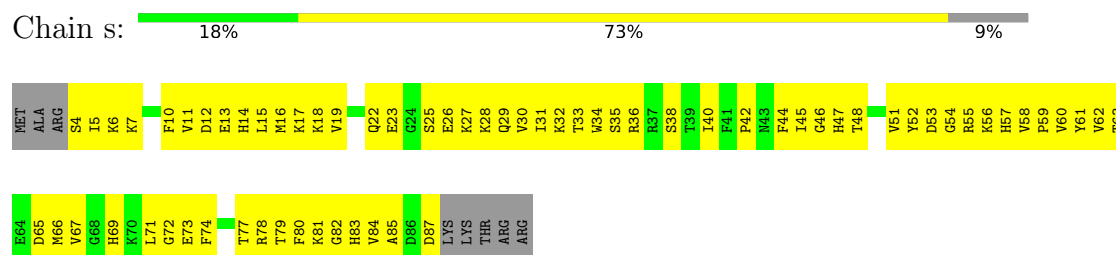
• Molecule 14: 30S ribosomal protein S13



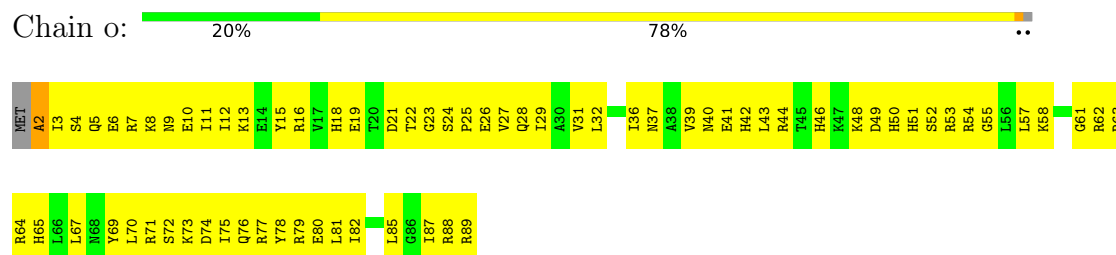
- Molecule 15: 30S ribosomal protein S14 type Z



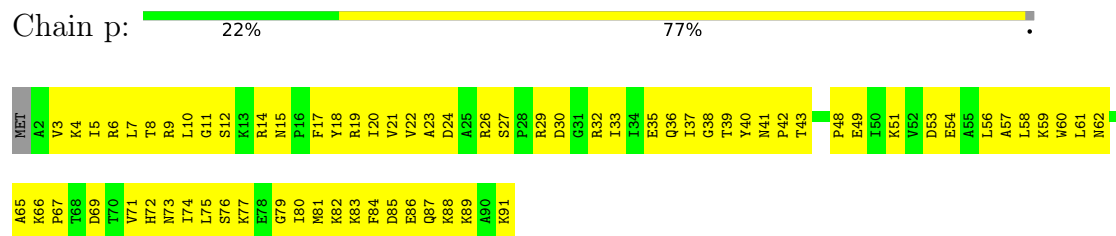
- Molecule 16: 30S ribosomal protein S19



- Molecule 17: 30S ribosomal protein S15

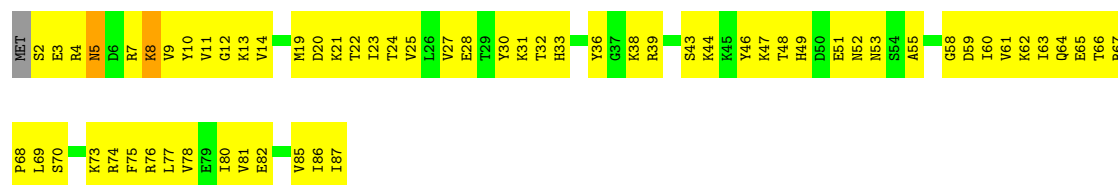


- Molecule 18: 30S ribosomal protein S16

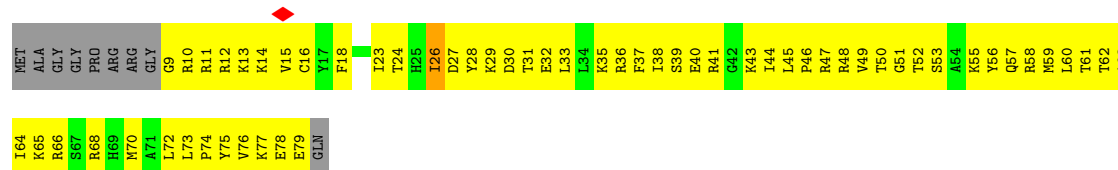


- Molecule 19: 30S ribosomal protein S17

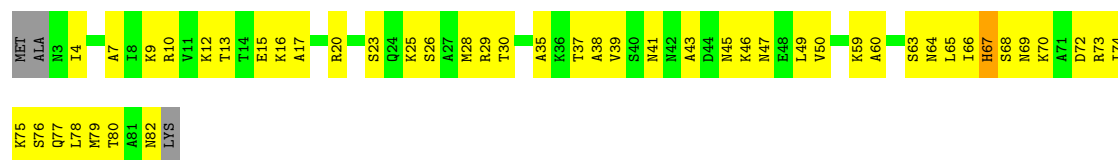




- Molecule 20: 30S ribosomal protein S18



- Molecule 21: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57677	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.7	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	21.928	Depositor
Minimum map value	-5.257	Depositor
Average map value	0.020	Depositor
Map value standard deviation	1.022	Depositor
Recommended contour level	2.74	Depositor
Map size (Å)	460.80002, 460.80002, 460.80002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.31	0/36954	0.51	0/57629
2	A	0.26	0/1261	0.65	1/1703 (0.1%)
3	b	0.19	0/1748	0.45	0/2345
4	d	0.24	0/1599	0.49	1/2146 (0.0%)
5	c	0.20	0/1661	0.43	0/2233
6	e	0.19	0/1192	0.43	0/1606
7	f	0.23	0/809	0.51	0/1085
8	g	0.20	0/1207	0.45	0/1625
9	h	0.21	0/1044	0.52	1/1401 (0.1%)
10	k	0.26	0/884	0.57	2/1193 (0.2%)
11	l	0.22	0/1079	0.51	0/1445
12	i	0.17	0/1033	0.41	0/1386
13	j	0.24	0/825	0.53	0/1110
14	m	0.27	0/952	0.66	2/1275 (0.2%)
15	n	0.20	0/512	0.55	1/678 (0.1%)
16	s	0.31	0/695	0.67	0/934
17	o	0.21	0/747	0.49	2/996 (0.2%)
18	p	0.21	0/723	0.51	0/971
19	q	0.23	0/715	0.57	0/955
20	r	0.23	0/598	0.68	2/797 (0.3%)
21	t	0.31	0/606	0.56	0/810
All	All	0.29	0/56844	0.51	12/84323 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	n	58	LYS	N-CA-C	6.95	119.13	108.42
14	m	28	SER	N-CA-C	-6.63	105.34	113.50
20	r	26	ILE	CA-C-N	6.21	132.87	121.70
20	r	26	ILE	C-N-CA	6.21	132.87	121.70
10	k	38	PHE	CA-C-N	5.78	132.10	121.70

There are no chirality outliers.

There are no planarity outliers.

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	a	33006	0	16616	3739	0
2	A	1242	0	1264	169	0
3	b	1725	0	1776	160	0
4	d	1570	0	1597	194	0
5	c	1638	0	1702	168	0
6	e	1178	0	1242	120	0
7	f	798	0	794	98	0
8	g	1189	0	1218	136	0
9	h	1032	0	1082	149	0
10	k	869	0	886	131	0
11	l	1062	0	1130	158	0
12	i	1017	0	1039	128	0
13	j	813	0	859	110	0
14	m	945	0	1001	136	0
15	n	502	0	527	69	0
16	s	677	0	672	129	0
17	o	738	0	769	111	0
18	p	712	0	744	91	0
19	q	707	0	749	93	0
20	r	589	0	628	92	0
21	t	606	0	650	54	0
All	All	52615	0	36945	5522	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 63.

The worst 5 of 5522 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)
4:d:138:THR:CG2	4:d:175:THR:HB	1.68	1.22
1:a:1064:U:H3	1:a:1218:C:N4	1.43	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1226:G:HO2'	15:n:2:ALA:N	1.48	1.10
4:d:138:THR:HG22	4:d:175:THR:CB	1.82	1.09
4:d:138:THR:CG2	4:d:175:THR:CB	2.33	1.07

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	
2	A	154/156 (99%)	141 (92%)	13 (8%)	0	100	100
3	b	212/255 (83%)	200 (94%)	12 (6%)	0	100	100
4	d	188/200 (94%)	175 (93%)	13 (7%)	0	100	100
5	c	206/217 (95%)	198 (96%)	8 (4%)	0	100	100
6	e	156/166 (94%)	147 (94%)	9 (6%)	0	100	100
7	f	94/98 (96%)	87 (93%)	7 (7%)	0	100	100
8	g	143/156 (92%)	132 (92%)	11 (8%)	0	100	100
9	h	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
10	k	115/129 (89%)	106 (92%)	9 (8%)	0	100	100
11	l	133/137 (97%)	113 (85%)	20 (15%)	0	100	100
12	i	126/132 (96%)	118 (94%)	8 (6%)	0	100	100
13	j	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
14	m	117/121 (97%)	104 (89%)	13 (11%)	0	100	100
15	n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
16	s	82/92 (89%)	69 (84%)	13 (16%)	0	100	100
17	o	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
18	p	88/91 (97%)	79 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	q	84/87 (97%)	74 (88%)	10 (12%)	0	100	100
20	r	69/80 (86%)	59 (86%)	10 (14%)	0	100	100
21	t	78/83 (94%)	73 (94%)	5 (6%)	0	100	100
All	All	2418/2584 (94%)	2229 (92%)	189 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	139/139 (100%)	137 (99%)	2 (1%)	59	71
3	b	186/221 (84%)	186 (100%)	0	100	100
4	d	169/175 (97%)	169 (100%)	0	100	100
5	c	169/175 (97%)	169 (100%)	0	100	100
6	e	124/131 (95%)	124 (100%)	0	100	100
7	f	84/86 (98%)	84 (100%)	0	100	100
8	g	126/132 (96%)	126 (100%)	0	100	100
9	h	112/113 (99%)	112 (100%)	0	100	100
10	k	93/104 (89%)	93 (100%)	0	100	100
11	l	117/119 (98%)	116 (99%)	1 (1%)	70	76
12	i	106/109 (97%)	106 (100%)	0	100	100
13	j	91/91 (100%)	91 (100%)	0	100	100
14	m	102/104 (98%)	101 (99%)	1 (1%)	68	75
15	n	52/53 (98%)	50 (96%)	2 (4%)	29	51
16	s	73/80 (91%)	73 (100%)	0	100	100
17	o	80/81 (99%)	80 (100%)	0	100	100
18	p	76/77 (99%)	76 (100%)	0	100	100
19	q	81/82 (99%)	79 (98%)	2 (2%)	42	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	r	63/68 (93%)	63 (100%)	0	100	100
21	t	67/69 (97%)	66 (98%)	1 (2%)	57	70
All	All	2110/2209 (96%)	2101 (100%)	9 (0%)	81	82

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	q	8	LYS
21	t	67	HIS
14	m	34	LEU
15	n	57	ARG
15	n	58	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
16	s	22	GLN
19	q	64	GLN
16	s	57	HIS
17	o	46	HIS
21	t	69	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1540/1547 (99%)	639 (41%)	0

5 of 639 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	G
1	a	10	G
1	a	11	A
1	a	15	U
1	a	17	A

There are no RNA pucker outliers to report.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

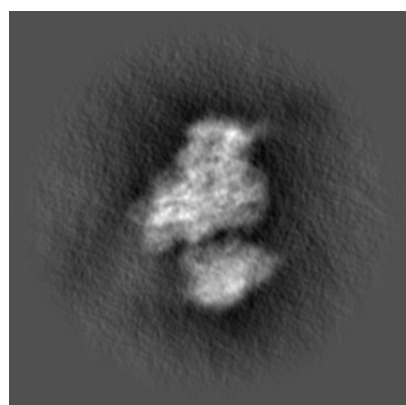
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16049. These allow visual inspection of the internal detail of the map and identification of artifacts.

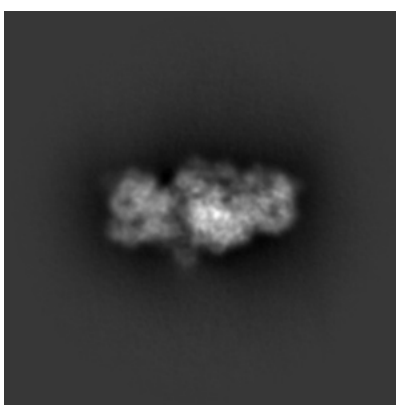
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

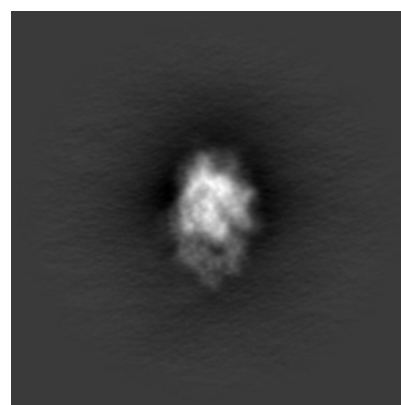
6.1.1 Primary map



X



Y

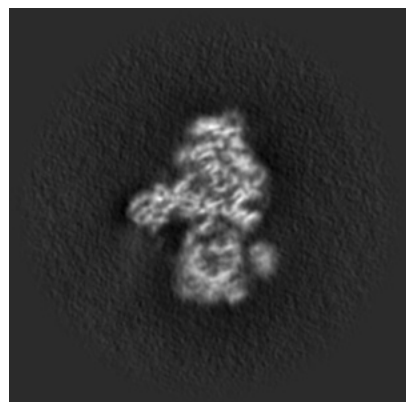


Z

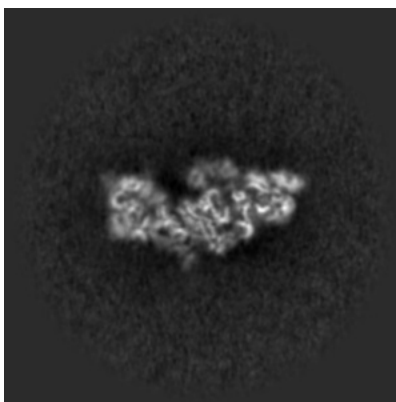
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

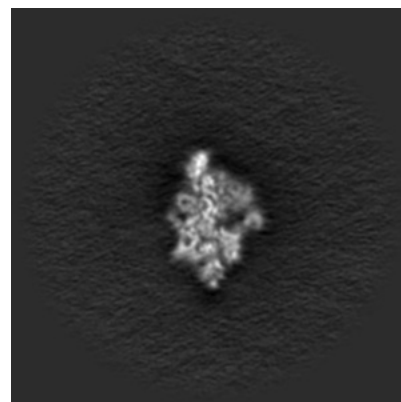
6.2.1 Primary map



X Index: 192



Y Index: 192

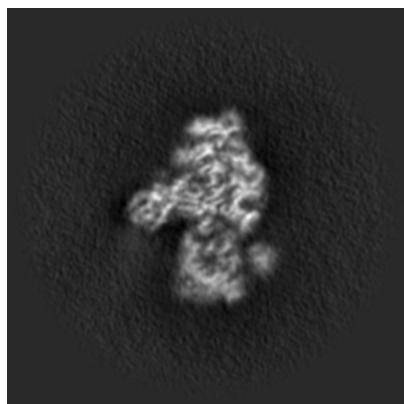


Z Index: 192

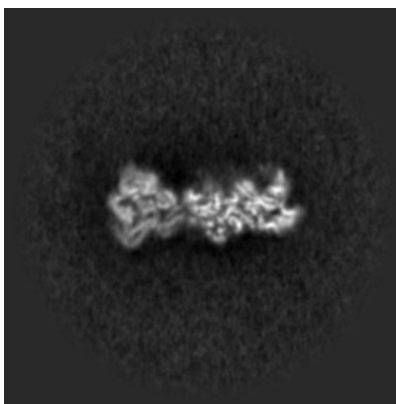
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

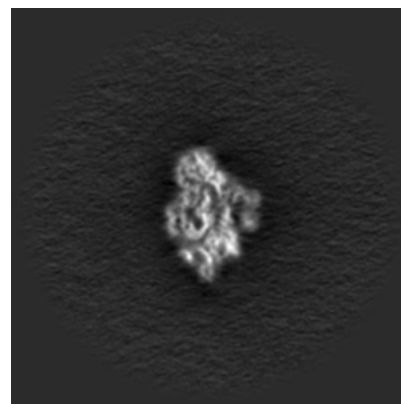
6.3.1 Primary map



X Index: 190



Y Index: 217

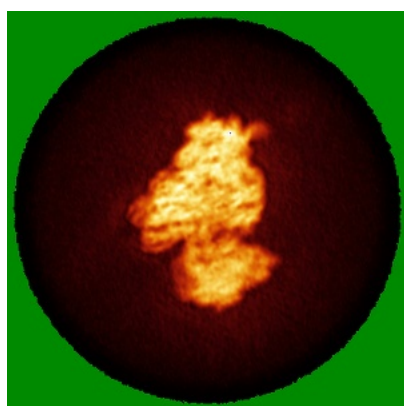


Z Index: 203

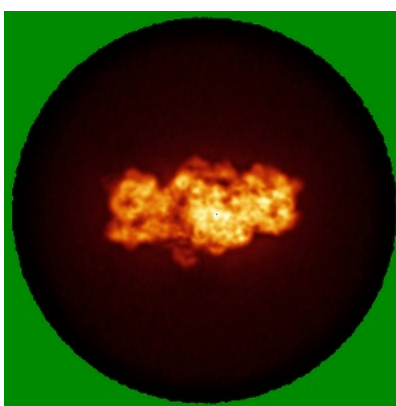
The images above show the largest variance slices of the map in three orthogonal directions.

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

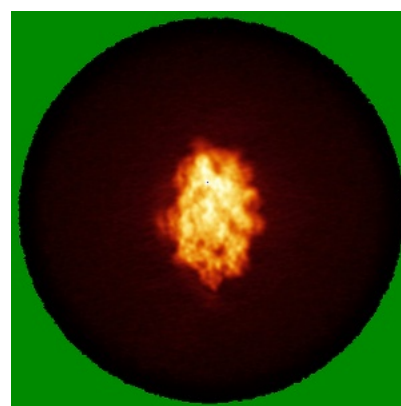
6.4.1 Primary map



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

This section was not generated.

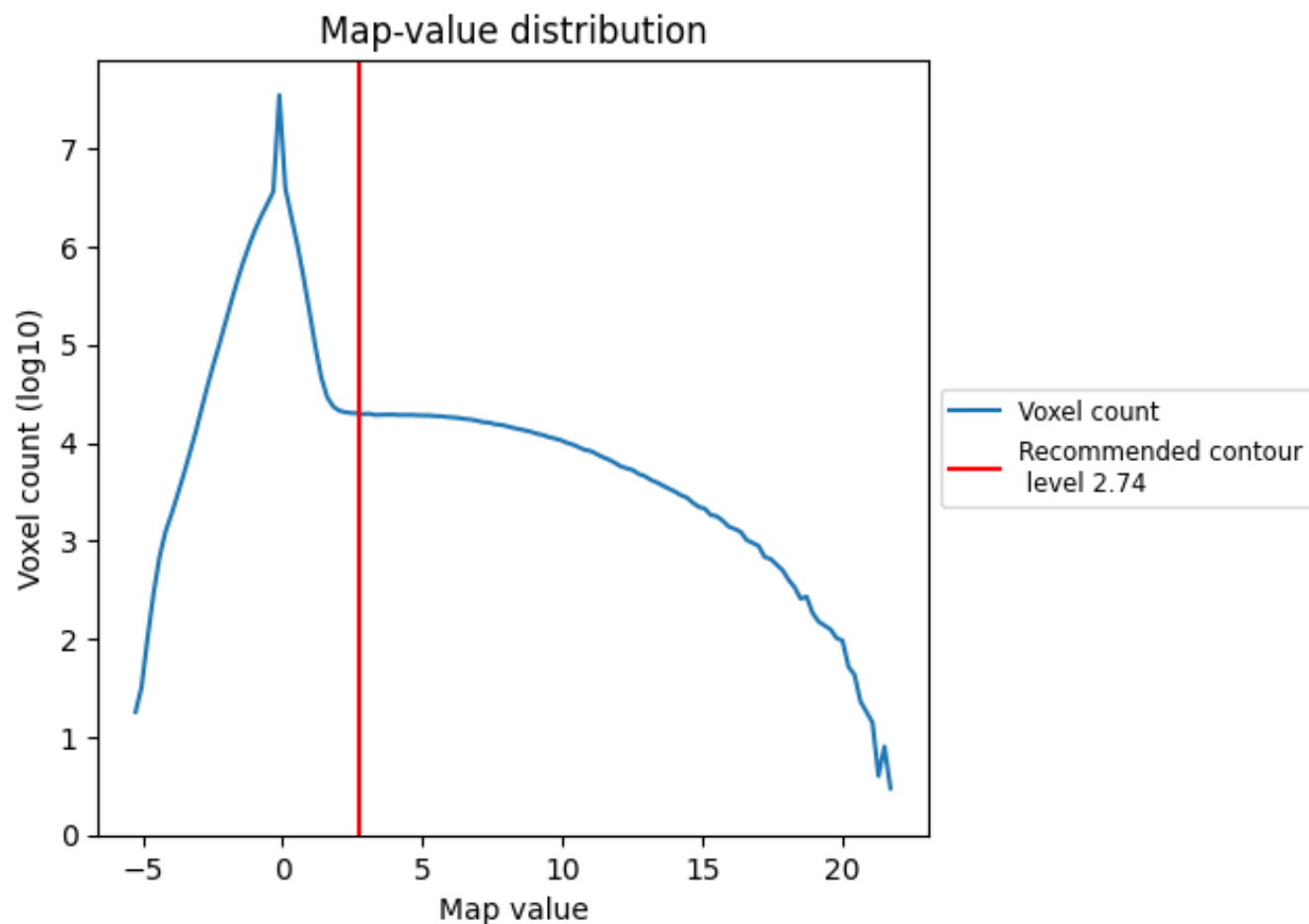
6.6 Mask visualisation

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

7 Map analysis [i](#)

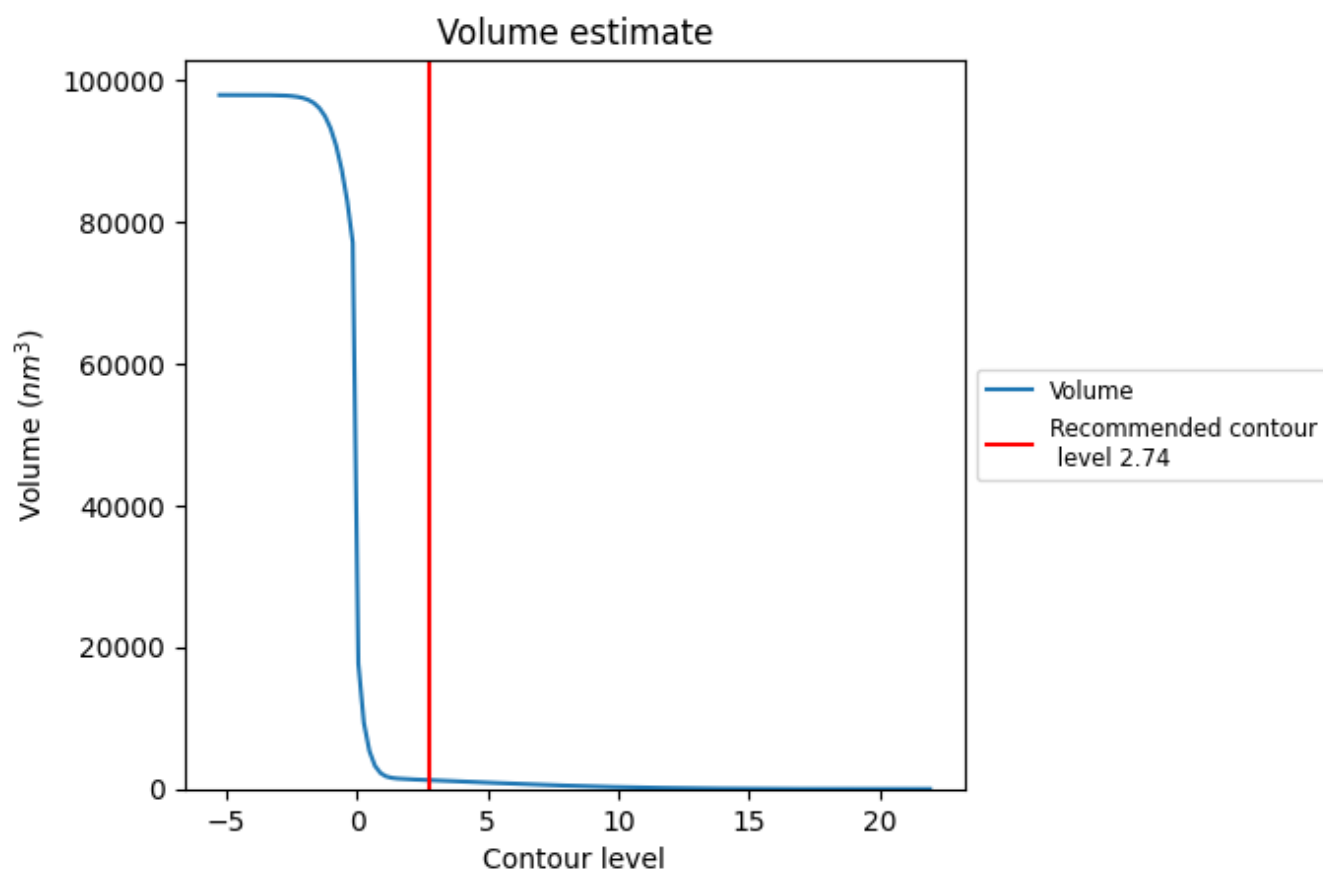
This section contains the results of statistical analysis of the map.

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.

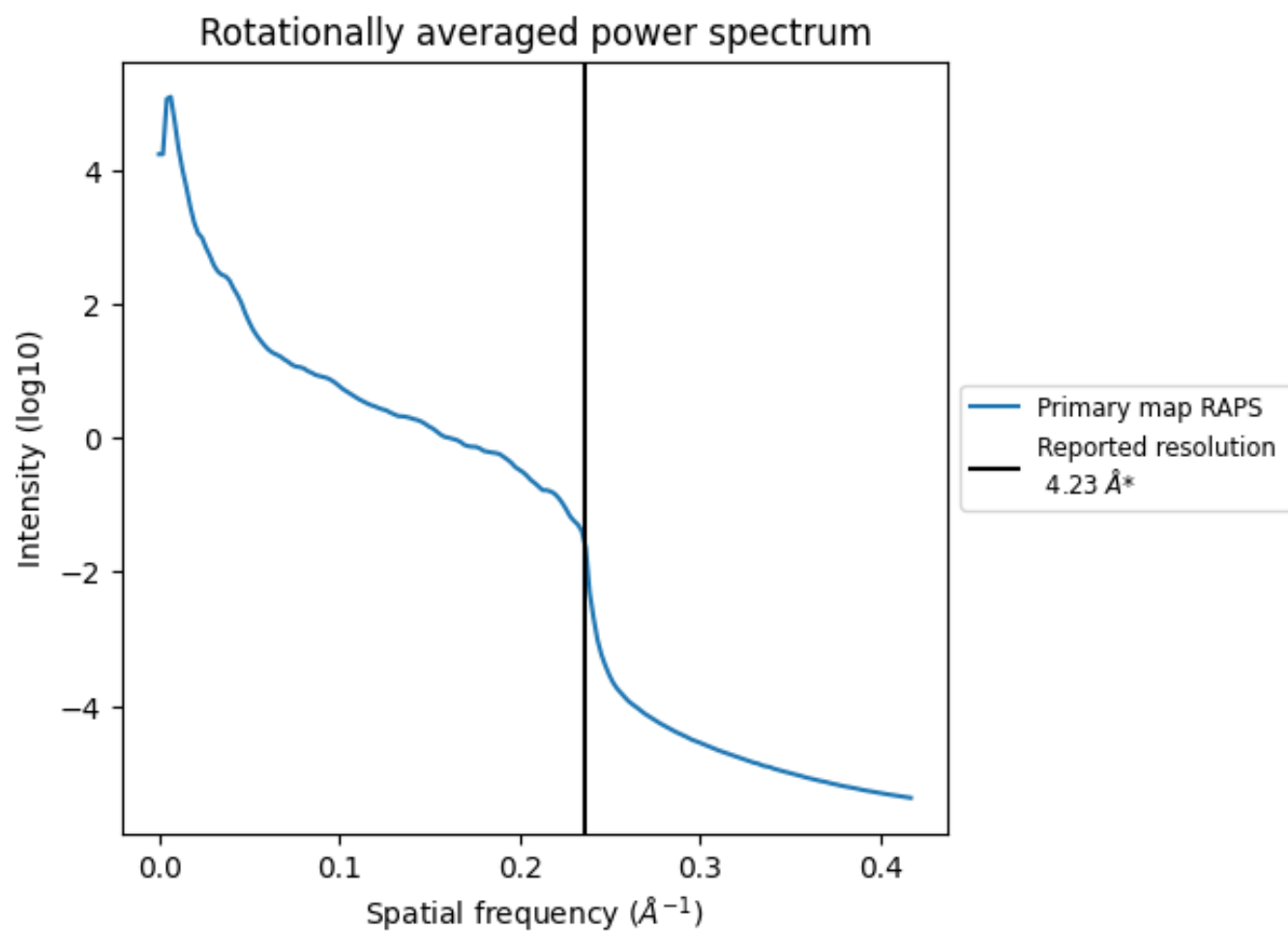
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1248 nm³; this corresponds to an approximate mass of 1127 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 0.236 Å⁻¹

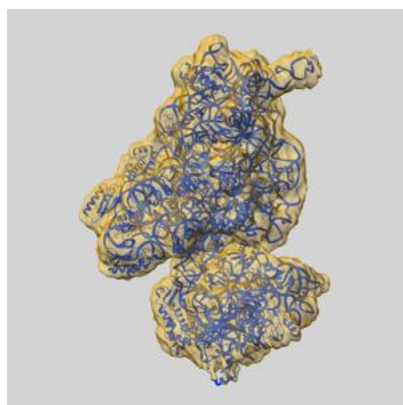
8 Fourier-Shell correlation

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

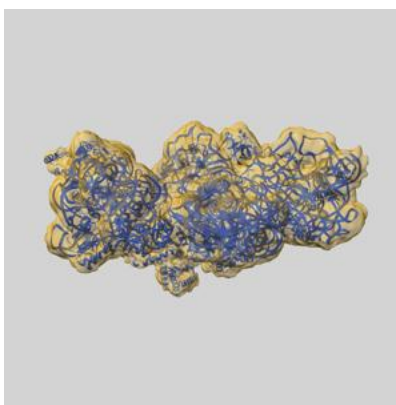
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16049 and PDB model 8BH7. Per-residue inclusion information can be found in section [3](#) on page [8](#).

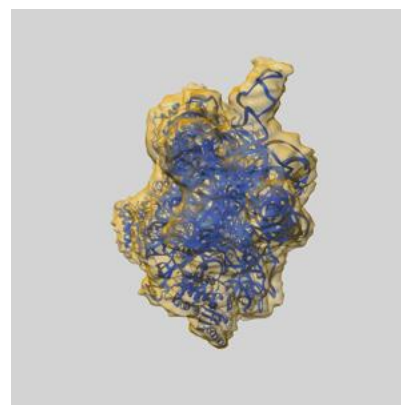
9.1 Map-model overlay [i](#)



X



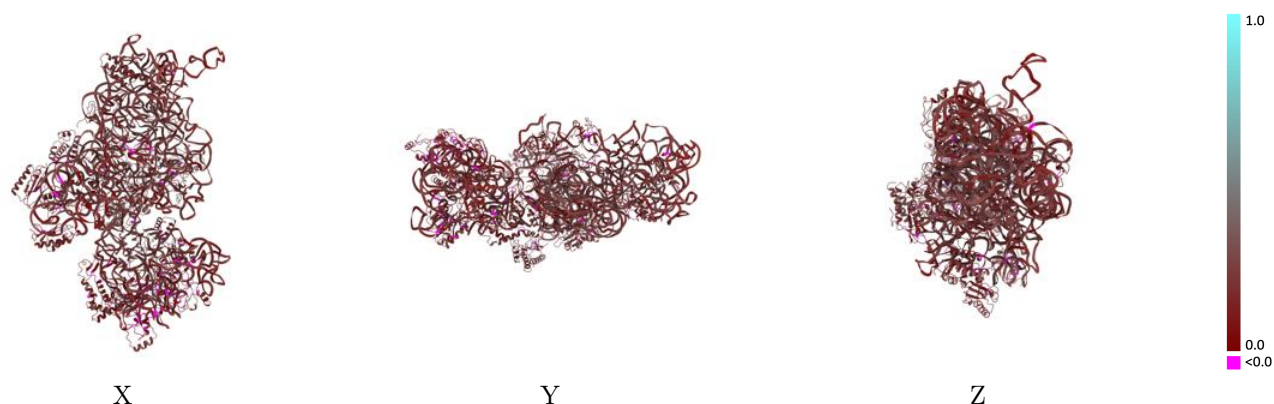
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.74 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

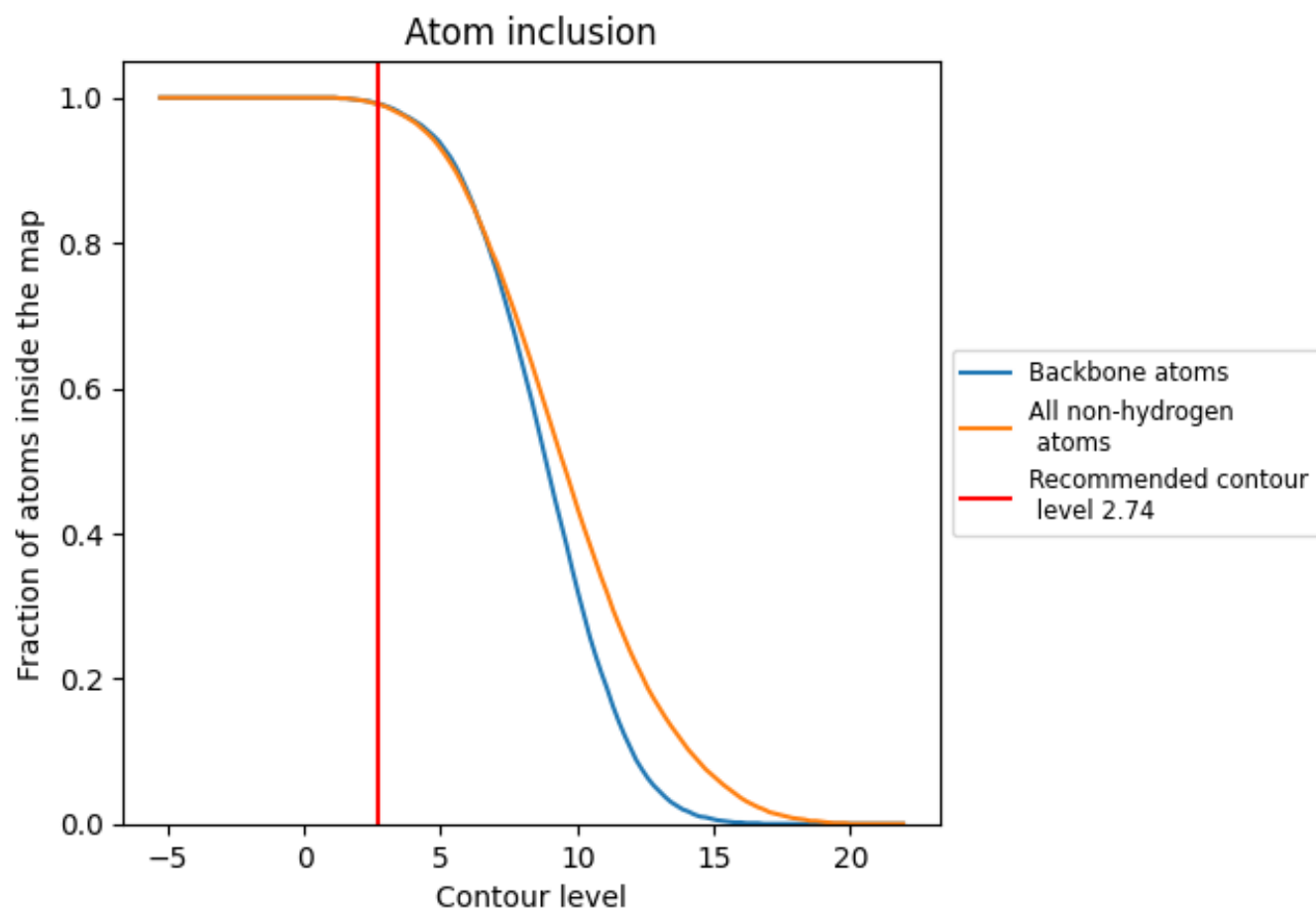


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (2.74) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9910	 0.2030
A	 0.9820	 0.1690
a	 1.0000	 0.2170
b	 0.8410	 0.1810
c	 0.9880	 0.2010
d	 1.0000	 0.2100
e	 0.9950	 0.2330
f	 0.9950	 0.1930
g	 0.9970	 0.1500
h	 0.9980	 0.1930
i	 1.0000	 0.1510
j	 0.9990	 0.1890
k	 0.9970	 0.1690
l	 0.9900	 0.1730
m	 0.8690	 0.0740
n	 1.0000	 0.1940
o	 1.0000	 0.1840
p	 1.0000	 0.2000
q	 1.0000	 0.2150
r	 0.9630	 0.1510
s	 1.0000	 0.1200
t	 0.9980	 0.2060

