



# wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 12:54 PM UTC

PDB ID : 4D61 / pdb\_00004d61  
EMDB ID : EMD-2813  
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state  
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.  
Deposited on : 2014-11-07  
Resolution : 9.00 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

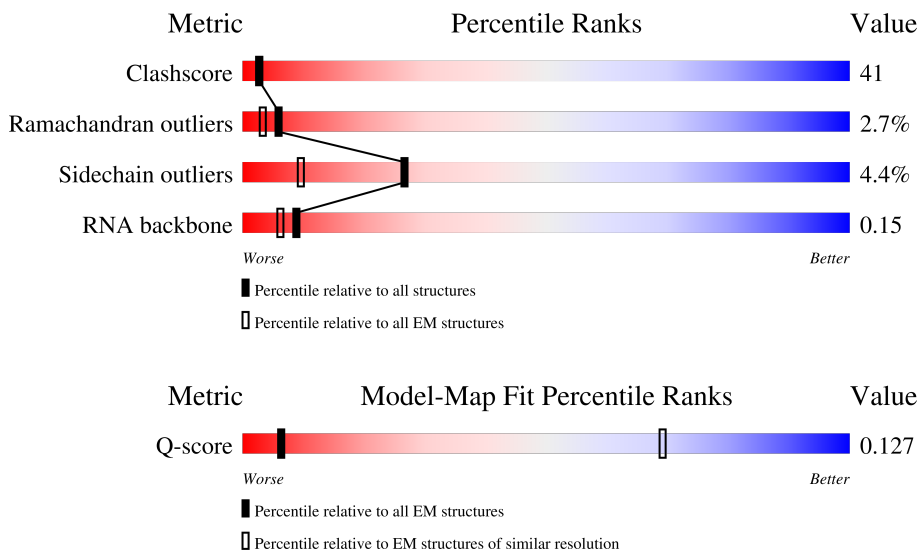
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 9.00 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	258 ( 8.40 - 9.40 )

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

Mol	Chain	Length	Quality of chain
1	1	1869	
2	A	295	
3	B	264	

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Mol	Chain	Length	Quality of chain
4	C	293	14% 47% 25% 24%
5	D	243	21% 49% 33% 5% 13%
6	E	263	16% 51% 41% 5%
7	F	204	20% 42% 44% 6% 8%
8	G	249	16% 49% 37% 7% 7%
9	H	194	54% 43% 52%
10	I	208	22% 49% 44% 6%
11	J	194	9% 49% 36% 7% 8%
12	K	165	12% 30% 21% 5% 43%
13	L	158	26% 51% 35% 6% 8%
14	M	132	54% 52% 33% 5% 9%
15	N	151	17% 56% 37% 6%
16	O	151	17% 51% 34% 5% 9%
17	P	145	23% 40% 37% 19%
18	Q	146	17% 51% 41% 5%
19	R	135	29% 42% 32% 7% 19%
20	S	152	18% 48% 37% 9% 7%
21	T	145	26% 43% 52%
22	U	119	29% 35% 45% 5% 15%
23	V	83	43% 63% 35%
24	W	130	21% 48% 47%
25	X	143	14% 48% 43% 6%
26	Y	133	17% 52% 32% 7% 8%
27	Z	125	11% 26% 29% 6% 39%
28	a	115	20% 28% 46% 8% 17%

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Mol	Chain	Length	Quality of chain
29	b	84	
30	c	69	
31	d	56	
32	e	59	
33	f	156	
34	g	317	
35	h	436	
36	i	426	
37	j	201	

## 2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 86384 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 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1742	37159	16589	6665	12164	1741	0	0

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	218	1719	1091	301	319	8	0	0

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	213	1729	1098	309	308	14	0	0

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	222	1724	1114	296	304	10	0	0

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	212	1646	1050	299	290	7	0	0

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	257	2031	1298	381	344	8	0	0

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	191	Total	C	N	O	S	0	0
			1535	978	282	274	1		

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	207	Total	C	N	O	S	0	0
			1695	1064	334	292	5		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	94	Total	C	N	O	S	0	0
			791	519	138	129	5		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	146	Total	C	N	O	S	0	0
			1199	764	224	205	6		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1207	773	229	204	1		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	137	Total	C	N	O	S	0	0
			1023	627	200	190	6		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	139	Total	C	N	O	S	0	0
			1108	704	210	191	3		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	109	Total	C	N	O	S	0	0
			893	561	170	159	3		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	T	143	1112	697	214	198	3	0	0

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	U	101	803	502	153	144	4	0	0

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	V	83	636	393	117	121	5	0	0

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	129	1033	659	193	175	6	0	0

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	X	134	1046	663	205	176	2	0	0

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	122	1002	635	196	166	5	0	0

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Z	76	605	387	112	105	1	0	0

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

- Molecule 33 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

- Molecule 34 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 35 is a protein called EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	h	436	3450	2193	582	663	12	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	438	LEU	-	expression tag	UNP P62495
h	439	GLU	-	expression tag	UNP P62495
h	440	HIS	-	expression tag	UNP P62495

- Molecule 36 is a protein called EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR GTP-BINDING SUBUNIT ERF3A.

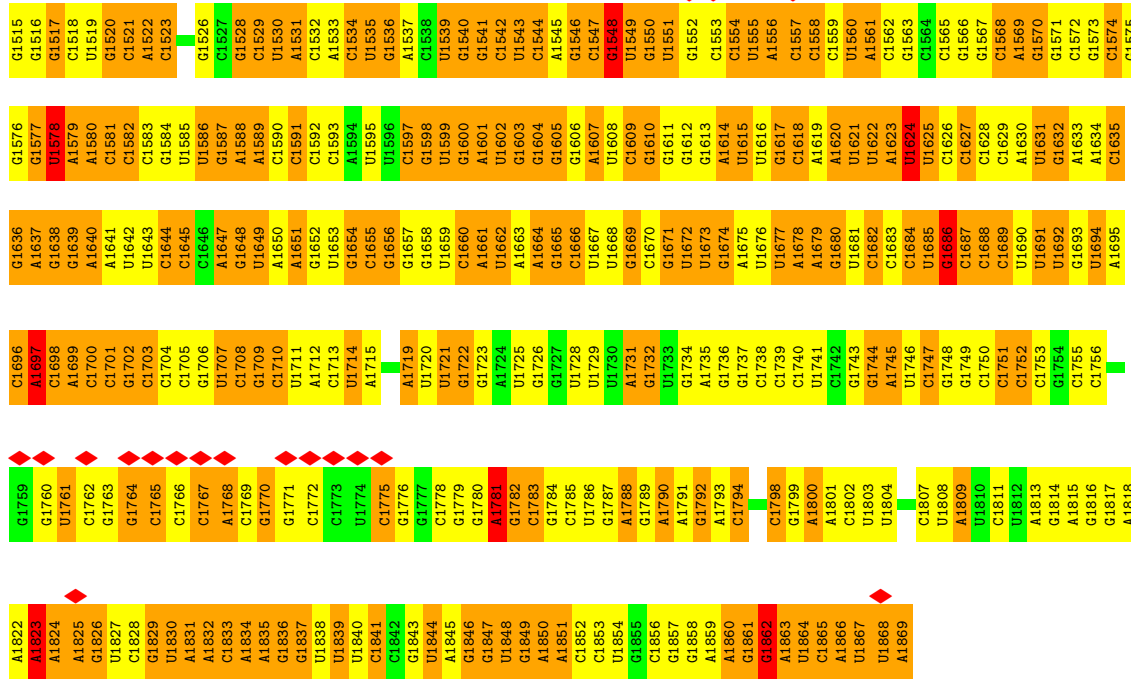
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	i	426	3357	2135	577	624	21	0	0

- Molecule 37 is a RNA chain called CRICKET PARALYSIS VIRUS IRES RNA.

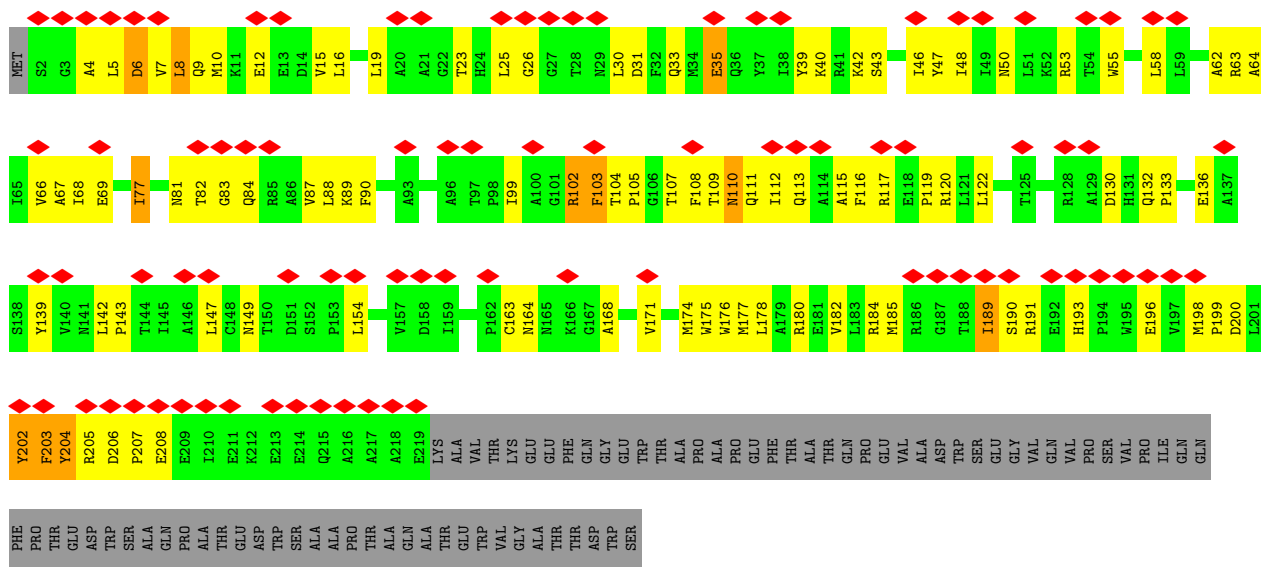
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	j	201	4257	1908	735	1413	201	0	0



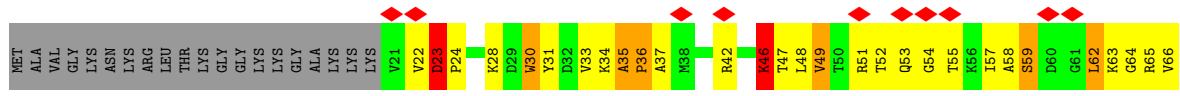
A1454	A1455	A1456	U1457	A1458	G1461	U1462	U1463	C1464	A1465	A1466	C1467	C1468	A1469	C1470	C1471	C1472	G1473	A1474	A1475	A1476	U1477	U1478	U1479	A1480	G1481	C1482	A1483	A1484	U1485	A1486	A1487	C1488	A1489	G1490	G1491	U1492	C1493	U1494	U1495	C1496	U1497	U1498	U1499	C1500	C1501	C1502	U1504	U1505	G1507	A1508	U1509	A1510	U1511	C1512	C1513	G1514	A604	A605	G606	U607	C608	U609	G610	U611	G612	G613	C614	C615	A616	G617	A618	C619	G620	C621	C622	G623	C624	G625	G626	U627	A628	A629	U630	U631	C632	C633	A634	G635	C636	U637	C638	C639	A640	A641	A642	A643	C644	C645	G646	U647	A648	U649	A650	U651	C652	C653	A654	G655	U656	A657	U658	C659	G660	U661	C662	C663																																																															
A1332	U1333	C1334	G1335	C1336	C1337	G1338	U1339	U1340	C1341	U1342	U1343	A1344	G1345	U1346	U1347	C1348	G1349	U1350	G1351	G1352	A1353	G1354	C1355	U1356	A1357	U1358	U1359	U1360	G1361	U1362	C1363	U1364	U1368	A1369	C1374	G1375	U1376	A1377	A1378	C1379	C1380	G1381	A1382	A1383	C1384	G1385	U1386	G1387	A1388	C1389	U1390	C1391	U1392	G1393	A1332	A1333	A1334	A1335	U1336	U1337	C1338	A1339	U1340	U1341	G1342	U1343	A1344	C1345	U1346	G1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355	U1356	U1357	U1358	U1359	U1360	U1361	U1362	U1363	U1364	U1365	U1366	U1367	U1368	U1369	U1370	U1371	U1372	U1373	U1374	U1375	U1376	U1377	U1378	U1379	U1380	U1381	U1382	U1383	U1384	U1385	U1386	U1387	U1388	U1389	U1390	U1391	U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453			
G1270	C1271	C1272	C1273	G1274	G1275	A1276	U1277	A1278	C1279	G1280	G1281	A1282	C1283	A1284	U1285	G1286	G1287	U1288	U1289	G1290	A1291	C1292	U1296	U1297	U1298	U1299	U1300	A1301	G1302	C1303	U1304	C1305	U1306	U1307	U1308	C1309	U1310	C1311	G1312	A1313	U1314	U1315	U1316	C1317	G1318	U1319	G1320	G1321	U1322	G1323	U1324	G1325	U1326	C1327	U1328	U1329	G1330	C1331	C1090	C1091	G1092	A1093	C1094	U1095	G1096	U1097	C1098	U1099	A1100	G1101	U1101	G1102	C1103	G1104	U1105	A1106	G1107	U1108	C1109	U1110	U1111	U1112	A1113	U1114	U1115	C1116	G1117	U1118	C1119	U1120	G1121	A1122	C1123	U1124	C1125	U1126	U1127	C1128	G1129	U1130	G1131	U1132	A1133	U1134	C1135	U1136	U1137	C1138	U1139	G1140	U1141	G1142	A1143	U1144	C1145	U1146	U1147	A1148	A1149																																																												
A1150	G1151	C1152	U1153	A1154	U1155	U1156	G1157	U1158	U1159	A1160	U1161	C1162	U1163	G1164	U1165	G1166	G1167	U1168	G1169	C1170	U1171	U1172	A1173	U1174	G1175	U1176	U1177	U1178	U1179	C1180	A1181	U1182	C1183	U1184	U1185	U1186	G1187	U1188	A1189	U1190	C1191	U1192	U1193	A1194	U1195	A1196	U1197	G1198	U1199	A1200	U1201	G1202	U1203	A1204	U1205	G1206	U1207	A1208	A1209																																																																																																																								
G1210	U1211	C1212	U1213	C1214	U1215	C1216	A1217	U1218	C1219	A1220	U1221	A1222	U1223	G1224	U1225	G1226	G1227	U1228	G1229	C1230	U1231	U1232	U1233	C1234	G1235	U1236	C1237	U1238	U1239	A1240	U1241	U1242	U1243	U1244	G1245	A1246	C1247	U1248	C1249	U1250	A1251	C1252	U1253	C1254	U1255	G1256	U1257	A1258	U1259	C1260	U1261	G1262	C1263	U1264	A1265	C1266	U1267	C1268	G1269																																																																																																																								
A1382	U1383	A1384	G1385	C1386	U1387	A1388	U1389	C1390	U1391	A1392	U1393	C1394	U1395	A1396	U1397	C1398	U1399	A1400	U1401	C1402	U1403	A1404	U1405	A1406	U1407	U1408	A1409	C1410	U1411	C1412	U1413	A1414	C1415	U1416	U1417	U1418	A1419	U1420	C1421	U1422	C1423	U1424	A1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453																																																																																																												
G1394	C1395	A1396	U1397	G1398	U1399	U1400	A1401	C1402	U1403	A1404	U1405	A1406	U1407	U1408	A1409	C1410	U1411	C1412	U1413	A1414	C1415	U1416	U1417	U1418	A1419	U1420	C1421	U1422	C1423	U1424	A1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453																																																																																																																								
A664	G665	U666	U667	A668	U669	G670	A671	U672	C673	G674	U675	C676	U677	U678	A679	G680	U681	U682	G683	U684	G685	U686	U687	U688	U689	G690	C691	G692	A693	U694	C695	G696	G697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843
A664	G665	U666	U667	A668	U669	G670	A671	U672	C673	G674	U675	C676	U677	U678	A679	G680	U681	U682	G683	U684	G685	U686	U687	U688	U689	G690	C691	G692	A693	U694	C695	G696	G697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843
A664	G665	U666	U667	A668	U669	G670	A671	U672	C673	G674	U675	C676	U677	U678	A679	G680	U681	U682	G683	U684	G685	U686	U687	U688	U689	G690	C691	G692	A693	U694	C695	G696	G697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843

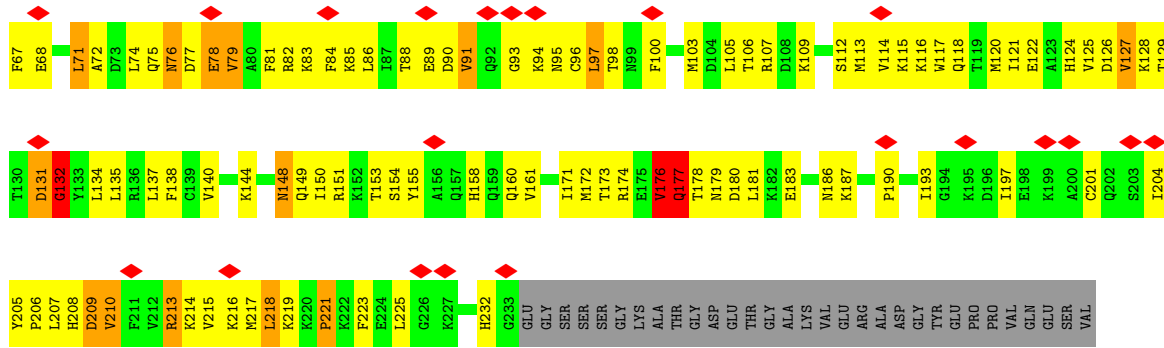


• Molecule 2: 40S RIBOSOMAL PROTEIN SA

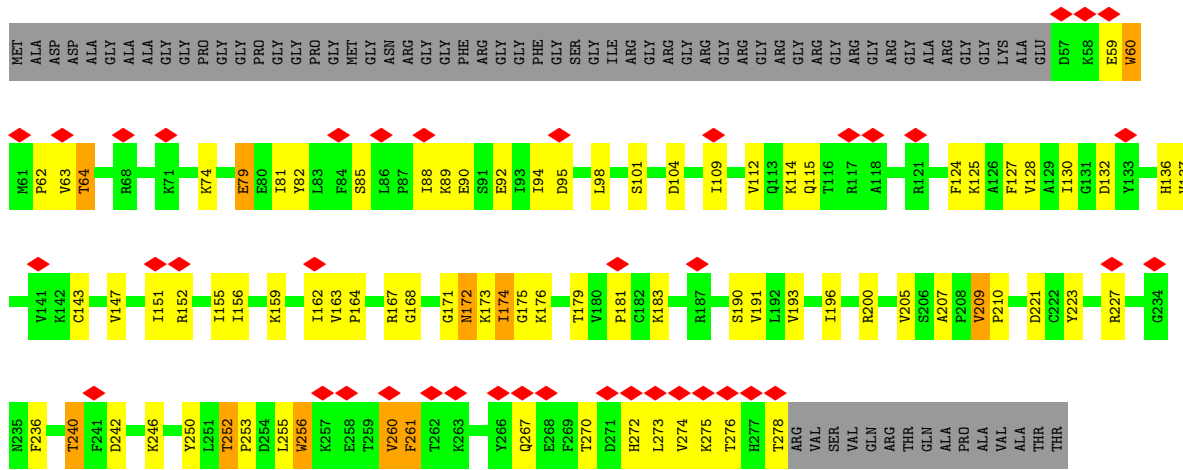


• Molecule 3: 40S RIBOSOMAL PROTEIN S3A

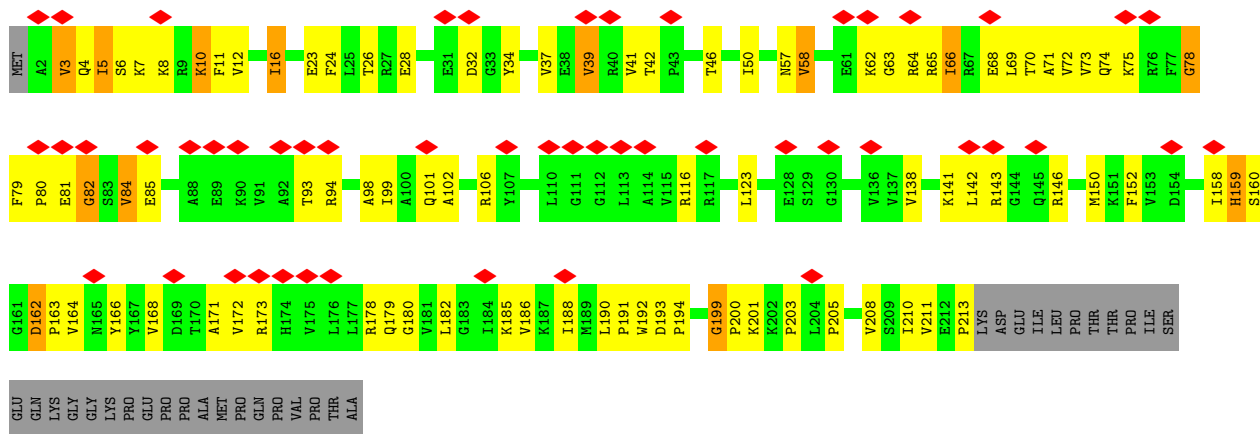




• Molecule 4: 40S RIBOSOMAL PROTEIN S2



• Molecule 5: 40S RIBOSOMAL PROTEIN S3



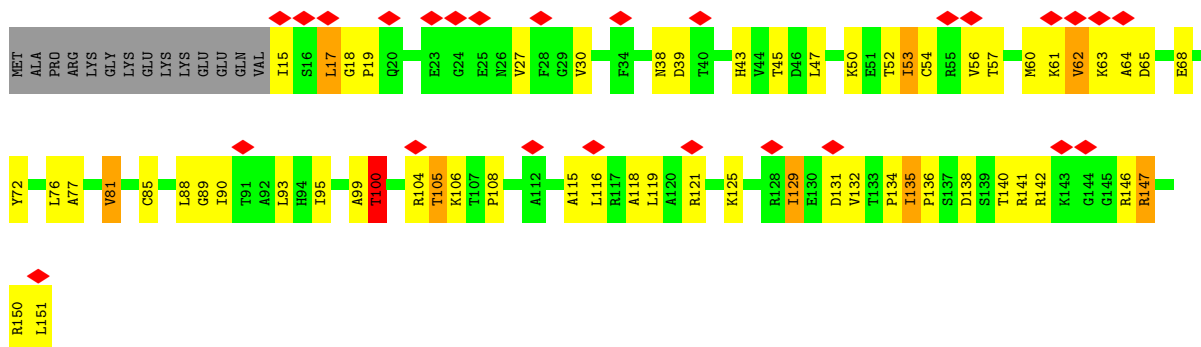
• Molecule 6: 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1



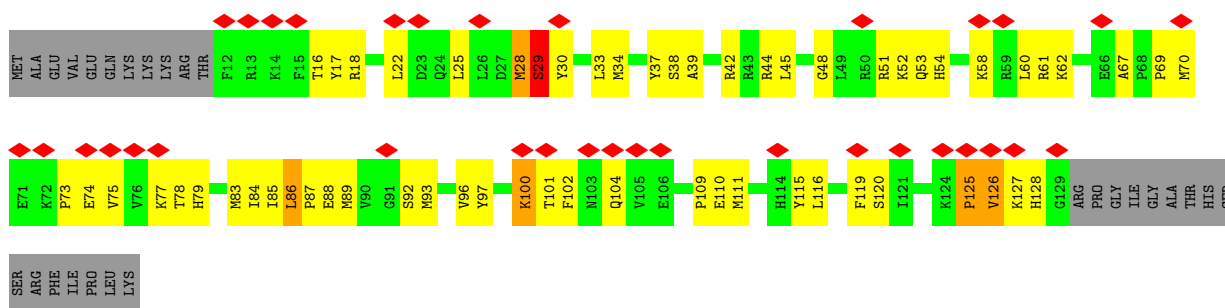




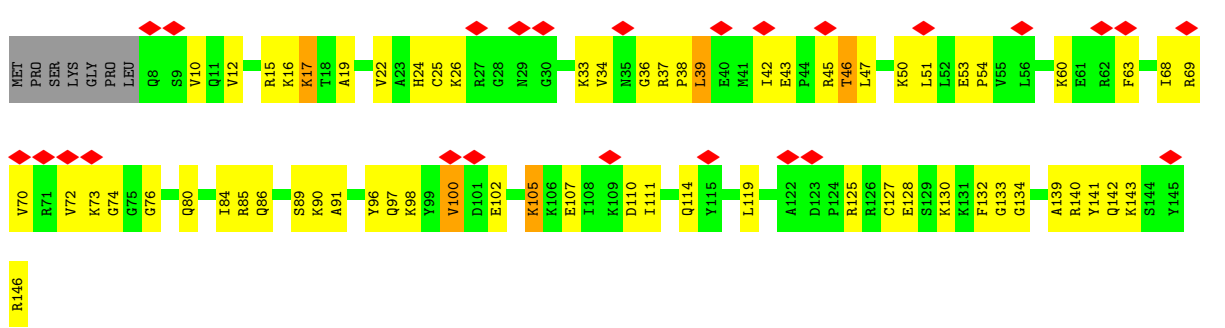




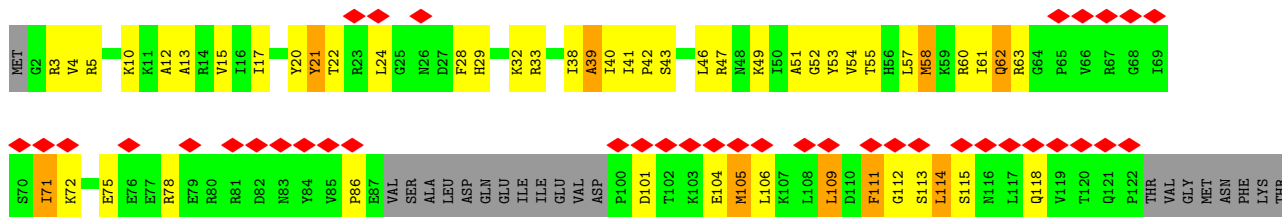
• Molecule 17: 40S RIBOSOMAL PROTEIN S15



• Molecule 18: 40S RIBOSOMAL PROTEIN S16

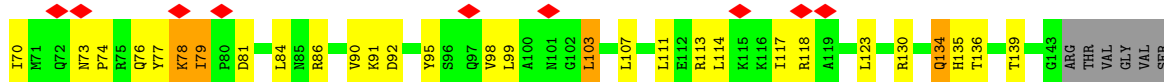
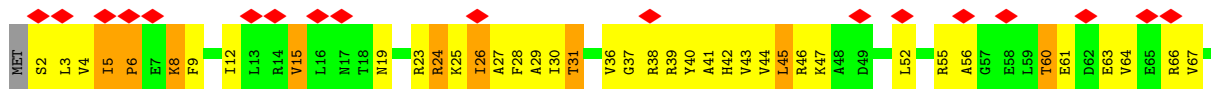


• Molecule 19: 40S RIBOSOMAL PROTEIN S17



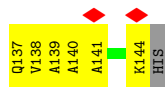
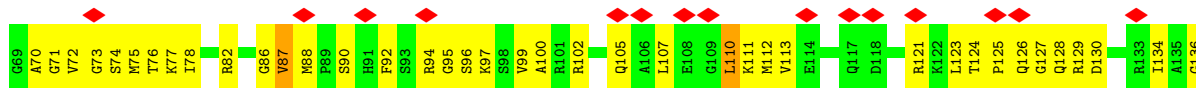
PRO  
ARG  
GLY  
PRO  
VAL

• Molecule 20: 40S RIBOSOMAL PROTEIN S18

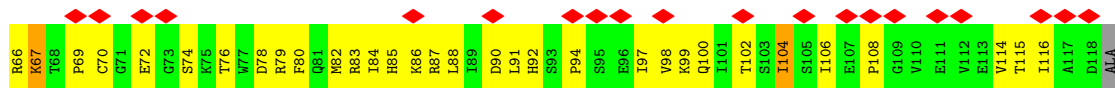
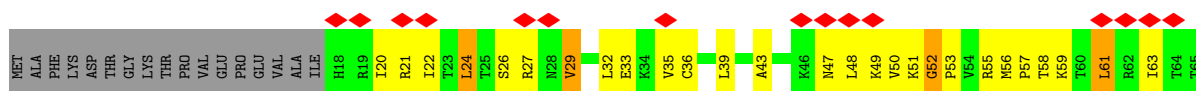


LYS  
LYS  
LYS

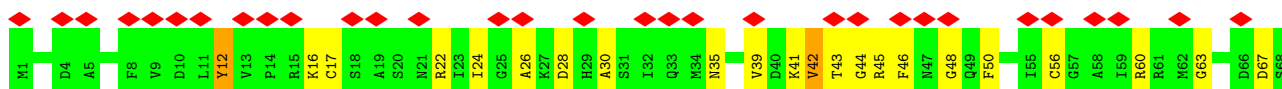
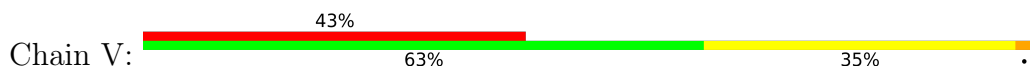
• Molecule 21: 40S RIBOSOMAL PROTEIN S19



• Molecule 22: 40S RIBOSOMAL PROTEIN S20

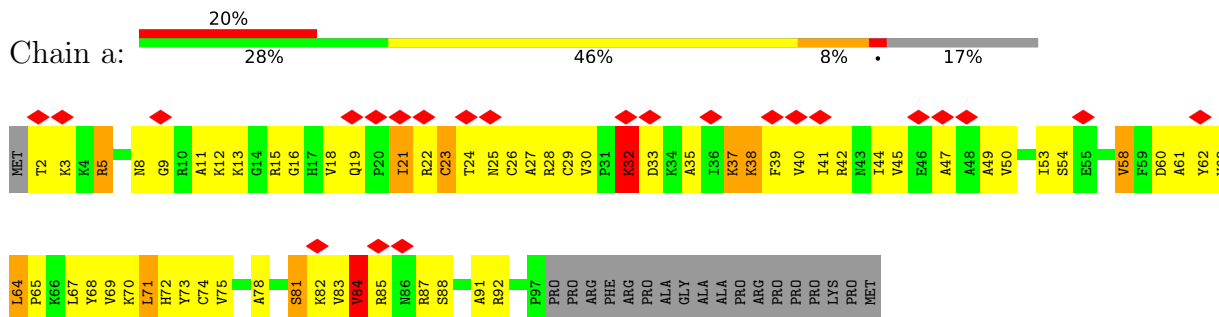


• Molecule 23: 40S RIBOSOMAL PROTEIN S21

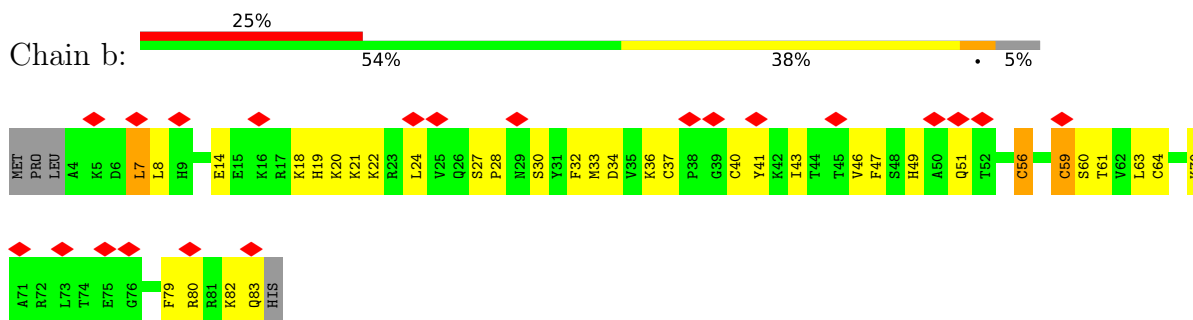




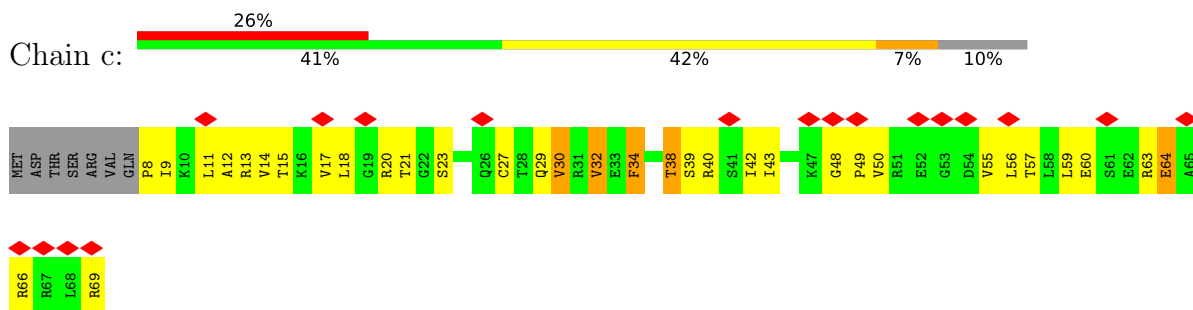
- Molecule 28: 40S RIBOSOMAL PROTEIN S26



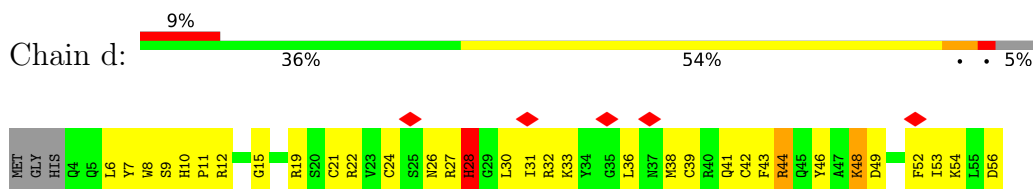
- Molecule 29: 40S RIBOSOMAL PROTEIN S27



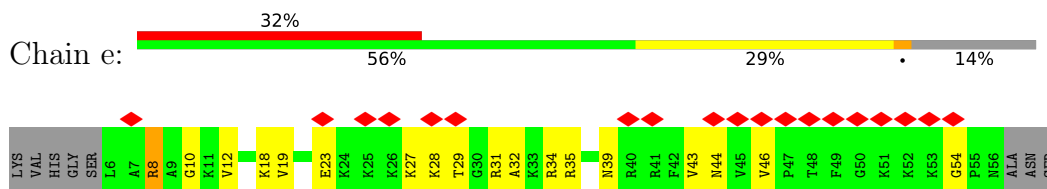
- Molecule 30: 40S RIBOSOMAL PROTEIN S28



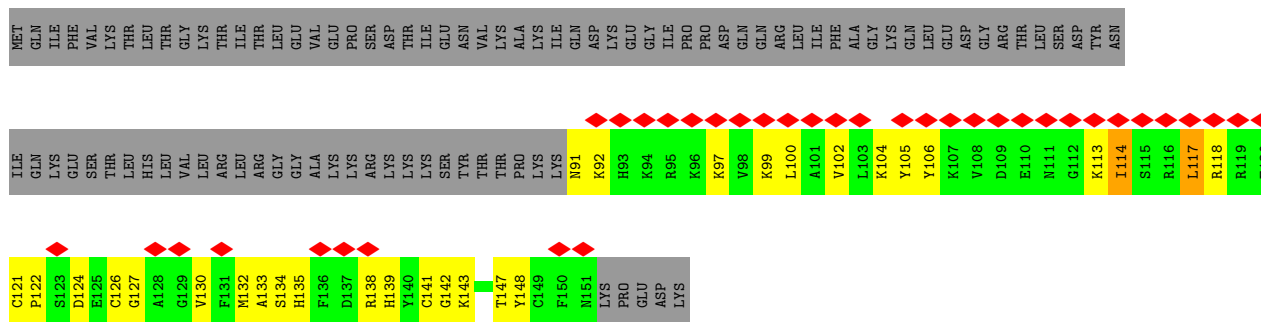
- Molecule 31: 40S RIBOSOMAL PROTEIN S29



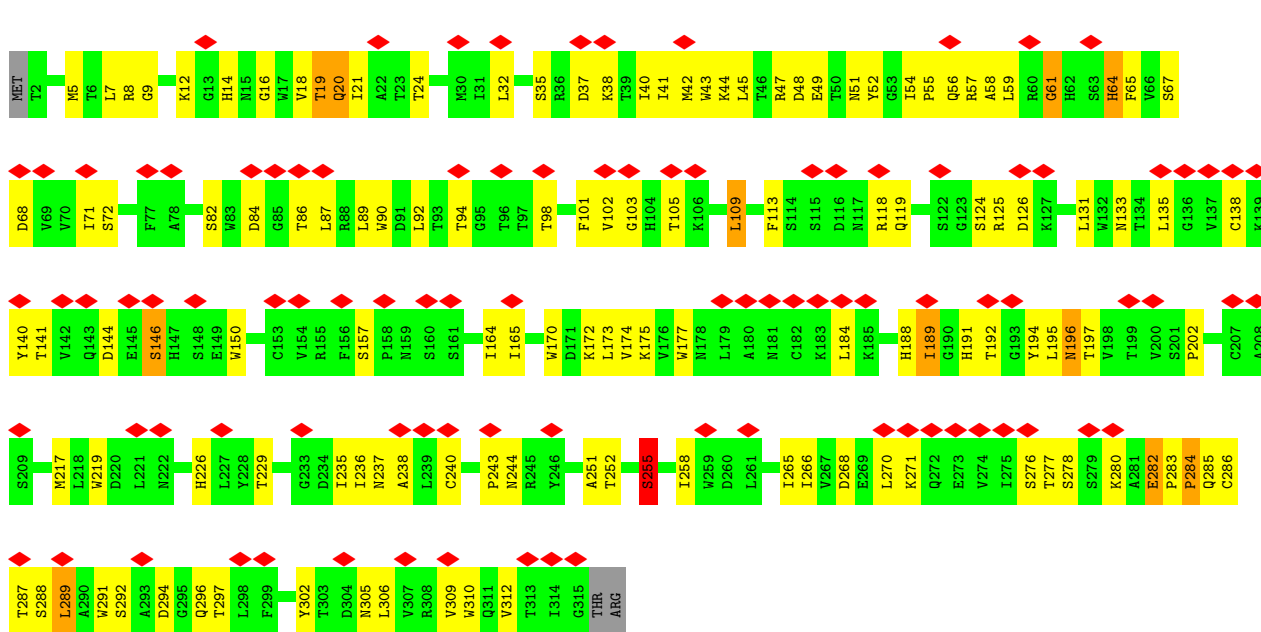
- Molecule 32: 40S RIBOSOMAL PROTEIN S30



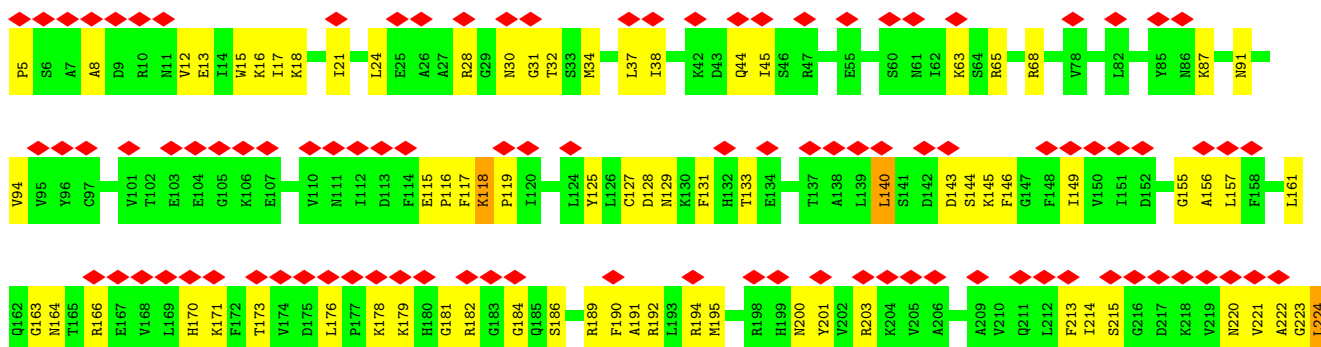
- Molecule 33: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

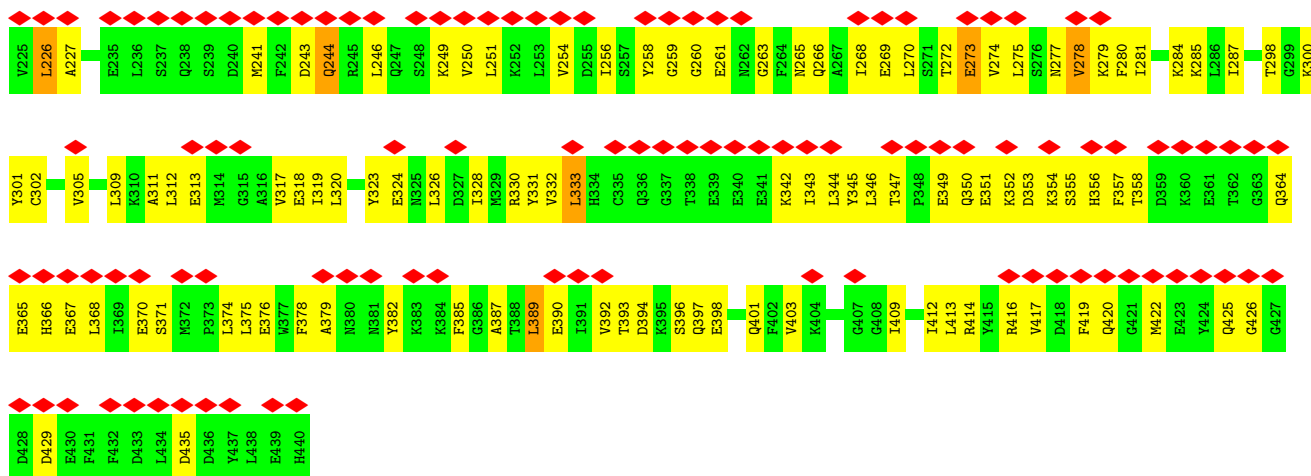


• Molecule 34: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1

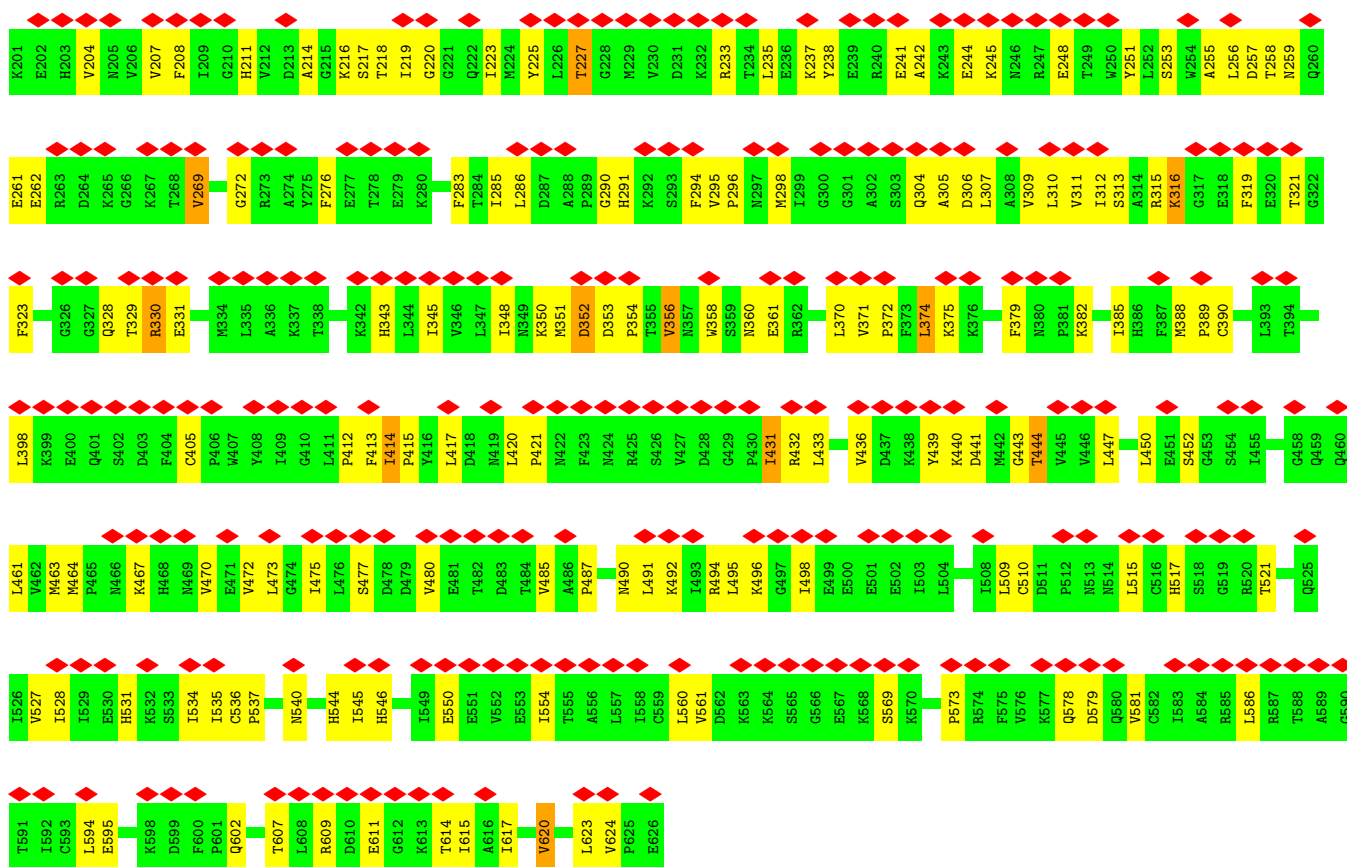


• Molecule 35: EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1



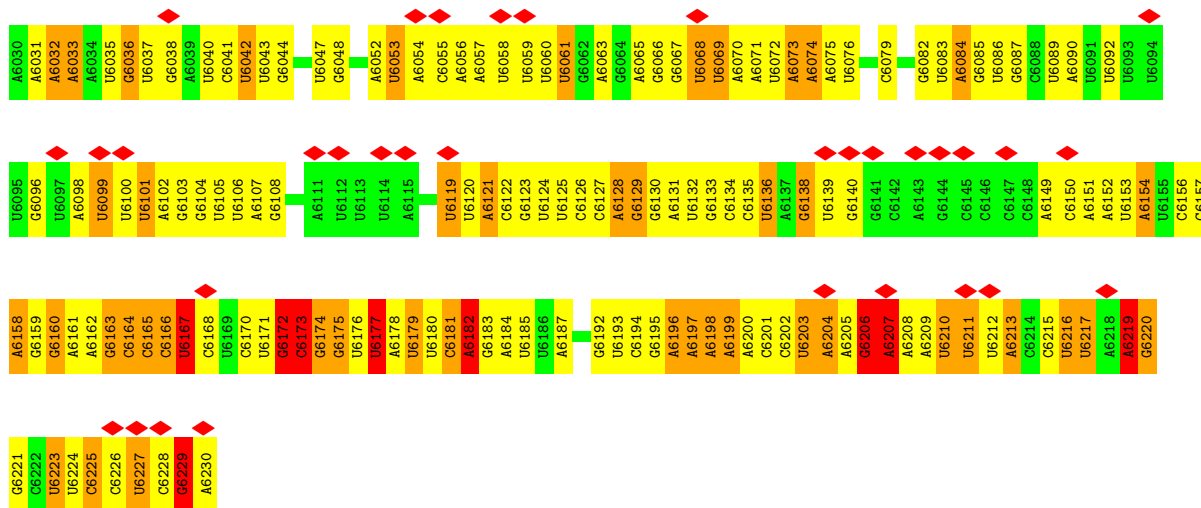


• Molecule 36: EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR GTP-BINDING SUB-UNIT ERF3A



• Molecule 37: CRICKET PARALYSIS VIRUS IRES RNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64902	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	194805	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	12.165	Depositor
Minimum map value	-4.363	Depositor
Average map value	0.164	Depositor
Map value standard deviation	0.954	Depositor
Recommended contour level	3	Depositor
Map size ( $\text{\AA}$ )	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.56, 1.56, 1.56	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	1	0.31	0/41550	0.66	11/64763 (0.0%)
2	A	0.89	4/1756 (0.2%)	1.16	11/2386 (0.5%)
3	B	0.83	0/1756	1.20	13/2350 (0.6%)
4	C	0.69	0/1761	1.10	5/2379 (0.2%)
5	D	0.63	0/1672	1.15	9/2250 (0.4%)
6	E	0.72	0/2072	1.16	10/2793 (0.4%)
7	F	0.68	0/1507	1.15	10/2026 (0.5%)
8	G	0.77	1/1907 (0.1%)	1.23	10/2538 (0.4%)
9	H	0.75	0/1558	1.26	12/2087 (0.6%)
10	I	0.75	0/1724	1.12	6/2298 (0.3%)
11	J	0.74	0/1520	1.25	13/2030 (0.6%)
12	K	0.77	0/815	1.10	5/1101 (0.5%)
13	L	0.69	0/1220	1.16	8/1633 (0.5%)
14	M	0.74	0/941	1.19	3/1264 (0.2%)
15	N	0.69	0/1231	1.21	12/1656 (0.7%)
16	O	0.73	0/1036	1.16	6/1391 (0.4%)
17	P	0.66	0/1000	1.07	2/1335 (0.1%)
18	Q	0.69	0/1125	1.10	3/1506 (0.2%)
19	R	0.69	0/904	1.11	6/1208 (0.5%)
20	S	0.69	0/1190	1.14	5/1594 (0.3%)
21	T	0.68	0/1131	1.10	3/1515 (0.2%)
22	U	0.76	0/813	1.17	3/1092 (0.3%)
23	V	0.70	0/643	1.16	2/860 (0.2%)
24	W	0.69	0/1050	1.12	6/1406 (0.4%)
25	X	0.76	0/1063	1.11	1/1421 (0.1%)
26	Y	0.71	0/1019	1.12	5/1354 (0.4%)
27	Z	0.68	0/611	1.14	3/820 (0.4%)
28	a	0.78	0/778	1.19	7/1041 (0.7%)
29	b	0.70	0/637	1.09	2/854 (0.2%)
30	c	0.71	0/492	1.15	5/657 (0.8%)
31	d	0.73	0/454	1.10	1/603 (0.2%)
32	e	0.70	0/417	1.09	0/548
33	f	0.76	0/507	1.33	5/673 (0.7%)
34	g	0.69	0/2497	1.06	7/3399 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	h	0.56	0/3506	0.97	5/4709 (0.1%)
36	i	0.64	1/3418 (0.0%)	0.96	4/4600 (0.1%)
37	j	0.86	21/4752 (0.4%)	0.67	18/7383 (0.2%)
All	All	0.58	27/92033 (0.0%)	0.90	237/133523 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	24
37	j	0	1
All	All	0	25

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	j	6173	C	O3'-P	-16.11	1.36	1.61
37	j	6229	G	O3'-P	15.71	1.84	1.61
37	j	6177	U	O3'-P	-14.71	1.39	1.61
37	j	6219	A	O3'-P	-12.77	1.42	1.61
37	j	6215	C	O3'-P	-12.45	1.42	1.61

The worst 5 of 237 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	37	ALA	N-CA-C	11.17	123.46	111.28
33	f	124	ASP	N-CA-C	-10.45	97.14	111.56
5	D	58	VAL	N-CA-C	10.33	120.34	110.42
15	N	24	THR	N-CA-C	9.81	121.73	111.14
4	C	60	TRP	N-CA-C	9.67	121.42	111.07

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	111	A	Sidechain
1	1	44	U	Sidechain
1	1	77	A	Sidechain
1	1	84	A	Sidechain

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Mol	Chain	Res	Type	Group
1	1	88	G	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	37159	0	18774	3845	0
2	A	1719	0	1717	132	0
3	B	1729	0	1803	143	0
4	C	1724	0	1808	83	0
5	D	1646	0	1736	123	0
6	E	2031	0	2138	118	0
7	F	1486	0	1545	121	0
8	G	1884	0	2044	156	0
9	H	1535	0	1632	133	0
10	I	1695	0	1785	116	0
11	J	1495	0	1615	94	0
12	K	791	0	811	53	0
13	L	1199	0	1269	74	0
14	M	931	0	961	44	0
15	N	1207	0	1294	67	0
16	O	1023	0	1050	61	0
17	P	981	0	1026	56	0
18	Q	1108	0	1174	88	0
19	R	893	0	946	65	0
20	S	1172	0	1229	77	0
21	T	1112	0	1146	117	0
22	U	803	0	866	80	0
23	V	636	0	637	43	0
24	W	1033	0	1080	65	0
25	X	1046	0	1110	73	0
26	Y	1002	0	1075	66	0
27	Z	605	0	665	57	0
28	a	767	0	816	101	0
29	b	625	0	642	38	0
30	c	490	0	520	35	0
31	d	444	0	442	53	0
32	e	412	0	463	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	f	497	0	497	47	0
34	g	2440	0	2396	120	0
35	h	3450	0	3446	217	0
36	i	3357	0	3398	165	0
37	j	4257	0	2143	311	0
All	All	86384	0	67699	6277	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 41.

The worst 5 of 6277 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)
5:D:116:ARG:NH1	37:j:6224:U:C6	1.68	1.61
1:1:478:G:O3'	36:i:443:GLY:CA	1.63	1.46
1:1:1684:C:H4'	37:j:6211:U:C4	1.55	1.41
1:1:1684:C:C4'	37:j:6211:U:C4	2.09	1.33
4:C:147:VAL:HG21	37:j:6224:U:P	1.69	1.33

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	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	14 51
3	B	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1 9
4	C	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	5 28
5	D	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	4 27
6	E	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6 31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	F	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	1	15
8	G	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	2	19
9	H	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	5	30
10	I	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	21
11	J	177/194 (91%)	168 (95%)	6 (3%)	3 (2%)	7	36
12	K	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	10
13	L	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	2	17
14	M	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	1	15
15	N	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	21
16	O	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	5	29
17	P	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	17
18	Q	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	8	40
19	R	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	6	32
20	S	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	14
21	T	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	9	40
22	U	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	12	49
23	V	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	4	26
24	W	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	7	38
25	X	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	1	15
26	Y	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	3	21
27	Z	74/125 (59%)	71 (96%)	0	3 (4%)	2	18
28	a	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	17
29	b	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
30	c	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	21
31	d	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
32	e	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	6	31
33	f	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
34	g	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	5	29
35	h	428/436 (98%)	410 (96%)	14 (3%)	4 (1%)	14	51
36	i	414/426 (97%)	403 (97%)	9 (2%)	2 (0%)	24	63
All	All	5553/6338 (88%)	5186 (93%)	215 (4%)	152 (3%)	6	25

5 of 152 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	76	ASN
3	B	132	GLY
3	B	148	ASN
3	B	154	SER
3	B	176	VAL

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	181/243 (74%)	177 (98%)	4 (2%)	45	64
3	B	194/231 (84%)	182 (94%)	12 (6%)	16	38
4	C	188/225 (84%)	179 (95%)	9 (5%)	23	44
5	D	175/202 (87%)	164 (94%)	11 (6%)	16	37
6	E	220/225 (98%)	207 (94%)	13 (6%)	18	39
7	F	158/170 (93%)	152 (96%)	6 (4%)	29	50
8	G	202/218 (93%)	196 (97%)	6 (3%)	36	57
9	H	171/174 (98%)	170 (99%)	1 (1%)	78	83
10	I	179/180 (99%)	167 (93%)	12 (7%)	15	36
11	J	160/168 (95%)	152 (95%)	8 (5%)	22	43
12	K	85/136 (62%)	81 (95%)	4 (5%)	23	45
13	L	133/142 (94%)	130 (98%)	3 (2%)	44	64
14	M	102/108 (94%)	96 (94%)	6 (6%)	18	39
15	N	130/131 (99%)	128 (98%)	2 (2%)	57	72
16	O	107/119 (90%)	99 (92%)	8 (8%)	12	33
17	P	107/130 (82%)	103 (96%)	4 (4%)	30	51
18	Q	115/121 (95%)	111 (96%)	4 (4%)	32	53
19	R	99/122 (81%)	92 (93%)	7 (7%)	13	35
20	S	123/132 (93%)	115 (94%)	8 (6%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	T	113/115 (98%)	106 (94%)	7 (6%)	16	38
22	U	93/107 (87%)	87 (94%)	6 (6%)	15	37
23	V	67/67 (100%)	67 (100%)	0	100	100
24	W	112/113 (99%)	108 (96%)	4 (4%)	31	52
25	X	108/115 (94%)	104 (96%)	4 (4%)	30	51
26	Y	107/115 (93%)	100 (94%)	7 (6%)	15	37
27	Z	67/103 (65%)	62 (92%)	5 (8%)	12	33
28	a	83/98 (85%)	76 (92%)	7 (8%)	10	30
29	b	72/76 (95%)	68 (94%)	4 (6%)	19	40
30	c	55/62 (89%)	52 (94%)	3 (6%)	19	41
31	d	47/49 (96%)	44 (94%)	3 (6%)	16	37
32	e	42/48 (88%)	39 (93%)	3 (7%)	13	35
33	f	54/140 (39%)	51 (94%)	3 (6%)	19	40
34	g	272/275 (99%)	260 (96%)	12 (4%)	25	47
35	h	376/376 (100%)	366 (97%)	10 (3%)	39	61
36	i	371/371 (100%)	361 (97%)	10 (3%)	39	61
All	All	4868/5407 (90%)	4652 (96%)	216 (4%)	27	47

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	R	58	MET
24	W	20	ARG
35	h	224	LEU
19	R	118	GLN
21	T	33	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
17	P	35	GLN
35	h	425	GLN
23	V	2	GLN
35	h	397	GLN
36	i	578	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1738/1869 (92%)	1041 (59%)	152 (8%)
37	j	196/201 (97%)	51 (26%)	0
All	All	1934/2070 (93%)	1092 (56%)	152 (7%)

5 of 1092 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	A
1	1	3	C
1	1	4	C
1	1	5	U
1	1	6	G

5 of 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1494	U
1	1	1824	A
1	1	1534	C
1	1	1637	A
1	1	1862	G

## 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
37	j	10
36	i	5
35	h	3

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	j	6150:C	O3'	6151:A	P	11.37
1	j	6065:A	O3'	6066:G	P	10.23
1	j	6106:U	O3'	6107:A	P	9.31
1	j	6136:U	O3'	6137:A	P	8.47
1	i	325:LYS	C	326:GLY	N	5.91

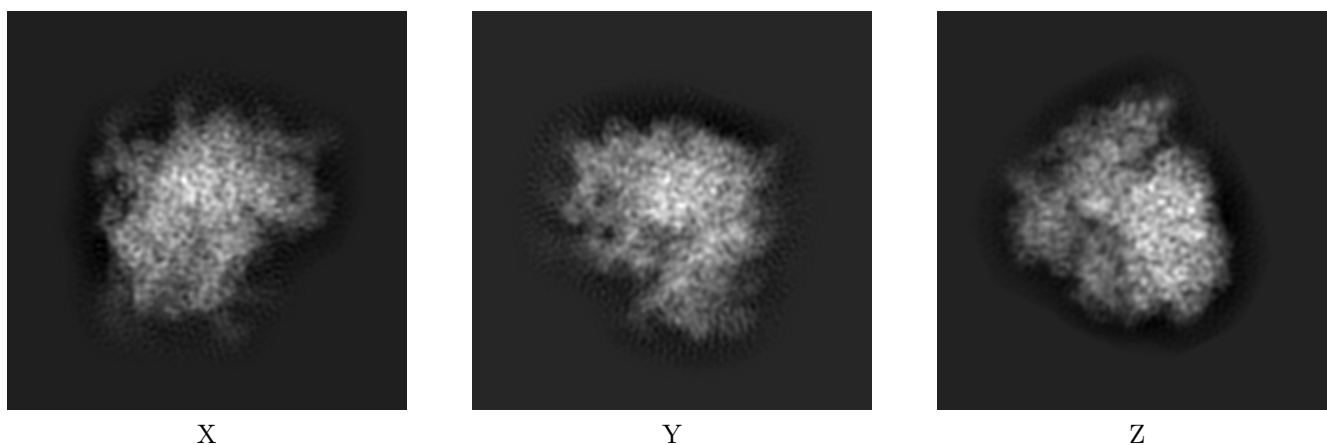
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2813. 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](#)

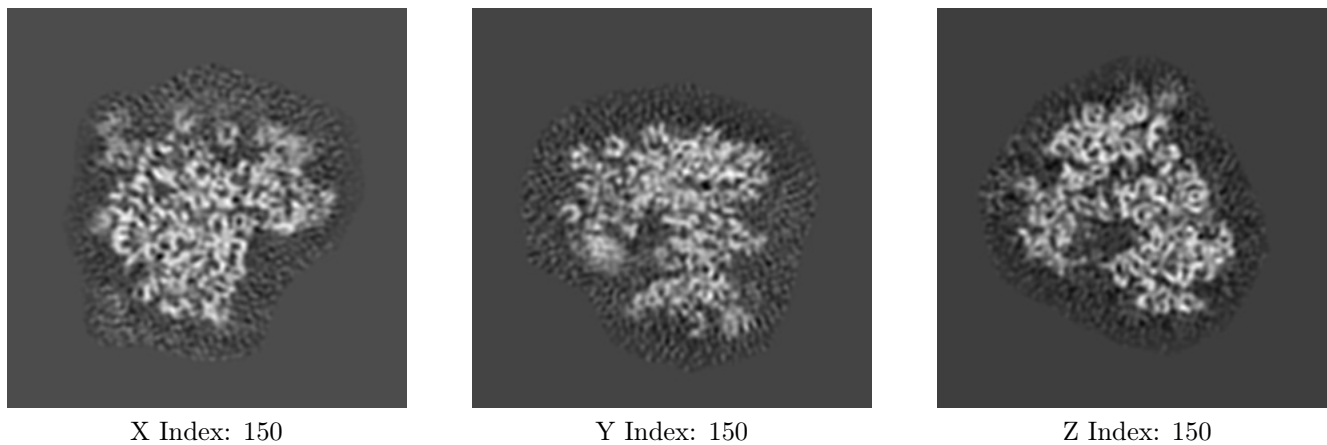
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

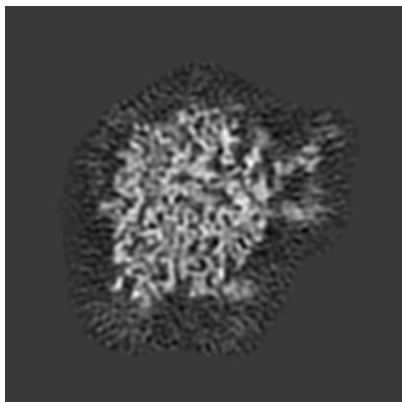
#### 6.2.1 Primary map



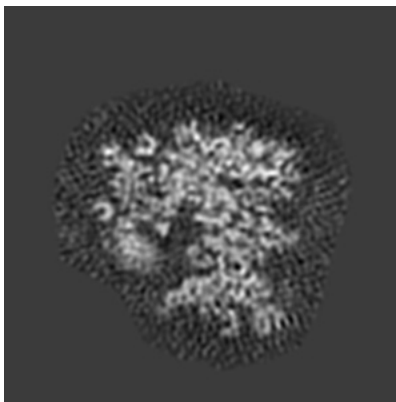
The images above show central slices of the map in three orthogonal directions.

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

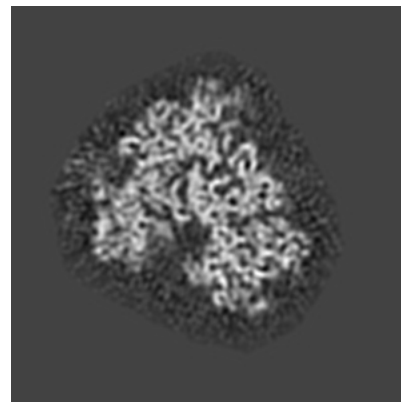
### 6.3.1 Primary map



X Index: 172



Y Index: 149

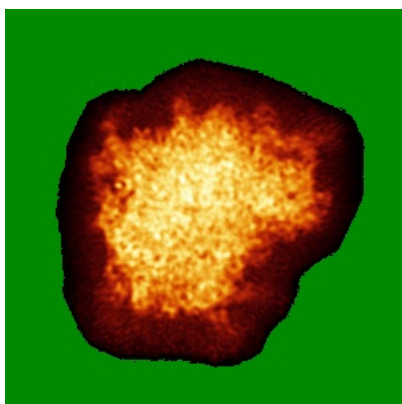


Z Index: 154

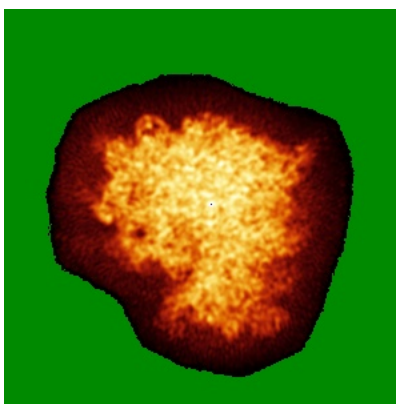
The images above show the largest variance slices of the map in three orthogonal directions.

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

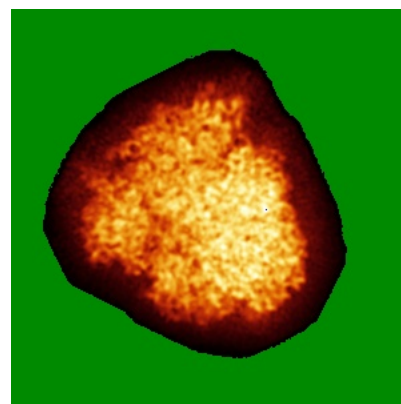
### 6.4.1 Primary map



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 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

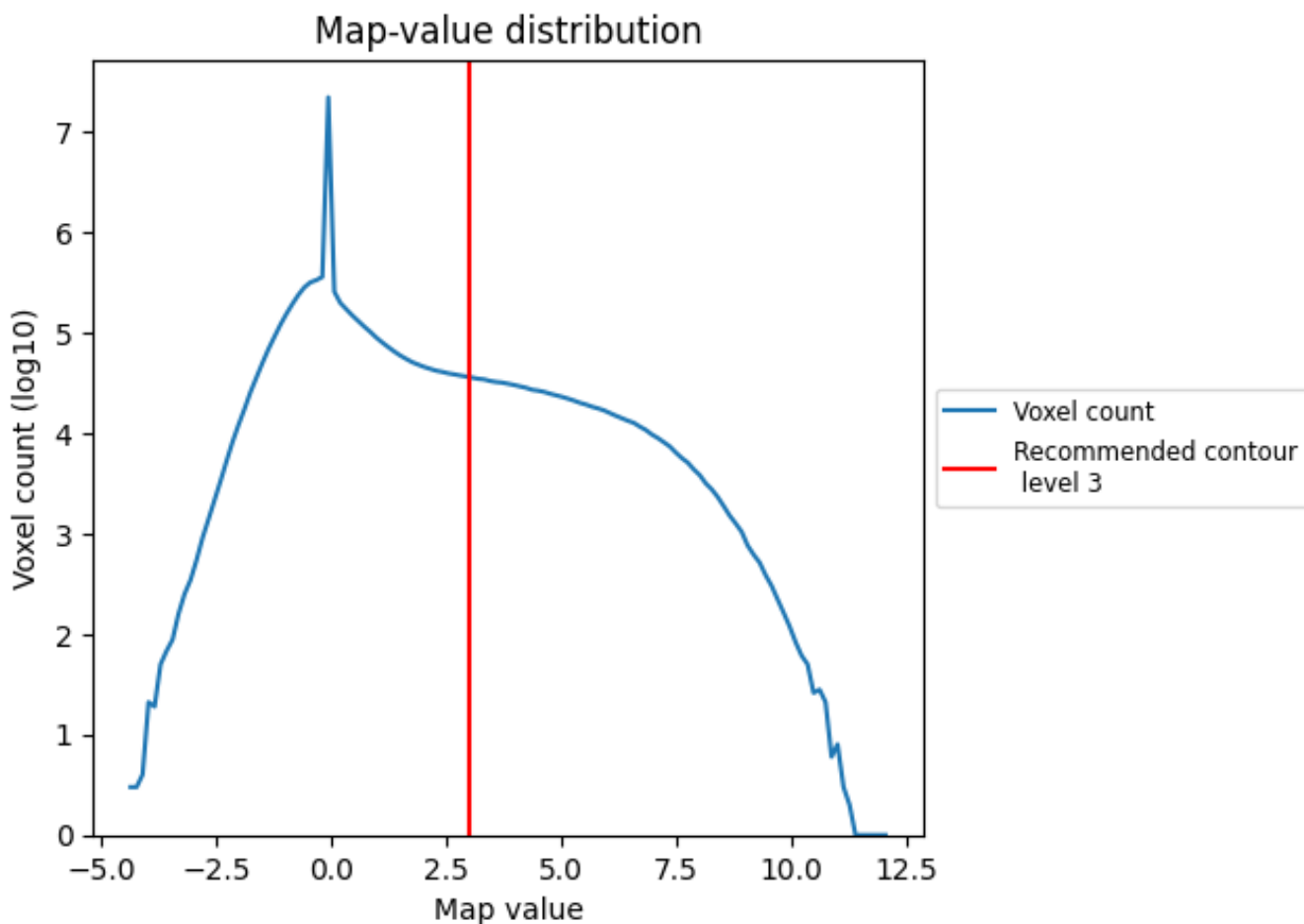
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

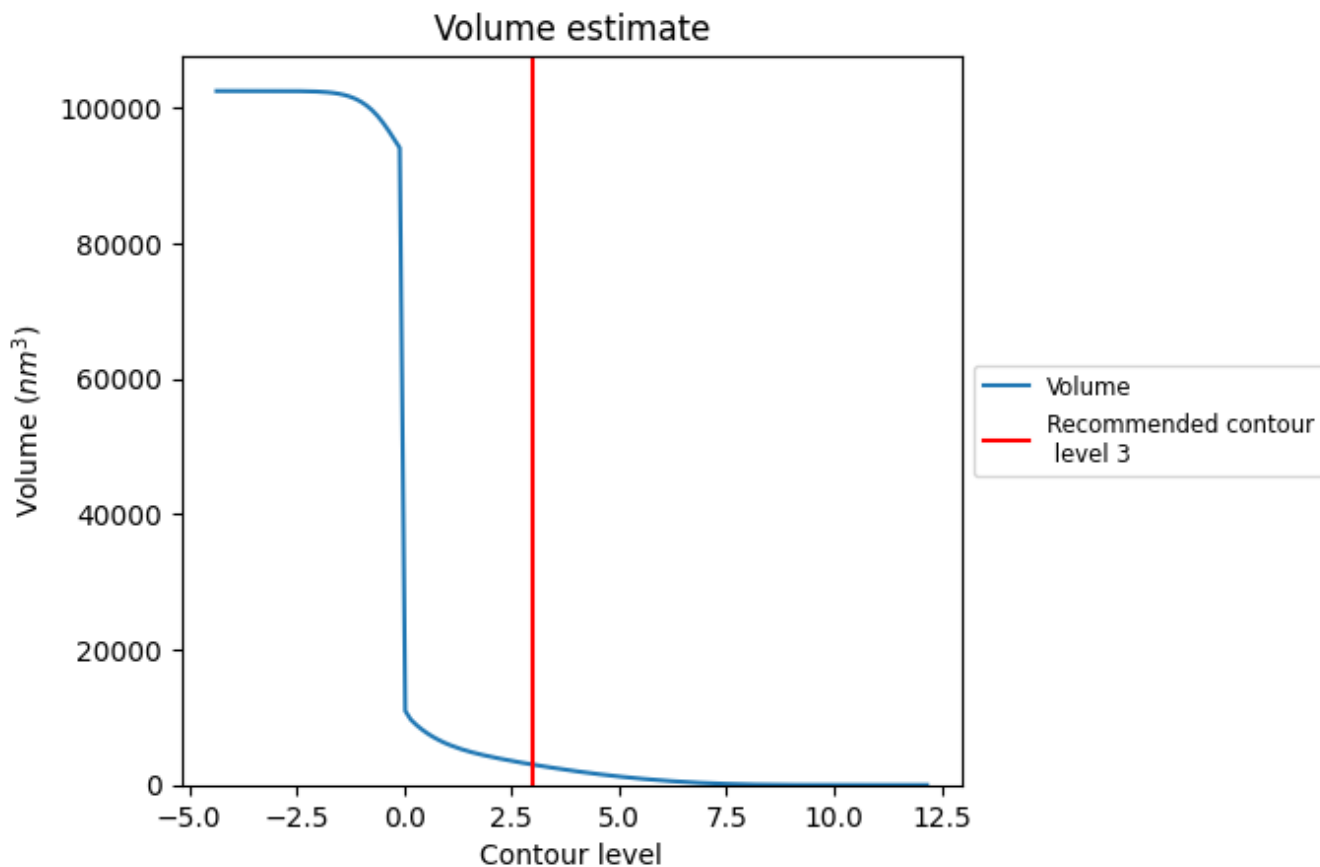
This section contains the results of statistical analysis of the map.

### 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.

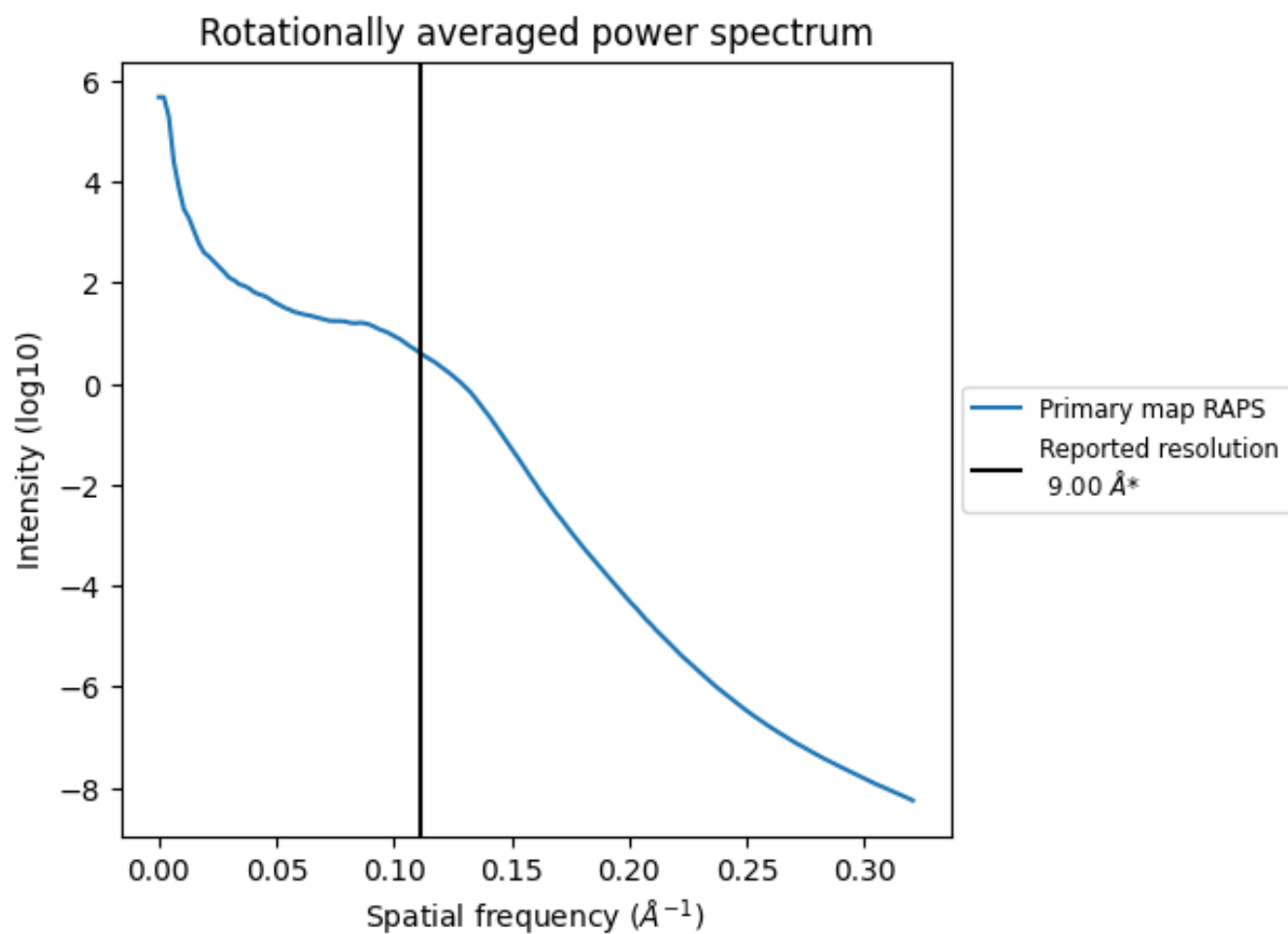
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3001 nm<sup>3</sup>; this corresponds to an approximate mass of 2711 kDa.

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

### 7.3 Rotationally averaged power spectrum i



\*Reported resolution corresponds to spatial frequency of 0.111 Å<sup>-1</sup>

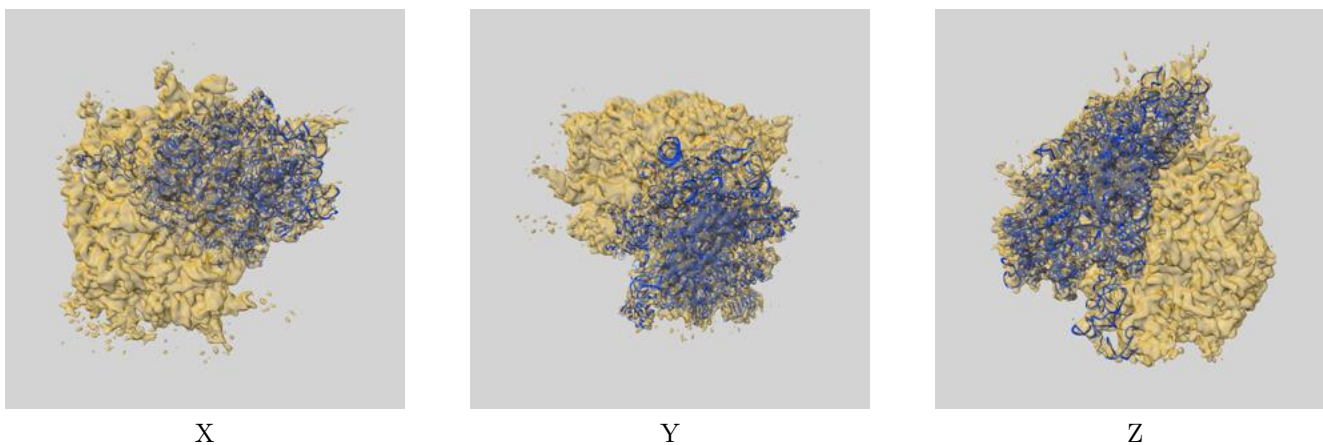
## 8 Fourier-Shell correlation

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

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

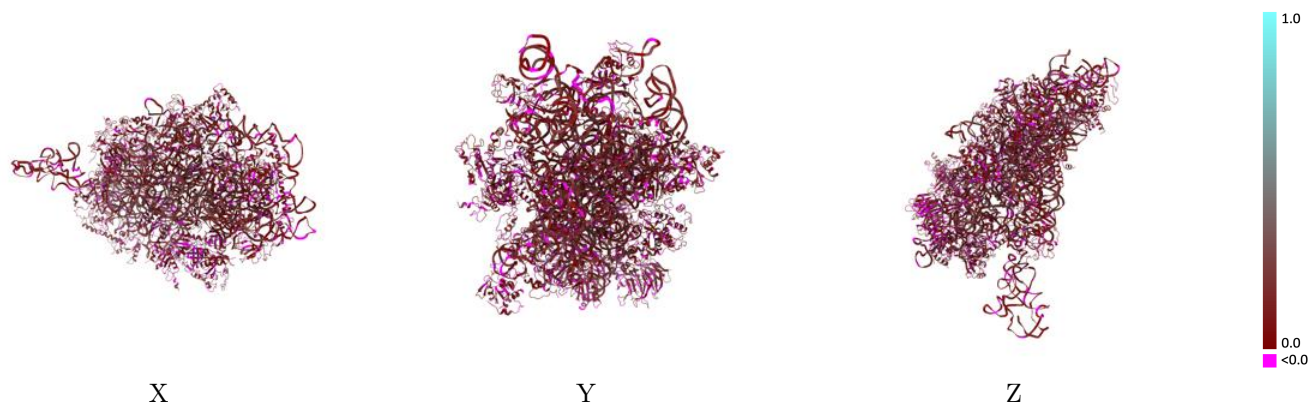
This section contains information regarding the fit between EMDB map EMD-2813 and PDB model 4D61. Per-residue inclusion information can be found in section 3 on page 11.

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



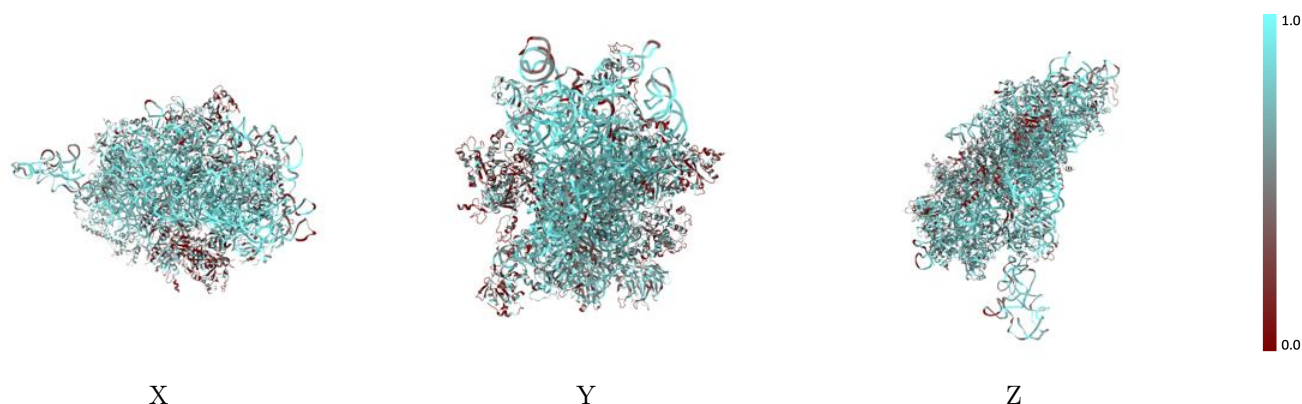
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



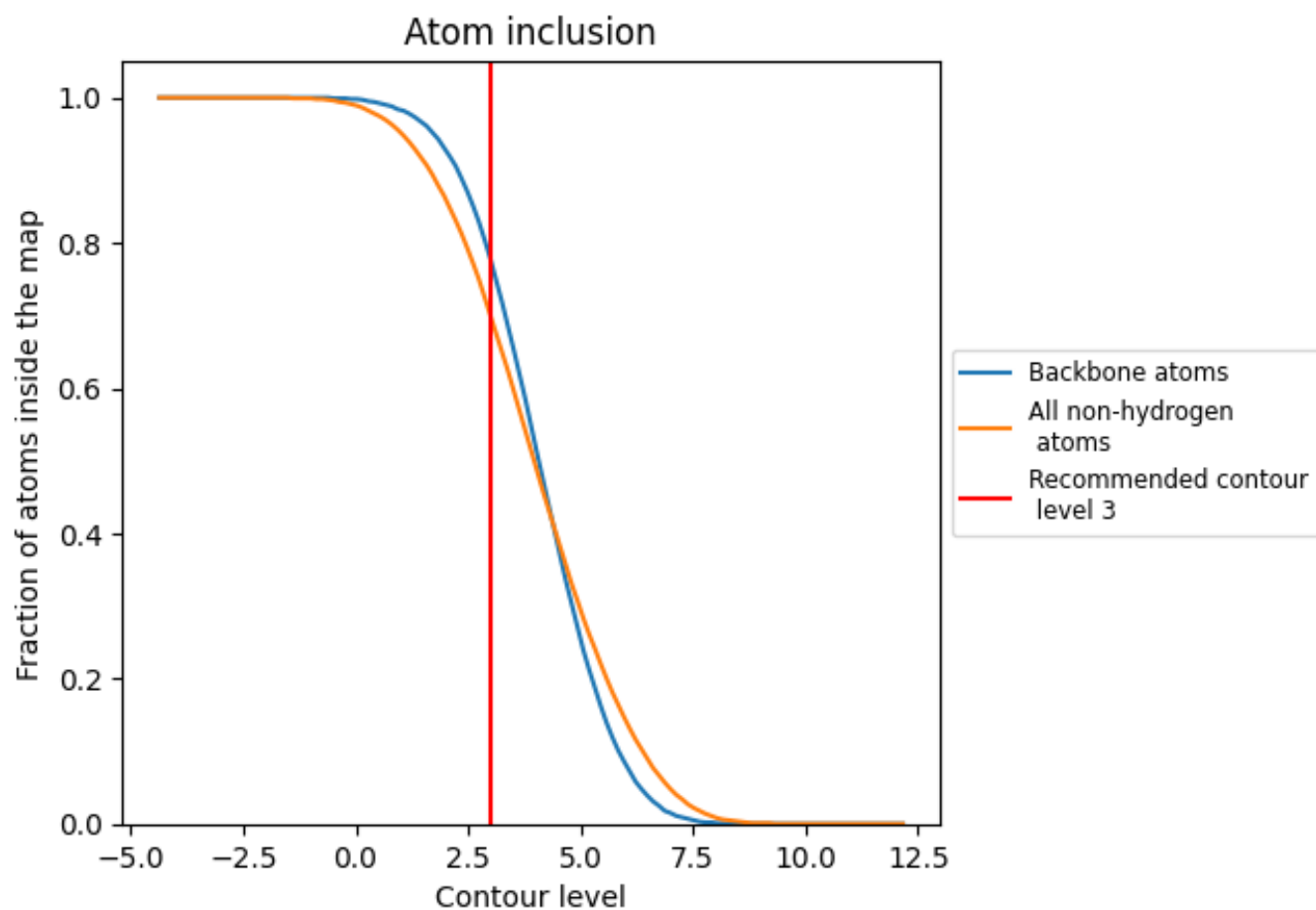
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 70% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7000	 0.1270
1	 0.8650	 0.1580
A	 0.4650	 0.1120
B	 0.6700	 0.1340
C	 0.6100	 0.1280
D	 0.5850	 0.1170
E	 0.6690	 0.1090
F	 0.6280	 0.0970
G	 0.6600	 0.0980
H	 0.3620	 0.1000
I	 0.6250	 0.0930
J	 0.6790	 0.1080
K	 0.6360	 0.0860
L	 0.6040	 0.1150
M	 0.3290	 0.0670
N	 0.6080	 0.1130
O	 0.6440	 0.1060
P	 0.5920	 0.0850
Q	 0.6790	 0.0870
R	 0.4920	 0.0900
S	 0.6550	 0.1070
T	 0.6320	 0.0850
U	 0.5370	 0.0690
V	 0.4850	 0.1050
W	 0.6240	 0.1050
X	 0.6260	 0.1140
Y	 0.6200	 0.1000
Z	 0.6560	 0.1180
a	 0.6210	 0.0910
b	 0.6020	 0.1140
c	 0.5680	 0.1030
d	 0.7160	 0.0630
e	 0.5210	 0.1160
f	 0.3710	 0.0750
g	 0.5860	 0.0860



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Chain	Atom inclusion	Q-score
h	 0.4200	 0.0970
i	 0.3540	 0.0920
j	 0.6870	 0.1270