



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 04:54 PM EST

PDB ID : 4V6S
EMDB ID : EMD-5360
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 3 of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-09
Resolution : 13.10 Å (reported)
Based on initial model : 2I2V

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:

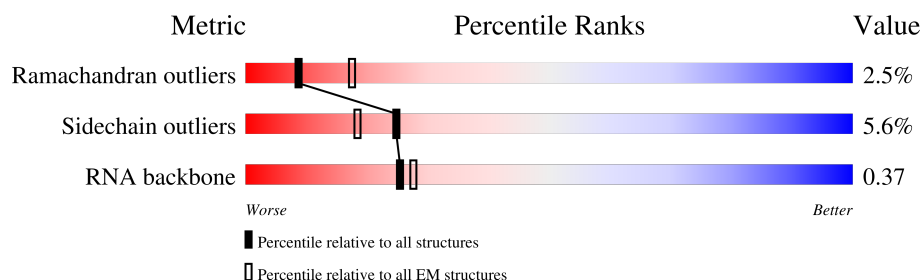
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 13.10 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AA	120	
2	AB	2904	
3	AC	234	
4	AD	272	
5	AE	209	
6	AF	201	
7	AG	178	
8	AH	176	



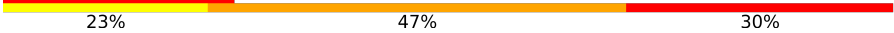









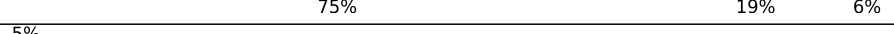
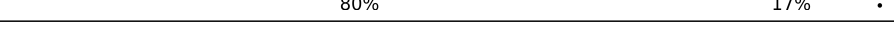

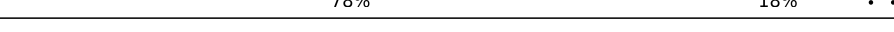



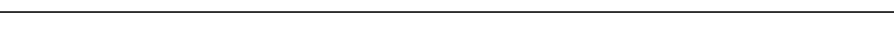




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Mol	Chain	Length	Quality of chain
9	AI	149	
10	AJ	164	
11	AK	141	
12	AL	142	
13	AM	123	
14	AN	144	
15	AO	136	
16	AP	127	
17	AQ	117	
18	AR	114	
19	AS	117	
20	AT	103	
21	AU	110	
22	AV	100	
23	AW	103	
24	AX	94	
25	AY	84	
26	AZ	77	
27	A0	63	
28	A1	58	
29	A2	70	
30	A3	56	
31	A4	54	
32	A5	46	
33	A6	64	

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Mol	Chain	Length	Quality of chain
34	A7	38	
35	BA	1542	
36	BB	47	
37	BC	77	
38	BD	240	
39	BE	232	
40	BF	205	
41	BG	166	
42	BH	135	
43	BI	178	
44	BJ	129	
45	BK	129	
46	BL	103	
47	BM	128	
48	BN	123	
49	BO	117	
50	BP	100	
51	BQ	88	
52	BR	82	
53	BS	83	
54	BT	74	
55	BU	91	
56	BV	86	
57	BW	70	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150700 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 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A4	54	Total	C	N	O		0	0
			441	284	81	76			

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	A6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 36 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 37 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	BC	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 40 is a protein called 30S ribosomal protein S4.

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

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BI	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

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

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BL	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BM	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BN	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BO	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 50 is a protein called 30S ribosomal protein S14.

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

- Molecule 51 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BQ	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

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

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BS	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BT	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BU	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BV	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

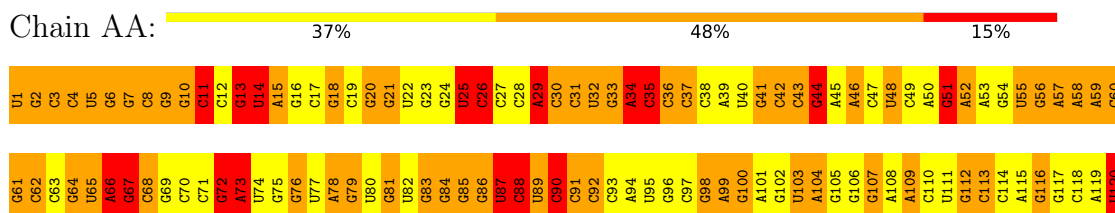
- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BW	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

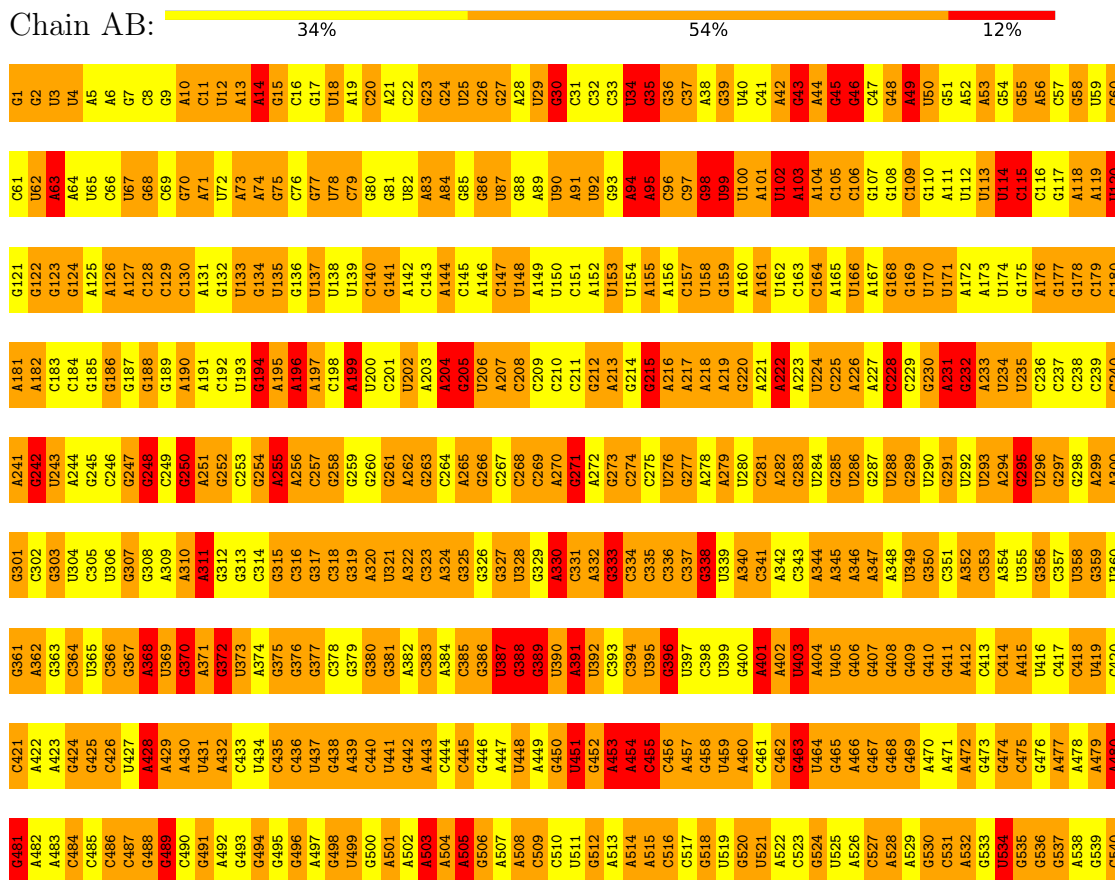
3 Residue-property plots

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: 5S ribosomal RNA



• Molecule 2: 23S ribosomal RNA

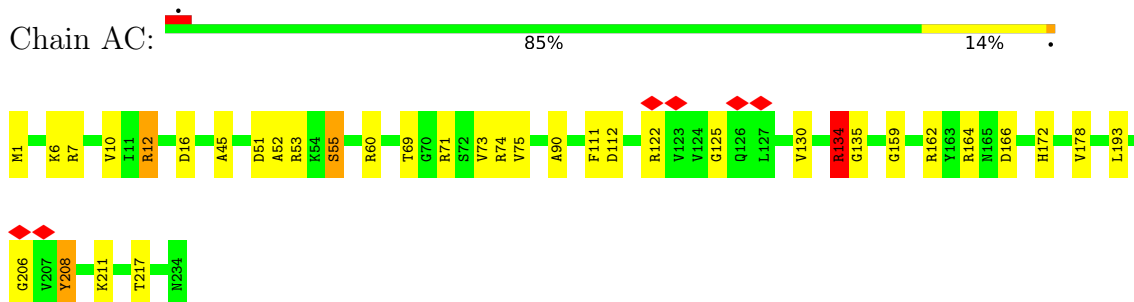


G1561	G1562	A1563	A1564	A1565	G1566	G1567	A1568	A1569	G1570	G1571	A1572	G1573	G1574	G1575	A1576	G1577	G1578	G1579	A1580	G1581	A1582	A1583	G1584	A1585	A1586	G1587	G1588	G1589	A1590	A1591	G1592	A1593	G1594	A1595	A1596	G1597	G1598	G1599	G1600	G1601	G1602	A1603	G1604	G1605	G1606	G1607	A1608	A1609	A1610	G1611	G1612	G1613	A1614	G1615	G1616	A1617	A1618	G1619	G1620						
G1441	U1442	U1443	U1444	G1445	U1446	U1447	U1448	U1449	U1450	G1451	G1452	A1453	G1454	G1455	G1456	U1457	U1458	G1459	U1460	G1461	G1462	G1463	G1464	G1465	U1466	U1467	U1468	U1469	U1470	G1471	G1472	G1473	G1474	G1475	U1476	A1477	G1478	U1479	U1480	U1481	G1482	U1483	U1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	A1492	U1493	U1494	G1495	U1496	U1497	U1498	U1499	U1500						
G1381	G1382	A1383	A1384	A1385	A1386	A1387	A1388	G1389	U1390	G1391	G1392	A1393	U1394	A1395	U1396	U1397	G1398	G1399	U1400	G1401	U1402	A1403	G1404	U1405	U1406	U1407	G1408	U1409	U1410	U1411	U1412	A1413	U1414	U1415	U1416	G1417	G1418	U1419	U1420	G1421	G1422	G1423	G1424	G1425	G1426	U1427	U1428	U1429	U1430	U1431	U1432	A1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440						
A1321	A1322	G1323	G1324	A1325	U1326	A1327	A1328	U1329	G1330	G1331	G1332	G1333	G1334	G1335	A1336	G1337	G1338	G1339	U1340	G1341	U1342	G1343	U1344	G1345	G1346	U1347	G1348	G1349	G1350	U1351	G1352	A1353	U1354	G1355	G1356	G1357	G1358	U1359	G1360	G1361	G1362	G1363	G1364	A1365	A1366	U1367	G1368	G1369	G1370	G1371	U1372	A1373	G1374	U1375	U1376	G1377	A1378	U1379	U1380						
G1261	A1262	U1263	A1264	A1265	U1266	U1267	A1268	U1269	G1270	G1271	A1272	U1273	A1274	A1275	U1276	G1277	G1278	G1279	U1280	G1281	U1282	G1283	U1284	U1285	A1286	A1287	G1288	G1289	U1290	G1291	U1292	G1293	U1294	G1295	G1296	G1297	G1298	U1299	G1300	A1301	A1302	G1303	A1304	G1305	G1306	A1307	A1308	G1309	G1310	G1311	U1312	U1313	G1314	U1315	U1316	G1317	U1318	G1319	G1320						
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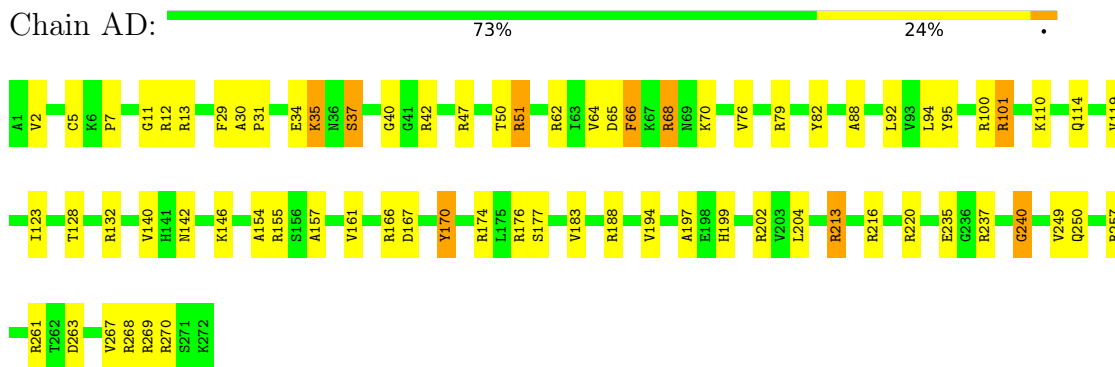
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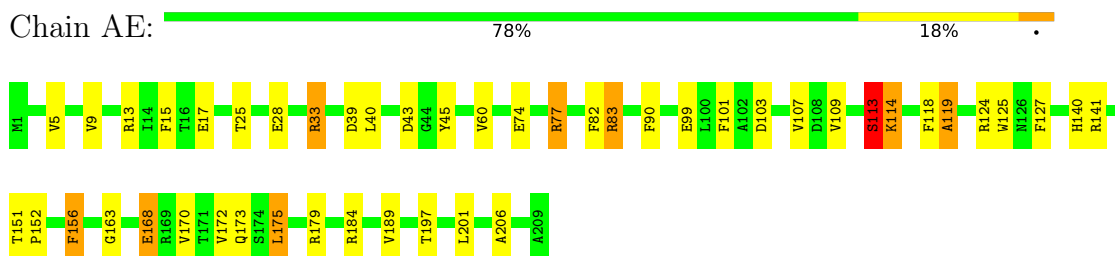
• Molecule 3: 50S ribosomal protein L1




• Molecule 4: 50S ribosomal protein L2

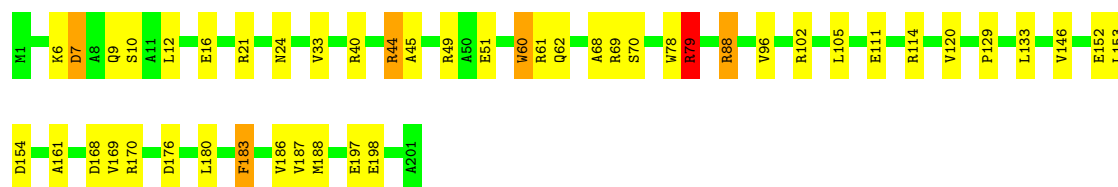


• Molecule 5: 50S ribosomal protein L3



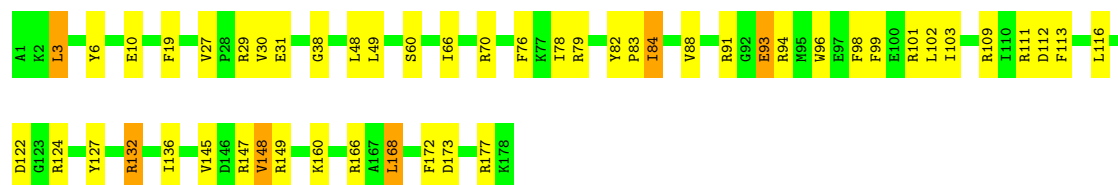
• Molecule 6: 50S ribosomal protein L4

Chain AF:  77% 20% .




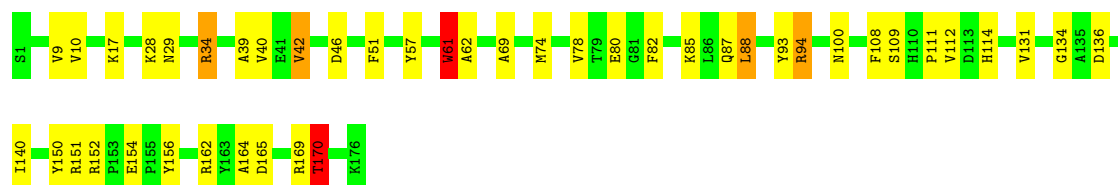
- Molecule 7: 50S ribosomal protein L5

Chain AG:  72% 25% .




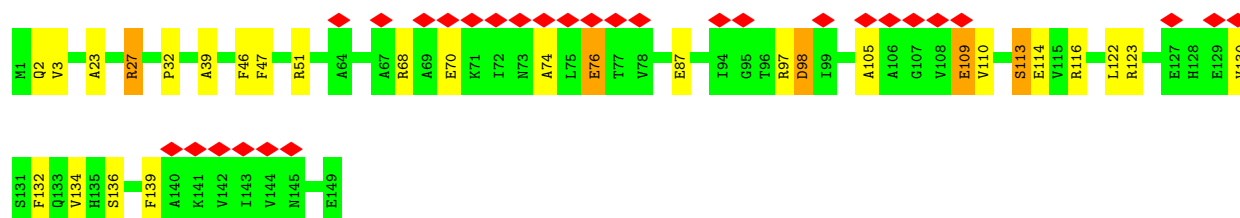
- Molecule 8: 50S ribosomal protein L6

Chain AH:  75% 22% ..




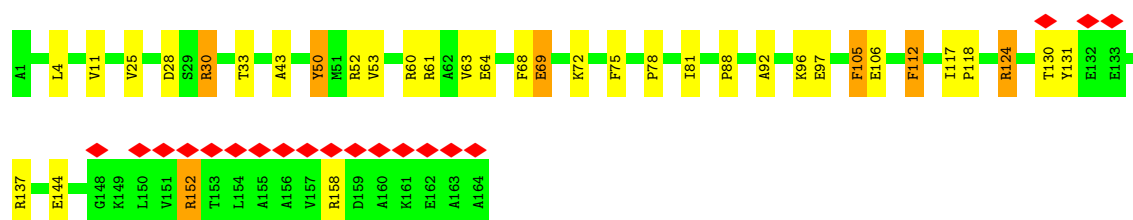
- Molecule 9: 50S ribosomal protein L9

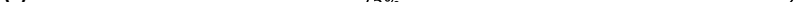
Chain AI:  19% 81% 16% .

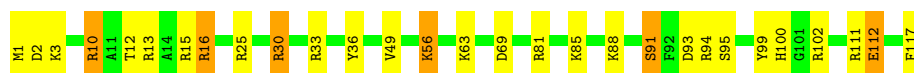


- Molecule 10: 50S ribosomal protein L10

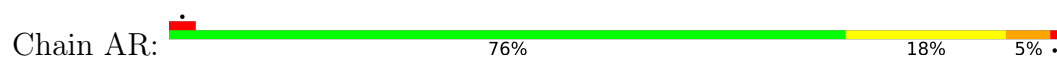
Chain AJ:  12% 78% 18% .



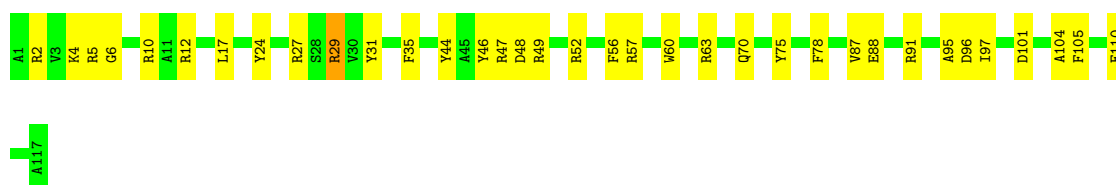
- Chain AQ: 



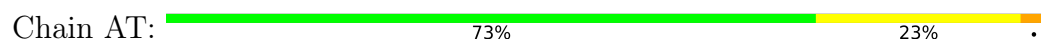
- Molecule 18: 50S ribosomal protein L19



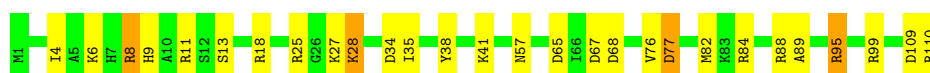
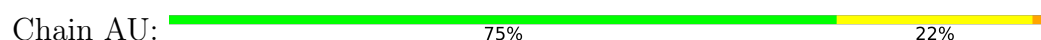
- Molecule 19: 50S ribosomal protein L20



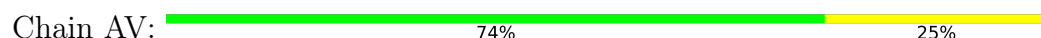
- Molecule 20: 50S ribosomal protein L21



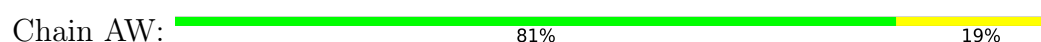
- Molecule 21: 50S ribosomal protein L22



- Molecule 22: 50S ribosomal protein L23



- Molecule 23: 50S ribosomal protein L24




- Molecule 24: 50S ribosomal protein L25

Chain AX:  71% 27% .



- Molecule 25: 50S ribosomal protein L27

Chain AY:  73% 24% .




- Molecule 26: 50S ribosomal protein L28

Chain AZ:  60% 36% .



- Molecule 27: 50S ribosomal protein L29

Chain A0:  79% 14% 6% .




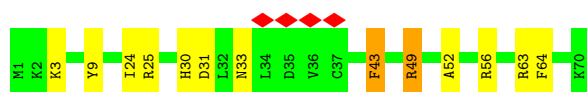
- Molecule 28: 50S ribosomal protein L30

Chain A1:  74% 19% 7% .




- Molecule 29: 50S ribosomal protein L31

Chain A2:  6% 81% 16% .




- Molecule 30: 50S ribosomal protein L32

Chain A3:  77% 18% . .



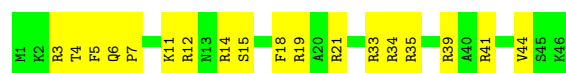
- Molecule 31: 50S ribosomal protein L33

Chain A4:  80% 17% .




- Molecule 32: 50S ribosomal protein L34

Chain A5:  61% 39%



- Molecule 33: 50S ribosomal protein L35

Chain A6:  83% 12% 5%



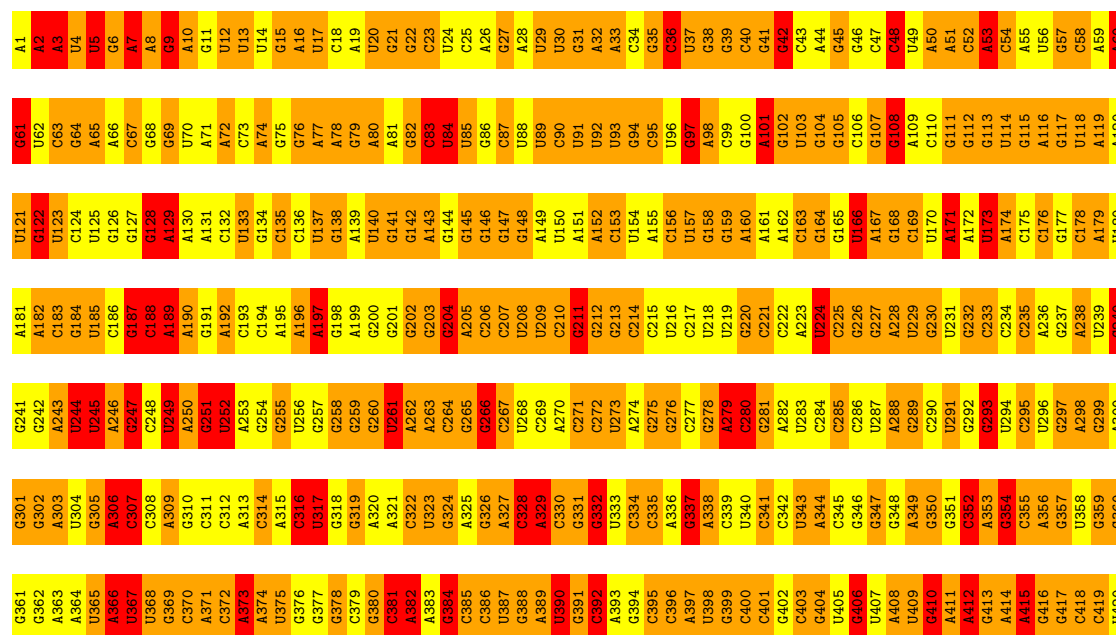
- Molecule 34: 50S ribosomal protein L36

Chain A7:  68% 29% .



- Molecule 35: 16S ribosomal RNA

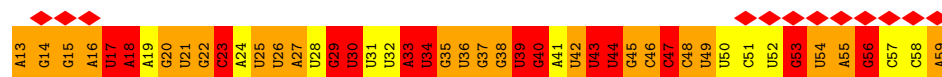
Chain BA:  33% 54% 13%



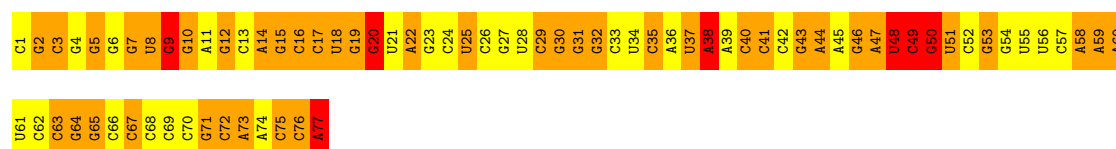
A1441	U1381	U1321	A1261	A1201	C1141	A1081	A1021	U961	A901	C841	A781	G721	G661	G601	G541	G481	U421
G1442	C1382	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782	G722	U662	A602	G542	A482	C422
C1443	C1383	G1323	U1263	C1203	G1143	U1083	A1023	G963	G903	U843	C783	U723	A663	U603	G543	C483	G423
U1444	C1384	A1324	U1264	A1204	G1144	G1084	G1024	A964	G904	G844	A784	U724	G664	G604	G544	C484	G424
U1445	G1385	C1325	C1265	U1205	A1145	U1085	U1025	U965	U905	A845	G785	G725	G665	U605	C545	U485	G425
A1446	G1386	U1326	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726	G666	G606	A546	U486	U426
A1447	G1387	C1327	C1267	G1207	C1147	G1087	C1027	C967	A907	G847	A787	G727	G667	A607	A547	A487	U427
C1448	C1388	C1328	G1268	C1208	U1148	G1088	C1028	A968	A908	C848	U788	A728	G668	A608	C548	C488	G428
C1449	A1389	A1329	A1269	C1209	C1149	G1089	U1029	A969	A909	G849	U789	A729	G669	A609	C549	C489	U429
U1450	U1390	U1330	G1270	C1210	A1150	U1090	C1030	C970	C910	U850	G790	G730	G670	U610	G550	A430	A430
U1451	U1391	U1331	A1271	C1211	A1151	U1091	C1031	G971	U911	G851	G791	G731	G671	U611	U551	A431	A431
C1452	G1392	A1332	U1272	U1212	A1152	A1092	G1032	G972	C912	G852	A792	G732	U672	C612	U552	A432	A432
G1453	U1393	C1333	C1273	A1213	G1153	A1093	G1033	G973	A913	C853	U793	G733	G673	C613	A553	G433	G433
A1454	A1394	G1334	A1274	C1214	G1154	G1094	G1034	A974	A914	U854	A794	G734	G674	C614	A554	C434	U434
G1455	C1395	U1335	A1275	G1215	A1155	U1095	A1035	A975	A915	U855	C795	G735	A675	G615	U555	A435	A435
A1456	A1396	C1336	G1276	A1216	G1156	C1096	A1036	G976	U916	C856	G796	G736	A676	G616	C556	A436	A436
G1457	C1397	G1337	C1277	C1217	A1157	C1097	C1037	A977	A917	C857	U797	G737	U677	G617	G557	A437	U437
G1458	A1398	G1338	G1278	A1218	C1158	C1098	C1038	A978	A918	C858	U798	G738	U678	G618	G558	A438	U438
G1459	C1399	A1339	G1279	A1219	U1159	G1099	G1039	C979	A919	C859	G799	G739	C679	U619	A559	U439	U439
A1460	C1400	A1340	A1280	G1220	G1160	C1100	U1040	C980	U920	A860	G800	U740	C680	C620	A560	C440	C440
G1461	C1281	U1341	C1281	G1221	C1161	A1101	G1041	C981	U921	G861	U801	G741	C681	A621	U561	C501	A441
C1462	C1402	C1342	C1282	G1222	C1162	A1102	A1042	U982	G922	C862	A802	G742	C682	A622	U562	A502	G442
U1463	C1403	C1343	C1283	C1223	A1163	C1103	G1043	U983	A923	U863	G803	A743	C683	C623	A563	C503	C443
U1464	G1404	U1344	A1284	U1224	G1164	G1104	A1044	C984	C924	A864	U804	C744	U684	C624	C564	C504	G444
A1465	A1405	C1345	A1285	A1225	U1165	A1105	U1045	C985	G925	A865	C805	G745	G685	U625	U565	G505	G445
C1466	U1406	A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746	U686	G626	C566	G506	G446
C1467	C1407	G1347	A1287	A1227	U1167	C1107	G1047	G987	G927	C867	A807	A747	A687	G627	G567	C507	G447
A1468	A1408	U1348	U1288	C1228	U1168	G1108	G1048	G988	G928	C868	C808	G748	C688	G628	G568	U508	A448
C1469	C1409	A1349	A1289	A1229	G1169	C1109	U1049	U989	G929	C869	G809	A749	C689	A629	C569	A509	G449
U1470	U1410	A1350	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C810	C750	C690	A630	G570	A510	G450
U1471	C1411	U1351	C1291	G1231	A1171	A1111	U1051	A991	C931	U871	C811	U751	G691	G631	U571	C511	A451
U1472	C1412	C1352	C1292	U1232	C1172	C1112	U1052	U992	C932	A872	G812	G752	U692	G632	A572	U512	A452
G1473	A1413	G1353	C1293	C1233	U1173	C1113	G1053	G993	G933	A873	U813	G753	C693	G633	A573	C513	G453
U1474	U1414	U1354	G1294	C1234	G1174	C1114	A1054	A994	C934	G874	A814	C754	A694	A634	A574	C514	G454
G1475	G1415	U1355	U1295	U1235	G1175	U1115	A1055	C995	A935	U875	A815	G755	A695	A635	G575	C515	G455
A1476	C1416	G1356	C1296	A1236	A1176	U1116	U1056	A996	C936	C876	A816	C756	A696	U636	C576	U516	A456
U1477	G1417	C1357	G1297	U1237	G1177	A1117	G1057	U997	A937	G877	C817	U757	U697	G637	G577	G517	G457
U1478	A1418	U1358	U1298	A1238	G1178	U1118	G1058	C998	A938	A878	G818	C758	C698	U638	C578	C518	U458
C1479	U1419	C1359	A1299	U1239	A1179	C1119	U1059	C999	G939	C879	A819	G759	C699	G639	A579	C519	A459
A1480	U1420	U1360	G1300	U1240	A1180	C1120	U1060	A1000	C940	C880	U820	G760	G700	A640	C580	A520	A460
U1481	G1421	G1361	C1301	C1241	G1181	U1121	G1061	C1001	G941	G881	G821	U761	U701	U641	G581	G521	A461
G1482	G1422	A1362	C1302	G1242	G1182	U1122	U1062	G1002	G942	C882	U822	U762	C702	A642	C582	C522	G462
A1483	G1423	A1363	C1303	C1243	U1183	U1123	G1063	G1003	U943	C883	G823	G763	C703	G643	A583	A523	U463
U1484	U1424	G1364	G1304	G1244	G1184	G1124	G1064	A1004	G944	U884	G824	C764	A704	U644	G584	G524	U464
U1485	U1425	G1365	G1305	C1245	G1185	U1125	U1065	A1005	G945	C885	A825	G765	G705	G645	G585	C525	A465
G1486	G1426	A1366	A1306	A1246	G1186	U1126	C1066	G1006	A946	G886	C826	A766	U706	G646	C586	C526	A466
G1487	C1427	C1367	U1307	U1247	G1187	G1127	A1067	U1007	G947	G887	U827	A767	U707	C647	G587	G527	U467
G1488	A1428	A1368	U1308	A1248	A1188	C1128	G1068	U1008	C948	C888	U828	A768	C708	A648	G588	C528	A468
G1489	A1429	C1369	G1309	C1249	U1189	G1129	C1069	U1009	A949	A889	G829	G769	U709	A649	U589	G529	C469
U1490	A1430	G1370	G1310	U1250	G1190	A1130	U1070	U1010	U950	C890	G830	C770	G710	G650	U590	G530	C470
G1491	A1431	G1371	A1311	A1251	A1191	G1131	C1071	C1011	G951	U891	A831	G771	G711	C651	U591	U531	U471
A1492	G1432	U1372	G1312	A1252	C1192	C1132	G1072	A1012	U952	A892	G832	U772	A712	G652	G592	A532	U472
A1493	A1433	G1373	U1313	G1253	G1193	G1133	U1073	G1013	G953	C893	G833	G773	G713	U653	U593	A533	U473
G1494	A1434	A1374	C1314	A1254	U1194	G1134	G1074	A1014	G954	G894	U834	G774	G714	G654	U594	U534	G474
U1495	G1435	A1375	U1315	G1255	C1195	U1135	U1075	G1015	U955	G895	A835	G775	A715	A655	A595	A535	U475
G1496	A1436	U1376	A1316	A1256	A1196	C1136	U1076	A1016	U956	C896	G836	G776	A716	G656	A596	C536	C476
G1497	A1437	A1377	G1317	A1257	A1197	C1137	G1077	U1017	U957	C897	U837	A777	U717	U657	G597	G537	C477
U1498	G1438	C1378	A1318	G1258	G1198	G1138	U1078	G1018	A958	G898	G838	G778	A718	C658	U598	G538	A478
A1499	A1439	G1379	A1319	C1259	U1199	G1139	U1079	A1019	A959	C899	G839	C779	A719	U659	C599	U539	U479
A1500	U1440	U1380	C1320	G1260	C1200	C1140	A1080	G1020	U960	A900	C840	A780	C720	C660	A600	G540	U480



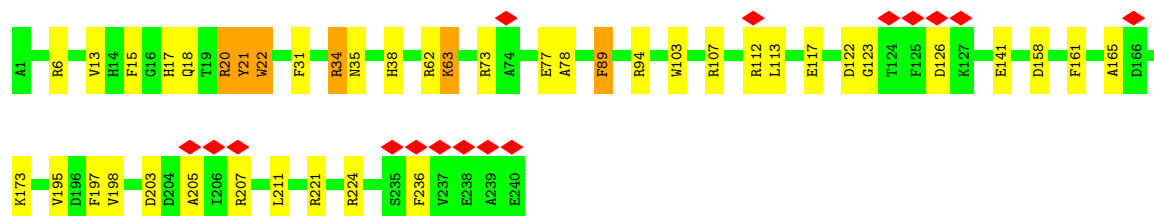
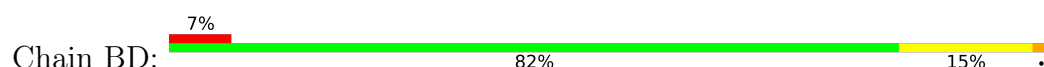
• Molecule 36: mRNA



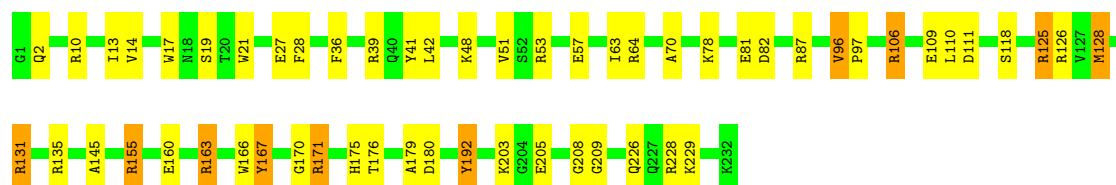
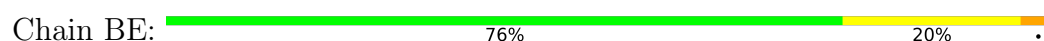
• Molecule 37: P site tRNA



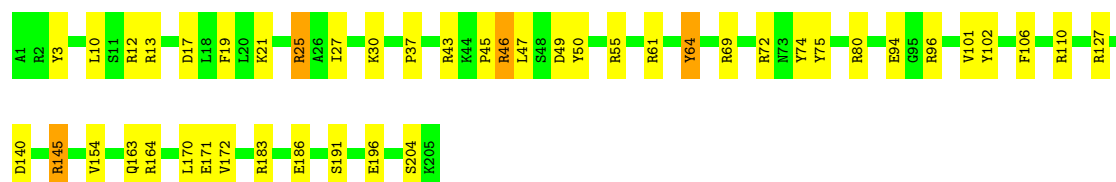
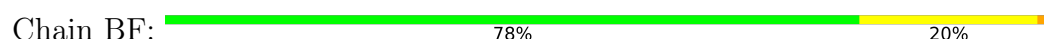
• Molecule 38: 30S ribosomal protein S2



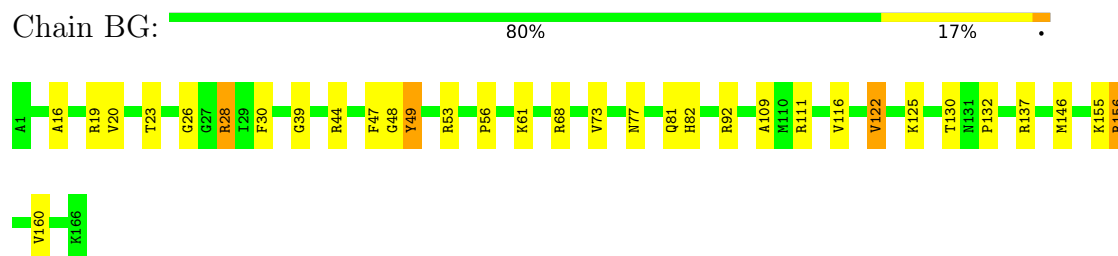
• Molecule 39: 30S ribosomal protein S3



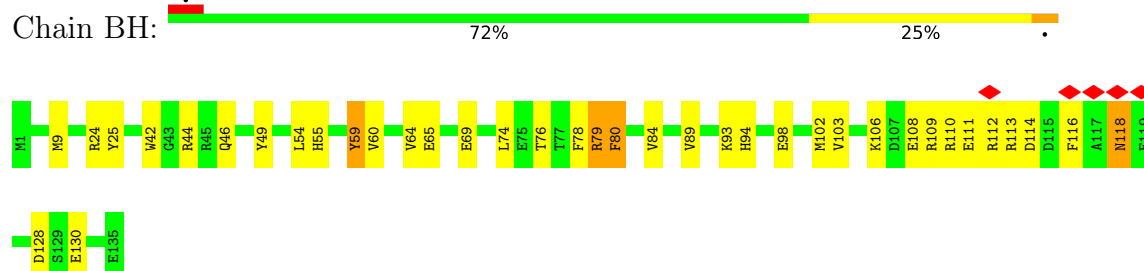
• Molecule 40: 30S ribosomal protein S4



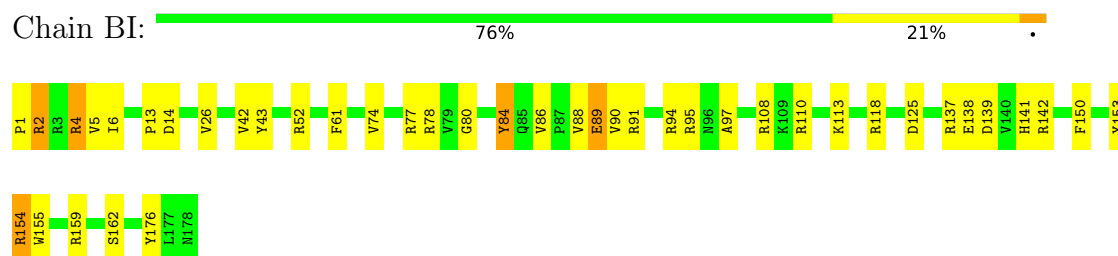
- Molecule 41: 30S ribosomal protein S5



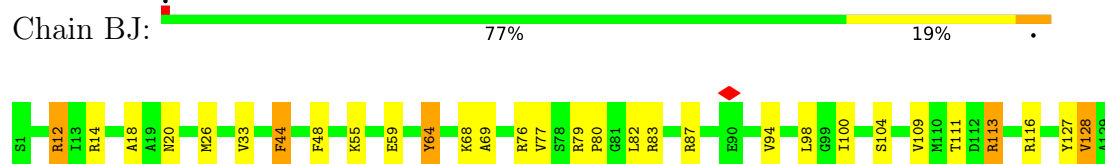
- Molecule 42: 30S ribosomal protein S6



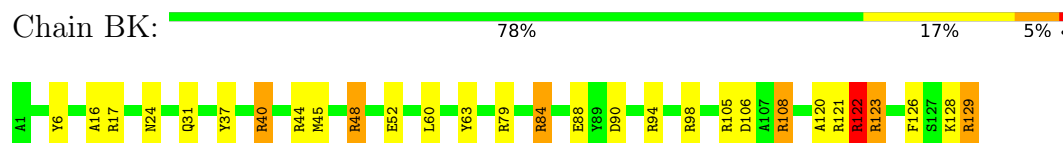
- Molecule 43: 30S ribosomal protein S7



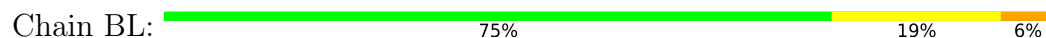
- Molecule 44: 30S ribosomal protein S8



- Molecule 45: 30S ribosomal protein S9

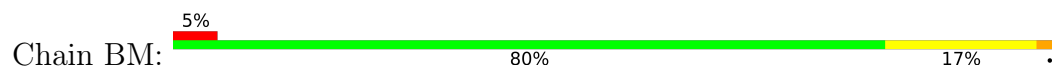


- Molecule 46: 30S ribosomal protein S10

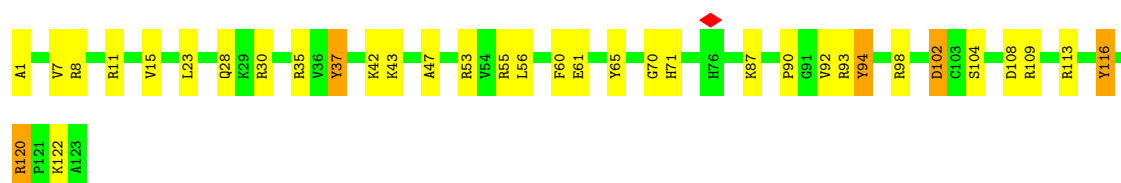




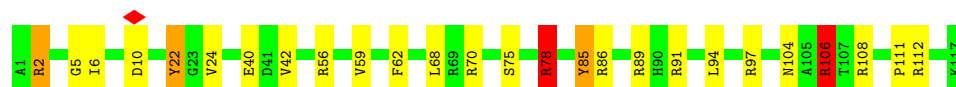
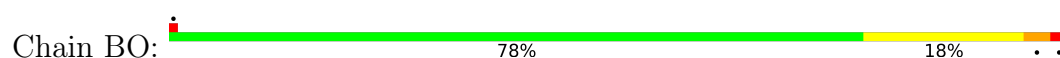
- Molecule 47: 30S ribosomal protein S11



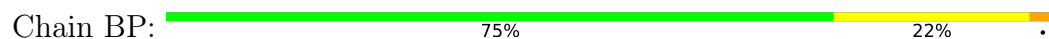
- Molecule 48: 30S ribosomal protein S12



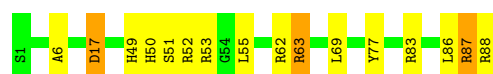
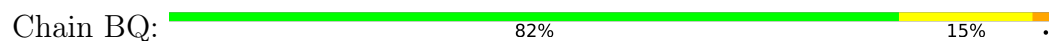
- Molecule 49: 30S ribosomal protein S13



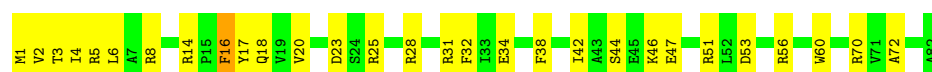
- Molecule 50: 30S ribosomal protein S14




- Molecule 51: 30S ribosomal protein S15

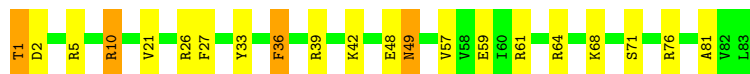


- Molecule 52: 30S ribosomal protein S16




- Molecule 53: 30S ribosomal protein S17

Chain BS:  75% 20% 5%



- Molecule 54: 30S ribosomal protein S18

Chain BT:  74% 20% 5%



- Molecule 55: 30S ribosomal protein S19

Chain BU:  70% 27% 3%



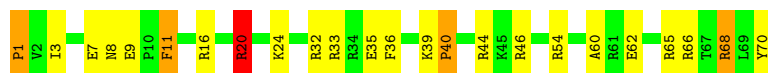
- Molecule 56: 30S ribosomal protein S20

Chain BV:  86% 13% 1%



- Molecule 57: 30S ribosomal protein S21

Chain BW:  66% 27% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	58269	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	1.443	Depositor
Minimum map value	-0.456	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.182	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 4SU, UR3, H2U, CH, 4OC, PSU, 2MG, 3TD, OMU, 6MZ, 5MU, 5MC, 7MG, 1MG, OMG, MA6, 2MA

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	AA	3.07	298/2869 (10.4%)	3.56	669/4474 (15.0%)
2	AB	3.08	7422/69257 (10.7%)	3.52	15483/108040 (14.3%)
3	AC	1.42	3/1748 (0.2%)	1.86	30/2355 (1.3%)
4	AD	1.56	11/2131 (0.5%)	2.03	60/2863 (2.1%)
5	AE	1.49	5/1586 (0.3%)	1.92	39/2134 (1.8%)
6	AF	1.52	7/1571 (0.4%)	1.92	42/2113 (2.0%)
7	AG	1.53	3/1444 (0.2%)	2.02	45/1937 (2.3%)
8	AH	1.53	6/1343 (0.4%)	1.96	35/1816 (1.9%)
9	AI	1.45	3/1122 (0.3%)	1.94	25/1515 (1.7%)
10	AJ	1.52	5/1247 (0.4%)	1.94	27/1679 (1.6%)
11	AK	1.44	5/1046 (0.5%)	1.86	18/1410 (1.3%)
12	AL	1.50	6/1152 (0.5%)	2.08	30/1551 (1.9%)
13	AM	1.53	5/956 (0.5%)	1.95	25/1279 (2.0%)
14	AN	1.52	5/1062 (0.5%)	1.89	20/1413 (1.4%)
15	AO	1.49	3/1093 (0.3%)	2.07	38/1460 (2.6%)
16	AP	1.48	5/1021 (0.5%)	2.09	28/1364 (2.1%)
17	AQ	1.57	4/910 (0.4%)	1.90	27/1219 (2.2%)
18	AR	1.54	2/929 (0.2%)	1.95	26/1242 (2.1%)
19	AS	1.52	6/960 (0.6%)	2.20	39/1278 (3.1%)
20	AT	1.60	5/829 (0.6%)	1.89	18/1107 (1.6%)
21	AU	1.49	1/864 (0.1%)	1.96	21/1156 (1.8%)
22	AV	1.54	3/794 (0.4%)	1.90	17/1060 (1.6%)
23	AW	1.44	2/797 (0.3%)	1.90	13/1062 (1.2%)
24	AX	1.49	5/766 (0.7%)	1.79	15/1025 (1.5%)
25	AY	1.48	2/642 (0.3%)	1.92	14/848 (1.7%)
26	AZ	1.50	3/635 (0.5%)	2.21	25/848 (2.9%)
27	A0	1.37	1/510 (0.2%)	1.90	12/677 (1.8%)
28	A1	1.52	2/453 (0.4%)	2.11	13/605 (2.1%)
29	A2	1.55	3/559 (0.5%)	1.96	12/745 (1.6%)
30	A3	1.49	1/450 (0.2%)	2.05	15/599 (2.5%)
31	A4	1.46	1/448 (0.2%)	1.82	7/594 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	A5	1.53	1/380 (0.3%)	2.15	14/498 (2.8%)
33	A6	1.55	4/513 (0.8%)	1.80	7/676 (1.0%)
34	A7	1.57	2/303 (0.7%)	1.98	6/397 (1.5%)
35	BA	3.07	3871/36769 (10.5%)	3.53	8462/57354 (14.8%)
36	BB	3.23	131/1108 (11.8%)	3.61	262/1724 (15.2%)
37	BC	3.09	176/1721 (10.2%)	3.61	392/2683 (14.6%)
38	BD	1.43	2/1904 (0.1%)	1.86	32/2565 (1.2%)
39	BE	1.55	11/1852 (0.6%)	1.94	38/2490 (1.5%)
40	BF	1.51	8/1665 (0.5%)	1.96	51/2227 (2.3%)
41	BG	1.54	5/1239 (0.4%)	2.01	27/1664 (1.6%)
42	BH	1.50	3/1121 (0.3%)	1.92	27/1509 (1.8%)
43	BI	1.54	5/1422 (0.4%)	2.05	48/1908 (2.5%)
44	BJ	1.49	3/989 (0.3%)	2.00	23/1326 (1.7%)
45	BK	1.55	5/1048 (0.5%)	2.08	34/1394 (2.4%)
46	BL	1.47	1/835 (0.1%)	2.19	25/1127 (2.2%)
47	BM	1.52	7/982 (0.7%)	2.02	28/1323 (2.1%)
48	BN	1.52	4/969 (0.4%)	2.10	39/1300 (3.0%)
49	BO	1.51	8/919 (0.9%)	1.98	30/1226 (2.4%)
50	BP	1.53	1/817 (0.1%)	2.02	23/1088 (2.1%)
51	BQ	1.43	1/724 (0.1%)	1.93	16/966 (1.7%)
52	BR	1.53	2/659 (0.3%)	2.14	25/884 (2.8%)
53	BS	1.55	6/681 (0.9%)	1.99	18/913 (2.0%)
54	BT	1.60	6/637 (0.9%)	2.07	18/851 (2.1%)
55	BU	1.53	3/744 (0.4%)	1.84	16/995 (1.6%)
56	BV	1.39	1/676 (0.1%)	1.86	14/895 (1.6%)
57	BW	1.46	5/598 (0.8%)	2.19	23/792 (2.9%)
All	All	2.69	12105/162469 (7.5%)	3.17	26586/242243 (11.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	69
2	AB	0	1654
3	AC	0	3
4	AD	0	11
5	AE	0	7
6	AF	0	2
7	AG	0	1
8	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	AI	0	3
10	AJ	0	8
11	AK	0	1
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	5
17	AQ	0	4
18	AR	0	6
19	AS	0	3
20	AT	0	5
21	AU	0	5
22	AV	0	1
24	AX	0	5
25	AY	0	4
26	AZ	0	2
27	A0	0	4
28	A1	0	4
29	A2	0	3
30	A3	0	1
31	A4	0	2
32	A5	0	2
33	A6	0	2
34	A7	0	2
35	BA	0	882
36	BB	0	30
37	BC	0	41
38	BD	0	4
39	BE	0	9
40	BF	0	3
41	BG	0	3
42	BH	0	9
43	BI	0	3
44	BJ	0	7
45	BK	0	5
46	BL	0	2
47	BM	0	1
48	BN	0	6
49	BO	0	4
50	BP	0	1
51	BQ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	BR	0	2
53	BS	0	1
54	BT	0	2
55	BU	0	4
57	BW	0	4
All	All	0	2857

The worst 5 of 12105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	504	A	N3-C4	18.22	1.45	1.34
2	AB	2682	A	N3-C4	18.21	1.45	1.34
2	AB	744	U	C2-N3	17.97	1.50	1.37
35	BA	1484	C	N1-C6	16.21	1.46	1.37
2	AB	2829	A	P-O5'	15.96	1.75	1.59

The worst 5 of 26586 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AL	120	ARG	NE-CZ-NH2	24.50	132.55	120.30
2	AB	1193	G	C8-N9-C4	-23.95	96.82	106.40
35	BA	581	G	N9-C4-C5	22.36	114.35	105.40
46	BL	45	ARG	NE-CZ-NH1	21.76	131.18	120.30
44	BJ	116	ARG	NE-CZ-NH2	-21.74	109.43	120.30

There are no chirality outliers.

5 of 2857 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	U	Sidechain
1	AA	2	G	Sidechain
1	AA	3	C	Sidechain
1	AA	4	C	Sidechain
1	AA	5	U	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	AA	2566	0	1299	0	0
2	AB	62351	0	31248	0	0
3	AC	1733	0	1824	0	0
4	AD	2092	0	2170	0	0
5	AE	1565	0	1616	0	0
6	AF	1552	0	1619	0	0
7	AG	1420	0	1460	0	0
8	AH	1323	0	1374	0	0
9	AI	1111	0	1148	0	0
10	AJ	1233	0	1283	0	0
11	AK	1032	0	1088	0	0
12	AL	1129	0	1162	0	0
13	AM	947	0	1023	0	0
14	AN	1053	0	1129	0	0
15	AO	1074	0	1157	0	0
16	AP	1008	0	1045	0	0
17	AQ	900	0	935	0	0
18	AR	917	0	965	0	0
19	AS	947	0	1022	0	0
20	AT	816	0	839	0	0
21	AU	857	0	922	0	0
22	AV	787	0	846	0	0
23	AW	789	0	847	0	0
24	AX	753	0	780	0	0
25	AY	634	0	656	0	0
26	AZ	625	0	655	0	0
27	A0	509	0	543	0	0
28	A1	449	0	491	0	0
29	A2	549	0	552	0	0
30	A3	444	0	461	0	0
31	A4	441	0	485	0	0
32	A5	377	0	418	0	0
33	A6	504	0	574	0	0
34	A7	302	0	343	0	0
35	BA	33089	0	16599	0	0
36	BB	993	0	501	0	0
37	BC	1641	0	841	0	0
38	BD	1872	0	1885	0	0
39	BE	1822	0	1913	0	0
40	BF	1643	0	1710	0	0
41	BG	1225	0	1273	0	0
42	BH	1101	0	1050	0	0
43	BI	1400	0	1449	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BJ	979	0	1034	0	0
45	BK	1036	0	1084	0	0
46	BL	825	0	865	0	0
47	BM	965	0	997	0	0
48	BN	955	0	1019	0	0
49	BO	910	0	981	0	0
50	BP	805	0	847	0	0
51	BQ	716	0	742	0	0
52	BR	649	0	666	0	0
53	BS	672	0	716	0	0
54	BT	626	0	651	0	0
55	BU	727	0	769	0	0
56	BV	670	0	722	0	0
57	BW	590	0	631	0	0
All	All	150700	0	102924	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	
3	AC	232/234 (99%)	215 (93%)	12 (5%)	5 (2%)	6	35
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	4	26
5	AE	207/209 (99%)	175 (84%)	24 (12%)	8 (4%)	3	23
6	AF	199/201 (99%)	173 (87%)	16 (8%)	10 (5%)	2	20
7	AG	176/178 (99%)	151 (86%)	15 (8%)	10 (6%)	1	18
8	AH	174/176 (99%)	159 (91%)	11 (6%)	4 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	147/149 (99%)	131 (89%)	12 (8%)	4 (3%)	5	31
10	AJ	162/164 (99%)	155 (96%)	6 (4%)	1 (1%)	25	66
11	AK	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	22	63
12	AL	140/142 (99%)	120 (86%)	15 (11%)	5 (4%)	3	25
13	AM	121/123 (98%)	105 (87%)	12 (10%)	4 (3%)	4	26
14	AN	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	7	36
15	AO	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	10	46
16	AP	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	19	60
17	AQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
18	AR	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	8	40
19	AS	115/117 (98%)	108 (94%)	3 (3%)	4 (4%)	3	25
20	AT	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
21	AU	108/110 (98%)	99 (92%)	5 (5%)	4 (4%)	3	24
22	AV	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	4	27
23	AW	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
24	AX	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	14	52
25	AY	82/84 (98%)	64 (78%)	14 (17%)	4 (5%)	2	20
26	AZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	3	23
27	A0	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	9	44
28	A1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	A2	68/70 (97%)	64 (94%)	3 (4%)	1 (2%)	10	46
30	A3	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	3	24
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	3	24
32	A5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	22
33	A6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	9	44
34	A7	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	1	12
38	BD	238/240 (99%)	218 (92%)	14 (6%)	6 (2%)	5	32
39	BE	230/232 (99%)	217 (94%)	9 (4%)	4 (2%)	9	42
40	BF	203/205 (99%)	186 (92%)	13 (6%)	4 (2%)	7	38
41	BG	164/166 (99%)	150 (92%)	12 (7%)	2 (1%)	13	50
42	BH	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	BI	176/178 (99%)	168 (96%)	5 (3%)	3 (2%)	9	42
44	BJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19	60
45	BK	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	6	33
46	BL	101/103 (98%)	91 (90%)	4 (4%)	6 (6%)	1	17
47	BM	126/128 (98%)	109 (86%)	15 (12%)	2 (2%)	9	44
48	BN	121/123 (98%)	103 (85%)	16 (13%)	2 (2%)	9	42
49	BO	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	17	57
50	BP	98/100 (98%)	85 (87%)	6 (6%)	7 (7%)	1	14
51	BQ	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	13	50
52	BR	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
53	BS	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	13	50
54	BT	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	3	22
55	BU	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	14	52
56	BV	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	50
57	BW	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	22
All	All	6319/6423 (98%)	5708 (90%)	453 (7%)	158 (2%)	9	32

5 of 158 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	94	LEU
6	AF	62	GLN
6	AF	188	MET
7	AG	136	ILE
9	AI	3	VAL

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	
3	AC	181/181 (100%)	176 (97%)	5 (3%)	43	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AD	217/217 (100%)	205 (94%)	12 (6%)	21	47
5	AE	164/164 (100%)	152 (93%)	12 (7%)	14	39
6	AF	165/165 (100%)	160 (97%)	5 (3%)	41	63
7	AG	149/149 (100%)	140 (94%)	9 (6%)	19	44
8	AH	137/137 (100%)	123 (90%)	14 (10%)	7	25
9	AI	114/114 (100%)	109 (96%)	5 (4%)	28	53
10	AJ	122/122 (100%)	115 (94%)	7 (6%)	20	45
11	AK	109/109 (100%)	104 (95%)	5 (5%)	27	52
12	AL	116/116 (100%)	107 (92%)	9 (8%)	12	36
13	AM	104/104 (100%)	98 (94%)	6 (6%)	20	45
14	AN	103/103 (100%)	102 (99%)	1 (1%)	76	86
15	AO	109/109 (100%)	101 (93%)	8 (7%)	14	39
16	AP	103/103 (100%)	99 (96%)	4 (4%)	32	56
17	AQ	87/87 (100%)	79 (91%)	8 (9%)	9	29
18	AR	99/99 (100%)	94 (95%)	5 (5%)	24	48
19	AS	89/89 (100%)	86 (97%)	3 (3%)	37	60
20	AT	84/84 (100%)	78 (93%)	6 (7%)	14	39
21	AU	93/93 (100%)	88 (95%)	5 (5%)	22	47
22	AV	84/84 (100%)	78 (93%)	6 (7%)	14	39
23	AW	84/84 (100%)	80 (95%)	4 (5%)	25	51
24	AX	78/78 (100%)	73 (94%)	5 (6%)	17	42
25	AY	62/62 (100%)	57 (92%)	5 (8%)	11	35
26	AZ	67/67 (100%)	60 (90%)	7 (10%)	7	24
27	A0	55/55 (100%)	52 (94%)	3 (6%)	21	47
28	A1	48/48 (100%)	42 (88%)	6 (12%)	4	19
29	A2	62/62 (100%)	61 (98%)	1 (2%)	62	79
30	A3	47/47 (100%)	45 (96%)	2 (4%)	29	53
31	A4	48/48 (100%)	44 (92%)	4 (8%)	11	34
32	A5	38/38 (100%)	35 (92%)	3 (8%)	12	35
33	A6	51/51 (100%)	50 (98%)	1 (2%)	55	74
34	A7	34/34 (100%)	33 (97%)	1 (3%)	42	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BD	198/198 (100%)	188 (95%)	10 (5%)	24	48
39	BE	189/189 (100%)	174 (92%)	15 (8%)	12	35
40	BF	172/172 (100%)	168 (98%)	4 (2%)	50	70
41	BG	125/125 (100%)	118 (94%)	7 (6%)	21	46
42	BH	116/116 (100%)	107 (92%)	9 (8%)	12	36
43	BI	146/146 (100%)	139 (95%)	7 (5%)	25	51
44	BJ	104/104 (100%)	99 (95%)	5 (5%)	25	51
45	BK	106/106 (100%)	100 (94%)	6 (6%)	20	45
46	BL	90/90 (100%)	83 (92%)	7 (8%)	12	36
47	BM	98/98 (100%)	96 (98%)	2 (2%)	55	74
48	BN	103/103 (100%)	99 (96%)	4 (4%)	32	56
49	BO	95/95 (100%)	89 (94%)	6 (6%)	18	43
50	BP	83/83 (100%)	79 (95%)	4 (5%)	25	51
51	BQ	76/76 (100%)	75 (99%)	1 (1%)	69	81
52	BR	65/65 (100%)	57 (88%)	8 (12%)	4	19
53	BS	77/77 (100%)	72 (94%)	5 (6%)	17	42
54	BT	64/64 (100%)	61 (95%)	3 (5%)	26	51
55	BU	78/78 (100%)	69 (88%)	9 (12%)	5	21
56	BV	65/65 (100%)	65 (100%)	0	100	100
57	BW	60/60 (100%)	55 (92%)	5 (8%)	11	34
All	All	5213/5213 (100%)	4919 (94%)	294 (6%)	25	46

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	BJ	68	LYS
55	BU	47	THR
45	BK	88	GLU
50	BP	66	THR
15	AO	136	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	119/120 (99%)	18 (15%)	13 (10%)
2	AB	2898/2904 (99%)	527 (18%)	180 (6%)
35	BA	1538/1542 (99%)	294 (19%)	112 (7%)
36	BB	46/47 (97%)	15 (32%)	6 (13%)
37	BC	76/77 (98%)	14 (18%)	1 (1%)
All	All	4677/4690 (99%)	868 (18%)	312 (6%)

5 of 868 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	13	G
1	AA	14	U
1	AA	25	U
1	AA	26	C

5 of 312 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	552	U
35	BA	1302	C
35	BA	681	A
35	BA	944	G
35	BA	1465	A

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

40 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	6MZ	AB	2030	2	18,25,26	1.85	3 (16%)	16,36,39	1.95	3 (18%)
2	5MU	AB	747	2	19,22,23	1.52	3 (15%)	28,32,35	2.79	17 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
37	4SU	BC	8	37	18,21,22	1.95	6 (33%)	26,30,33	1.77	7 (26%)
2	2MA	AB	2503	2	17,25,26	1.22	2 (11%)	17,37,40	1.78	3 (17%)
2	2MG	AB	2445	2	18,26,27	1.77	4 (22%)	16,38,41	1.76	4 (25%)
35	PSU	BA	516	35	18,21,22	1.67	4 (22%)	22,30,33	2.34	4 (18%)
2	OMU	AB	2552	2	19,22,23	0.82	1 (5%)	26,31,34	1.36	3 (11%)
2	5MU	AB	1939	2	19,22,23	1.35	2 (10%)	28,32,35	2.31	9 (32%)
35	MA6	BA	1518	35	19,26,27	1.51	2 (10%)	18,38,41	1.32	3 (16%)
2	OMC	AB	2498	2	19,22,23	1.30	5 (26%)	26,31,34	1.57	6 (23%)
2	PSU	AB	1911	2	18,21,22	2.38	8 (44%)	22,30,33	1.33	4 (18%)
2	H2U	AB	2449	2	18,21,22	1.23	1 (5%)	21,30,33	2.82	9 (42%)
2	6MZ	AB	1618	2	18,25,26	1.81	6 (33%)	16,36,39	1.60	4 (25%)
35	5MC	BA	967	35	18,22,23	1.05	1 (5%)	26,32,35	1.33	4 (15%)
2	2MG	AB	1835	2	18,26,27	1.79	4 (22%)	16,38,41	1.83	3 (18%)
2	PSU	AB	1917	2	18,21,22	1.39	4 (22%)	22,30,33	1.82	5 (22%)
2	PSU	AB	2580	2	18,21,22	1.85	5 (27%)	22,30,33	1.48	4 (18%)
2	OMG	AB	2251	2	18,26,27	1.71	5 (27%)	19,38,41	1.37	1 (5%)
35	2MG	BA	966	35	18,26,27	1.87	6 (33%)	16,38,41	1.50	4 (25%)
2	1MG	AB	745	2	18,26,27	2.01	9 (50%)	19,39,42	1.89	6 (31%)
2	PSU	AB	2605	2	18,21,22	1.79	3 (16%)	22,30,33	1.92	7 (31%)
2	PSU	AB	746	2	18,21,22	2.04	5 (27%)	22,30,33	2.03	6 (27%)
35	7MG	BA	527	35	22,26,27	3.39	7 (31%)	29,39,42	1.61	2 (6%)
35	5MC	BA	1407	35	18,22,23	1.58	3 (16%)	26,32,35	1.49	6 (23%)
37	PSU	BC	56	37	18,21,22	2.23	5 (27%)	22,30,33	1.22	1 (4%)
2	5MC	AB	1962	2	18,22,23	1.31	2 (11%)	26,32,35	1.51	6 (23%)
35	2MG	BA	1207	35	18,26,27	1.59	4 (22%)	16,38,41	1.44	2 (12%)
37	H2U	BC	21	37	18,21,22	1.65	6 (33%)	21,30,33	2.23	9 (42%)
35	4OC	BA	1402	35	20,23,24	1.24	4 (20%)	26,32,35	1.97	8 (30%)
37	OMC	BC	33	37	19,22,23	1.24	3 (15%)	26,31,34	1.38	5 (19%)
2	3TD	AB	1915	2	18,22,23	1.38	3 (16%)	22,32,35	2.17	7 (31%)
35	2MG	BA	1516	35	18,26,27	1.64	4 (22%)	16,38,41	1.47	3 (18%)
2	7MG	AB	2069	2	22,26,27	4.67	4 (18%)	29,39,42	1.64	5 (17%)
2	PSU	AB	2457	2	18,21,22	1.56	3 (16%)	22,30,33	2.33	5 (22%)
2	CH	AB	2575	2	16,21,22	1.64	2 (12%)	20,30,33	1.55	4 (20%)
2	PSU	AB	2504	2	18,21,22	1.71	3 (16%)	22,30,33	2.17	5 (22%)
35	UR3	BA	1498	35	19,22,23	1.23	3 (15%)	26,32,35	1.91	7 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	AB	955	2	18,21,22	1.90	3 (16%)	22,30,33	1.56	4 (18%)
37	5MU	BC	55	37	19,22,23	1.01	1 (5%)	28,32,35	1.97	8 (28%)
35	MA6	BA	1519	35	19,26,27	1.46	4 (21%)	18,38,41	2.25	5 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6MZ	AB	2030	2	-	0/5/27/28	0/3/3/3
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
37	4SU	BC	8	37	-	0/7/25/26	0/2/2/2
2	2MA	AB	2503	2	-	0/3/25/26	0/3/3/3
2	2MG	AB	2445	2	-	0/5/27/28	0/3/3/3
35	PSU	BA	516	35	-	1/7/25/26	0/2/2/2
2	OMU	AB	2552	2	-	1/9/27/28	0/2/2/2
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
35	MA6	BA	1518	35	-	0/7/29/30	0/3/3/3
2	OMC	AB	2498	2	-	0/9/27/28	0/2/2/2
2	PSU	AB	1911	2	-	2/7/25/26	0/2/2/2
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
2	6MZ	AB	1618	2	-	1/5/27/28	0/3/3/3
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
2	2MG	AB	1835	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	1917	2	-	3/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	3/7/25/26	0/2/2/2
2	OMG	AB	2251	2	-	0/5/27/28	0/3/3/3
35	2MG	BA	966	35	-	0/5/27/28	0/3/3/3
2	1MG	AB	745	2	-	0/3/25/26	0/3/3/3
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	746	2	-	1/7/25/26	0/2/2/2
35	7MG	BA	527	35	-	1/7/37/38	0/3/3/3
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
37	PSU	BC	56	37	-	0/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
35	2MG	BA	1207	35	-	0/5/27/28	0/3/3/3
37	H2U	BC	21	37	-	0/7/38/39	0/2/2/2
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
37	OMC	BC	33	37	-	0/9/27/28	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	2MG	BA	1516	35	-	0/5/27/28	0/3/3/3
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
2	PSU	AB	2504	2	-	2/7/25/26	0/2/2/2
35	UR3	BA	1498	35	-	0/7/25/26	0/2/2/2
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
37	5MU	BC	55	37	-	0/7/25/26	0/2/2/2
35	MA6	BA	1519	35	-	0/7/29/30	0/3/3/3

The worst 5 of 153 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	2069	7MG	C8-N9	-20.69	1.34	1.46
35	BA	527	7MG	C8-N9	-14.00	1.38	1.46
2	AB	2030	6MZ	C6-N1	5.79	1.42	1.34
2	AB	1911	PSU	C2'-C1'	-5.36	1.46	1.53
2	AB	955	PSU	C2'-C1'	-5.26	1.46	1.53

The worst 5 of 208 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	2457	PSU	C6-C5-C4	7.75	123.62	118.20
35	BA	516	PSU	C3'-C2'-C1'	7.65	110.55	101.64
2	AB	2449	H2U	O2-C2-N1	-7.16	114.12	123.11
2	AB	1939	5MU	C5M-C5-C4	6.70	126.14	118.77
2	AB	2504	PSU	C6-C5-C4	6.64	122.84	118.20

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	746	PSU	C2'-C1'-C5-C4
2	AB	2552	OMU	C1'-C2'-O2'-CM2
2	AB	1917	PSU	O4'-C4'-C5'-O5'
2	AB	1917	PSU	C3'-C4'-C5'-O5'
35	BA	527	7MG	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AB	2831:G	O3'	2832:U	P	1.76

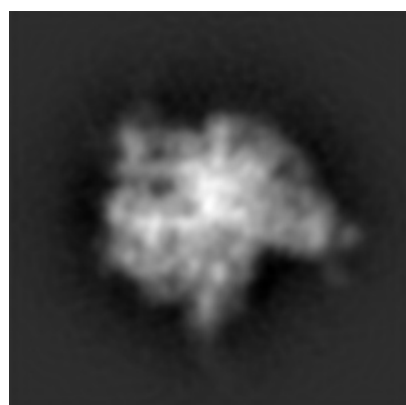
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5360. These allow visual inspection of the internal detail of the map and identification of artifacts.

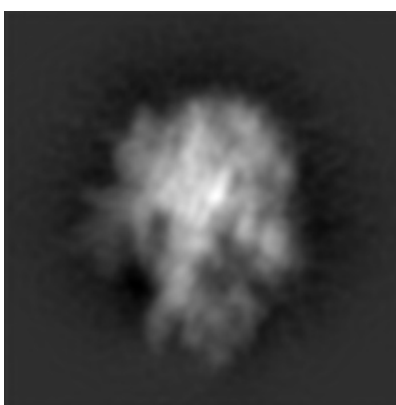
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

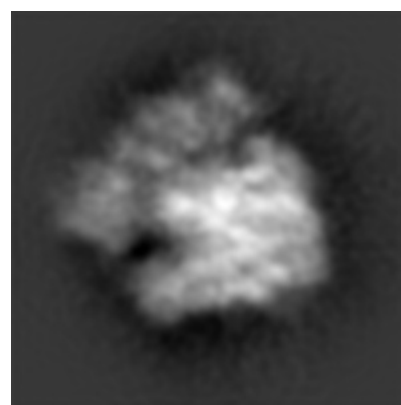
6.1.1 Primary map



X



Y

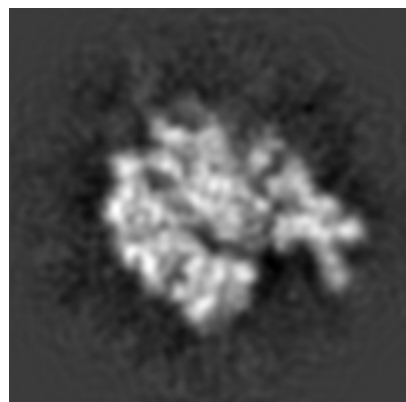


Z

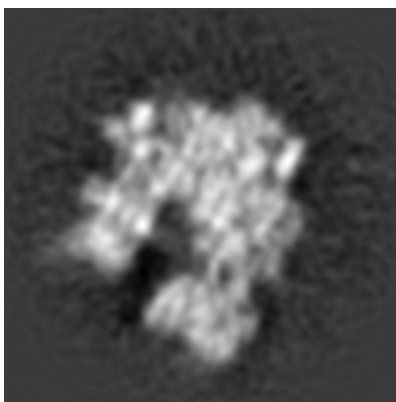
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

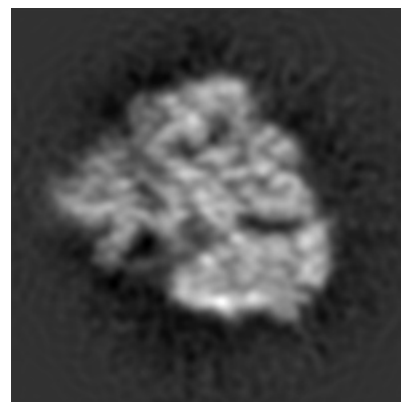
6.2.1 Primary map



X Index: 125



Y Index: 125

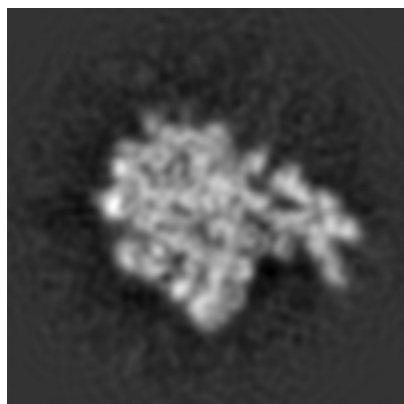


Z Index: 125

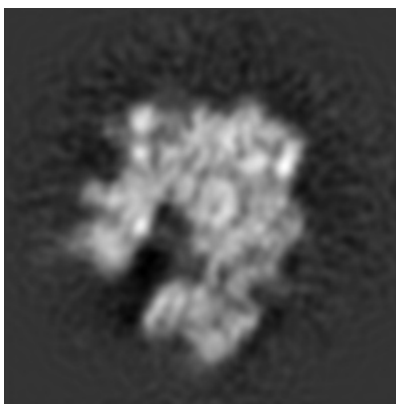
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

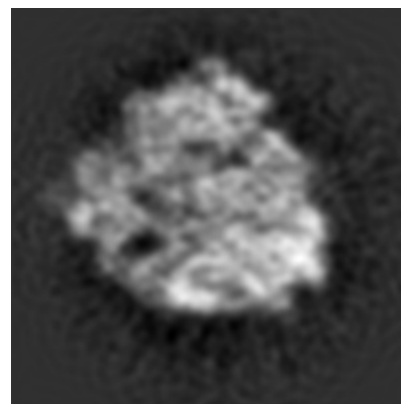
6.3.1 Primary map



X Index: 131



Y Index: 128

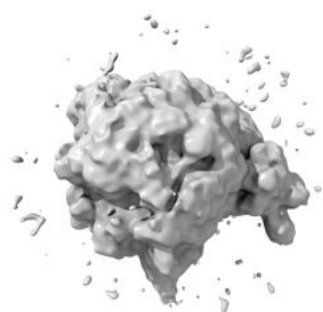


Z Index: 118

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

6.4 Orthogonal surface views [i](#)

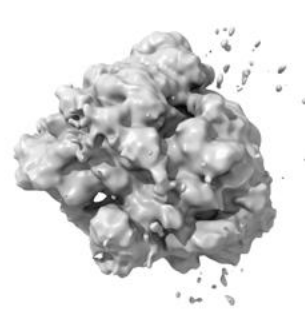
6.4.1 Primary map



X



Y



Z

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

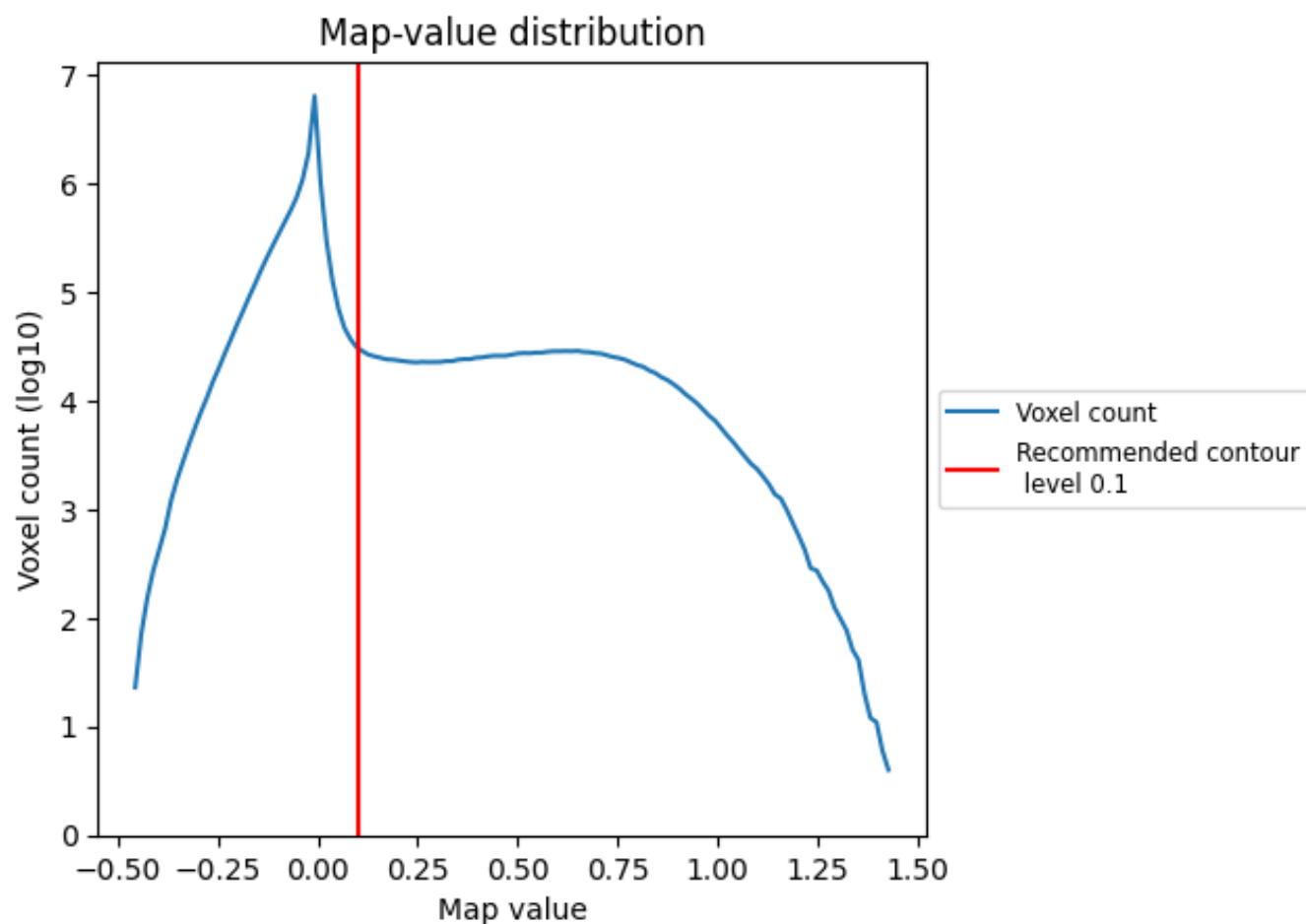
6.5 Mask visualisation

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

7 Map analysis [i](#)

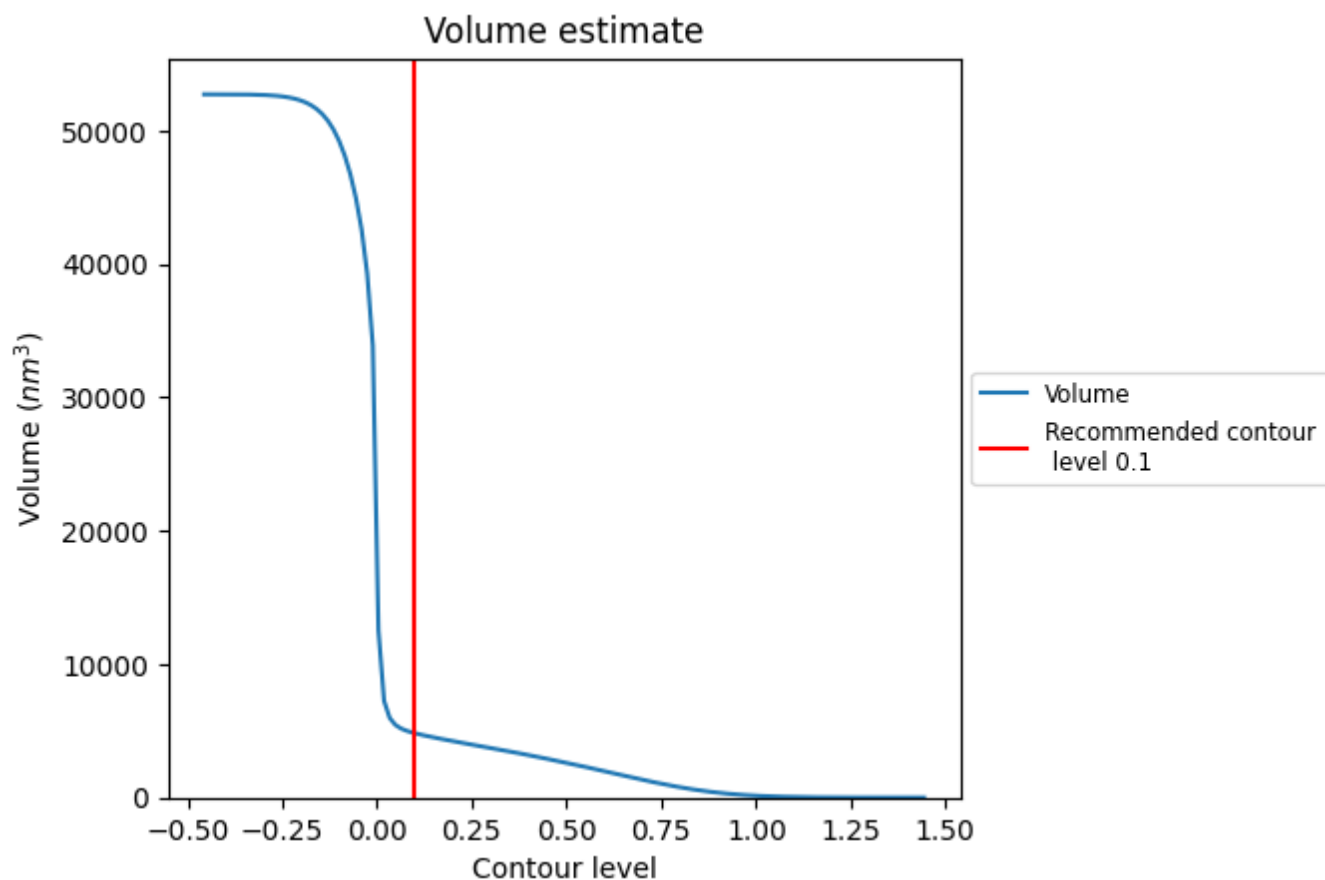
This section contains the results of statistical analysis of the map.

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.

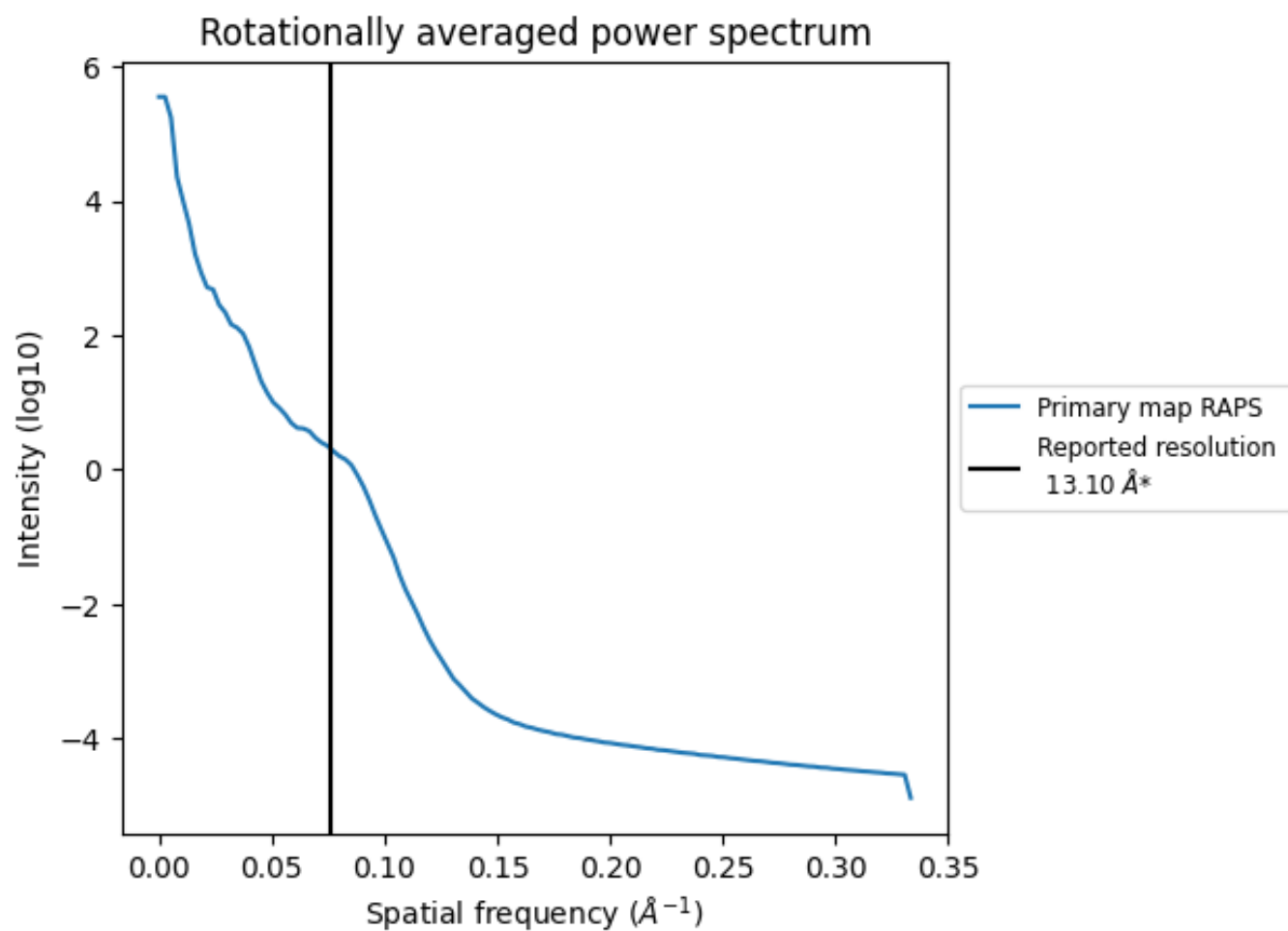
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4825 nm^3 ; this corresponds to an approximate mass of 4359 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 0.076 \AA^{-1}

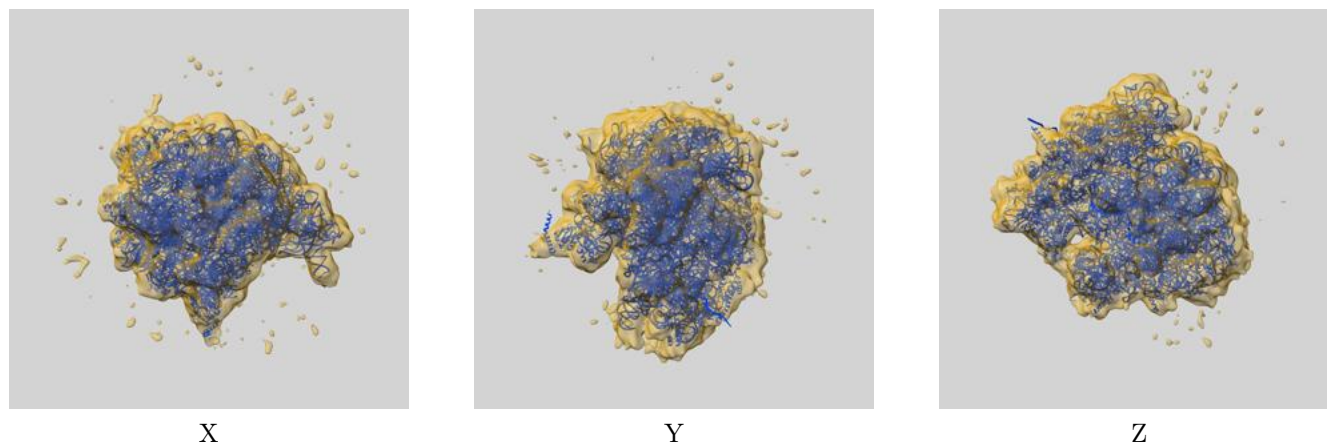
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

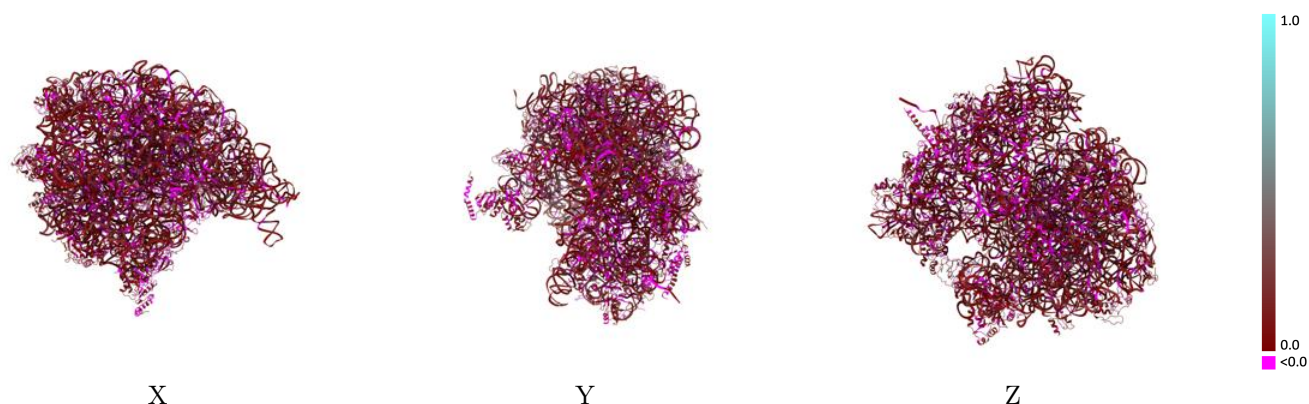
This section contains information regarding the fit between EMDB map EMD-5360 and PDB model 4V6S. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



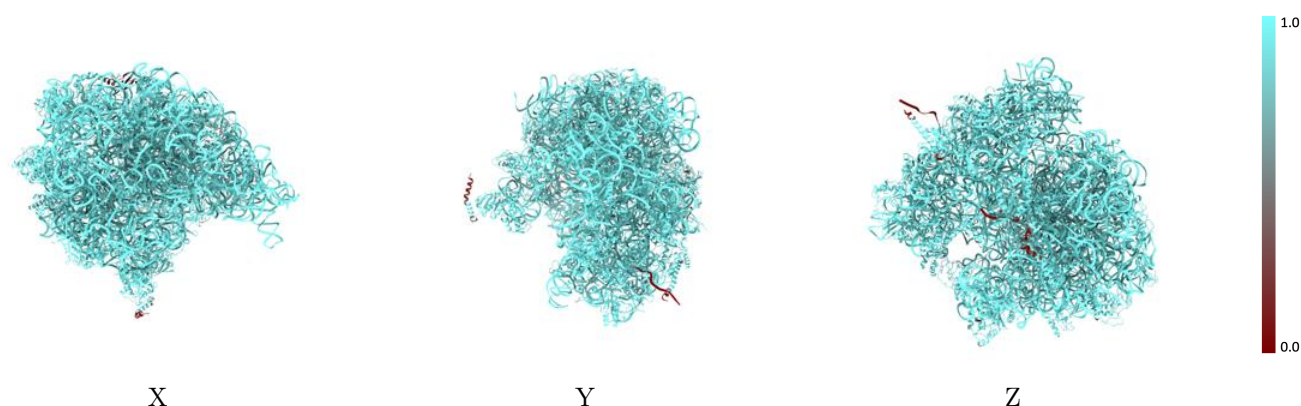
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



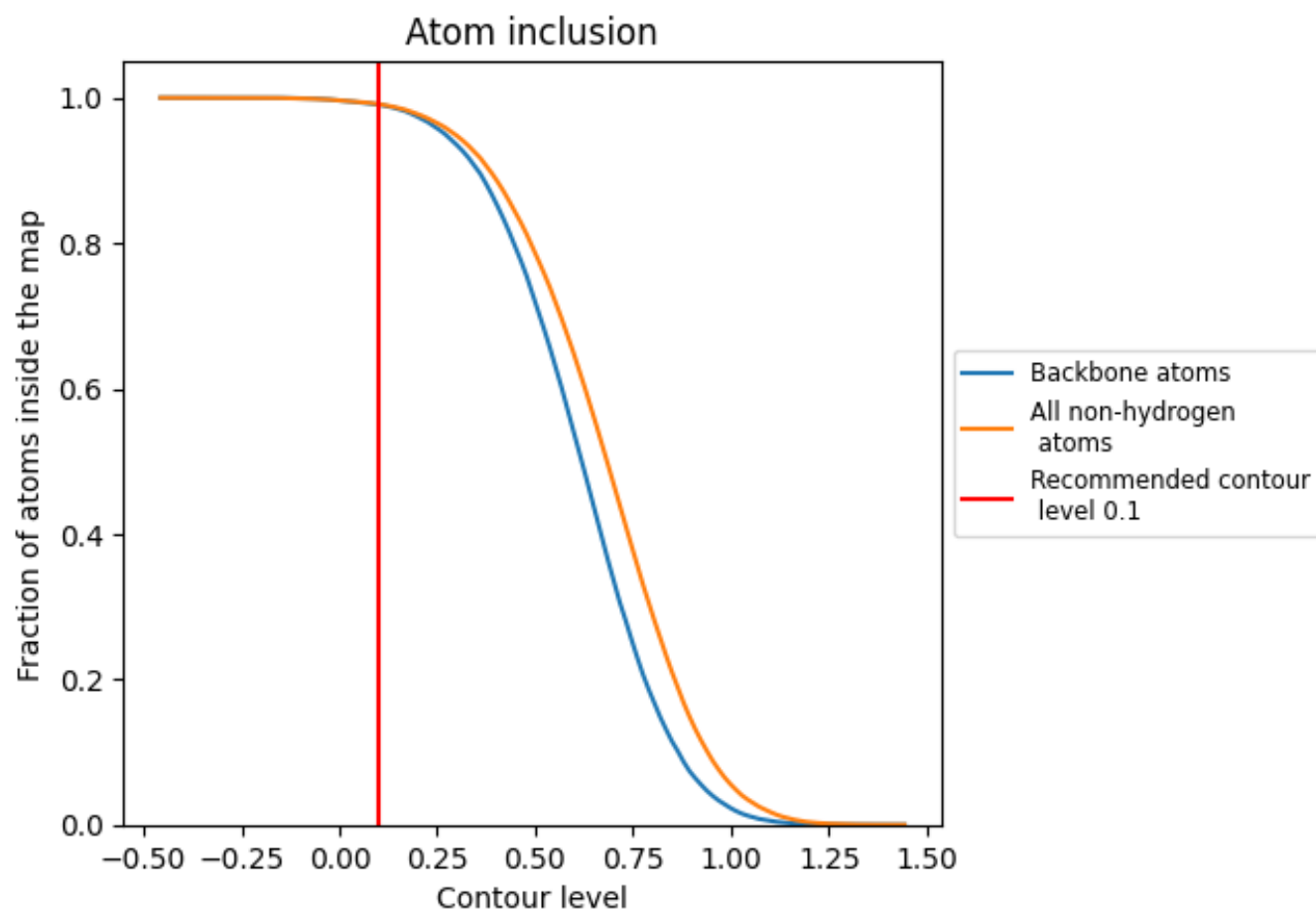
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion ⓘ



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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9912	0.0680
A0	1.0000	0.0510
A1	0.9954	0.0290
A2	0.9108	0.0270
A3	1.0000	0.0260
A4	1.0000	0.0490
A5	1.0000	-0.0180
A6	1.0000	-0.0250
A7	1.0000	0.0160
AA	0.9996	0.0850
AB	0.9991	0.0850
AC	0.9614	0.0370
AD	1.0000	0.0210
AE	0.9961	0.0150
AF	0.9974	0.0470
AG	0.9978	0.0730
AH	0.9992	0.0210
AI	0.7901	0.0300
AJ	0.8698	0.0350
AK	0.9795	0.0440
AL	0.9991	0.0250
AM	0.9902	0.0340
AN	0.9941	0.0100
AO	1.0000	0.0310
AP	1.0000	0.0080
AQ	0.9931	0.0550
AR	0.9786	0.0230
AS	0.9978	0.0170
AT	1.0000	0.0470
AU	1.0000	0.0140
AV	1.0000	0.0310
AW	1.0000	0.0770
AX	1.0000	0.0740
AY	0.9984	0.0080
AZ	1.0000	0.0600



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Chain	Atom inclusion	Q-score
BA	 0.9992	 0.0840
BB	 0.7341	 -0.0130
BC	 1.0000	 0.0980
BD	 0.9093	 0.0220
BE	 0.9983	 0.0640
BF	 1.0000	 0.0460
BG	 0.9967	 0.0420
BH	 0.9618	 0.0290
BI	 0.9926	 0.0680
BJ	 0.9729	 0.0280
BK	 0.9879	 0.0480
BL	 1.0000	 0.0400
BM	 0.9369	 0.0550
BN	 0.9772	 0.0330
BO	 0.9715	 0.0480
BP	 1.0000	 0.0270
BQ	 1.0000	 0.0410
BR	 1.0000	 0.0480
BS	 1.0000	 0.0660
BT	 1.0000	 0.0540
BU	 0.9817	 0.0270
BV	 1.0000	 0.0460
BW	 0.9964	 0.0570