wwPDB EM Validation Summary Report (i)

Dec 10, 2022 – 12:00 pm GMT

PDB ID	:	6QIK
EMDB ID	:	EMD-4560
Title	:	Cryo-EM structures of Lsg1-TAP pre-60S ribosomal particles
Authors	:	Kargas, V.; Warren, A.J.
Deposited on	:	2019-01-20
Resolution	:	3.10 Å(reported)
Based on initial model	:	4V88

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 (i) 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 (i)) were used in the production of this report:

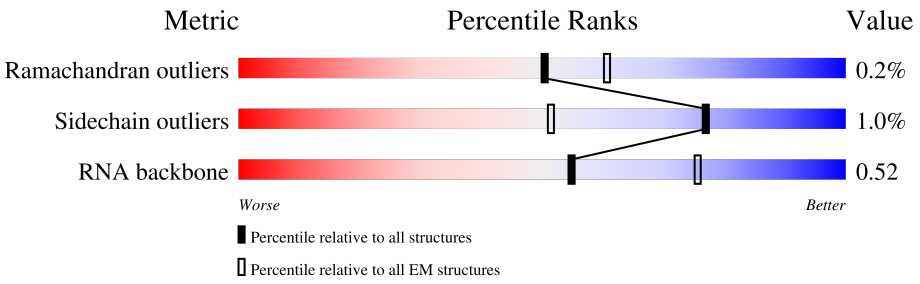
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3396	7% 71% 22% 7%
2	B	254	95%
3	C	387	97%
4	D	362	99%
5	E	174	6% 97%
6	F	191	10% 99%
7	G	176	21% 99%
8	H	256	7% 87% 13%

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Mol	Chain	Length	Quality of chain
9	J	198	99%
10	K	199	7% 92% 7%
11	L	137	98%
12	M	138	7% 96%
13	N	149	99%
14	O	204	100%
15	P	297	91% 9%
16	Q	186	98%
17	R	189	78% 21%
18	S	172	99%
19	T	160	99%
20	U	154	99%
21	V	121	82% 18%
22	W	142	85% 15%
23	X	127	98%
24	Y	136	99%
25	Z	120	97%
26	a	59	7% 88% 12%
27	b	244	89% 10%
28	c	105	8% 92% 8%
29	d	113	8% 93% 5%
30	e	130	5% 97%
31	f	107	98%
32	g	121	82% 15%
33	h	100	21% 98%

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Mol	Chain	Length	Quality of chain
34	i	88	93% 5%
35	j	78	97%
36	k	51	98%
37	l	106	86% 11%
38	m	92	96%
39	n	245	91% 9%
40	z	432	5% 13% 87%
41	w	518	28% 72% 25%
42	v	155	39% 61%
43	o	640	49% 47% 50%
44	p	210	30% 100%
45	t	128	41% 41% 59%
46	x	121	84% 16%
47	y	158	73% 25%

2 Entry composition (i)

There are 48 unique types of molecules in this entry. The entry contains 128569 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3146	67292	30062	12142	21944	3144	0	0

- Molecule 2 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	247	1878	1170	381	326	1	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	381	3039	1928	577	526	8	0	0

- Molecule 4 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	361	2748	1730	522	493	3	0	0

- Molecule 5 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	169	1352	847	253	248	4	0	0

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	189	1502	953	272	273	4	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	175	1399	902	251	245	1	0	0

- Molecule 8 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	223	1742	1117	309	313	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	197	1563	1005	292	265	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	K	186	1486	929	304	253	0	0

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	136	1002	628	189	178	7	0	0

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	135	1045	669	197	177	2	0	0

- Molecule 13 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	148	1172	749	231	189	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	203	1719	1077	361	280	1	0	0

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	269	2176	1378	375	421	2	0	0

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	185	1440	908	290	240	2	0	0

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	R	150	1209	752	257	200	0	0

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	171	1436	925	266	242	3	0	0

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	159	1275	805	246	220	4	0	0

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	U	154	1222	761	237	224	0	0

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	V	99	786	510	129	147	0	0

- Molecule 22 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	120	958	617	168	171	2	0	0

- Molecule 23 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	X	125	984	620	191	173	0	0

- Molecule 24 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	Y	135	1091	710	202	179	0	0

- Molecule 25 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Z	118	963	612	185	165	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	a	52	415	259	90	66	0	0

- Molecule 27 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	b	219	1760	1138	320	301	1	0	0

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	97	741	479	124	137	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	107	872	553	165	153	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	127	1020	646	205	167	2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	106	849	540	165	143	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	g	103	812	504	167	137	4	0	0

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	h	98	763	477	155	129	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	i	84	665	405	145	110	5	0	0

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	j	77	611	391	115	105	0	0

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	k	50	435	272	97	64	2	0	0

- Molecule 37 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	l	94	756	476	153	122	5	0	0

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	m	89	680	421	136	117	6	0	0

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	n	224	1691	1051	293	340	7	0	0

- Molecule 40 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	z	58	491	301	100	87	3	0	0

- Molecule 41 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	w	389	3076	1955	530	571	20	0	0

- Molecule 42 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	v	60	500	322	98	79	1	0	0

- Molecule 43 is a protein called Large subunit GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	o	322	2593	1660	449	477	7	0	0

- Molecule 44 is a protein called uL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	p	210	1050	630	210	210	0	0

- Molecule 45 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
46	x	121	2576	1152	461	843	120	0	0

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	y	156	3310	1482	582	1091	155	0	0

- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
48	g	1	1	1	0
48	i	1	1	1	0
48	l	1	1	1	0

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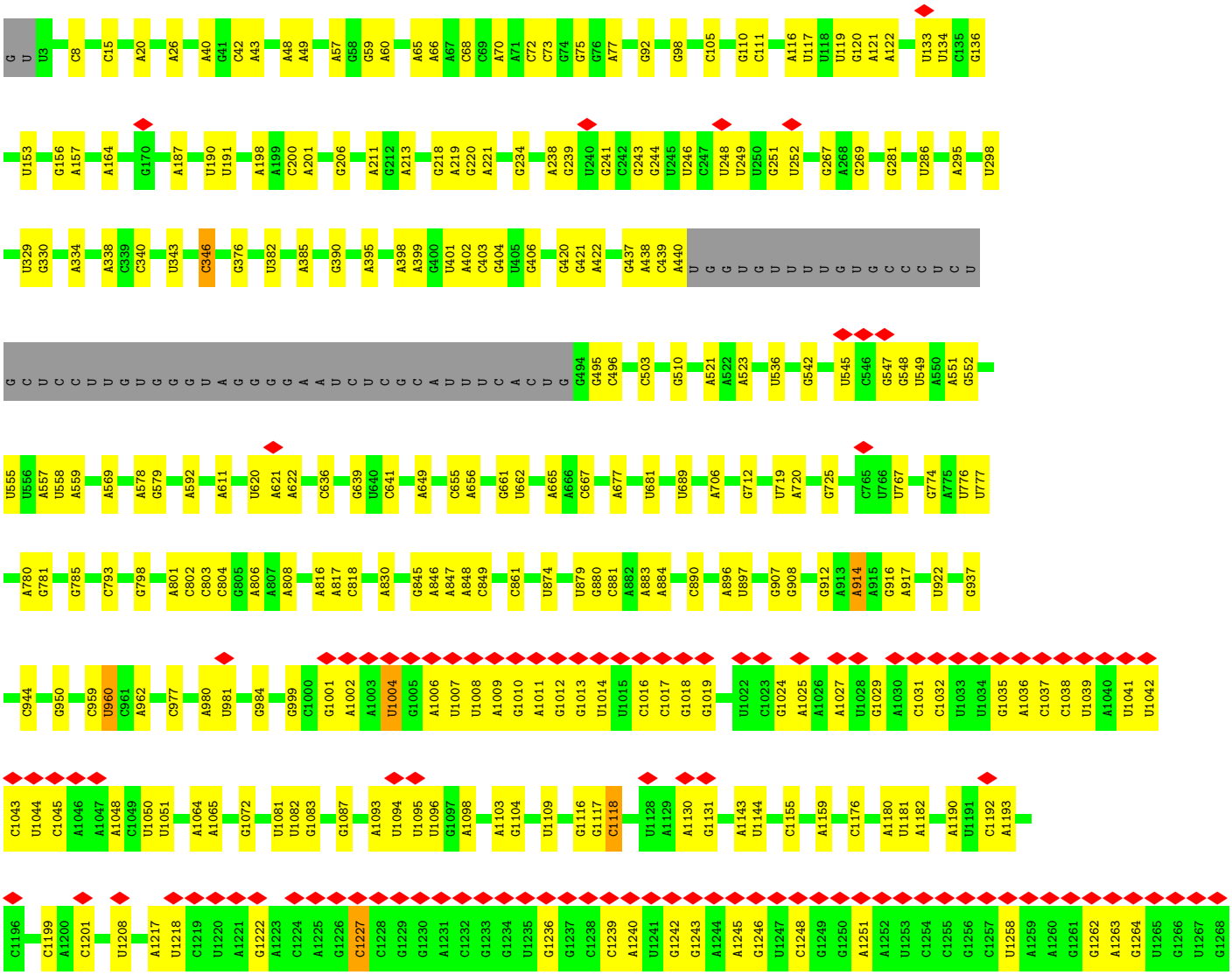
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
48	m	1	1	1	0
			Total	Zn	
48	w	2	2	2	0
			Total	Zn	
48	t	1	1	1	0

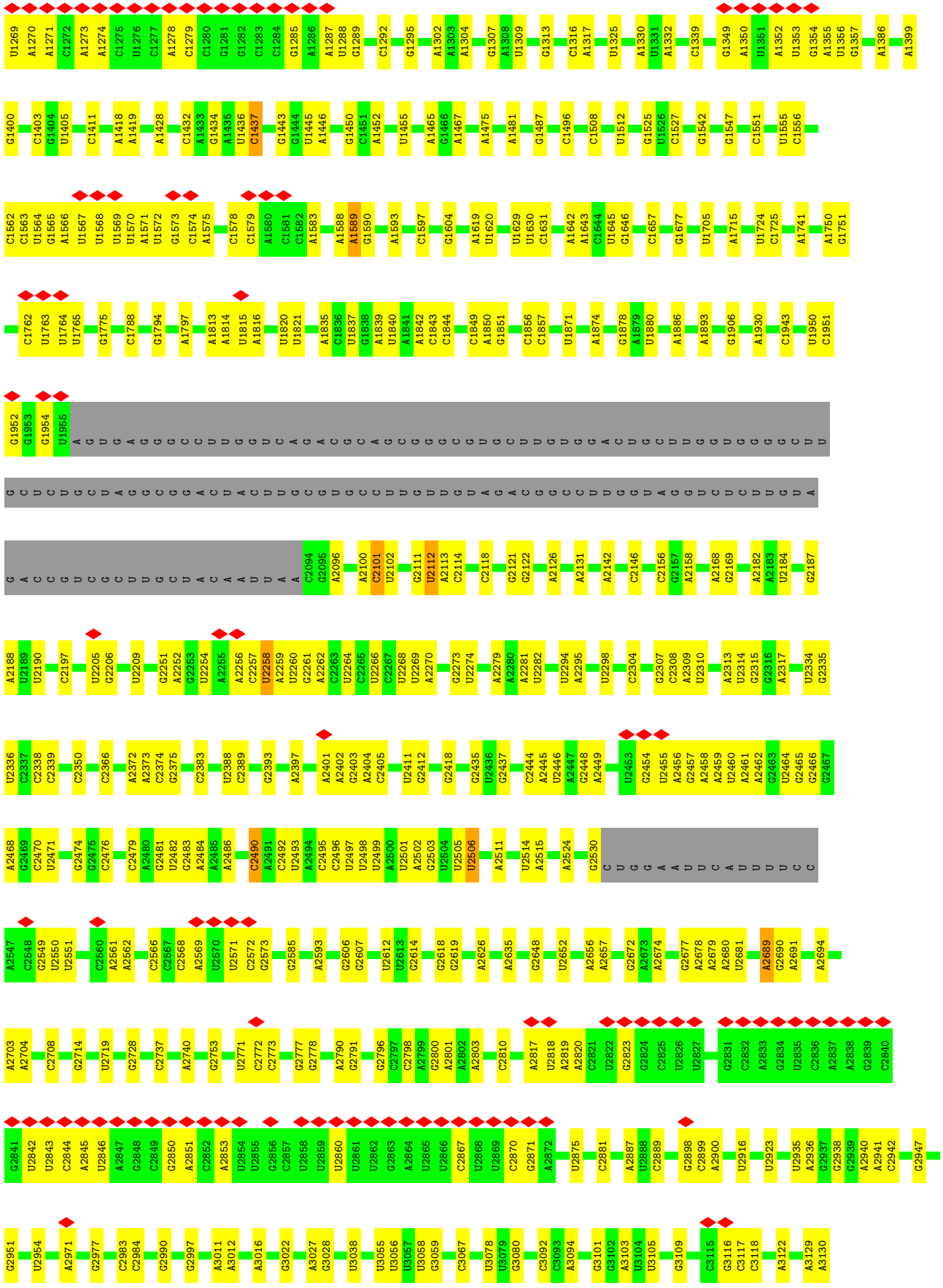
3 Residue-property plots (i)

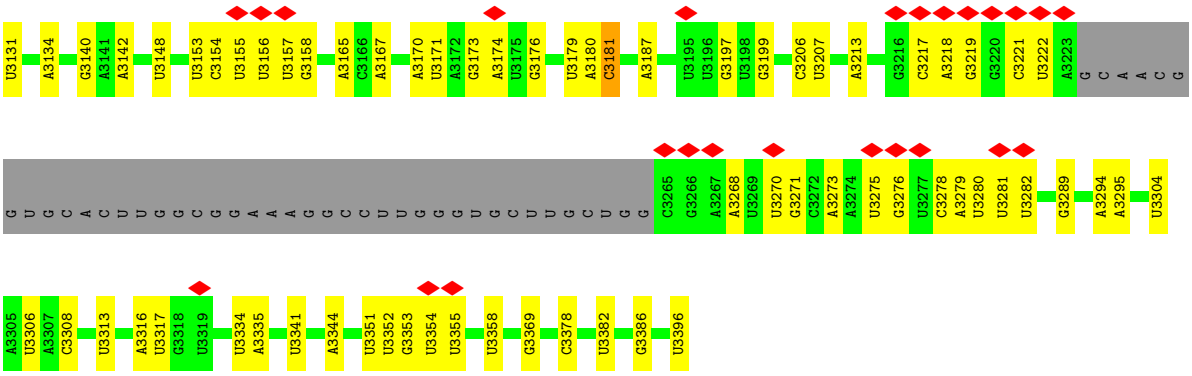
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S ribosomal RNA

Chain A: 7% 71% 22% 7%

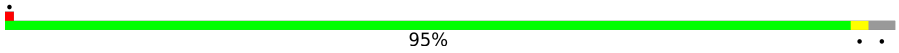


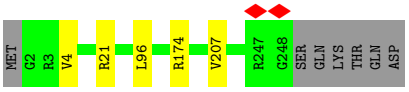

U1269 A1270 A1271 C1272 A1273 A1274 C1275 U1276 C1277 A1278 C1279 C1280 G1281 G1282 C1283 C1284 G1285 A1286 A1287 U1288 G1289 C1292 G1295 A1302 A1303 A1304 G1307 A1308 U1309 G1313 C1316 A1317 U1325 A1330 U1331 A1332 C1339 G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 A1386 A1399
G1400 C1403 G1404 U1405 C1411 A1418 A1419 A1428 C1432 A1433 G1434 A1435 U1436 C1437 G1443 G1444 U1445 A1446 G1450 C1451 A1452 U1455 A1465 G1466 A1467 A1475 A1481 G1487 C1496 C1508 U1512 G1525 U1526 C1527 G1542 G1547 C1551 U1555 C1556
C1562 C1563 U1564 G1565 A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1573 C1574 A1575 C1578 C1579 A1580 C1581 C1582 A1583 A1588 A1589 G1590 A1593 C1597 G1604 A1619 U1620 U1629 U1630 C1631 A1642 A1643 C1644 U1645 G1646 C1657 G1677 U1705 A1715 U1724 C1725 A1741 A1750 G1751
C1762 U1763 U1764 U1765 G1775 C1788 G1794 A1797 A1813 A1814 U1815 A1816 U1820 U1821 A1835 C1836 U1837 G1838 A1839 U1840 A1841 A1842 C1843 C1844 C1849 A1850 G1851 C1856 C1857 U1871 A1874 G1878 A1879 U1880 A1886 A1893 G1906 A1930 C1943 U1950 C1951
G1952 G1953 G1954 U1955 A G U G A G G G C C U U G G G U G C A G A C G C G G G C U G U U G U G G A C U G C C C U C C U A A C C C G U G G C C C U G G G U A G G G U C U C U U G U A
G A C C G U C G C U C U G C G C U A C A A U U A A C C G C G U U G C G G C C C U G U U G G G C C G G U G G C C U U G G G C U U G G G C U U G G G



- Molecule 2: 60S ribosomal protein L2-A

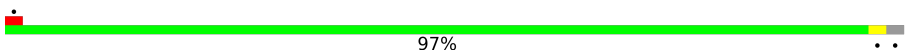
Chain B:





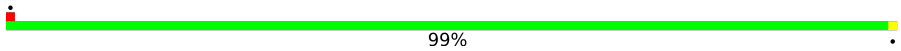
- Molecule 3: 60S ribosomal protein L3

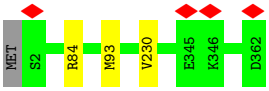
Chain C:



- Molecule 4: 60S ribosomal protein L4-A

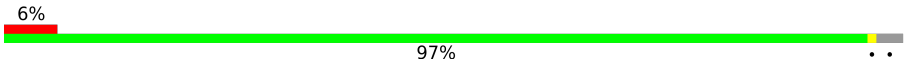
Chain D:

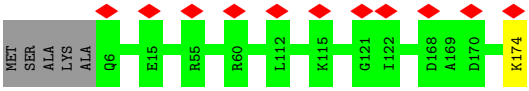




- Molecule 5: 60S ribosomal protein L11-A

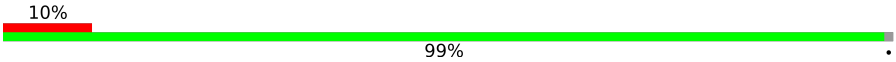
Chain E:

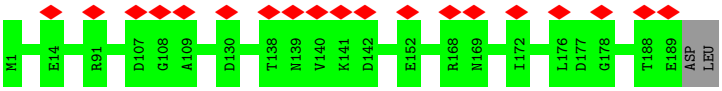




- Molecule 6: 60S ribosomal protein L9-A

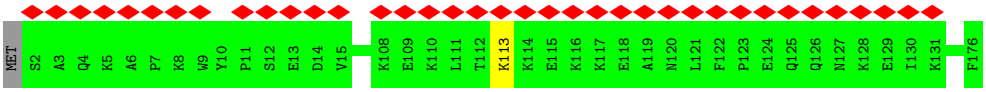
Chain F:





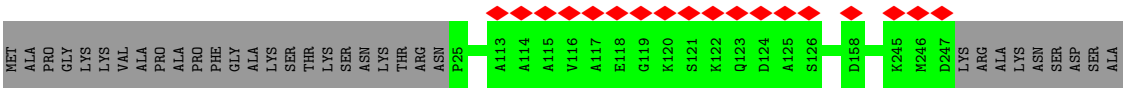
- Molecule 7: 60S ribosomal protein L6-A

Chain G: 21% 99%



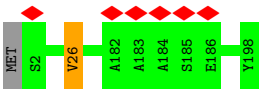
• Molecule 8: 60S ribosomal protein L8-A

Chain H: 7% 87% 13%



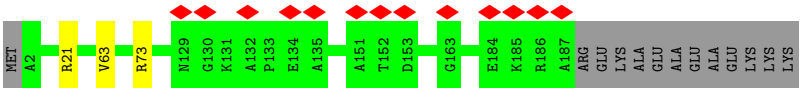
• Molecule 9: 60S ribosomal protein L16-B

Chain J: 99%



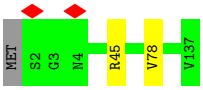
• Molecule 10: 60S ribosomal protein L13-A

Chain K: 7% 92% 7%



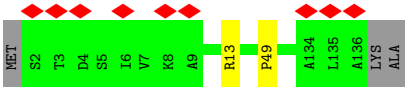
• Molecule 11: 60S ribosomal protein L23-A

Chain L: 98%



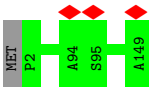
• Molecule 12: 60S ribosomal protein L14-A

Chain M: 7% 96%



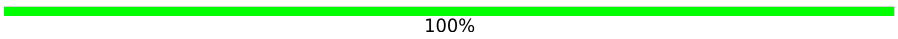
• Molecule 13: 60S ribosomal protein L28

Chain N: 99%



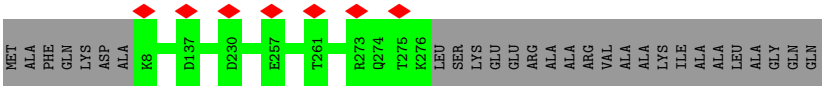
- Molecule 14: 60S ribosomal protein L15-A

Chain O:



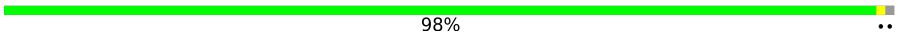
- Molecule 15: 60S ribosomal protein L5

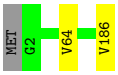
Chain P:



- Molecule 16: 60S ribosomal protein L18-A

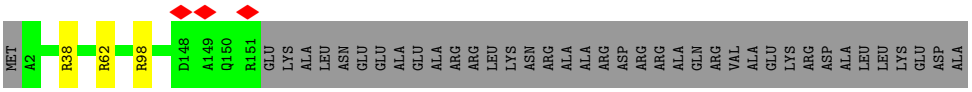
Chain Q:





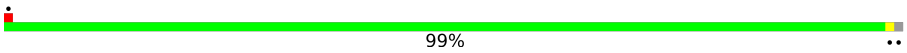
- Molecule 17: 60S ribosomal protein L19-A

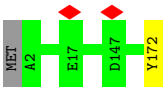
Chain R:



- Molecule 18: 60S ribosomal protein L20-A

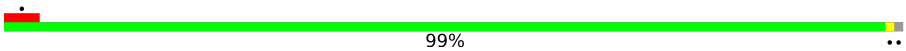
Chain S:

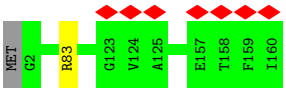




- Molecule 19: 60S ribosomal protein L21-A

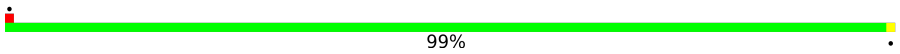
Chain T:

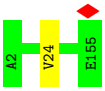




- Molecule 20: 60S ribosomal protein L17-A

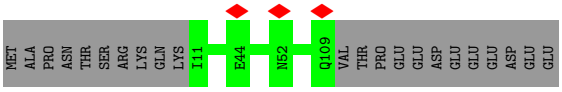
Chain U:





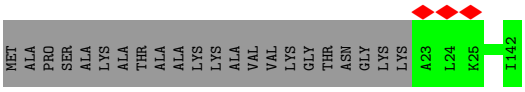
• Molecule 21: 60S ribosomal protein L22-A

Chain V:

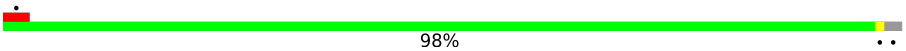


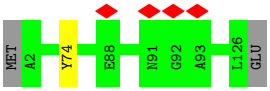
• Molecule 22: 60S ribosomal protein L25

Chain W:

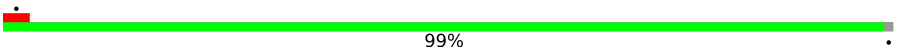


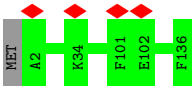
• Molecule 23: 60S ribosomal protein L26-A

Chain X: 

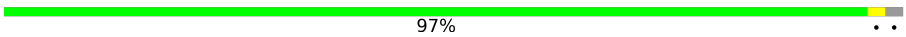


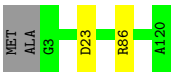
• Molecule 24: 60S ribosomal protein L27-A

Chain Y: 



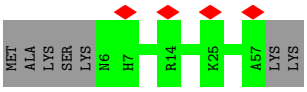
• Molecule 25: 60S ribosomal protein L35-A

Chain Z: 



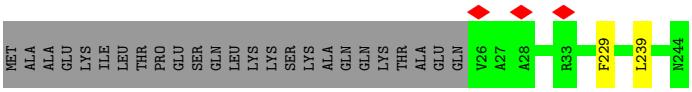
• Molecule 26: 60S ribosomal protein L29

Chain a:



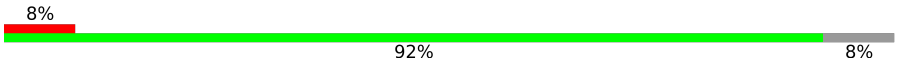
• Molecule 27: 60S ribosomal protein L7-A

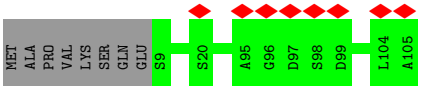
Chain b:



• Molecule 28: 60S ribosomal protein L30

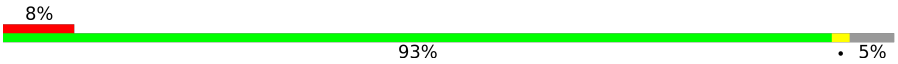
Chain c:

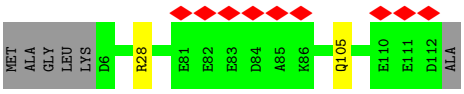




• Molecule 29: 60S ribosomal protein L31-A

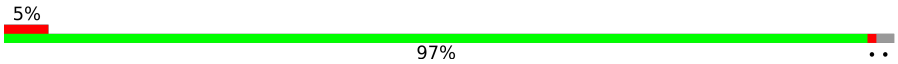
Chain d:

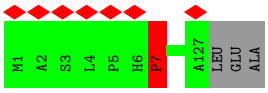




• Molecule 30: 60S ribosomal protein L32

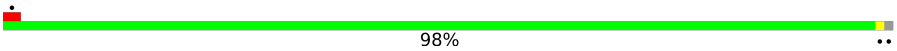
Chain e:

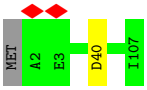




• Molecule 31: 60S ribosomal protein L33-A

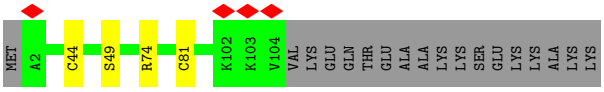
Chain f:





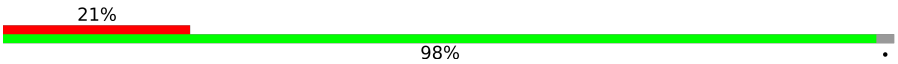
• Molecule 32: 60S ribosomal protein L34-A

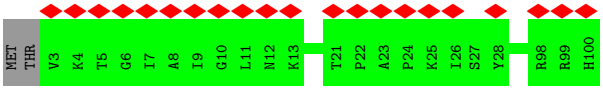
Chain g:



• Molecule 33: 60S ribosomal protein L36-A

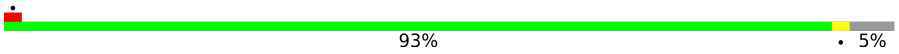
Chain h:

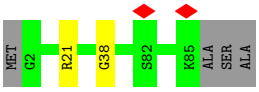




- Molecule 34: 60S ribosomal protein L37-A

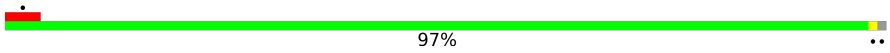
Chain i:

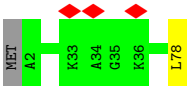




- Molecule 35: 60S ribosomal protein L38

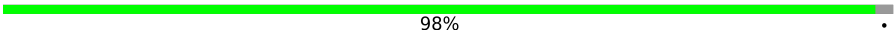
Chain j:





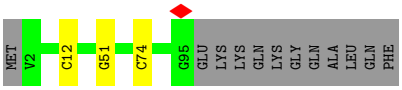
- Molecule 36: 60S ribosomal protein L39

Chain k:



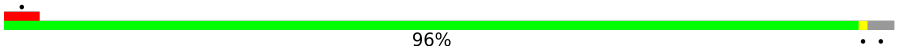
- Molecule 37: 60S ribosomal protein L42-A

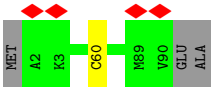
Chain l:



- Molecule 38: 60S ribosomal protein L43-A

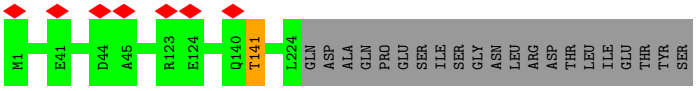
Chain m:





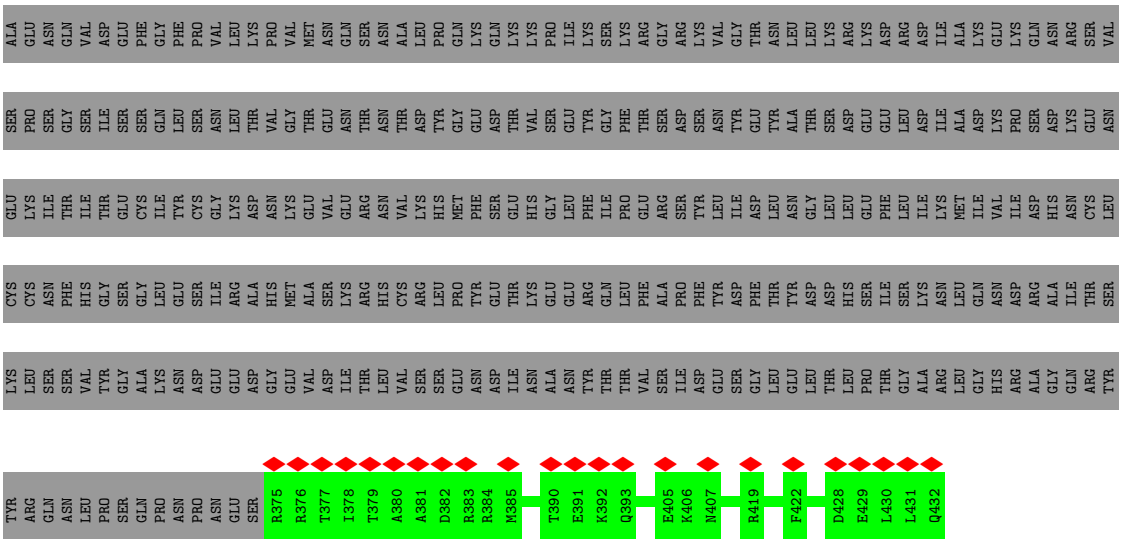
- Molecule 39: Eukaryotic translation initiation factor 6

Chain n:



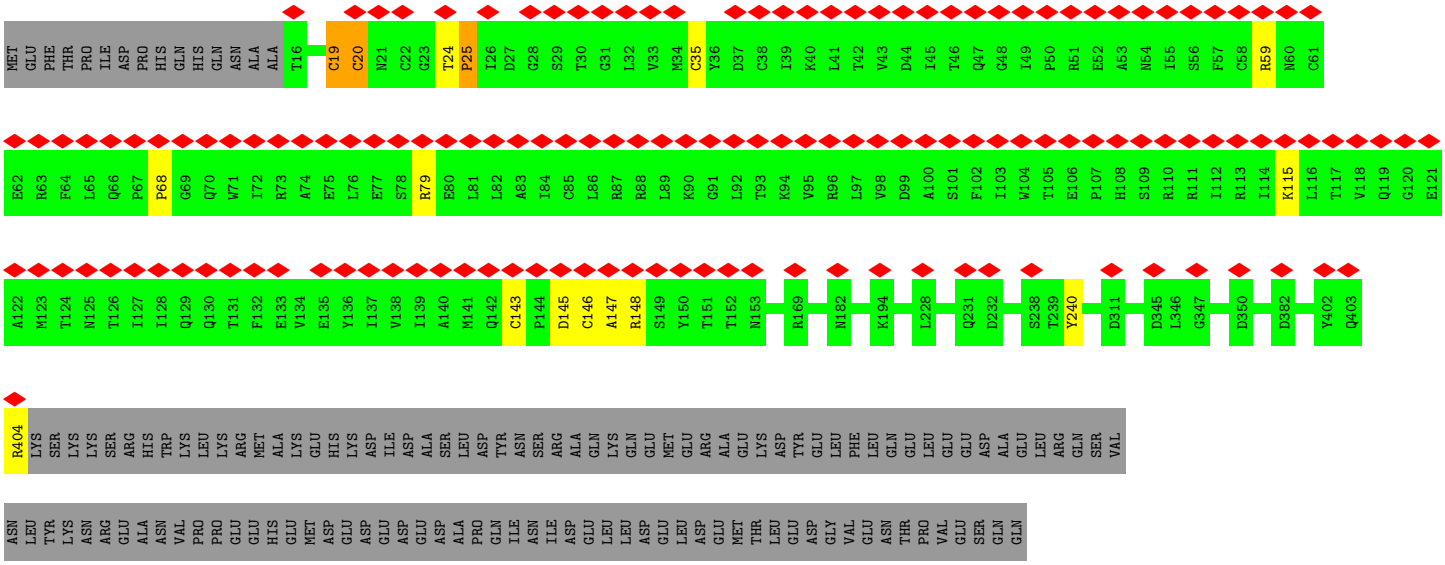
- Molecule 40: Cytoplasmic 60S subunit biogenesis factor REH1

Chain z:



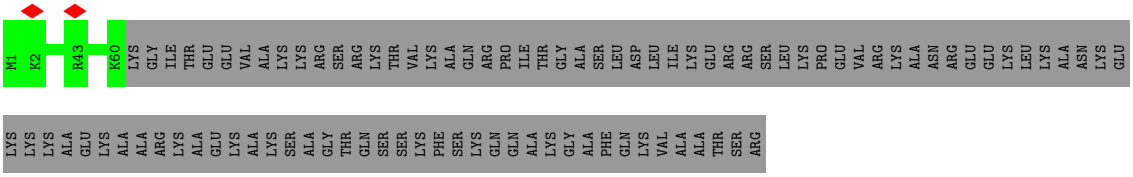
- Molecule 41: 60S ribosomal export protein NMD3

Chain w:



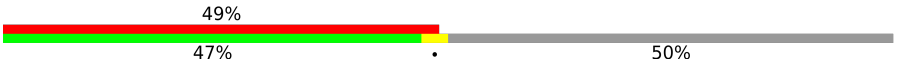
- Molecule 42: 60S ribosomal protein L24-A

Chain v:



- Molecule 43: Large subunit GTPase 1

Chain o:



MET PRO PRO LYS GLU ALA PRO LYS LYS TRP LYS ALA PRO LYS GLY PRO LYS PRO THR HIS ARG LYS ASN LYS ASN LYS LEU GLU LEU GLY ARG ALA ILE LYS TYR ALA ARG GLN LYS GLU ASN ALA ILE GLU TYR LEU PRO ASP GLY GLU MET ARG PHE THR THR ASP LYS HIS GLU ALA

ASN TRP VAL LYS LEU ARG SER VAL THR GLN GLU SER ALA LEU ASP GLU PHE LEU SER THR ALA ALA LEU ALA ASP LYS ASP PHE THR ALA ASP ARG HIS SER ASN VAL LYS ILE ILE ARG MET ASP SER GLY ASN ASP SER ALA THR SER GLN GLY PHE SER MET THR ASN GLU GLN ARG

GLY ASN LEU ASN ALA LYS GLN ARG ALA LEU ALA LYS D133 L134 I135 V136 P137 R138 R139 P140 E141 W142 N143 E144 G145 M146 S147 K148 F149 Q150 L151 D152 R153 Q154 E155 K156 E157 A158 F159 L160 E161 W162 R163 R164 K165 L166 A167 H168 L169 Q170 E171 S172 N173 E174 D175 L176 L177 L178 T179 P180

F181 E182 R183 N184 I185 E186 V187 W188 K189 Q190 L191 W192 V195 E196 R197 S198 D199 L200 V201 V202 Q203 I204 V205 D206 A207 R208 N209 P210 L211 L212 F213 R214 S215 V216 D217 L218 E219 R220 Y221 V222 K223 E224 S225 D226 D227 R228 K229 A230 M231 L232 L233 L234 V235 M236 K237 A238 D239 L240 L241

T242 K243 K244 Q245 R246 I247 A248 W249 A250 K251 Y252 F253 I254 S255 K256 N257 I258 S259 F260 T261 F262 Y263 S264 A265 L266 R267 ALA ASN GLN LEU LEU GLU LYS GLN LYS GLU MET GLY GLU ASP TYR ARG GLU GLN ASP PHE GLU GLU ALA ASP LYS GLU GLY PHE ASP ALA ASP GLU LYS V301

M302 E303 K304 V305 K306 I307 L308 S309 I310 D311 GLN LEU GLU GLU LEU PHE LEU SER LYS ALA PRO ASN GLU PRO LEU LEU PRO PRO LEU PRO GLY GLN PRO PRO LEU I337 N338 I339 G340 L341 V342 G343 Y344 P345 N346 V347 G348 K349 S350 S351 T352 I353 N354 S355 L356 V357 G358 A359 K360 K361

V362 S363 V364 S365 S366 T367 P368 G369 K370 T371 K372 H373 F374 Q375 T376 I377 K378 L379 S380 D381 S382 V383 M384 L385 C386 D387 C388 P389 G390 L391 V392 F393 P394 N395 F396 A397 Y398 N399 K400 G401 E402 L403 V404 C405 N406 G407 V408 L409 P410 I411 D412 Q413 L414 R415 D416 Y417 I418 G419 P420 A421

G422 L423 V424 A425 E426 R427 I428 P429 K430 Y431 Y432 I433 E434 A435 I436 Y437 G438 I439 H440 I441 Q442 T443 K444 S445 R446 D447 E448 G449 G450 N451 G452 D453 I454 P455 T456 A457 Q458 E459 L460 L461 V462 A463 Y464 A465 R466 A467 R468 G469 Y470 M471 T472 Q473 G474 Y475 G476 S477 A478 D479 E480 P481

R482 A483 S484 R485 Y486 I487 L488 K489 D490 Y491 V492 N493 G494 K495 L496 L497 Y498 V499 N500 P501 P502 P503 H504 L505 E506 D507 D508 T509 P510 Y511 T512 ARG GLU GLU CYS GLU GLU PHE ASN LYS ASP LEU TYR VAL PHE ASP ARG LEU PRO ASP THR ARG LYS GLU GLN VAL GLN ASN ALA ALA

LYS ALA LYS GLY ILE ASP ILE VAL ASP LEU ALA ARG ASP LEU ASN GLN LEU THR PHE SER ALA HIS THR GLY GLY ASP THR GLN LYS GLU ALA LYS SER VAL THR HIS GLY GLY LYS GLN ALA ALA LEU TYR ASN ALA ALA GLU ASP LEU ASP ARG ASP PHE PHE LYS MET ASN ASN VAL

GLU GLY ARG LEU SER THR PRO PHE HIS LYS VAL GLN ASN SER SER ALA GLY LYS ARG HIS ASN LYS LYS ASN LYS SER LYS ASN ALA LYS SER LYS VAL PHE SER ILE GLU ASN ASN

- Molecule 44: uL1

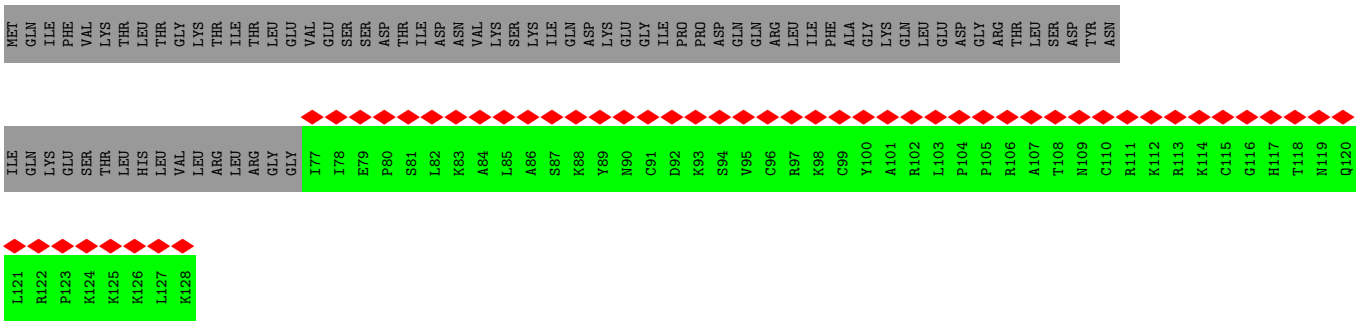
Chain p: 30% 100%

X1 X2 X3 X4 X5 X25 X26 X27 X32 X35 X36 X40 X41 X42 X45 X46 X47 X58 X64 X65 X66 X67 X68 X69 X70 X71 X72 X73 X74 X75 X76 X81 X82 X87 X88 X89 X90 X104 X105 X110 X117 X118 X119 X125 X126 X133

X136 X137 X138 X139 X148 X160 X161 X165 X166 X167 X168 X169 X170 X175 X178 X179 X180 X187 X188 X197 X198 X199 X200 X201 X202 X203 X204 X207 X208 X209 X210

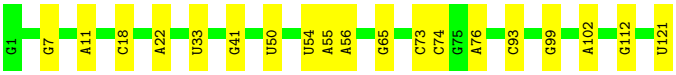
- Molecule 45: Ubiquitin-60S ribosomal protein L40

Chain t: 41% 41% 59%



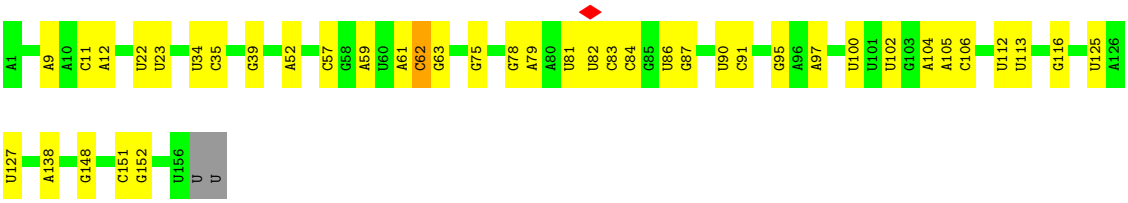
- Molecule 46: 5S ribosomal RNA

Chain x:



- Molecule 47: 5.8S ribosomal RNA

Chain y:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	260853	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.560	Depositor
Minimum map value	-0.287	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	383.40002, 383.40002, 383.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	1.25	40/75327 (0.1%)	1.14	104/117440 (0.1%)
2	B	0.89	2/1912 (0.1%)	0.78	3/2569 (0.1%)
3	C	0.87	0/3110	0.80	3/4184 (0.1%)
4	D	0.86	1/2800 (0.0%)	0.68	1/3791 (0.0%)
5	E	0.45	0/1373	0.63	0/1841
6	F	0.44	0/1523	0.61	0/2051
7	G	0.57	0/1423	0.63	0/1911
8	H	0.68	0/1774	0.62	0/2395
9	J	0.86	1/1593 (0.1%)	0.69	0/2137
10	K	0.79	0/1511	0.77	1/2031 (0.0%)
11	L	0.81	1/1017 (0.1%)	0.74	1/1368 (0.1%)
12	M	0.62	0/1060	0.66	0/1428
13	N	0.89	0/1203	0.70	0/1611
14	O	1.00	0/1756	0.79	0/2353
15	P	0.65	0/2225	0.61	0/3004
16	Q	0.86	1/1464 (0.1%)	0.74	0/1964
17	R	0.83	0/1226	0.75	4/1637 (0.2%)
18	S	0.76	0/1472	0.63	0/1979
19	T	0.78	0/1299	0.66	0/1742
20	U	0.94	1/1245 (0.1%)	0.71	0/1676
21	V	0.60	0/802	0.60	0/1087
22	W	0.80	0/973	0.65	0/1313
23	X	0.77	0/995	0.73	0/1329
24	Y	0.59	0/1117	0.65	0/1496
25	Z	0.72	0/972	0.71	2/1293 (0.2%)
26	a	0.62	0/426	0.61	0/570
27	b	0.87	0/1797	0.67	0/2419
28	c	0.68	0/749	0.63	0/1007
29	d	0.80	0/886	0.75	1/1190 (0.1%)
30	e	0.81	0/1041	0.70	1/1393 (0.1%)
31	f	0.91	0/867	0.79	1/1167 (0.1%)
32	g	0.87	0/822	0.77	1/1099 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	h	0.56	0/770	0.67	0/1023
34	i	0.90	0/680	0.81	0/901
35	j	0.58	0/617	0.63	0/825
36	k	0.86	0/442	0.73	0/587
37	l	0.79	0/768	0.77	0/1016
38	m	0.85	0/687	0.76	0/915
39	n	0.48	0/1712	0.60	0/2330
40	z	0.41	0/494	0.67	0/654
41	w	0.59	3/3135 (0.1%)	0.63	1/4255 (0.0%)
42	v	0.57	0/512	0.61	0/680
43	o	0.49	3/2647 (0.1%)	0.67	2/3582 (0.1%)
45	t	0.29	0/423	0.56	0/562
46	x	1.08	0/2880	1.08	0/4487
47	y	1.40	5/3699 (0.1%)	1.19	7/5760 (0.1%)
All	All	1.07	58/137226 (0.0%)	1.00	133/202052 (0.1%)

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	w	25	PRO	N-CA	14.19	1.71	1.47
43	o	394	PRO	N-CA	13.54	1.70	1.47
43	o	179	THR	C-N	8.59	1.50	1.34
1	A	42	C	C4-C5	-6.82	1.37	1.43
1	A	346	C	N1-C6	-6.18	1.33	1.37

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	18	PRO	CA-N-CD	-15.99	89.11	111.50
1	A	962	A	N1-C6-N6	8.65	123.79	118.60
43	o	394	PRO	CA-N-CD	-8.28	99.91	111.50
1	A	962	A	C5-C6-N6	-7.93	117.36	123.70
1	A	406	G	O4'-C1'-N9	7.53	114.22	108.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	B	245/254 (96%)	221 (90%)	24 (10%)	0	100	100
3	C	379/387 (98%)	347 (92%)	31 (8%)	1 (0%)	41	73
4	D	359/362 (99%)	332 (92%)	27 (8%)	0	100	100
5	E	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
6	F	187/191 (98%)	175 (94%)	12 (6%)	0	100	100
7	G	173/176 (98%)	156 (90%)	17 (10%)	0	100	100
8	H	221/256 (86%)	204 (92%)	17 (8%)	0	100	100
9	J	195/198 (98%)	187 (96%)	8 (4%)	0	100	100
10	K	184/199 (92%)	173 (94%)	11 (6%)	0	100	100
11	L	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
12	M	133/138 (96%)	123 (92%)	9 (7%)	1 (1%)	19	54
13	N	146/149 (98%)	123 (84%)	23 (16%)	0	100	100
14	O	201/204 (98%)	184 (92%)	17 (8%)	0	100	100
15	P	267/297 (90%)	253 (95%)	14 (5%)	0	100	100
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	148/189 (78%)	146 (99%)	2 (1%)	0	100	100
18	S	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
20	U	152/154 (99%)	142 (93%)	10 (7%)	0	100	100
21	V	97/121 (80%)	88 (91%)	9 (9%)	0	100	100
22	W	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
23	X	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
24	Y	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
25	Z	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
26	a	50/59 (85%)	43 (86%)	7 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	b	217/244 (89%)	200 (92%)	17 (8%)	0	100	100
28	c	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
29	d	105/113 (93%)	91 (87%)	14 (13%)	0	100	100
30	e	125/130 (96%)	110 (88%)	14 (11%)	1 (1%)	19	54
31	f	104/107 (97%)	96 (92%)	8 (8%)	0	100	100
32	g	101/121 (84%)	88 (87%)	13 (13%)	0	100	100
33	h	96/100 (96%)	88 (92%)	8 (8%)	0	100	100
34	i	82/88 (93%)	70 (85%)	11 (13%)	1 (1%)	13	44
35	j	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
36	k	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
37	l	92/106 (87%)	85 (92%)	6 (6%)	1 (1%)	14	46
38	m	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
39	n	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	29	64
40	z	56/432 (13%)	48 (86%)	8 (14%)	0	100	100
41	w	387/518 (75%)	340 (88%)	41 (11%)	6 (2%)	9	37
42	v	58/155 (37%)	57 (98%)	1 (2%)	0	100	100
43	o	316/640 (49%)	246 (78%)	68 (22%)	2 (1%)	25	59
45	t	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
All	All	6753/8141 (83%)	6178 (92%)	561 (8%)	14 (0%)	50	79

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	18	PRO
41	w	148	ARG
41	w	20	CYS
41	w	68	PRO
30	e	7	PRO

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	B	189/196 (96%)	189 (100%)	0	100	100
3	C	317/323 (98%)	312 (98%)	5 (2%)	62	84
4	D	288/289 (100%)	287 (100%)	1 (0%)	92	96
5	E	147/150 (98%)	146 (99%)	1 (1%)	84	93
6	F	169/171 (99%)	169 (100%)	0	100	100
7	G	152/153 (99%)	151 (99%)	1 (1%)	84	93
8	H	183/208 (88%)	183 (100%)	0	100	100
9	J	163/164 (99%)	162 (99%)	1 (1%)	86	94
10	K	149/159 (94%)	147 (99%)	2 (1%)	69	87
11	L	104/105 (99%)	104 (100%)	0	100	100
12	M	107/109 (98%)	106 (99%)	1 (1%)	78	91
13	N	118/119 (99%)	118 (100%)	0	100	100
14	O	175/176 (99%)	175 (100%)	0	100	100
15	P	227/245 (93%)	227 (100%)	0	100	100
16	Q	150/151 (99%)	149 (99%)	1 (1%)	84	93
17	R	124/154 (80%)	124 (100%)	0	100	100
18	S	155/156 (99%)	154 (99%)	1 (1%)	86	94
19	T	136/137 (99%)	135 (99%)	1 (1%)	84	93
20	U	125/125 (100%)	125 (100%)	0	100	100
21	V	86/107 (80%)	86 (100%)	0	100	100
22	W	104/118 (88%)	104 (100%)	0	100	100
23	X	108/110 (98%)	107 (99%)	1 (1%)	78	91
24	Y	115/116 (99%)	115 (100%)	0	100	100
25	Z	104/105 (99%)	104 (100%)	0	100	100
26	a	41/47 (87%)	41 (100%)	0	100	100
27	b	184/205 (90%)	182 (99%)	2 (1%)	73	89
28	c	81/88 (92%)	81 (100%)	0	100	100
29	d	94/97 (97%)	93 (99%)	1 (1%)	73	89
30	e	109/111 (98%)	108 (99%)	1 (1%)	78	91
31	f	90/91 (99%)	90 (100%)	0	100	100
32	g	88/103 (85%)	85 (97%)	3 (3%)	37	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	80/82 (98%)	80 (100%)	0	100	100
34	i	69/71 (97%)	68 (99%)	1 (1%)	67	86
35	j	68/69 (99%)	67 (98%)	1 (2%)	65	85
36	k	45/46 (98%)	45 (100%)	0	100	100
37	l	81/91 (89%)	79 (98%)	2 (2%)	47	75
38	m	70/72 (97%)	69 (99%)	1 (1%)	67	86
39	n	192/211 (91%)	191 (100%)	1 (0%)	88	94
40	z	53/392 (14%)	53 (100%)	0	100	100
41	w	348/467 (74%)	338 (97%)	10 (3%)	42	72
42	v	53/129 (41%)	53 (100%)	0	100	100
43	o	284/555 (51%)	266 (94%)	18 (6%)	18	48
45	t	47/116 (40%)	47 (100%)	0	100	100
All	All	5772/6889 (84%)	5715 (99%)	57 (1%)	77	90

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	n	141	THR
43	o	400	LYS
41	w	145	ASP
43	o	395	ASN
43	o	179	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
43	o	395	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3141/3396 (92%)	664 (21%)	22 (0%)
46	x	120/121 (99%)	19 (15%)	0
47	y	155/158 (98%)	34 (21%)	0
All	All	3416/3675 (92%)	717 (20%)	22 (0%)

5 of 717 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	15	C
1	A	26	A
1	A	40	A
1	A	43	A
1	A	48	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2404	A
1	A	2497	U
1	A	2459	A
1	A	3027	A
1	A	1287	A

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

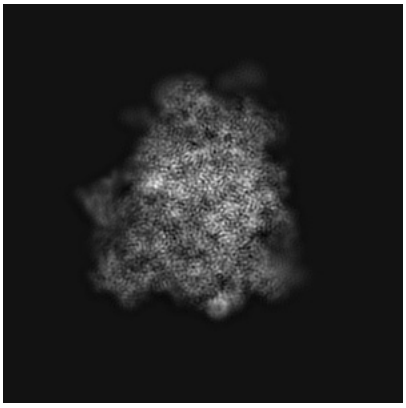
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4560. These allow visual inspection of the internal detail of the map and identification of artifacts.

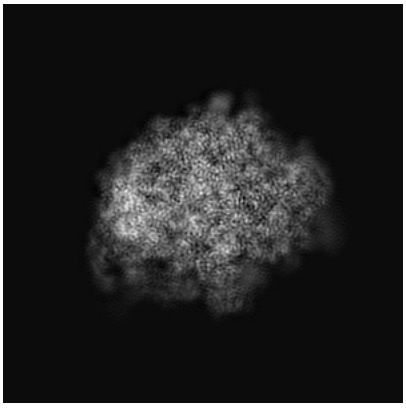
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

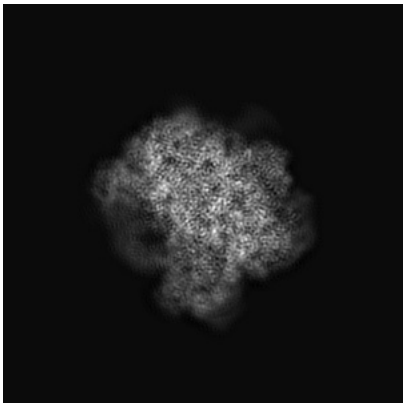
6.1.1 Primary map



X



Y

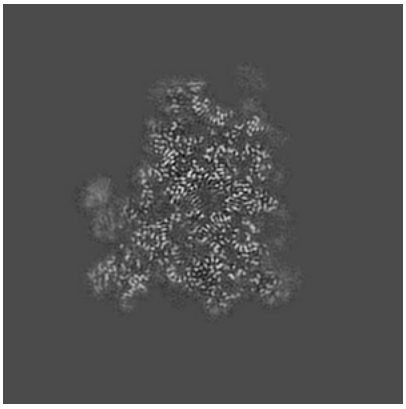


Z

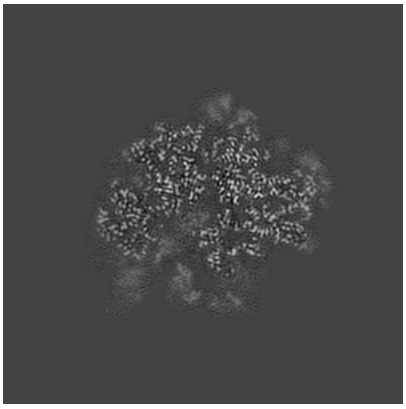
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 180



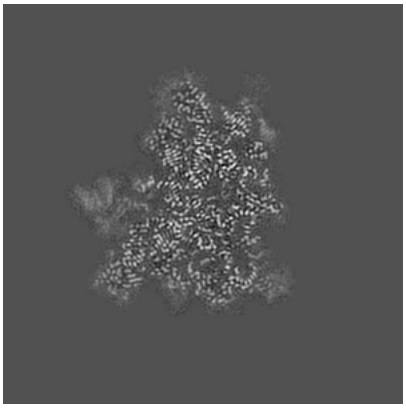
Y Index: 180

Z Index: 180

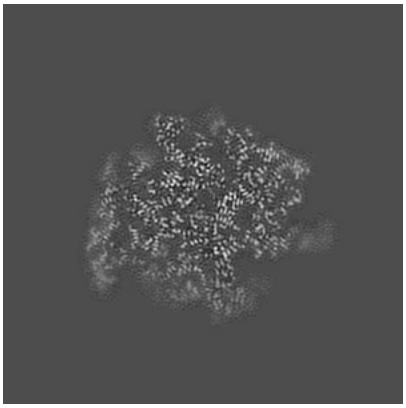
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

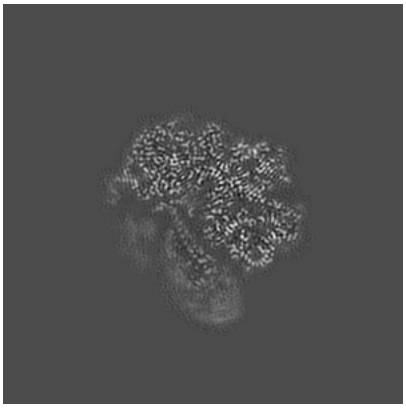
6.3.1 Primary map



X Index: 189



Y Index: 196

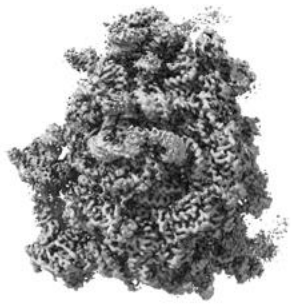


Z Index: 177

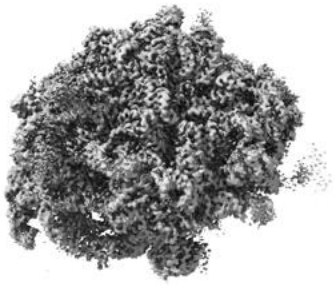
The images above show the largest variance slices of the map in three orthogonal directions.

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

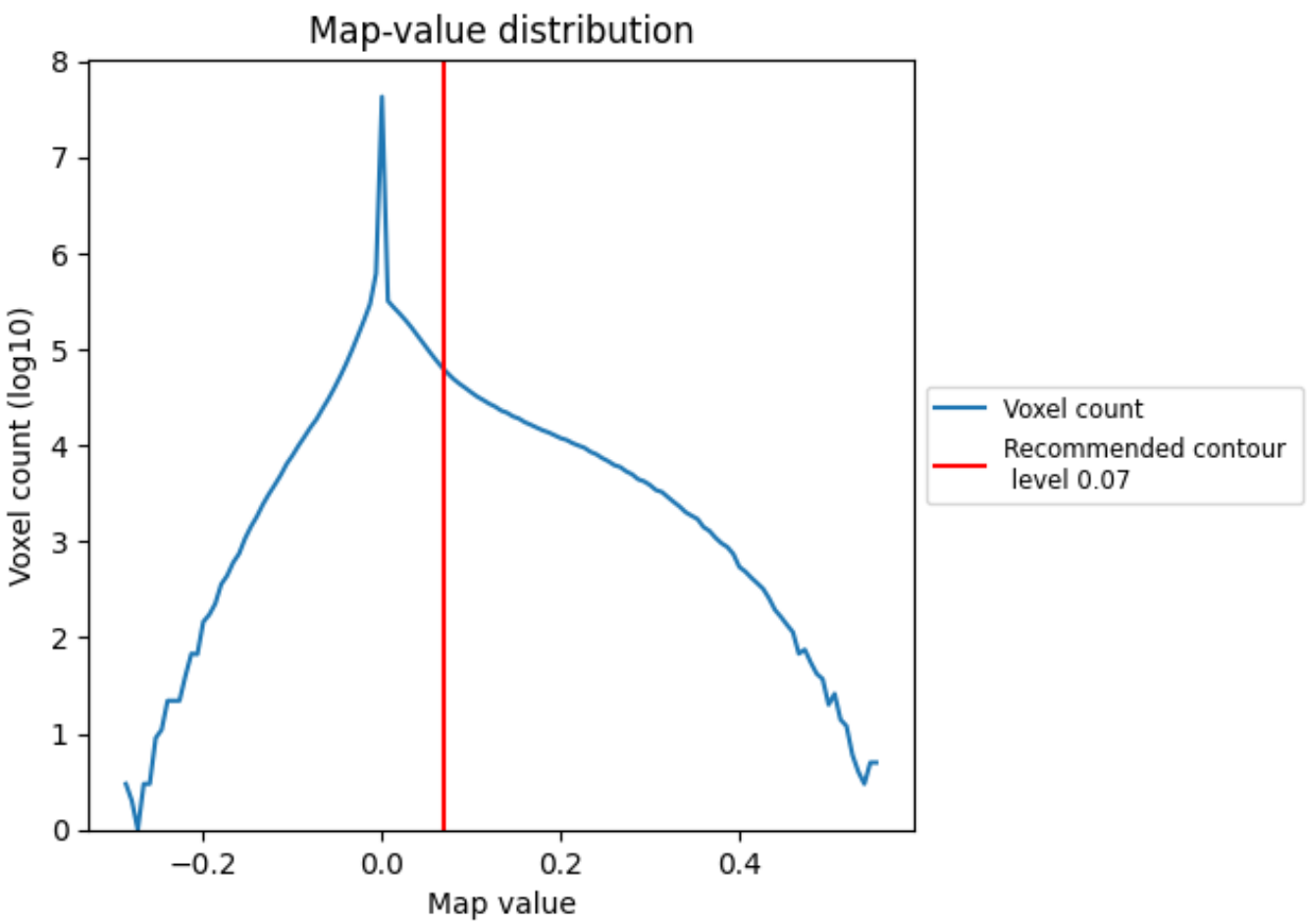
6.5 Mask visualisation (i)

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

7 Map analysis (i)

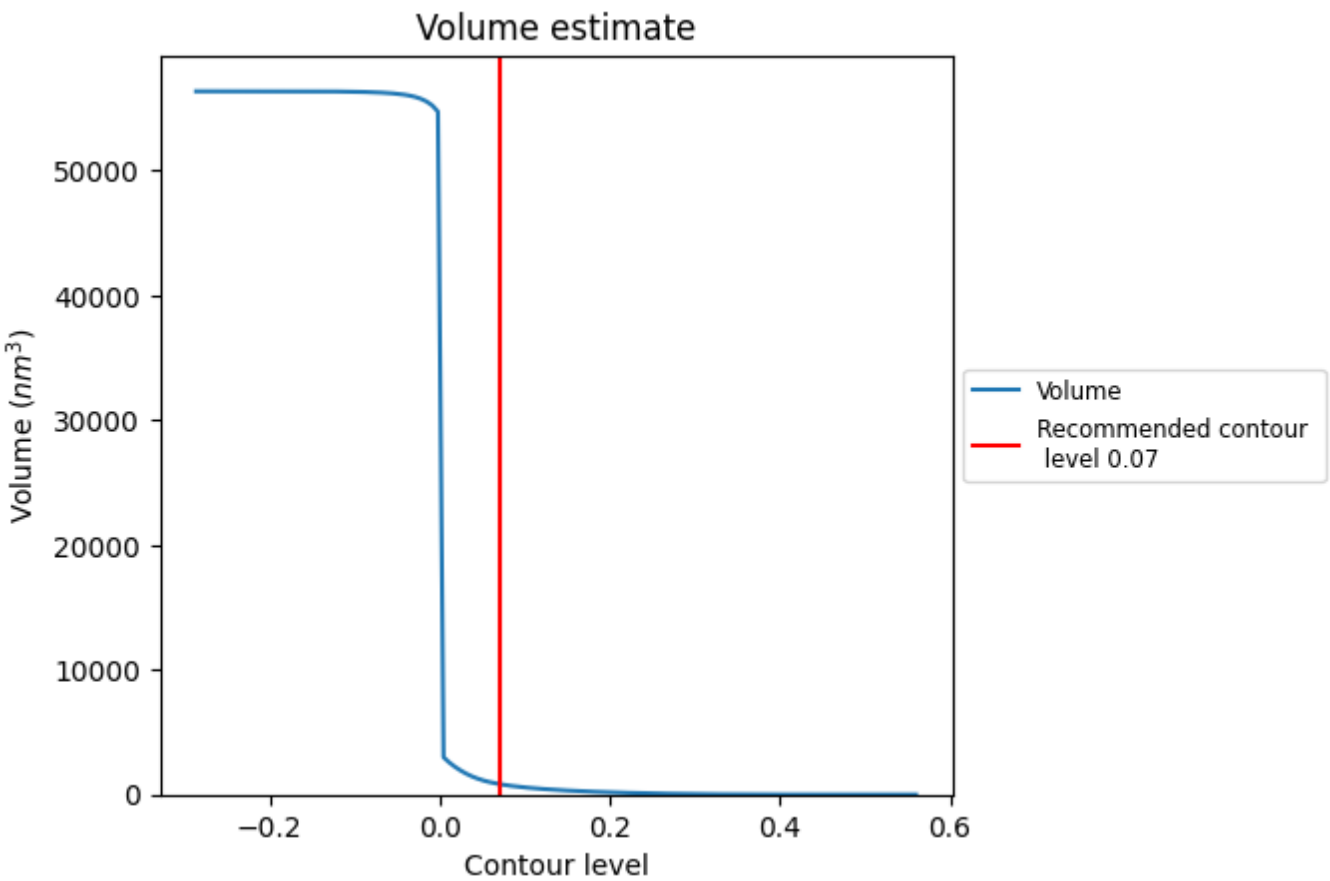
This section contains the results of statistical analysis of the map.

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.

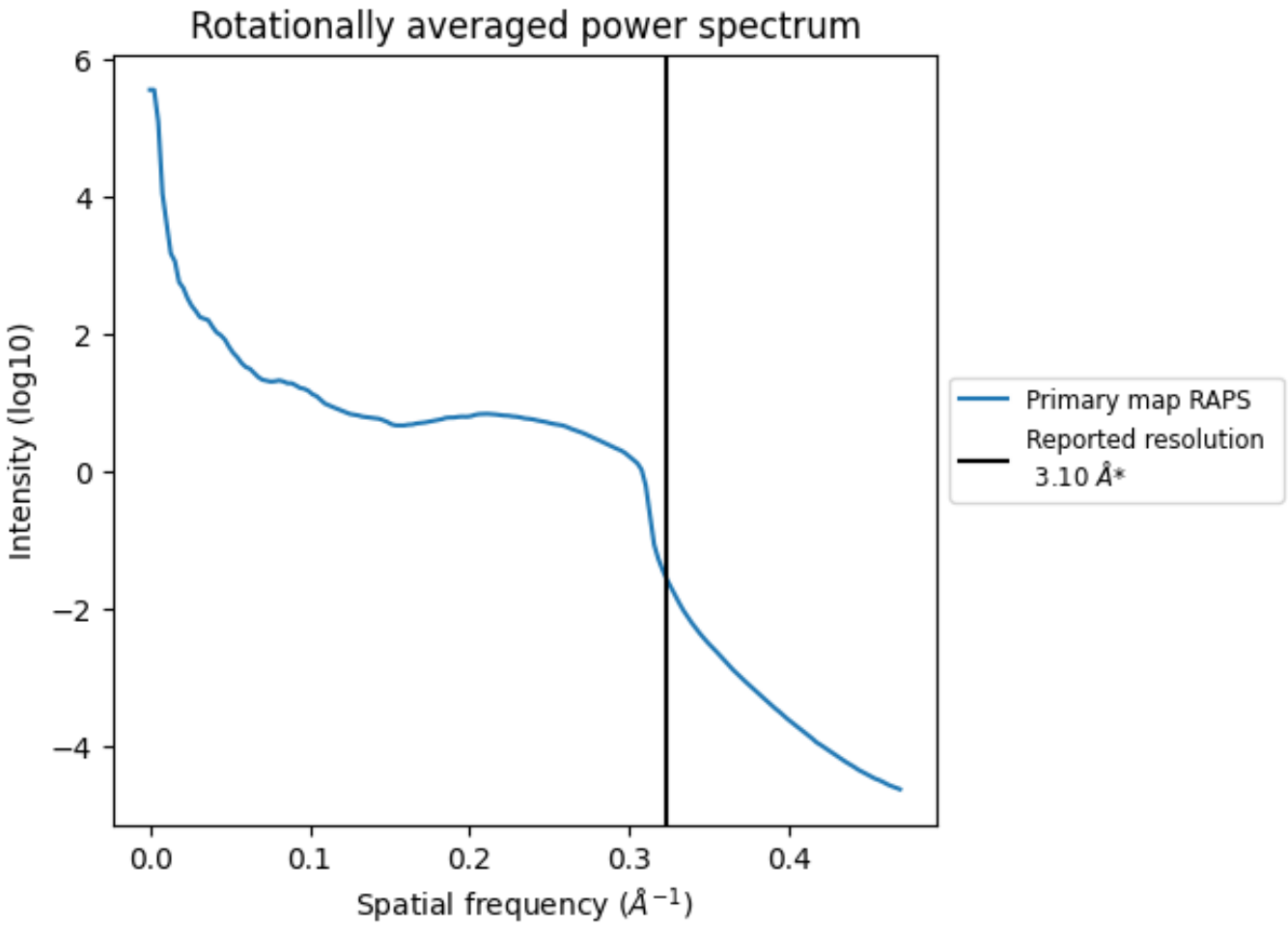
7.2 Volume estimate (i)



The volume at the recommended contour level is 838 nm^3; this corresponds to an approximate mass of 757 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 0.323 Å^{-1}

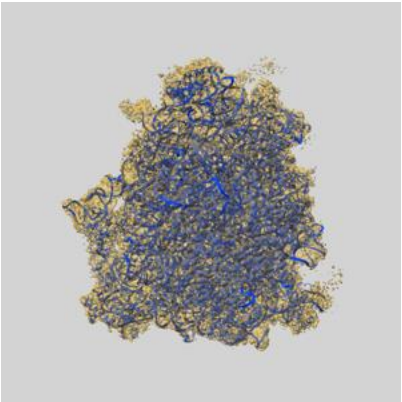
8 Fourier-Shell correlation (i)

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

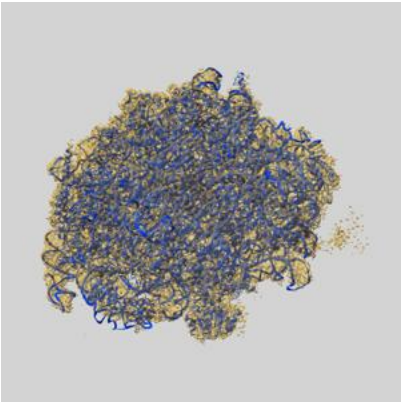
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4560 and PDB model 6QIK. Per-residue inclusion information can be found in section 3 on page 13.

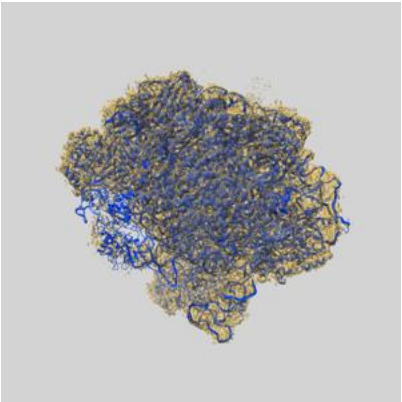
9.1 Map-model overlay (i)



X



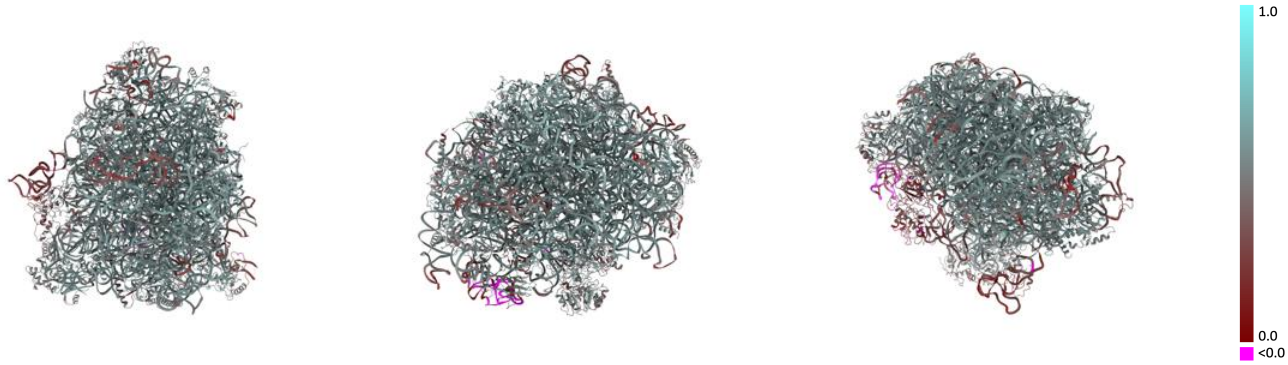
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07 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.

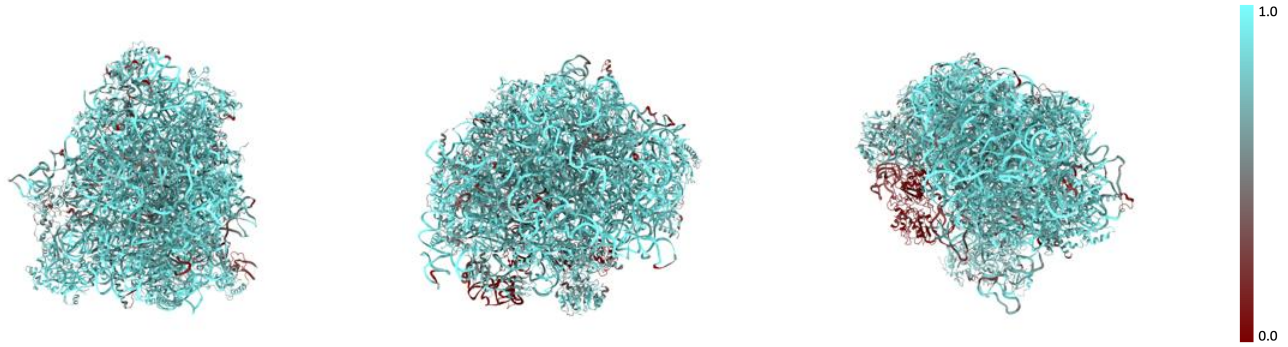
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

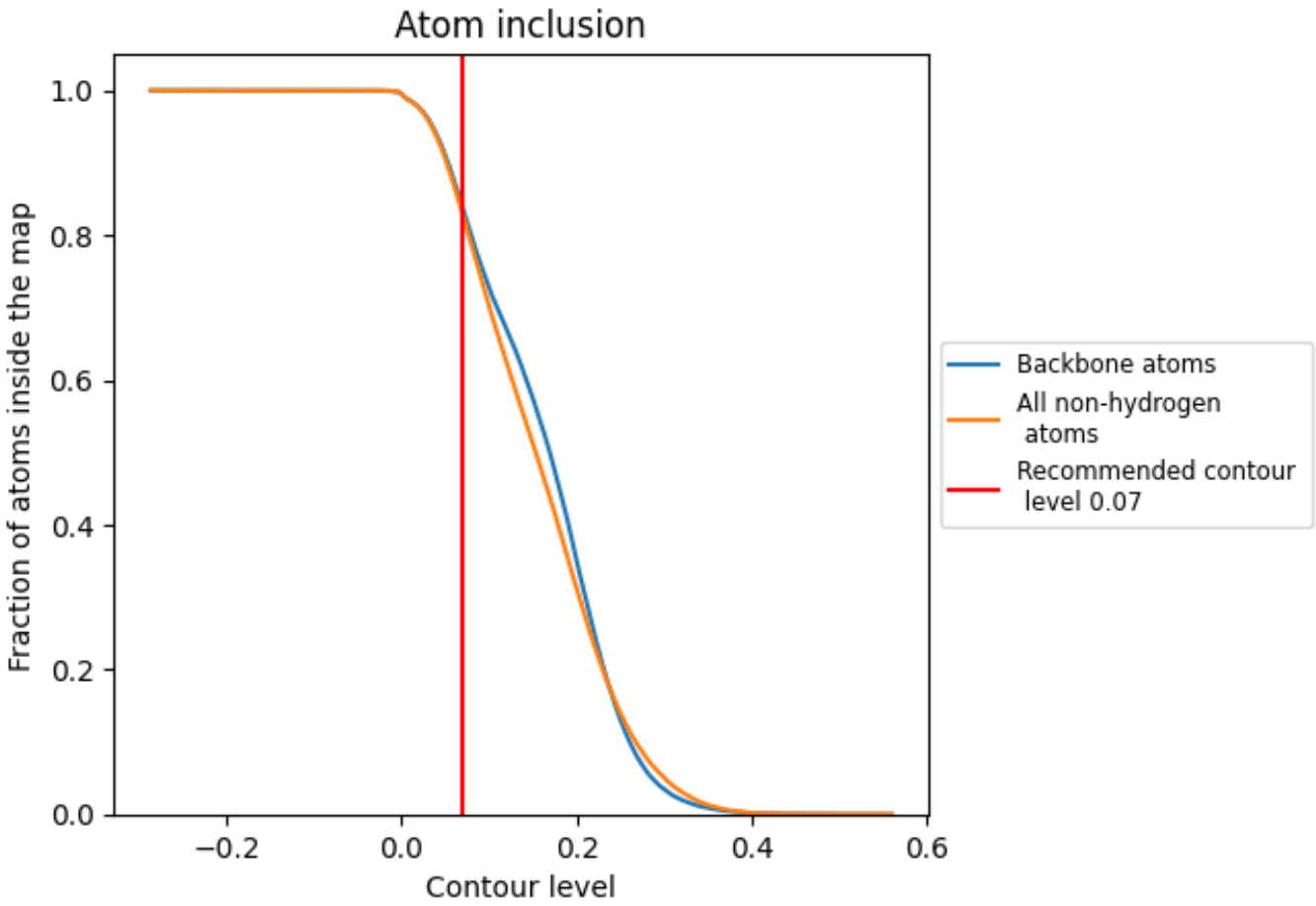
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.07).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8278	0.5190
A	0.8778	0.5150
B	0.8614	0.5770
C	0.8639	0.5630
D	0.8518	0.5690
E	0.7489	0.4610
F	0.6791	0.4980
G	0.6781	0.4830
H	0.7845	0.5170
J	0.8336	0.5540
K	0.8031	0.5460
L	0.8292	0.5690
M	0.7967	0.5290
N	0.8764	0.5670
O	0.8796	0.5860
P	0.8356	0.5290
Q	0.8716	0.5780
R	0.8349	0.5530
S	0.8435	0.5580
T	0.8039	0.5440
U	0.8592	0.5720
V	0.8070	0.5060
W	0.8333	0.5540
X	0.8433	0.5640
Y	0.8159	0.5130
Z	0.8335	0.5500
a	0.7802	0.5470
b	0.8527	0.5570
c	0.7805	0.5000
d	0.7920	0.5430
e	0.8119	0.5700
f	0.8451	0.5750
g	0.8431	0.5660
h	0.6472	0.5110
i	0.8688	0.5840

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	0.7977	0.5120
k	0.8502	0.5830
l	0.8550	0.5810
m	0.8201	0.5570
n	0.7449	0.4860
o	0.0668	0.2950
p	0.6143	0.3640
t	0.0025	0.3180
v	0.7335	0.5290
w	0.4819	0.4100
x	0.9686	0.5410
y	0.9677	0.5680
z	0.4609	0.5160