



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:19 PM UTC

PDB ID : 7Q0F / pdb_00007q0f
EMDB ID : EMD-13744
Title : Structure of Candida albicans 80S ribosome in complex with phyllanthoside
Authors : Zgadzay, Y.; Kolosova, O.; Stetsenko, A.; Jenner, L.; Guskov, A.; Yusupova, G.; Yusupov, M.
Deposited on : 2021-10-14
Resolution : 2.64 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

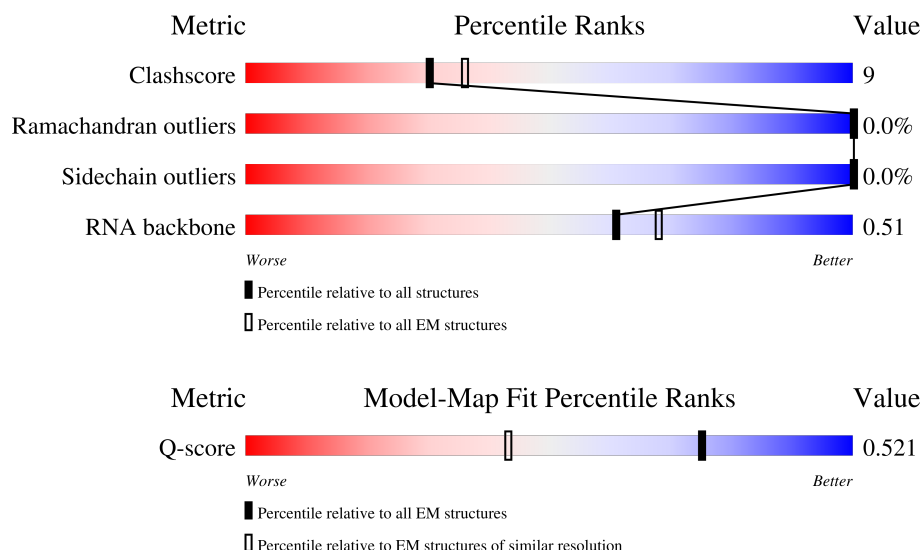
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.64 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



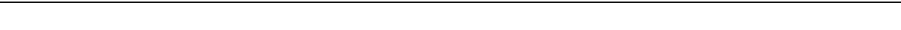
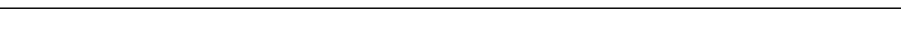
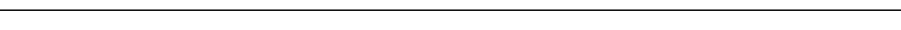
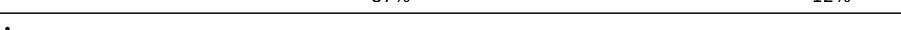
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8968 (2.14 - 3.14)

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	1	3359	
2	3	121	
3	4	158	

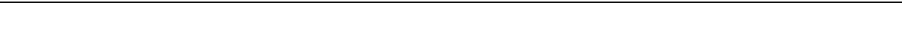
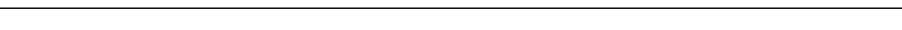
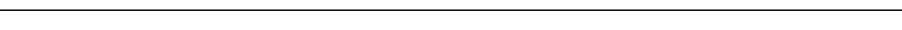
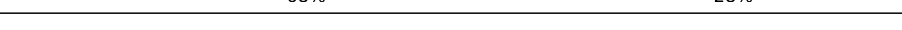
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Mol	Chain	Length	Quality of chain
4	j	254	 82% 16% .
5	k	389	 81% 19% .
6	l	363	 87% 13% .
7	m	298	 85% 13% .
8	n	176	 74% 14% 12%
9	o	241	 82% 15% .
10	p	262	 76% 15% 9%
11	q	191	 79% 21% .
12	r	220	 79% 16% 5%
13	s	174	 76% 22% ..
14	t	202	 89% 10% .
15	u	131	 82% 17% .
16	v	204	 85% 14%
17	w	200	 87% 12%
18	x	185	 78% 15% 7%
19	y	186	 83% 16% .
20	z	190	 82% 13% 6%
21	0	172	 83% 16% .
22	2	160	 87% 12% .
23	5	124	 63% 20% 17%
24	6	137	 80% 15% .
25	7	155	 34% 7% 59%
26	8	142	 75% 11% 15%
27	9	127	 84% 15% .
28	AA	136	 84% 15% .

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Mol	Chain	Length	Quality of chain
29	AB	149	 83% 17% .
30	AC	63	 83% 17% .
31	AD	106	 80% 10% 9%
32	AE	112	 84% 13% .
33	AF	131	 85% 11% 5%
34	AG	107	 90% 9% .
35	AH	122	 80% 11% 8%
36	AI	120	 82% 18% .
37	AJ	99	 93% 6% .
38	AK	90	 82% 13% .
39	AL	78	 76% 23% .
40	AM	51	 73% 25% .
41	AN	52	 85% 15%
42	AO	25	 68% 28% .
43	AP	106	 75% 22% . .
44	AQ	92	 84% 15% .
45	i	267	 7% 31% 11% 58%
46	A	1787	 37% 45% 13% 5%
47	B	261	 57% 23% 20%
48	C	256	 65% 18% 16%
49	D	249	 67% 20% 13%
50	E	251	 16% 65% 24% 11%
51	F	262	 77% 22% .
52	G	225	 18% 60% 32% 8%
53	H	236	 69% 27% .

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Mol	Chain	Length	Quality of chain
54	I	186	
55	J	206	
56	K	189	
57	L	118	
58	M	155	
59	N	143	
60	O	151	
61	P	132	
62	Q	142	
63	R	142	
64	S	137	
65	T	145	
66	U	145	
67	V	119	
68	W	87	
69	X	130	
70	Y	145	
71	Z	135	
72	a	105	
73	b	119	
74	c	82	
75	d	67	
76	e	56	
77	f	63	
78	g	193	

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Mol	Chain	Length	Quality of chain
79	h	317	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
81	3K5	1	3402	X	-	-	-

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 199317 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
1	1	3209	Total	C	N	O	P	0	0
			68595	30642	12317	22427	3209		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1153	463	842	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	585	1110	158		

- Molecule 4 is a protein called Ribosomal 60S subunit protein L2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	249	Total	C	N	O	S	1	0
			1894	1185	377	330	2		

- Molecule 5 is a protein called Ribosomal 60S subunit protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	k	386	Total	C	N	O	S	1	0
			3084	1955	584	538	7		

- Molecule 6 is a protein called Ribosomal 60S subunit protein L4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	l	361	Total	C	N	O	S	0	0
			2751	1729	529	490	3		

- Molecule 7 is a protein called Ribosomal 60S subunit protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	m	292	Total	C	N	O	S	0	0
			2394	1526	416	450	2		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	n	155	Total	C	N	O	S	1	0
			1237	794	226	217			

- Molecule 9 is a protein called Ribosomal 60S subunit protein L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	o	234	Total	C	N	O	S	1	0
			1893	1213	348	331	1		

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	p	238	Total	C	N	O	S	0	0
			1839	1175	327	334	3		

- Molecule 11 is a protein called Ribosomal 60S subunit protein L9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	190	Total	C	N	O	S	0	0
			1519	958	276	281	4		

- Molecule 12 is a protein called Ribosomal 60S subunit protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	r	208	Total	C	N	O	S	0	0
			1689	1069	322	291	7		

- Molecule 13 is a protein called Ribosomal 60S subunit protein L11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	s	172	Total	C	N	O	S	1	0
			1385	864	262	255	4		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	200	Total	C	N	O	0	0
			1610	1009	318	283		

- Molecule 15 is a protein called Ribosomal 60S subunit protein L14B.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	u	130	Total	C	N	O	S	0
			1029	660	193	175	1	0

- Molecule 16 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	v	203	Total	C	N	O	S	0
			1713	1075	356	280	2	0

- Molecule 17 is a protein called Ribosomal 60S subunit protein L16A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	w	199	Total	C	N	O	S	0
			1590	1025	294	269	2	0

- Molecule 18 is a protein called Ribosomal 60S subunit protein L17B.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	x	172	Total	C	N	O	0	0
			1375	850	279	246		

- Molecule 19 is a protein called Ribosomal 60S subunit protein L18A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	y	185	Total	C	N	O	3	0
			1478	930	302	246		

- Molecule 20 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	z	179	Total	C	N	O	S	1
			1462	904	311	244	3	0

- Molecule 21 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 22 is a protein called Ribosomal 60S subunit protein L21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 23 is a protein called Ribosomal 60S subunit protein L22B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5	103	Total	C	N	O	S	2	0
			848	553	139	156			

- Molecule 24 is a protein called Ribosomal 60S subunit protein L23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 25 is a protein called Ribosomal 60S subunit protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	63	Total	C	N	O	S	0	0
			524	334	103	86	1		

- Molecule 26 is a protein called Ribosomal 60S subunit protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	121	Total	C	N	O	S	0	0
			974	622	175	176	1		

- Molecule 27 is a protein called Ribosomal 60S subunit protein L26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	9	126	Total	C	N	O	S	0	0
			989	618	190	181			

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AA	135	Total	C	N	O	S	0	0
			1087	705	197	183	2		

- Molecule 29 is a protein called Ribosomal 60S subunit protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AB	148	Total	C	N	O	S	0	0
			1170	741	231	197	1		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AC	63	Total	C	N	O	S	1	0
			509	317	109	82	1		

- Molecule 31 is a protein called Ribosomal 60S subunit protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AD	96	Total	C	N	O	S	0	0
			729	469	121	137	2		

- Molecule 32 is a protein called Ribosomal 60S subunit protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AE	109	Total	C	N	O	S	0	0
			889	562	167	158	2		

- Molecule 33 is a protein called Ribosomal 60S subunit protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AF	125	Total	C	N	O	S	1	0
			1015	649	197	168	1		

- Molecule 34 is a protein called Ribosomal 60S subunit protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AG	106	Total	C	N	O	S	3	0
			867	558	166	142	1		

- Molecule 35 is a protein called Ribosomal 60S subunit protein L34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AH	112	Total	C	N	O	S	4	0
			913	567	188	154	4		

- Molecule 36 is a protein called Ribosomal 60S subunit protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AI	119	Total	C	N	O		1	0
			990	629	195	166			

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AJ	98	Total	C	N	O	S	1	0
			772	481	158	131	2		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AK	86	Total	C	N	O	S	0	0
			677	413	148	110	6		

- Molecule 39 is a protein called Ribosomal 60S subunit protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AL	77	Total	C	N	O		1	0
			623	398	116	109			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AM	50	Total	C	N	O		1	0
			446	280	100	66			

- Molecule 41 is a protein called Rpl40bp.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AN	52	Total	C	N	O	S	1	0
			427	265	89	67	6		

- Molecule 42 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AO	24	Total	C	N	O	S	0	0
			227	138	61	27	1		

- Molecule 43 is a protein called Ribosomal 60S subunit protein L42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AP	103	Total	C	N	O	S	2	0
			843	533	168	137	5		

- Molecule 44 is a protein called Ribosomal 60S subunit protein L43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AQ	91	Total	C	N	O	S	0	0
			698	430	140	124	4		

- Molecule 45 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	113	Total	C	N	O		0	0
			853	512	155	186			

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	1692	Total	C	N	O	P	0	0
			36083	16130	6412	11849	1692		

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	208	Total	C	N	O	S	0	0
			1627	1041	284	297	5		

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	C	214	Total	C	N	O	S	0	0
			1724	1094	313	313	4		

- Molecule 49 is a protein called Ribosomal 40S subunit protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	D	216	Total	C	N	O	S	0	0
			1620	1033	287	295	5		

- Molecule 50 is a protein called Ribosomal 40S subunit protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E	223	Total	C	N	O	S	0	0
			1707	1087	311	305	4		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F	260	Total	C	N	O	S	0	0
			2055	1306	386	358	5		

- Molecule 52 is a protein called Ribosomal 40S subunit protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	G	206	Total	C	N	O	S	0	0
			1614	1008	301	301	4		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H	226	Total	C	N	O	S	0	0
			1820	1133	351	330	6		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	I	182	Total	C	N	O	S	0	0
			1466	939	264	263			

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J	203	Total	C	N	O	S	0	0
			1579	973	322	283	1		

- Molecule 56 is a protein called Ribosomal 40S subunit protein S9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	K	178	Total	C	N	O	S	0	0
			1453	918	286	248	1		

- Molecule 57 is a protein called Ribosomal 40S subunit protein S10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	L	93	Total	C	N	O	S	0	0
			783	511	129	142	1		

- Molecule 58 is a protein called Ribosomal 40S subunit protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	M	141	Total	C	N	O	S	0	0
			1129	722	212	192	3		

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N	116	Total	C	N	O	S	0	0
			885	550	158	172	5		

- Molecule 60 is a protein called Ribosomal 40S subunit protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O	150	Total	C	N	O	S	0	0
			1187	757	219	210	1		

- Molecule 61 is a protein called Ribosomal 40S subunit protein S14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	P	127	Total	C	N	O	S	0	0
			942	579	186	174	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	119	IAS	ASP	modified residue	UNP A0A1D8PDT3

- Molecule 62 is a protein called Ribosomal 40S subunit protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Q	118	Total	C	N	O	S	0	0
			935	598	169	162	6		

- Molecule 63 is a protein called Ribosomal 40S subunit protein S16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	R	140	Total	C	N	O	S	0	0
			1091	700	198	192	1		

- Molecule 64 is a protein called Ribosomal 40S subunit protein S17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S	125	Total	C	N	O	S	0	0
			1002	631	184	186	1		

- Molecule 65 is a protein called Ribosomal 40S subunit protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	T	142	Total	C	N	O	S	0	0
			1169	733	228	205	3		

- Molecule 66 is a protein called Ribosomal 40S subunit protein S19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	U	141	Total	C	N	O	S	0	0
			1100	689	210	200	1		

- Molecule 67 is a protein called Ribosomal 40S subunit protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V	100	Total	C	N	O	S	0	0
			790	499	146	143	2		

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	W	87	Total	C	N	O	S	0	0
			676	415	126	133	2		

- Molecule 69 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	X	129	Total	C	N	O	S	0	0
			1032	655	191	183	3		

- Molecule 70 is a protein called Ribosomal 40S subunit protein S23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Y	143	Total	C	N	O	S	0	0
			1110	701	219	188	2		

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Z	132	Total	C	N	O		0	0
			1072	670	216	186			

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	a	72	Total	C	N	O		0	0
			578	369	103	106			

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	b	100	Total	C	N	O	S	0	0
			799	494	169	130	6		

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	c	81	Total	C	N	O	S	0	0
			614	383	110	114	7		

- Molecule 75 is a protein called Ribosomal 40S subunit protein S28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	d	62	Total	C	N	O	S	0	0
			487	299	98	88	2		

- Molecule 76 is a protein called Ribosomal 40S subunit protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	e	55	Total	C	N	O	S	0	0
			454	281	94	75	4		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	f	56	Total	C	N	O	S	0	0
			444	278	89	75	2		

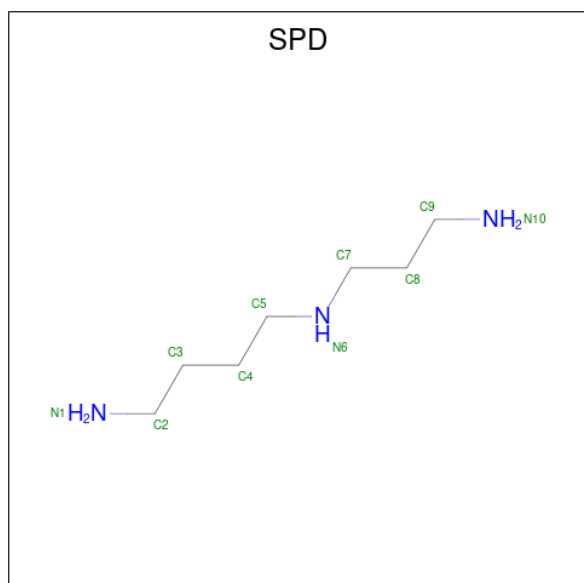
- Molecule 78 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	g	70	Total	C	N	O	S	0	0
			574	362	113	93	6		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

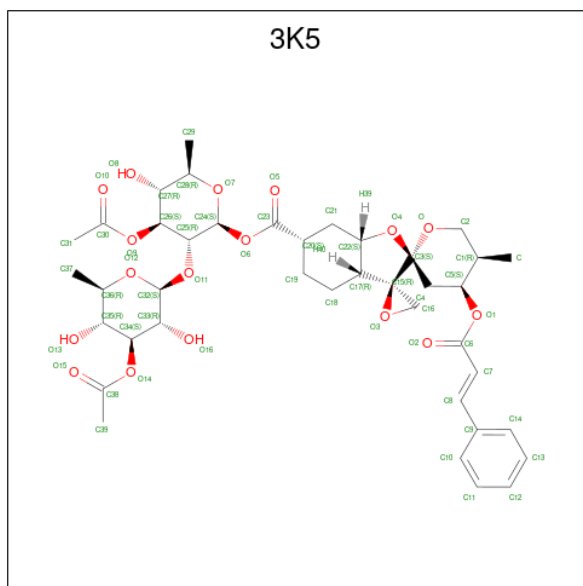
Mol	Chain	Residues	Atoms					AltConf	Trace
79	h	311	Total	C	N	O	S	0	0
			2398	1519	412	462	5		

- Molecule 80 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
80	1	1	Total	C	N	0
			10	7	3	

- Molecule 81 is 3-O-acetyl-2-O-(3-O-acetyl-6-deoxy-beta-D-glucopyranosyl)-6-deoxy-1-O-{[(2R,2'S,3a'R,4''S,5''R,6'S,7a'S)-5''-methyl-4''-{[(2E)-3-phenylprop-2-enoyl]oxy}decahydrodispiro[oxirane-2,3'-[1]benzofuran-2',2''-pyran]-6'-yl]carbonyl}-beta-D-glucopyranose (CCD ID: 3K5) (formula: C₄₀H₅₂O₁₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
81	1	1	Total	C	O	0
			57	40	17	

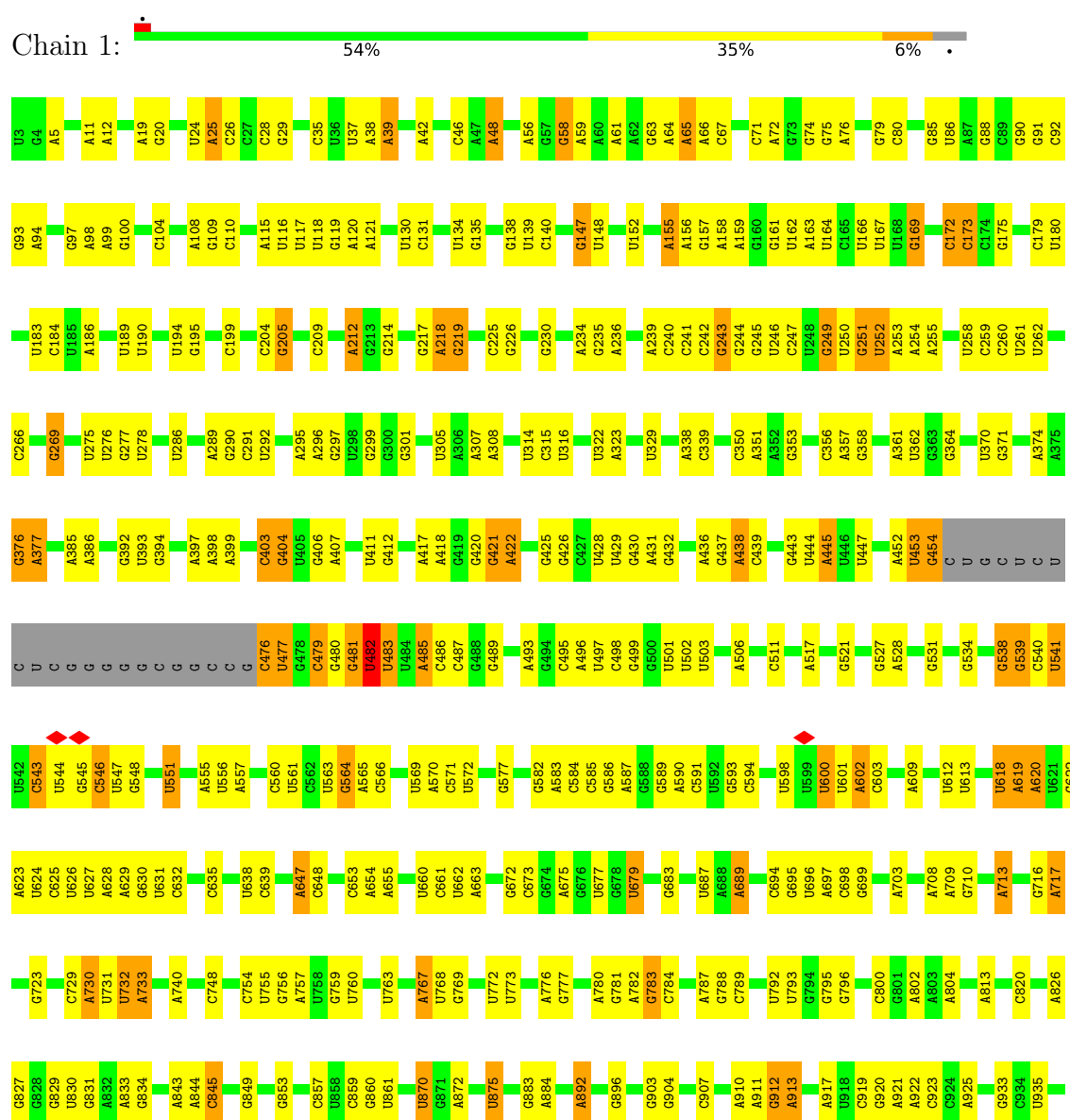
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	AK	1	Total	Zn	0
			1	1	
82	AN	1	Total	Zn	0
			1	1	
82	AP	1	Total	Zn	0
			1	1	
82	AQ	1	Total	Zn	0
			1	1	
82	b	1	Total	Zn	0
			1	1	
82	c	1	Total	Zn	0
			1	1	
82	e	1	Total	Zn	0
			1	1	
82	g	1	Total	Zn	0
			1	1	

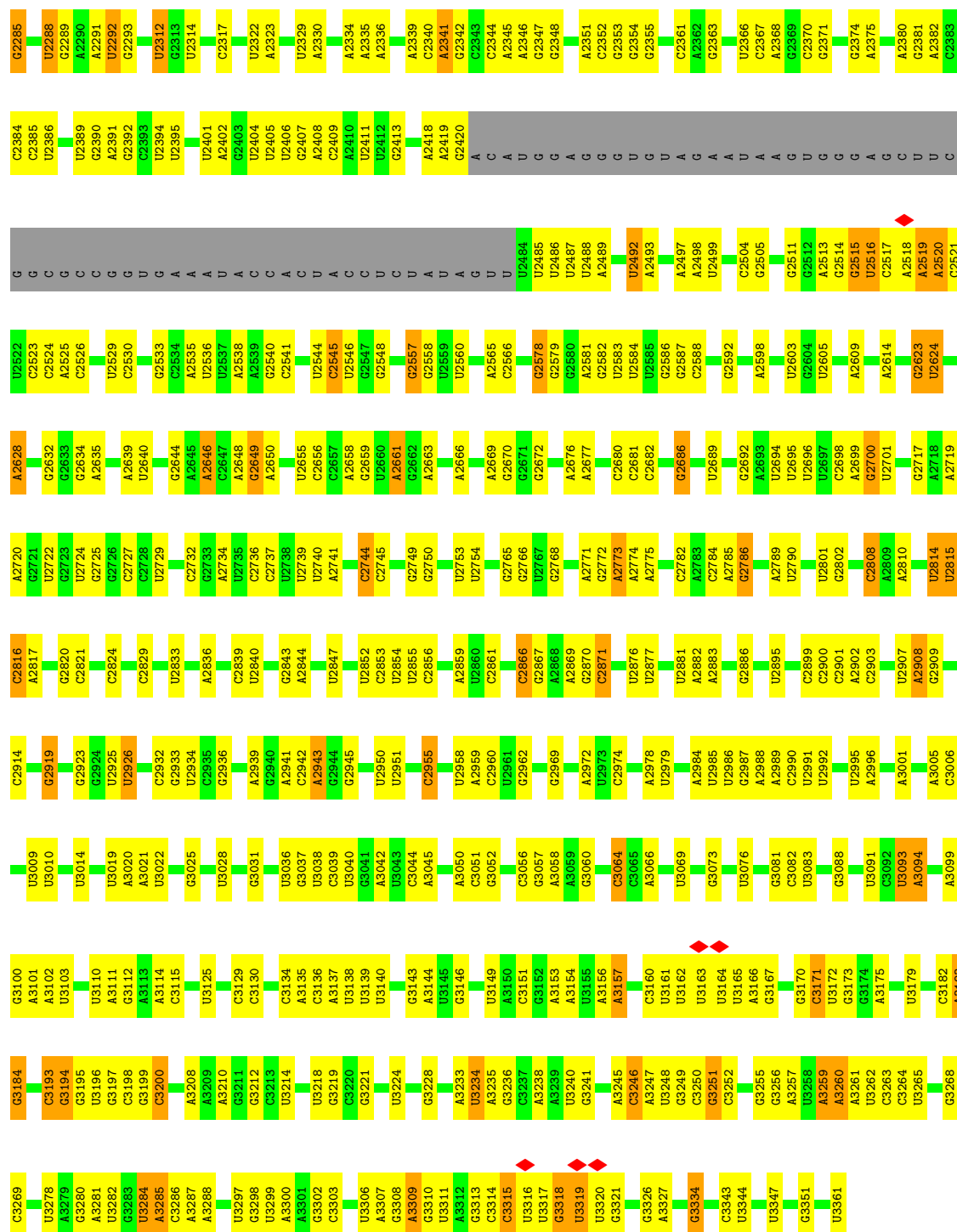
3 Residue-property plots [i](#)

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



U2181	A2082	U1955	A1746	C1694	A1531	A1386	A1283	A1221	U1029	C940
C2182	G2083	U1956	G1747	U1625	G1532	C1387	A1286	G1222	U1030	C941
U2183	A2084	G1957	U1755	G1631	A1533	G1388	A1287	C1223	A1031	U942
G2184	C2086	U1958	A1756	G1634	G1534	U1395	C1288	G1225	A1032	A948
A2185	G2087	G1959	A1757	C1635	C1547	G1400	G1291	A1226	C1033	U951
A2186	C2088	U1960	U1758	G1636	G1548	U1403	C1292	A1227	U1034	U952
U2187	G2089	U1961	U1759	U1637	U1549	G1408	U1301	G1228	U1035	U955
G2188	C2090	U1962	U1760	U1638	U1550	U1408	G1302	G1229	A1042	C955
A2191	U2091	U1963	U1761	A1639	U1551	U1408	G1303	U1230	A1043	U956
A2192	C2092	U1964	G1762	C1640	C1552	A1414	A1304	G1232	A1044	A961
G2196	A2098	U1965	C1763	U1641	G1556	A1415	U1305	G1234	C1045	U962
A2197	G2099	U1966	G1767	G1648	U1557	U1421	C1308	C1235	A1050	A963
U2201	U2107	U1967	U1768	G1648	G1558	U1421	G1309	A1236	U1058	C964
A2202	C2108	A1968	G1771	C1653	C1559	G1427	C1310	U1237	A1058	C965
U2203	A2109	U1969	G1774	U1655	U1561	U1430	G1312	G1238	U1059	U972
U2204	G2114	U1970	C1775	C1656	A1564	G1433	A1313	A1240	A1060	C973
C2205	U2115	C1971	G1776	G1657	U1565	U1442	A1314	A1241	G1061	C974
A2206	A2116	U1972	U1777	G1658	U1566	U1443	A1322	G1242	U1062	U975
A2207	U2117	G1973	U1778	C1659	U1567	U1444	C1323	U1243	U1063	A976
G2210	A2118	C1974	U1779	U1660	U1568	G1442	A1326	C1244	G1068	U977
A2211	U2119	U1975	A1780	U1661	U1569	U1443	U1327	G1245	U1069	C978
A2222	A2120	U1976	G1781	G1662	C1570	U1444	A1328	G1246	U1077	U981
G2227	A2121	U1977	G1782	A1663	G1571	G1446	C1329	A1247	U1078	U982
A2230	U2126	U1978	U1787	U1668	G1572	U1457	G1336	C1250	U1079	U984
A2234	A2127	C1979	C1788	U1678	C1573	A1457	U1337	C1251	A1080	G988
C2235	U2130	A1793	A1793	A1679	A1575	U1466	C1343	G1252	A1081	C989
G2239	A2134	U1794	A1794	U1680	C1576	U1467	U1344	U1254	A1089	U991
A2240	U2135	A1795	A1795	C1689	C1578	U1468	G1345	A1255	G995	C996
C2241	G2136	U1796	A1796	U1690	A1579	G1469	U1346	G1257	U1091	C997
G2243	A2137	G1804	G1804	U1691	U1580	A1470	U1347	A1258	U1092	A996
U2244	G2138	A1805	A1805	A1692	C1581	A1471	U1348	C1259	A1094	U999
C2245	U2139	U1806	A1806	A1693	U1585	C1474	U1349	G1260	A1099	G1006
A2145	A2145	G1807	G1807	C1705	A1586	U1475	U1352	U1261	A1100	A1007
A2146	G2147	U1808	U1808	C1706	G1587	U1476	G1353	G1262	A1008	A1008
G2147	U2148	A1809	A1809	U1713	G1588	A1477	U1354	G1263	G1009	U1010
U2148	G2149	U1810	U1810	G1714	C1592	G1482	U1355	U1264	U1011	C1011
G2149	A2155	A1811	A1811	G1715	C1593	G1483	U1356	U1265	U1012	U1012
G2155	G2155	G1813	G1813	U1720	G1594	U1484	U1357	A1268	U1013	U1013
A2158	A2158	U1814	U1814	C1721	A1601	A1494	C1358	A1269	G1014	G1014
C2159	C2159	U1815	U1815	G1732	U1611	U1495	U1363	U1270	G1017	U1017
G2163	G2163	U1816	U1816	A1737	U1612	A1502	U1364	C1273	U1018	U1018
A2166	A2166	U1817	U1817	U1738	G1613	G1503	G1376	U1274	U1019	U1019
U2171	U2171	A1824	A1824	G1739	U1616	C1504	A1377	C1276	G1020	G1020
G2172	G2172	A1825	A1825	U1740	U1618	A1520	A1382	G1277	A1021	A1021
A2281	A2281	C1827	C1827	C1741	U1618	G1521	A1382	C1278	A1022	A1022
U2276	U2276	U1828	U1828	A1745	U1623	A1530	G1385	G1281	A1023	A1023
A2277	A2277	U1835	U1835	U1745	U1623	A1530	G1385	A1282	U1024	U1024
U2281	U2281	U1836	U1836	U1745	U1623	A1530	G1385	A1282	G1025	G1025



• Molecule 2: 5S ribosomal RNA

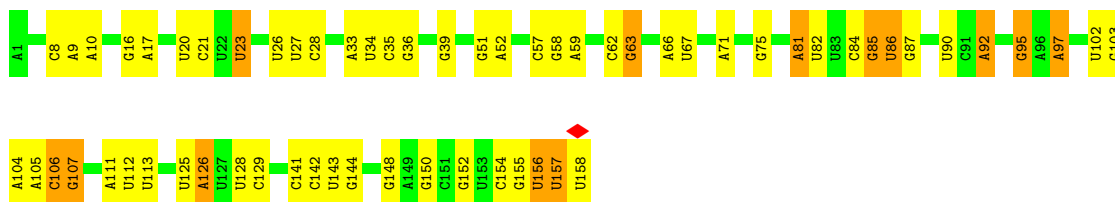
Chain 3: 66% 31%





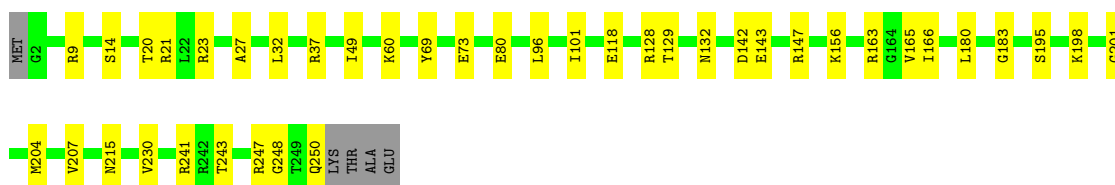
- Molecule 3: 5.8S ribosomal RNA

Chain 4: 



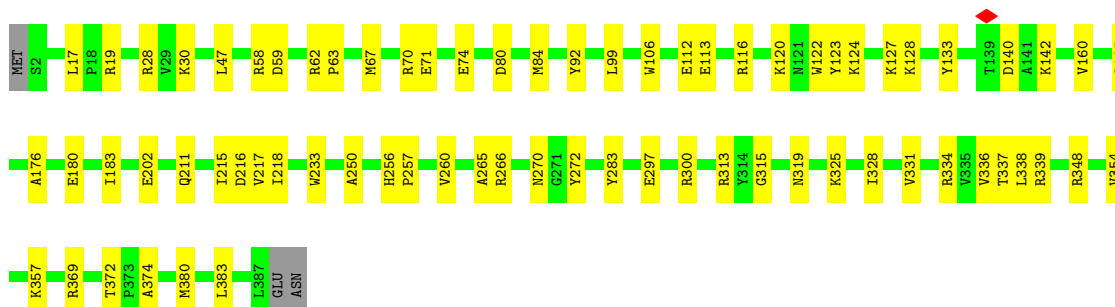
- Molecule 4: Ribosomal 60S subunit protein L2A

Chain j: 



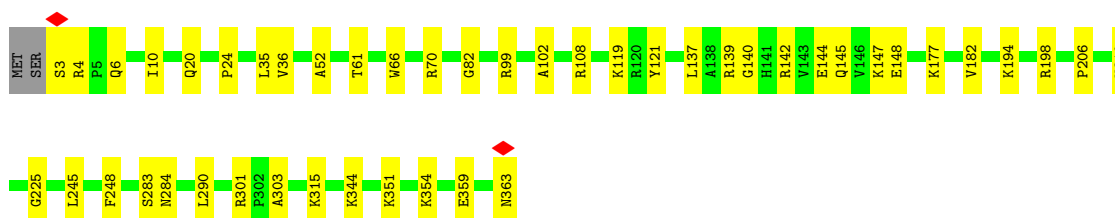
- Molecule 5: Ribosomal 60S subunit protein L3

Chain k: 



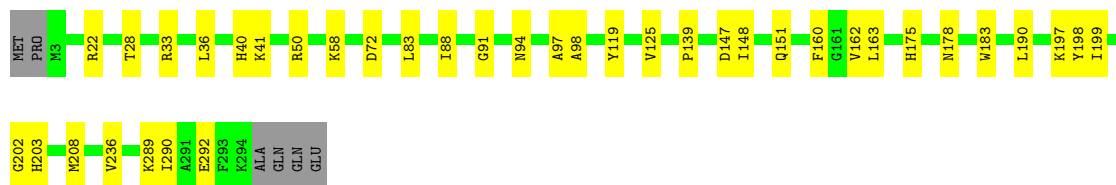
- Molecule 6: Ribosomal 60S subunit protein L4B

Chain l: 



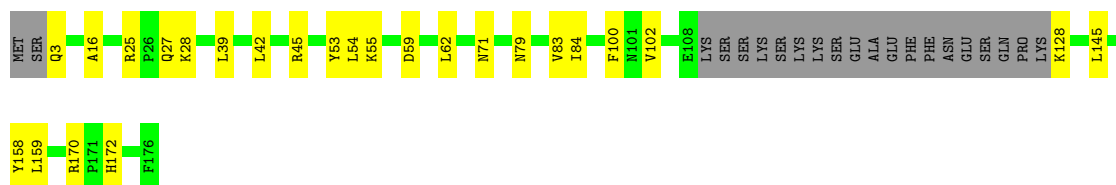
- Molecule 7: Ribosomal 60S subunit protein L5

Chain m:  85% 13%



• Molecule 8: 60S ribosomal protein L6

Chain n:  74% 14% 12%



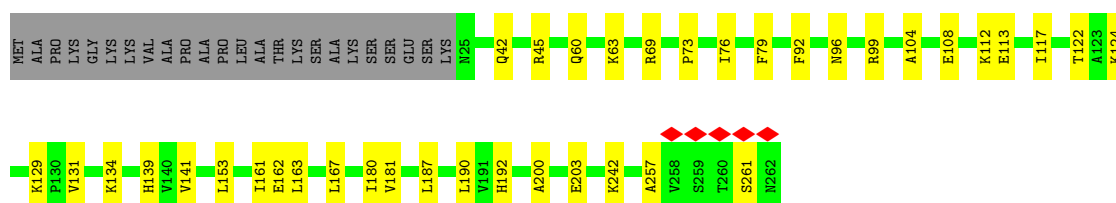
• Molecule 9: Ribosomal 60S subunit protein L7A

Chain o:  82% 15%



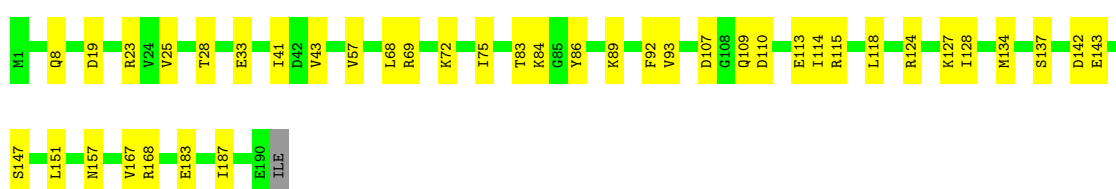
• Molecule 10: 60S ribosomal protein L8

Chain p:  76% 15% 9%



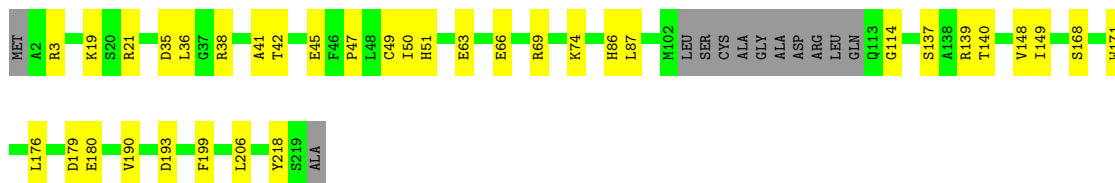
• Molecule 11: Ribosomal 60S subunit protein L9B

Chain q:  79% 21%



- Molecule 12: Ribosomal 60S subunit protein L10

Chain r:  79% 16% 5%



- Molecule 13: Ribosomal 60S subunit protein L11B

Chain s:  76% 22% ..



- Molecule 14: 60S ribosomal protein L13

Chain t:  89% 10% .



- Molecule 15: Ribosomal 60S subunit protein L14B

Chain u:  82% 17% .



- Molecule 16: Ribosomal protein L15

Chain v:  85% 14%

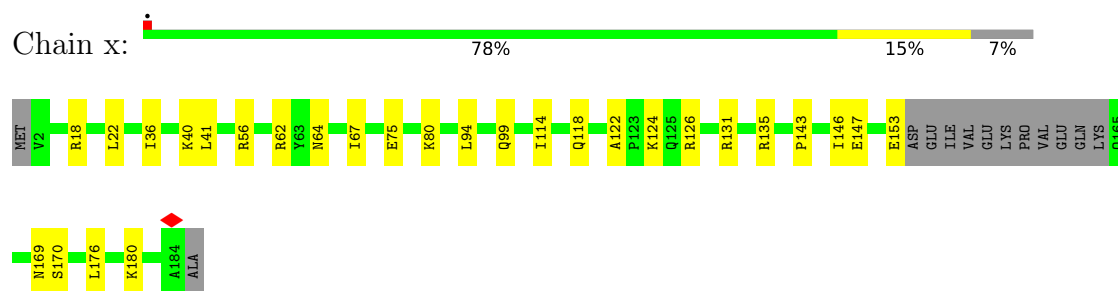


- Molecule 17: Ribosomal 60S subunit protein L16A

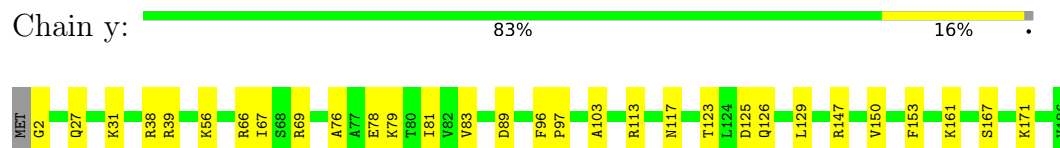
Chain w:  87% 12%



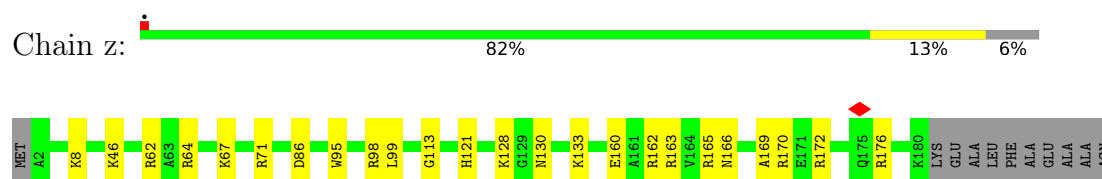
- Molecule 18: Ribosomal 60S subunit protein L17B



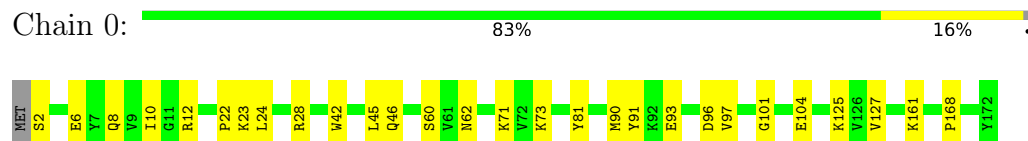
- Molecule 19: Ribosomal 60S subunit protein L18A



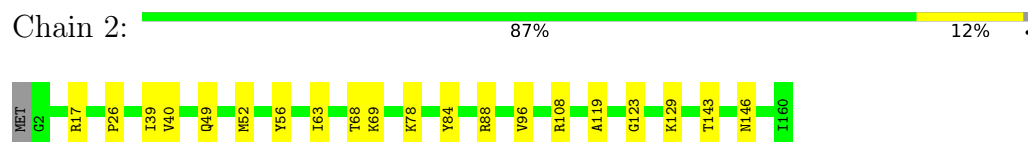
- Molecule 20: Ribosomal protein L19



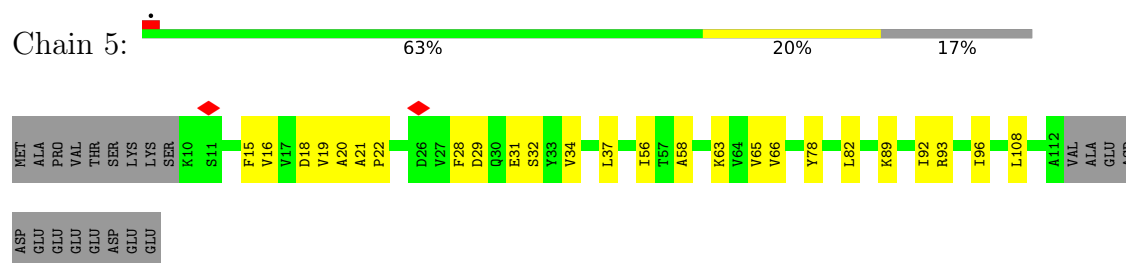
- Molecule 21: 60S ribosomal protein L20



- Molecule 22: Ribosomal 60S subunit protein L21A

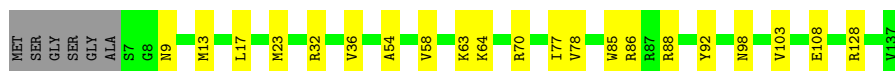


- Molecule 23: Ribosomal 60S subunit protein L22B



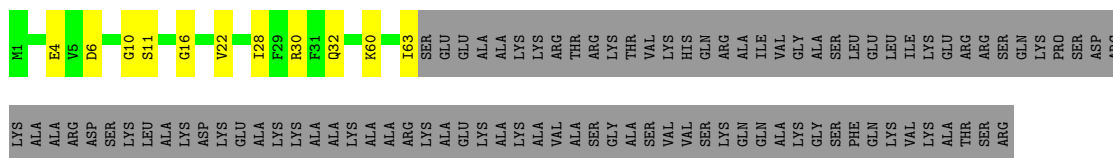
- Molecule 24: Ribosomal 60S subunit protein L23B

Chain 6:  80% 15%



- Molecule 25: Ribosomal 60S subunit protein L24A

Chain 7:  34% 7% 59%



- Molecule 26: Ribosomal 60S subunit protein L25

Chain 8:  75% 11% 15%



- Molecule 27: Ribosomal 60S subunit protein L26B

Chain 9:  84% 15%



- Molecule 28: 60S ribosomal protein L27

Chain AA:  84% 15%



- Molecule 29: Ribosomal 60S subunit protein L28

Chain AB:  83% 17%



- Molecule 30: 60S ribosomal protein L29

Chain AC:  83% 17%



- Molecule 31: Ribosomal 60S subunit protein L30

Chain AD:  80% 10% 9%



- Molecule 32: Ribosomal 60S subunit protein L31B

Chain AE:  84% 13% 3%



- Molecule 33: Ribosomal 60S subunit protein L32

Chain AF:  85% 11% 5%



- Molecule 34: Ribosomal 60S subunit protein L33A

Chain AG:  90% 9% 1%



- Molecule 35: Ribosomal 60S subunit protein L34B

Chain AH:  80% 11% 8%

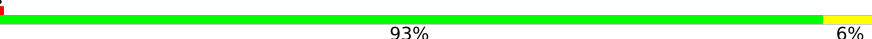


- Molecule 36: Ribosomal 60S subunit protein L35A

Chain AI:  82% 18% 0%



- Molecule 37: 60S ribosomal protein L36

Chain AJ:  93% 6% 1%



- Molecule 38: Ribosomal protein L37

Chain AK:  82% 13%



- Molecule 39: Ribosomal 60S subunit protein L38

Chain AL:  76% 23%



- Molecule 40: 60S ribosomal protein L39

Chain AM:  73% 25%



- Molecule 41: Rpl40bp

Chain AN:  85% 15%



- Molecule 42: 60S ribosomal protein eL41

Chain AO:  68% 28%



- Molecule 43: Ribosomal 60S subunit protein L42A

Chain AP:  75% 22%

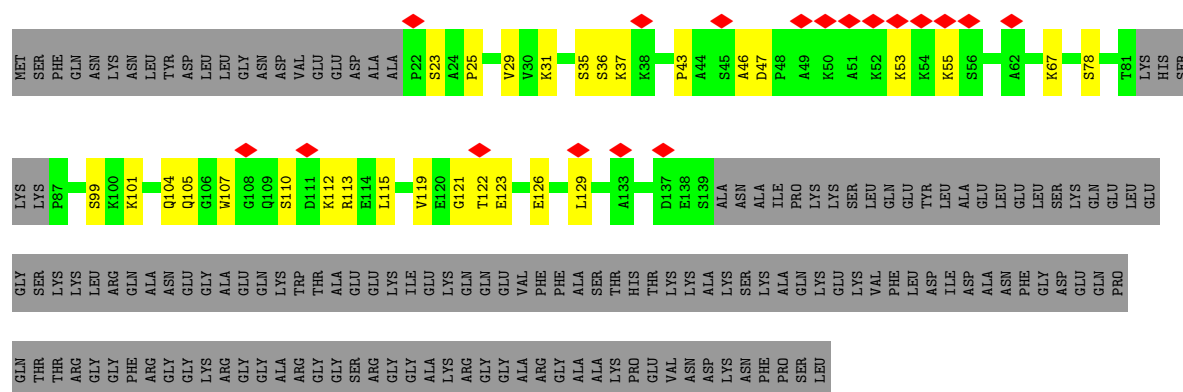


- Molecule 44: Ribosomal 60S subunit protein L43A

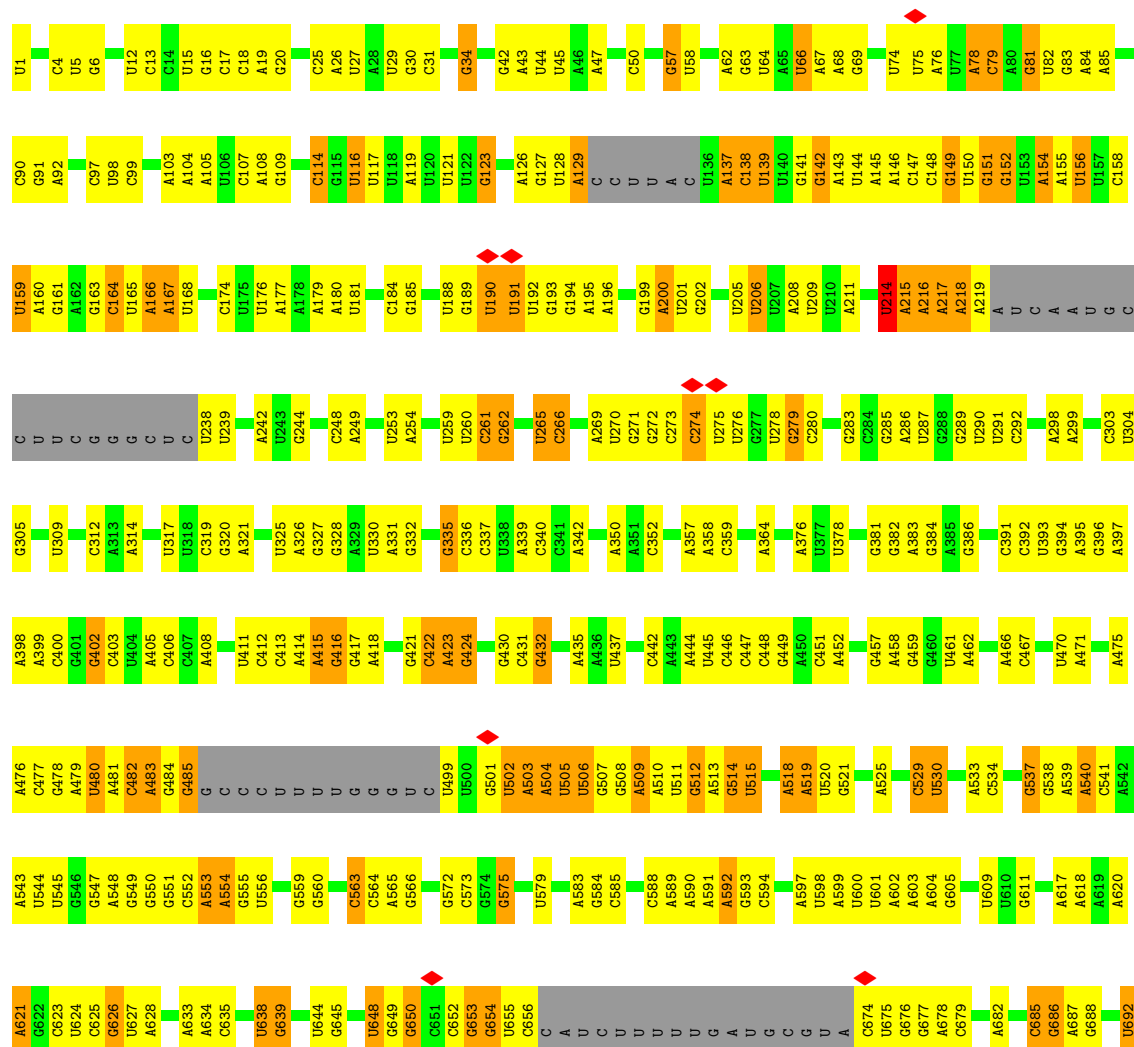
Chain AQ:  84% 15%



Chain i:

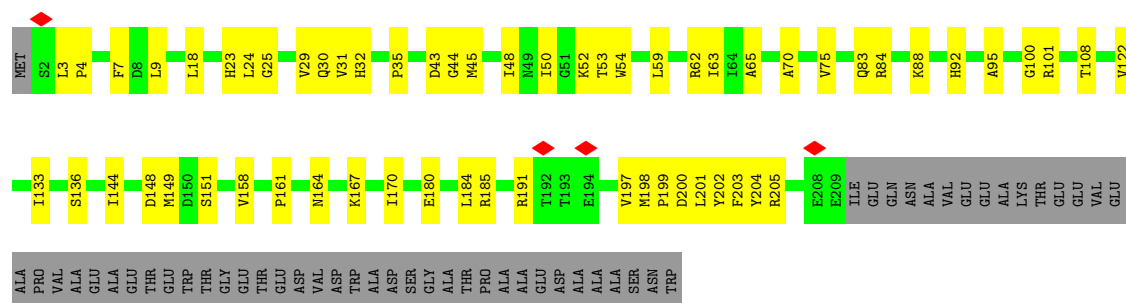


Chain A: 37% 45% 13% 5%

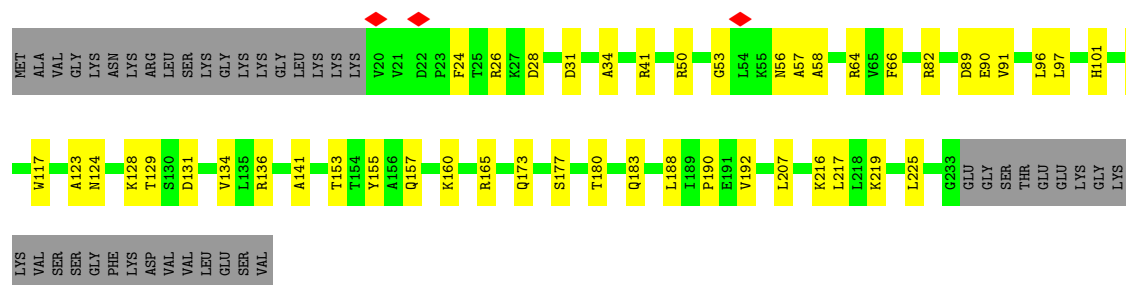


C1661	A1580	U1509	C1449	C1375	A1307	U1234	G1164	A1077	A1011	A909	C833	U693
C1662	G1561	G1510	G1450	U1376	C1308	U1235	C1165	A1078	A1012	G910	C834	C694
U1663	U1582	A1511	G1451	C1379	G1309	U1236	U1166	C1081	C1013	A911	A835	C695
C1664	C1583	A1512	C1452	C1380	G1313	U1237	U1167	C1082	C1014	C912	U836	U696
C1665	A1587	A1513	U1453	G1381	A1314	U1238	A1168	G1085	U1015	A913	C837	U697
C1666	G1588	G1518	U1454	A1382	G1315	U1239	A1169	G1086	U1016	U914	C838	C698
C1667	C1589	U1519	A1455	U1382	A1316	U1240	U1170	G1087	G1017	A915	U839	U699
A1668	U1590	G1519	C1456	U1383	G1317	U1241	A1174	U1088	C1018	C916	A840	G700
U1669	U1591	G1523	A1457	U1384	A1320	U1242	A1179	U1089	G1019	U917	A841	G701
U1670	U1592	G1524	C1458	A1385	A1321	U1243	C1180	G1092	G1020	A918	G843	G
G1671	C1593	U1525	U1459	A1386	C1322	U1247	A1181	G1093	A1021	C919	A844	A
C1672	G1594	G1526	A1461	A1387	C1324	G1249	G1184	G1094	C1022	U920	U845	G
U1673	U1595	G1529	C1462	G1391	A1326	G1250	G1185	G1099	U1025	A924	U846	C
U1674	U1596	A1530	G1463	G1395	U1326	U1251	G1186	G1099	A1024	A925	A847	C
U1675	U1597	G1530	A1465	A1396	A1330	G1252	G1187	G1099	G1025	A929	U848	A
A1676	U1598	G1533	G1466	A1397	A1331	U1253	A1188	U1102	G1026	U930	U849	U
G1677	U1600	A1534	C1467	U1398	U1332	G1254	A1189	G1103	G1027	U931	A850	U
G	A1601	G1535	C1468	U1399	A1333	G1255	A1190	G1104	A1028	U932	G853	A
A	A1602	C1536	U1469	U1400	U1334	U1256	C1190	U1105	U1029	U933	A854	U
A	G1603	A1537	G1470	U1401	G1335	U1257	U1191	C1106	C1030	A933	G855	U
G	U1604	U1538	C1471	G1402	U1336	G1258	C1192	G1115	G1031	C934	G856	G
C	C1605	U1539	G1472	G1403	G1337	G1259	A1193	G1115	G1032	C935	G857	G
C	G1606	G1540	A1473	A1410	C1344	A1260	A1194	U1129	U1043	G938	G857	C
G	G1609	U1541	G1474	A1413	U1345	A1261	C1195	U1130	U1044	G939	A796	G
C	C1610	A1542	U1475	A1414	A1346	U1262	C1196	A1122	U1045	A940	U797	A
C	C1611	U1544	U1476	G1415	C1347	G1263	A1196	A1123	A1046	C941	A798	A
A	C1612	U1545	U1477	G1416	U1348	G1264	G1197	A1127	U1047	U942	A799	
C	U1613	U1546	A1478	U1416	U1349	C1265	G1198	A1128	U1048	U943	C868	
C	U1614	U1547	G1479	U1417	C1350	G1266	C1201	U1129	A1049	U944	A869	
U	U1615	U1548	G1480	U1420	U1351	A1270	A1202	U1130	U1050	U945	G870	
C	G1616	G1549	C1481	G1421	A1345	U1271	G1203	A1132	C1051	A949	G871	
U	A1622	C1550	U1482	U1422	U1346	A1272	A1206	A1133	A1046	U951	A872	
U	U1623	U1551	G1483	U1423	U1347	U1273	C1207	A1144	U1047	A952	U874	
C	C1626	C1552	U1484	G1424	U1348	U1275	A1208	A1145	U1048	U953	A875	
U	G1627	C1555	G1485	C1425	U1349	G1276	A1209	C1146	G1049	C954	G877	
G	U1630	A1556	C1486	C1426	C1350	U1279	A1211	G1149	A1050	A955	U878	
A1701	C1631	G1559	C1487	U1427	U1351	G1279	A1212	G1150	C1052	A956	U879	
A1702	G1632	A1560	G1488	U1428	G1352	G1282	G1213	C1143	A1055	G965	U880	
C1704	A1635	G1561	G1489	A1430	G1353	U1283	G1214	A1144	U1056	A973	U881	
G1705	C1636	G1562	G1491	A1431	U1354	G1284	A1215	A1145	C1057	U974	A814	
	U1644	U1565	G1492	C1432	U1355	A1285	U1216	C1146	G1058	C975	U815	
U1709	A1638	U1566	G1493	C1433	A1357	U1286	U1217	G1149	G1059	G976	U816	
U1710	C1645	U1567	U1494	G1434	G1358	U1292	G1218	A1151	C1060	A977	U817	
C1711	U1648	C1568	U1495	U1435	U1359	G1293	A1219	G1152	A1061	C985	U818	
U1712	G1649	A1570	U1496	U1436	C1360	C1294	A1220	U1153	C1062	A989	U819	
G1713	U1656	U1571	G1497	U1437	U1361	U1297	A1221	G1154	U1063	U989	G822	
U1714	C1657	U1572	U1498	U1438	C1362	U1298	A1222	G1155	U1064	U997	G823	
U1715	A1658	A1573	U1499	G1439	C1365	U1299	A1223	U1156	U1065	A998	U824	
C1716	U1659	U1574	G1500	G1440	U1366	U1300	G1226	G1157	A1066	U1003	U825	
A1717	C1657	G1575	A1503	C1442	U1367	G1301	G1227	C1158	C1067	A904	U826	
U1718	U1658	C1576	U1504	C1443	G1368	C1302	G1228	C1159	G1068	C905	A827	
A1719	C1659	U1578	G1505	C1444	A1370	G1303	U1229	U1160	U1069	U906	U828	
C1720	G1660	C1579	A1446	A1445	G1371	U1304	U1230	G1161	A1072	A907	G830	
			U1507	G1448	G1372	U1305	C1231	G1163	A1073	A1004	A754	
G1724			A1448	A1374	A1374	A1306	U1232			A1005	A755	
											A756	
											G757	
											C758	
											G831	
											A832	

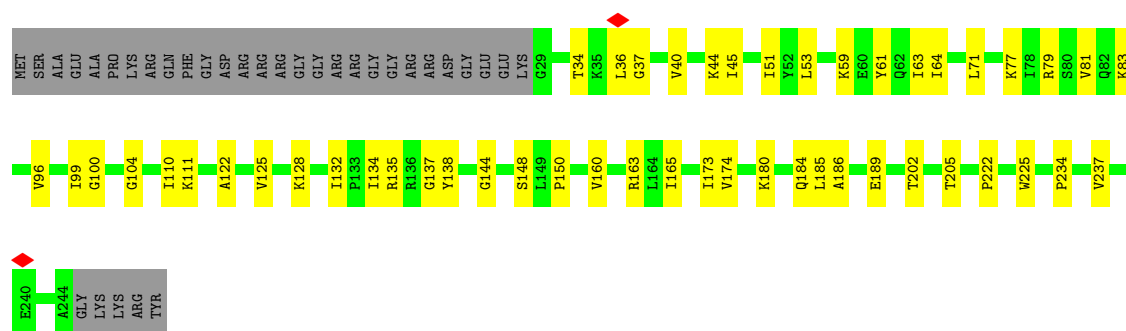
- Molecule 47: 40S ribosomal protein S0



- Molecule 48: 40S ribosomal protein S1

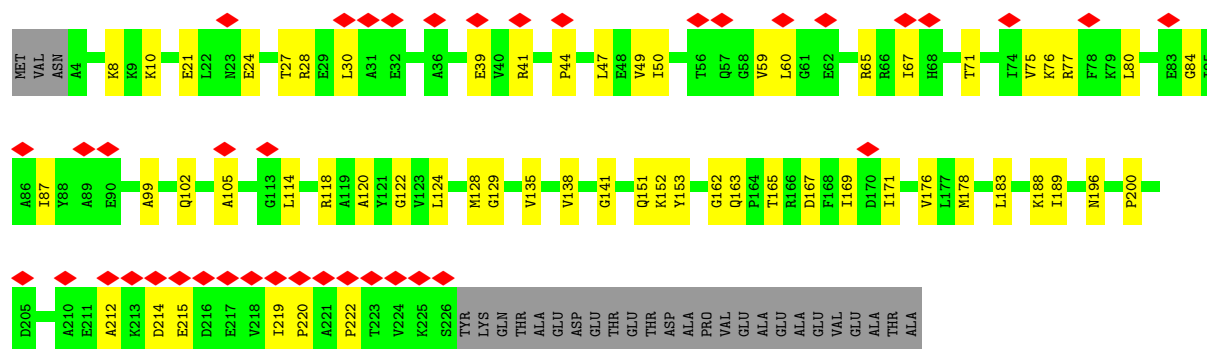


- Molecule 49: Ribosomal 40S subunit protein S2

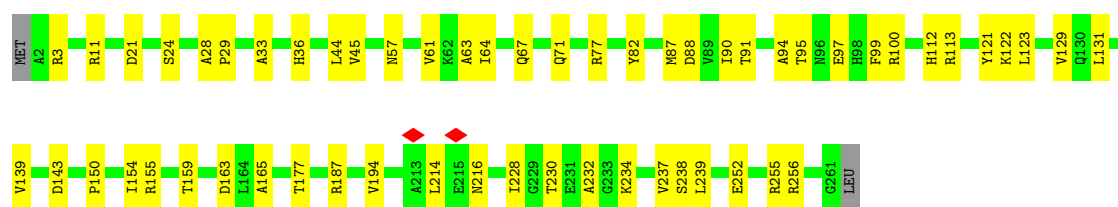
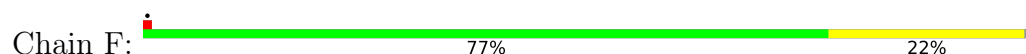


- Molecule 50: Ribosomal 40S subunit protein S3

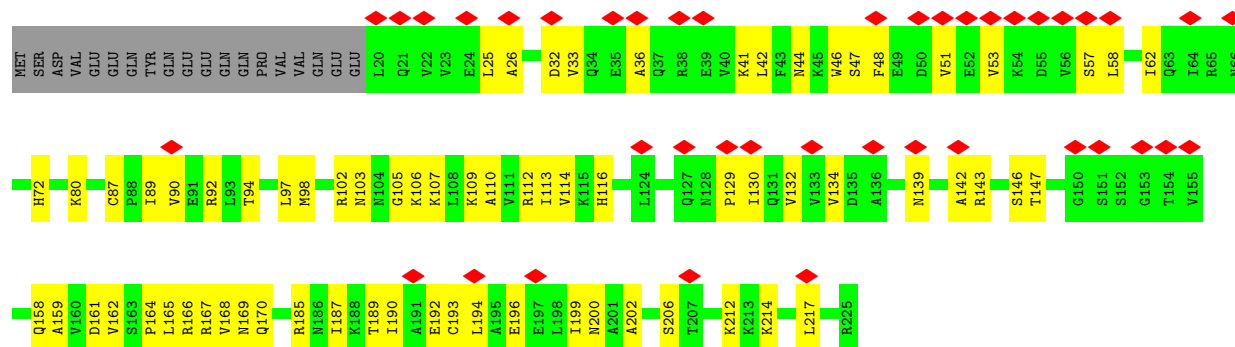




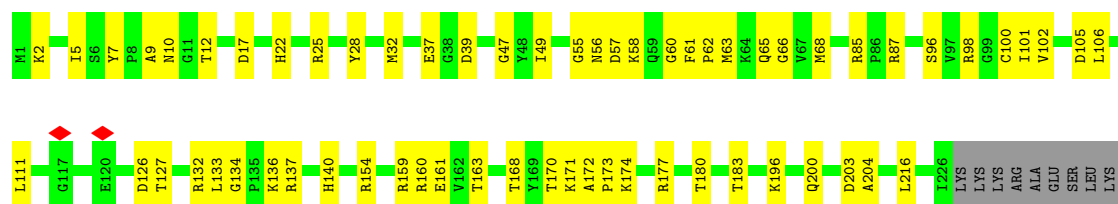
- Molecule 51: 40S ribosomal protein S4



- Molecule 52: Ribosomal 40S subunit protein S5

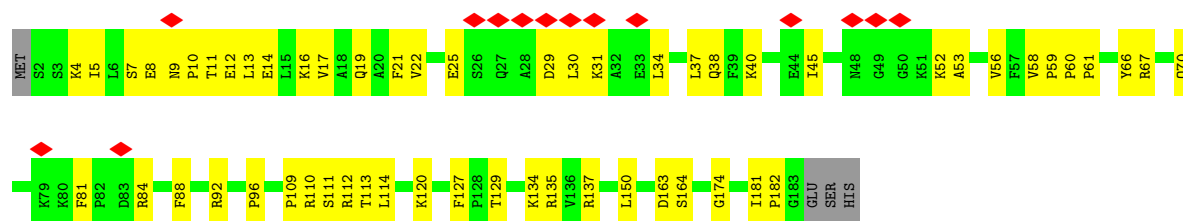


- Molecule 53: 40S ribosomal protein S6



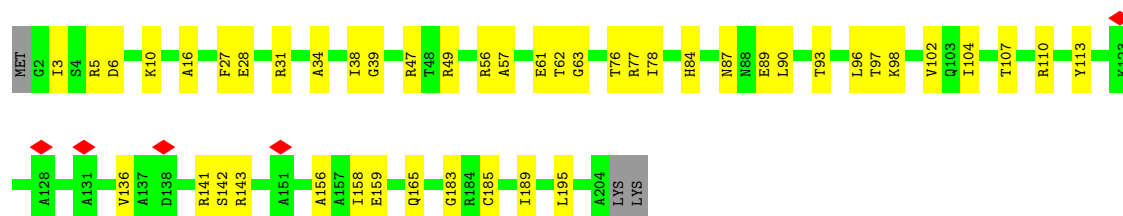
- Molecule 54: 40S ribosomal protein S7





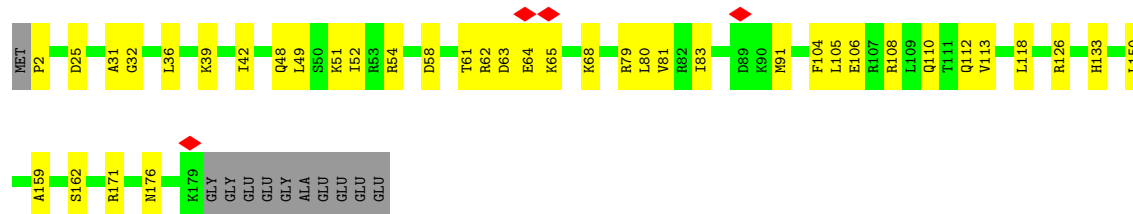
- Molecule 55: 40S ribosomal protein S8

Chain J: 76% 22%



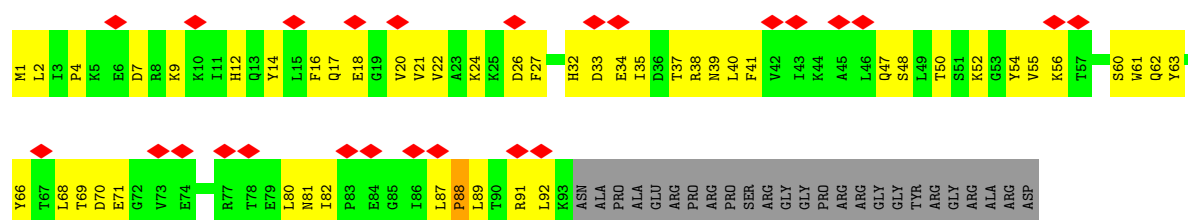
- Molecule 56: Ribosomal 40S subunit protein S9B

Chain K: 74% 21% 6%



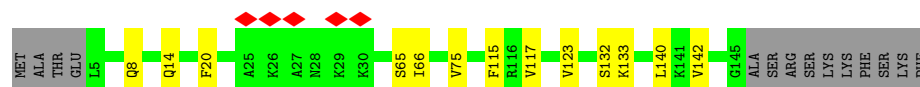
- Molecule 57: Ribosomal 40S subunit protein S10A

Chain L: 21% 37% 41% 21%

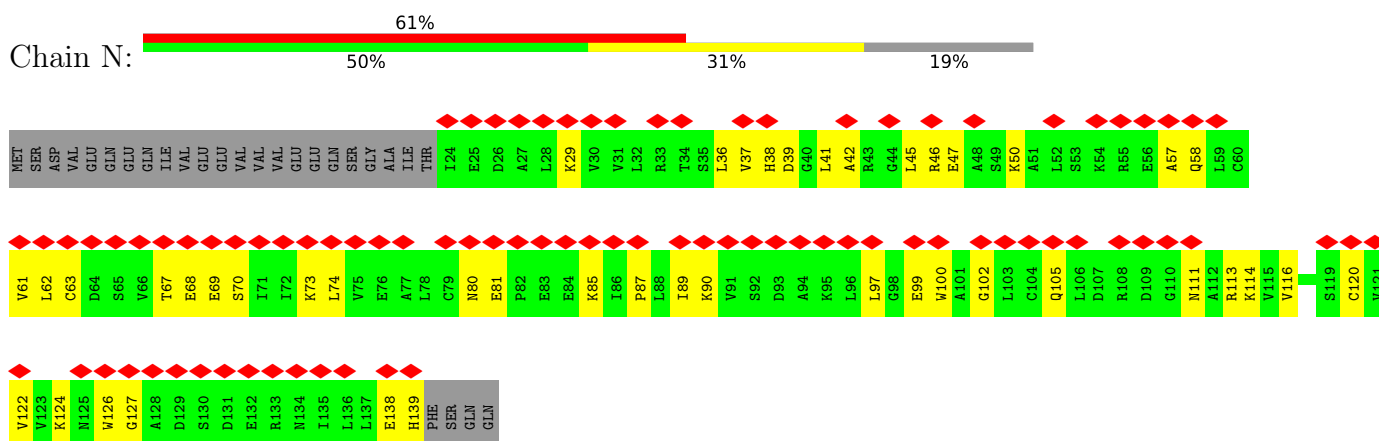


- Molecule 58: Ribosomal 40S subunit protein S11A

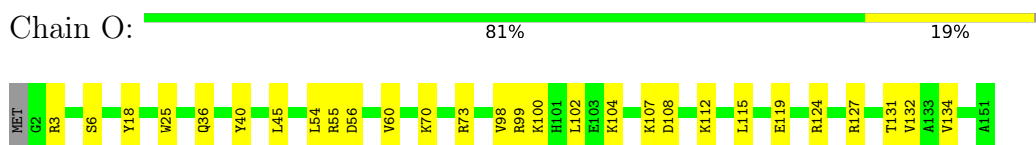
Chain M: 83% 8% 9%



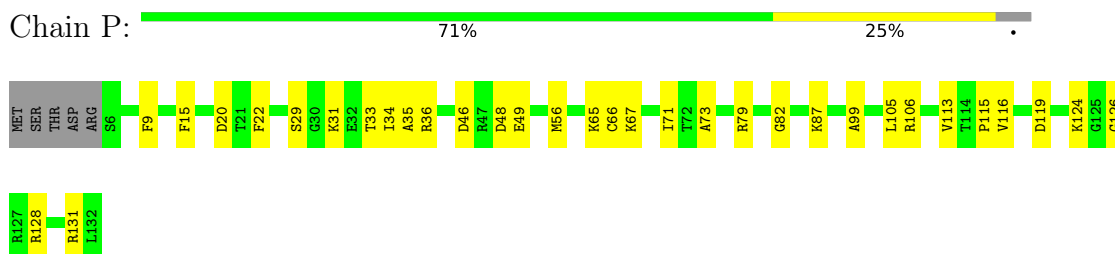
- Molecule 59: 40S ribosomal protein S12



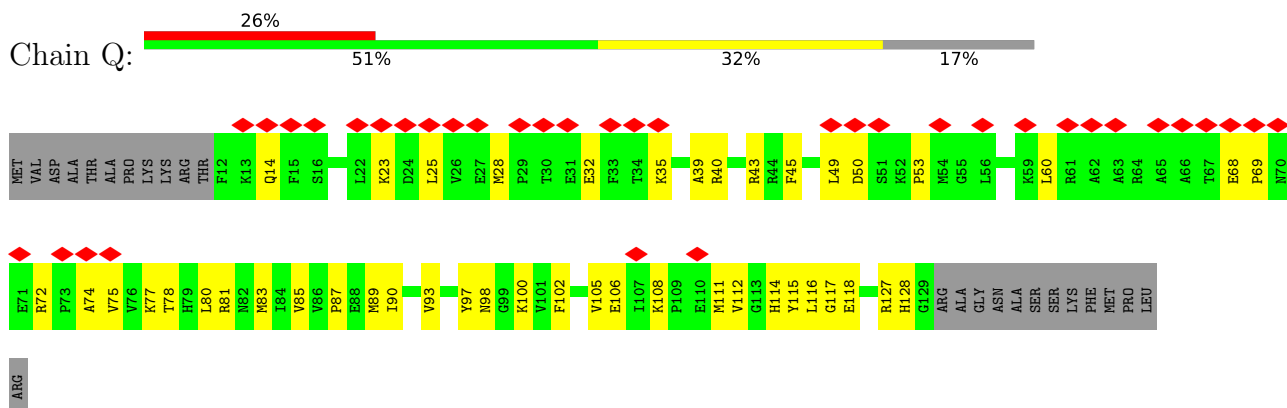
- Molecule 60: Ribosomal 40S subunit protein S13



- Molecule 61: Ribosomal 40S subunit protein S14B

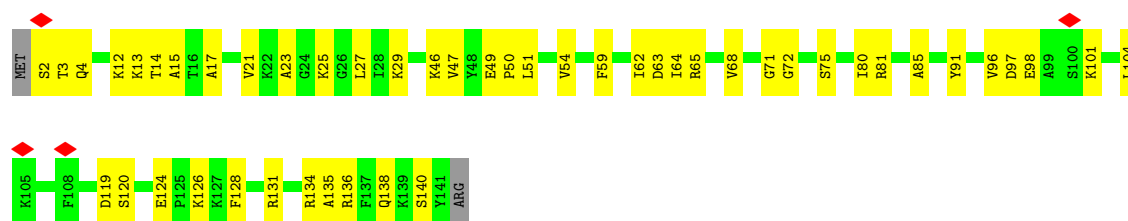


- Molecule 62: Ribosomal 40S subunit protein S15

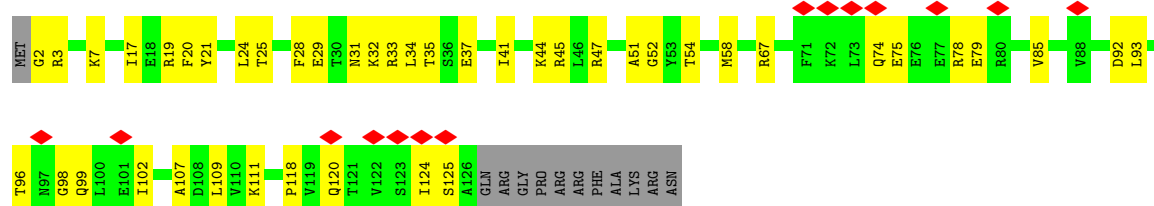


- Molecule 63: Ribosomal 40S subunit protein S16A

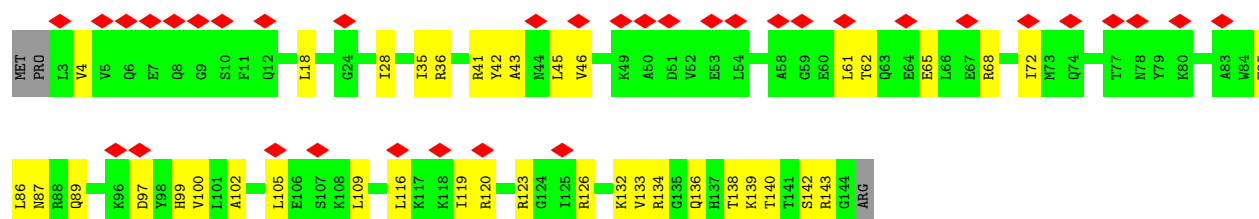




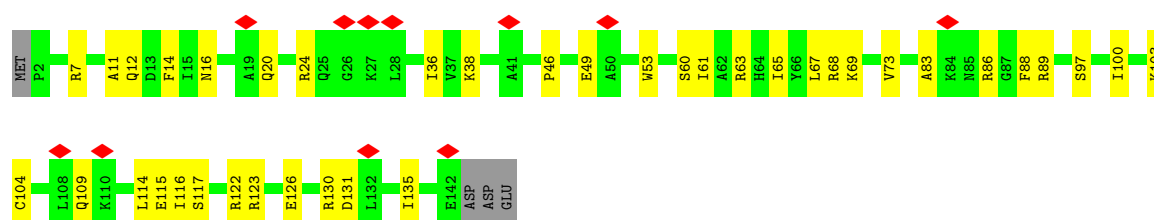
• Molecule 64: Ribosomal 40S subunit protein S17B



• Molecule 65: Ribosomal 40S subunit protein S18B

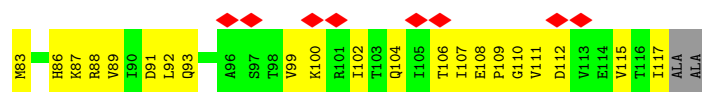


• Molecule 66: Ribosomal 40S subunit protein S19A

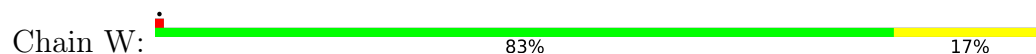


• Molecule 67: Ribosomal 40S subunit protein S20





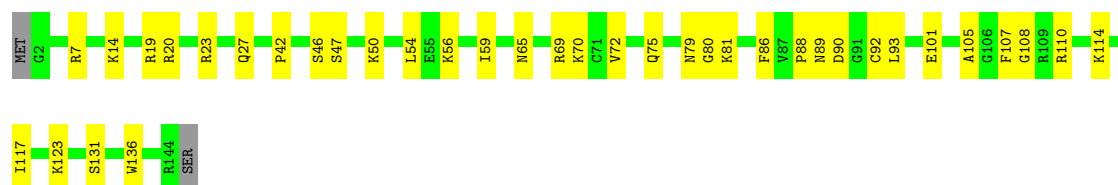
- Molecule 68: 40S ribosomal protein S21



- Molecule 69: 40S ribosomal protein S22-A



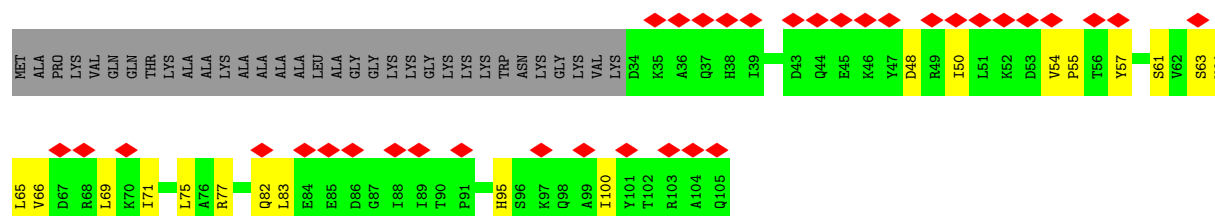
- Molecule 70: Ribosomal 40S subunit protein S23B



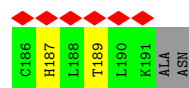
- Molecule 71: 40S ribosomal protein S24



- Molecule 72: 40S ribosomal protein S25

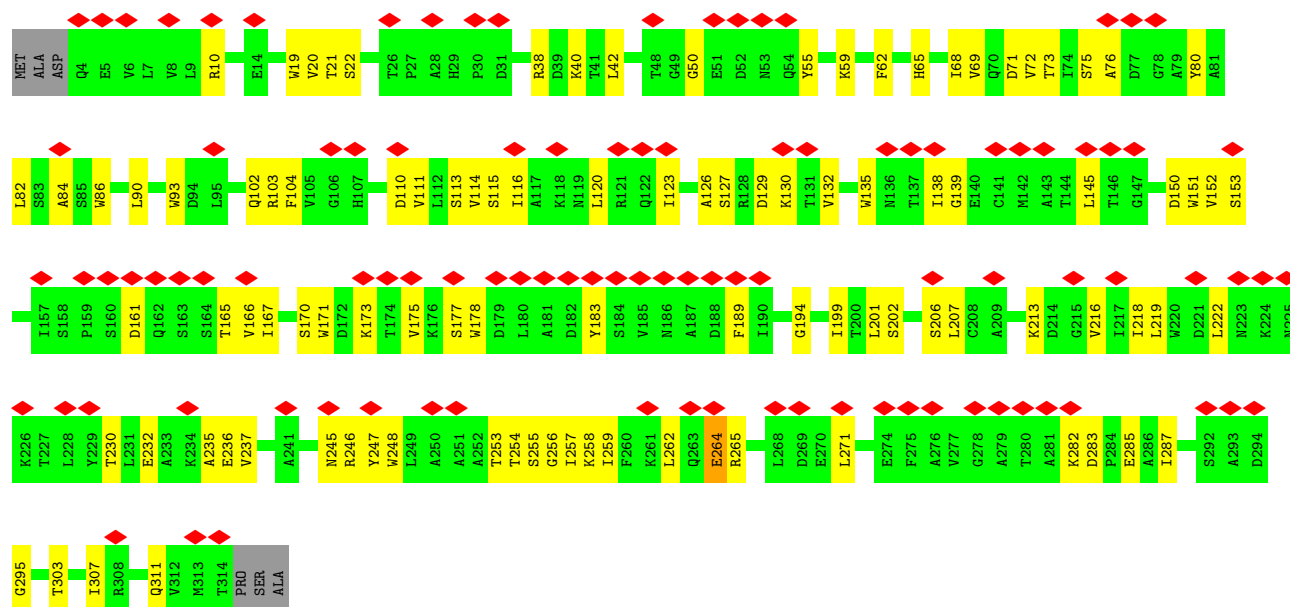


- lys K122 K123 K124 K125 K126 K127 K128 K129 K130 K131 K132 K133 K134 K135 K136 K137 K138 K139 K140 K141 K142 K143 K144 K145 K146 K147 K148 K149 K150 K151 K152 K153 K154 K155 K156 K157 K158 K159 K160 K161 K162 K163 K164 K165 K166 K167 K168 K169 K170 K171 K172 K173 K174 K175 K176 K177 K178 K179 K180 K181 K182 K183 K184 K185 K186 K187 K188 K189 K190 K191 K192 K193 K194 K195 K196 K197 K198 K199 K200



- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

Chain h: 32% 66% 32%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132328	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.771	Depositor
Minimum map value	-1.536	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	426.36002, 426.36002, 426.36002	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.836, 0.836, 0.836	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IAS, MLZ, SPD, OMC, OMG, 3K5

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.22	9/76718 (0.0%)	0.30	4/119600 (0.0%)
2	3	0.17	0/2884	0.22	0/4492
3	4	0.19	0/3746	0.26	0/5832
4	j	0.19	0/1931	0.32	0/2592
5	k	0.20	0/3156	0.35	0/4246
6	l	0.17	0/2799	0.33	0/3777
7	m	0.15	0/2447	0.30	0/3294
8	n	0.15	0/1258	0.29	0/1696
9	o	0.18	0/1929	0.32	0/2589
10	p	0.15	0/1869	0.30	0/2519
11	q	0.15	0/1537	0.30	0/2067
12	r	0.17	0/1724	0.32	0/2314
13	s	0.35	1/1404 (0.1%)	0.56	4/1880 (0.2%)
14	t	0.16	0/1637	0.32	0/2195
15	u	0.16	0/1044	0.29	0/1407
16	v	0.21	0/1753	0.31	0/2347
17	w	0.18	0/1620	0.30	0/2167
18	x	0.17	0/1398	0.31	0/1879
19	y	0.17	0/1511	0.28	0/2022
20	z	0.14	0/1483	0.25	0/1972
21	0	0.18	0/1483	0.30	0/1997
22	2	0.17	0/1305	0.28	0/1749
23	5	0.15	0/871	0.38	0/1175
24	6	0.17	0/994	0.33	0/1339
25	7	0.16	0/536	0.31	0/712
26	8	0.17	0/990	0.31	0/1337
27	9	0.15	0/999	0.30	0/1334
28	AA	0.15	0/1112	0.31	0/1488
29	AB	0.19	0/1199	0.30	0/1607
30	AC	0.16	0/522	0.31	0/692
31	AD	0.14	0/738	0.27	0/994
32	AE	0.17	0/902	0.29	0/1212

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AF	0.17	0/1039	0.31	0/1390
34	AG	0.19	0/895	0.31	0/1201
35	AH	0.16	0/934	0.36	0/1242
36	AI	0.15	0/1004	0.33	0/1337
37	AJ	0.13	0/780	0.27	0/1033
38	AK	0.19	0/690	0.32	0/916
39	AL	0.16	0/632	0.35	0/842
40	AM	0.18	0/458	0.27	0/609
41	AN	0.15	0/436	0.35	0/577
42	AO	0.12	0/228	0.29	0/293
43	AP	0.19	0/840	0.40	0/1108
44	AQ	0.17	0/705	0.31	0/940
45	i	0.13	0/864	0.36	0/1156
46	A	0.14	0/40362	0.32	7/62888 (0.0%)
47	B	0.13	0/1666	0.32	0/2273
48	C	0.12	0/1750	0.30	0/2354
49	D	0.14	0/1648	0.32	0/2237
50	E	0.13	0/1731	0.36	0/2324
51	F	0.12	0/2096	0.32	0/2822
52	G	0.11	0/1631	0.34	0/2199
53	H	0.12	0/1845	0.31	0/2464
54	I	0.14	0/1490	0.34	0/2004
55	J	0.16	0/1606	0.36	0/2150
56	K	0.11	0/1478	0.29	0/1978
57	L	0.18	0/801	0.49	0/1081
58	M	0.14	0/1154	0.32	0/1553
59	N	0.15	0/892	0.47	0/1203
60	O	0.12	0/1210	0.30	0/1631
61	P	0.13	0/944	0.32	0/1265
62	Q	0.16	0/954	0.44	0/1282
63	R	0.12	0/1109	0.37	0/1486
64	S	0.12	0/1014	0.38	0/1361
65	T	0.13	0/1186	0.33	0/1590
66	U	0.13	0/1120	0.34	0/1508
67	V	0.17	0/800	0.40	0/1082
68	W	0.13	0/683	0.35	0/918
69	X	0.17	0/1049	0.39	0/1412
70	Y	0.13	0/1128	0.33	0/1505
71	Z	0.10	0/1086	0.30	0/1447
72	a	0.12	0/585	0.30	0/789
73	b	0.14	0/811	0.35	0/1085
74	c	0.13	0/624	0.32	0/843
75	d	0.13	0/489	0.41	0/654

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	e	0.15	0/466	0.40	0/620
77	f	0.18	0/451	0.49	0/601
78	g	0.16	0/585	0.48	0/778
79	h	0.18	0/2451	0.42	0/3337
All	All	0.18	10/213899 (0.0%)	0.32	15/313891 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1737	A	O3'-P	-12.69	1.42	1.61
13	s	118	PRO	CG-CD	-9.73	1.17	1.50
1	1	482	U	C1'-N1	6.32	1.57	1.48
1	1	477	U	C1'-N1	6.31	1.57	1.48
1	1	483	U	C1'-N1	6.12	1.57	1.48

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1017	G	P-O3'-C3'	21.59	152.59	120.20
46	A	822	G	O3'-P-O5'	18.80	132.21	104.00
13	s	118	PRO	CA-N-CD	-12.09	95.08	112.00
46	A	822	G	P-O3'-C3'	12.05	138.28	120.20
46	A	214	U	OP2-P-O3'	-12.00	71.99	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68595	0	34479	879	0
2	3	2579	0	1304	27	0
3	4	3353	0	1694	45	0
4	j	1894	0	1975	31	0
5	k	3084	0	3173	55	0
6	l	2751	0	2879	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	m	2394	0	2362	25	0
8	n	1237	0	1316	20	0
9	o	1893	0	1990	21	0
10	p	1839	0	1957	27	0
11	q	1519	0	1588	23	0
12	r	1689	0	1731	24	0
13	s	1385	0	1418	36	0
14	t	1610	0	1686	20	0
15	u	1029	0	1116	15	0
16	v	1713	0	1764	22	0
17	w	1590	0	1705	17	0
18	x	1375	0	1403	20	0
19	y	1478	0	1590	24	0
20	z	1462	0	1570	24	0
21	0	1442	0	1500	22	0
22	2	1276	0	1333	18	0
23	5	848	0	864	17	0
24	6	986	0	1040	14	0
25	7	524	0	545	8	0
26	8	974	0	1032	10	0
27	9	989	0	1064	13	0
28	AA	1087	0	1154	14	0
29	AB	1170	0	1203	21	0
30	AC	509	0	545	8	0
31	AD	729	0	775	6	0
32	AE	889	0	936	9	0
33	AF	1015	0	1095	11	0
34	AG	867	0	932	7	0
35	AH	913	0	1002	14	0
36	AI	990	0	1094	16	0
37	AJ	772	0	863	6	0
38	AK	677	0	697	9	0
39	AL	623	0	688	11	0
40	AM	446	0	488	9	0
41	AN	427	0	473	8	0
42	AO	227	0	272	6	0
43	AP	843	0	914	19	0
44	AQ	698	0	734	11	0
45	i	853	0	830	26	0
46	A	36083	0	18151	841	0
47	B	1627	0	1644	46	0
48	C	1724	0	1805	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	D	1620	0	1715	35	0
50	E	1707	0	1807	45	0
51	F	2055	0	2137	40	0
52	G	1614	0	1688	55	0
53	H	1820	0	1896	52	0
54	I	1466	0	1561	45	0
55	J	1579	0	1602	31	0
56	K	1453	0	1532	26	0
57	L	783	0	799	40	0
58	M	1129	0	1183	10	0
59	N	885	0	915	31	0
60	O	1187	0	1249	23	0
61	P	942	0	980	27	0
62	Q	935	0	970	42	0
63	R	1091	0	1155	39	0
64	S	1002	0	1058	35	0
65	T	1169	0	1216	35	0
66	U	1100	0	1114	37	0
67	V	790	0	855	36	0
68	W	676	0	677	17	0
69	X	1032	0	1066	22	0
70	Y	1110	0	1182	32	0
71	Z	1072	0	1123	32	0
72	a	578	0	613	16	0
73	b	799	0	860	15	0
74	c	614	0	627	8	0
75	d	487	0	523	25	0
76	e	454	0	431	21	0
77	f	444	0	483	24	0
78	g	574	0	606	24	0
79	h	2398	0	2374	83	0
80	1	10	0	19	0	0
81	1	57	0	52	6	0
82	AK	1	0	0	0	0
82	AN	1	0	0	0	0
82	AP	1	0	0	0	0
82	AQ	1	0	0	0	0
82	b	1	0	0	0	0
82	c	1	0	0	0	0
82	e	1	0	0	0	0
82	g	1	0	0	0	0
All	All	199317	0	148441	3064	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 3064 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A:215:A:H62	46:A:830:G:C1'	1.14	1.55
46:A:215:A:N6	46:A:830:G:H1'	1.09	1.38
1:1:445:A:N6	1:1:485:A:N1	2.00	1.08
77:f:50:THR:OG1	77:f:53:LYS:HB2	1.56	1.04
70:Y:89:ASN:ND2	70:Y:92:CYS:SG	2.36	0.99

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	
4	j	248/254 (98%)	240 (97%)	8 (3%)	0	100	100
5	k	385/389 (99%)	376 (98%)	9 (2%)	0	100	100
6	l	359/363 (99%)	354 (99%)	5 (1%)	0	100	100
7	m	290/298 (97%)	283 (98%)	7 (2%)	0	100	100
8	n	152/176 (86%)	148 (97%)	4 (3%)	0	100	100
9	o	233/241 (97%)	225 (97%)	8 (3%)	0	100	100
10	p	236/262 (90%)	232 (98%)	4 (2%)	0	100	100
11	q	188/191 (98%)	185 (98%)	3 (2%)	0	100	100
12	r	204/220 (93%)	204 (100%)	0	0	100	100
13	s	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
14	t	198/202 (98%)	193 (98%)	5 (2%)	0	100	100
15	u	128/131 (98%)	124 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	v	201/204 (98%)	200 (100%)	1 (0%)	0	100	100
17	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
18	x	168/185 (91%)	165 (98%)	3 (2%)	0	100	100
19	y	186/186 (100%)	182 (98%)	4 (2%)	0	100	100
20	z	178/190 (94%)	176 (99%)	2 (1%)	0	100	100
21	0	171/172 (99%)	170 (99%)	1 (1%)	0	100	100
22	2	159/160 (99%)	158 (99%)	1 (1%)	0	100	100
23	5	103/124 (83%)	97 (94%)	6 (6%)	0	100	100
24	6	129/137 (94%)	128 (99%)	1 (1%)	0	100	100
25	7	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
26	8	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
27	9	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
28	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
29	AB	146/149 (98%)	141 (97%)	5 (3%)	0	100	100
30	AC	62/63 (98%)	62 (100%)	0	0	100	100
31	AD	94/106 (89%)	94 (100%)	0	0	100	100
32	AE	107/112 (96%)	106 (99%)	1 (1%)	0	100	100
33	AF	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
34	AG	107/107 (100%)	104 (97%)	3 (3%)	0	100	100
35	AH	114/122 (93%)	113 (99%)	1 (1%)	0	100	100
36	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
37	AJ	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
38	AK	84/90 (93%)	83 (99%)	1 (1%)	0	100	100
39	AL	76/78 (97%)	72 (95%)	4 (5%)	0	100	100
40	AM	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
41	AN	51/52 (98%)	50 (98%)	1 (2%)	0	100	100
42	AO	22/25 (88%)	22 (100%)	0	0	100	100
43	AP	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
44	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	i	109/267 (41%)	104 (95%)	5 (5%)	0	100	100
47	B	206/261 (79%)	200 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	C	212/256 (83%)	209 (99%)	3 (1%)	0	100	100
49	D	214/249 (86%)	212 (99%)	2 (1%)	0	100	100
50	E	221/251 (88%)	214 (97%)	7 (3%)	0	100	100
51	F	258/262 (98%)	256 (99%)	2 (1%)	0	100	100
52	G	204/225 (91%)	195 (96%)	9 (4%)	0	100	100
53	H	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
54	I	180/186 (97%)	177 (98%)	3 (2%)	0	100	100
55	J	201/206 (98%)	199 (99%)	2 (1%)	0	100	100
56	K	176/189 (93%)	174 (99%)	2 (1%)	0	100	100
57	L	91/118 (77%)	83 (91%)	7 (8%)	1 (1%)	11	16
58	M	139/155 (90%)	136 (98%)	3 (2%)	0	100	100
59	N	114/143 (80%)	100 (88%)	14 (12%)	0	100	100
60	O	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
61	P	123/132 (93%)	120 (98%)	3 (2%)	0	100	100
62	Q	116/142 (82%)	106 (91%)	10 (9%)	0	100	100
63	R	138/142 (97%)	131 (95%)	7 (5%)	0	100	100
64	S	123/137 (90%)	117 (95%)	6 (5%)	0	100	100
65	T	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
66	U	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
67	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
68	W	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
69	X	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
70	Y	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
71	Z	130/135 (96%)	130 (100%)	0	0	100	100
72	a	70/105 (67%)	68 (97%)	2 (3%)	0	100	100
73	b	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
74	c	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
75	d	60/67 (90%)	56 (93%)	4 (7%)	0	100	100
76	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
77	f	54/63 (86%)	53 (98%)	1 (2%)	0	100	100
78	g	68/193 (35%)	60 (88%)	8 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
79	h	309/317 (98%)	294 (95%)	15 (5%)	0	100	100
All	All	11010/12138 (91%)	10737 (98%)	272 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	L	88	PRO

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	
4	j	191/194 (98%)	191 (100%)	0	100	100
5	k	326/328 (99%)	326 (100%)	0	100	100
6	l	290/292 (99%)	290 (100%)	0	100	100
7	m	247/252 (98%)	247 (100%)	0	100	100
8	n	135/154 (88%)	135 (100%)	0	100	100
9	o	199/204 (98%)	199 (100%)	0	100	100
10	p	198/216 (92%)	198 (100%)	0	100	100
11	q	169/170 (99%)	169 (100%)	0	100	100
12	r	178/186 (96%)	178 (100%)	0	100	100
13	s	148/149 (99%)	148 (100%)	0	100	100
14	t	166/168 (99%)	166 (100%)	0	100	100
15	u	108/109 (99%)	108 (100%)	0	100	100
16	v	177/178 (99%)	177 (100%)	0	100	100
17	w	166/167 (99%)	166 (100%)	0	100	100
18	x	142/154 (92%)	142 (100%)	0	100	100
19	y	156/154 (101%)	156 (100%)	0	100	100
20	z	147/153 (96%)	147 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	0	158/157 (101%)	158 (100%)	0	100	100
22	2	135/134 (101%)	135 (100%)	0	100	100
23	5	95/112 (85%)	93 (98%)	2 (2%)	47	67
24	6	101/103 (98%)	101 (100%)	0	100	100
25	7	57/127 (45%)	57 (100%)	0	100	100
26	8	108/121 (89%)	108 (100%)	0	100	100
27	9	111/112 (99%)	111 (100%)	0	100	100
28	AA	117/118 (99%)	117 (100%)	0	100	100
29	AB	120/121 (99%)	120 (100%)	0	100	100
30	AC	50/49 (102%)	50 (100%)	0	100	100
31	AD	81/90 (90%)	81 (100%)	0	100	100
32	AE	98/100 (98%)	98 (100%)	0	100	100
33	AF	111/115 (96%)	111 (100%)	0	100	100
34	AG	94/92 (102%)	94 (100%)	0	100	100
35	AH	99/102 (97%)	99 (100%)	0	100	100
36	AI	106/106 (100%)	106 (100%)	0	100	100
37	AJ	79/79 (100%)	79 (100%)	0	100	100
38	AK	70/73 (96%)	70 (100%)	0	100	100
39	AL	69/69 (100%)	69 (100%)	0	100	100
40	AM	47/47 (100%)	47 (100%)	0	100	100
41	AN	48/47 (102%)	48 (100%)	0	100	100
42	AO	23/24 (96%)	23 (100%)	0	100	100
43	AP	88/89 (99%)	86 (98%)	2 (2%)	44	65
44	AQ	72/73 (99%)	72 (100%)	0	100	100
45	i	92/212 (43%)	92 (100%)	0	100	100
47	B	176/215 (82%)	176 (100%)	0	100	100
48	C	194/229 (85%)	194 (100%)	0	100	100
49	D	174/198 (88%)	174 (100%)	0	100	100
50	E	174/196 (89%)	174 (100%)	0	100	100
51	F	218/220 (99%)	218 (100%)	0	100	100
52	G	178/197 (90%)	178 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	H	195/204 (96%)	195 (100%)	0	100	100
54	I	163/167 (98%)	163 (100%)	0	100	100
55	J	157/160 (98%)	157 (100%)	0	100	100
56	K	153/160 (96%)	153 (100%)	0	100	100
57	L	87/104 (84%)	87 (100%)	0	100	100
58	M	122/134 (91%)	122 (100%)	0	100	100
59	N	98/123 (80%)	98 (100%)	0	100	100
60	O	129/130 (99%)	129 (100%)	0	100	100
61	P	96/101 (95%)	96 (100%)	0	100	100
62	Q	102/121 (84%)	102 (100%)	0	100	100
63	R	114/116 (98%)	114 (100%)	0	100	100
64	S	112/122 (92%)	112 (100%)	0	100	100
65	T	126/129 (98%)	126 (100%)	0	100	100
66	U	113/117 (97%)	113 (100%)	0	100	100
67	V	90/105 (86%)	90 (100%)	0	100	100
68	W	71/71 (100%)	71 (100%)	0	100	100
69	X	112/113 (99%)	112 (100%)	0	100	100
70	Y	116/118 (98%)	116 (100%)	0	100	100
71	Z	109/112 (97%)	109 (100%)	0	100	100
72	a	64/85 (75%)	64 (100%)	0	100	100
73	b	86/102 (84%)	86 (100%)	0	100	100
74	c	72/73 (99%)	72 (100%)	0	100	100
75	d	54/58 (93%)	54 (100%)	0	100	100
76	e	47/48 (98%)	46 (98%)	1 (2%)	47	67
77	f	48/54 (89%)	48 (100%)	0	100	100
78	g	62/175 (35%)	62 (100%)	0	100	100
79	h	259/263 (98%)	258 (100%)	1 (0%)	84	91
All	All	9443/10220 (92%)	9437 (100%)	6 (0%)	100	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	AP	24[B]	LYS

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Mol	Chain	Res	Type
76	e	27	HIS
79	h	264	GLU
23	5	31[B]	GLU
23	5	31[A]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
51	F	98	HIS
57	L	81	ASN
51	F	157	ASN
55	J	132	HIS
65	T	21	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3205/3359 (95%)	549 (17%)	32 (0%)
2	3	120/121 (99%)	9 (7%)	0
3	4	157/158 (99%)	26 (16%)	2 (1%)
46	A	1685/1787 (94%)	402 (23%)	42 (2%)
All	All	5167/5425 (95%)	986 (19%)	76 (1%)

5 of 986 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	A
1	1	24	U
1	1	25	A
1	1	29	G
1	1	39	A

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	A	855	C
46	A	1523	G
46	A	876	A
46	A	1396	A
46	A	1581	G

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

6 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
1	OMC	1	2808	1	19,22,23	2.97	8 (42%)	25,31,34	1.15	2 (8%)
61	IAS	P	119	61	6,7,8	1.06	0	3,8,10	1.79	0
43	MLZ	AP	55	43	8,9,10	0.71	0	4,9,11	0.93	0
24	MLZ	6	110	24	8,9,10	0.72	0	4,9,11	0.87	0
1	OMG	1	2765	1	23,26,27	2.35	9 (39%)	32,38,41	1.89	8 (25%)
43	MLZ	AP	40	43	8,9,10	0.71	0	4,9,11	0.95	0

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
1	OMC	1	2808	1	-	3/9/27/28	0/2/2/2
61	IAS	P	119	61	-	0/7/7/8	-
43	MLZ	AP	55	43	-	2/7/8/10	-
24	MLZ	6	110	24	-	3/7/8/10	-
1	OMG	1	2765	1	-	0/9/27/28	0/3/3/3
43	MLZ	AP	40	43	-	0/7/8/10	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2765	OMG	C4-N3	6.36	1.48	1.34
1	1	2808	OMC	C2-N3	6.25	1.48	1.36
1	1	2808	OMC	C6-C5	5.88	1.48	1.35
1	1	2765	OMG	C2-N3	5.48	1.46	1.33
1	1	2808	OMC	C2-N1	4.88	1.50	1.40

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2765	OMG	C5-C4-N3	-4.96	120.49	128.39
1	1	2765	OMG	C2-N3-C4	4.48	120.02	112.30
1	1	2765	OMG	N9-C8-N7	-3.22	107.42	113.40
1	1	2808	OMC	O2-C2-N3	-3.13	117.40	122.33
1	1	2765	OMG	C2-N1-C6	-3.05	119.58	125.11

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	2808	OMC	O4'-C1'-N1-C2
1	1	2808	OMC	O4'-C1'-N1-C6
1	1	2808	OMC	C1'-C2'-O2'-CM2
24	6	110	MLZ	C-CA-CB-CG
43	AP	55	MLZ	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2808	OMC	2	0
61	P	119	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
81	3K5	1	3402	-	63,63,63	0.33	0	84,95,95	0.68	3 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
80	SPD	1	3401	-	9,9,9	0.32	0	8,8,8	0.78	0

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
81	3K5	1	3402	-	1/1/21/23	8/29/121/121	0/7/7/7
80	SPD	1	3401	-	-	3/7/7/7	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	1	3402	3K5	O-C3-C15	2.53	112.25	107.32
81	1	3402	3K5	C20-C21-C22	-2.22	107.20	111.93
81	1	3402	3K5	C4-C3-C15	-2.07	110.82	114.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
81	1	3402	3K5	C15

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	1	3402	3K5	C39-C38-O14-C34
81	1	3402	3K5	C35-C34-O14-C38
81	1	3402	3K5	O15-C38-O14-C34
81	1	3402	3K5	C6-C7-C8-C9
81	1	3402	3K5	O1-C6-C7-C8

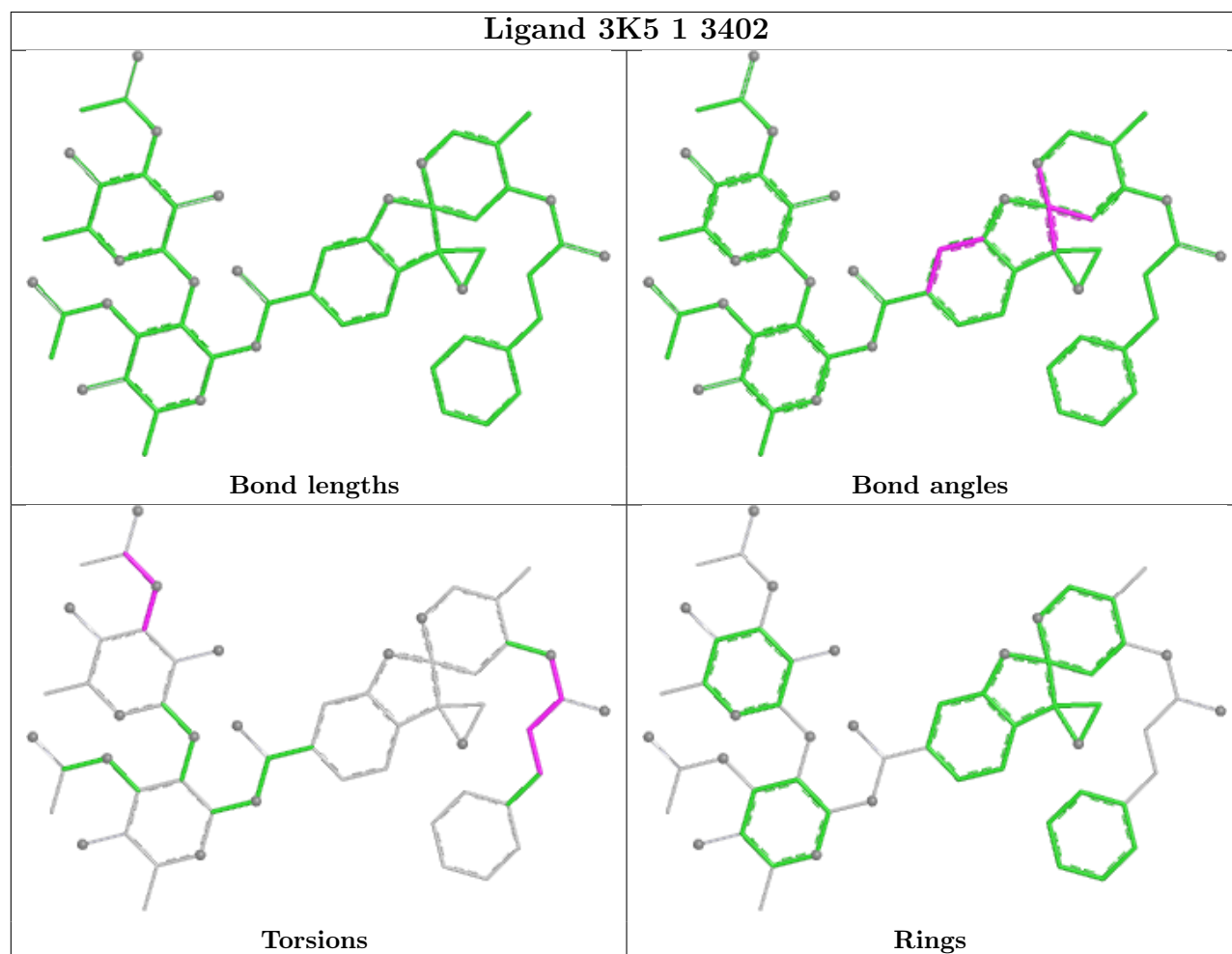
There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	1	3402	3K5	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

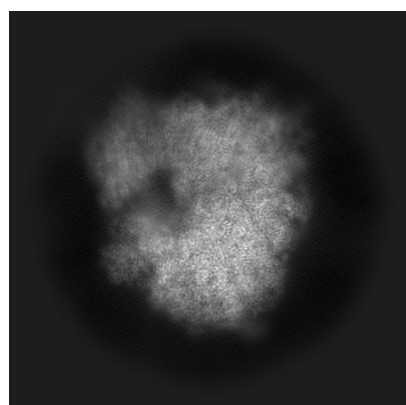
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13744. These allow visual inspection of the internal detail of the map and identification of artifacts.

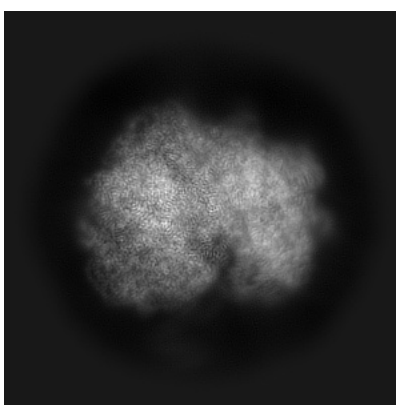
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

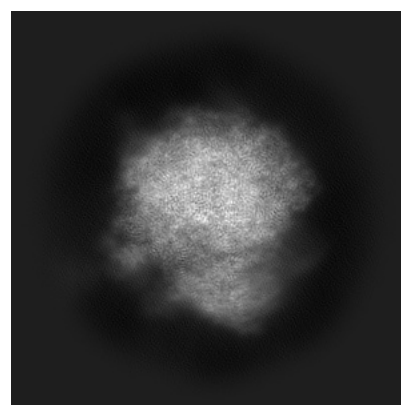
6.1.1 Primary map



X



Y

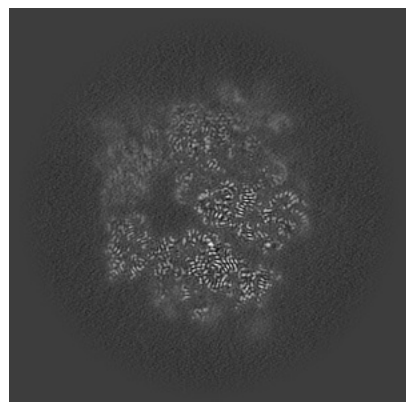


Z

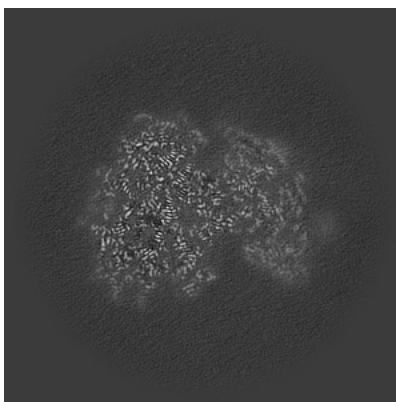
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

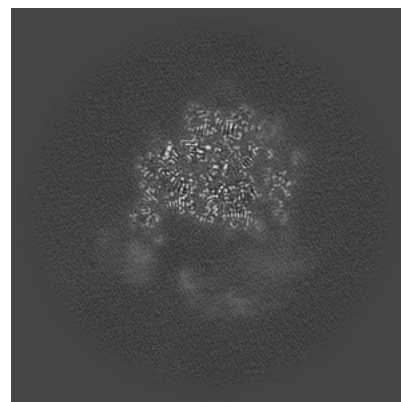
6.2.1 Primary map



X Index: 255



Y Index: 255

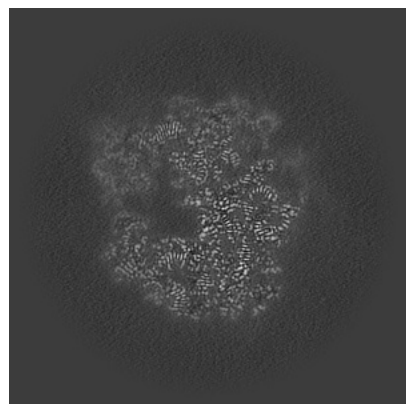


Z Index: 255

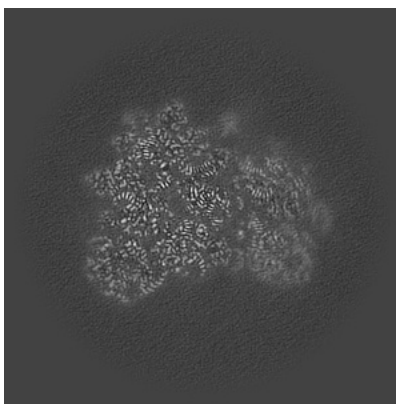
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

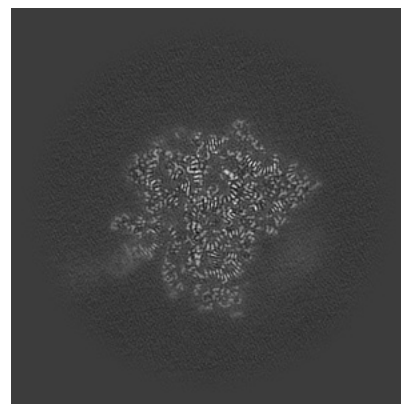
6.3.1 Primary map



X Index: 274



Y Index: 274

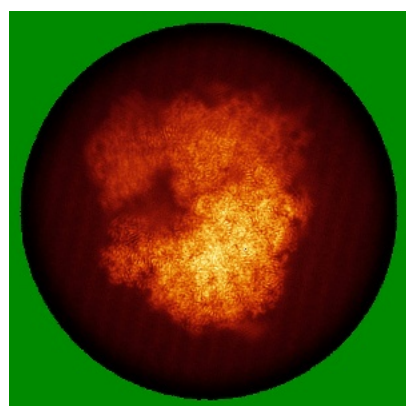


Z Index: 206

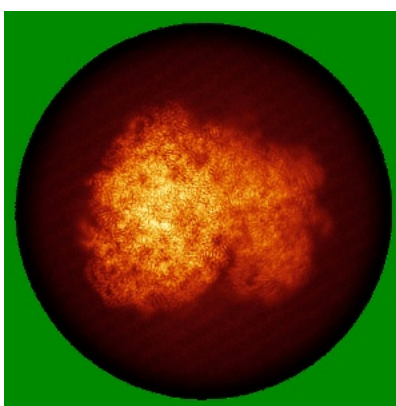
The images above show the largest variance slices of the map in three orthogonal directions.

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

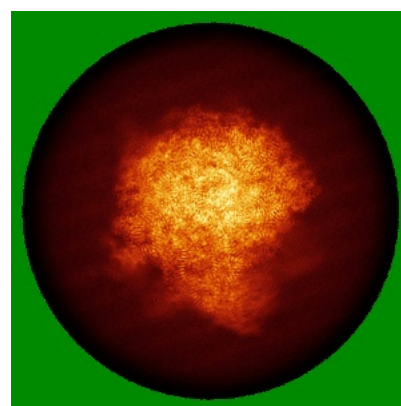
6.4.1 Primary map



X



Y

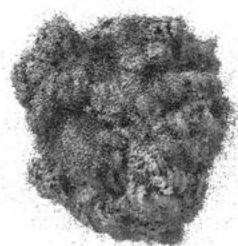


Z

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

6.5 Orthogonal surface views [i](#)

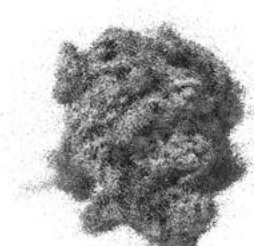
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

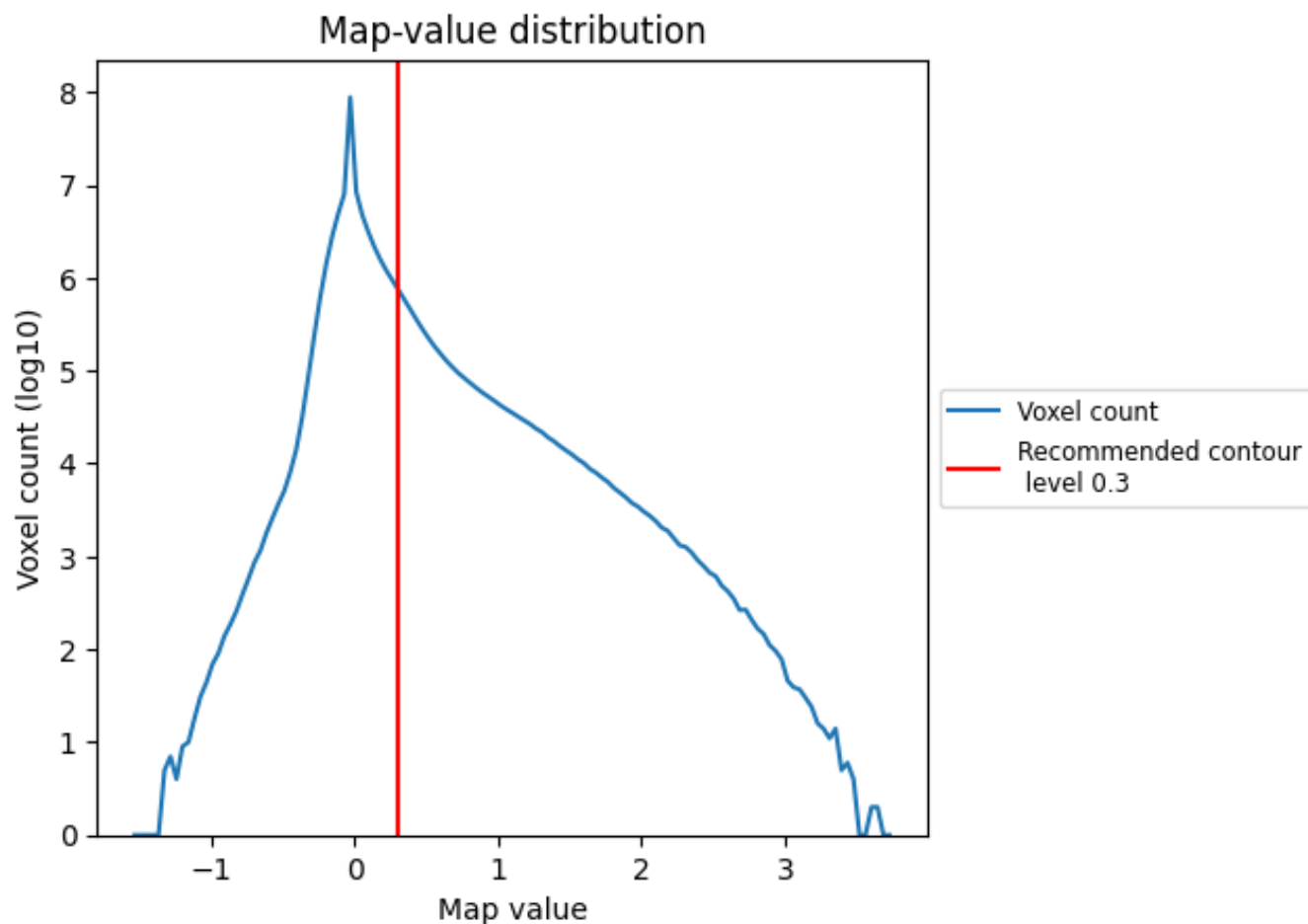
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

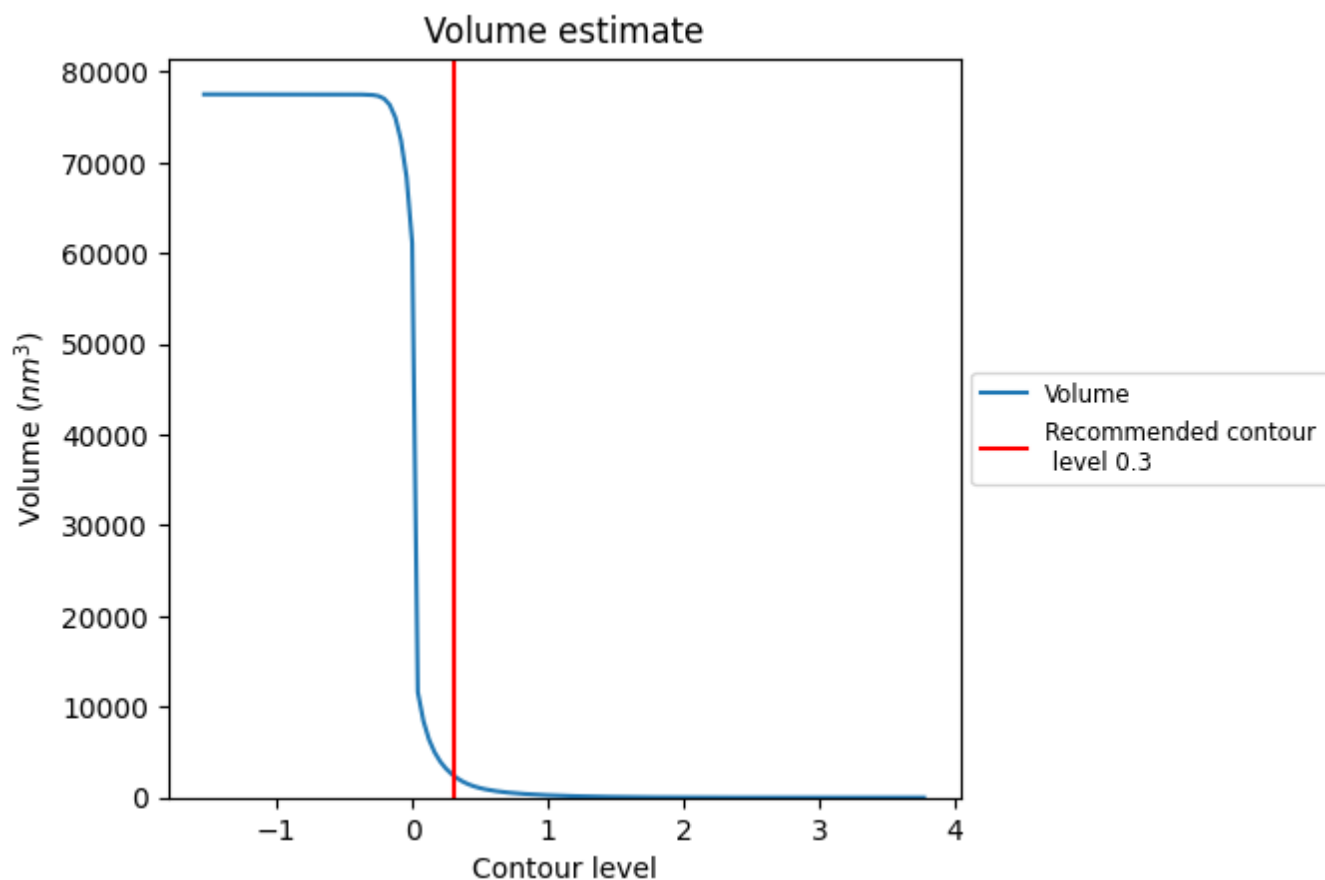
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

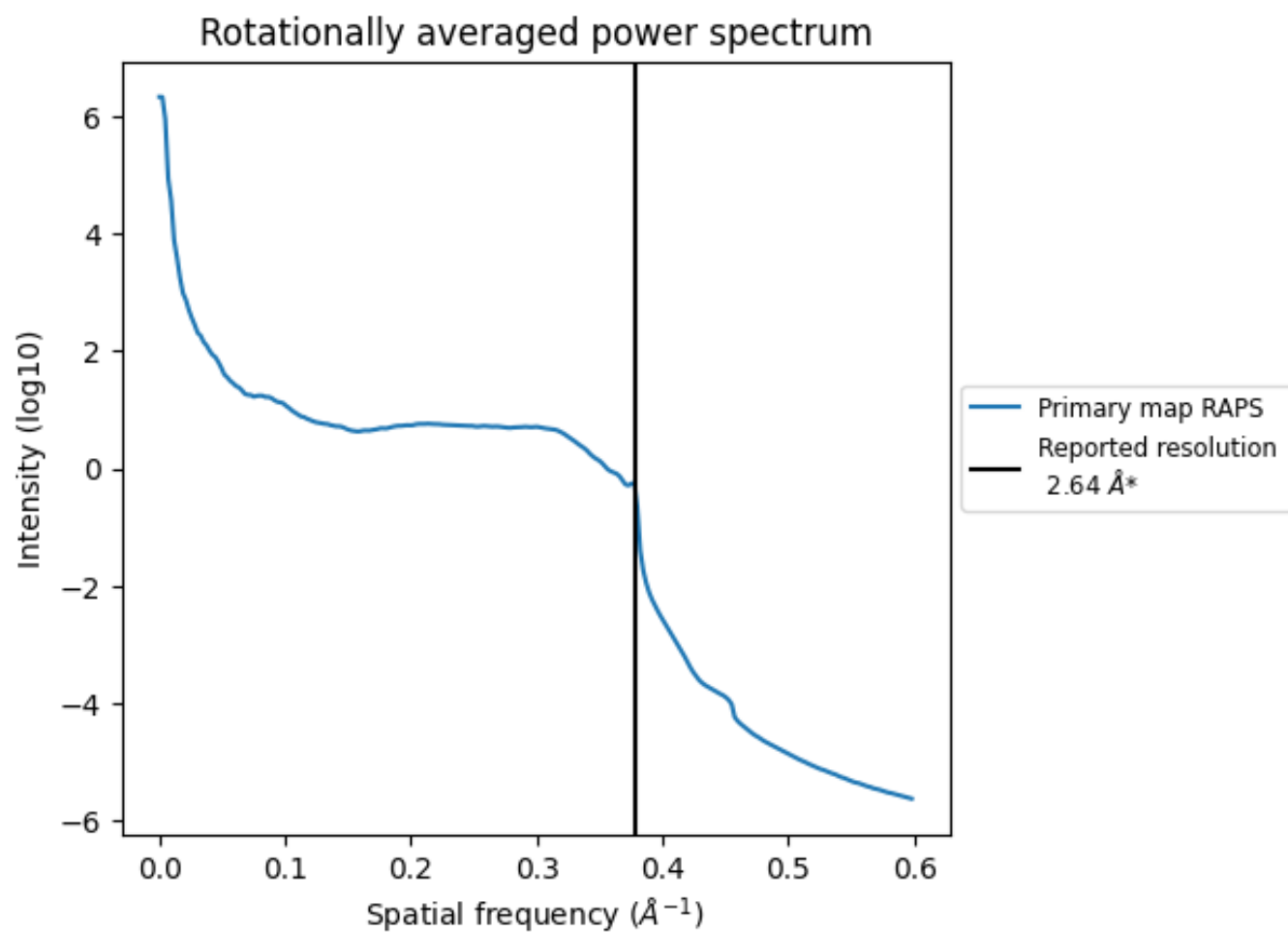
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2466 nm³; this corresponds to an approximate mass of 2228 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 ⓘ

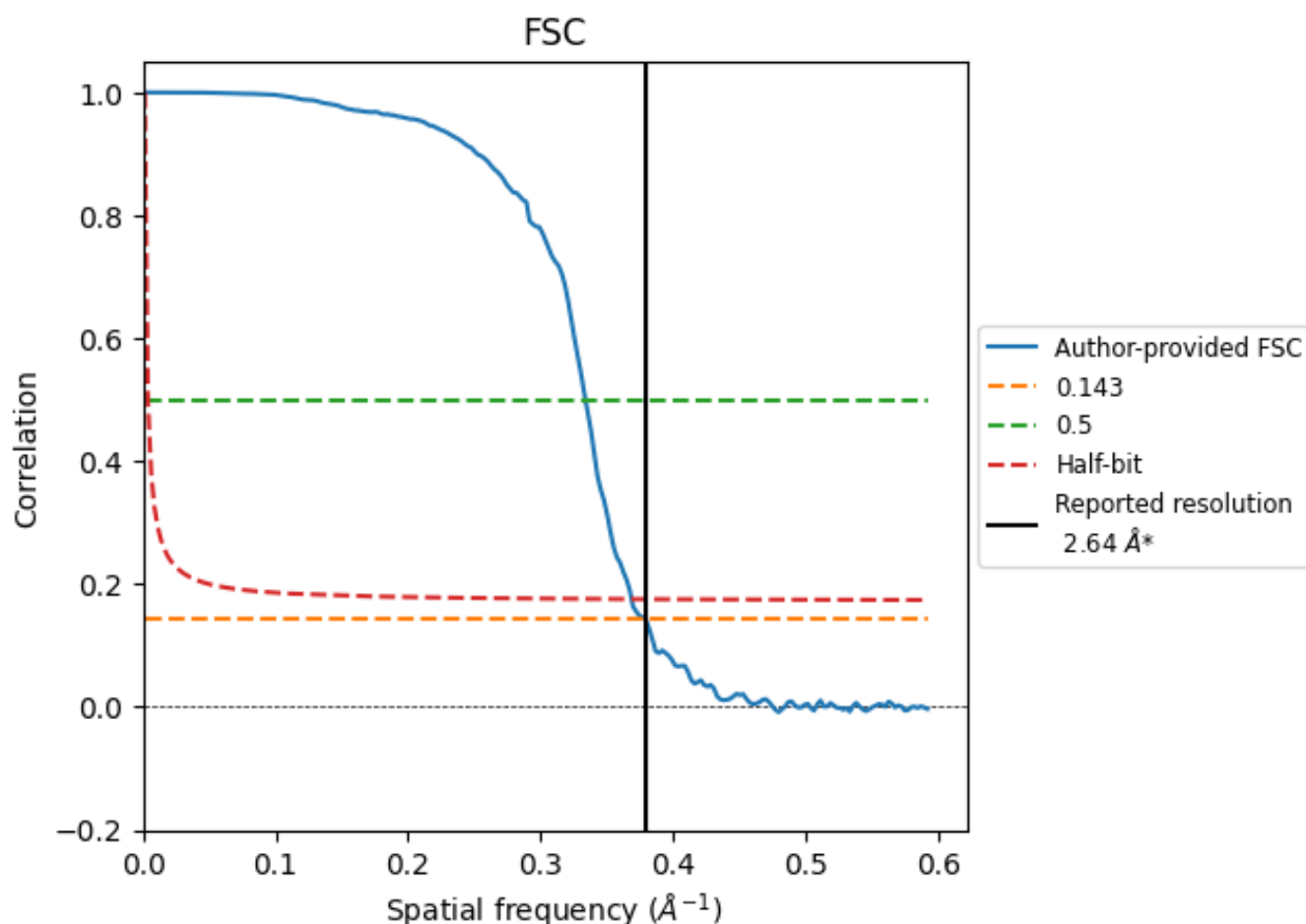


*Reported resolution corresponds to spatial frequency of 0.379 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.379 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

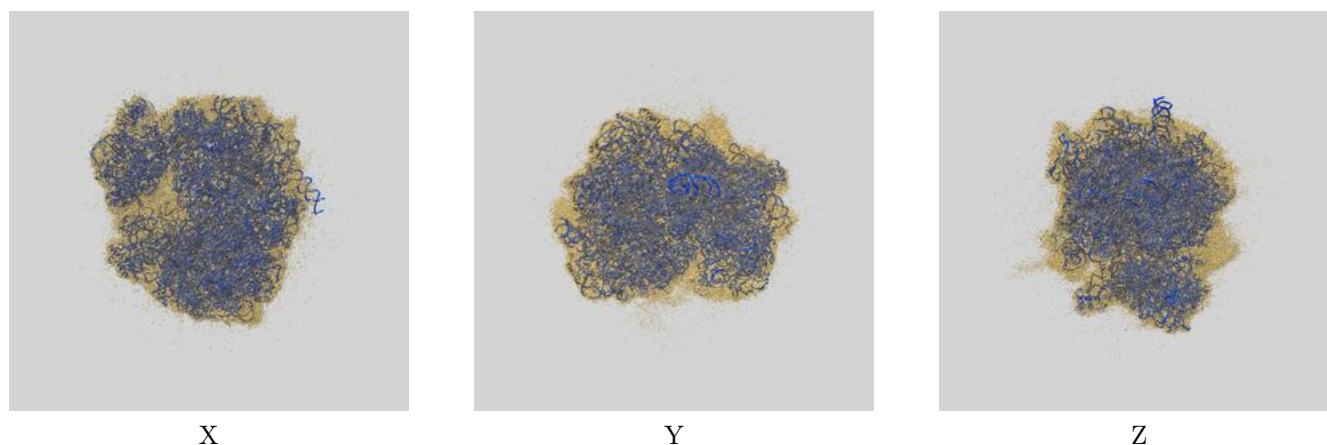
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.64	-	-
Author-provided FSC curve	2.64	2.99	2.71
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

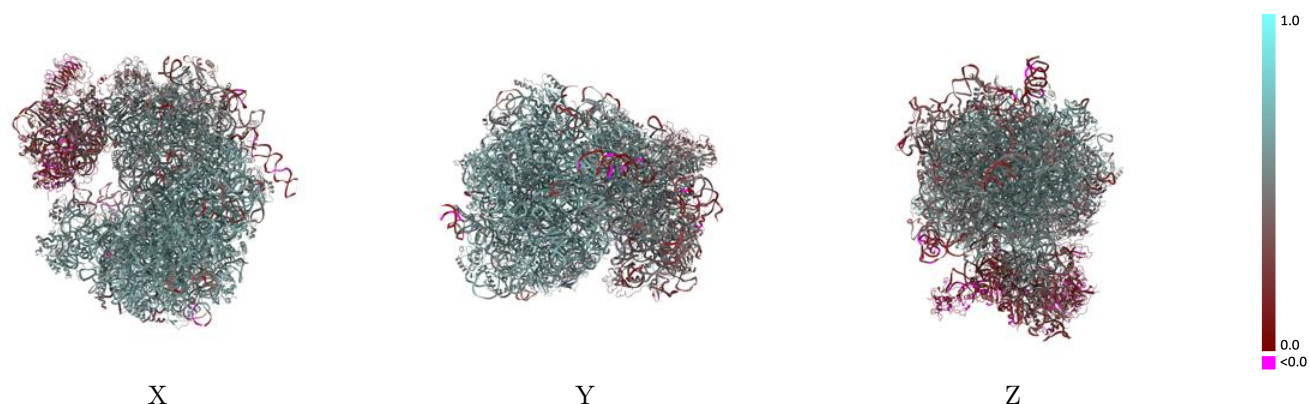
This section contains information regarding the fit between EMDB map EMD-13744 and PDB model 7Q0F. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

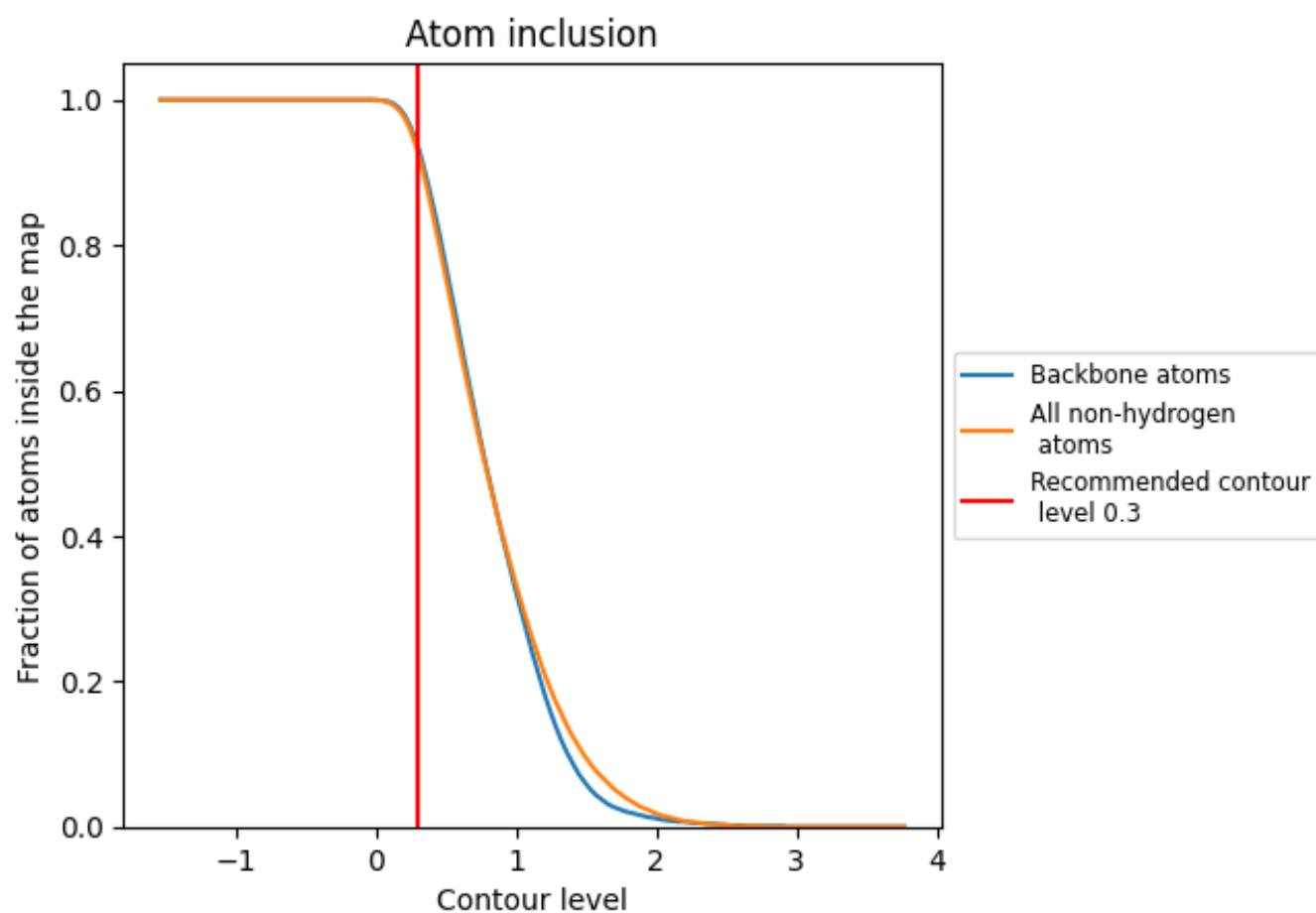


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.5210
0	 0.9830	 0.6200
1	 0.9680	 0.5830
2	 0.9750	 0.6010
3	 0.9940	 0.6120
4	 0.9870	 0.6080
5	 0.9050	 0.5050
6	 0.9770	 0.6110
7	 0.9800	 0.5980
8	 0.9750	 0.6000
9	 0.9660	 0.5910
A	 0.9370	 0.4450
AA	 0.9570	 0.5860
AB	 0.9840	 0.6260
AC	 0.9550	 0.5650
AD	 0.9830	 0.5830
AE	 0.9450	 0.5910
AF	 0.9830	 0.6110
AG	 0.9850	 0.6400
AH	 0.9650	 0.6000
AI	 0.9750	 0.5870
AJ	 0.9530	 0.5710
AK	 0.9850	 0.6310
AL	 0.9340	 0.5450
AM	 0.9860	 0.6100
AN	 0.9510	 0.5910
AO	 0.9130	 0.5560
AP	 0.9680	 0.6130
AQ	 0.9790	 0.6050
B	 0.8830	 0.4450
C	 0.9220	 0.4850
D	 0.9240	 0.5010
E	 0.6850	 0.2600
F	 0.9330	 0.4690
G	 0.6520	 0.2120



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Chain	Atom inclusion	Q-score
H	 0.8620	 0.3860
I	 0.8140	 0.4280
J	 0.9110	 0.5140
K	 0.9010	 0.4540
L	 0.6040	 0.1490
M	 0.9220	 0.5440
N	 0.2430	 0.1120
O	 0.9620	 0.5350
P	 0.9400	 0.5080
Q	 0.5490	 0.1730
R	 0.8180	 0.3210
S	 0.7360	 0.3370
T	 0.6170	 0.1970
U	 0.7690	 0.2830
V	 0.7300	 0.2890
W	 0.8960	 0.4770
X	 0.9520	 0.5410
Y	 0.9450	 0.4910
Z	 0.8830	 0.3990
a	 0.4310	 0.1500
b	 0.9570	 0.5350
c	 0.9180	 0.4730
d	 0.5590	 0.2020
e	 0.8380	 0.2810
f	 0.8400	 0.3820
g	 0.3040	 0.1310
h	 0.5440	 0.2200
i	 0.6460	 0.2820
j	 0.9950	 0.6360
k	 0.9800	 0.6180
l	 0.9680	 0.5950
m	 0.9550	 0.5620
n	 0.9470	 0.5650
o	 0.9490	 0.5920
p	 0.9320	 0.5640
q	 0.9530	 0.5800
r	 0.9700	 0.6030
s	 0.9270	 0.5300
t	 0.9490	 0.5850
u	 0.9710	 0.5900
v	 0.9950	 0.6400
w	 0.9850	 0.6210

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Chain	Atom inclusion	Q-score
x	 0.9890	 0.6220
y	 0.9920	 0.6180
z	 0.9630	 0.5840