



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:25 AM UTC

PDB ID : 9OFV / pdb_00009ofv
EMDB ID : EMD-70444
Title : Consensus reconstruction of the eukaryotic Ribosome-associated Quality Control complex
Authors : Li, W.; Cahoon, T.; Shen, P.S.
Deposited on : 2025-04-30
Resolution : 3.16 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

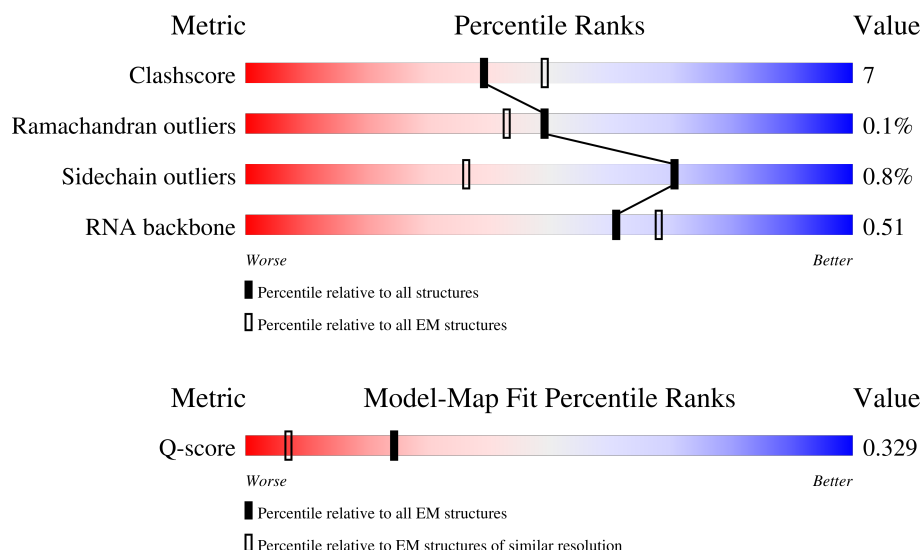
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 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	14474 (2.66 - 3.66)

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

Mol	Chain	Length	Quality of chain
1	A	835	
1	B	835	
1	C	835	

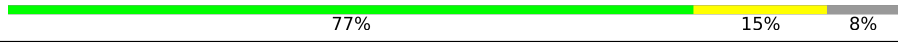
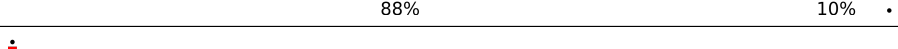
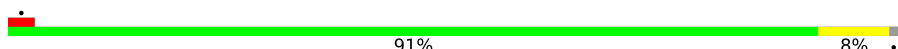
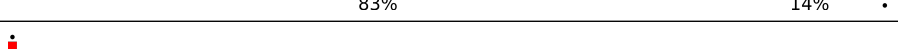
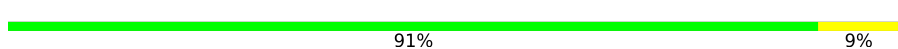
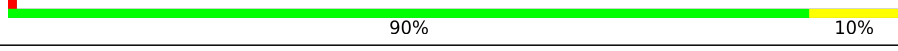
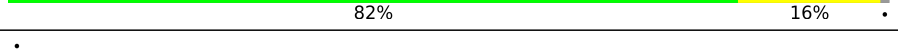
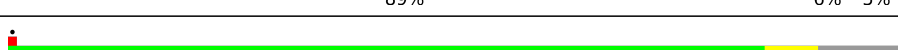
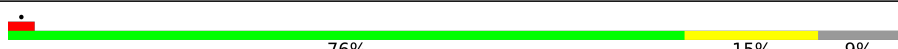
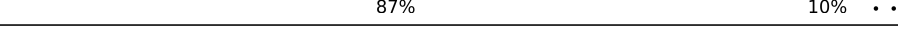
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Mol	Chain	Length	Quality of chain
1	D	835	
1	E	835	
1	F	835	
2	H	76	
2	J	76	
2	K	76	
3	G	580	
4	3	184	
5	4	186	
6	5	189	
7	6	172	
8	7	160	
9	8	121	
10	I	137	
11	9	155	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	

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Mol	Chain	Length	Quality of chain
22	V	100	
23	W	88	
24	Y	51	
25	Z	128	
26	b	106	
27	c	92	
28	d	25	
29	f	3395	
30	h	121	
31	i	158	
32	j	254	
33	k	387	
34	l	362	
35	m	297	
36	n	176	
37	o	244	
38	p	256	
39	q	191	
40	r	221	
41	s	174	
42	t	199	
43	u	138	
44	a	1038	
45	e	1562	
46	g	245	

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Mol	Chain	Length	Quality of chain
47	x	76	
47	y	76	
48	z	165	
49	0	312	
50	1	17	
51	w	217	
52	X	78	
53	v	753	
54	2	76	
55	a0	199	
56	b0	142	

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
57	ATP	A	901	-	-	X	-
57	ATP	C	1001	-	-	X	-
57	ATP	C	1003	-	-	X	-
57	ATP	D	901	-	-	X	-
57	ATP	D	902	-	-	X	-
57	ATP	E	902	-	-	X	-
57	ATP	F	901	-	-	X	-
58	ADP	E	901	-	-	X	-

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 183852 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 protein called Cell division control protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	547	Total	C	N	O	S	0	0
			4206	2641	732	814	19		
1	B	654	Total	C	N	O	S	0	0
			5049	3184	880	964	21		
1	C	492	Total	C	N	O	S	0	0
			3759	2363	656	723	17		
1	D	489	Total	C	N	O	S	0	0
			3747	2354	659	717	17		
1	E	496	Total	C	N	O	S	0	0
			3786	2380	660	729	17		
1	F	533	Total	C	N	O	S	0	0
			4093	2567	720	787	19		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	588	GLN	GLU	conflict	UNP P25694
B	588	GLN	GLU	conflict	UNP P25694
C	588	GLN	GLU	conflict	UNP P25694
D	588	GLN	GLU	conflict	UNP P25694
E	588	GLN	GLU	conflict	UNP P25694
F	588	GLN	GLU	conflict	UNP P25694

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	48	Total	C	N	O		0	0
			376	237	63	76			
2	H	76	Total	C	N	O	S	0	0
			601	375	105	120	1		
2	J	76	Total	C	N	O	S	0	0
			601	375	105	120	1		

- Molecule 3 is a protein called Nuclear protein localization protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	468	Total	C	N	O	S	0	0
			3762	2381	628	732	21		

- Molecule 4 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 5 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 6 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 7 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 8 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 9 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 10 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 11 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	9	63	Total	C	N	O	S	0	0
			518	333	102	82	1		

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 15 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 24 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 25 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 26 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 27 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 28 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 29 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	f	3216	Total	C	N	O	P	1	0
			68802	30732	12391	22462	3217		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	?	-	G	deletion	GB 1262303
f	1956	U	-	insertion	GB 1262303
f	?	-	A	deletion	GB 1262303
f	2255	U	-	insertion	GB 1262303
f	?	-	G	deletion	GB 1262303

- Molecule 30 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 31 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 32 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 33 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	k	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 34 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 35 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 36 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	167	Total	C	N	O		0	0
			1307	843	234	230			

- Molecule 37 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 38 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 39 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	q	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 40 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 41 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 42 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 43 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 44 is a protein called Ribosome quality control complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	a	848	Total	C	N	O	S	0	0
			6573	4191	1139	1226	17		

- Molecule 45 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	e	1530	Total	C	N	O	S	0	0
			11556	7383	1946	2189	38		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

- Molecule 47 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	74	Total	C	N	O	P	0	0
			1579	702	278	525	74		
47	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

- Molecule 48 is a protein called Large ribosomal subunit protein uL11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	z	148	Total	C	N	O		0	0
			728	432	148	148			

- Molecule 49 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 50 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	17	Total	C	N	O		0	0
			85	51	17	17			

- Molecule 51 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 52 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	X	76	Total	C	N	O		0	0
			608	388	114	106			

- Molecule 53 is a protein called Ribosome quality control complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	531	Total	C	N	O	S	0	0
			4376	2824	729	807	16		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	724	THR	-	expression tag	UNP Q05468
v	725	SER	-	expression tag	UNP Q05468
v	726	GLY	-	expression tag	UNP Q05468
v	727	SER	-	expression tag	UNP Q05468
v	728	PRO	-	expression tag	UNP Q05468
v	729	GLY	-	expression tag	UNP Q05468
v	730	ASP	-	expression tag	UNP Q05468
v	731	TYR	-	expression tag	UNP Q05468
v	732	LYS	-	expression tag	UNP Q05468
v	733	ASP	-	expression tag	UNP Q05468
v	734	ASP	-	expression tag	UNP Q05468
v	735	ASP	-	expression tag	UNP Q05468
v	736	ASP	-	expression tag	UNP Q05468
v	737	LYS	-	expression tag	UNP Q05468
v	738	ASP	-	expression tag	UNP Q05468
v	739	TYR	-	expression tag	UNP Q05468
v	740	LYS	-	expression tag	UNP Q05468
v	741	ASP	-	expression tag	UNP Q05468
v	742	ASP	-	expression tag	UNP Q05468
v	743	ASP	-	expression tag	UNP Q05468
v	744	ASP	-	expression tag	UNP Q05468
v	745	LYS	-	expression tag	UNP Q05468
v	746	ASP	-	expression tag	UNP Q05468
v	747	TYR	-	expression tag	UNP Q05468
v	748	LYS	-	expression tag	UNP Q05468

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Chain	Residue	Modelled	Actual	Comment	Reference
v	749	ASP	-	expression tag	UNP Q05468
v	750	ASP	-	expression tag	UNP Q05468
v	751	ASP	-	expression tag	UNP Q05468
v	752	ASP	-	expression tag	UNP Q05468
v	753	LYS	-	expression tag	UNP Q05468

- Molecule 54 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	76	Total	C	N	O	S	0	0
			602	378	105	118	1		

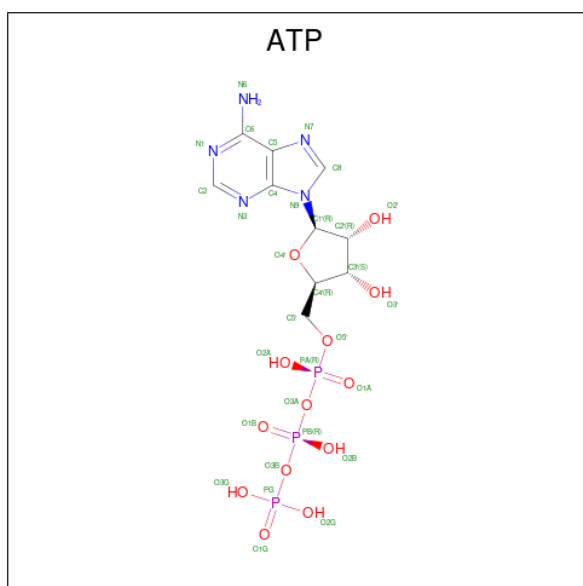
- Molecule 55 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	a0	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 56 is a protein called 60S ribosomal protein L25.

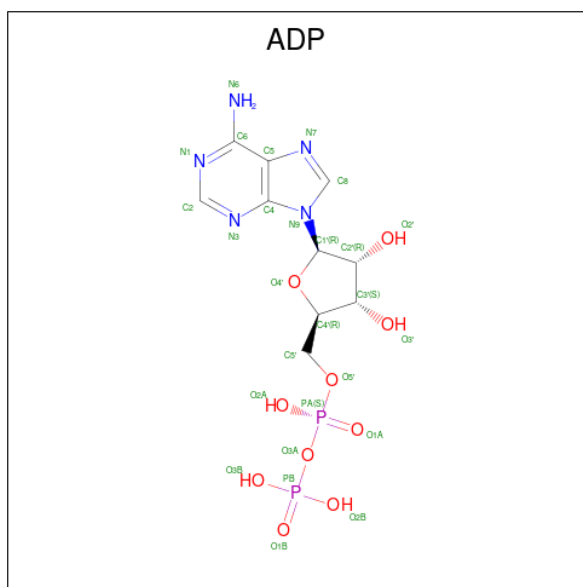
Mol	Chain	Residues	Atoms					AltConf	Trace
56	b0	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 57 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
57	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
57	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 58 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
58	E	1	Total	C	N	O	P	0
			27	10	5	10	2	

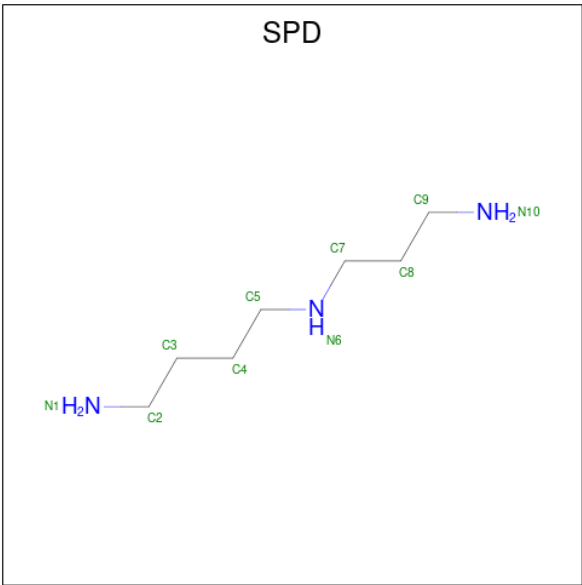
- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	G	2	Total 2	Zn 2	0
59	T	1	Total 1	Zn 1	0
59	W	1	Total 1	Zn 1	0
59	Z	1	Total 1	Zn 1	0
59	b	1	Total 1	Zn 1	0
59	c	1	Total 1	Zn 1	0

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total 1	Mg 1	0
60	5	1	Total 1	Mg 1	0
60	I	1	Total 1	Mg 1	0
60	R	1	Total 1	Mg 1	0
60	T	1	Total 1	Mg 1	0
60	f	3	Total 3	Mg 3	0
60	h	1	Total 1	Mg 1	0
60	j	2	Total 2	Mg 2	0
60	k	1	Total 1	Mg 1	0

- Molecule 61 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).

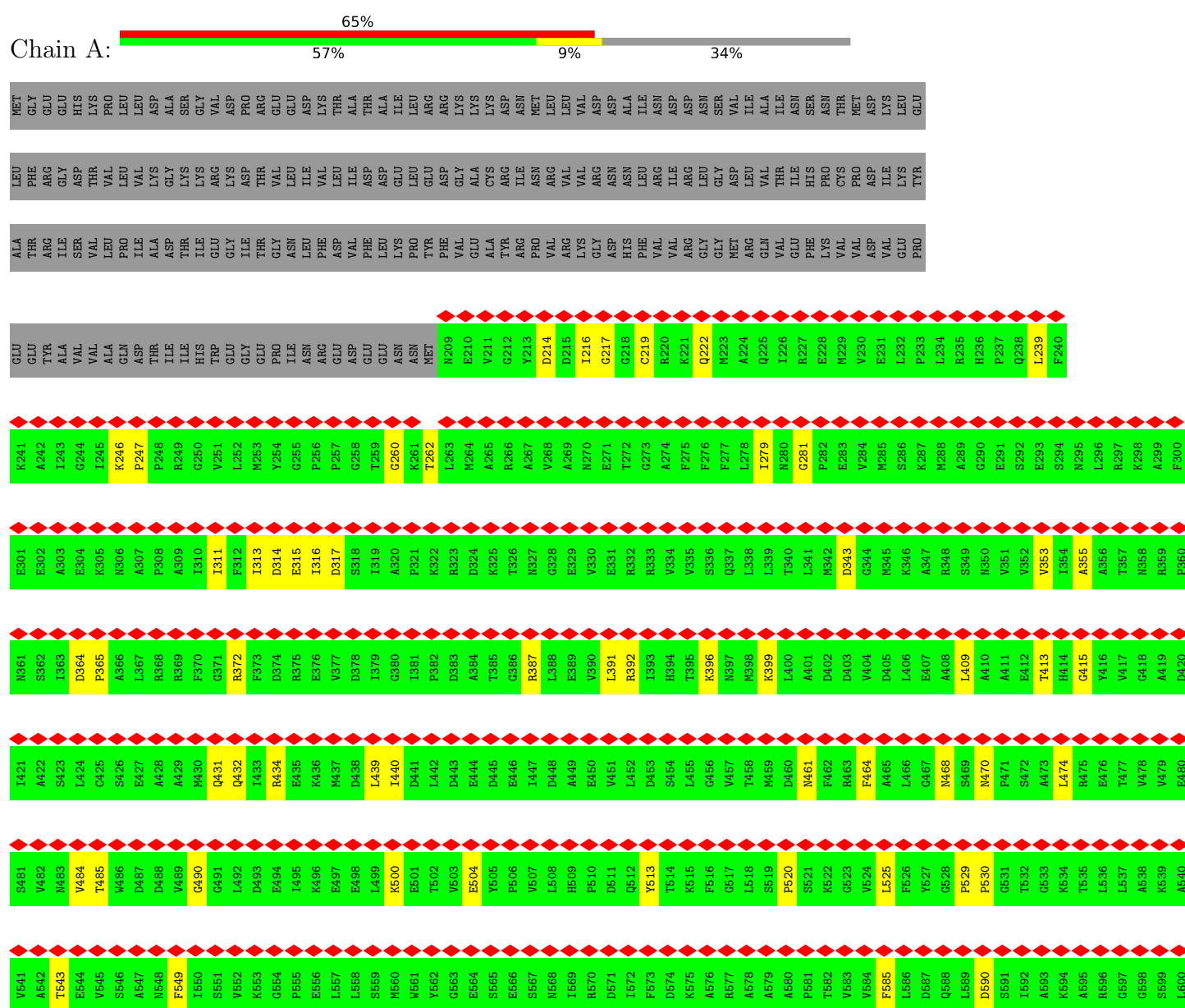


Mol	Chain	Residues	Atoms			AltConf
61	f	1	Total	C	N	0
			10	7	3	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Cell division control protein 48



V541	G601	N661	ALA	SER
A542	D602	A662	GLY	GLN
T543	A603	R663	GLY	GLU
E544	G604	L664	VAL	LYS
V545	G605	S665	VAL	ALA
S546	A606	I666	VAL	SER
A547	S607	L667	GLY	ARG
N548	D608	N668	GLY	GLN
F549	R609	A669	ASP	PHE
I550	V610	Q670	VAL	SER
S551	V611	L671	VAL	ASN
V552	N612	R672	THR	PHE
K553	Q613	K673	ASP	ASN
G554	L614	T674	GLY	ASP
P555	L615	P675	ALA	ALA
E556	T616	L676	LYS	PRO
L557	E617	E677	ALA	LEU
L558	M618	P678	GLN	THR
S559	D619	G679	GLU	THR
M560	G620	L680	PRO	ALA
W561	M621	E681	GLY	THR
Y562	N622	L682	VAL	ASP
G563	A623	T683	ASP	ASN
E564	K624	A684	VAL	PRO
S565	K625	I685	LYS	ASN
E566	N626	A686	ASP	ASN
S567	V627	K687	THR	SER
N568	F628	A688	LYS	ALA
I569	E629	T689	GLU	PRO
R570	I630	Q690	LEU	GLY
D571	G631	G691	VAL	ALA
I572	A632	F692	ASP	GLY
F573	T633	S693	ALA	ALA
D574	N634	G694	LYS	PHE
K575	R635	A695	THR	GLY
A576	P636	D696	ALA	SER
R577	D637	L697	LYS	ASN
A578	Q638	L698	ARG	ALA
A579	I639	Y699	VAL	GLU
A580	D640	I700	SER	ASP
P581	P641	V701	ASP	ASP
T582	A642	Q702	GLU	LEU
V583	I643	R703	TYR	TYR
V584	L644	A704	ARG	ARG
F585	R645	A705	TYR	TYR
L586	P646	K706	GLU	GLU
D587	G647	Y707	ALA	ALA
Q588	R648	A708	LYS	GLN
L589	L649	I709	SER	HIS
D590	D650	K710	ASP	GLN
S591	Q651	D711	ASP	GLU
I592	L652	S712	TYR	HIS
A593	I653	I713	SER	GLU
K594	Y654	GLU	ALA	ALA
A595	V655	ALA	GLY	ALA
R596	P656	HIS	THR	THR
G597	L657	ARG	ARG	ARG
Q598	P658	GLN	GLN	GLN
S599	D659	HIS	GLU	GLU
L600	E660			

● Molecule 1: Cell division control protein 48



MET	LEU	ALA	GLU	K241	E301	N361	I421	S481
GLY	PHE	THR	GLY	A242	E302	S362	A422	V482
GLU	ARG	ILE	TYR	I243	A303	I363	S423	N483
HIS	ASP	SER	VAL	G244	E304	D364	L424	V484
LYS	THR	VAL	VAL	I245	K305	P365	C425	T485
PRO	LEU	LEU	PRO	K246	N306	A366	S426	W486
LEU	VAL	PRO	GLN	P247	A307	L367	E427	D487
LEU	VAL	ASP	ASP	R248	P308	R368	A428	D488
ALA	GLY	ALA	THR	R249	A309	R369	A429	V489
LYS	LYS	LYS	ILE	G250	I310	F370	M430	G490
GLY	ARG	GLY	TRP	V251	I311	G371	Q431	G491
VAL	VAL	THR	GLY	L252	F312	R372	Q432	L492
ASP	ASP	THR	GLY	M253	I313	F373	T433	D493
PRO	THR	THR	PRO	Y254	D314	D374	R434	E494
GLY	GLY	ASN	ILE	G255	E315	R375	E435	I495
ASP	LEU	LEU	ASN	P256	I316	E376	K436	K496
ASP	ASP	PHE	ARG	P257	D317	V377	M437	E497
THR	THR	VAL	ASP	G258	S318	D378	D438	E498
ALA	ASP	PHE	GLY	T259	I319	I379	LEU	L499
ILE	GLY	LEU	ASN	G260	A320	G380	ILE	K500
LEU	LEU	PRO	GLU	K261	P321	I381	ASP	E501
ARG	ARG	TYR	TYR	T262	K322	P382	ASP	T502
LYS	LYS	VAL	VAL	L263	R323	D383	ASP	V503
ALA	ALA	GLY	ALA	M264	D324	A384	GLU	E504
LYS	LYS	ALA	ALA	A265	K325	T385	GLU	I505
ASP	ASP	TYR	TYR	R266	T326	G386	ASP	P506
ILE	ILE	ARG	ARG	A267	N327	R387	ALA	V507
ASN	ASN	PRO	VAL	V268	G328	L388	VAL	L508
THR	LEU	VAL	GLY	A269	E329	E389	L452	H509
LEU	VAL	VAL	GLY	N270	V330	V390	D453	P510
VAL	ARG	ARG	ASP	E271	E331	L391	S454	D511
ASP	ASP	ASN	ASP	T272	R332	I392	L455	Q512
ILE	ILE	PHE	LEU	G273	R333	I393	G456	Y513
ASN	ASN	ILE	ILE	A274	V334	H394	V457	T514
THR	THR	VAL	VAL	F275	V335	T395	T458	K515
ALA	ASP	ARG	ARG	F276	S336	K396	N459	F516
ASN	ASN	GLY	GLY	F277	Q337	N397	D460	G517
VAL	VAL	MET	MET	L278	L338	M398	A461	L518
ILE	ILE	LEU	ARG	I279	L339	K399	F462	S519
ALA	ALA	VAL	GLN	G280	T340	L400	R463	P520
ILE	ILE	THR	VAL	G281	L341	A401	F464	S521
ASN	ASN	ILE	PHE	E282	M342	D402	A465	S521
SER	SER	PRO	LYS	E283	D343	D403	L466	K522
ASP	ASP	VAL	VAL	V284	G344	V404	G467	G523
LYS	LYS	ASP	ASP	M285	M345	D405	M468	V524
LEU	LEU	ILE	VAL	S286	K346	L406	M469	L525
TYR	TYR	LYS	LYS	K287	A347	E407	S469	F526
		GLU	GLU	M288	R348	A408	M470	Y527
		ASP	ASP	A289	S349	L409	P471	G528
		ILE	ILE	G290	N350	A410	S472	P529
		ASP	ASP	E291	V351	A411	A473	P530
		LYS	LYS	S292	V352	E412	L474	G531
		THR	THR	E293	V353	T413	R475	T532
		VAL	VAL	S294	I354	H414	E476	G533
		ASP	ASP	N295	A355	G415	T477	K534
		LYS	LYS	L296	A356	Y416	V478	T535
		GLU	GLU	R297	T357	V417	V479	L536
		PRO	PRO	K298	N358	G418	E480	L537
				A299	R359	A419		A538
				F300	P360	D420		K539
								A540



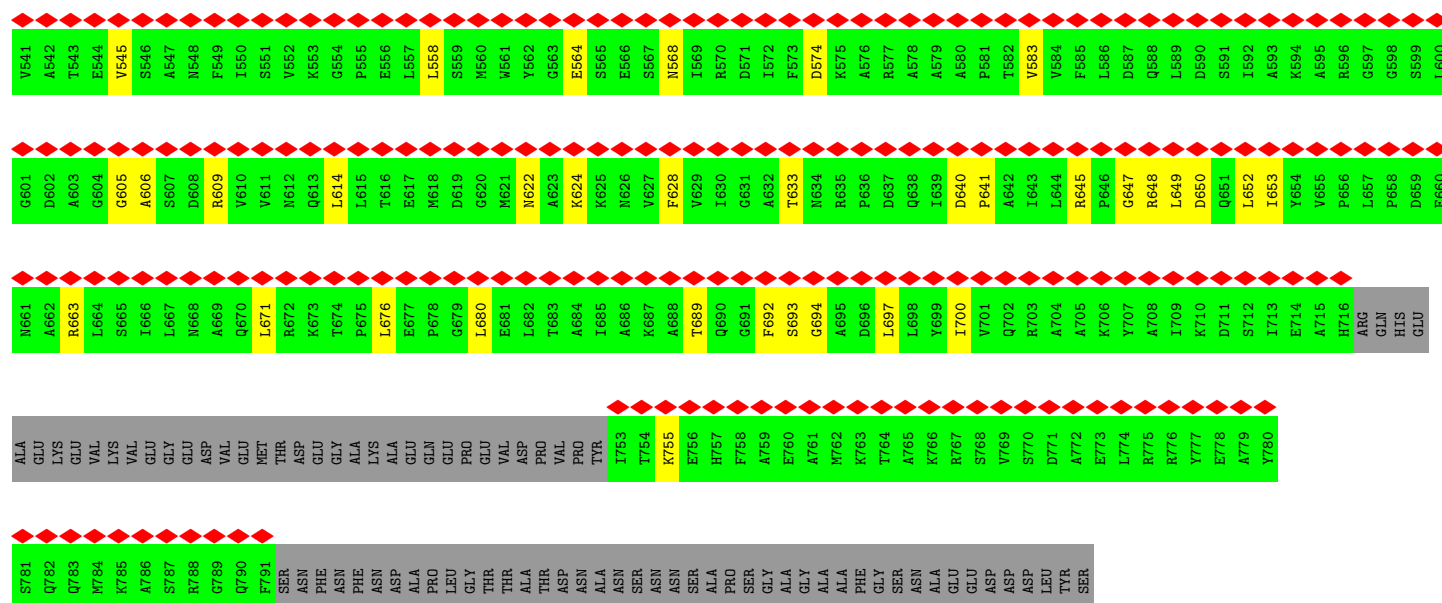
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T543	A603	R663	GLU	MET
E544	G604	L664	VAL	LYS
V545	S665	S665	LYS	ALA
S546	A606	I666	VAL	SER
A547	S607	L667	GLY	ARG
N548	D608	N668	GLU	GLN
F549	R609	A669	ASP	PHE
I550	V610	G670	VAL	SER
S551	V611	L671	MET	ASN
V552	N612	R672	THR	PHE
K553	Q613	T673	ASP	ASN
G554	L614	K674	GLU	ASN
P555	L615	P675	ALA	ALA
E556	T616	L676	LYS	PRO
L557	T617	L677	LEU	LEU
L558	M618	P678	GLY	THR
S559	D619	G679	THR	THR
M560	G620	L680	ALA	PRO
W561	M621	E681	GLU	THR
Y562	N622	L682	ASP	ASP
G563	A623	T683	PRO	ALA
E564	K624	A684	VAL	ASN
S565	K625	I685	SER	SER
E566	N626	A686	ASN	ASN
S567	V627	K687	THR	THR
N568	F628	A688	ALA	LYS
I569	V629	T689	GLU	PRO
R570	I630	Q690	PHE	SER
D571	G631	G691	GLY	GLY
I572	A632	F692	ALA	ALA
F573	T633	S693	MET	ALA
D574	N634	G694	LYS	PHE
K575	R635	A695	THR	GLY
A576	P636	D696	ALA	SER
R577	D637	L697	ARG	ASN
A578	Q638	L698	SER	ALA
A579	I639	Y699	VAL	GLU
A580	D640	I700	ASP	ASP
P581	P641	V701	ALA	ASP
T582	A642	Q702	GLU	LEU
V583	I643	R703	LEU	TYR
V584	L644	A704	ARG	ARG
F585	R645	A705	THR	THR
L586	P646	K706	ALA	ASP
D587	G647	Y707	GLU	GLY
Q588	R648	A708	TYR	TYR
L589	L649	I709	ALA	SER
D590	D650	K710	ASP	ASP
S591	Q651	D711	THR	THR
I592	L652	S712	ALA	ALA
A593	I653	I713	LYS	LYS
K594	Y654	E714	ARG	ARG
A595	V655	A715	THR	THR
R596	P656	H716	ASP	ASP
G597	L657	R717	LYS	LYS
G598	P658	Q718	LEU	LEU
S599	D659	HIS	GLU	GLU
L600	E660	GLU	TYR	TYR

• Molecule 1: Cell division control protein 48

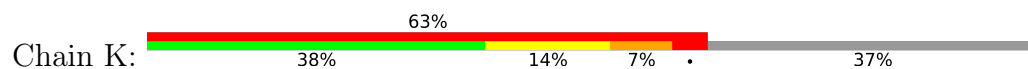


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GLY	PHE	THR	GLU	A242	E302	S362	A422	V482
GLU	ARG	ILE	TYR	I243	A303	I363	A423	N483
HIS	GLY	ILE	ALA	G244	E304	D364	L424	V484
LYS	ASP	SER	VAL	I245	K305	P365	C425	T485
PRO	THR	VAL	LEU	K246	N306	A366	S426	K486
LEU	LEU	PRO	GLN	P247	A307	L367	E427	D487
LEU	VAL	ALA	ALA	P248	P308	R368	A428	D488
LEU	VAL	ASP	ASP	R249	A309	R369	A429	V489
LEU	LYS	LYS	ILE	G250	I310	F370	M430	G490
GLY	ARG	ILE	TRP	V251	I311	G371	Q431	G491
VAL	ASP	GLY	GLY	L252	F312	R372	Q432	L492
PRO	PRO	THR	GLU	M253	I313	F373	I433	D493
GLU	VAL	THR	PRO	Y254	D314	D374	R434	E494
ASP	LEU	ASN	ILE	G255	E315	R375	E435	I495
ASP	TLE	LEU	ASN	P256	I316	R376	E436	K496
THR	VAL	PHE	ARG	G257	D317	E376	K436	E497
THR	ILE	VAL	GLU	T258	S318	V377	M437	E498
ALA	ASP	PHE	ASP	G260	I319	I378	LEU	L499
GLU	GLU	LEU	GLU	G261	A320	G380	ASP	K500
ILE	ALA	LYS	ASN	T262	P321	I381	LEU	E501
LEU	LEU	PRO	GLU	L263	K322	P382	ASP	T502
ARG	ARG	PHE	TYR	M264	R323	D383	GLU	V503
LYS	LYS	GLU	VAL	A265	K324	A384	ASP	E504
LYS	LYS	ALA	ALA	G266	D325	T385	ILE	Y505
ASP	ARG	TYR	TYR	R267	T326	G386	ASP	P506
ASP	ILE	ARG	ARG	A267	N327	R387	A449	V507
MET	ASN	VAL	ASN	V268	G328	L388	E450	L508
LEU	VAL	VAL	VAL	A269	E329	E389	V451	H509
VAL	VAL	ARG	VAL	N270	V330	V390	L452	P510
VAL	ARG	LYS	LYS	E271	E331	L391	D453	D511
ASP	ASP	GLY	GLY	T272	R332	R392	S454	Q512
ASP	ASP	ASN	ASN	G273	R333	I393	L455	Y513
ILE	ILE	LEU	PHE	A274	V334	H394	G456	T514
ASN	ASN	ARG	VAL	F275	V335	T395	V457	K515
THR	THR	TLE	ARG	F276	S336	K396	T458	F516
VAL	VAL	ASP	VAL	F277	Q337	N397	M459	G517
ILE	ILE	VAL	ARG	L278	L338	M398	D460	L518
ALA	ALA	LEU	GLN	I279	L339	K399	M461	S519
ASP	ASP	VAL	VAL	N280	T340	L400	F462	P520
ASP	ASP	THR	VAL	G281	L341	A401	R463	S521
ASN	ASN	ILE	GLU	P282	M342	D402	F464	K522
TYR	ASN	PRO	PHE	E283	D343	D403	A465	G523
ARG	ASN	VAL	LYS	M284	G344	V404	L466	V524
ARG	PRO	ASP	VAL	M285	M345	D405	G467	L525
ASP	ASP	ILE	ASP	S286	K346	L406	M468	F526
LYS	LYS	LYS	VAL	K287	A347	E407	S469	Y527
LEU	LEU	GLU	GLU	M288	R348	A408	M470	G528
TYR	TYR	THR	THR	A289	S349	L409	P471	P529
ASP	ASP	PRO	VAL	G290	N350	A410	S472	P530
LYS	LYS	ASP	VAL	E291	V351	A411	A473	G531
LEU	LEU	ILE	ASP	S292	V352	E412	L474	T532
LEU	LEU	LYS	VAL	E293	V353	T413	R475	G533
TYR	TYR	GLU	GLU	S294	I354	H414	E476	K534
		PRO	PRO	L296	A355	G415	T477	T535
		ASP	ASP	R297	A356	Y416	V478	L536
		GLU	GLU	A299	T357	V417	V479	L537
		PRO	PRO	F300	N358	G418	E480	A540
					R359	A419		K539
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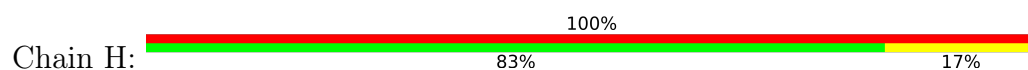




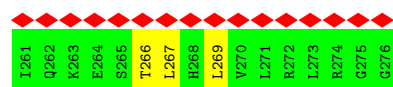
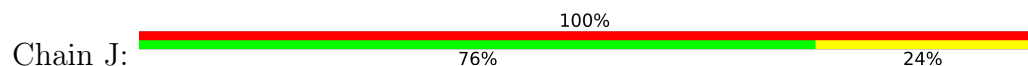
• Molecule 2: Ubiquitin



• Molecule 2: Ubiquitin

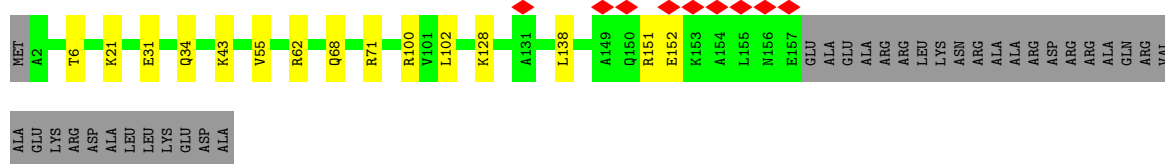
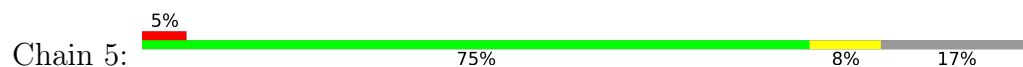


• Molecule 2: Ubiquitin

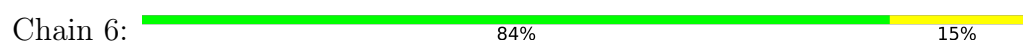




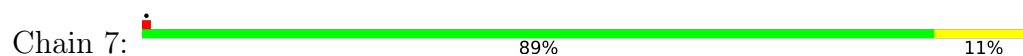
- Molecule 6: 60S ribosomal protein L19-A



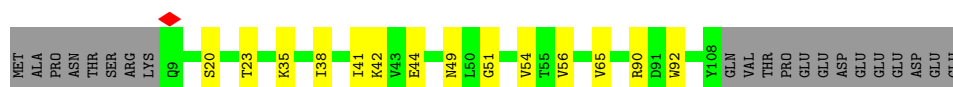
- Molecule 7: 60S ribosomal protein L20-A



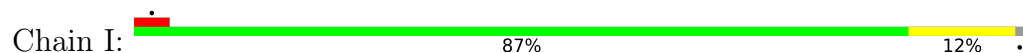
- Molecule 8: 60S ribosomal protein L21-A



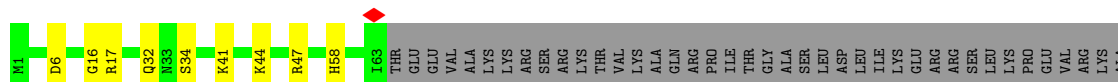
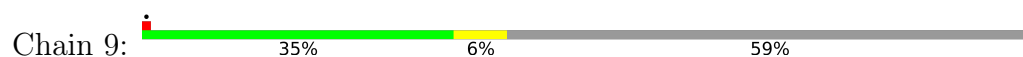
- Molecule 9: 60S ribosomal protein L22-A



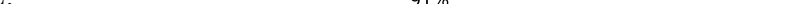
- Molecule 10: 60S ribosomal protein L23-A

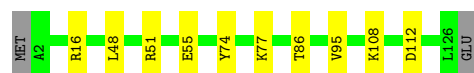


- Molecule 11: Large ribosomal subunit protein eL24A



- Molecule 12: 60S ribosomal protein L26-A

Chain L:  91% 8%



- Molecule 13: 60S ribosomal protein L27-A

Chain M: 89% 10%



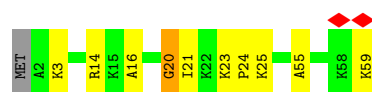
- Molecule 14: 60S ribosomal protein L28

Chain N: 85% 14% .



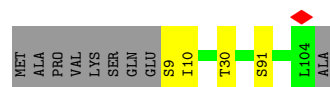
- Molecule 15: Large ribosomal subunit protein eL29

Chain 0:  81% 15% ..

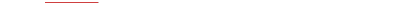


- Molecule 16: 60S ribosomal protein L30

Chain P:  88% . 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  6% 80% 17%



- Molecule 18: Large ribosomal subunit protein eL32

Chain R: 91% 7%



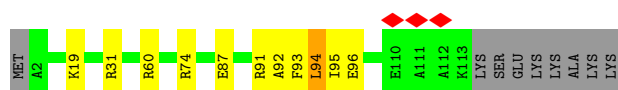
- Molecule 19: 60S ribosomal protein L33-A

Chain S: 89% 10% .



- Molecule 20: 60S ribosomal protein L34-A

Chain T: 83% 8% 7% .



- Molecule 21: 60S ribosomal protein L35-A

Chain U: 93% 6% .



- Molecule 22: 60S ribosomal protein L36-A

Chain V: 91% 8% .



- Molecule 23: 60S ribosomal protein L37-A

Chain W: 77% 15% 8% .



- Molecule 24: 60S ribosomal protein L39

Chain Y: 88% 10% .



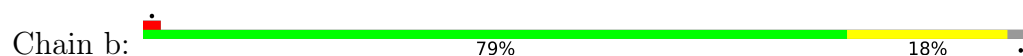
- Molecule 25: Ubiquitin-60S ribosomal protein L40



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

ILE GLN LYS GLU SER THR LEU HIS VAL LEU LEU ARG ARG GLY I77 Y100 R113 K124 K125 K128

- Molecule 26: 60S ribosomal protein L42-A



MET V2 T7 T10 H20 T21 Q22 Y28 K29 A30 S34 L35 R41 R45 K61 A62 K63 V69 L72 V75 K76 H90 G95 K100 L104 GLN PHE

- Molecule 27: 60S ribosomal protein L43-A



MET A2 K3 R4 R17 Y18 H20 K44 R49 G66 R87 E91 A92

- Molecule 28: 60S ribosomal protein L41-A



M4 H5 A6 K7 H8 H9 K10 K11 K12 T13 R14 K17 R18 R19 R20 R21 R22 V23 R24 A25 ARG SER LYS

- Molecule 29: 25S rRNA



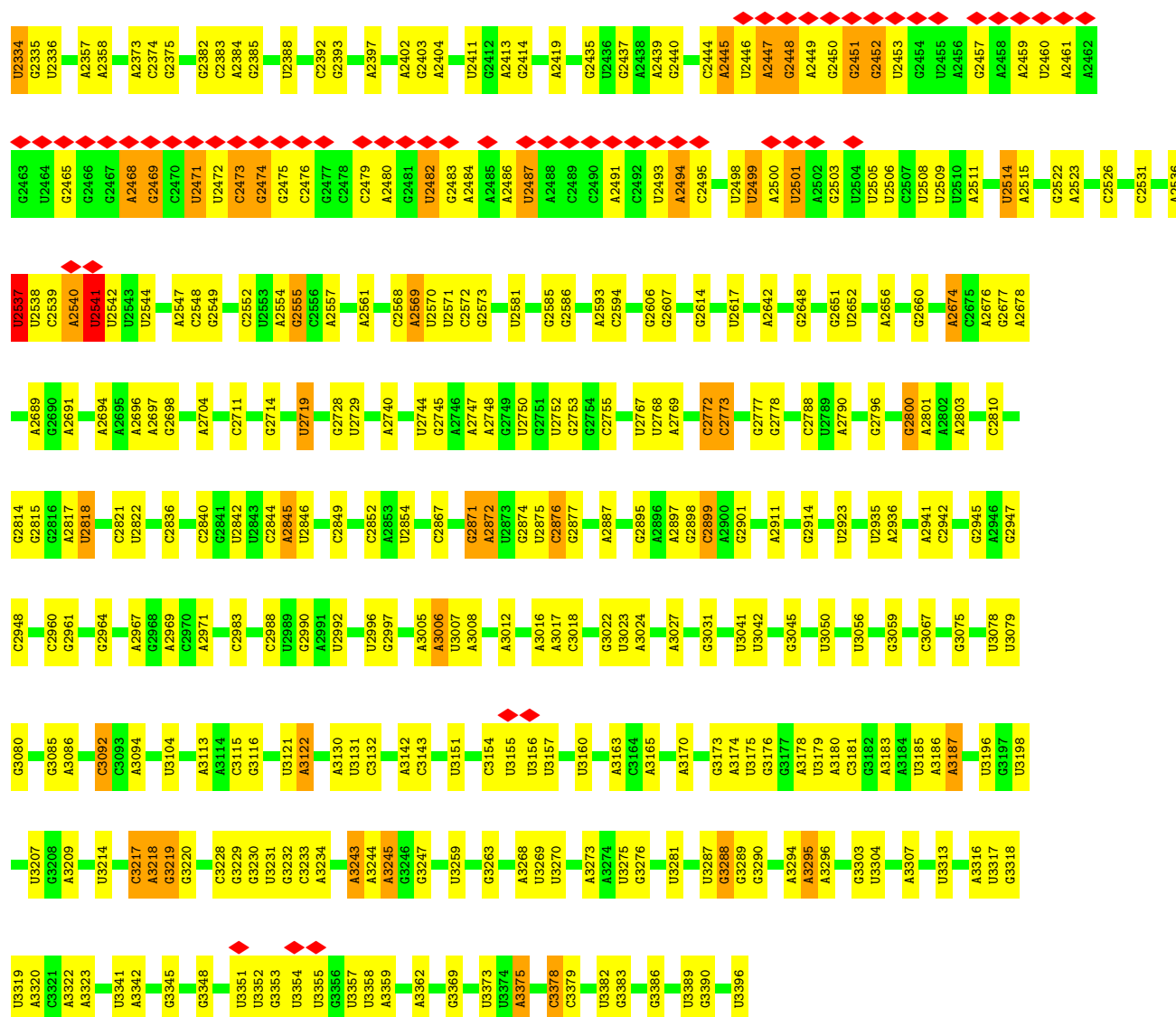
G U U3 A6 A13 A15 A16 U19 A20 G21 A26 A40 A43 A49 G59 A60 A65 A66 A67 C68 G76 G86 G92 G93 G94 A95 G98 A99 A109 G110 C111 A116 G120 A121 A122 A123 U129 A130 U133 U134 C135

G136 G139 G156 A157 G158 A159 A165 C166 G172 G173 U182 G183 A187 U190 U191 C200 G206 U210 A211 G212 A213 G216 U217 G218 A219 A220 G234 U240 G241 C242 G243 G244 U245 U249 U252 G269 G282 G283 A284 A285 U286 A295

A286 G297 G301 U305 A306 A307 A308 A323 U329 C339 A348 A349 C350 A351 A352 G358 A361 A365 A374 A375 G376 G394 A397 A398 A399 G400 U401 A402 C403 U411 G412 A417 A418 G421 A422 C439 U440 U441 U442 G443 U444 U445 U446 U447

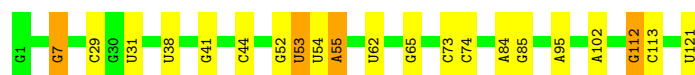
U448 U449 G450 U451 G A C C C U U G C U U C C U C U A G G G G A U U C U U C G C U486 U487 U488 U489 U490 G494 G495 G505 G518 A519 U520 A521 A522 A523 U528 A529 G530 G531 A532





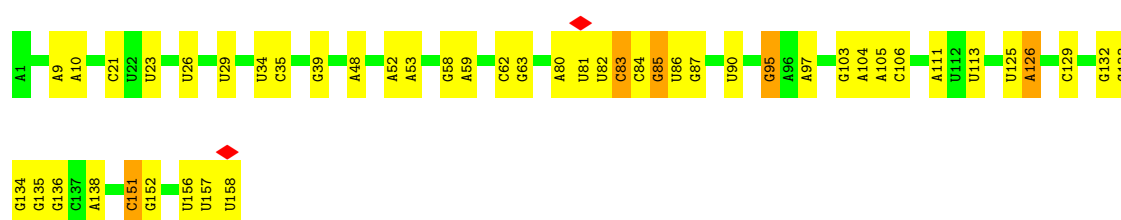
• Molecule 30: 5S rRNA

Chain h: 83% 14%



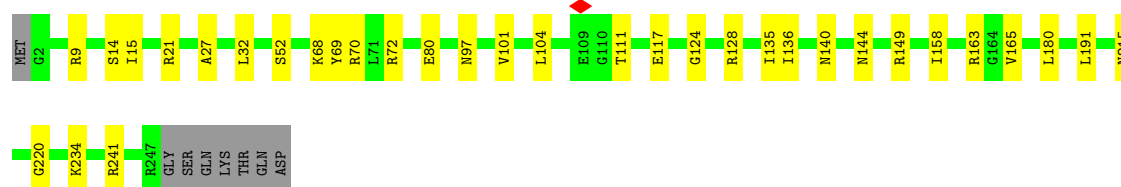
• Molecule 31: 5.8S rRNA

Chain i: 70% 27%



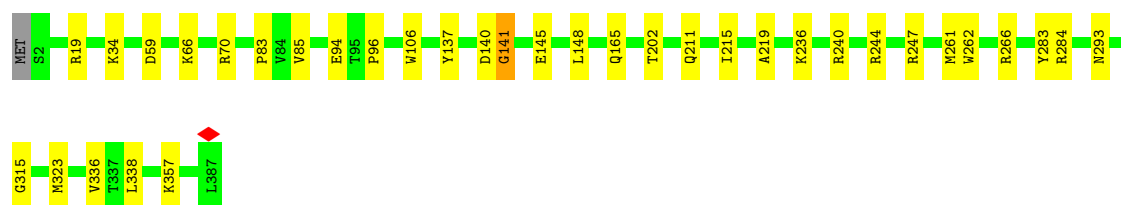
- Molecule 32: 60S ribosomal protein L2-A

Chain j:  84% 13%



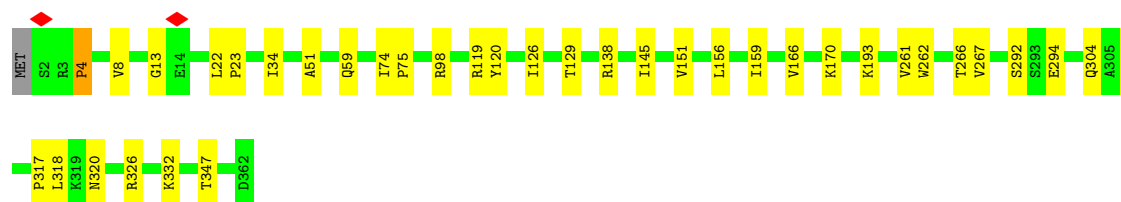
- Molecule 33: Large ribosomal subunit protein uL3

Chain k:  91% 9%



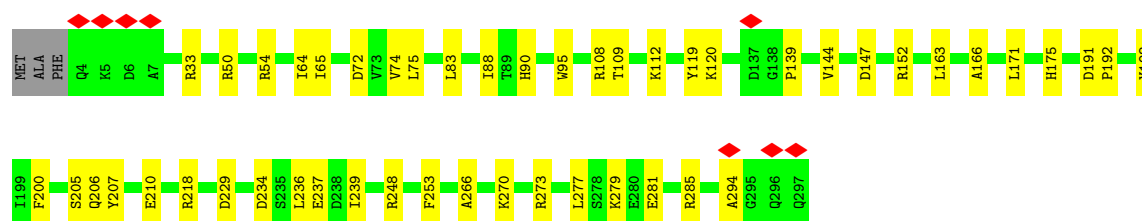
- Molecule 34: Large ribosomal subunit protein uL4A

Chain l:  90% 10%



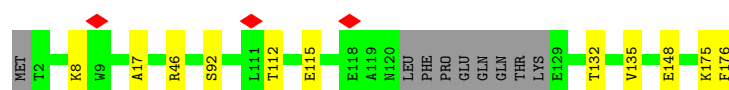
- Molecule 35: Large ribosomal subunit protein uL18

Chain m:  82% 16%

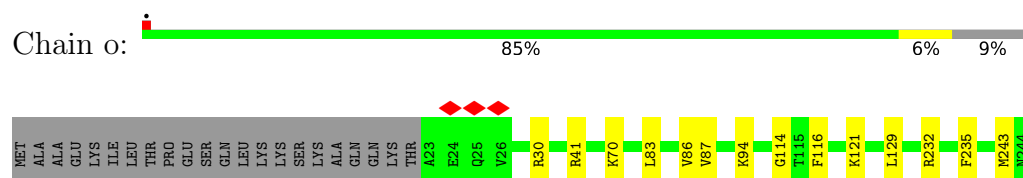


- Molecule 36: Large ribosomal subunit protein eL6B

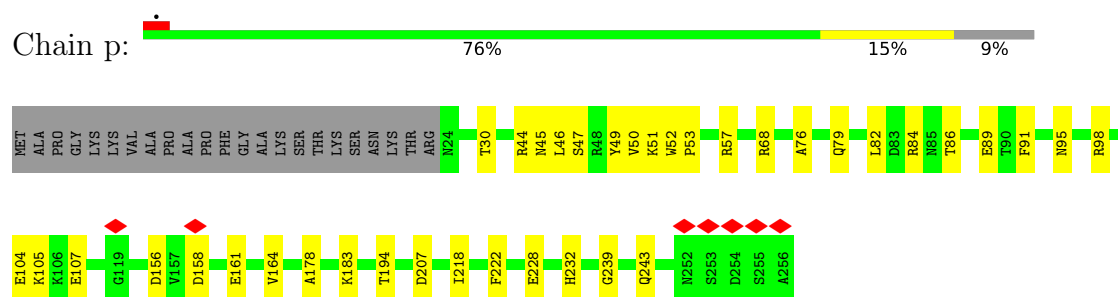
Chain n:  89% 6% 5%



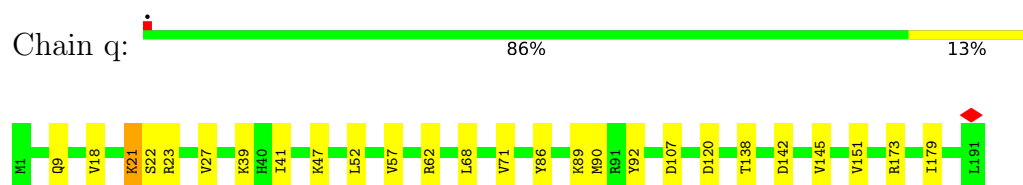
- Molecule 37: 60S ribosomal protein L7-A



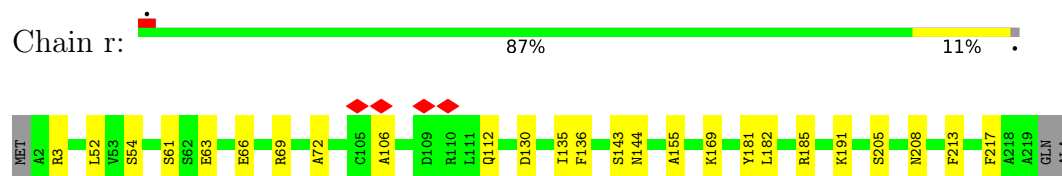
- Molecule 38: 60S ribosomal protein L8-A



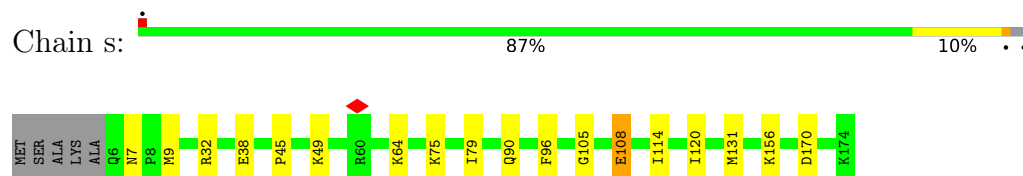
- Molecule 39: 60S ribosomal protein L9-A



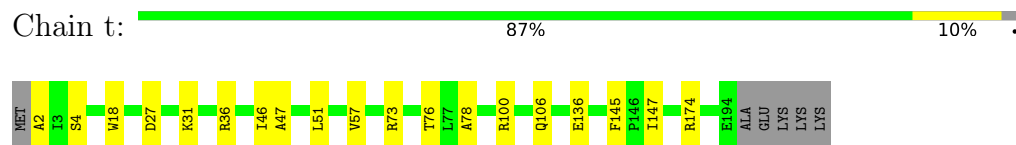
- Molecule 40: Large ribosomal subunit protein uL16



- Molecule 41: Large ribosomal subunit protein uL5A



- Molecule 42: 60S ribosomal protein L13-A



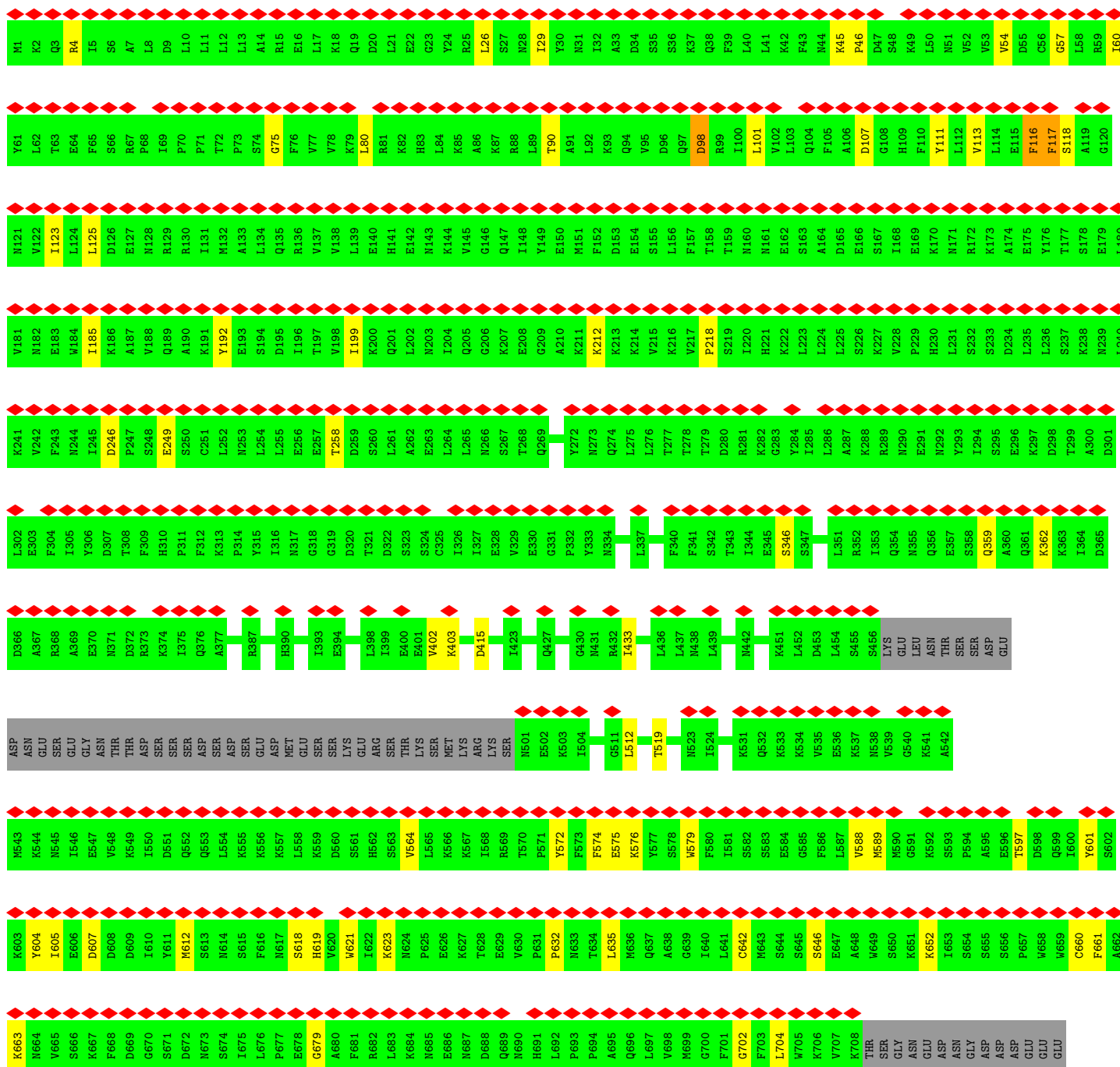
- Molecule 43: 60S ribosomal protein L14-A

Chain u: 

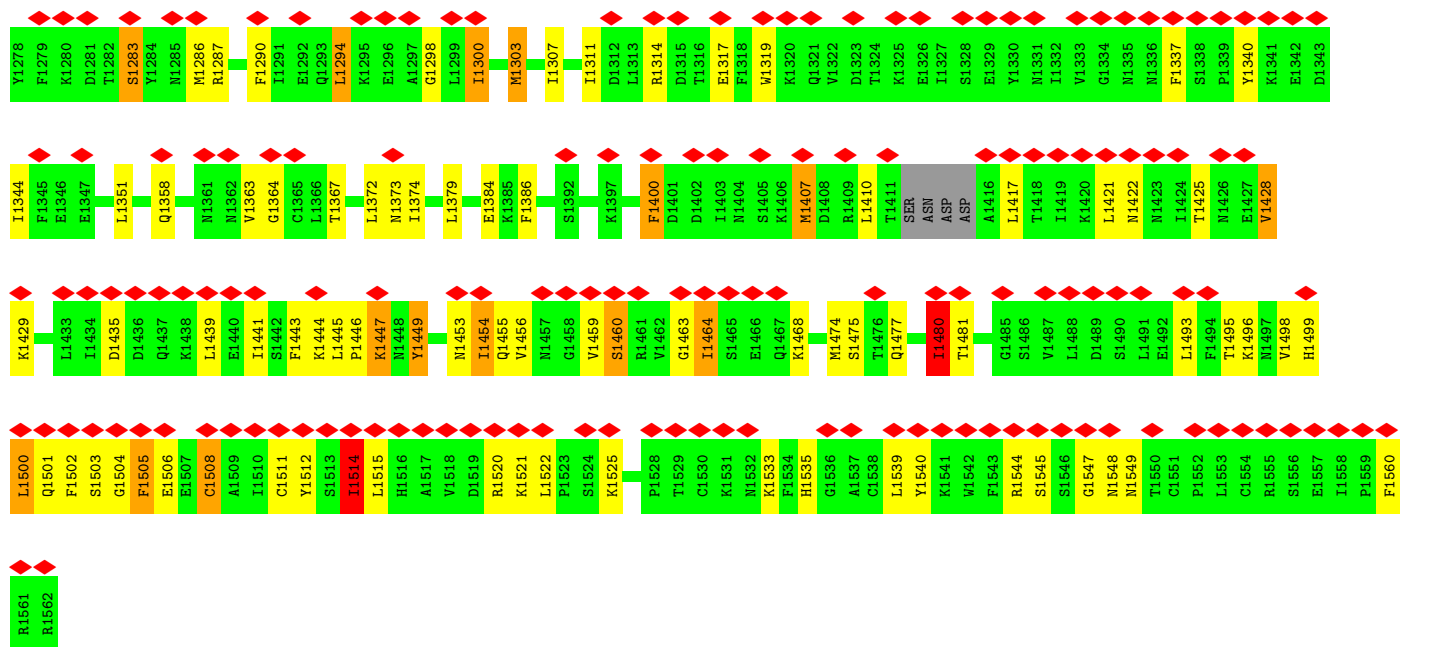


• Molecule 44: Ribosome quality control complex subunit 2

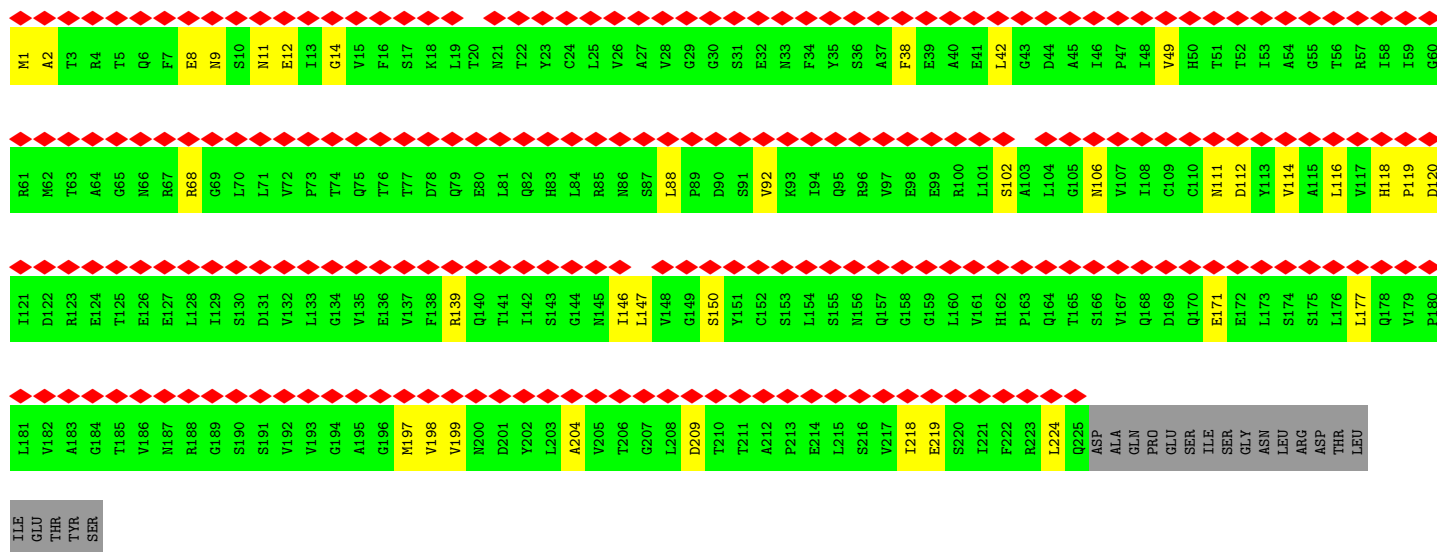
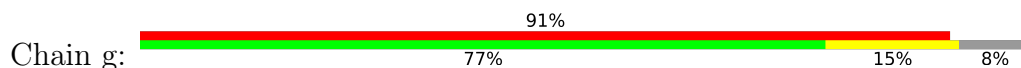
Chain a: 



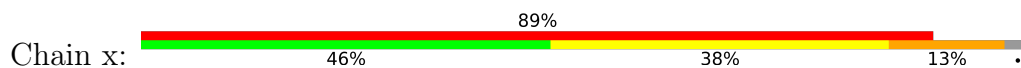
E1214	L1215	R1216	I1217	GLN	LYS	GLN	THR	GLY	SER	SER	ASP	ASP	VAL	M1235	S1236	K1237	F1238	K1239	L1240	P1241	Q1242	K1243	L1244	Q1245	K1246	K1247	D1250	E1251	V1252	F1253	K1254	L1257	E1258	Y1259	E1260	M1261	K1262	N1263	S1264	F1265	Y1268	L1269	V1270	H1273	L1274	I1275	L1276	M1277													
Y1152	Q1153	K1154	L1155	Y1156	K1157	V1158	I1159	S1160	S1161	M1162	E1163	L1164	K1165	K1166	L1167	E1168	S1169	Q1170	Y1171	K1172	R1173	L1174	F1175	L1176	V1177	L1178	N1179	M1180	D1181	K1182	D1183	I1184	G1185	S1186	M1187	I1188	N1189	R1192	L1193	L1194	T1195	L1196	L1197	L1198	G1199	S1200	L1201	V1202	V1203	K1204	T1205	Q1206	Q1207	D1208	I1209	I1210	I1211	E1212	Y1213		
T1092	L1093	Y1094	L1095	L1096	E1097	L1098	R1099	S1100	S1101	C1102	L1103	N1104	L1105	Y1106	E1107	T1108	L1109	S1110	Q1111	GLY	VAL	SER	LYS	ASN	GLY	GLU	ILE	N1180	D1181	K1182	D1183	I1184	G1185	S1186	M1187	I1188	N1189	R1192	L1193	L1194	T1195	L1196	L1197	L1198	G1199	S1200	L1201	V1202	V1203	K1204	T1205	Q1206	Q1207	D1208	I1209	I1210	I1211	E1212	Y1213		
L1032	K1033	M1034	L1035	D1036	S1037	D1038	L1039	A1040	Y1041	E1042	P1043	S1044	F1045	S1046	T1047	R1048	R1049	L1050	L1051	L1052	L1053	D1054	F1055	F1056	T1057	K1058	L1059	M1060	R1061	F1062	E1063	G1064	V1065	R1066	D1067	M1068	G1069	I1070	T1071	A1072	F1073	E1074	L1075	S1076	E1077	R1078	L1079	L1080	A1081	D1082	S1083	L1084	S1085	M1086	C1087	Q1088	I1089	D1090			
E972	I973	T974	K975	L976	R977	T978	L979	L980	A981	S982	Q983	L984	I985	G986	I987	R988	E989	V990	E991	L992	V993	D994	Q995	E996	F997	K998	S999	L1000	A1001	L1002	L1003	N1004	L1005	L1006	D1007	D1008	I1009	P1010	Q1011	A1012	D1013	K1014	Q1015	F1016	V1017	P1018	I1019	A1020	P1021	Q1022	R1023	L1024	N1025	M1026	I1027	F1028	R1029	S1030			
V912	L913	Y914	K915	Y916	L917	L918	N919	S920	I921	D922	T923	Y924	S925	S926	T927	T928	L929	N930	G931	L932	L933	A934	S935	V936	E937	S938	F939	Y940	T941	K942	T943	Y944	R945	D946	Q947	K948	S949	T950	D951	K952	D953	Y954	L955	L956	C957	A958	P959	L960	L961	N962	L963	F964	N965	R966	S967	N968	S969	K970			
S852	E853	E854	P855	N856	D857	L858	Y859	Y860	D861	F862	G863	H864	T865	F866	F867	K868	H869	G870	K871	V872	N873	L874	N875	F876	S877	D878	I879	V880	G881	N882	V883	I884	Q885	P886	A887	N888	G889	G890	D891	A892	M893	L894	T895	P896	D897	I898	A899	E900	S901	N902	S903	Y904	Y905	F906	F907	Y908	Y909	S910	R911		
T792	N793	T794	H795	L796	L797	L798	T799	D800	D801	F802	G803	I804	N805	L806	K807	N808	M809	Q810	K811	L812	I813	R814	Y815	A816	L817	F818	L819	D820	A821	L822	L823	D824	A825	L826	P827	E828	R829	V830	N831	N832	H833	I834	V835	A836	F837	I838	T839	V840	V841	S842	E843	L844	V845	T846	D847	Y848	N849	C850	L851		
Q732	H733	A734	Q735	V736	Y737	F738	S739	P740	G741	A742	K743	E744	K745	Y746	T747	T748	H749	A750	V751	E752	L753	I754	N755	G756	C757	N758	D759	T760	S761	Q762	I763	F764	F765	P766	A767	N768	A769	I770	E771	V772	F773	A774	R775	Y776	M777	P778	I779	I780	D781	Y782	R783	S784	S785	L786	H787	S788	S789	L790	S791		
C672	A673	V674	L675	S676	K677	L678	D679	E680	T681	F682	F683	S684	T685	L686	I687	L688	N689	T690	D691	F692	L693	S694	C695	A696	L697	Y698	V700	T701	E702	I703	T704	N705	E706	K707	L708	F709	K710	S712	L713	Q714	L715	A716	K717	G718	N719	S720	E721	I722	A723	N724	K725	L726	A727	Q728	V729	I730	L731				
Y612	Q613	Q614	L615	M616	K617	S618	D619	S620	L621	E622	K743	L623	E624	L625	Y626	I627	E628	D629	F630	M631	K632	N633	Y634	K635	F636	D637	D638	S639	G640	E641	I642	F643	K644	G645	N646	N647	K648	F649	L650	N651	Q652	R653	T654	L655	T656	K657	L658	Y659	R660	S661	A662	V663	A664	N665	G666	Q667	V668	E669	Q670	I611	
V552	Q553	E554	S555	T556	Y557	Q558	N559	F560	A561	G562	I563	L563	M564	A565	Q566	Y567	S568	N569	S570	K571	F572	F573	K574	M575	N576	T577	D578	A579	I580	G521	Y522	S582	L583	E584	A525	F586	F587	I588	V589	L590	D591	S592	F593	M594	I595	F596	K597	T598	I599	K600	L601	A602	T603	M604	N605	E606	L607	D608	N609	D610	I611
N492	N493	E494	S495	A496	I497	S498	R499	L500	F501	D502	F503	F504	V505	Q506	L507	I508	E509	T510	D511	P512	S513	N514	V515	F516	N517	K518	Y519	D520	G521	Y522	Y523	D524	A525	L526	N527	Y528	F529	L530	D531	S532	D533	M534	I535	F536	L537	N538	G539	K540	I541	G542	K543	F544	I545	N546	E547	P548	T550	L551			



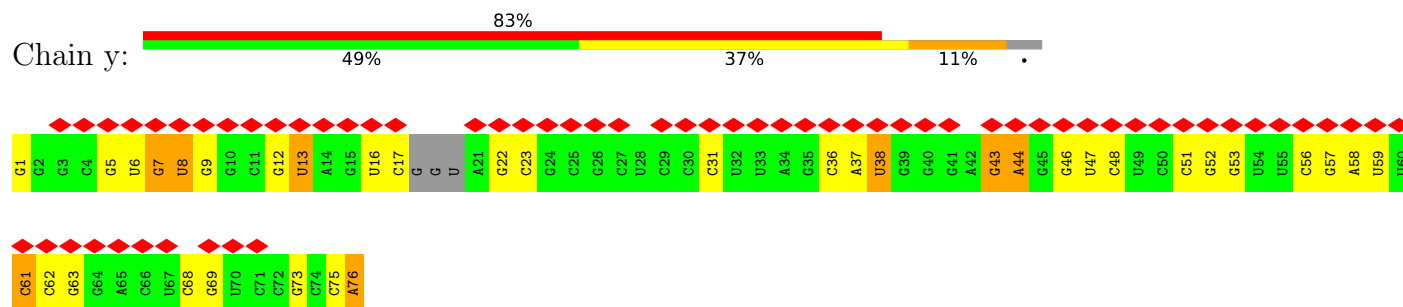
• Molecule 46: Eukaryotic translation initiation factor 6



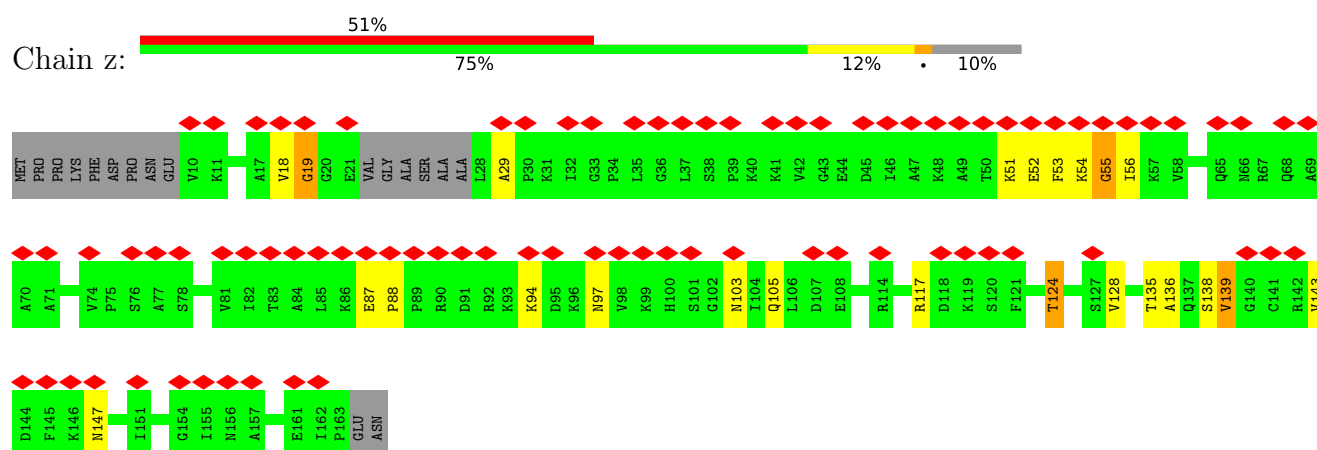
• Molecule 47: Ala tRNA



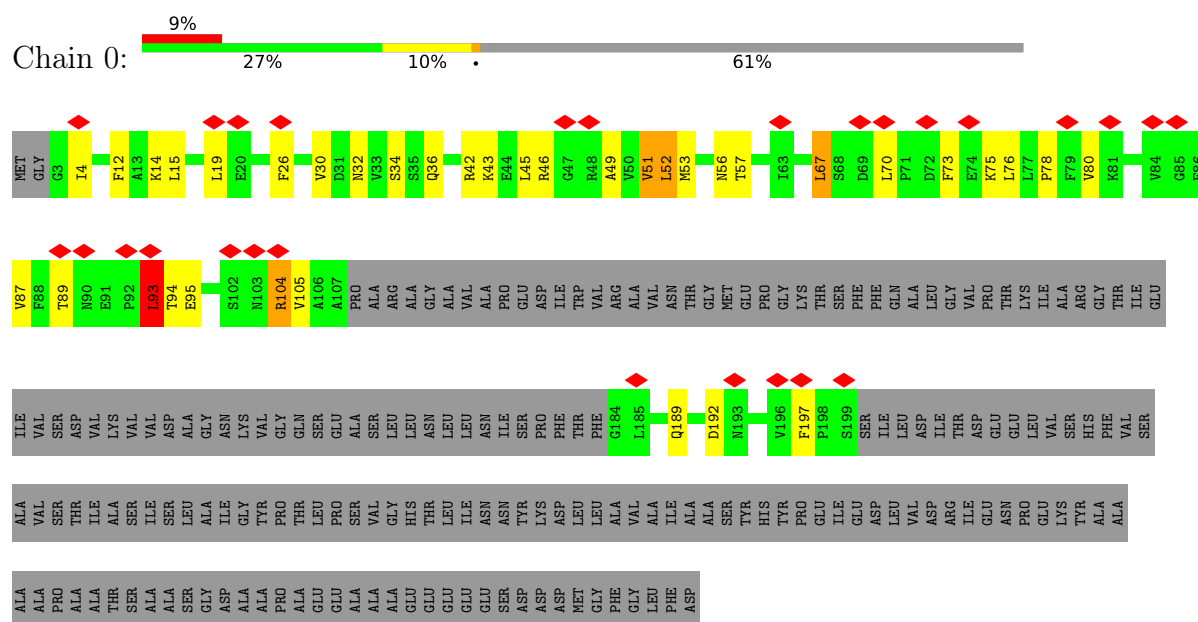
- Molecule 47: Ala tRNA



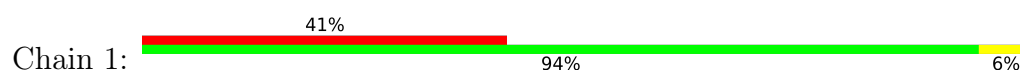
- Molecule 48: Large ribosomal subunit protein uL11A



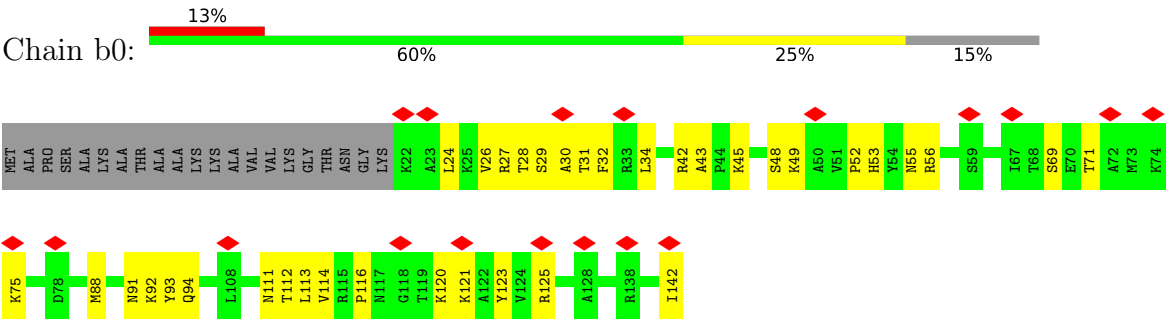
- Molecule 49: 60S acidic ribosomal protein P0



- Molecule 50: CAT-tailed nascent peptide



• Molecule 56: 60S ribosomal protein L25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28262	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.553	Depositor
Minimum map value	-0.788	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.187	Depositor
Map size (Å)	677.12, 677.12, 677.12	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, MG, ZN, ADP, SPD

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.15	0/4273	0.42	0/5775
1	B	0.37	0/5129	0.63	0/6942
1	C	0.18	0/3819	0.46	0/5165
1	D	0.18	0/3808	0.46	0/5148
1	E	0.21	1/3846 (0.0%)	0.45	4/5202 (0.1%)
1	F	0.15	0/4158	0.41	0/5614
2	H	0.17	0/606	0.43	0/812
2	J	0.14	0/606	0.38	0/812
2	K	0.65	0/379	1.15	5/509 (1.0%)
3	G	0.20	0/3851	0.53	2/5201 (0.0%)
4	3	0.30	0/1439	0.61	0/1938
5	4	0.28	0/1465	0.58	0/1965
6	5	0.30	0/1275	0.56	0/1702
7	6	0.31	0/1473	0.56	0/1980
8	7	0.27	0/1296	0.56	0/1739
9	8	0.29	0/812	0.75	2/1099 (0.2%)
10	I	0.27	0/1018	0.50	0/1369
11	9	0.27	0/530	0.52	0/703
12	L	0.27	0/995	0.53	0/1329
13	M	0.27	0/1106	0.56	0/1485
14	N	0.32	0/1200	0.56	1/1607 (0.1%)
15	O	0.26	0/473	0.62	0/629
16	P	0.26	0/745	0.60	0/1001
17	Q	0.31	0/890	0.68	2/1196 (0.2%)
18	R	0.26	0/1034	0.47	0/1385
19	S	0.30	0/868	0.47	0/1168
20	T	0.29	0/890	0.58	2/1189 (0.2%)
21	U	0.27	0/978	0.53	0/1301
22	V	0.28	0/772	0.57	0/1026
23	W	0.32	0/660	0.60	0/875
24	Y	0.29	0/443	0.46	0/588
25	Z	0.28	0/416	0.60	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	b	0.28	0/836	0.53	0/1104
27	c	0.27	0/701	0.56	0/934
28	d	0.22	0/208	0.81	2/267 (0.7%)
29	f	0.31	0/77011	0.40	5/120065 (0.0%)
30	h	0.26	0/2883	0.32	0/4491
31	i	0.30	0/3746	0.36	0/5832
32	j	0.31	0/1908	0.54	0/2564
33	k	0.29	0/3146	0.53	0/4228
34	l	0.29	0/2800	0.57	4/3790 (0.1%)
35	m	0.27	0/2400	0.56	0/3239
36	n	0.28	0/1329	0.60	0/1794
37	o	0.31	0/1821	0.58	0/2451
38	p	0.27	0/1836	0.58	1/2481 (0.0%)
39	q	0.30	0/1529	0.64	2/2060 (0.1%)
40	r	0.25	0/1801	0.49	0/2416
41	s	0.27	0/1367	0.69	4/1834 (0.2%)
42	t	0.29	0/1568	0.62	1/2106 (0.0%)
43	u	0.30	0/1068	0.53	0/1438
44	a	0.26	0/6683	0.55	2/9016 (0.0%)
45	e	0.66	0/11755	0.97	58/15956 (0.4%)
46	g	0.24	0/1672	0.59	1/2281 (0.0%)
47	x	0.35	0/1761	0.61	0/2742
47	y	0.37	0/1735	0.64	0/2701
48	z	0.67	0/726	1.24	13/1006 (1.3%)
49	0	0.49	0/976	0.95	3/1313 (0.2%)
51	w	0.27	0/1736	0.61	0/2332
52	X	0.45	0/614	0.50	0/819
53	v	0.84	3/4492 (0.1%)	1.12	7/6087 (0.1%)
54	2	0.72	0/608	1.02	0/816
55	a0	0.32	0/1585	0.54	0/2128
56	b0	0.31	0/979	0.57	0/1321
All	All	0.35	4/194533 (0.0%)	0.55	121/280619 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	G	0	1
15	O	0	1
21	U	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	k	0	1
34	l	0	2
38	p	0	3
39	q	0	1
43	u	0	1
45	e	0	1
46	g	0	1
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	v	439	GLN	C-N	21.17	1.61	1.33
53	v	372	LEU	C-N	18.31	1.58	1.33
53	v	286	GLU	C-N	8.53	1.45	1.33
1	E	261	LYS	N-CA	-6.29	1.38	1.46

The worst 5 of 121 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	36	ILE	C-N-CD	-13.24	70.72	125.00
45	e	1364	GLY	N-CA-C	12.27	127.34	112.49
53	v	440	ARG	O-C-N	11.96	136.70	122.34
45	e	1514	ILE	CA-C-N	-10.41	106.69	122.09
45	e	1514	ILE	C-N-CA	-10.41	106.69	122.09

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	510	ASN	Peptide
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
33	k	141	GLY	Peptide
34	l	13	GLY	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4206	0	4232	63	0
1	B	5049	0	5118	110	0
1	C	3759	0	3798	86	0
1	D	3747	0	3784	127	0
1	E	3786	0	3827	126	0
1	F	4093	0	4121	70	0
2	H	601	0	622	8	0
2	J	601	0	622	10	0
2	K	376	0	392	64	0
3	G	3762	0	3638	45	0
4	3	1416	0	1433	12	0
5	4	1441	0	1543	14	0
6	5	1258	0	1342	18	0
7	6	1437	0	1475	21	0
8	7	1272	0	1312	12	0
9	8	796	0	812	8	0
10	I	1003	0	1048	11	0
11	9	518	0	542	7	0
12	L	984	0	1075	7	0
13	M	1080	0	1122	10	0
14	N	1169	0	1211	16	0
15	O	462	0	491	8	0
16	P	737	0	792	2	0
17	Q	876	0	912	10	0
18	R	1013	0	1077	6	0
19	S	850	0	880	7	0
20	T	880	0	942	9	0
21	U	969	0	1078	4	0
22	V	766	0	842	6	0
23	W	645	0	645	11	0
24	Y	436	0	475	6	0
25	Z	410	0	442	4	0
26	b	824	0	888	12	0
27	c	694	0	734	8	0
28	d	207	0	250	3	0
29	f	68802	0	34573	604	0
30	h	2579	0	1304	9	0
31	i	3353	0	1695	41	0
32	j	1874	0	1943	24	0
33	k	3075	0	3142	26	0
34	l	2748	0	2859	23	0
35	m	2351	0	2294	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	n	1307	0	1377	8	0
37	o	1784	0	1862	10	0
38	p	1804	0	1877	55	0
39	q	1508	0	1572	17	0
40	r	1764	0	1804	16	0
41	s	1346	0	1370	9	0
42	t	1543	0	1608	15	0
43	u	1053	0	1149	51	0
44	a	6573	0	6471	60	0
45	e	11556	0	10822	475	0
46	g	1651	0	1613	22	0
47	x	1579	0	800	24	0
47	y	1556	0	788	16	0
48	z	728	0	337	20	0
49	0	961	0	979	48	0
50	1	85	0	21	1	0
51	w	1709	0	1797	15	0
52	X	608	0	677	66	0
53	v	4376	0	4289	116	0
54	2	602	0	629	26	0
55	a0	1555	0	1659	133	0
56	b0	964	0	1025	187	0
57	A	31	0	12	23	0
57	B	31	0	12	2	0
57	C	93	0	32	64	0
57	D	62	0	22	49	0
57	E	31	0	10	14	0
57	F	31	0	12	18	0
58	E	27	0	11	23	0
59	G	2	0	0	0	0
59	T	1	0	0	0	0
59	W	1	0	0	0	0
59	Z	1	0	0	0	0
59	b	1	0	0	0	0
59	c	1	0	0	0	0
60	3	1	0	0	0	0
60	5	1	0	0	0	0
60	I	1	0	0	0	0
60	R	1	0	0	0	0
60	T	1	0	0	0	0
60	f	3	0	0	0	0
60	h	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	j	2	0	0	0	0
60	k	1	0	0	0	0
61	f	10	0	19	1	0
All	All	183852	0	145983	2352	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 7.

The worst 5 of 2352 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)
45:e:917:LEU:HD13	45:e:963:MET:SD	1.21	1.74
45:e:272:TYR:HA	45:e:277:MET:SD	1.28	1.66
45:e:277:MET:SD	45:e:278:PRO:HD3	1.34	1.65
1:E:536:LEU:HD22	58:E:901:ADP:C5'	1.23	1.60
1:E:536:LEU:CD2	58:E:901:ADP:H3'	1.14	1.60

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	
1	A	543/835 (65%)	522 (96%)	21 (4%)	0	100	100
1	B	648/835 (78%)	612 (94%)	36 (6%)	0	100	100
1	C	488/835 (58%)	448 (92%)	40 (8%)	0	100	100
1	D	485/835 (58%)	449 (93%)	36 (7%)	0	100	100
1	E	492/835 (59%)	463 (94%)	27 (6%)	2 (0%)	30	59
1	F	527/835 (63%)	501 (95%)	26 (5%)	0	100	100
2	H	74/76 (97%)	73 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	74/76 (97%)	74 (100%)	0	0	100	100
2	K	46/76 (60%)	31 (67%)	10 (22%)	5 (11%)	0	1
3	G	466/580 (80%)	421 (90%)	44 (9%)	1 (0%)	43	71
4	3	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
5	4	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
6	5	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
7	6	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
8	7	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
9	8	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
10	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
11	9	61/155 (39%)	61 (100%)	0	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	29
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
24	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
25	Z	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
26	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
27	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
28	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
32	j	244/254 (96%)	226 (93%)	18 (7%)	0	100	100
33	k	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
34	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	36	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
36	n	163/176 (93%)	154 (94%)	9 (6%)	0	100	100
37	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
38	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
39	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	24	55
40	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
41	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	21	52
42	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	24	55
43	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
44	a	842/1038 (81%)	827 (98%)	15 (2%)	0	100	100
45	e	1518/1562 (97%)	1486 (98%)	30 (2%)	2 (0%)	48	76
46	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	z	144/165 (87%)	135 (94%)	7 (5%)	2 (1%)	9	34
49	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	43
51	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
52	X	74/78 (95%)	74 (100%)	0	0	100	100
53	v	527/753 (70%)	510 (97%)	16 (3%)	1 (0%)	43	71
54	2	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
55	a0	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
56	b0	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
All	All	13416/16565 (81%)	12793 (95%)	604 (4%)	19 (0%)	49	76

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	561	TRP
2	K	37	PRO
2	K	38	PRO
2	K	41	GLN
48	z	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	
1	A	448/695 (64%)	447 (100%)	1 (0%)	87	87
1	B	545/695 (78%)	543 (100%)	2 (0%)	84	84
1	C	401/695 (58%)	399 (100%)	2 (0%)	81	82
1	D	398/695 (57%)	397 (100%)	1 (0%)	86	85
1	E	403/695 (58%)	399 (99%)	4 (1%)	68	76
1	F	434/695 (62%)	433 (100%)	1 (0%)	87	87
2	H	69/69 (100%)	69 (100%)	0	100	100
2	J	69/69 (100%)	69 (100%)	0	100	100
2	K	44/69 (64%)	42 (96%)	2 (4%)	24	53
3	G	420/516 (81%)	419 (100%)	1 (0%)	87	87
4	3	138/146 (94%)	138 (100%)	0	100	100
5	4	150/151 (99%)	150 (100%)	0	100	100
6	5	129/154 (84%)	129 (100%)	0	100	100
7	6	155/156 (99%)	155 (100%)	0	100	100
8	7	135/137 (98%)	135 (100%)	0	100	100
9	8	87/107 (81%)	87 (100%)	0	100	100
10	I	104/105 (99%)	104 (100%)	0	100	100
11	9	54/129 (42%)	54 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	46 (100%)	0	100	100
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	95 (100%)	0	100	100
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	67/71 (94%)	67 (100%)	0	100	100
24	Y	45/46 (98%)	45 (100%)	0	100	100
25	Z	45/116 (39%)	45 (100%)	0	100	100
26	b	87/91 (96%)	87 (100%)	0	100	100
27	c	71/72 (99%)	71 (100%)	0	100	100
28	d	20/23 (87%)	20 (100%)	0	100	100
32	j	189/196 (96%)	189 (100%)	0	100	100
33	k	320/323 (99%)	320 (100%)	0	100	100
34	l	288/289 (100%)	288 (100%)	0	100	100
35	m	241/245 (98%)	241 (100%)	0	100	100
36	n	139/155 (90%)	139 (100%)	0	100	100
37	o	186/205 (91%)	186 (100%)	0	100	100
38	p	187/208 (90%)	187 (100%)	0	100	100
39	q	168/171 (98%)	168 (100%)	0	100	100
40	r	185/187 (99%)	184 (100%)	1 (0%)	81	82
41	s	145/150 (97%)	145 (100%)	0	100	100
42	t	154/159 (97%)	154 (100%)	0	100	100
43	u	107/109 (98%)	107 (100%)	0	100	100
44	a	677/949 (71%)	676 (100%)	1 (0%)	88	89
45	e	1157/1451 (80%)	1102 (95%)	55 (5%)	23	52
46	g	180/211 (85%)	180 (100%)	0	100	100
49	0	104/254 (41%)	94 (90%)	10 (10%)	8	28
51	w	197/198 (100%)	197 (100%)	0	100	100
52	X	68/69 (99%)	68 (100%)	0	100	100
53	v	492/686 (72%)	484 (98%)	8 (2%)	55	71
54	2	68/68 (100%)	68 (100%)	0	100	100
55	a0	160/162 (99%)	160 (100%)	0	100	100
56	b0	104/118 (88%)	104 (100%)	0	100	100
All	All	11066/14029 (79%)	10977 (99%)	89 (1%)	70	78

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	e	1367	THR
49	0	30	VAL
45	e	1379	LEU
45	e	1441	ILE
49	0	76	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
45	e	189	ASN
53	v	198	GLN
45	e	397	ASN
45	e	1141	GLN
53	v	610	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	f	3211/3395 (94%)	601 (18%)	0
30	h	120/121 (99%)	12 (10%)	0
31	i	157/158 (99%)	32 (20%)	0
47	x	72/76 (94%)	26 (36%)	0
47	y	71/76 (93%)	26 (36%)	0
All	All	3631/3826 (94%)	697 (19%)	0

5 of 697 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	f	6	A
29	f	13	A
29	f	14	U
29	f	26	A
29	f	40	A

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 19 are monoatomic - leaving 11 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
57	ATP	C	1001	-	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)
57	ATP	C	1003	-	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)
57	ATP	B	901	-	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)
57	ATP	C	1002	-	32,33,33	1.41	4 (12%)	48,52,52	1.77	9 (18%)
57	ATP	D	902	-	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)
58	ADP	E	901	-	28,29,29	1.43	4 (14%)	43,45,45	1.85	9 (20%)
57	ATP	E	902	-	32,33,33	1.40	4 (12%)	48,52,52	1.78	9 (18%)
57	ATP	A	901	-	32,33,33	1.41	4 (12%)	48,52,52	1.78	9 (18%)
57	ATP	F	901	-	32,33,33	1.41	4 (12%)	48,52,52	1.77	9 (18%)
61	SPD	f	3401	-	9,9,9	0.31	0	8,8,8	0.85	0
57	ATP	D	901	-	32,33,33	1.42	4 (12%)	48,52,52	1.79	9 (18%)

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
57	ATP	C	1001	-	-	9/22/38/38	0/3/3/3
57	ATP	C	1003	-	-	9/22/38/38	0/3/3/3
57	ATP	B	901	-	-	6/22/38/38	0/3/3/3
57	ATP	C	1002	-	-	9/22/38/38	0/3/3/3
57	ATP	D	902	-	-	9/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	ADP	E	901	-	-	3/16/32/32	0/3/3/3
57	ATP	E	902	-	-	9/22/38/38	0/3/3/3
57	ATP	A	901	-	-	9/22/38/38	0/3/3/3
57	ATP	F	901	-	-	3/22/38/38	0/3/3/3
61	SPD	f	3401	-	-	5/7/7/7	-
57	ATP	D	901	-	-	6/22/38/38	0/3/3/3

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	D	901	ATP	C5-C4	4.81	1.47	1.39
57	D	902	ATP	C5-C4	4.81	1.47	1.39
57	B	901	ATP	C5-C4	4.76	1.47	1.39
57	C	1002	ATP	C5-C4	4.75	1.47	1.39
57	C	1003	ATP	C5-C4	4.75	1.47	1.39

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	C	1001	ATP	C5-C4-N3	-5.89	118.61	126.72
57	B	901	ATP	C5-C4-N3	-5.86	118.64	126.72
57	E	902	ATP	C5-C4-N3	-5.86	118.65	126.72
57	D	901	ATP	C5-C4-N3	-5.86	118.65	126.72
57	C	1003	ATP	C5-C4-N3	-5.86	118.65	126.72

There are no chirality outliers.

5 of 77 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	A	901	ATP	O4'-C4'-C5'-O5'
57	A	901	ATP	C3'-C4'-C5'-O5'
57	C	1001	ATP	O4'-C4'-C5'-O5'
57	C	1001	ATP	C3'-C4'-C5'-O5'
57	C	1002	ATP	O4'-C4'-C5'-O5'

There are no ring outliers.

11 monomers are involved in 194 short contacts:

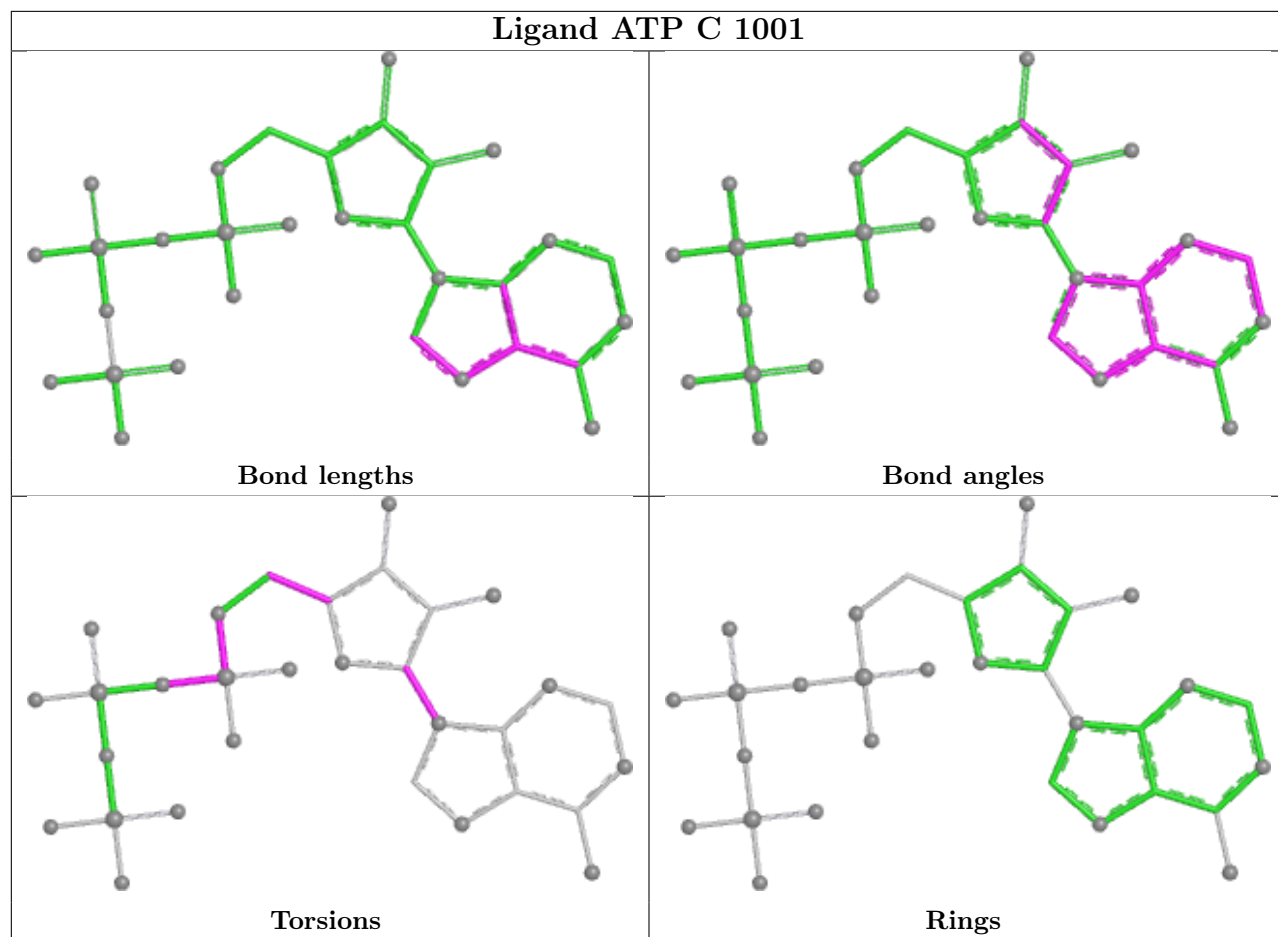
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	C	1001	ATP	42	0

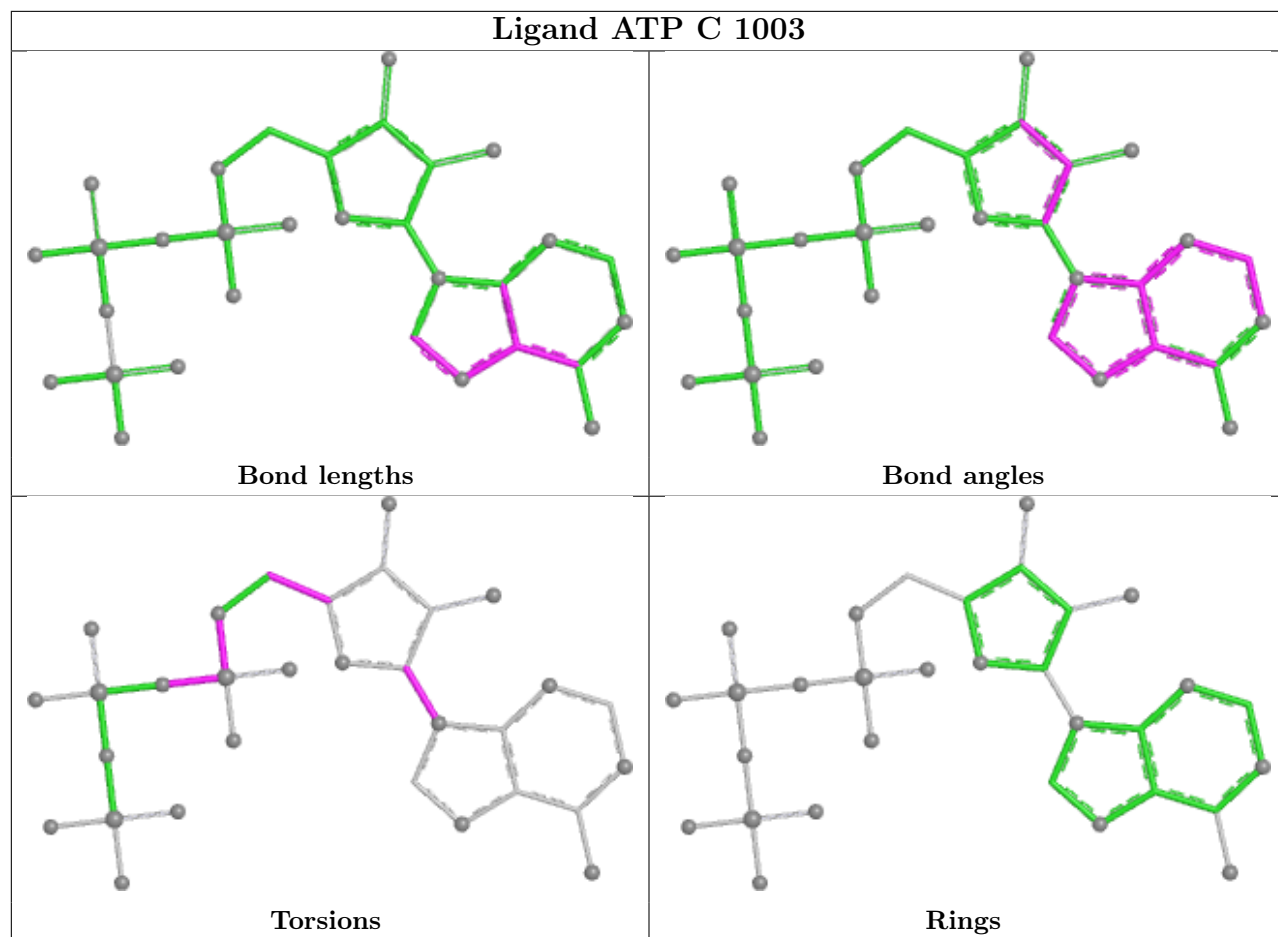
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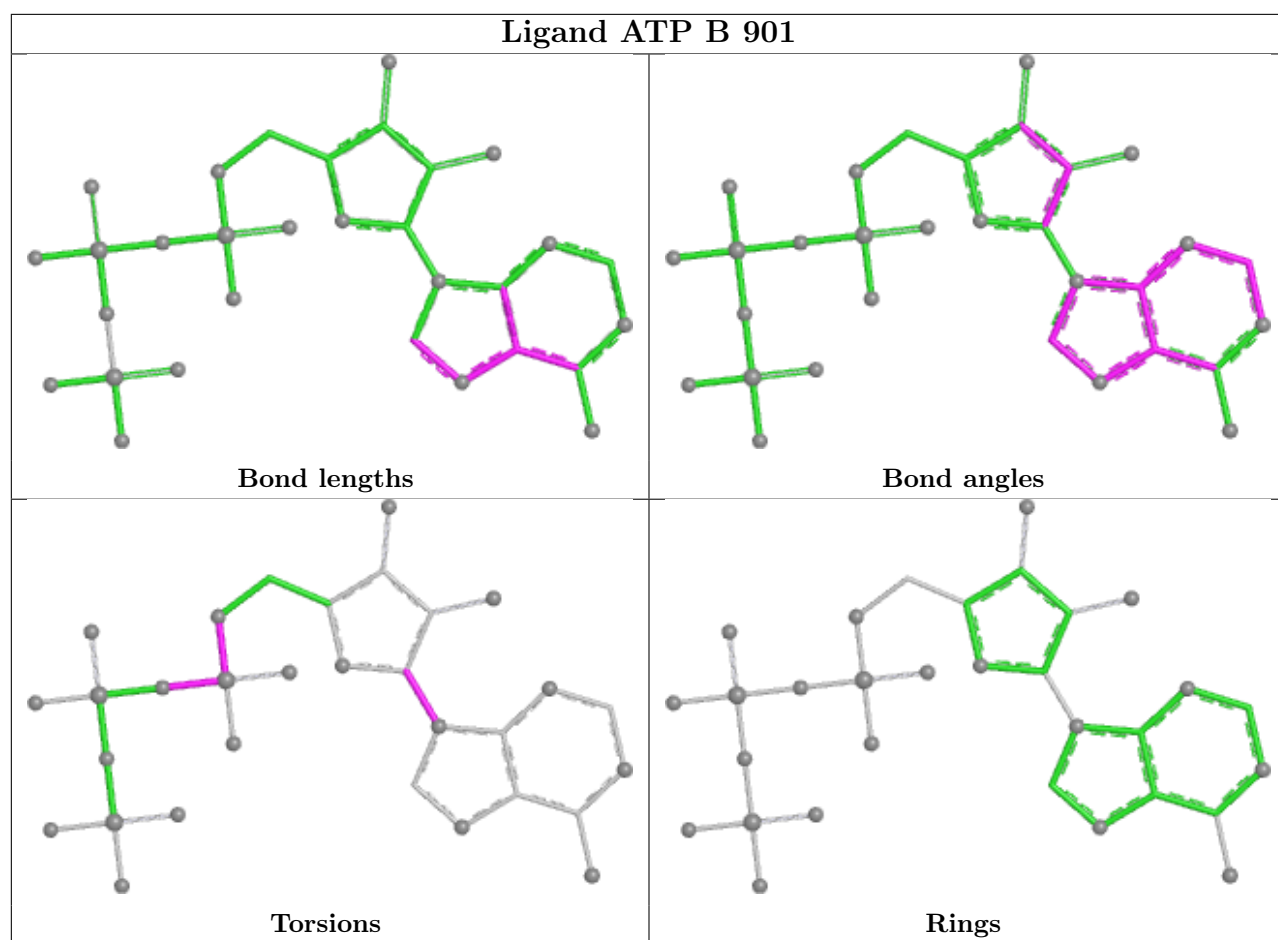
Continued from previous page...

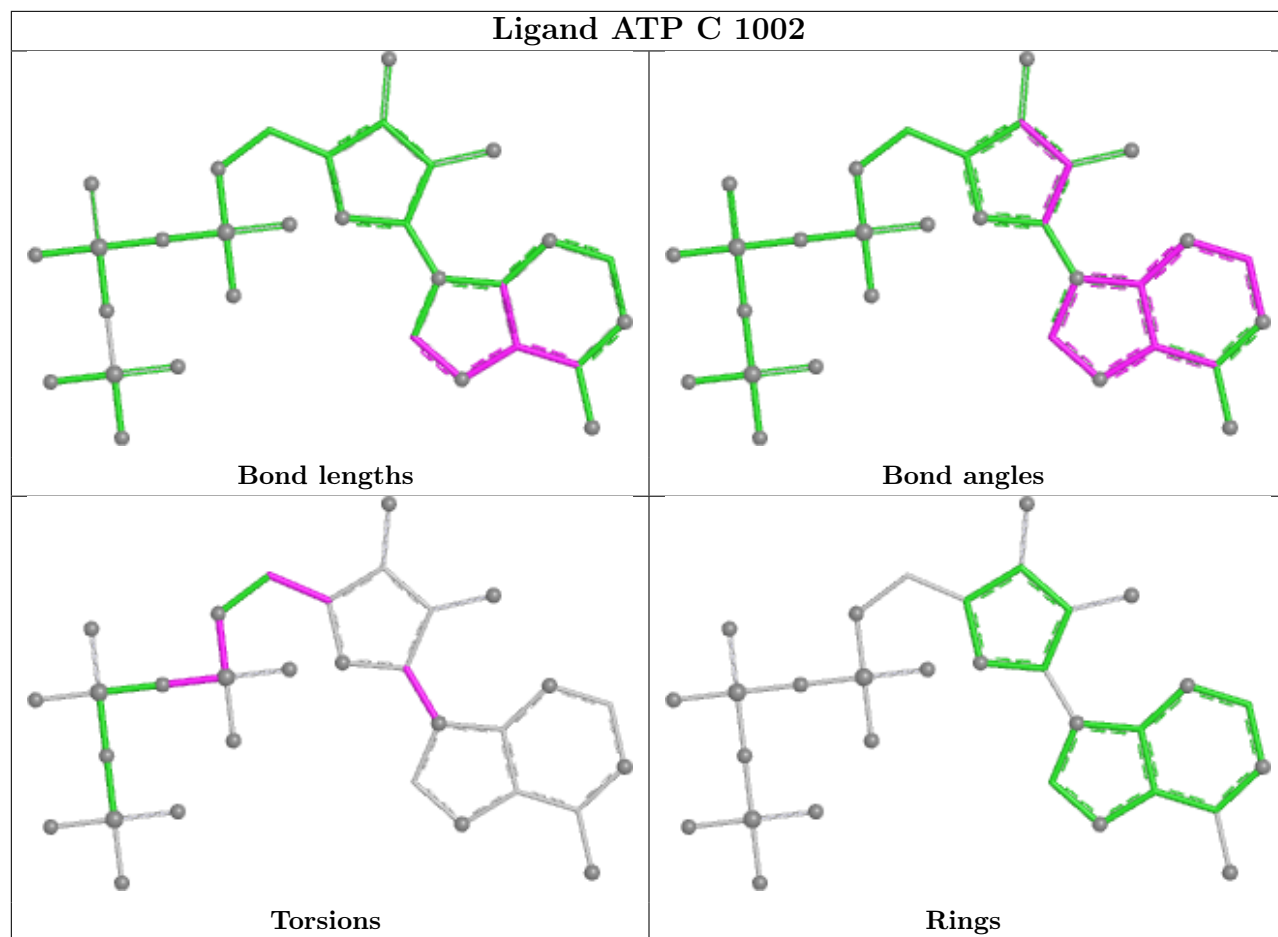
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	C	1003	ATP	18	0
57	B	901	ATP	2	0
57	C	1002	ATP	4	0
57	D	902	ATP	29	0
58	E	901	ADP	23	0
57	E	902	ATP	14	0
57	A	901	ATP	23	0
57	F	901	ATP	18	0
61	f	3401	SPD	1	0
57	D	901	ATP	20	0

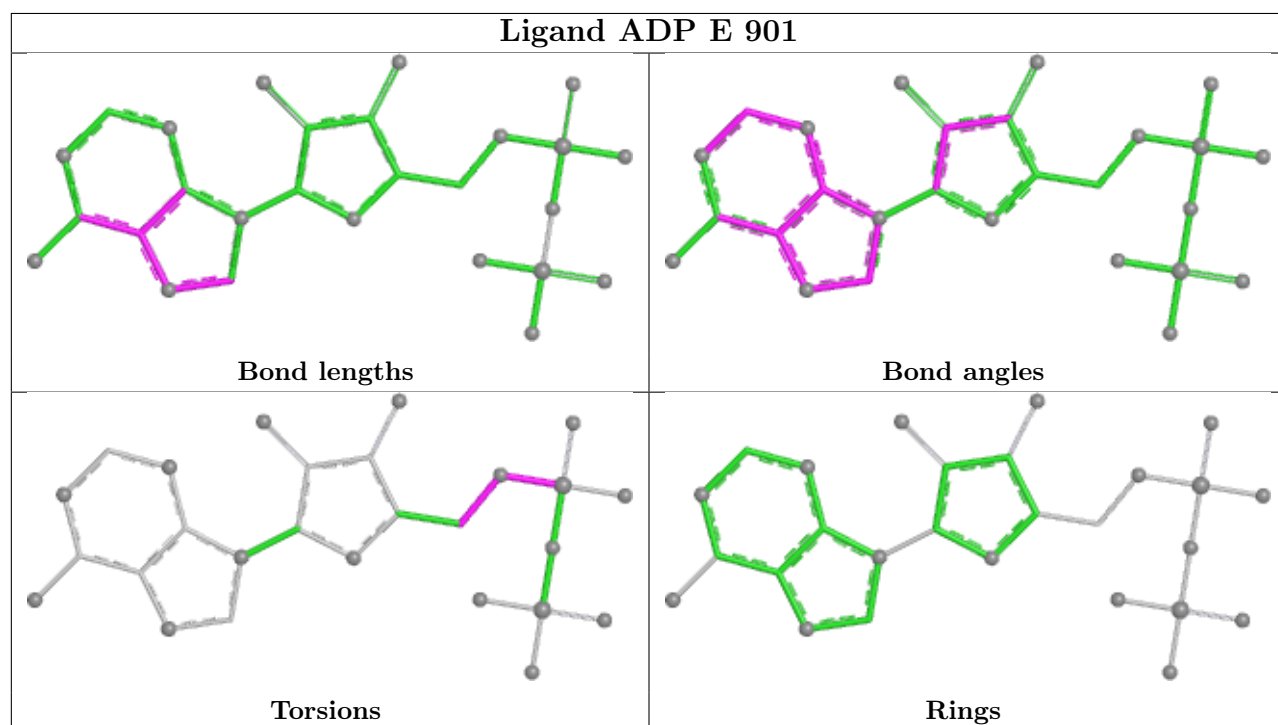
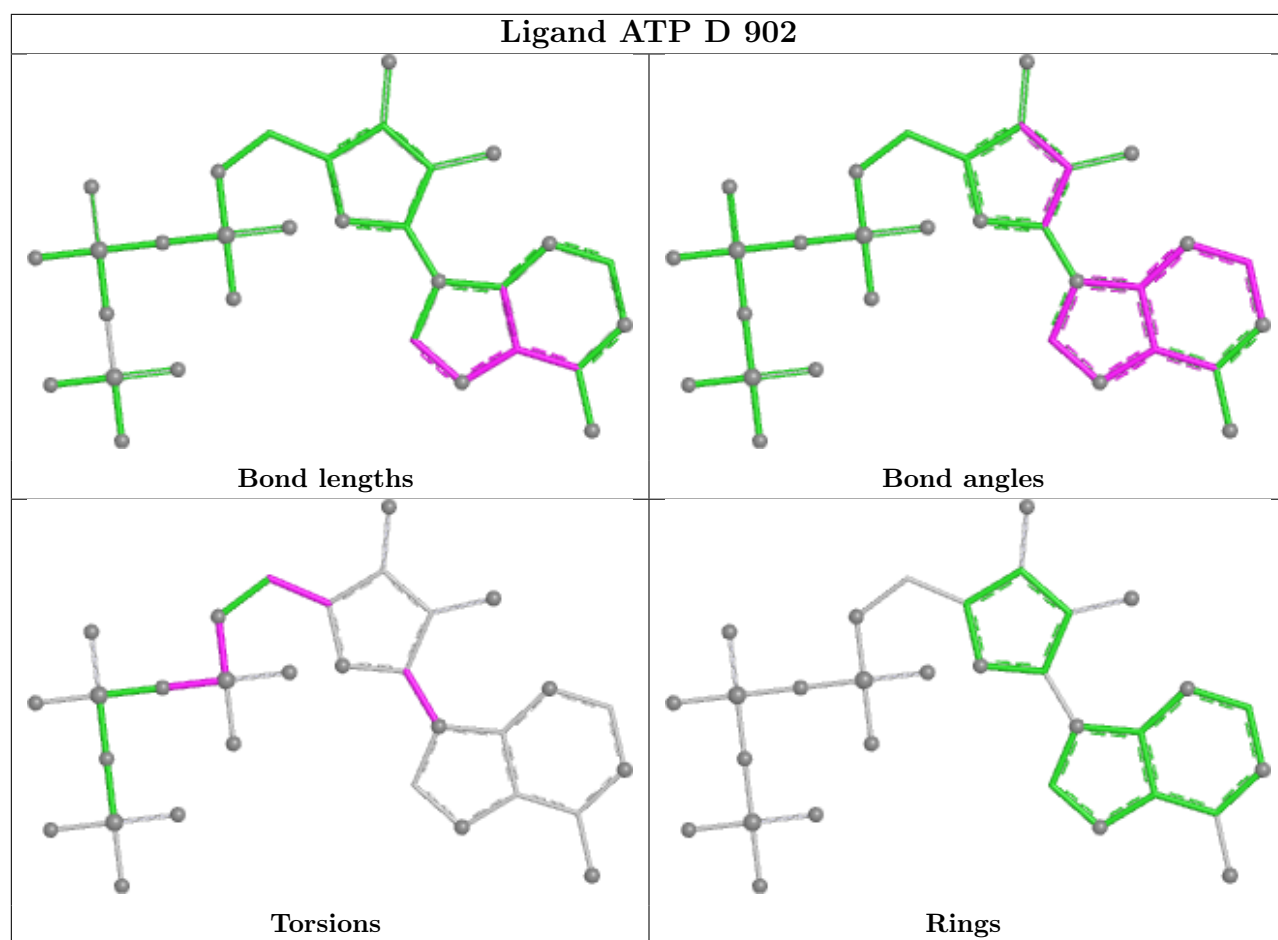
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

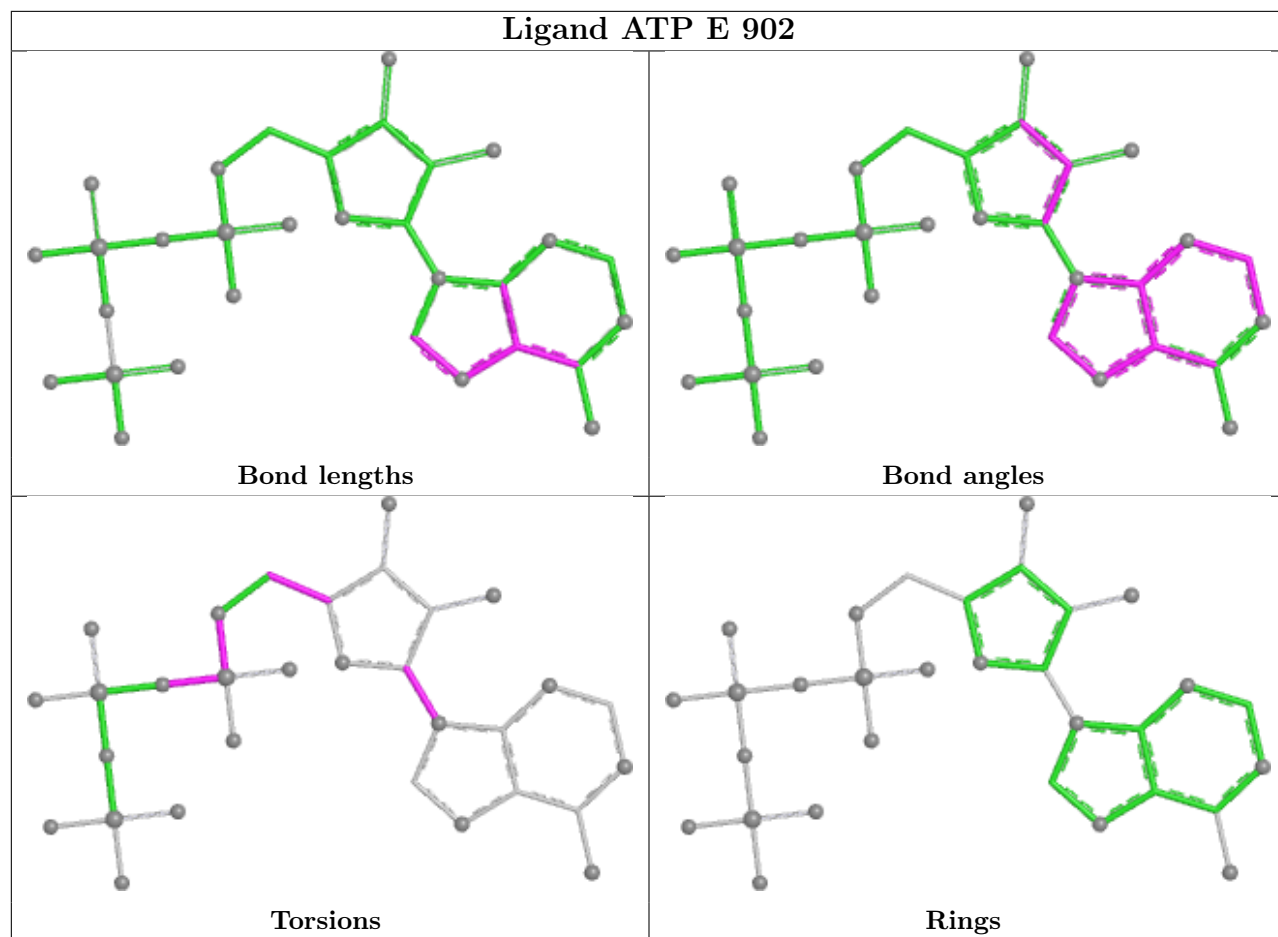


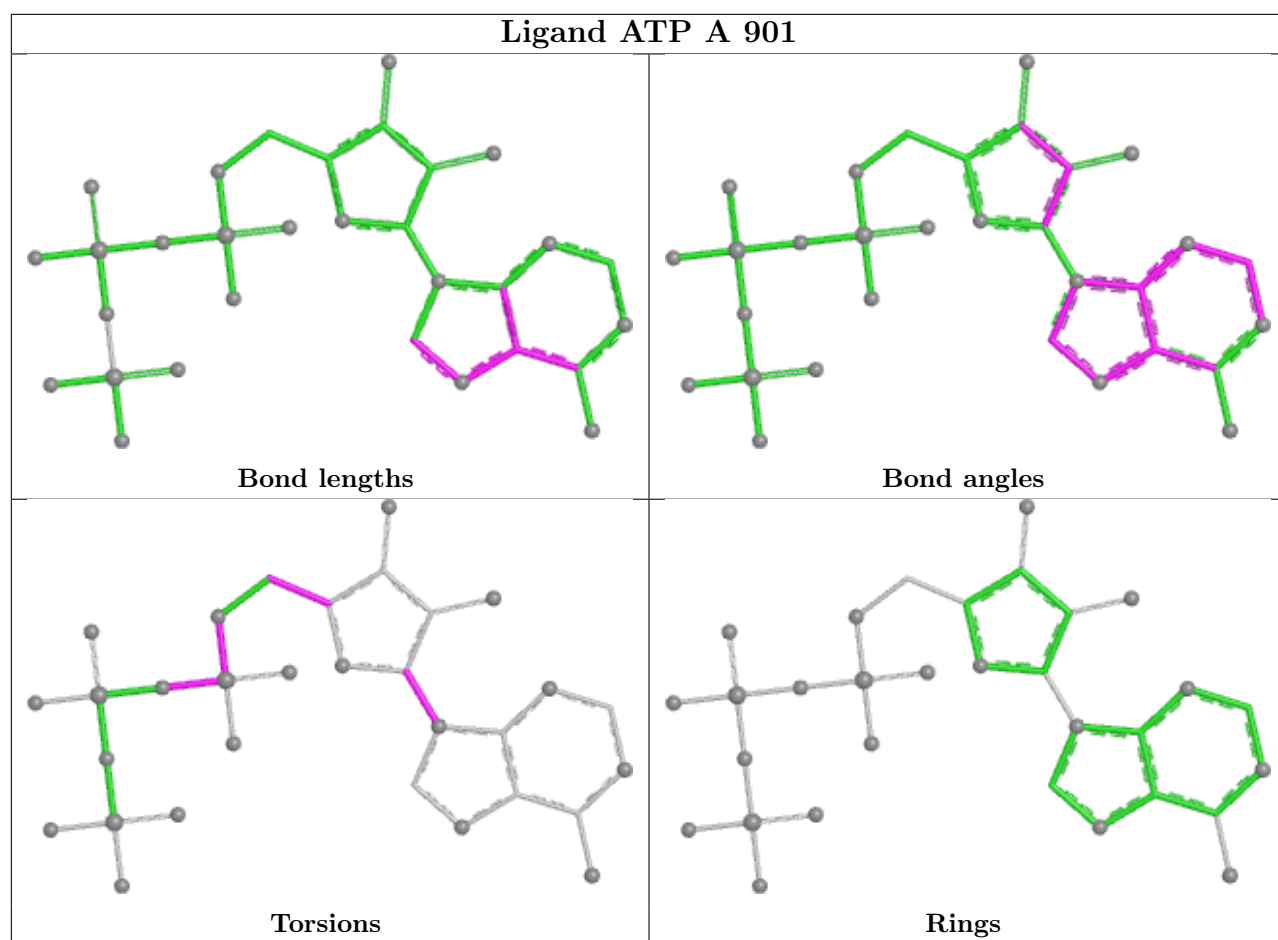


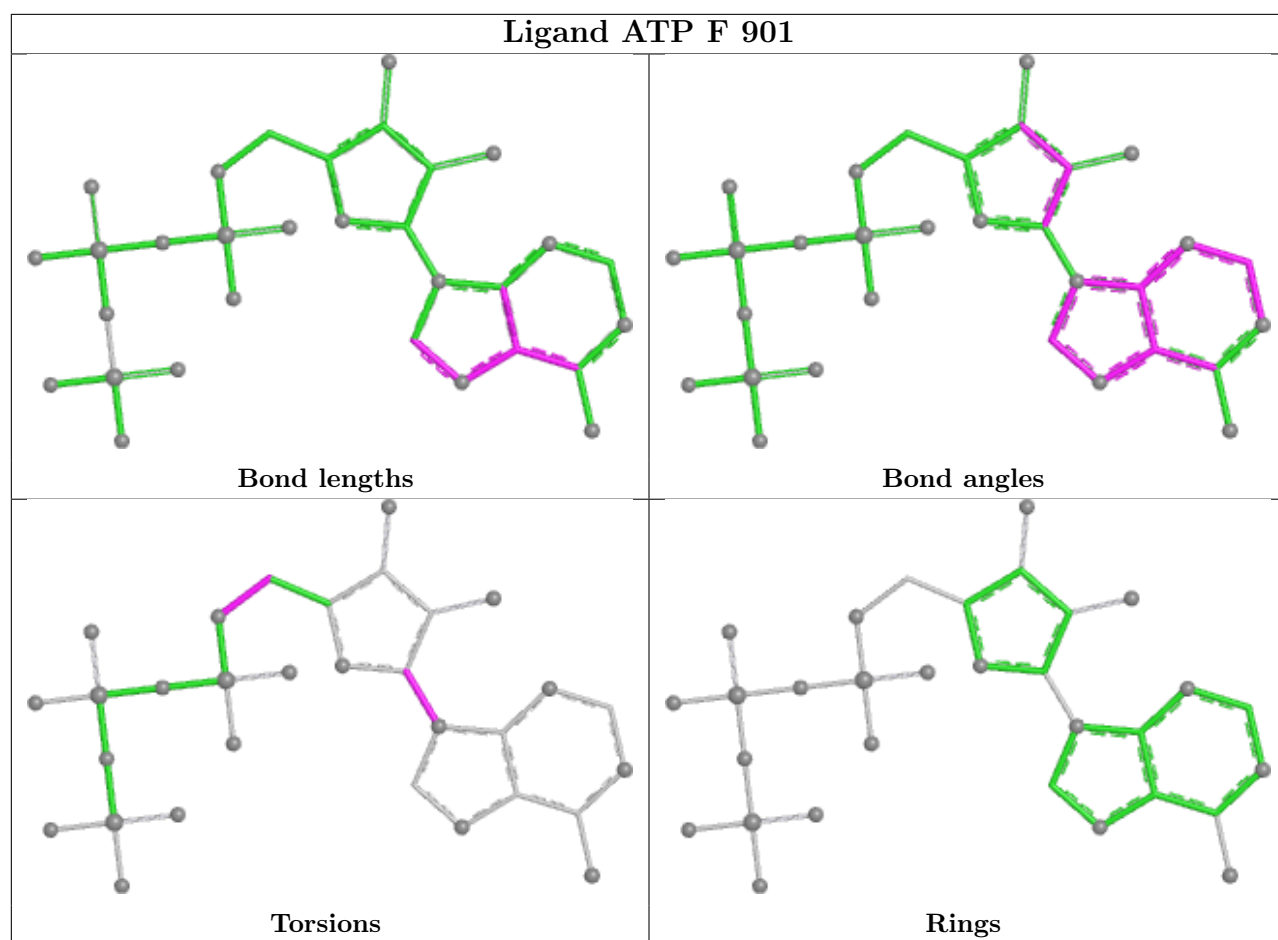


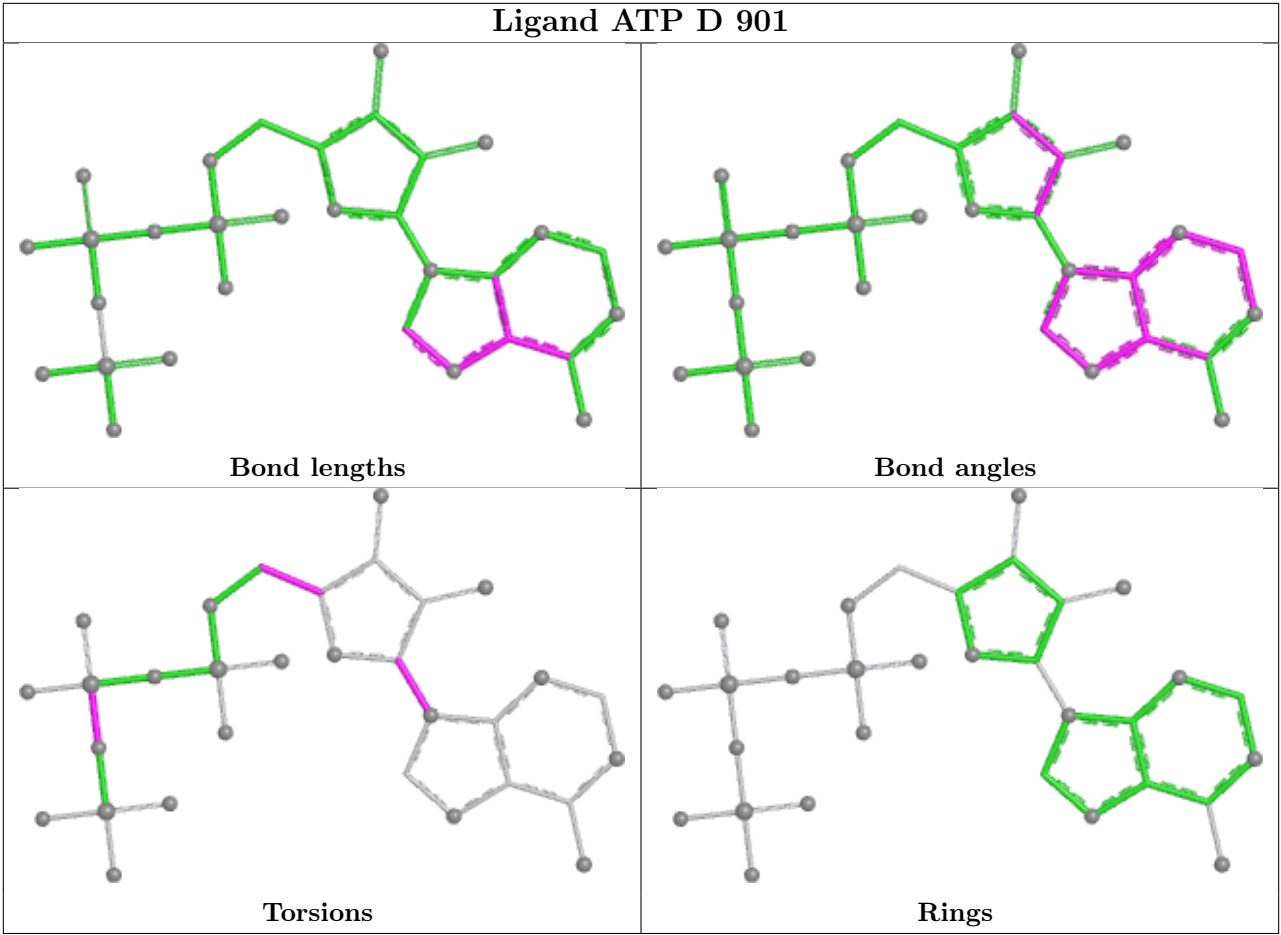












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	e	2
53	v	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	e	1071:THR	C	1072:ALA	N	3.98
1	e	932:LEU	C	933:LEU	N	2.01
1	v	439:GLN	C	440:ARG	N	1.62

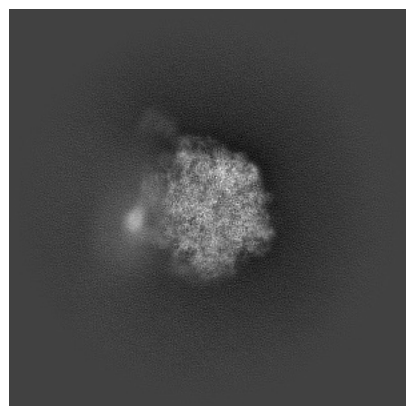
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70444. These allow visual inspection of the internal detail of the map and identification of artifacts.

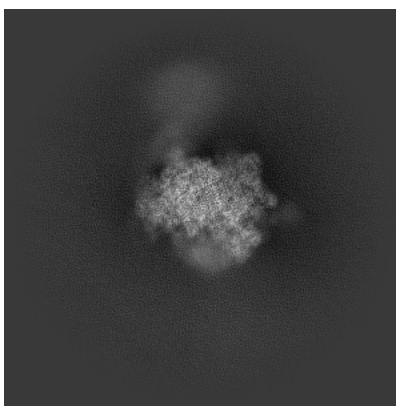
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

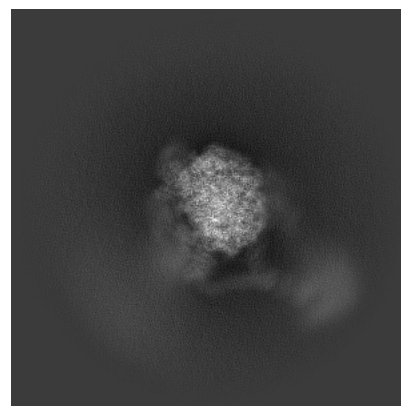
6.1.1 Primary map



X

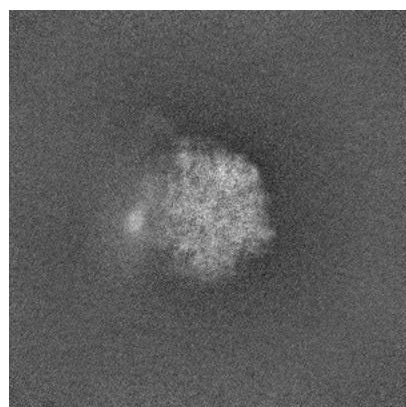


Y

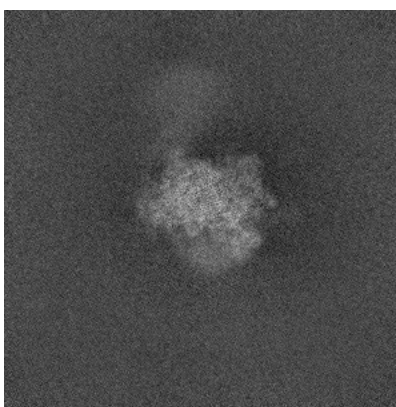


Z

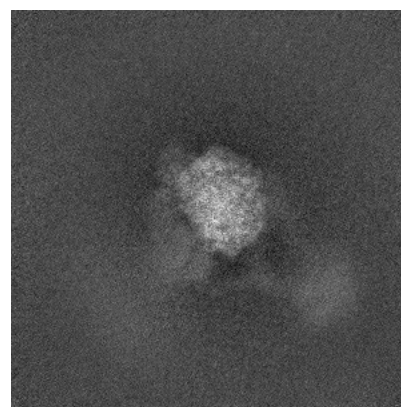
6.1.2 Raw map



X



Y

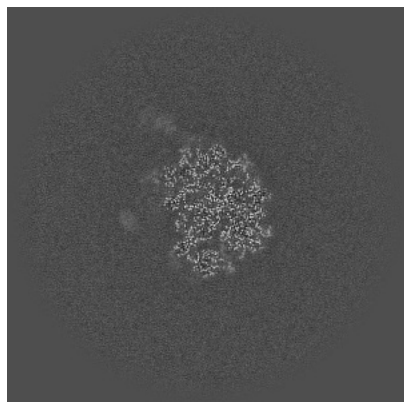


Z

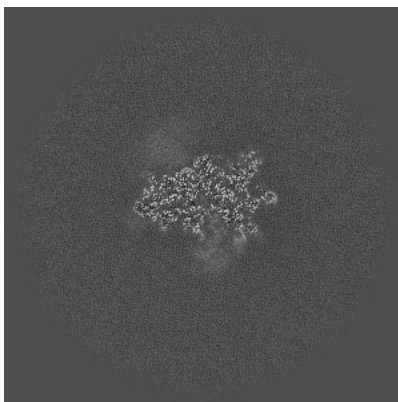
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

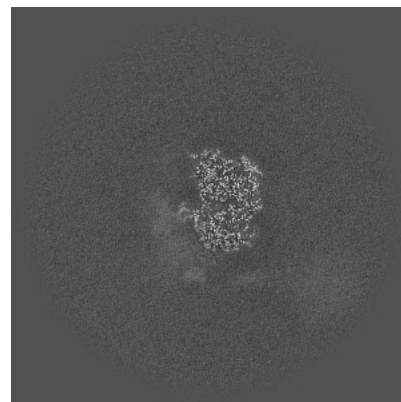
6.2.1 Primary map



X Index: 320

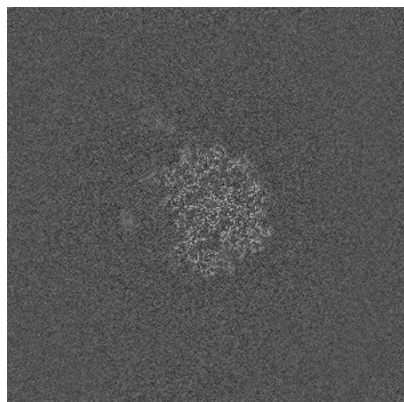


Y Index: 320

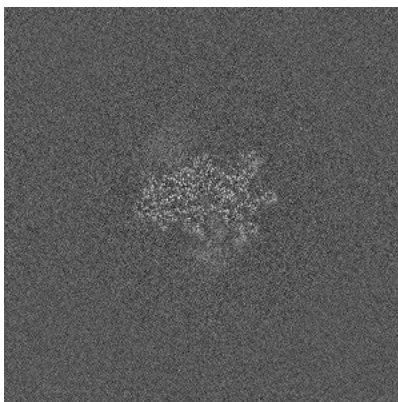


Z Index: 320

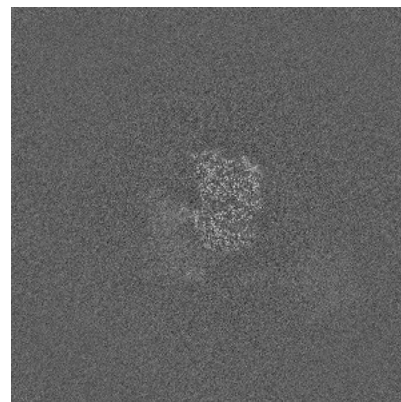
6.2.2 Raw map



X Index: 320



Y Index: 320

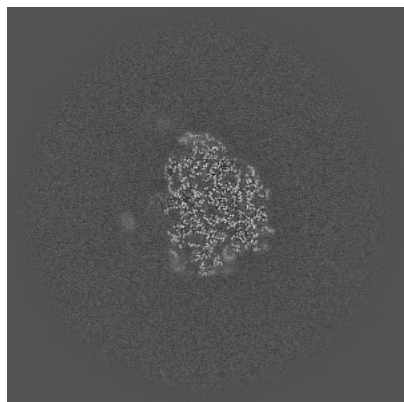


Z Index: 320

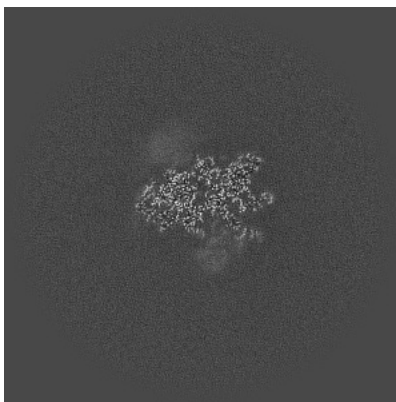
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

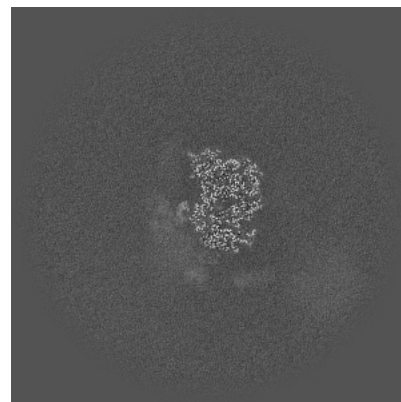
6.3.1 Primary map



X Index: 331

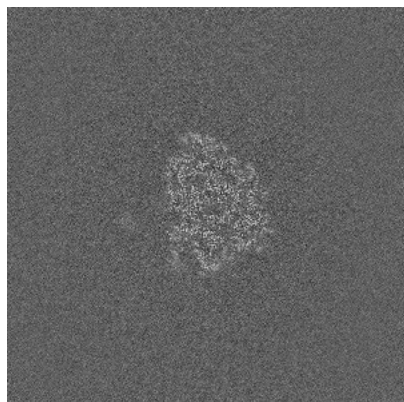


Y Index: 325

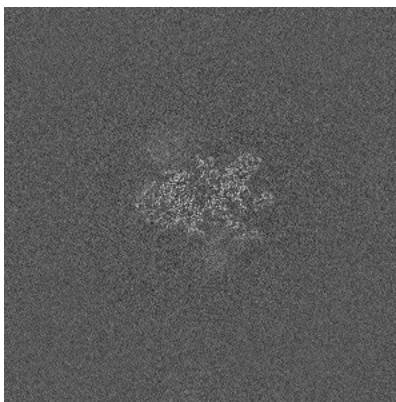


Z Index: 318

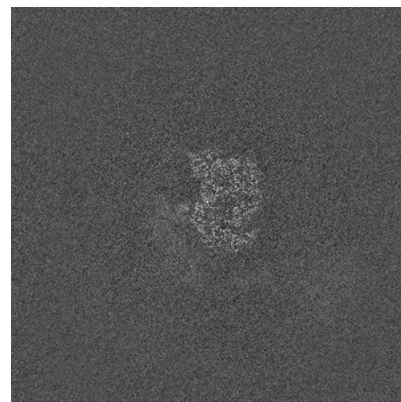
6.3.2 Raw map



X Index: 333



Y Index: 326

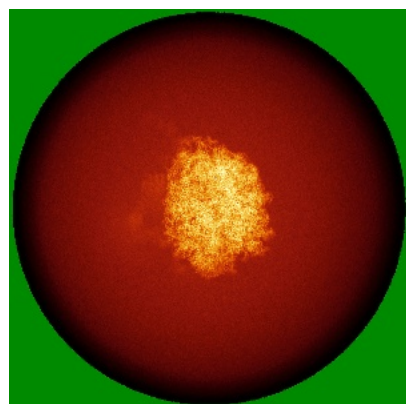


Z Index: 317

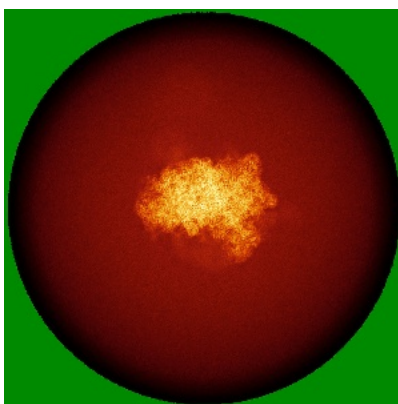
The images above show the largest variance slices of the map in three orthogonal directions.

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

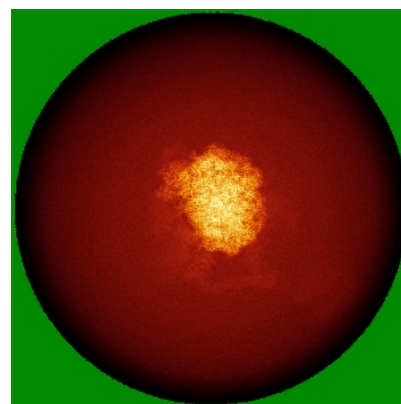
6.4.1 Primary map



X

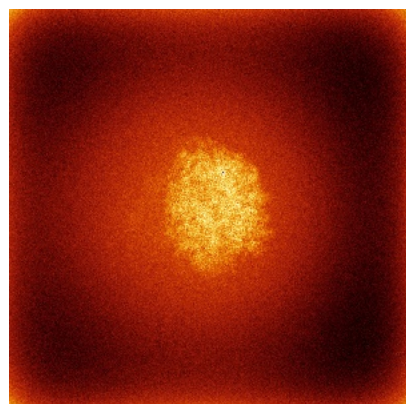


Y

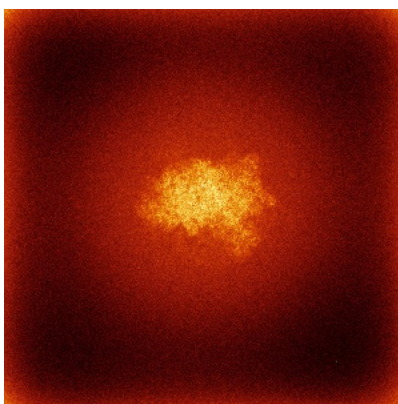


Z

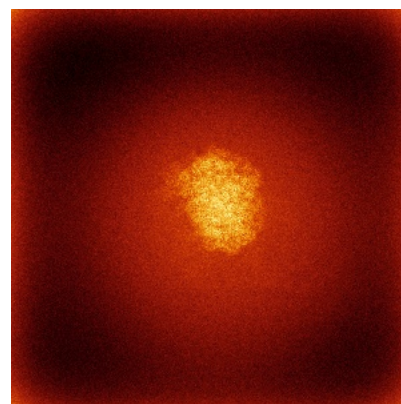
6.4.2 Raw map



X



Y

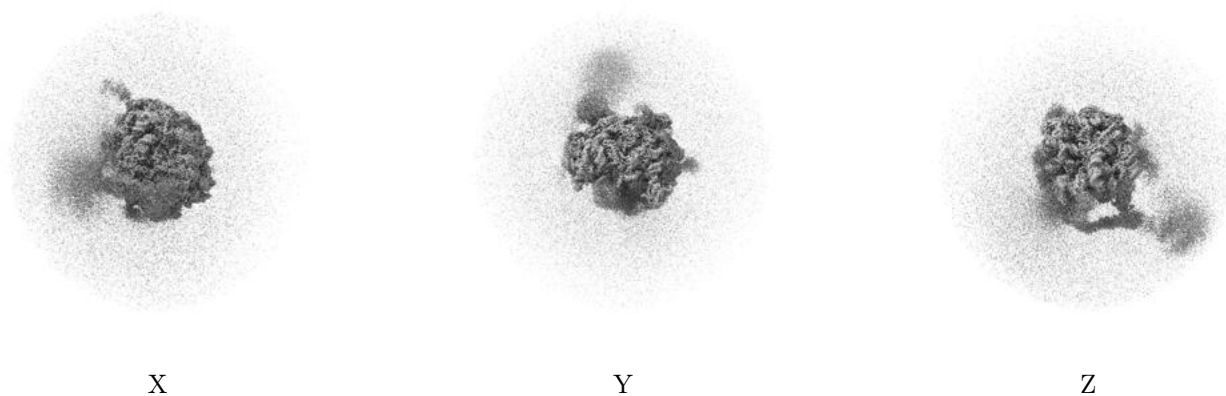


Z

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

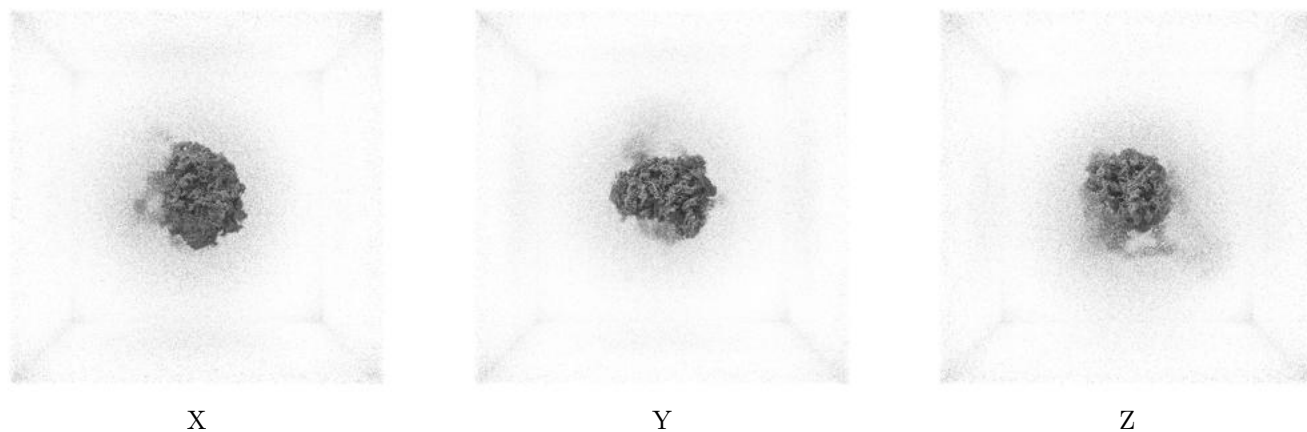
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.187. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

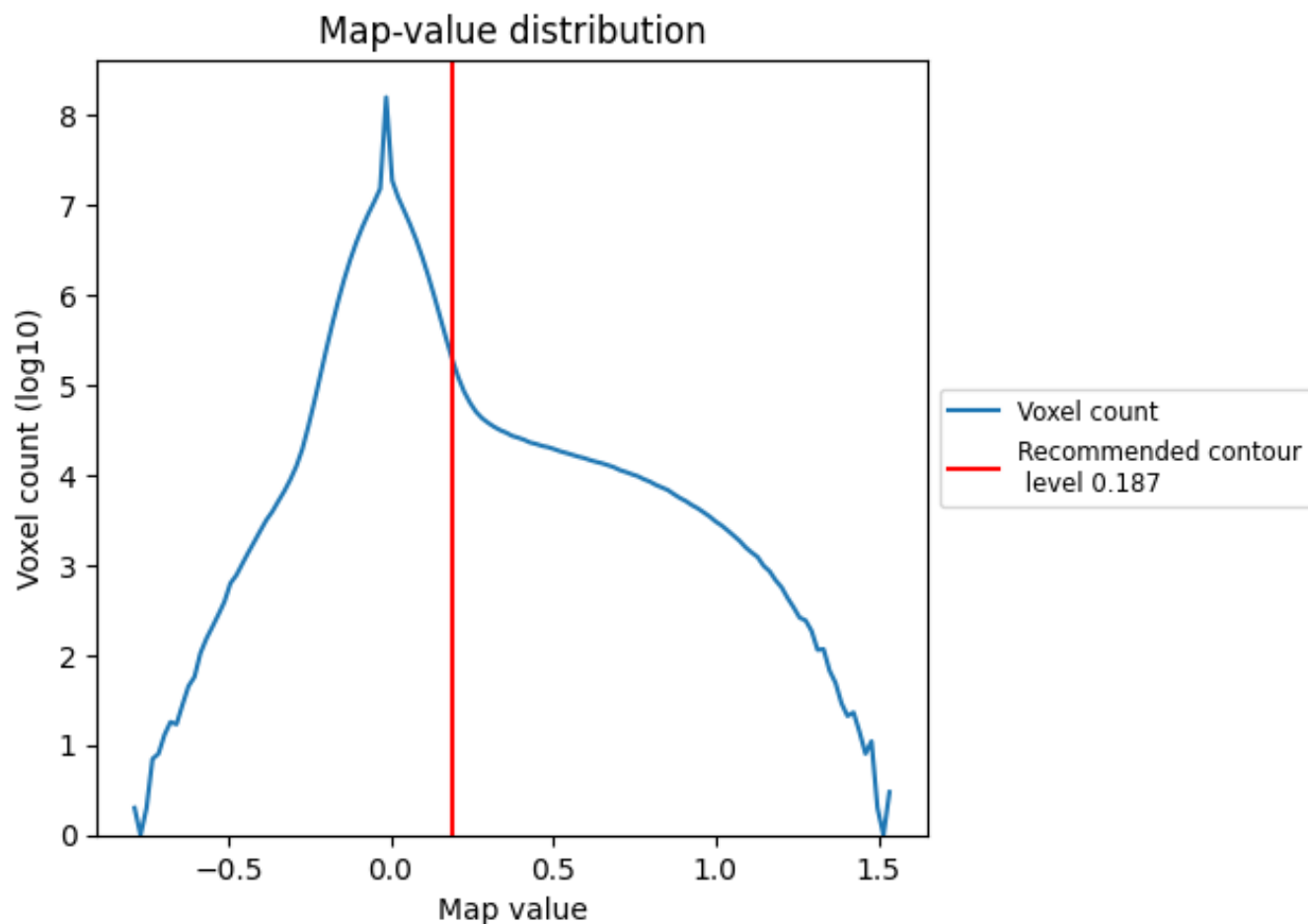
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

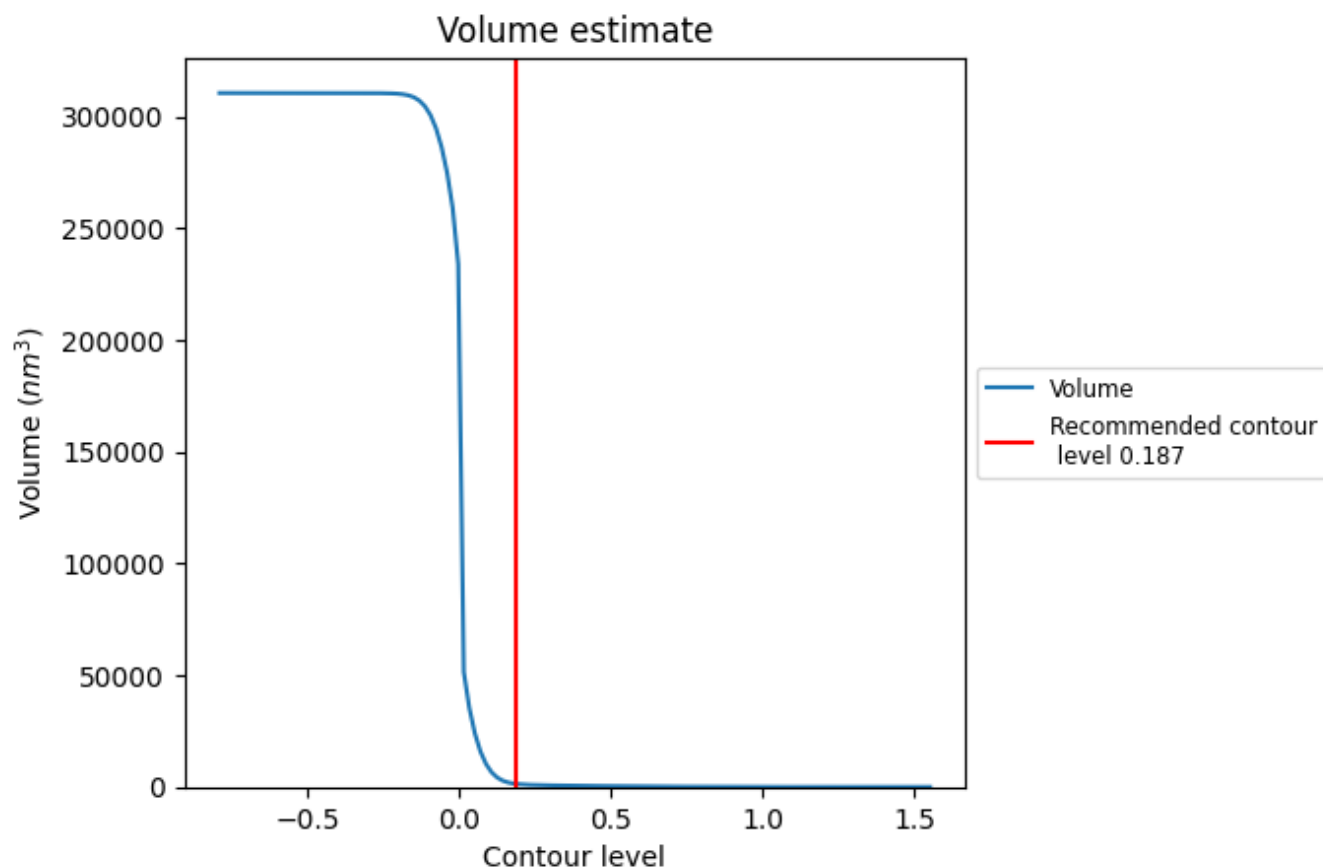
This section contains the results of statistical analysis of the map.

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.

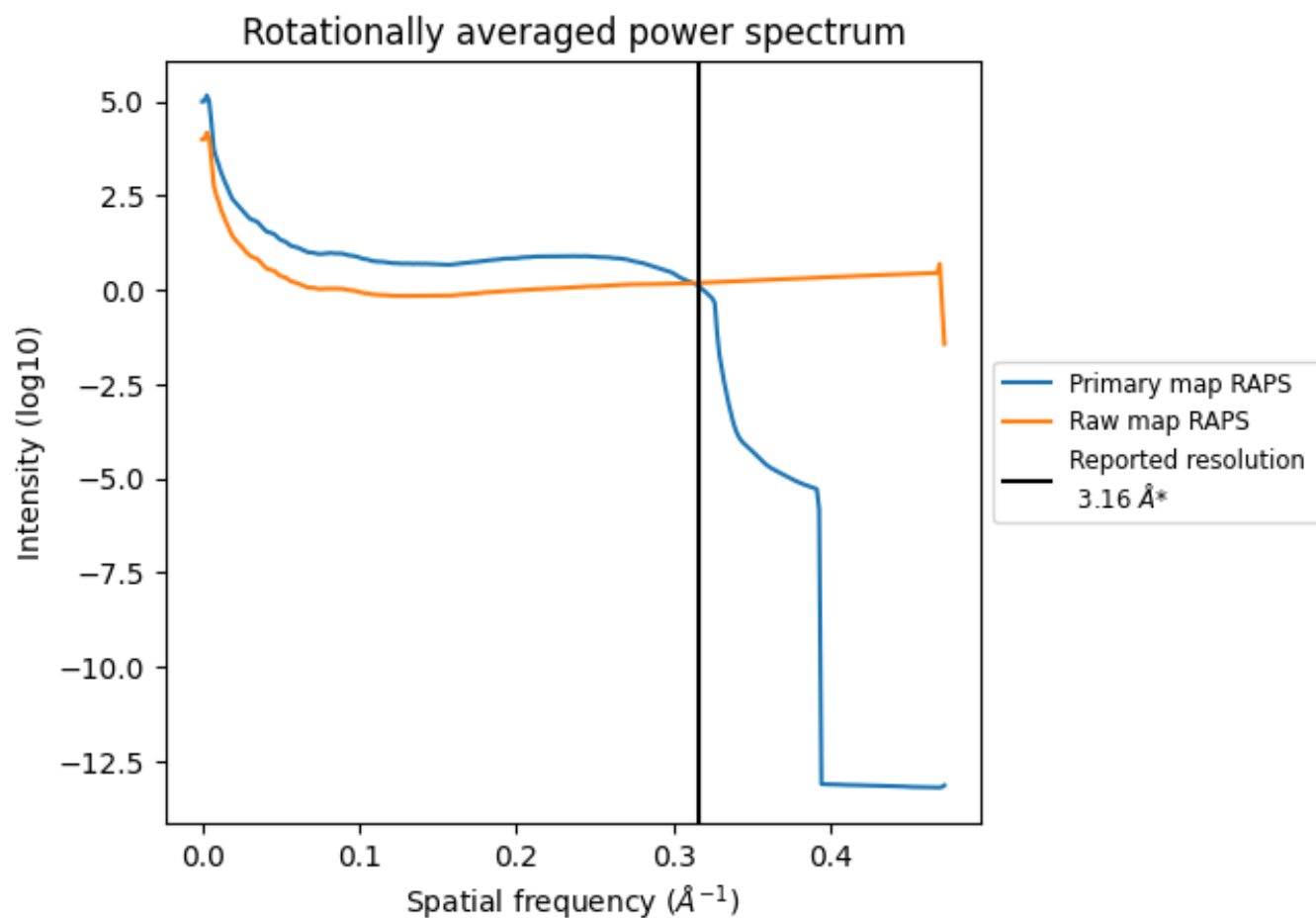
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1424 nm³; this corresponds to an approximate mass of 1287 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 ⓘ

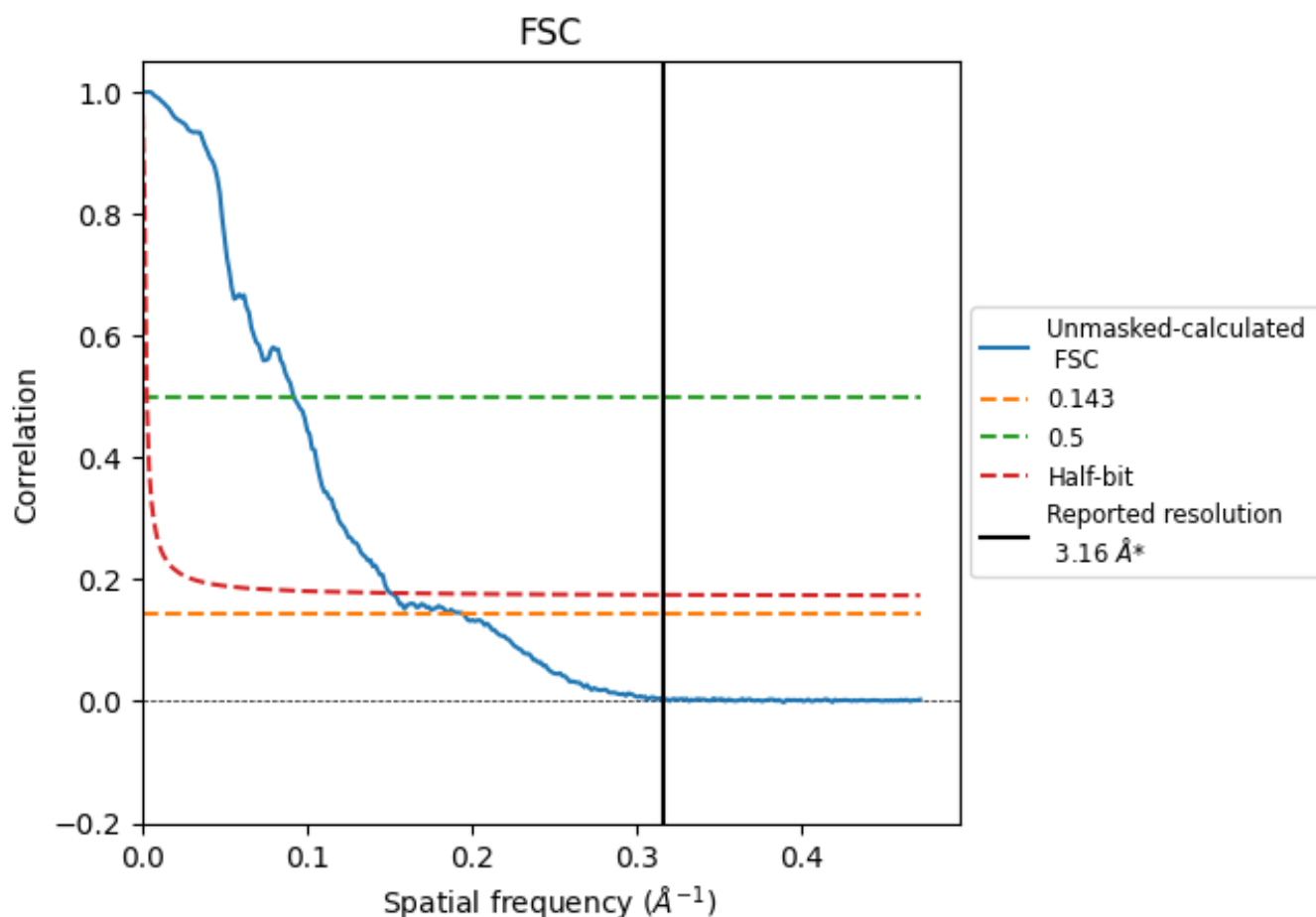


*Reported resolution corresponds to spatial frequency of 0.316 Å⁻¹

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 0.316 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.12	10.83	6.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.12 differs from the reported value 3.16 by more than 10 %

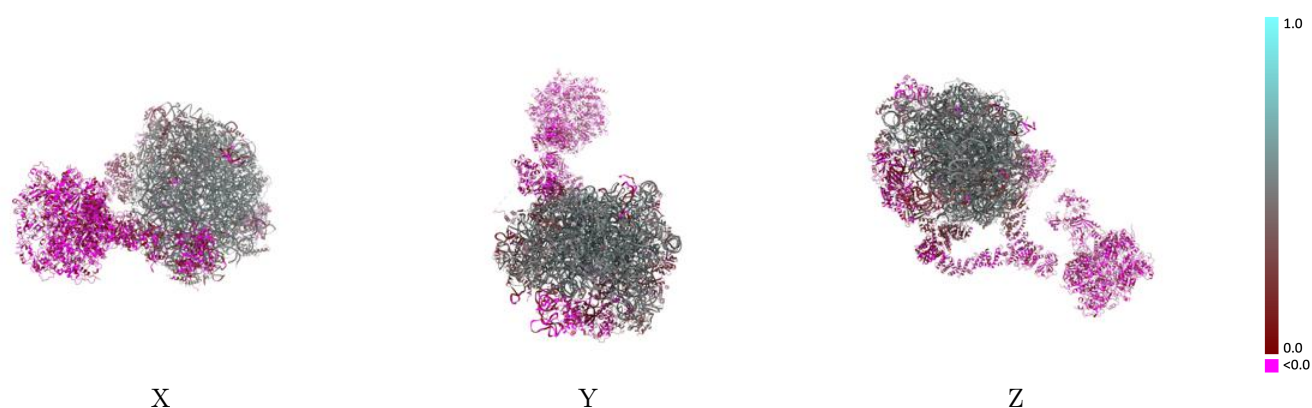
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70444 and PDB model 9OFV. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)

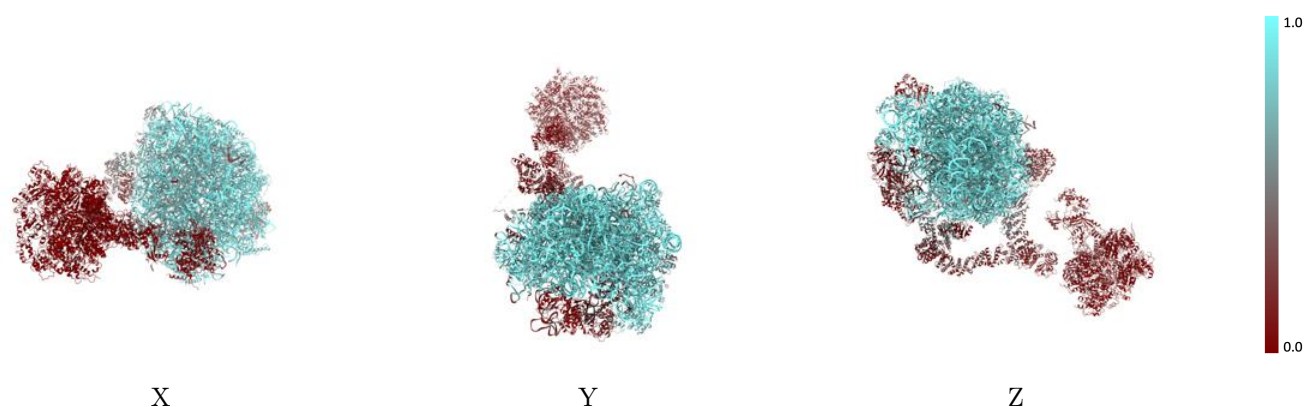
This section was not generated.

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



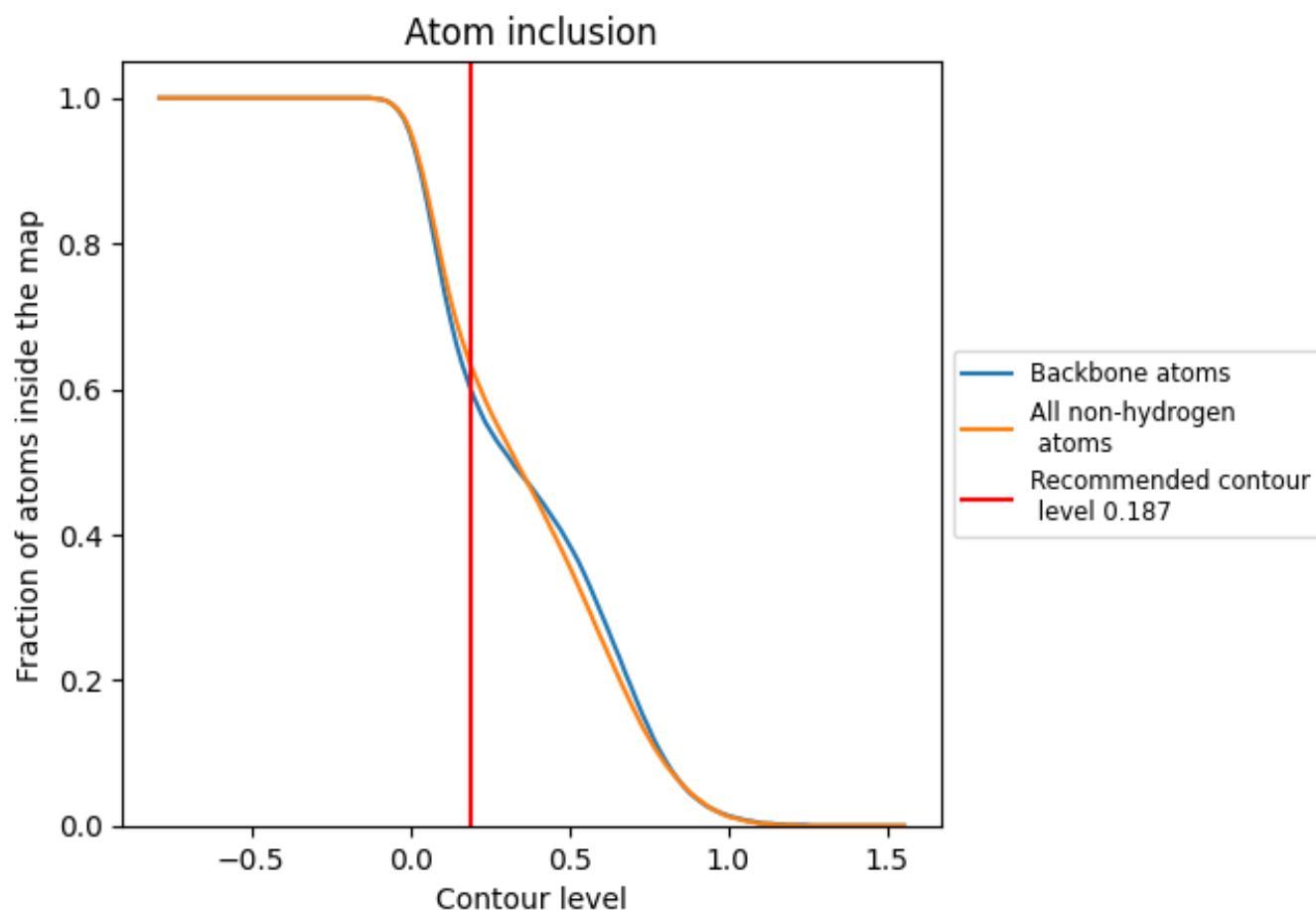
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.187).

9.4 Atom inclusion [i](#)



At the recommended contour level, 60% of all backbone atoms, 64% 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 (0.187) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6360	 0.3290
0	 0.5700	 0.2150
1	 0.5770	 0.3690
2	 0.0370	 -0.0080
3	 0.8750	 0.5180
4	 0.9070	 0.5240
5	 0.8230	 0.4600
6	 0.8890	 0.5070
7	 0.8730	 0.5020
8	 0.7950	 0.4250
9	 0.8670	 0.4790
A	 0.0140	 0.0070
B	 0.0140	 0.0020
C	 0.0070	 -0.0160
D	 0.0080	 -0.0000
E	 0.0070	 0.0060
F	 0.0070	 0.0010
G	 0.0030	 0.0110
H	 0.0000	 0.0090
I	 0.8320	 0.4920
J	 0.0020	 0.0010
K	 0.0000	 0.0050
L	 0.8780	 0.4980
M	 0.8280	 0.4230
N	 0.9090	 0.5300
O	 0.8500	 0.4880
P	 0.8180	 0.4310
Q	 0.8330	 0.4800
R	 0.8980	 0.5310
S	 0.9000	 0.5270
T	 0.8420	 0.4740
U	 0.8560	 0.4850
V	 0.8450	 0.4450
W	 0.9210	 0.5440
X	 0.7280	 0.3320



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Chain	Atom inclusion	Q-score
Y	 0.9060	 0.5280
Z	 0.8720	 0.4990
a	 0.1590	 0.0670
a0	 0.7390	 0.3180
b	 0.8670	 0.5000
b0	 0.6670	 0.2380
c	 0.8510	 0.4680
d	 0.2180	 0.2700
e	 0.2610	 0.0850
f	 0.9320	 0.4770
g	 0.0740	 0.2270
h	 0.9720	 0.4930
i	 0.9530	 0.4990
j	 0.8840	 0.5060
k	 0.8870	 0.5090
l	 0.8930	 0.5050
m	 0.8370	 0.4270
n	 0.8270	 0.4420
o	 0.8820	 0.4900
p	 0.8250	 0.4280
q	 0.8530	 0.4740
r	 0.8410	 0.4820
s	 0.8110	 0.3930
t	 0.8930	 0.4940
u	 0.8530	 0.4610
v	 0.0890	 0.0090
w	 0.0490	 0.0010
x	 0.1830	 0.0950
y	 0.2690	 0.0980
z	 0.4600	 0.1380