



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Feb 18, 2018 – 07:23 am GMT

PDB ID : 5T2C
EMDB ID: : EMD-8345
Title : CryoEM structure of the human ribosome at 3.6 Angstrom resolution
Authors : Zhang, X.; Lai, M.; Zhou, Z.H.
Deposited on : 2016-08-23
Resolution : 3.60 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

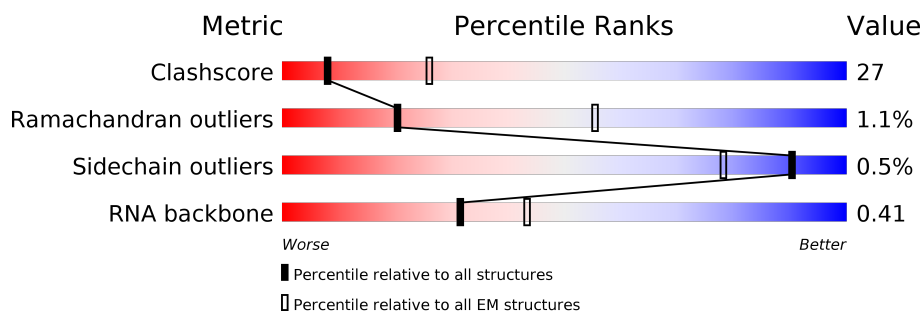
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.

















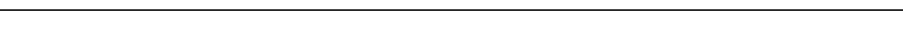
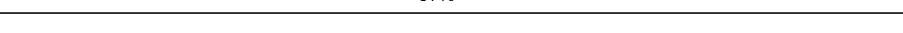

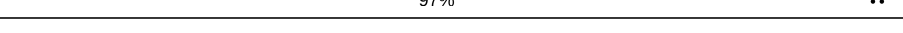
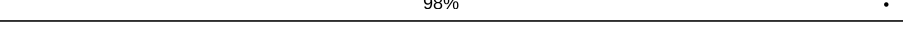
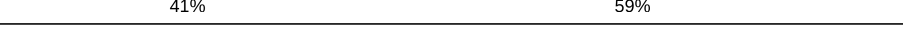
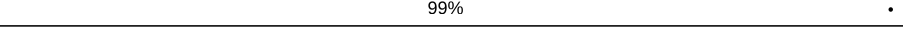



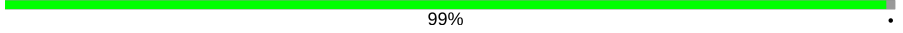
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136279	1886
Ramachandran outliers	132675	1663
Sidechain outliers	132484	1531
RNA backbone	3744	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	B	121	71% 25% . .
2	C	157	67% 23% 10% .
3	D	257	70% 26% .
4	E	403	74% 26%
5	F	427	64% 22% 14%
6	G	297	71% 27% .
7	I	203	79% 20% .
8	J	160	78% 18% .

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Mol	Chain	Length	Quality of chain
9	L	196	
10	N	160	
11	O	128	
12	P	140	
13	Q	157	
14	S	145	
15	T	136	
16	U	148	
17	V	159	
18	X	125	
19	Y	135	
20	Z	110	
21	a	117	
22	b	123	
23	c	105	
24	d	97	
25	e	70	
26	f	51	
27	g	128	
28	j	92	
29	k	137	
30	m	248	
31	n	266	
32	o	192	
33	s	215	




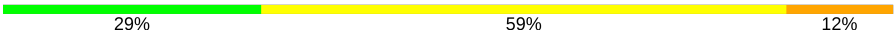


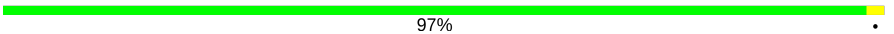

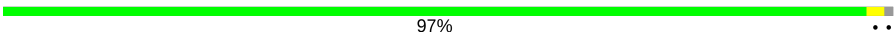

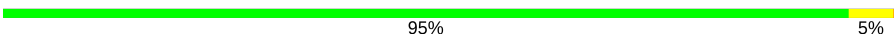
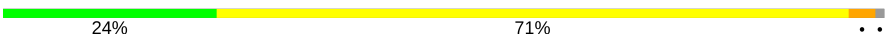





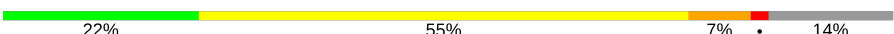





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Mol	Chain	Length	Quality of chain
34	t	204	99%
35	h	25	92%
36	r	211	97%
37	A	5070	41% 25% 8% 26%
38	H	288	53% 26% 16%
39	i	106	97%
40	K	188	71% 28%
41	l	217	98%
42	M	176	73% 24%
43	p	214	98%
44	q	178	96%
45	R	156	63% 13% 23%
46	W	115	60% 25% 15%
47	AA	1869	32% 46% 11% 7%
48	AC	83	36% 60%
49	AD	143	41% 55%
50	AE	115	34% 54% 12%
51	AF	69	30% 59% 9%
52	AH	156	22% 21% 54%
53	AJ	293	20% 54% 24%
54	AK	249	27% 67% 5%
55	AL	194	32% 63% 5%
56	AN	151	35% 62%
57	AP	130	32% 63% 5%
58	AQ	133	23% 73%

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Mol	Chain	Length	Quality of chain
59	AR	125	
60	AT	59	
61	AV	84	
62	An	75	
63	Ap	264	
64	Aq	243	
65	Ar	263	
66	At	194	
67	Au	208	
68	Av	165	
69	Ay	146	
70	A0	152	
71	Ao	295	
72	As	204	
73	Aw	158	
74	Ax	145	
75	Az	135	
76	AB	119	
77	AG	56	
78	AI	317	
79	AM	132	
80	AO	151	
81	AU	145	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 217989 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	367	Total	C	N	O	S	0	0
			2919	1835	582	488	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 7 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 8 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 9 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 10 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 11 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 12 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 13 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	64	Total	C	N	O	S	0	0
			534	340	104	87	3		

- Molecule 14 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 15 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 16 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 17 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 18 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	X	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 19 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 20 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 21 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 22 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 23 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 24 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	d	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 25 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	e	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 26 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 28 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 30 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	m	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 31 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	n	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 32 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	o	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 33 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 34 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	t	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 35 is a protein called 60S Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 36 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 37 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A	3776	Total	C	N	O	P	0	0
			80184	35672	14597	26140	3775		

- Molecule 38 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 39 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 40 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 41 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 42 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	M	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 43 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 44 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 45 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	R	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 46 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AA	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a protein called 40S ribosomal protein S21.

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

- Molecule 49 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AD	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 50 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AE	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 51 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AF	63	Total	C	N	O	S	0	0
			498	302	101	93	2		

- Molecule 52 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AH	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AJ	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AK	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 55 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AL	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 57 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AP	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 58 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AQ	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 59 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AR	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 60 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 61 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AV	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 62 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	An	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 63 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ap	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 64 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Aq	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 65 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ar	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 66 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	At	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 67 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Au	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 68 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Av	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 69 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ay	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	A0	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ao	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 72 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	As	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 73 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Aw	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 74 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ax	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Az	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AB	102	Total	C	N	O	S	0	0
			807	507	153	143	4		

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AG	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AI	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 79 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	52	GLN	LEU	conflict	UNP P25398
AM	69	LEU	CYS	conflict	UNP P25398
AM	99	ASN	LYS	conflict	UNP P25398

- Molecule 80 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

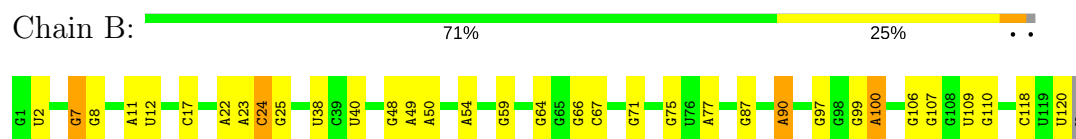
- Molecule 81 is a protein called 40S ribosomal protein S19.

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

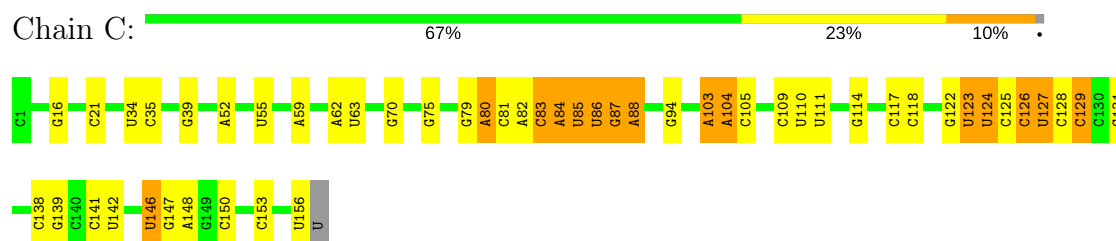
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

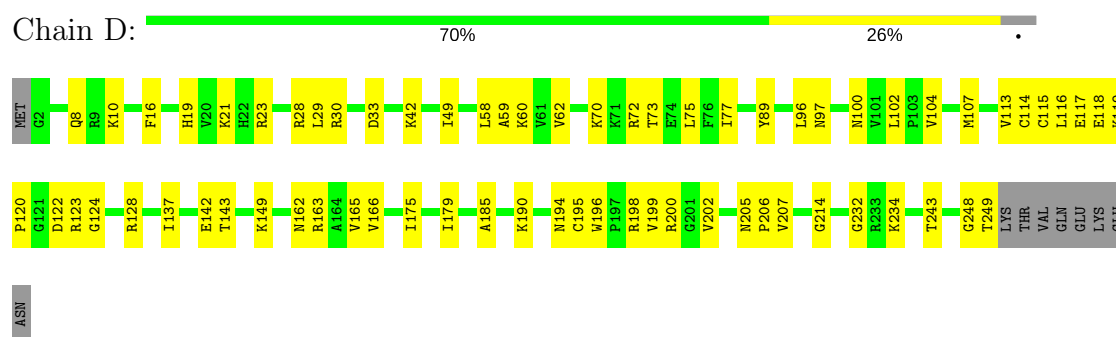
• Molecule 1: 5S rRNA



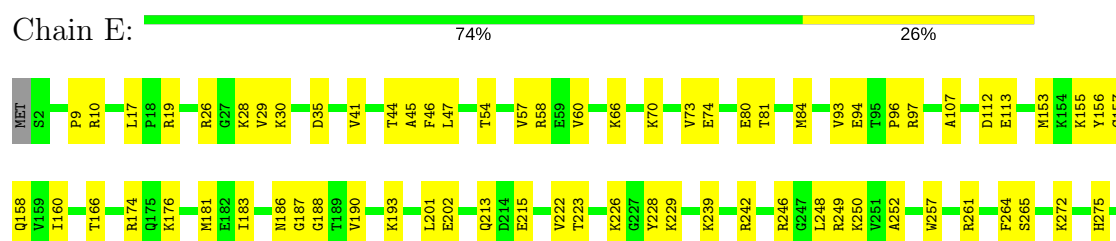
• Molecule 2: 5.8S rRNA



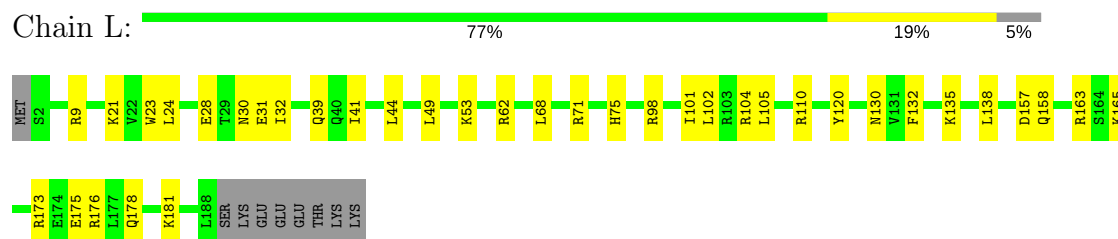
• Molecule 3: 60S ribosomal protein L8



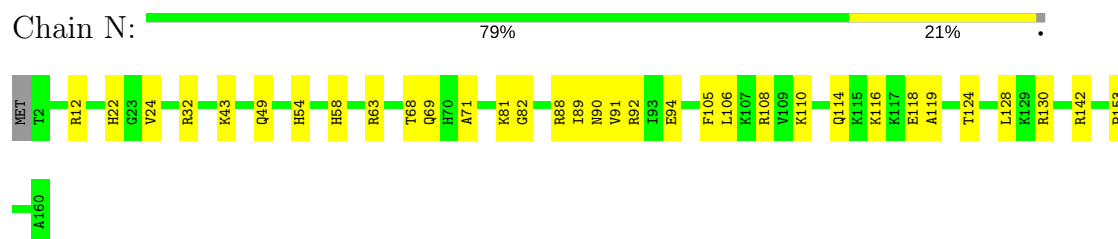
• Molecule 4: 60S ribosomal protein L3



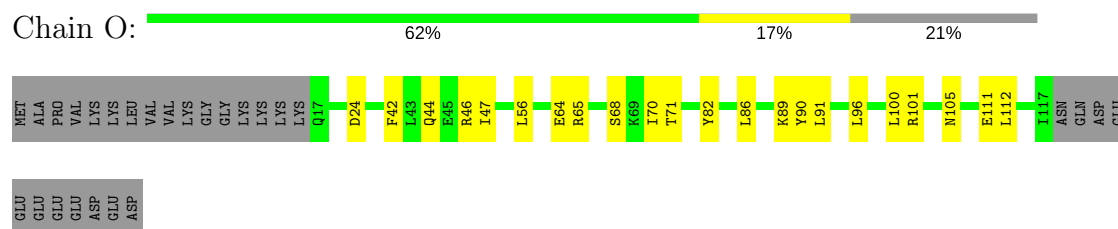
- Molecule 9: 60S ribosomal protein L19



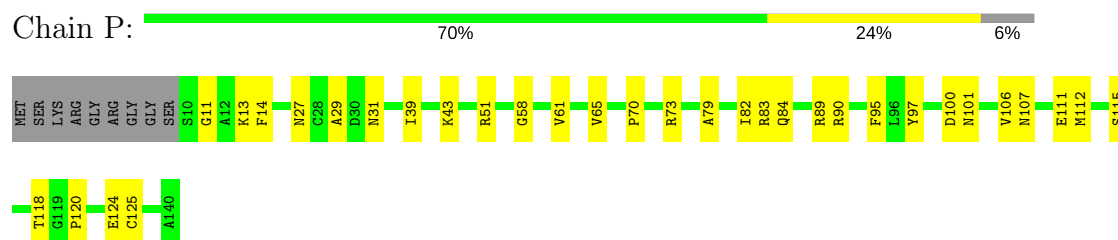
- Molecule 10: 60S ribosomal protein L21



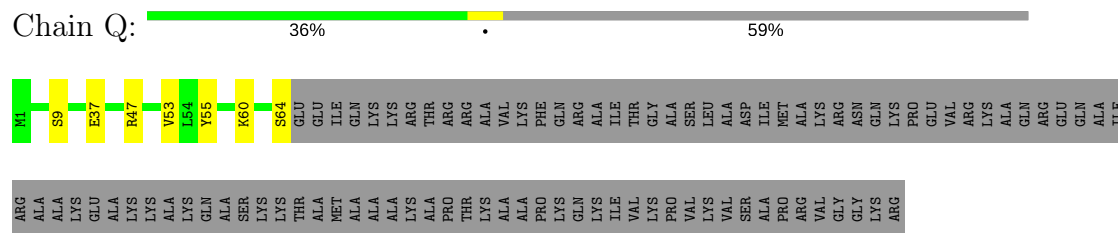
- Molecule 11: 60S ribosomal protein L22



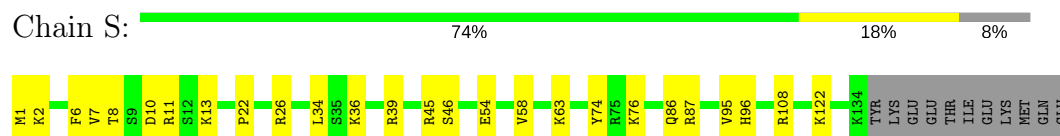
- Molecule 12: 60S ribosomal protein L23



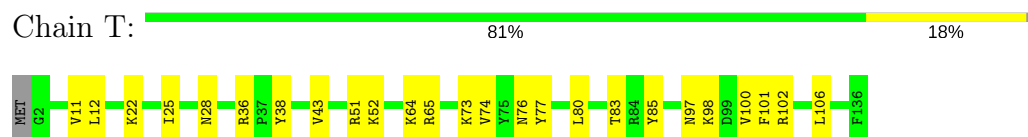
- Molecule 13: 60S ribosomal protein L24



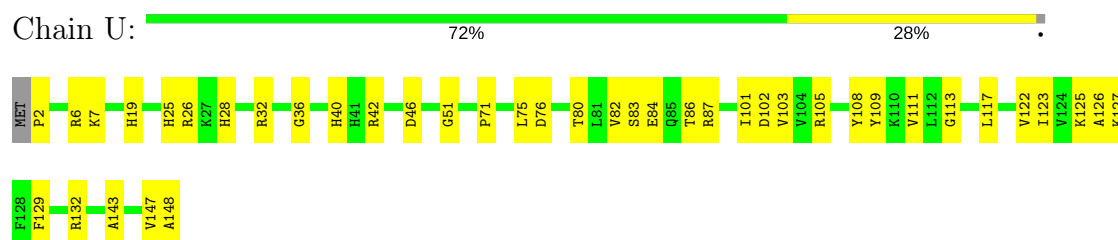
- Molecule 14: 60S ribosomal protein L26



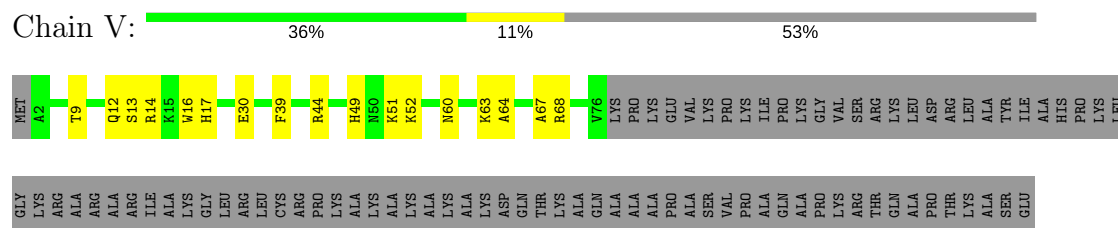
- Molecule 15: 60S ribosomal protein L27



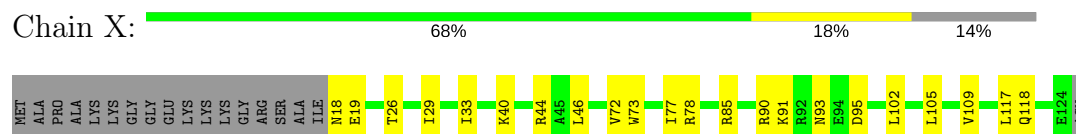
- Molecule 16: 60S ribosomal protein L27a



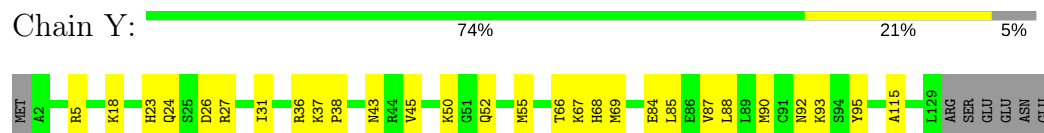
- Molecule 17: 60S ribosomal protein L29



- Molecule 18: 60S ribosomal protein L31

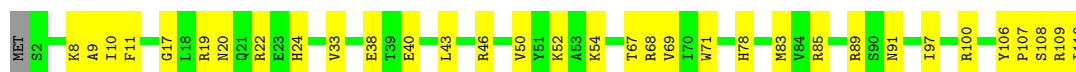


- Molecule 19: 60S ribosomal protein L32



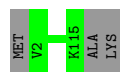
- Molecule 20: 60S ribosomal protein L35a





- Molecule 21: 60S ribosomal protein L34

Chain a: 97%



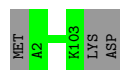
- Molecule 22: 60S ribosomal protein L35

Chain b: 99%



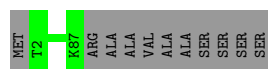
- Molecule 23: 60S ribosomal protein L36

Chain c: 97%



- Molecule 24: 60S ribosomal protein L37

Chain d: 89% 11%



- Molecule 25: 60S ribosomal protein L38

Chain e: 97%



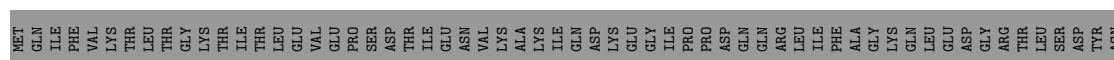
- Molecule 26: 60S ribosomal protein L39

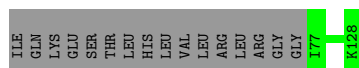
Chain f: 98%



- Molecule 27: Ubiquitin-60S ribosomal protein L40

Chain g: 41% 59%





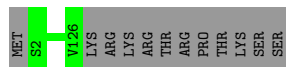
- Molecule 28: 60S ribosomal protein L37a

Chain j: 99%



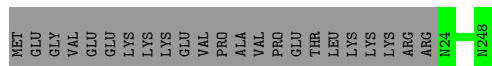
- Molecule 29: 60S ribosomal protein L28

Chain k: 91% 9%



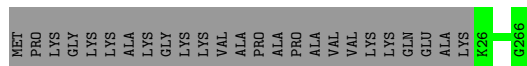
- Molecule 30: 60S ribosomal protein L7

Chain m: 91% 9%



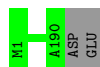
- Molecule 31: 60S ribosomal protein L7a

Chain n: 91% 9%



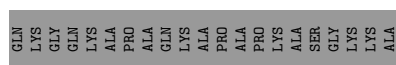
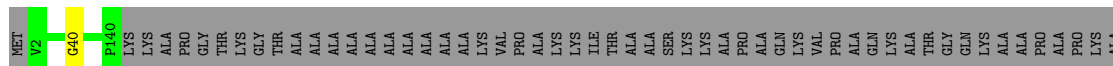
- Molecule 32: 60S ribosomal protein L9

Chain o: 99%



- Molecule 33: 60S ribosomal protein L14

Chain s: 64% 35%



- Molecule 34: 60S ribosomal protein L15

Chain t: 99%



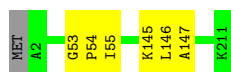
- Molecule 35: 60S Ribosomal protein L41

Chain h: 92% . .



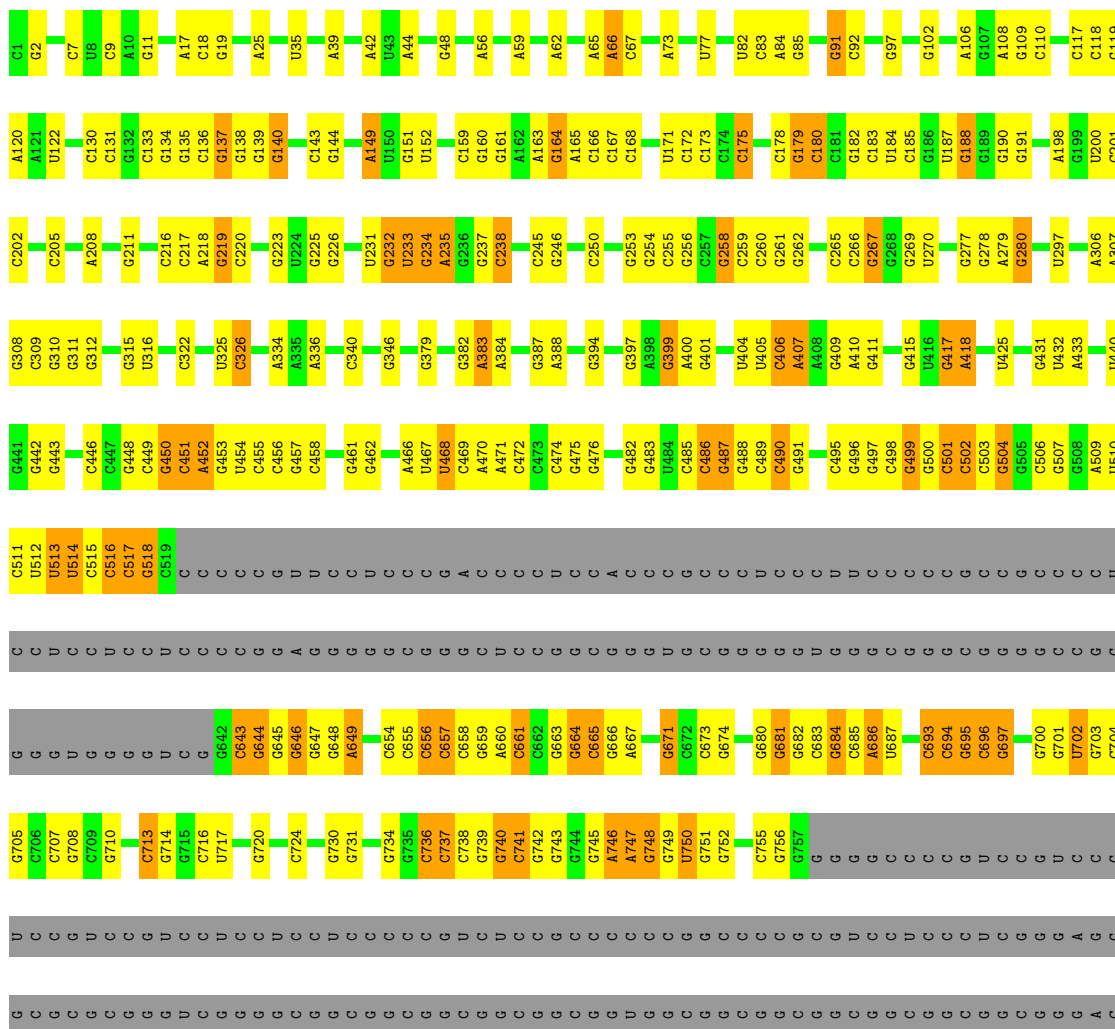
- Molecule 36: 60S ribosomal protein L13

Chain r:  97%



- Molecule 37: 28S rRNA

Chain A: 41% 25% 8% 26%

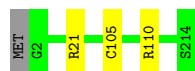


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G2114	A1766	A1554	G1448	A1372	G1277	C1216	G	G	G965	G
G2115	A1767	A1563	C1449	C1375	C1278	G1217	C	G	A966	A
G2116	C1768	A1563	C1450	C1376	G1279	G1218	G	G	C967	A
G2117	G1769	A1564	G1451	G1377	G1280	C1219	C	G	A968	A
G2118	A1770	A1565	C1455	C1378	G1281	G1220	C	G	C969	C
G2119	U1771	C1566	C1456	C1379	G1282	G1221	C	G	G970	C
G2120	C1772	G1573	G1457	C1380	G1283	A1222	C	G	C971	C
G2121	U1773	G1573	C1457	U1381	G1284	G	C	C	C972	C
G2122	A1774	G1577	C1468	C1382	G1285	U	C	C	C973	C
G2123	A1775	U1578	C1468	A1387	G1286	U	C	C	C974	C
G2124	A1776	C1586	G1474	C1388	G1288	U	C	C	C975	C
G2125	C1777	G1586	G1475	A1387	C1289	U	C	C	C976	C
G2126	C1778	C	C1476	C1387	G1290	U	C	C	C977	C
G2127	U1781	C	C1477	C1390	G1291	C	C	C	C978	C
G2128	U1782	C	C1478	A1391	G1292	C	C	C	G979	C
G2129	C1783	C	C1479	A1392	G1293	G1232	C	C	U980	C
G2130	G1879	C	C1480	A1393	C1294	G1233	C	C	U981	C
G2131	C1879	C	C1481	G1394	C1295	G1234	C	C	U982	C
G2132	A1787	C	C1482	U1395	G1296	G1235	C	C	C983	C
G2133	A1788	C	C1483	G1396	U1297	C1236	C	C	C984	C
G2134	A1789	C	C1484	A1397	G1298	C1237	C	C	C985	C
G2135	A1794	C	C1485	A1398	G1299	A1238	C	C	C986	C
G2136	A1802	C	C1486	G1399	C1300	C1239	C	C	C987	C
G2137	G1803	C	C1487	G1400	C1301	G1240	C	C	C988	C
G2138	A1804	C	C1488	C1401	U1302	C1241	C	C	C989	C
G2139	A1805	C	C1489	C1404	G1311	C1242	C	C	C990	C
G2140	G1806	C	C1490	G1405	U1311	G1243	C	C	C991	C
G2141	C1807	C	C1491	G1406	U1312	C1244	C	C	C992	C
G2142	G1811	C	C1492	C1407	U1313	G1245	C	C	C993	C
G2143	G1815	C	C1493	G1408	G1321	C1246	C	C	C994	C
G2144	C1816	C	C1494	C1409	A1322	U1247	C	C	C995	C
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G2147	G1819	C	C1503	G1412	C1325	C1250	C	C	C998	C
G2148	C1820	C	C1504	C1413	A1326	C1251	C	C	C999	C
G2149	G1821	C	C1505	C1414	G1329	C1252	C	C	C999	C
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G2152	G1823	C	C1508	C1417	U1339	A1255	C	C	C999	C
G2153	A1825	C	C1509	C1418	C1340	G1256	C	C	C999	C
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G2158	G1832	C	C1514	G1423	G1358	A1263	C	C	C999	C
G2159	U1833	C	C1515	A1433	G1359	G1265	C	C	C999	C
G2160	C1834	C	C1516	G1434	G1360	G1266	C	C	C999	C
G2161	G1835	C	C1517	C1435	G1361	G1267	C	C	C999	C
G2162	G1836	C	C1518	C1436	G1365	G1268	C	C	C999	C
G2163	G1837	C	C1519	C1437	G1366	G1269	C	C	C999	C
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G2168	G1842	C	C1524	C1442	A1370	G1274	C	C	C999	C
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G2170	G1846	C	C1526	G1434	G1371	G1276	C	C	C999	C
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G2172	G1848	C	C1528	C1436	G1373	G1278	C	C	C999	C
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G2174	G1850	C	C1530	C1438	G1375	G1280	C	C	C999	C
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G2176	G1852	C	C1532	C1440	G1377	G1282	C	C	C999	C
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G2181	G1857	C	C1537	C1445	G1382	G1287	C	C	C999	C
G2182	U1858	C	C1538	C1446	G1383	G1288	C	C	C999	C
G2183	A1859	C	C1539	C1447	G1384	G1289	C	C	C999	C
G2184	G1860	C	C1540	C1448	G1385	G1290	C	C	C999	C
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G2190	G1866	C	C1546	C1454	G1391	G1296	C	C	C999	C
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G2194	C1869	C	C1550	C1458	G1395	G1300	C	C	C999	C
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G2201	G1876	C	C1557	C1465	G1402	G1321	C	C	C999	C
G2202	C1877	C	C1558	C1466	G1403	A1322	C	C	C999	C
G2203	G1878	C	C1559	C1467	G1404	A1323	C	C	C999	C
G2204	U1879	C	C1560	C1468	G1405	C1249	C	C	C999	C
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G2206	C1881	C	C1562	C1470	G1407	C1251	C	C	C999	C
G2207	A1882	C	C1563	C1471	G1408	C1252	C	C	C999	C
G2208	G1883	C	C1564	C1472	G1409	G1253	C	C	C999	C
G2209	U1884	C	C1565	C1473	G1410	A1254	C	C	C999	C
G2210	C1885	C	C1566	C1474	G1411	A1255	C	C	C999	C
G2211	G1886	C	C1567	C1475	G1412	G1256	C	C	C999	C
G2212	U1887	C	C1568	C1476	G1413	A1257	C	C	C999	C
G2213	G1888	C	C1569	C1477	G1414	G1260	C	C	C999	C
G2214	C1889	C	C1570	C1478	G1415	G1261	C	C	C999	C
G2215	G1889	C	C1571	C1479	G1416	G1262	C	C	C999	C
G2216	U1890	C	C1572	C1480	G1417	A1263	C	C	C999	C
G2217	G1890	C	C1573	C1481	G1418	G1265	C	C	C999	C
G2218	C1891	C	C1574	C1482	G1419	G1266	C	C	C999	C
G2219	G1892	C	C1575	C1483	G1420	G1267	C	C	C999	C
G2220	A1893	C	C1576	C1484	G1421	G1268	C	C	C999	C
G2221	G1894	C	C1577	C1485	G1422	G1269	C	C	C999	C
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G2223	G1896	C	C1579	C1487	G1424	G1271	C	C	C999	C
G2224	U1897	C	C1580	C1488	G1425	G1272	C	C	C999	C
G2225	G1898	C	C1581	C1489	G1426	G1273	C	C	C999	C
G2226	C1899	C	C1582	C1490	G1427	G1274	C	C	C999	C
G2227	A1899	C	C1583	C1491	G1428	G1275	C	C	C999	C
G2228	G1900	C	C1584	C1492	G1429	G1276	C	C	C999	C
G2229	U1901	C	C1585	C1493	G1430	G1277	C	C	C999	C
G2230	C1902	C	C1586	C1494	G1431	G1278	C	C	C999	C
G2231	G1903	C	C1587	C1495	G1432	G1279	C	C	C999	C
G2232	U1904	C	C1588	C1496	G1433	G1280	C	C	C999	C
G2233	G1905	C	C1589	C1497	G1434	G1281	C	C	C999	C
G2234	C1906	C	C1590	C1498	G1435	G1282	C	C	C999	C
G2235	A1907	C	C1591	C1499	G1436	G1283	C	C	C999	C
G2236	G1908	C	C1592	C1500	G1437	G1284	C	C	C999	C
G2237	U1909	C	C1593	C1501	G1438	G1285	C	C	C999	C
G2238	C1910	C	C1594	C1502	G1439	G1286	C	C	C999	C
G2239	G1911	C	C1595	C1503	G1440	G1287	C	C	C999	C
G2240	U1912	C	C1596	C1504	G1441	G1288	C	C	C999	C
G2241	C1913	C	C1597	C1505	G1442	G1289	C	C	C999	C
G2242	G1914	C	C1598	C1506	G1443	G1290	C	C	C999	C
G2243	U1915	C	C1599	C1507	G1444	G1291	C	C	C999	C
G2244	G1916	C	C1600	C1508	G1445	G1292	C	C	C999	C
G2245	C1917	C	C1601	C1509	G1446	G1293	C	C	C999	C
G2246	U1918	C	C1602	C1510	G1447	G1294	C	C	C999	C
G2247	G1919	C	C1603	C1511	G1448	G1295	C	C	C999	C
G2248	C1920	C	C1604	C1512	G1449	G1296	C	C	C999	C
G2249	G1921	C	C1605	C1513	G1450	G1297	C	C	C999	C
G2250	U1922	C	C1606	C1514	G1451	G1298	C	C	C999	C
G2251	G1923	C	C1607	C1515	G1452	G1299	C	C	C999	C
G2252	C1924	C	C1608	C1516	G1453	G1300	C	C	C999	C
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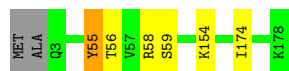

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G5068	G4975	G4904	G	G3776	A4669	U4542	C4429	U4301	U4190	G4104	G3974	C3896	U3772	C3697	C3594
U5069	U4976	G4909	U	C	G4670	G4543	C4444	U4302	G4191	G4107	C3975	C3897	A3774	G3698	C3595
		G4910	G	U	A4672	G4545		G4305			C3977	G3898	A3775	C3699	A3596
A4979	A4911	C4913	C	U	U4677	A4548	G4448	U4306	G4200	G4110	G4034	G3899	G3776	C3700	C3597
C4980	C4912	C4913	C	U	G4678	G4549	A4449		G4201	U4111	G4035	G3900	G3777	C3598	C3599
G4913	G4914	C4915	C	U	G4679	G4550	A4452	A4313	A4213	U4112	G4036	A3901			
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C4986	C4917	C4918	C	C	U4552	U4551		C4318	A4219	G4115	G4038	G3907	A3784	U3707	U3607
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U4989	C4919	C4920	G	C	C4695	U4558	U4459		G4221	U4118	C4041		U3786	U3709	
C4990	C4920	C4921	G	C	C4704	C4560	A4464	A4325	G4222	G4119	G4042	C3913	C3780		
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C4923	C4923	C4922	G	C	U4707	A4568	C4466	G4330	G4226	G4121	U4044	U3915	U3790	A3712	G3626
		C4923	C	G	A4708	A4568		G4331		G4122	G4045	G3916	U3713	U3713	
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U5002	U5002	C4927	G	C	U4757	U4574	A4471	C4337	U4232	A4127	A4047	C3919	U3715	U3715	
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C5004	C5004	C4929	A	C	A4734	G4587	G4475	G4338	A4233	G4131	U4049	C3810	U4049	A3717	A3636
G5005	G5005	C4930	C	C	G4581	G4581	C4476	A4339	A4234	C4132	A4050	G3922	G3811	U3637	U3637
U5006	U5006	C4931	C	C	C4622	C4582	A4477			C4132	C4051		C3812	C3838	C3838
A5007	A5007	C4932	C	C	G4731	C4582				C4052	C4052	A3928	A3723	U3639	U3639
		C4932	C	C	C4732	C4583		C4349	U4242	G4135	A4053		A3724	G3725	U3640
A5011	A5011	C4933	C	C	C4733	C4587	U4481	C4350	G4261	G4136	C4054	C3938	G3725	U3641	U3641
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U5014	U5014	C4936	C	C	A4589	A4589	C4489		A4251	C4139	C4057	C3941	G3819	U3729	U3644
G5015	G5015	C4937	C	C	C4590	A4590	C4490	G4355		C4140	U4058	A3942	U3730	U3645	U3645
A5016	A5016	C4938	C	C	G4740	A4590	G4491		G4254	G4141	C4059			U3730	A3646
G5017	G5017	C4939	C	U	C4741	G4600	U4492	A4376	U4260	C4142	C4064	G3944	U3838	A3733	A3647
		C	G	U	G4742	G4601	U4493	A4377	G4261	C4143	G4065	G3946	G3839	U3734	A3648
		G	C	A	A4744	A4617		A4378		C4144	U4066	A3947	U3840	G3735	
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C5023	C4942	C4942	C	C	C4746	U4620	U4500	A4380		C4147	U4068	A3949	C3843	A3746	G3661
C5024	C4944	C4944	C	G	G4749	G4620	U4501	A4381		C4148	U4069	U3950	U3843		A3662
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G5028	C4948	C4948	C	C	U4754	U4629	C4508	A4385	A4273	G4152	C4073	G3955	G3857	C3753	C3667
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G5031	U4951	U4950	C	G	U4757	A4635	A4510	C4387	G4275	C4154	U4075	U3957	G3859	C3755	C3669
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A5034	C4952	C4952	C	C	U4759	G4637	U4512	A4394	G4277	C4158		U3959	A3860	G3757	G3671
		G4952	C	C	G4760	U4638	A4513	U4395	C4278			A3960	A3867	U3758	C3672
U5037	A4955	C4955	C	C	G4761	G4643	C4518	A4396	A4279	C4162	G4081	A3961	A3867	U3758	C3673
		U4956	G	C	A4762	G4644		A4397	U4280	U4163	G4082	A3962	A3759	G3673	C3674
U5040	C4957	C4957	C	C	U4763	G4644	C4522	C4398	A4281	U4163	C4083	A3963	U3760	G3674	C3675
G5041	U4958	C4958	C	C	A4764	A4648	G4522	C4398			C4084	A3963	A3877	C3761	
		U4959	C	C	G4765	A4648	A4523	C4398		G4168	A4085	U3964	C3878	U3762	
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		C4961	C	C	G4767	A4657	C4525	C4413	G4288	A4170	C4088	A3966	U3764	C3763	C3881
C5054	C4962	C4962	G	C	C4768	U4657	C4526	U4419				A3967	G3880	U3764	C3881
G5055	G4963	C4963	A	C	G4769	U4658	U4527	U4420	G4291	C4171	G4093	A3968	A3765	C3765	A3682
A5056	A5056	C4964	G	C	C4770	G4659	C4527	C4421	U4296	U4174	G4093	G3969	G3888	C3767	C3683
C5057	U4965	U4965	C	C	U4771	C4771	G4528	A4422	U4297	C4175	C4094	G3970	G3889	C3768	C3689
A5058		C4966	C	C	C4772	G4663	C4531	A4426	U4298			G3971	A3890	C3769	C3692
		C4967	C	C	C4773	U4667	U4531	C4427	U4299	C4182	C4102	G3972	A3891	U3770	A3693

Chain p:  98% .



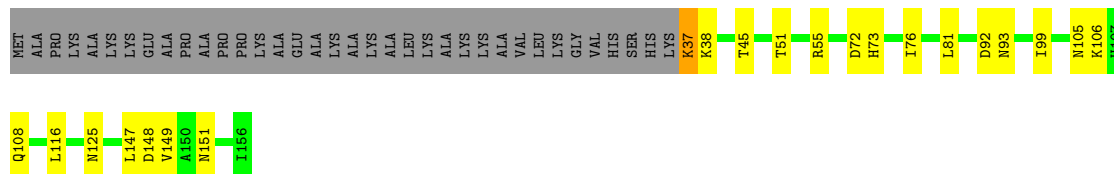
- Molecule 44: 60S ribosomal protein L11

Chain q:  96% . . .



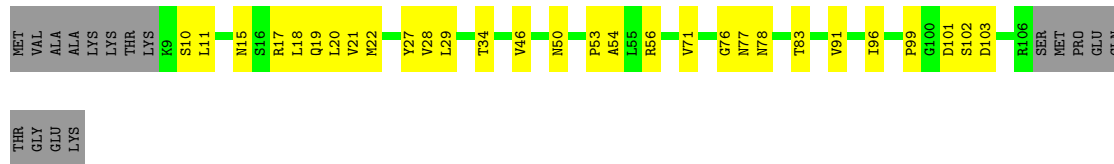
- Molecule 45: 60S ribosomal protein L23a

Chain R:  63% 13% 23%



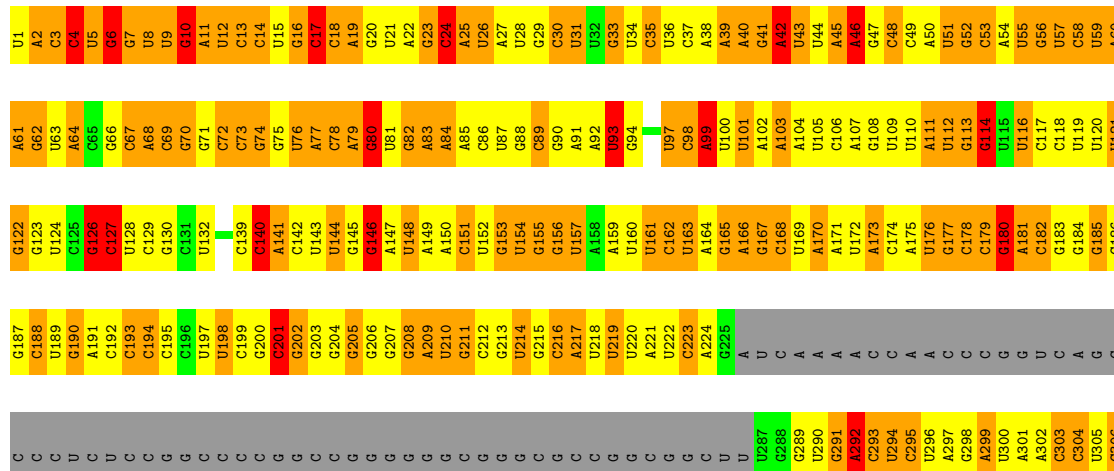
- Molecule 46: 60S ribosomal protein L30

Chain W:  60% 25% 15%



- Molecule 47: 18S rRNA

Chain AA:  32% 46% 11% 7%



C1271	G1211	G1151	C1091	A1030	G970	G910	C850	C790	C730	A670	G610	C550	C490	C429	U368	G307
C1272	G1212	U1152	G1092	A1031	G971	C911	C851	C791	G731	A671	G611	U551	C491	C430	C369	G308
C1273	C1213	C1153	A1093	C1032	A972	C912	C852	C792	U732	A672	U612	G552	C492	G431	G370	C309
C1274	A1214	U1154	C1094	G1033	C973	G913	C853	C793	C733	G673	G613	U553	A493	G432	A371	C310
G1275	C1215	U1155	U1095	A1034	C974	U914	A854	A794	C734	C674	C614	C494	C494	G433	U372	C311
A1276	C1216	U1156	G1096	A1035	G975	G915	C855	A795	C735	U675	C615	A555	U495	G434	G373	G312
C1277	A1217	G1157	G1097	A1036	G976	A916	C856	C796	C736	C676	A616	U556	C496	A435	G374	A313
A1278	C1218	U1158	C1098	G1037	C977	U917	U857	C797	G737	U677	G617	U557	C497	G436	U375	U314
C1279	C1219	G1159	G1099	U1038	G978	U918	A858	A798	C738	U678	A618	G558	C498	G437	A376	G315
C1280	A1220	U1160	A1100	C1039	C979	A919	G859	U799	C739	A679	A619	G559	G499	G438	G377	G316
G1281	G1221	U1161	U1101	G1040	A980	A920	G860	U800	C	G680	G620	A560	A500	A439	U378	C317
A1282	C1222	C1162	G1102	G1041	A981	G921	A861	U801	C	U681	C621	A561	C501	A440	C379	A318
C1283	A1223	C1163	C1103		G982	A922	A862	A802	U	U682	C622	U562	C502	C441	G380	C319
G1284	G1224	G1164	A1084	G1044	A983	G923	U863	C803	U	G683	G623	G563	C503	C442	C381	G320
G1285	U1225	G1165	G1105	U1045	A984	G924	A864	U804	G744	G684	C624	A564	G504	U443	C382	C321
G1286	G1226	G1166	C1106	U1046	G985	G925	A865	U805	C745	A685	G625	G565	G505	G444	G383	C322
A1287	G1227	G1167	G1107	C1047	U986	A926	U866	U806	C746	U686	G626	G566	G506	A445	U384	C323
C1288	A1228	G1168	G1108	G1048	A987	C927	G867	G807	U747	C687	U627	C567	G507	G446	G385	C324
U1289	G1229	G1169	C1109	A1049	C988	G928	U868	A808	U748	U688	A628	C568	A508	A447	C386	C325
G1290	C1230	U1170	G1110	A1100	A989	G929	U869	A809	U749	U689	A629	A569	G509	A448	C387	C326
A1291	G1231	G1171	U1111	G1051	A990	C930	A870	A810	C750	G690	U630	C570	G510	U449	U388	G327
C1292	U1232	U1172	U1112	A1052	G991	C931	U871	A811	G751	G691	U631	U571	U511	G450	A389	U328
G1293	G1233	A1173	C1113	C1053	A992	G932	A872	A812	C752	G692	C632	U572	A512	G451	C390	G329
A1294	C1234	U1174	U1114	G1054	G993	G933	C873	A813	C753	A693	C633	U573	G513	G452	C391	G330
A1295	G1235	G1175	U1115	A1055	C994	G934	A874	U814	G	G694	A634	A574	U514	C453	A392	C331
G1296	G1236	G1176	C1116	U1056	G995	G935	A875	U815	C	C695	G635	A575	G515	U454	U393	G332
C1297	U1237	U1177	C1117	C1057	A996	G936	C876	A816	C	G696	C636	A576	A516	A455	G394	G333
G1298	U1238	U1178	A1118	A1058	A997	C937	C877	G817	C	G697	U637	U577	G517	G456	G395	C334
A1299	U1239	G1179	C1119	G1059	A998	A938	G878	A818	C	G698	C638	C578	G518	C457	U396	G335
U1300	A1240	C1180	U1120	A1060	G999	U939	C879	G819	C	C	C839	C579	A519	A458	G397	A336
A1301	U1241	A1181	G1121	U1061	C1000	U940	G880	U820	U	G	A640	U580	A520	C459	A398	C337
C1302	A1242	A1182	A1122	A1062	A1001	C941	G881	G821	C	G	A641	U581	A521	A460	C399	G338
C1303	U1243	G1183	C1123	C1063	A1002	G942	U882	U823	C	G	A642	C582	A522	U461	C400	A339
U1304	U1244	A1184	C1124	C1064	C1124	U943	U883	U823	A	G	A643	C583	A523	C462	A401	C340
G1245	G1245	C1185	C1125	G1065	U1004	A944	C884	C824	U	G	G644	G584	U524	C463	C402	C341
A1246	U1306	U1186	C1126	U1066	G1005	U945	U885	A825	G	G	C845	C585	A525	A464	G403	C342
G1247	C1247	G1187	C1127	C1067	C1006	U946	A886	A826	U	C	G646	G586	A526	A465	G404	A343
U1308	U1248	A1188	C1128	A1068	C1007	G947	U887	G827	U	C	U647	A587	C527	G466	G405	U344
C1309	C1249	A1189	G1129	U1069	C948	C948	U888	G828	C	G	A648	G588	A528	C467	U406	G345
U1310	A1250	A1190	G1130	A1070	A1008	G949	U889	C829	U	G	A649	G589	A529	A468	A407	C346
C1311	U1251	C1191	G1131	G1071	G1010	C950	U890	A830	U	C	A650	A590	U530	A469	A408	G347
G1312	C1252	U1192	C1132	U1072	A1011	C951	G891	G831	A	C	U851	U591	A531	C469	C409	A348
A1253	C1253	U1193	A1133	C1073	A1012	G952	U892	G832	C	G	U652	C592	C532	C472	G410	A349
U1314	G1254	A1194	C1134	U1074	U1013	C953	U893	G833	C	C	A653	C593	A533	A473	G411	C350
G1255	C1255	A1195	C1135	C1075	G1014	U954	G894	C834	U	G	A654	A594	G534	G474	G412	G351
G1256	G1256	A1196	U1136	G1076	U1015	A955	G895	C835	G	A	A655	U595	G535	C475	C413	U352
G1257	C1257	U1197	U1137	A1077	G1016	G956	U896	G836	A	G	G656	U596	A536	A476	A414	
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C1259	A1259	U1199	C1139	C1079	U1018	G958	U898	G838	C	G	U658	G598	U538	C478	U416	C356
U1320	G1260	A1200	A1180	U1080	C1019	G959	U899	C839	U	G	G659	A599	C539	C479	C417	G357
C1261	C1261	U1201	G1141	U1081	A1020	U960	C900	C840	U	A	C660	G600	U540	G480	A418	C358
G1322	C1262	U1202	G1142	A1082	U1021	G961	G901	G841	C	G	U661	G601	U541	C481	C419	U359
U1263	C1263	G1203	C1143	A1083	U1022	A962	G902	C842	C	C	G662	G602	U542	G482	C420	A360
C1324	C1264	A1204	A1144	A1084	A1023	A963	A903	C843	C	C	C663	C603	C543	C483	G421	U361
G1325	A1265	C1205	A1145	C1085	A1024	A964	A904	U844	C	A	A664	A604	G544	A484	C424	C362
C1266	G1266	G1206	C1146	G1086	U1025	U965	C905	G845	C785	A	G665	A605	A545	A485	A363	
C1267	C1267	G1207	A1147	U1087	C1026	U966	U906	G846	C	C	U666	G606	G546	A486	G425	A364
G1328	C1268	A1208	C1148	A1088	A1027	G967	G907	A847	G787	G	U667	U607	G547	U487	A426	G327
U1329	G1269	C1209	A1149	G1089	A1028	U968	A908	U848	G788	C	A668	C608	C548	U488	U427	U366
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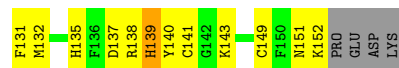
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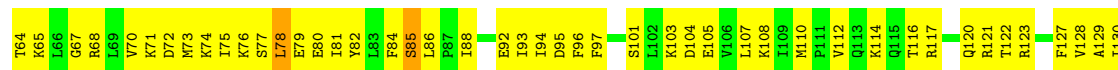
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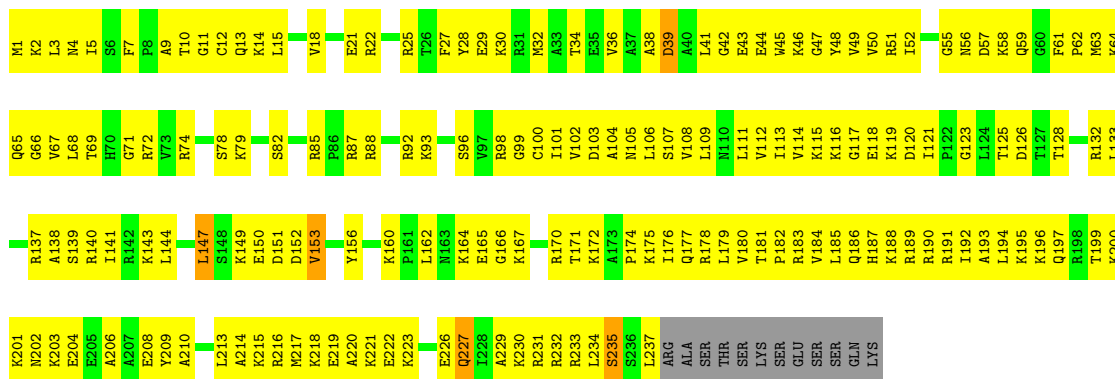
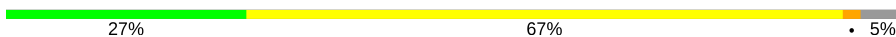
V131	D132	D133	D134	G135	H136	V137	G138	V139	G140	V141	K142	G143	K144	K145	V146	V147	A148	T149	A150	V151	V152	G153	V154	V155	V156	L157	A158	V159	L160	V161	L162	V163	P164	V165	V166	R167	G168	V169	W170	W171	G172	K173	V174	G175	K176	P177	V178	T179	V180	P181	C182	K183	V184	V185	R187	C188	G189	S190	V191	V192	V193	V194	V195	V196	V197	V198	V199	V200	V201	V202	V203	V204	V205	V206	V207	V208	V209	V210	V211	V212	V213	V214	V215	V216	V217	V218	V219	V220	V221	V222	V223	V224	V225	V226	V227	V228	V229	V230	V231	V232	V233	V234	V235	V236	V237	V238	V239	V240	V241	V242	V243	V244	V245	V246	V247	V248	V249	V250	V251	V252	V253	V254	V255	V256	V257	V258	V259	V260	V261	V262	V263	V264	V265	V266	V267	V268	V269	V270	V271	V272	V273	V274	V275	V276	V277	V278	V279	V280	V281	V282	V283	V284	V285	V286	V287	V288	V289	V290	V291	V292	V293	V294	V295	V296	V297	V298	V299	V300	V301	V302	V303	V304	V305	V306	V307	V308	V309	V310	V311	V312	V313	V314	V315	V316	V317	V318	V319	V320	V321	V322	V323	V324	V325	V326	V327	V328	V329	V330	V331	V332	V333	V334	V335	V336	V337	V338	V339	V340	V341	V342	V343	V344	V345	V346	V347	V348	V349	V350	V351	V352	V353	V354	V355	V356	V357	V358	V359	V360	V361	V362	V363	V364	V365	V366	V367	V368	V369	V370	V371	V372	V373	V374	V375	V376	V377	V378	V379	V380	V381	V382	V383	V384	V385	V386	V387	V388	V389	V390	V391	V392	V393	V394	V395	V396	V397	V398	V399	V400	V401	V402	V403	V404	V405	V406	V407	V408	V409	V410	V411	V412	V413	V414	V415	V416	V417	V418	V419	V420	V421	V422	V423	V424	V425	V426	V427	V428	V429	V430	V431	V432	V433	V434	V435	V436	V437	V438	V439	V440	V441	V442	V443	V444	V445	V446	V447	V448	V449	V450	V451	V452	V453	V454	V455	V456	V457	V458	V459	V460	V461	V462	V463	V464	V465	V466	V467	V468	V469	V470	V471	V472	V473	V474	V475	V476	V477	V478	V479	V480	V481	V482	V483	V484	V485	V486	V487	V488	V489	V490	V491	V492	V493	V494	V495	V496	V497	V498	V499	V500	V501	V502	V503	V504	V505	V506	V507	V508	V509	V510	V511	V512	V513	V514	V515	V516	V517	V518	V519	V520	V521	V522	V523	V524	V525	V526	V527	V528	V529	V530	V531	V532	V533	V534	V535	V536	V537	V538	V539	V540	V541	V542	V543	V544	V545	V546	V547	V548	V549	V550	V551	V552	V553	V554	V555	V556	V557	V558	V559	V560	V561	V562	V563	V564	V565	V566	V567	V568	V569	V570	V571	V572	V573	V574	V575	V576	V577	V578	V579	V580	V581	V582	V583	V584	V585	V586	V587	V588	V589	V590	V591	V592	V593	V594	V595	V596	V597	V598	V599	V600	V601	V602	V603	V604	V605	V606	V607	V608	V609	V610	V611	V612	V613	V614	V615	V616	V617	V618	V619	V620	V621	V622	V623	V624	V625	V626	V627	V628	V629	V630	V631	V632	V633	V634	V635	V636	V637	V638	V639	V640	V641	V642
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L192	L193	L194	L195	L196	L197	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L233	L234	L235	L236	L237	L238	L239	L240	L241	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L259
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V260	V261	T262	K263	S264	P265	Y266	Q267	E268	F269	T270	D271	H272	L273	V274	K275	T276	H277	T278	V280	SER	VAL	GLN	ARG	THR	GLN	ALA	PRO	ALA	VAL	ALA	THR	THR
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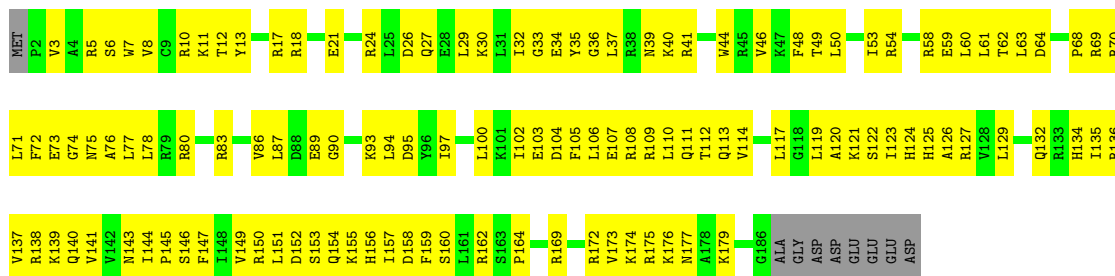
- 


Chain AK:



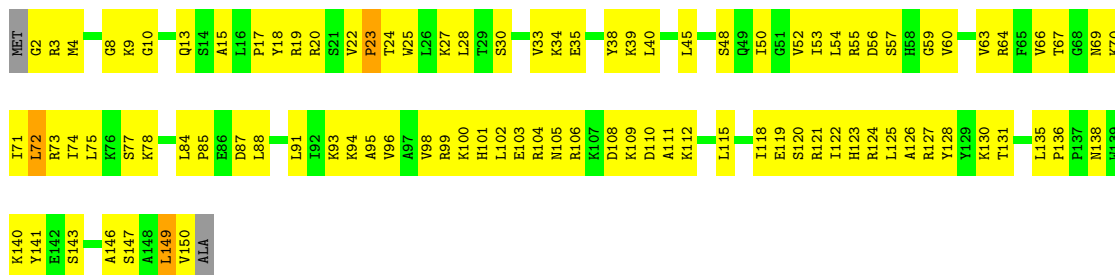
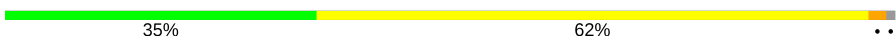
- Molecule 55: 40S ribosomal protein S9

Chain AL:



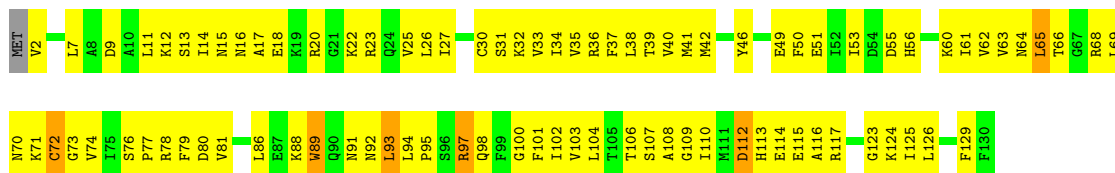
- Molecule 56: 40S ribosomal protein S13

Chain AN:



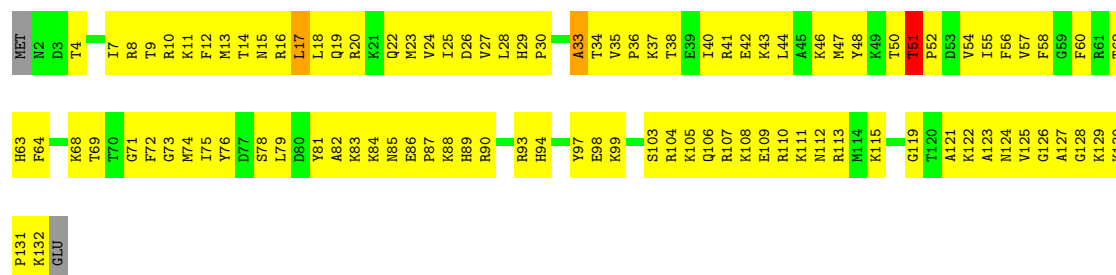
- Molecule 57: 40S ribosomal protein S15a

Chain AP:




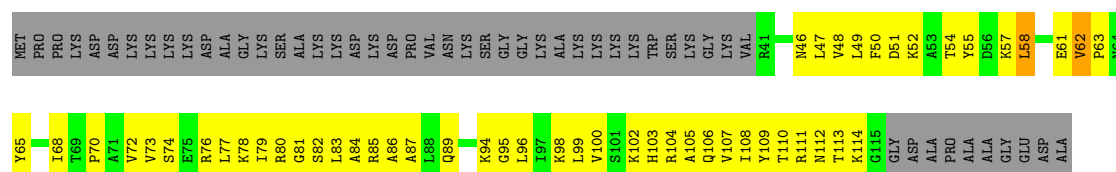
- Molecule 58: 40S ribosomal protein S24

Chain AQ:  23% 73% ..



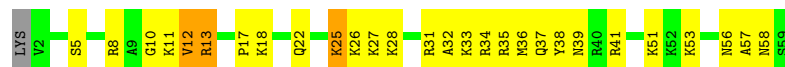
- Molecule 59: 40S ribosomal protein S25

Chain AR: 



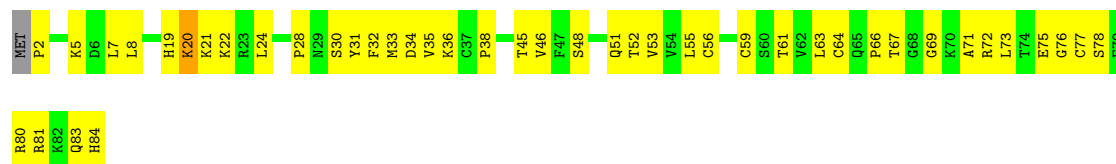
- Molecule 60: 40S ribosomal protein S30

Chain AT:  51% 42% 5%



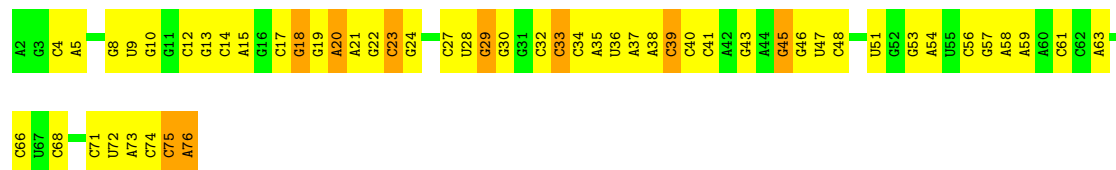
- Molecule 61: 40S ribosomal protein S27

Chain AV:  46% 51% ...




- Molecule 62: tRNA

Chain An:  29% 59% 12%



- Molecule 63: 40S ribosomal protein S3a

Chain Ap:  78% .. 19%

- Molecule 64: 40S ribosomal protein S3

Chain Aq: 89% • 7%



- Molecule 65: 40S ribosomal protein S4, X isoform

Chain Ar:  97%



- Molecule 66: 40S ribosomal protein S7

Chain At: 93% . .



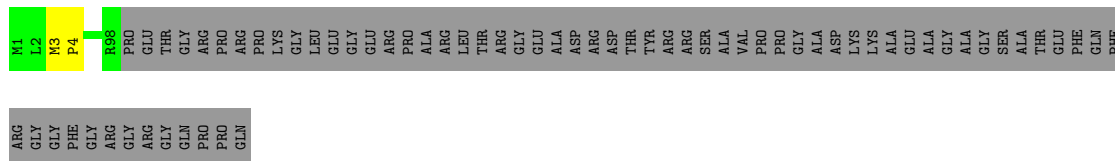
- Molecule 67: 40S ribosomal protein S8

Chain Au: 97%



- Molecule 68: 40S ribosomal protein S10

Chain Av:  58% 41%



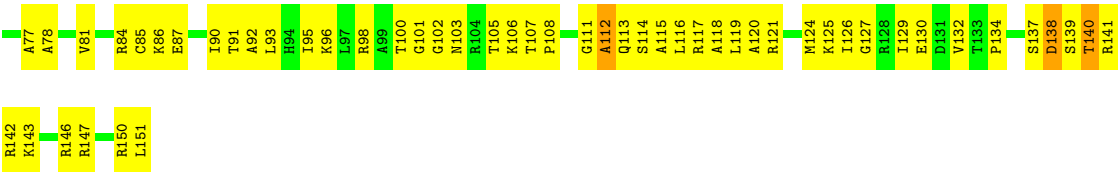
- Molecule 69: 40S ribosomal protein S16

Chain Av:  95% 5%

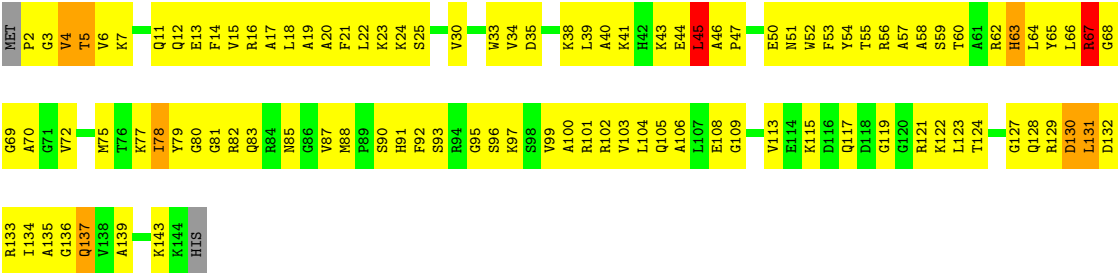


- Molecule 70: 40S ribosomal protein S18

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| NET | ALA | PRO | ARG | LYS | GLY | LYS | GLU | LYS | LYS | LYS | GLU | E12 | Q13 | V14 | I15 | S16 | L17 | G18 | P19 | E23 | G24 | V27 | C31 | H32 | I33 | F34 | D39 | T40 | F41 | V42 | H43 | V44 | L47 | K50 | E51 | C54 | R55 | V56 | T57 | M60 | A64 | D65 | R66 | D67 | E68 | S69 | S70 | P71 | V72 | A73 | L74 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



• Molecule 81: 40S ribosomal protein S19



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	175708	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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 > 2$	RMSZ	# $ Z > 2$
1	B	0.22	0/2858	0.68	0/4455
10	N	0.26	0/1326	0.44	0/1770
11	O	0.27	0/839	0.46	0/1126
12	P	0.27	0/993	0.47	0/1332
13	Q	0.26	0/547	0.44	0/728
14	S	0.25	0/1132	0.46	0/1504
15	T	0.27	0/1130	0.47	0/1507
16	U	0.28	0/1191	0.51	0/1591
17	V	0.24	0/620	0.41	0/819
18	X	0.25	0/903	0.44	0/1216
19	Y	0.26	0/1071	0.46	0/1429
2	C	0.23	0/3701	0.71	3/5766 (0.1%)
20	Z	0.27	0/895	0.50	0/1198
21	a	0.25	0/916	0.46	0/1220
22	b	0.24	0/1023	0.43	0/1351
23	c	0.25	0/843	0.44	0/1115
24	d	0.25	0/720	0.48	0/952
25	e	0.26	0/575	0.51	0/761
26	f	0.24	0/454	0.41	0/599
27	g	0.23	0/435	0.44	0/575
28	j	0.29	0/718	0.45	0/953
29	k	0.26	0/1017	0.49	0/1364
3	D	0.28	0/1936	0.50	0/2596
30	m	0.26	0/1905	0.42	0/2539
31	n	0.25	0/1960	0.45	0/2637
32	o	0.25	0/1537	0.49	0/2066
33	s	0.28	0/1161	0.45	0/1554
34	t	0.26	0/1746	0.48	1/2338 (0.0%)
35	h	0.21	0/231	0.36	0/294
36	r	0.29	0/1732	0.51	2/2315 (0.1%)
37	A	0.24	0/89645	0.73	17/139764 (0.0%)
38	H	0.34	0/1996	0.86	9/2673 (0.3%)
39	i	0.26	0/876	0.47	0/1156
4	E	0.26	0/3306	0.49	0/4424

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	K	0.27	0/1537	0.70	1/2052 (0.0%)
41	l	0.29	0/1769	0.52	1/2371 (0.0%)
42	M	0.32	0/1493	0.50	0/2003
43	p	0.26	0/1751	0.48	0/2340
44	q	0.25	0/1432	0.46	0/1912
45	R	0.25	0/1002	0.44	0/1345
46	W	0.26	0/774	0.46	0/1038
47	AA	1.45	406/41243 (1.0%)	1.53	695/64257 (1.1%)
48	AC	0.64	0/643	0.79	0/860
49	AD	0.83	0/1116	0.85	1/1490 (0.1%)
5	F	0.25	0/2973	0.47	0/3992
50	AE	0.75	0/828	0.78	0/1109
51	AF	0.50	0/500	0.83	1/669 (0.1%)
52	AH	0.51	0/593	0.80	1/786 (0.1%)
53	AJ	0.75	0/1762	0.83	3/2381 (0.1%)
54	AK	0.48	0/1946	0.75	1/2590 (0.0%)
55	AL	0.61	0/1550	0.77	0/2069
56	AN	0.67	0/1226	0.79	2/1649 (0.1%)
57	AP	0.74	0/1051	0.93	4/1406 (0.3%)
58	AQ	0.59	1/1083 (0.1%)	0.79	1/1438 (0.1%)
59	AR	0.42	0/604	0.80	1/810 (0.1%)
6	G	0.26	0/2428	0.45	0/3252
60	AT	0.54	0/465	0.73	0/612
61	AV	0.58	0/665	0.75	1/891 (0.1%)
62	An	1.24	10/1795 (0.6%)	1.64	46/2798 (1.6%)
63	Ap	0.66	0/1765	0.78	1/2362 (0.0%)
64	Aq	0.54	2/1793 (0.1%)	0.77	2/2414 (0.1%)
65	Ar	0.60	0/2118	0.72	0/2849
66	At	0.53	0/1544	0.79	3/2068 (0.1%)
67	Au	0.69	0/1715	0.76	1/2287 (0.0%)
68	Av	0.45	0/851	0.79	0/1147
69	Ay	0.49	0/1177	0.74	0/1575
7	I	0.26	0/1682	0.45	0/2250
70	A0	0.50	0/1253	0.84	1/1676 (0.1%)
71	Ao	0.68	0/1784	0.76	1/2424 (0.0%)
72	As	0.48	0/1531	0.76	1/2059 (0.0%)
73	Aw	0.79	1/1268 (0.1%)	0.83	1/1696 (0.1%)
74	Ax	0.44	0/815	0.78	1/1087 (0.1%)
75	Az	0.55	0/1086	0.84	0/1457
76	AB	0.47	0/817	0.84	2/1097 (0.2%)
77	AG	0.52	0/455	0.68	0/603
78	AI	0.46	0/2493	0.75	3/3394 (0.1%)
79	AM	0.41	0/962	0.80	1/1290 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	J	0.26	0/1268	0.45	0/1701
80	AO	0.61	0/1062	0.83	0/1425
81	AU	0.52	0/1131	0.82	2/1515 (0.1%)
9	L	0.24	0/1582	0.45	0/2091
All	All	0.69	420/234319 (0.2%)	0.92	811/344274 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	O	0	1
33	s	0	1
38	H	0	1
39	i	0	1
40	K	0	1
48	AC	0	1
49	AD	0	3
5	F	0	1
52	AH	0	2
53	AJ	0	1
54	AK	0	5
55	AL	0	1
56	AN	0	1
59	AR	0	1
60	AT	0	3
61	AV	0	1
63	Ap	0	3
64	Aq	0	3
65	Ar	0	2
66	At	0	3
67	Au	0	1
68	Av	0	1
69	Ay	0	5
70	A0	0	4
71	Ao	0	4
72	As	0	6
75	Az	0	4
76	AB	0	4
78	AI	0	5
79	AM	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
80	AO	0	2
81	AU	0	4
All	All	0	78

The worst 5 of 420 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1031	A	N9-C4	-10.37	1.31	1.37
47	AA	1170	A	N9-C4	-9.35	1.32	1.37
47	AA	1815	A	N9-C4	-9.17	1.32	1.37
47	AA	1815	A	N3-C4	-8.95	1.29	1.34
47	AA	1173	A	N9-C4	-8.77	1.32	1.37

The worst 5 of 811 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	K	158	THR	C-N-CD	-21.62	73.03	120.60
38	H	96	VAL	N-CA-C	-18.95	59.84	111.00
38	H	89	LEU	N-CA-C	-15.05	70.37	111.00
47	AA	1130	G	N3-C4-C5	12.10	134.65	128.60
47	AA	1861	G	N3-C4-C5	-11.49	122.85	128.60

There are no chirality outliers.

5 of 78 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	290	SER	Peptide
38	H	88	VAL	Mainchain
11	O	65	ARG	Peptide
39	i	58	LYS	Peptide
33	s	40	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	B	2558	0	1296	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	3314	0	1683	26	0
3	D	1898	0	1993	59	0
4	E	3238	0	3376	79	0
5	F	2919	0	3092	77	0
6	G	2382	0	2410	59	0
7	I	1650	0	1794	43	0
8	J	1242	0	1269	22	0
9	L	1566	0	1727	46	0
10	N	1298	0	1366	30	0
11	O	825	0	850	13	0
12	P	979	0	1039	25	0
13	Q	534	0	546	5	0
14	S	1115	0	1205	23	0
15	T	1107	0	1182	16	0
16	U	1162	0	1213	28	0
17	V	610	0	650	13	0
18	X	888	0	930	14	0
19	Y	1053	0	1147	19	0
20	Z	876	0	912	29	0
21	a	906	0	1002	0	0
22	b	1015	0	1148	0	0
23	c	832	0	917	0	0
24	d	705	0	741	0	0
25	e	569	0	637	0	0
26	f	444	0	483	0	0
27	g	429	0	469	0	0
28	j	708	0	760	0	0
29	k	1002	0	1068	0	0
30	m	1870	0	1996	0	0
31	n	1927	0	2074	0	0
32	o	1518	0	1601	0	0
33	s	1138	0	1204	0	0
34	t	1701	0	1749	0	0
35	h	230	0	275	0	0
36	r	1701	0	1818	0	0
37	A	80184	0	40389	914	0
38	H	1958	0	2125	138	0
39	i	862	0	933	0	0
40	K	1513	0	1628	43	0
41	l	1741	0	1854	0	0
42	M	1453	0	1490	55	0
43	p	1711	0	1749	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	q	1410	0	1440	0	0
45	R	985	0	1066	34	0
46	W	764	0	804	23	0
47	AA	36900	0	18591	3377	0
48	AC	636	0	637	57	0
49	AD	1098	0	1167	106	0
50	AE	814	0	867	84	0
51	AF	498	0	525	51	0
52	AH	581	0	597	63	0
53	AJ	1725	0	1813	212	0
54	AK	1923	0	2089	210	0
55	AL	1525	0	1640	166	0
56	AN	1202	0	1289	121	0
57	AP	1034	0	1080	126	0
58	AQ	1065	0	1142	132	0
59	AR	598	0	656	74	0
60	AT	459	0	503	38	0
61	AV	651	0	672	47	0
62	An	1604	0	813	0	0
63	Ap	1738	0	1808	0	0
64	Aq	1765	0	1864	0	0
65	Ar	2076	0	2177	0	0
66	At	1521	0	1616	0	0
67	Au	1686	0	1772	0	0
68	Av	827	0	854	0	0
69	Ay	1158	0	1232	0	0
70	A0	1235	0	1307	171	0
71	Ao	1747	0	1751	0	0
72	As	1509	0	1563	0	0
73	Aw	1247	0	1323	0	0
74	Ax	804	0	841	0	0
75	Az	1072	0	1129	0	0
76	AB	807	0	874	158	0
77	AG	445	0	442	42	0
78	AI	2436	0	2392	289	0
79	AM	952	0	983	65	0
80	AO	1049	0	1073	118	0
81	AU	1112	0	1146	203	0
All	All	217989	0	161328	6816	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 27.

The worst 5 of 6816 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)
76:AB:49:LYS:HG2	76:AB:92:HIS:CE1	1.36	1.55
38:H:84:LYS:HB3	38:H:89:LEU:CD2	1.32	1.53
38:H:84:LYS:CB	38:H:89:LEU:HD23	1.01	1.48
76:AB:49:LYS:HE3	76:AB:51:LYS:NZ	1.29	1.44
7:I:22:ILE:HD12	42:M:166:ARG:NH1	1.15	1.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	246/257 (96%)	227 (92%)	19 (8%)	0	100	100
4	E	400/403 (99%)	378 (94%)	22 (6%)	0	100	100
5	F	365/427 (86%)	331 (91%)	33 (9%)	1 (0%)	43	78
6	G	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	43	78
7	I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
8	J	151/160 (94%)	145 (96%)	5 (3%)	1 (1%)	24	66
9	L	185/196 (94%)	177 (96%)	8 (4%)	0	100	100
10	N	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
11	O	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
12	P	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
13	Q	62/157 (40%)	58 (94%)	4 (6%)	0	100	100
14	S	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
15	T	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
16	U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	V	73/159 (46%)	65 (89%)	8 (11%)	0	100	100
18	X	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
19	Y	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
20	Z	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
21	a	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
22	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
23	c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
24	d	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
25	e	67/70 (96%)	62 (92%)	4 (6%)	1 (2%)	11	52
26	f	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
27	g	50/128 (39%)	45 (90%)	5 (10%)	0	100	100
28	j	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
29	k	123/137 (90%)	110 (89%)	13 (11%)	0	100	100
30	m	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
31	n	239/266 (90%)	228 (95%)	11 (5%)	0	100	100
32	o	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
33	s	137/215 (64%)	124 (90%)	13 (10%)	0	100	100
34	t	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
35	h	22/25 (88%)	19 (86%)	2 (9%)	1 (4%)	3	27
36	r	208/211 (99%)	189 (91%)	17 (8%)	2 (1%)	17	60
38	H	238/288 (83%)	203 (85%)	30 (13%)	5 (2%)	8	45
39	i	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
40	K	185/188 (98%)	177 (96%)	7 (4%)	1 (0%)	31	72
41	l	215/217 (99%)	188 (87%)	25 (12%)	2 (1%)	19	61
42	M	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	14	57
43	p	211/214 (99%)	196 (93%)	14 (7%)	1 (0%)	31	72
44	q	172/178 (97%)	163 (95%)	6 (4%)	3 (2%)	10	49
45	R	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
46	W	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
48	AC	81/83 (98%)	70 (86%)	8 (10%)	3 (4%)	4	32
49	AD	139/143 (97%)	117 (84%)	22 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	AE	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
51	AF	61/69 (88%)	55 (90%)	6 (10%)	0	100	100
52	AH	69/156 (44%)	54 (78%)	13 (19%)	2 (3%)	5	38
53	AJ	220/293 (75%)	195 (89%)	25 (11%)	0	100	100
54	AK	235/249 (94%)	206 (88%)	27 (12%)	2 (1%)	19	61
55	AL	183/194 (94%)	161 (88%)	21 (12%)	1 (0%)	31	72
56	AN	147/151 (97%)	125 (85%)	22 (15%)	0	100	100
57	AP	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
58	AQ	129/133 (97%)	118 (92%)	8 (6%)	3 (2%)	7	43
59	AR	73/125 (58%)	61 (84%)	12 (16%)	0	100	100
60	AT	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
61	AV	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	14	57
63	Ap	212/264 (80%)	184 (87%)	25 (12%)	3 (1%)	12	53
64	Aq	225/243 (93%)	195 (87%)	26 (12%)	4 (2%)	9	48
65	Ar	260/263 (99%)	226 (87%)	31 (12%)	3 (1%)	14	57
66	At	187/194 (96%)	155 (83%)	30 (16%)	2 (1%)	16	59
67	Au	204/208 (98%)	179 (88%)	22 (11%)	3 (2%)	11	52
68	Av	96/165 (58%)	77 (80%)	18 (19%)	1 (1%)	17	60
69	Ay	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	8	45
70	A0	148/152 (97%)	121 (82%)	21 (14%)	6 (4%)	3	29
71	Ao	220/295 (75%)	190 (86%)	28 (13%)	2 (1%)	19	61
72	As	189/204 (93%)	158 (84%)	23 (12%)	8 (4%)	3	28
73	Aw	151/158 (96%)	130 (86%)	18 (12%)	3 (2%)	8	46
74	Ax	95/145 (66%)	60 (63%)	21 (22%)	14 (15%)	0	4
75	Az	130/135 (96%)	93 (72%)	26 (20%)	11 (8%)	1	12
76	AB	100/119 (84%)	82 (82%)	14 (14%)	4 (4%)	3	30
77	AG	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	3	31
78	AI	311/317 (98%)	261 (84%)	44 (14%)	6 (2%)	9	47
79	AM	120/132 (91%)	91 (76%)	26 (22%)	3 (2%)	6	41
80	AO	138/151 (91%)	112 (81%)	21 (15%)	5 (4%)	4	33
81	AU	141/145 (97%)	116 (82%)	18 (13%)	7 (5%)	2	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	11449/12881 (89%)	10266 (90%)	1060 (9%)	123 (1%)	20 59

5 of 123 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	H	100	LYS
38	H	225	PRO
40	K	159	PRO
44	q	55	TYR
44	q	59	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	D	190/199 (96%)	190 (100%)	0	100 100
4	E	348/349 (100%)	348 (100%)	0	100 100
5	F	305/348 (88%)	305 (100%)	0	100 100
6	G	246/250 (98%)	246 (100%)	0	100 100
7	I	173/174 (99%)	173 (100%)	0	100 100
8	J	134/141 (95%)	134 (100%)	0	100 100
9	L	166/175 (95%)	166 (100%)	0	100 100
10	N	139/140 (99%)	139 (100%)	0	100 100
11	O	91/115 (79%)	91 (100%)	0	100 100
12	P	101/107 (94%)	101 (100%)	0	100 100
13	Q	56/126 (44%)	56 (100%)	0	100 100
14	S	124/135 (92%)	124 (100%)	0	100 100
15	T	117/118 (99%)	117 (100%)	0	100 100
16	U	120/121 (99%)	120 (100%)	0	100 100
17	V	63/126 (50%)	63 (100%)	0	100 100
18	X	98/110 (89%)	98 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	Y	114/121 (94%)	114 (100%)	0	100	100
20	Z	88/89 (99%)	88 (100%)	0	100	100
21	a	98/100 (98%)	98 (100%)	0	100	100
22	b	109/110 (99%)	109 (100%)	0	100	100
23	c	86/89 (97%)	86 (100%)	0	100	100
24	d	73/80 (91%)	73 (100%)	0	100	100
25	e	64/65 (98%)	64 (100%)	0	100	100
26	f	47/48 (98%)	47 (100%)	0	100	100
27	g	48/116 (41%)	48 (100%)	0	100	100
28	j	74/75 (99%)	74 (100%)	0	100	100
29	k	109/121 (90%)	109 (100%)	0	100	100
30	m	194/215 (90%)	194 (100%)	0	100	100
31	n	203/223 (91%)	203 (100%)	0	100	100
32	o	169/171 (99%)	169 (100%)	0	100	100
33	s	118/161 (73%)	118 (100%)	0	100	100
34	t	171/172 (99%)	171 (100%)	0	100	100
35	h	23/24 (96%)	23 (100%)	0	100	100
36	r	176/177 (99%)	174 (99%)	2 (1%)	76	90
38	H	215/252 (85%)	209 (97%)	6 (3%)	47	78
39	i	93/94 (99%)	92 (99%)	1 (1%)	76	90
40	K	164/165 (99%)	164 (100%)	0	100	100
41	l	195/196 (100%)	194 (100%)	1 (0%)	90	96
42	M	156/157 (99%)	154 (99%)	2 (1%)	71	89
43	p	180/181 (99%)	178 (99%)	2 (1%)	76	90
44	q	148/149 (99%)	144 (97%)	4 (3%)	48	78
45	R	108/133 (81%)	107 (99%)	1 (1%)	81	92
46	W	83/97 (86%)	83 (100%)	0	100	100
48	AC	67/67 (100%)	67 (100%)	0	100	100
49	AD	113/115 (98%)	113 (100%)	0	100	100
50	AE	88/98 (90%)	88 (100%)	0	100	100
51	AF	56/62 (90%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AH	64/140 (46%)	64 (100%)	0	100	100
53	AJ	188/225 (84%)	186 (99%)	2 (1%)	76	90
54	AK	207/218 (95%)	207 (100%)	0	100	100
55	AL	161/168 (96%)	161 (100%)	0	100	100
56	AN	130/131 (99%)	130 (100%)	0	100	100
57	AP	112/113 (99%)	110 (98%)	2 (2%)	62	85
58	AQ	113/115 (98%)	113 (100%)	0	100	100
59	AR	66/103 (64%)	66 (100%)	0	100	100
60	AT	47/48 (98%)	47 (100%)	0	100	100
61	AV	75/76 (99%)	75 (100%)	0	100	100
63	Ap	195/231 (84%)	193 (99%)	2 (1%)	78	90
64	Aq	190/202 (94%)	190 (100%)	0	100	100
65	Ar	224/225 (100%)	223 (100%)	1 (0%)	92	97
66	At	169/174 (97%)	169 (100%)	0	100	100
67	Au	178/180 (99%)	178 (100%)	0	100	100
68	Av	89/136 (65%)	89 (100%)	0	100	100
69	Ay	121/121 (100%)	120 (99%)	1 (1%)	83	93
70	A0	130/132 (98%)	130 (100%)	0	100	100
71	Ao	184/243 (76%)	184 (100%)	0	100	100
72	As	161/170 (95%)	159 (99%)	2 (1%)	74	89
73	Aw	137/142 (96%)	136 (99%)	1 (1%)	85	94
74	Ax	87/130 (67%)	84 (97%)	3 (3%)	40	74
75	Az	120/122 (98%)	115 (96%)	5 (4%)	32	69
76	AB	93/107 (87%)	89 (96%)	4 (4%)	32	68
77	AG	47/49 (96%)	46 (98%)	1 (2%)	56	83
78	AI	272/275 (99%)	270 (99%)	2 (1%)	85	94
79	AM	104/108 (96%)	103 (99%)	1 (1%)	78	90
80	AO	110/119 (92%)	110 (100%)	0	100	100
81	AU	113/115 (98%)	112 (99%)	1 (1%)	81	92
All	All	9988/10975 (91%)	9941 (100%)	47 (0%)	90	96

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	AP	72	CYS
69	Ay	100	VAL
78	AI	54	ILE
63	Ap	90	ASP
72	As	44	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
42	M	146	HIS
55	AL	75	ASN
78	AI	237	ASN
44	q	155	HIS
50	AE	19	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	119/121 (98%)	16 (13%)	0
2	C	155/157 (98%)	34 (21%)	1 (0%)
37	A	3707/5070 (73%)	1071 (28%)	50 (1%)
47	AA	1716/1869 (91%)	906 (52%)	48 (2%)
62	An	74/75 (98%)	37 (50%)	0
All	All	5771/7292 (79%)	2064 (35%)	99 (1%)

5 of 2064 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	2	U
1	B	7	G
1	B	17	C
1	B	22	A
1	B	24	C

5 of 99 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
37	A	4889	G
47	AA	400	C
47	AA	1606	G
37	A	4913	G

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Mol	Chain	Res	Type
37	A	5027	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	151:ILE	C	152:GLY	N	2.01