



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 17, 2017 – 09:38 PM EST

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

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

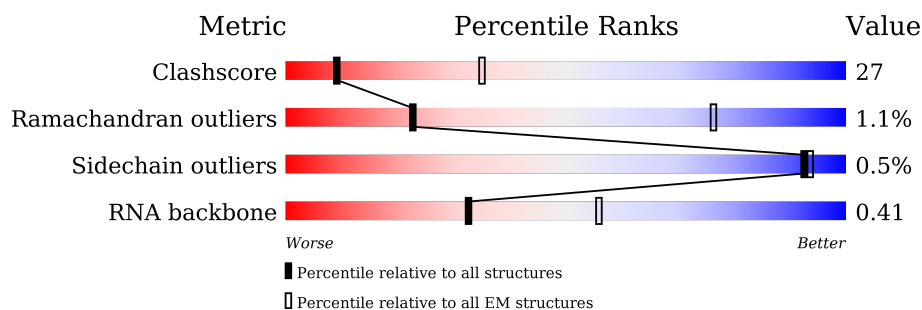
1 Overall quality at a glance

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.















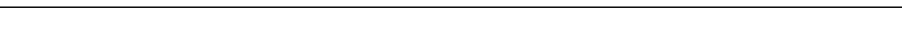

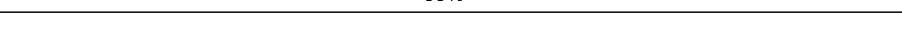
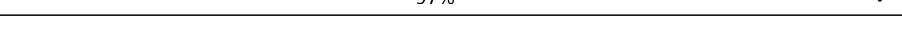
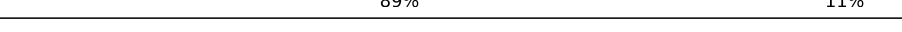
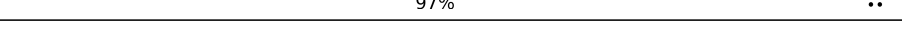
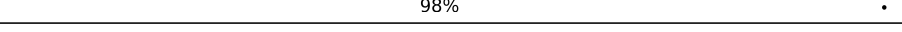

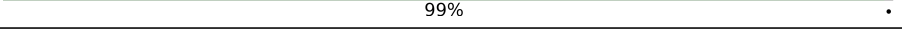



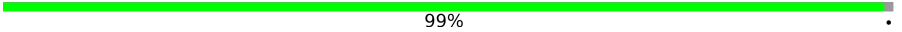
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	




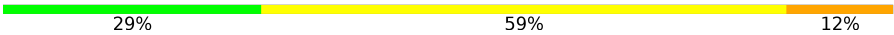


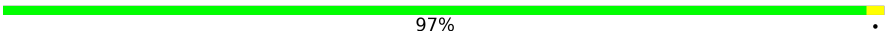
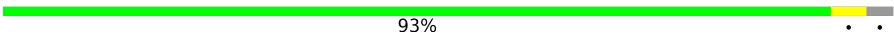
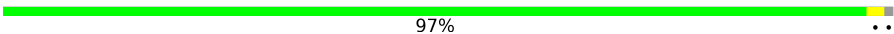

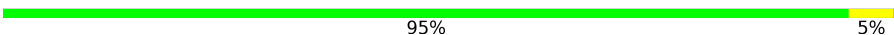
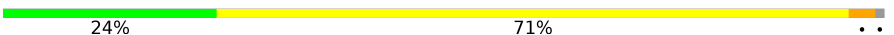





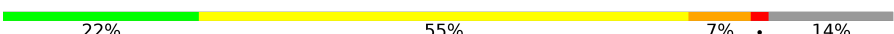





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Mol	Chain	Length	Quality of chain
34	t	204	99%
35	h	25	92%
36	r	211	97%
37	A	5070	41% 25% 8% 26%
38	H	288	53% 26% 16%
39	i	106	97%
40	K	188	71% 28%
41	l	217	98%
42	M	176	73% 24%
43	p	214	98%
44	q	178	96%
45	R	156	63% 13% 23%
46	W	115	60% 25% 15%
47	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		

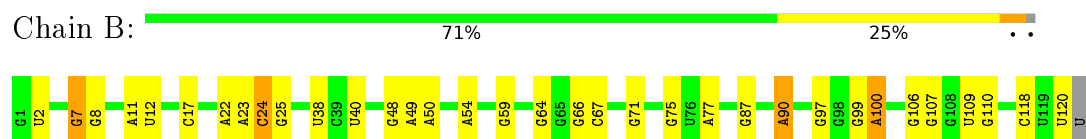
- Molecule 81 is a protein called 40S ribosomal protein S19.

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

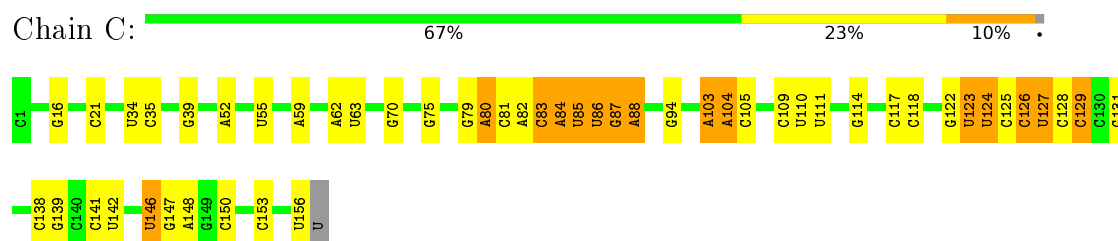
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

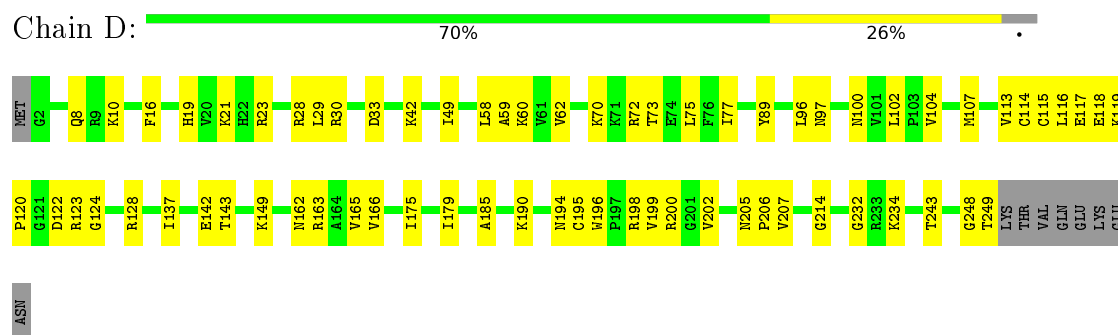
- Molecule 1: 5S rRNA



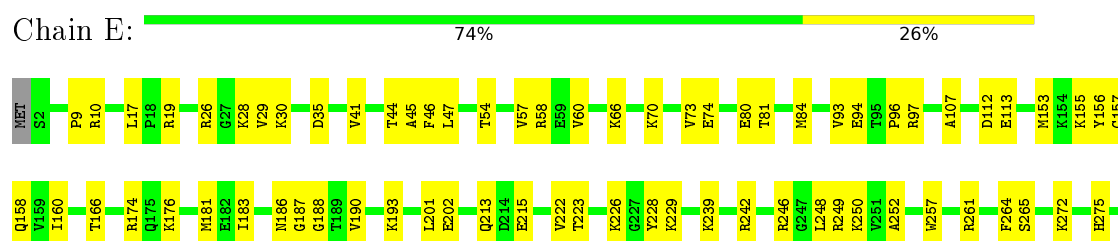
- Molecule 2: 5.8S rRNA



- Molecule 3: 60S ribosomal protein L8



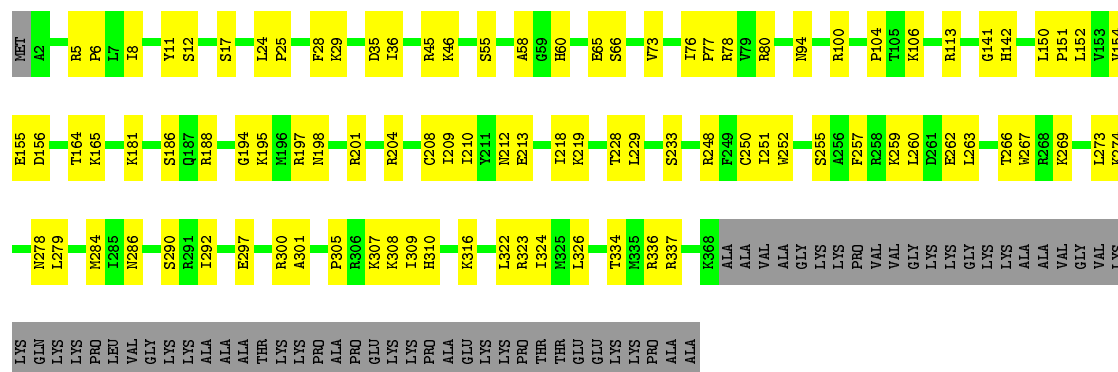
- Molecule 4: 60S ribosomal protein L3





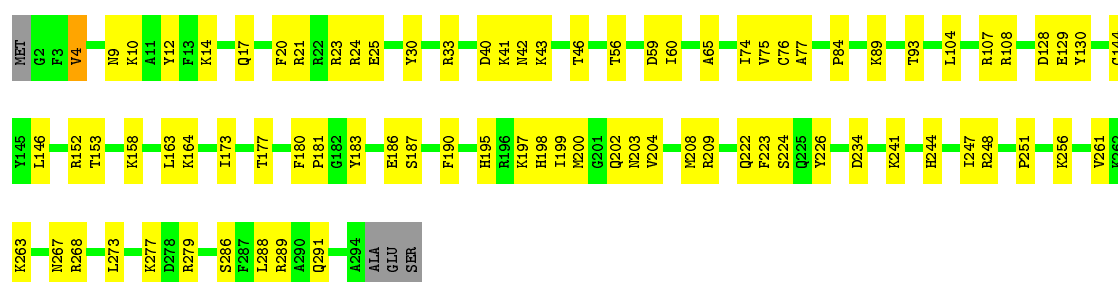
• Molecule 5: 60S ribosomal protein L4

Chain F: 64% 22% 14%



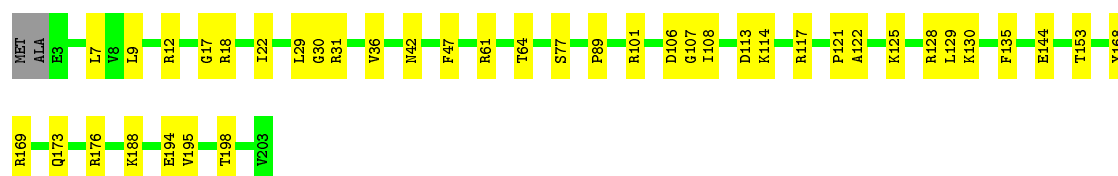
• Molecule 6: 60S ribosomal protein L5

Chain G: 71% 27% .



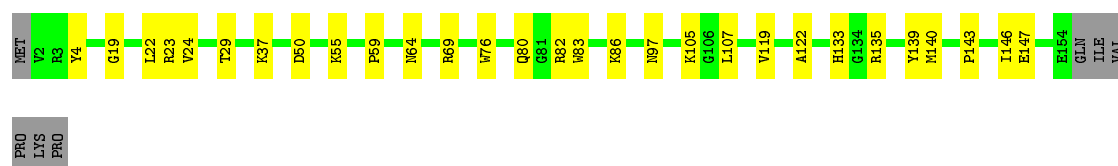
• Molecule 7: 60S ribosomal protein L13a

Chain I: 79% 20% .

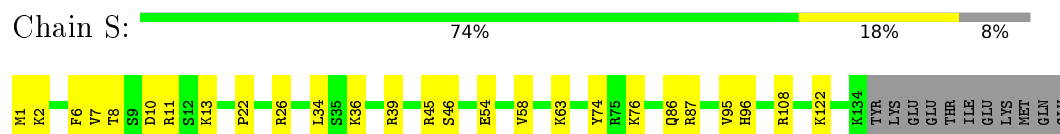


• Molecule 8: 60S ribosomal protein L17

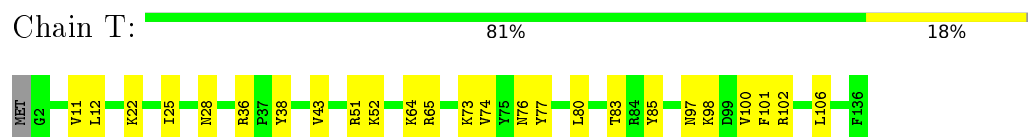
Chain J: 78% 18% .



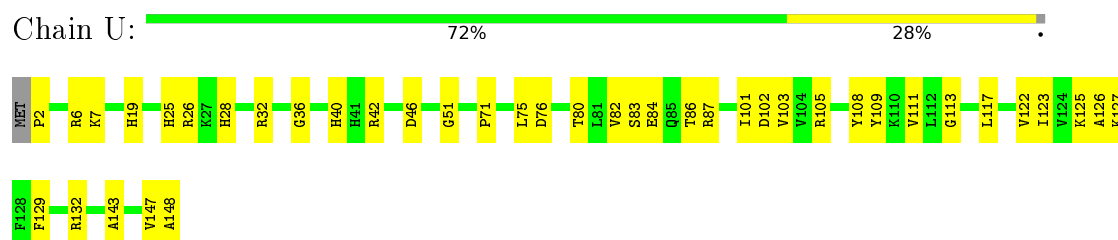
- Molecule 14: 60S ribosomal protein L26



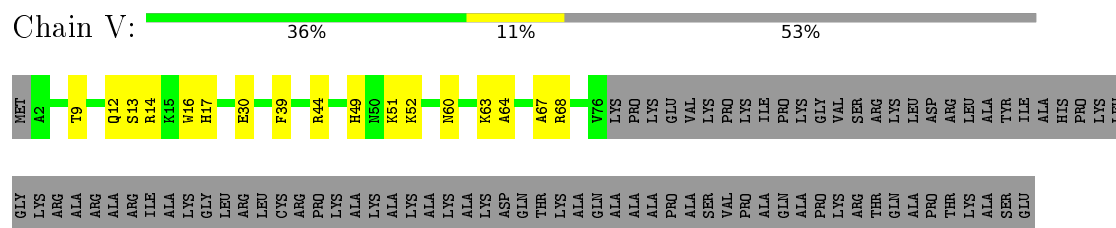
- Molecule 15: 60S ribosomal protein L27



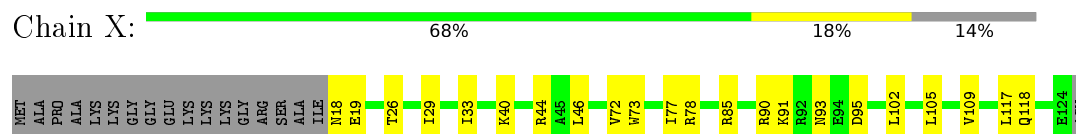
- Molecule 16: 60S ribosomal protein L27a



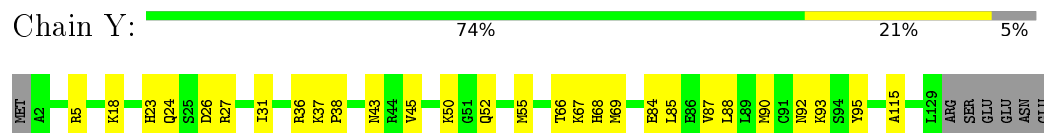
- Molecule 17: 60S ribosomal protein L29



- Molecule 18: 60S ribosomal protein L31

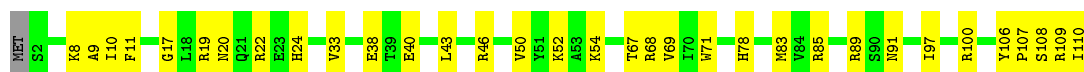


- Molecule 19: 60S ribosomal protein L32



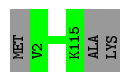
- Molecule 20: 60S ribosomal protein L35a





- Molecule 21: 60S ribosomal protein L34

Chain a: 97%



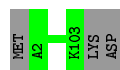
- Molecule 22: 60S ribosomal protein L35

Chain b: 99%



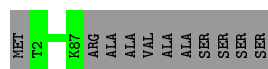
- Molecule 23: 60S ribosomal protein L36

Chain c: 97%



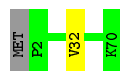
- Molecule 24: 60S ribosomal protein L37

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%





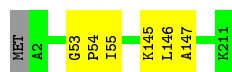
- Molecule 35: 60S Ribosomal protein L41

Chain h: 92% . .



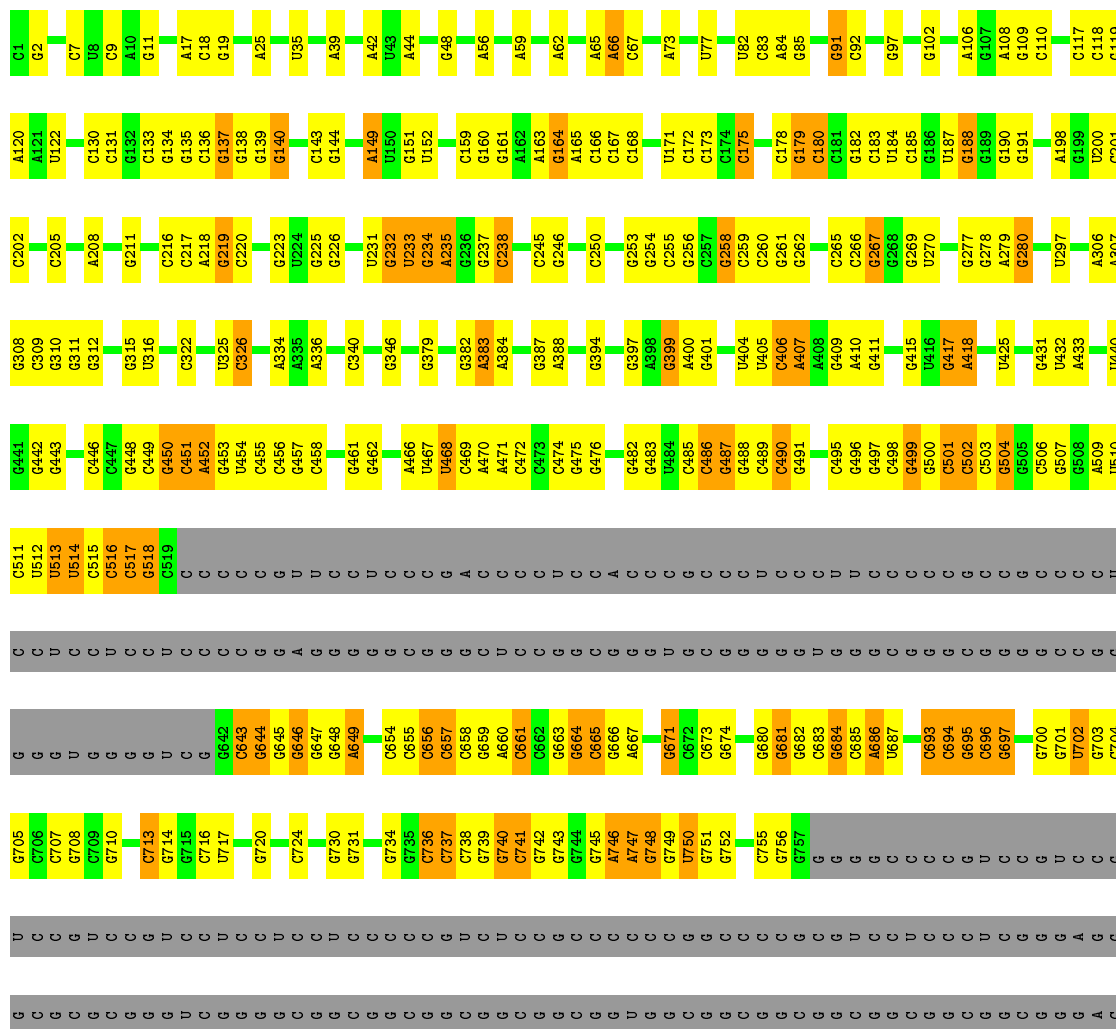
- Molecule 36: 60S ribosomal protein L13

Chain r:  97% .



- Molecule 37: 28S rRNA

Chain A: 41% 25% 8% 26%



G2113	G2024	A1960	G1846	A1765	A1553	G1447	A1371	G1276	G1215	G	G1090	G	A964	C
G2114	A2025	G1961	G1846	A1766	A1554	G1448	A1372	G1277	G1216	G	G1091	G	G965	G
G2115	A2026	A1962	U1852	A1767	A1555	G1449	G1375	G1278	G1217	G	G1092	G	A966	A
G2116	U2027	G1768	G1855	C1768	A1563	C1450	C1376	G1279	G1218	G	G1093	G	C967	A
G2117	G2028	G1769	G1856	A1770	A1564	G1451	G1377	G1280	G1219	C	C1094	U	C968	A
G2118	G2034	U1771	G1856	U1771	C1566	G1455	C1378	G1282	G1220	C	A1095	U	C969	C
G2119	G2034	C1772	U1860	C1772	G1456	G1457	C1379	G1283	G1221	C	C1096	C	G970	C
G2120	G2045	C1773	U1860	C1773	G1457	G1457	C1380	G1284	A1222	U	C1097	U	U971	C
G2121	G2046	C1774	U1866	C1774	G1457	G1457	C1381	U1285	G	C	G1098	C	C974	C
G2122	A2047	A1775	A1867	A1775	G1458	G1458	C1382	G1286	U	C	G1099	C	C975	C
G2123	U2048	A1776	A1868	A1776	G1459	G1459	C1383	G1287	U	C	U1100	C	G976	C
G2124	G2059	C1777	G1869	C1777	G1460	G1460	C1384	U1288	U	C	C1099	C	C977	C
G2125	G2060	C1778	G1869	C1778	G1461	G1461	C1385	G1289	U	C	C1099	C	C978	C
G2126	G2062	G1779	G1870	C1779	G1462	G1462	C1386	G1290	U	C	C1099	C	G979	C
G2127	G2063	G1780	G1871	C1780	G1463	G1463	C1387	G1291	U	C	C1099	C	G980	C
G2128	G2064	U1781	G1872	U1781	G1464	G1464	C1388	G1292	U	C	C1099	C	G981	C
G2129	G2065	C1782	G1873	C1782	G1465	G1465	C1389	G1293	C	C	C1099	C	U982	C
G2130	G2066	A1783	C1783	A1783	G1466	G1466	C1390	G1294	G	C	C1099	C	C983	C
G2131	G2067	G1784	G1874	G1784	G1467	G1467	C1391	G1295	G	C	C1099	C	C984	C
G	G2068	C1785	G1875	C1785	G1468	G1468	C1392	G1296	G	C	C1099	C	C985	C
C	G2069	A1786	G1876	A1786	G1469	G1469	C1393	G1297	G	C	C1099	C	C986	C
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U	G2071	U1788	G1878	U1788	G1471	G1471	C1395	G1299	G	C	C1099	C	C988	C
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U	G2074	U1791	G1881	U1791	G1474	G1474	C1398	U1302	G	C	C1099	C	C991	C
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U	G2076	A1793	G1883	A1793	G1476	G1476	C1400	G1304	G	C	C1099	C	C993	C
U	G2077	U1794	G1884	U1794	G1477	G1477	C1401	U1305	G	C	C1099	C	C994	C
U	G2078	C1795	G1885	C1795	G1478	G1478	C1402	G1306	G	C	C1099	C	C995	C
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U	G2083	C1800	G1890	C1800	G1483	G1483	C1407	G1311	G	C	C1099	C	C1000	C
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U	G2085	A1802	G1892	A1802	G1485	G1485	C1409	G1313	G	C	C1099	C	C1002	C
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U	G2087	U1804	G1894	U1804	G1487	G1487	C1411	G1315	G	C	C1099	C	C1004	C
U	G2088	C1805	G1895	C1805	G1488	G1488	C1412	G1316	G	C	C1099	C	C1005	C
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U	G2093	U1810	G1900	U1810	G1493	G1493	C1417	G1321	G	C	C1099	C	C1010	C
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U	G2107	U1824	G1914	U1824	G1507	G1507	C1431	G1335	G	C	C1099	C	C1024	C
U	G2108	C1825	G1915	C1825	G1508	G1508	C1432	G1336	G	C	C1099	C	C1025	C
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U	G2110	U1827	G1917	U1827	G1510	G1510	C1434	G1338	G	C	C1099	C	C1027	C
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U	G2123	C1840	G1930	C1840	G1523	G1523	C1447	G1351	G	C	C1099	C	C1040	C
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U	G2132	C1849	G1939	C1849	G1532	G1532	C1456	G1360	G	C	C1099	C	C1049	C
U	G2133	A1850	G1940	A1850	G1533	G1533	C1457	G1361	G	C	C1099	C	C1050	C
U	G2134	U1851	G1941	U1851	G1534	G1534	C1458	G1362	G	C	C1099	C	C1051	C
U	G2135	C1852	G1942	C1852	G1535	G1535	C1459	G1363	G	C	C1099	C	C1052	C
U	G2136	A1853	G1943	A1853	G1536	G1536	C1460	G1364	G	C	C1099	C	C1053	C
U	G2137	U1854	G1944	U1854	G1537	G1537	C1461	G1365	G	C	C1099	C	C1054	C
U	G2138	C1855	G1945	C1855	G1538	G1538	C1462	G1366	G	C	C1099	C	C1055	C
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U	G2140	U1857	G1947	U1857	G1540	G1540	C1464	G1368	G	C	C1099	C	C1057	C
U	G2141	C1858	G1948	C1858	G1541	G1541	C1465	G1369	G	C	C1099	C	C1058	C
U	G2142	A1859	G1949	A1859	G1542	G1542	C1466	G1370	G	C	C1099	C	C1059	C
U	G2143	U1860	G1950	U1860	G1543	G1543	C1467	G1371	G	C	C1099	C	C1060	C
U	G2144	C1861	G1951	C1861	G1544	G1544	C1468	G1372	G	C	C1099	C	C1061	C
U	G2145	A1862	G1952	A1862	G1545	G1545	C1469	G1373	G	C	C1099	C	C1062	C
U	G2146	U1863	G1953	U1863	G1546	G1546	C1470	G1374	G	C	C1099	C	C1063	C
U	G2147	C1864	G1954	C1864	G1547	G1547	C1471	G1375	G	C	C1099	C	C1064	C
U	G2148	A1865	G1955	A1865	G1548	G1548	C1472	G1376	G	C	C1099	C	C1065	C
U	G2149	U1866	G1956	U1866	G1549	G1549	C1473	G1377	G	C	C1099	C	C1066	

[illegible]

A5061	C4974	G4903	G4541	U4668	G4541	A4428	U4300	G4184	C4103	G3973	U3892	C3771	C3593
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U5069	C	C	G4543	C4670	G4543	C4444	U4302	U4191	G	C3975	C3897	U3773	U3595
C	U	U	A4544	A4672	A4544	G4449	U4305	G4200	G4107	C3976	G3898	A3774	A3596
A4979	C	C	G4545	U4677	G4545	A4449	U4306	G4201	C4110	C3977	G3900	G3775	G3597
C4980	C	U	A4548	G4678	A4548	A4449	U4313	A4213	U4111	G4034	A3901	G3776	C3598
G4981	C	C	G4549	C	G4549	U4452	A4313	A4214	U4112	G4035	C3901	G3777	A3599
C4982	C	C	U4551	U4683	U4551	C4453	C4314	A4215	C4113	C4036	A3905	G3780	C3605
U4985	C	C	U4552	C	U4552	U4457	C4318	A4219	C4114	C4037	A3906	G3705	U3606
C4987	C	C	U4555	G4694	U4555	U4458	G4322	A4220	U4115	G4038	G3907	U3707	U3607
U4988	C	C	U4560	C4695	U4560	U4459	A4325	A4221	U4116	G4039	A3908	G3708	A3608
C4990	C	C	U4567	C	U4567	U4464	G4329	G4222	U4117	C4040	C3913	G3709	A3624
U4991	C	C	U4568	C	U4568	U4465	G4330	G4223	U4118	G4041	U3914	G3710	G3625
G4992	C	C	G4573	A4708	U4573	U4471	G4332	G4224	C4119	G4042	G3915	A3712	G3626
C4996	C	C	G4574	U4709	U4574	U4472	C4337	U4225	U4120	G4043	G3916	U3713	A3629
U5002	C	C	G4581	C	U4581	U4473	U4338	U4226	U4121	U4044	G3917	U3714	A3635
C5003	C	C	U4582	C4730	U4582	U4474	G4339	U4227	G4122	U4045	G3918	U3715	C3636
C5004	C	C	U4583	G4731	U4583	U4475	U4340	U4228	G4123	U4046	C3919	U3716	U3637
G5005	C	C	G4587	G4732	U4587	U4476	A4349	A4234	C4132	C4051	G3922	A3723	G5638
U5006	C	C	G4588	G4733	U4588	U4477	C4349	U4242	G4135	C4052	A3928	A3724	U3639
A5007	C	C	G4589	G4734	U4589	U4478	C4350	U4243	G4136	A4053	G3938	G3725	U3640
A5011	C	C	G4590	C4741	U4590	U4479	U4351	U4244	U4137	U4054	G3939	A3726	U3641
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C5013	C	C	U4601	G4743	U4601	U4481	U4353	U4246	U4139	U4056	U3941	U3728	A3643
A5014	C	C	G4617	G4744	U4617	U4482	U4354	U4247	C4140	C4057	A3942	U3729	U3644
G5015	C	C	U4620	C4745	U4620	U4483	U4355	U4248	G4141	U4058	A3943	U3730	U3645
C5016	C	C	G4627	G4746	U4627	U4484	A4376	U4249	C4142	C4059	G3944	A3733	A3646
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G4949	C	C	G4637	C4755	U4637	U4486	U4378	U4251	C4144	G4065	G3946	G3735	A3648
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G4951	C	C	U4639	C4757	U4639	U4488	A4380	U4253	G4146	U4067	C3948	A3746	G3661
A5034	C	C	U4640	G4758	U4640	U4489	U4381	U4254	C4147	U4068	A3949	G3750	A3662
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C5040	C	C	U4642	G4760	U4642	U4491	U4383	U4256	G4149	U4070	G3951	G3752	C3666
G5041	C	C	U4643	C4761	U4643	U4492	U4384	U4257	C4150	U4071	A3954	G3753	C3667
C5050	C	C	U4644	G4762	U4644	U4493	U4385	U4258	G4151	A4072	G3955	G3754	C3668
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G5065	C	C	U4646	G4764	U4646	U4495	U4387	U4260	C4153	U4074	U3957	A3756	C3670
A5066	C	C	U4647	C4765	U4647	U4496	U4394	U4261	G4154	U4075	U3958	G3757	G3671
C5057	C	C	U4648	G4766	U4648	U4497	U4395	U4262	C4155	G4081	U3959	U3758	C3672
A5058	C	C	U4649	C4767	U4649	U4498	U4396	U4263	C4156	U4082	G3961	A3759	G3673
C	C	C	U4650	G4768	U4650	U4499	U4397	U4264	U4162	U4083	A3962	A3760	G3674
C	C	C	U4651	C4769	U4651	U4500	U4398	U4265	U4163	U4084	A3963	C3761	G3675
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C	C	C	U4653	C4771	U4653	U4502	U4403	U4267	G4169	A4086	A3965	A3763	G3681
C	C	C	U4654	G4772	U4654	U4503	U4404	U4268	C4170	C4087	A3966	U3764	A3682
C	C	C	U4655	C4773	U4655	U4504	U4405	U4269	C4171	C4088	G3967	G3765	C3683
C	C	C	U4656	G4774	U4656	U4505	U4406	U4270	U4174	G4089	G3968	C3767	G3689
C	C	C	U4657	C4775	U4657	U4506	U4407	U4271	G4175	C4101	G3969	U3768	A3692
C	C	C	U4658	G4776	U4658	U4507	U4408	U4272	C4183	C4102	A3972	U3770	A3692

Chain p:  98%



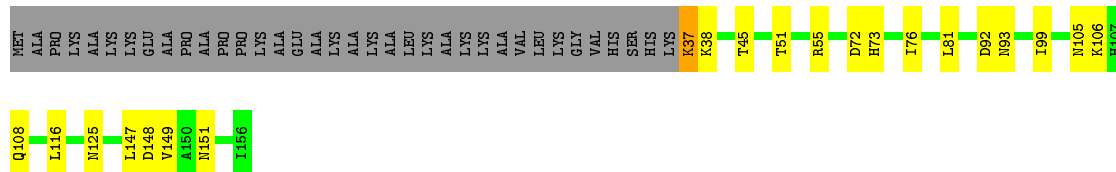
- Molecule 44: 60S ribosomal protein L11

Chain q:  96%



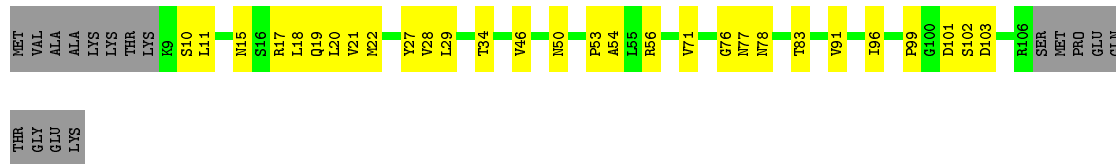
- Molecule 45: 60S ribosomal protein L23a

Chain R:  63% 13% 23%



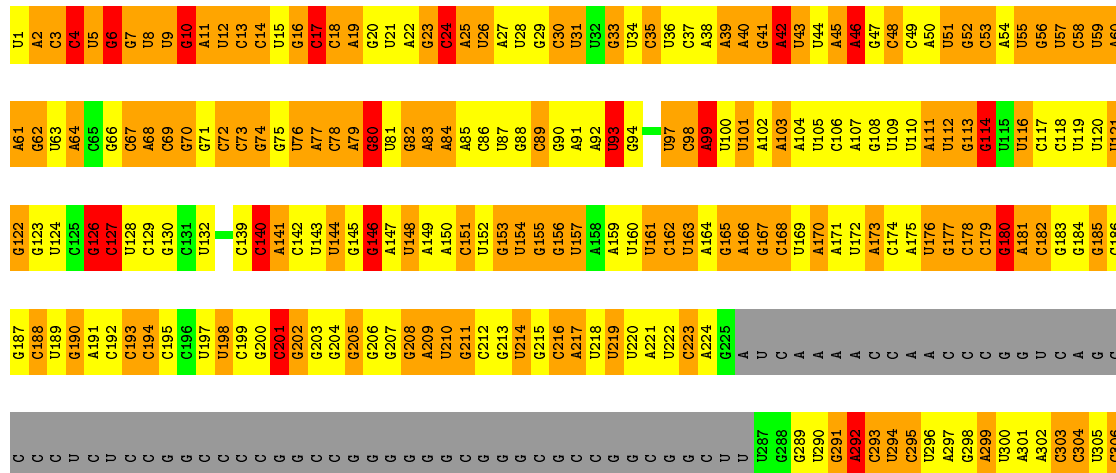
- Molecule 46: 60S ribosomal protein L30

Chain W:  60% 25% 15%

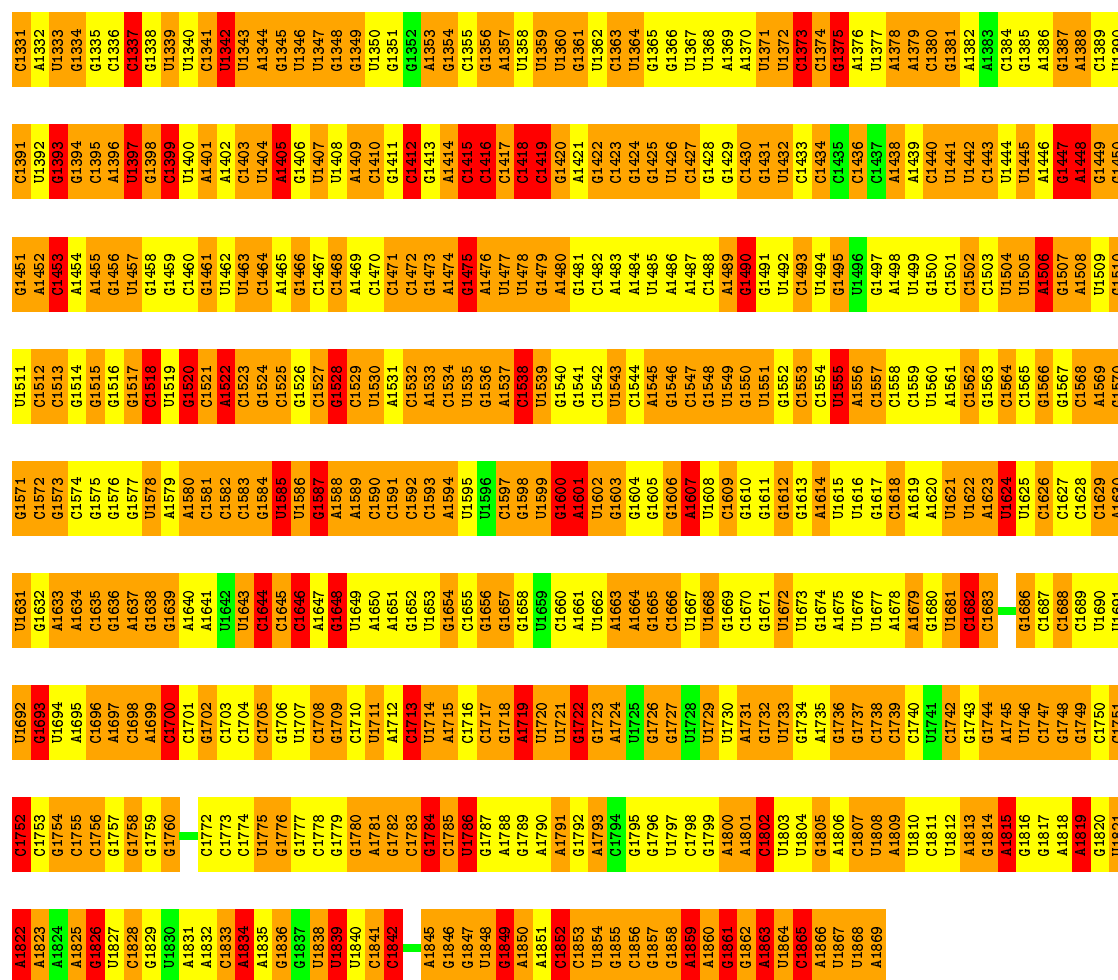


- Molecule 47: 18S rRNA

Chain AA:  32% 46% 11% 7%

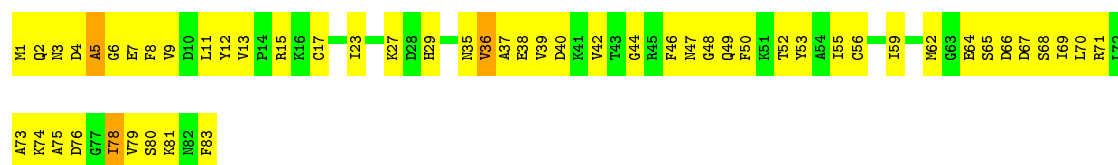


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C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725
C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C	C	C	C	C	C	C746	C747	C748	C749	C750	C751	C752	C753	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C</																																																																																																																																					



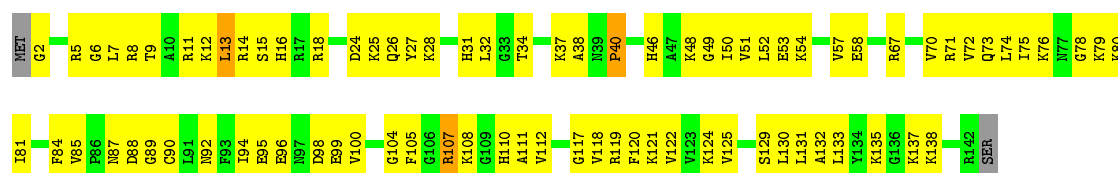
• Molecule 48: 40S ribosomal protein S21

Chain AC: 36% 60%



• Molecule 49: 40S ribosomal protein S23

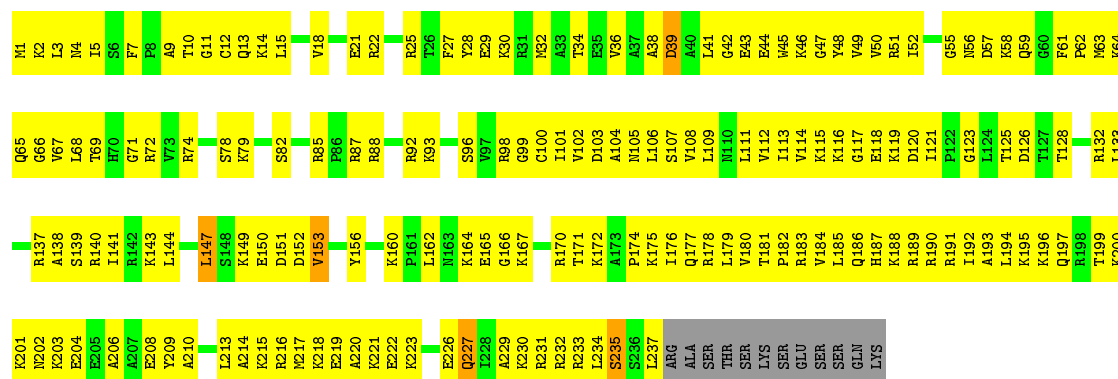
Chain AD: 41% 55%



• Molecule 50: 40S ribosomal protein S26

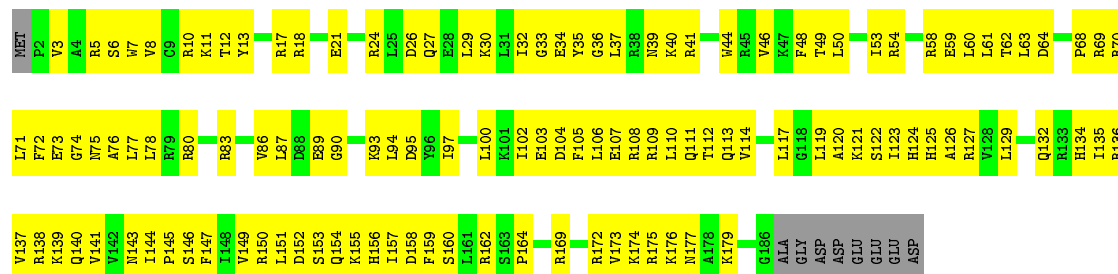
- Molecule 54: 40S ribosomal protein S6

Chain AK:  27% 67% 5%



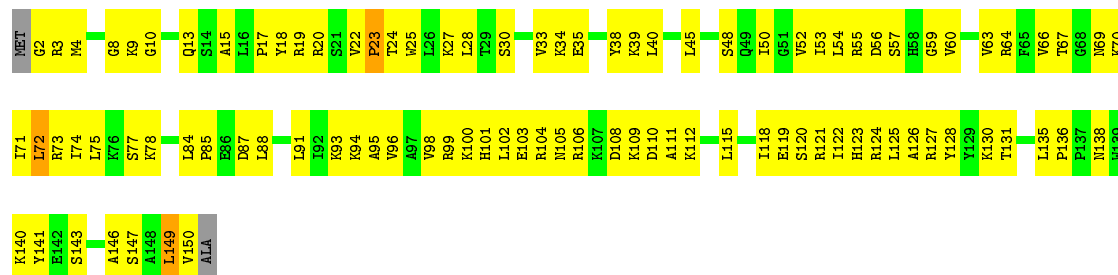
- Molecule 55: 40S ribosomal protein S9

Chain AL:  32% 63% 5%



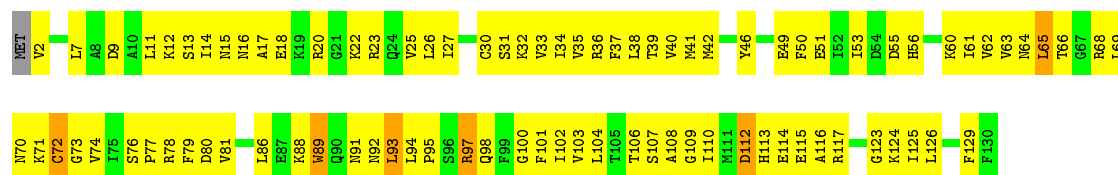
- Molecule 56: 40S ribosomal protein S13

Chain AN:  35% 62% 2%

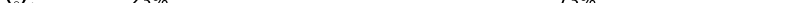


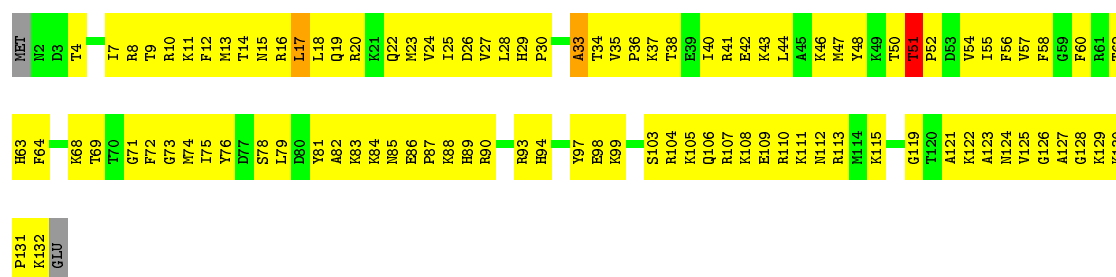
- Molecule 57: 40S ribosomal protein S15a

Chain AP:  32% 63% 5%




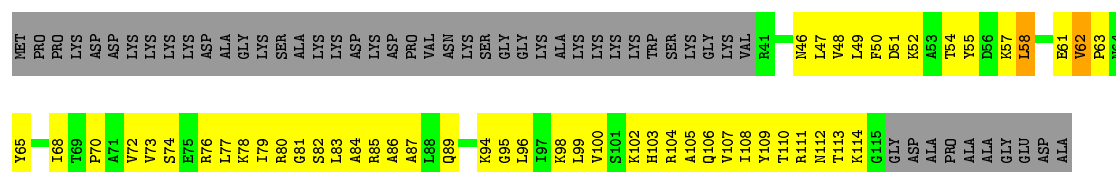
- Molecule 58: 40S ribosomal protein S24

Chain AQ:  23% 73% ..



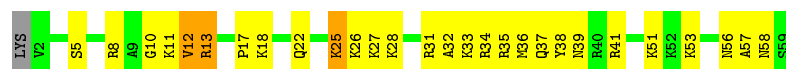
- Molecule 59: 40S ribosomal protein S25

Chain AR: 



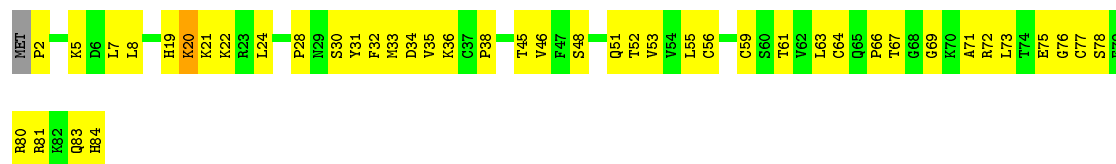
- Molecule 60: 40S ribosomal protein S30

Chain AT:  51% 42% 5%



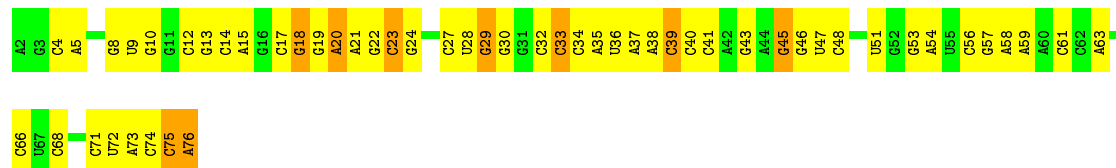
- Molecule 61: 40S ribosomal protein S27

Chain AV:  46% 51% ...



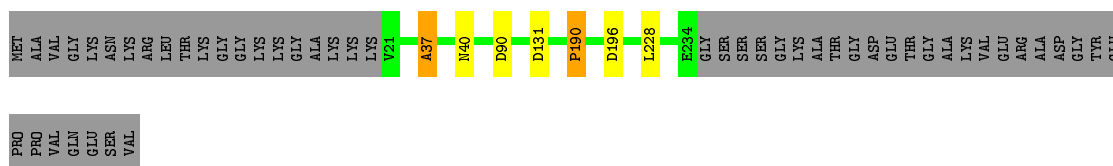
- Molecule 62: tRNA

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%



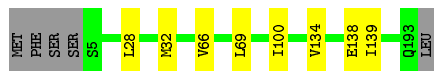
- Molecule 65: 40S ribosomal protein S4, X isoform

Chain Ar: 97%



- Molecule 66: 40S ribosomal protein S7

Chain At: 93%



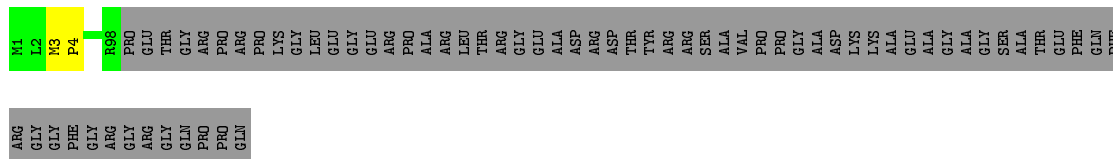
- Molecule 67: 40S ribosomal protein S8

Chain Au: 97%



- Molecule 68: 40S ribosomal protein S10

Chain Av: 58% 41%



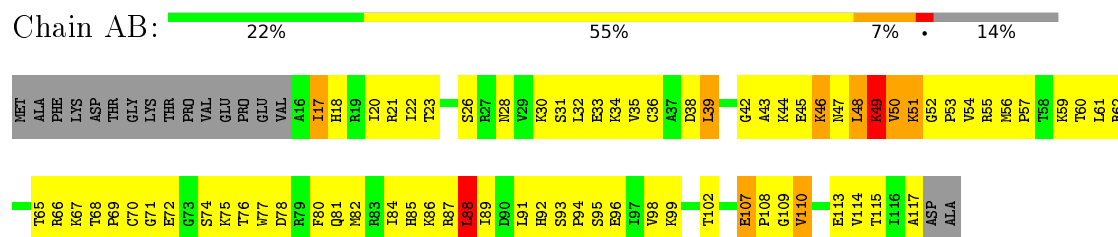
- Molecule 69: 40S ribosomal protein S16

Chain Ay: 95% 5%

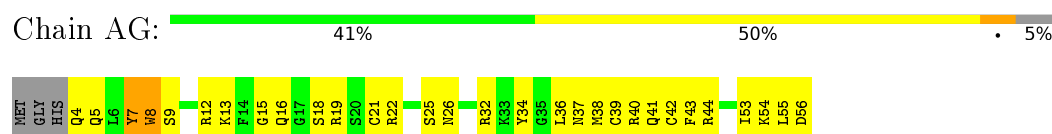


- Molecule 70: 40S ribosomal protein S18

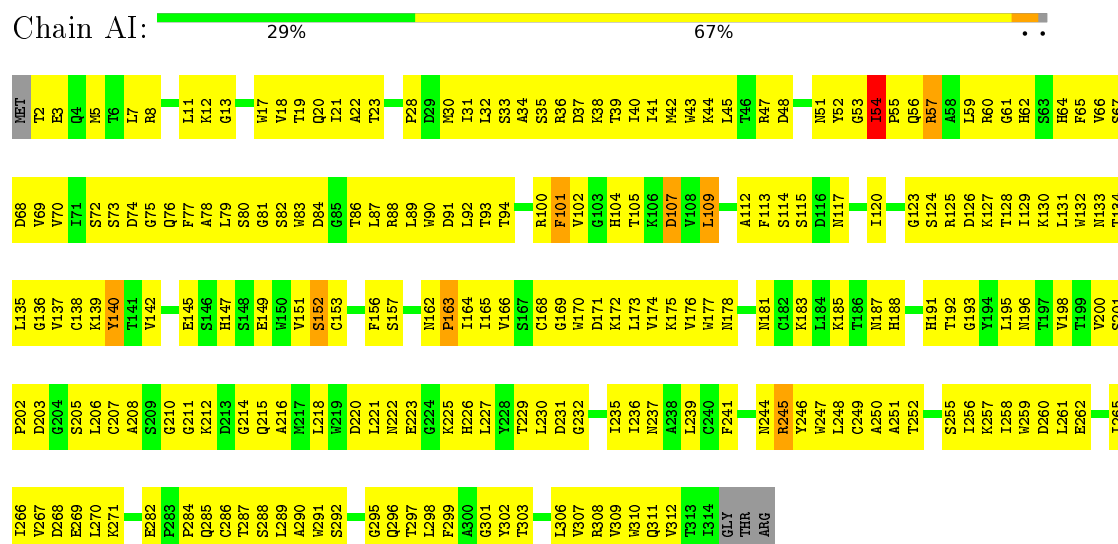
- Molecule 76: 40S ribosomal protein S20



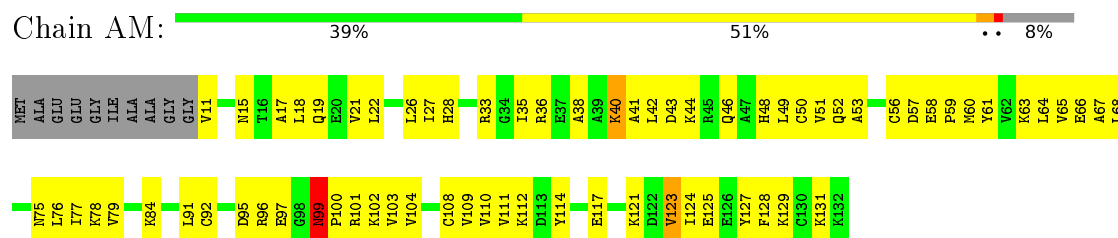
- Molecule 77: 40S ribosomal protein S29



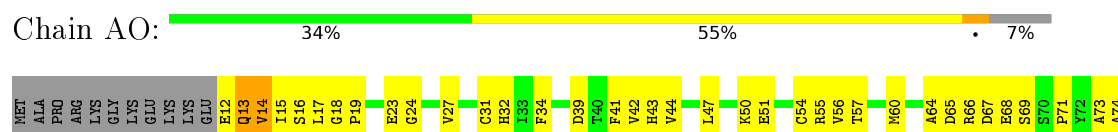
- Molecule 78: Receptor of activated protein C kinase 1

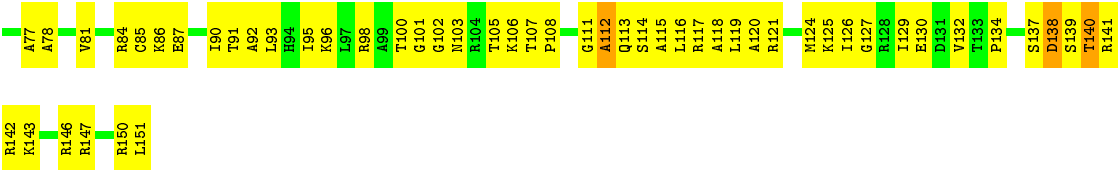


- Molecule 79: 40S ribosomal protein S12



- Molecule 80: 40S ribosomal protein S14





● 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	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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%)	46	83
6	G	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	46	83
7	I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
8	J	151/160 (94%)	145 (96%)	5 (3%)	1 (1%)	26	72
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%)	13	57
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	31
36	r	208/211 (99%)	189 (91%)	17 (8%)	2 (1%)	19	66
38	H	238/288 (83%)	203 (85%)	30 (13%)	5 (2%)	9	52
39	i	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
40	K	185/188 (98%)	177 (96%)	7 (4%)	1 (0%)	34	77
41	l	215/217 (99%)	188 (87%)	25 (12%)	2 (1%)	21	67
42	M	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	16	62
43	p	211/214 (99%)	196 (93%)	14 (7%)	1 (0%)	34	77
44	q	172/178 (97%)	163 (95%)	6 (4%)	3 (2%)	11	55
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	38
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%)	6	44
53	AJ	220/293 (75%)	195 (89%)	25 (11%)	0	100	100
54	AK	235/249 (94%)	206 (88%)	27 (12%)	2 (1%)	21	67
55	AL	183/194 (94%)	161 (88%)	21 (12%)	1 (0%)	34	77
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%)	8	50
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%)	16	62
63	Ap	212/264 (80%)	184 (87%)	25 (12%)	3 (1%)	14	59
64	Aq	225/243 (93%)	195 (87%)	26 (12%)	4 (2%)	11	54
65	Ar	260/263 (99%)	226 (87%)	31 (12%)	3 (1%)	16	62
66	At	187/194 (96%)	155 (83%)	30 (16%)	2 (1%)	17	64
67	Au	204/208 (98%)	179 (88%)	22 (11%)	3 (2%)	13	57
68	Av	96/165 (58%)	77 (80%)	18 (19%)	1 (1%)	19	66
69	Ay	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	9	52
70	A0	148/152 (97%)	121 (82%)	21 (14%)	6 (4%)	3	34
71	Ao	220/295 (75%)	190 (86%)	28 (13%)	2 (1%)	21	67
72	As	189/204 (93%)	158 (84%)	23 (12%)	8 (4%)	3	33
73	Aw	151/158 (96%)	130 (86%)	18 (12%)	3 (2%)	9	53
74	Ax	95/145 (66%)	60 (63%)	21 (22%)	14 (15%)	0	5
75	Az	130/135 (96%)	93 (72%)	26 (20%)	11 (8%)	1	14
76	AB	100/119 (84%)	82 (82%)	14 (14%)	4 (4%)	4	35
77	AG	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	4	36
78	AI	311/317 (98%)	261 (84%)	44 (14%)	6 (2%)	10	53
79	AM	120/132 (91%)	91 (76%)	26 (22%)	3 (2%)	7	48
80	AO	138/151 (91%)	112 (81%)	21 (15%)	5 (4%)	4	39
81	AU	141/145 (97%)	116 (82%)	18 (13%)	7 (5%)	3	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11449/12881 (89%)	10266 (90%)	1060 (9%)	123 (1%)	23	64

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%)	80	92
38	H	215/252 (85%)	209 (97%)	6 (3%)	51	82
39	i	93/94 (99%)	92 (99%)	1 (1%)	80	92
40	K	164/165 (99%)	164 (100%)	0	100	100
41	l	195/196 (100%)	194 (100%)	1 (0%)	92	97
42	M	156/157 (99%)	154 (99%)	2 (1%)	76	91
43	p	180/181 (99%)	178 (99%)	2 (1%)	80	92
44	q	148/149 (99%)	144 (97%)	4 (3%)	52	83
45	R	108/133 (81%)	107 (99%)	1 (1%)	84	94
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%)	80	92
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%)	66	89
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%)	82	93
64	Aq	190/202 (94%)	190 (100%)	0	100	100
65	Ar	224/225 (100%)	223 (100%)	1 (0%)	93	98
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%)	86	95
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%)	78	92
73	Aw	137/142 (96%)	136 (99%)	1 (1%)	88	96
74	Ax	87/130 (67%)	84 (97%)	3 (3%)	44	80
75	Az	120/122 (98%)	115 (96%)	5 (4%)	36	75
76	AB	93/107 (87%)	89 (96%)	4 (4%)	35	75
77	AG	47/49 (96%)	46 (98%)	1 (2%)	61	87
78	AI	272/275 (99%)	270 (99%)	2 (1%)	88	96
79	AM	104/108 (96%)	103 (99%)	1 (1%)	82	93
80	AO	110/119 (92%)	110 (100%)	0	100	100
81	AU	113/115 (98%)	112 (99%)	1 (1%)	84	94
All	All	9988/10975 (91%)	9941 (100%)	47 (0%)	92	97

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