



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Oct 13, 2019 – 08:09 PM EDT

PDB ID : 4V8T  
EMDB ID: : EMD-2169  
Title : Cryo-EM Structure of the 60S Ribosomal Subunit in Complex with Arx1 and Re1  
Authors : Greber, B.J.; Boehringer, D.; Montellese, C.; Ban, N.  
Deposited on : 2012-08-07  
Resolution : 8.10 Å(reported)  
Based on PDB ID : 3U5I, 3U5H

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](mailto: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.

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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) : 2.4

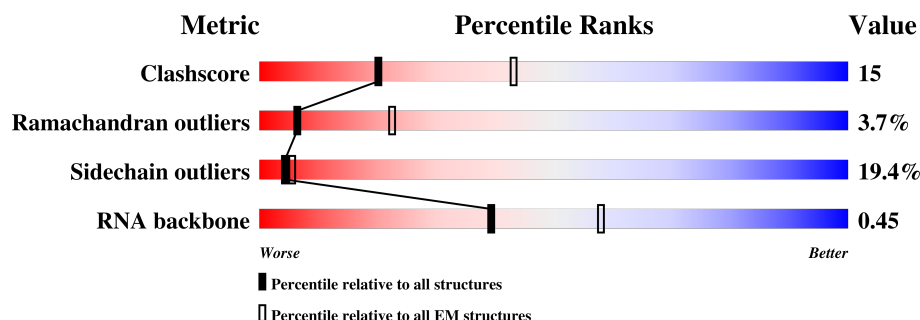
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.10 Å.

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














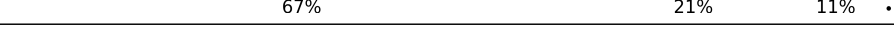







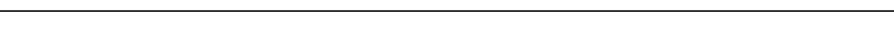

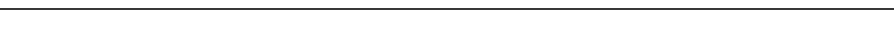
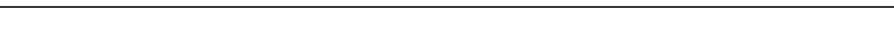


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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  $\geq 3$ , 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	A	254	59% 29% 10% ..
2	B	387	58% 28% 11% .
3	C	362	54% 33% 11% .
4	D	297	59% 31% 8% ..
5	E	176	63% 18% 7% . 11%
6	F	244	60% 25% 6% . 9%
7	G	256	44% 32% 13% . 10%
8	H	191	50% 36% 13% .









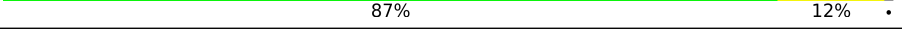

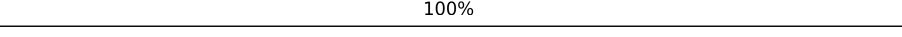
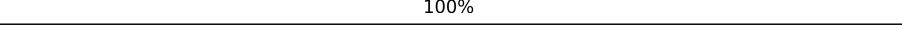
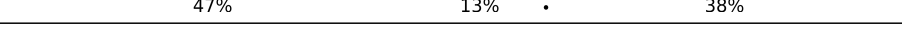
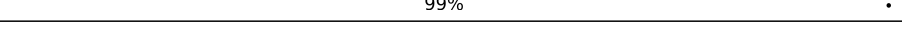

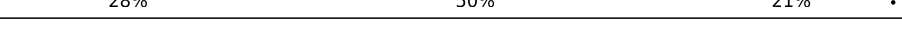

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Mol	Chain	Length	Quality of chain
9	I	221	
10	J	174	
11	K	155	
12	L	199	
13	M	138	
14	N	204	
15	O	219	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	155	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	59	
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	

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Mol	Chain	Length	Quality of chain
34	h	120	
35	i	100	
36	j	88	
37	k	78	
38	l	51	
39	m	128	
40	n	25	
41	o	106	
42	p	92	
43	q	312	
44	r	47	
45	s	46	
46	t	614	
47	1	114	
48	5	3396	
49	7	121	
50	8	158	

## 2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 130050 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S RIBOSOMAL PROTEIN L2-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L3.

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

- Molecule 3 is a protein called 60S RIBOSOMAL PROTEIN L4-A.

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

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	3	ALA	THR	conflict	UNP Q3E757

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	150	Total	C	N	O		0	0
			750	450	150	150			

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	194	Total	C	N	O		0	0
			1548	965	316	267			

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	197	0
			3119	2008	581	528	2		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	3	SER	VAL	microheterogeneity	UNP P26784
O	4	GLN	GLU	microheterogeneity	UNP P26784
O	11	ALA	GLY	microheterogeneity	UNP P26784
O	13	ASP	GLY	microheterogeneity	UNP P26784
O	16	LEU	VAL	microheterogeneity	UNP P26784
O	22	THR	VAL	microheterogeneity	UNP P26784
O	23	ILE	VAL	microheterogeneity	UNP P26784
O	27	VAL	LEU	microheterogeneity	UNP P26784
O	40	ALA	GLU	microheterogeneity	UNP P26784
O	80	LEU	PHE	microheterogeneity	UNP P26784
O	84	ILE	LEU	microheterogeneity	UNP P26784
O	104	ILE	VAL	microheterogeneity	UNP P26784
O	158	ASP	ALA	microheterogeneity	UNP P26784
O	163	ARG	SER	microheterogeneity	UNP P26784
O	179	SER	ALA	microheterogeneity	UNP P26784
O	182	SER	ASN	microheterogeneity	UNP P26784
O	184	ALA	THR	microheterogeneity	UNP P26784
O	186	ALA	SER	microheterogeneity	UNP P26784
O	196	ALA	SER	microheterogeneity	UNP P26784
O	197	LEU	PHE	microheterogeneity	UNP P26784

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	155	Total	C	N	O	0	0
			1227	764	238	225		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L18-B.

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

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L19-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	188	Total	C	N	O		0
			1521	935	326	260		0

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	172	Total	C	N	O	S	0
			1445	930	267	244	4	0

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	159	Total	C	N	O	S	0
			1276	805	246	221	4	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	98	Total	C	N	O		0
			778	505	127	146		0

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L23-A.

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

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L24-A.



Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	135	Total	C	N	O	S	0	0
			1038	651	206	180	1		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L29.

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

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L33-A.

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

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L34-A.

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

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L40.

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

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L43-A.

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

- Molecule 43 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	143	Total	C	N	O	S	0	0
			1077	687	192	195	3		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	199	UNK	SER	SEE REMARK 999	UNP P05317
q	200	UNK	SER	SEE REMARK 999	UNP P05317
q	201	UNK	ILE	SEE REMARK 999	UNP P05317
q	202	UNK	LEU	SEE REMARK 999	UNP P05317
q	203	UNK	ASP	SEE REMARK 999	UNP P05317
q	204	UNK	ILE	SEE REMARK 999	UNP P05317
q	205	UNK	THR	SEE REMARK 999	UNP P05317
q	206	UNK	ASP	SEE REMARK 999	UNP P05317
q	207	UNK	GLU	SEE REMARK 999	UNP P05317
q	208	UNK	GLU	SEE REMARK 999	UNP P05317
q	209	UNK	LEU	SEE REMARK 999	UNP P05317
q	210	UNK	VAL	SEE REMARK 999	UNP P05317
q	211	UNK	SER	SEE REMARK 999	UNP P05317
q	212	UNK	HIS	SEE REMARK 999	UNP P05317
q	213	UNK	PHE	SEE REMARK 999	UNP P05317
q	214	UNK	VAL	SEE REMARK 999	UNP P05317
q	215	UNK	SER	SEE REMARK 999	UNP P05317
q	216	UNK	ALA	SEE REMARK 999	UNP P05317
q	217	UNK	VAL	SEE REMARK 999	UNP P05317
q	218	UNK	SER	SEE REMARK 999	UNP P05317
q	219	UNK	THR	SEE REMARK 999	UNP P05317
q	220	UNK	ILE	SEE REMARK 999	UNP P05317
q	221	UNK	ALA	SEE REMARK 999	UNP P05317

- Molecule 44 is a protein called RIBOSOMAL PROTEIN P1 ALPHA.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	47	Total	C	N	O	0	0
			235	141	47	47		

- Molecule 45 is a protein called RIBOSOMAL PROTEIN P2 BETA.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	46	Total	C	N	O	0	0
			230	138	46	46		

- Molecule 46 is a protein called PROBABLE METALLOPROTEASE ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	380	Total	C	N	O	S	0	0
			2938	1853	511	563	11		

- Molecule 47 is a RNA chain called ES27 OF THE 25S RRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
47	1	114	Total P 114 114	0	114

- Molecule 48 is a RNA chain called 25S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3150	Total	C	N	O	P	0	0
			67376	30095	12145	21987	3149		

- Molecule 49 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 50 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

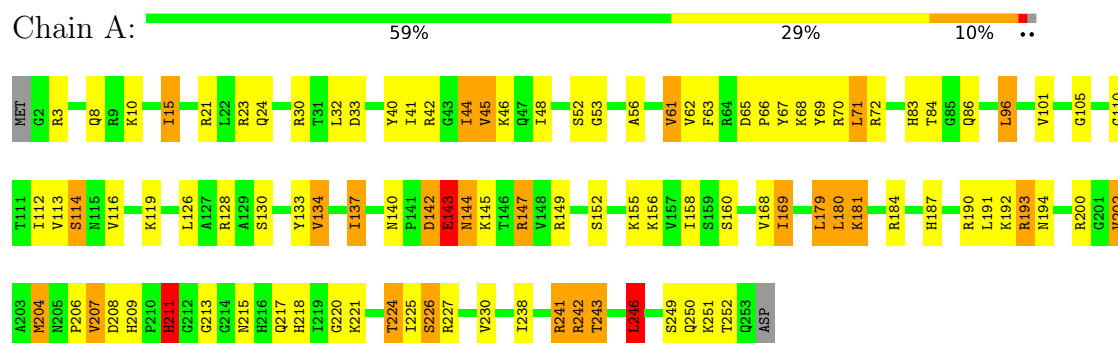
- Molecule 51 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
51	p	1	Total Zn 1 1	0
51	o	1	Total Zn 1 1	0
51	j	1	Total Zn 1 1	0
51	m	1	Total Zn 1 1	0

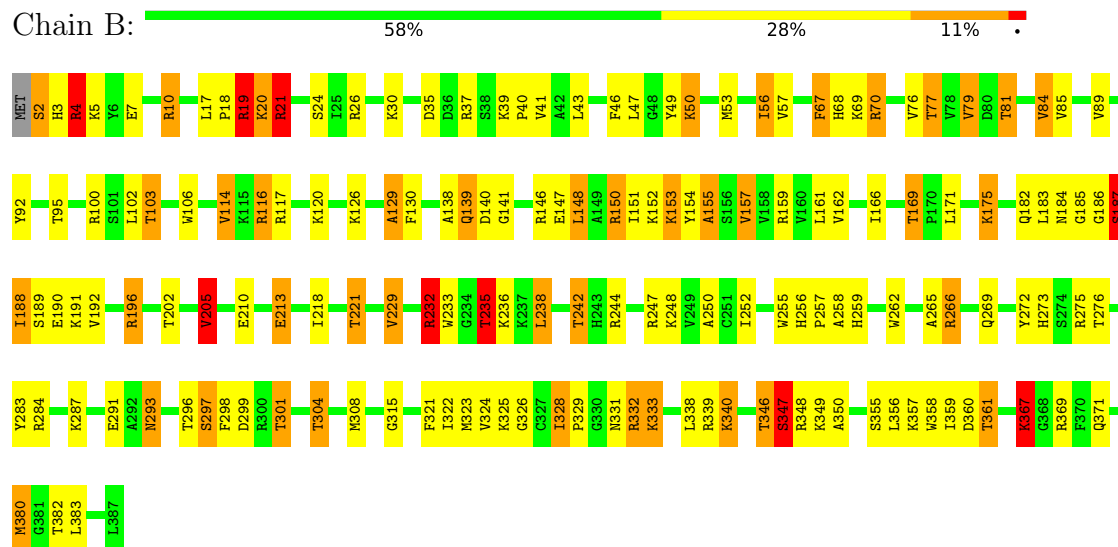
### 3 Residue-property plots

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.

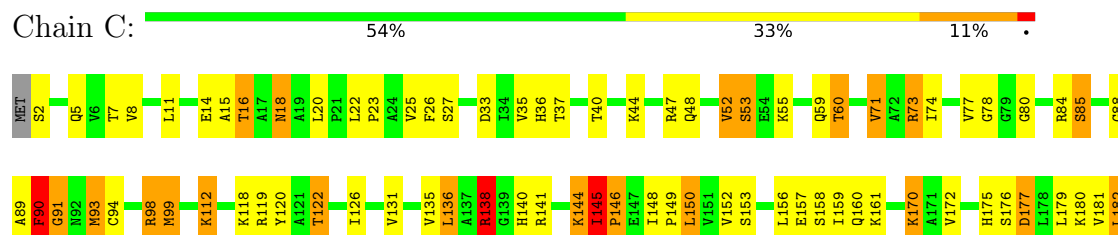
#### • Molecule 1: 60S RIBOSOMAL PROTEIN L2-B

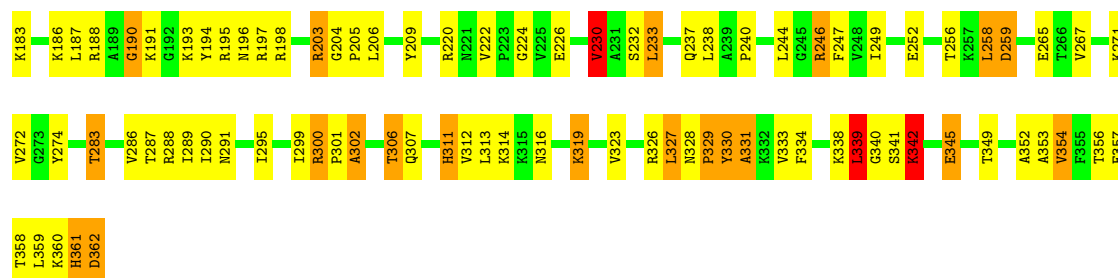


#### • Molecule 2: 60S RIBOSOMAL PROTEIN L3

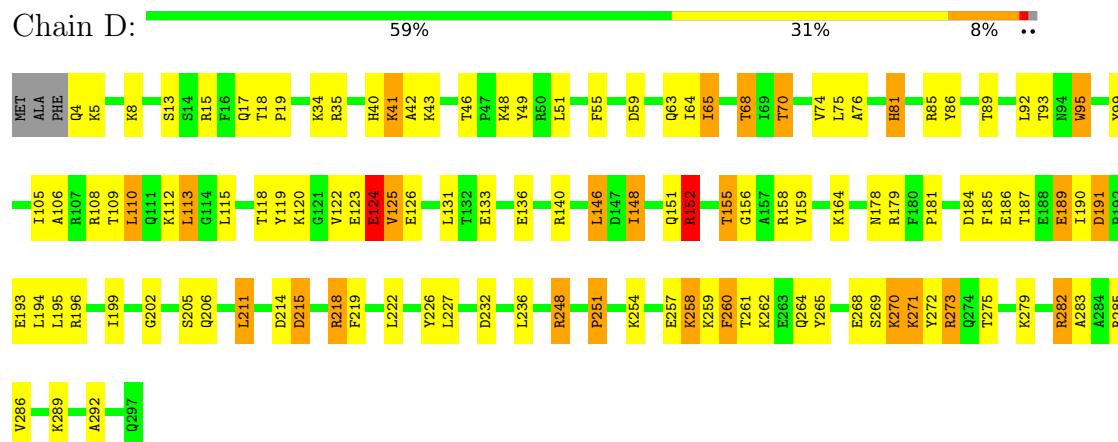


#### • Molecule 3: 60S RIBOSOMAL PROTEIN L4-A

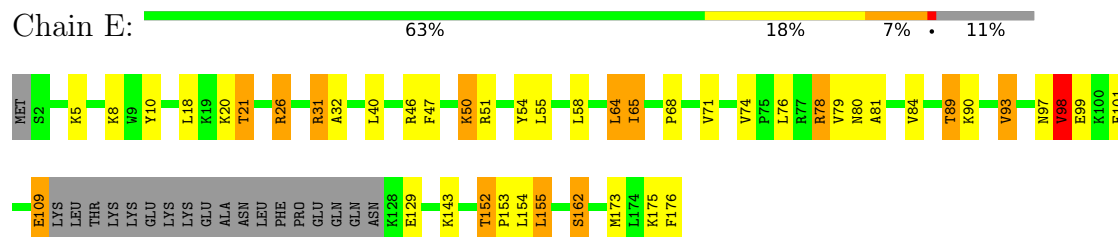




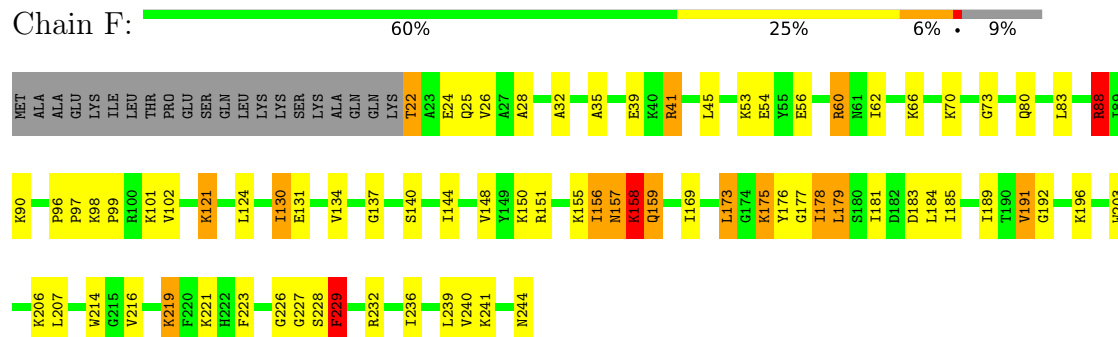
• Molecule 4: 60S RIBOSOMAL PROTEIN L5



• Molecule 5: 60S RIBOSOMAL PROTEIN L6-A

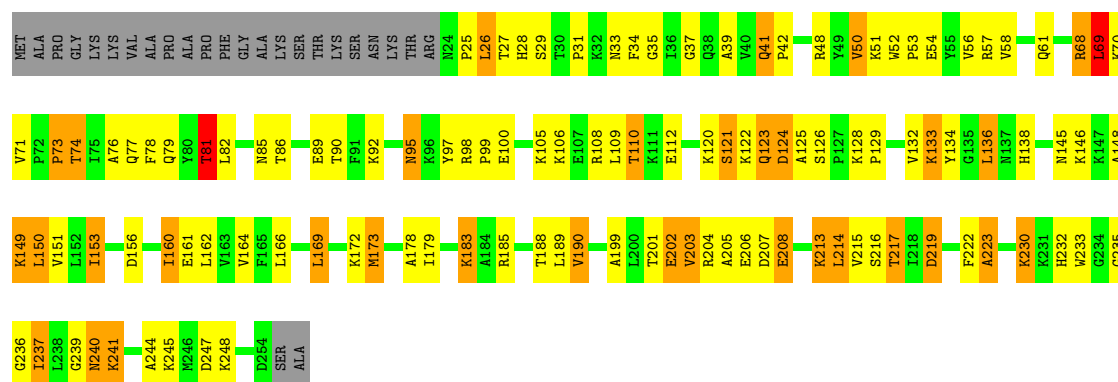


• Molecule 6: 60S RIBOSOMAL PROTEIN L7-A



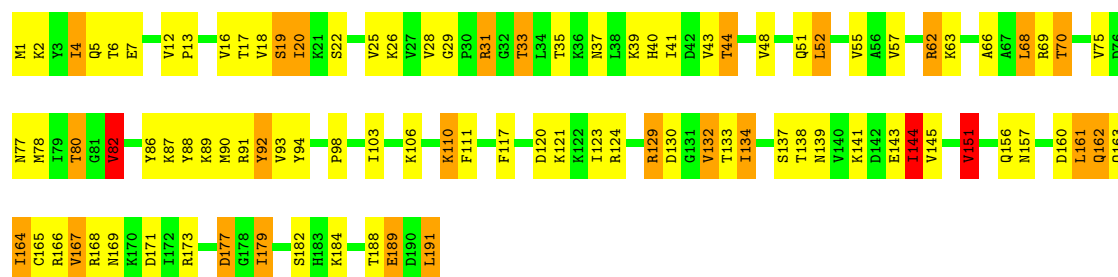
• Molecule 7: 60S RIBOSOMAL PROTEIN L8-A





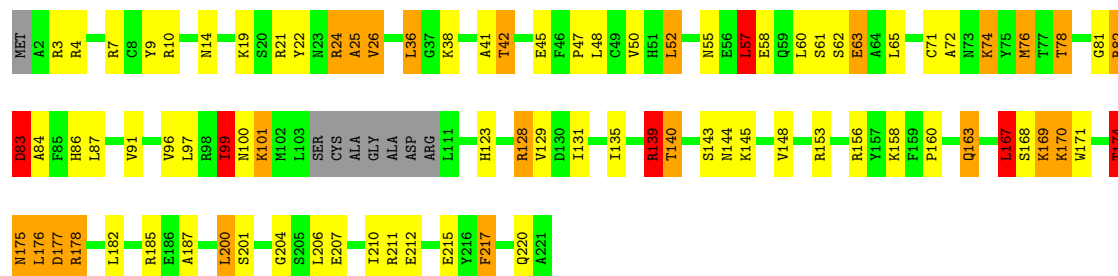
• Molecule 8: 60S RIBOSOMAL PROTEIN L9-A

Chain H: 50% 36% 13% .



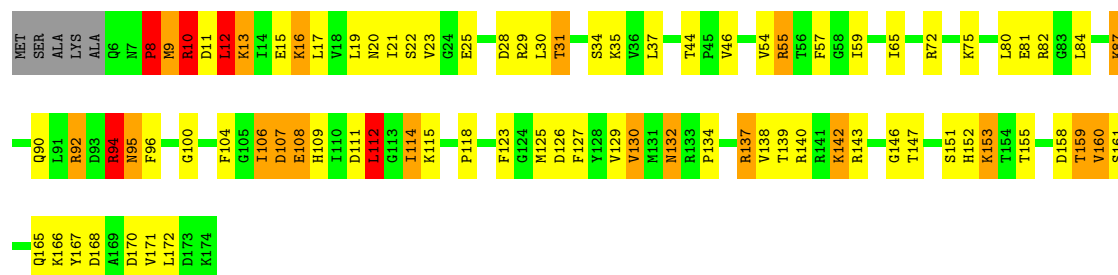
• Molecule 9: 60S RIBOSOMAL PROTEIN L10

Chain I: 57% 26% 10% . .




• Molecule 10: 60S RIBOSOMAL PROTEIN L11-B

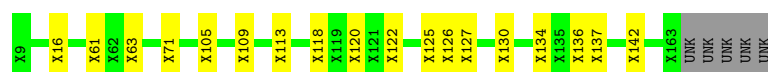
Chain J: 49% 34% 11% . .



• Molecule 11: 60S RIBOSOMAL PROTEIN L12

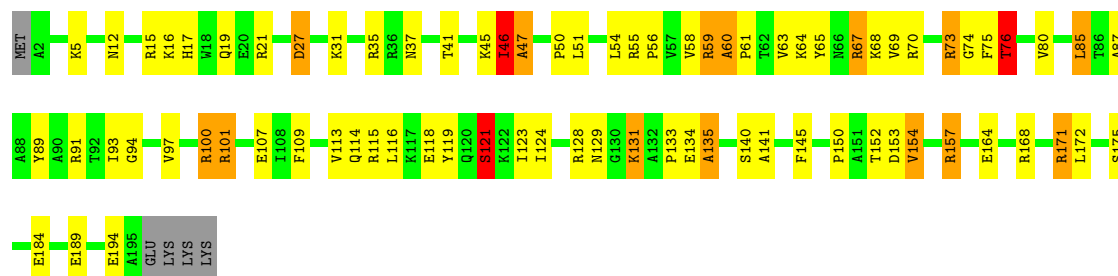


Chain K:  85% 12%



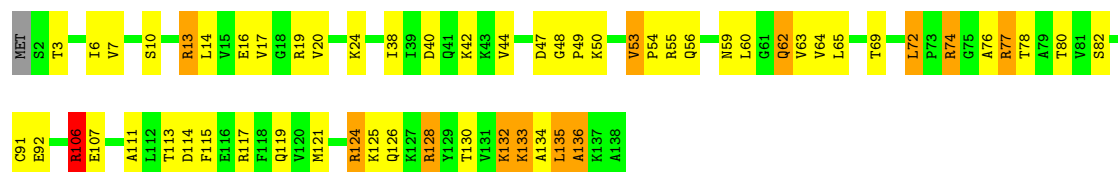
• Molecule 12: 60S RIBOSOMAL PROTEIN L13-A

Chain L:  58% 31% 7%



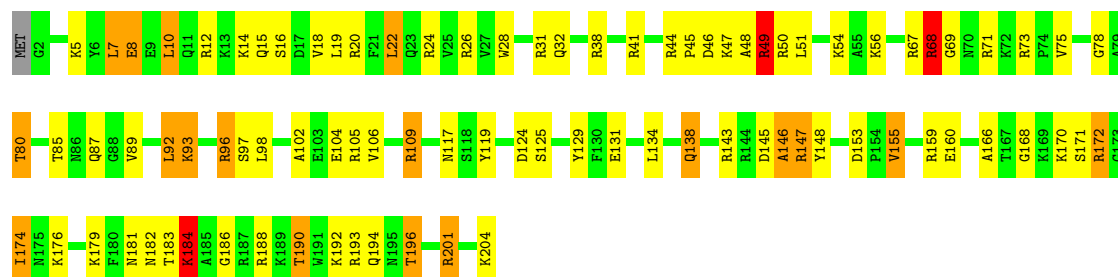
• Molecule 13: 60S RIBOSOMAL PROTEIN L14-A

Chain M:  57% 33% 9%



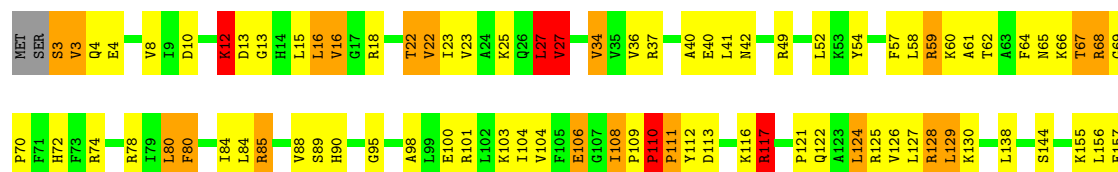
• Molecule 14: 60S RIBOSOMAL PROTEIN L15-A

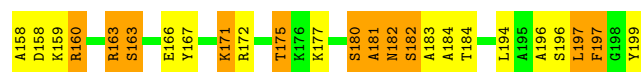
Chain N:  56% 33% 9%



• Molecule 15: 60S RIBOSOMAL PROTEIN L16-A

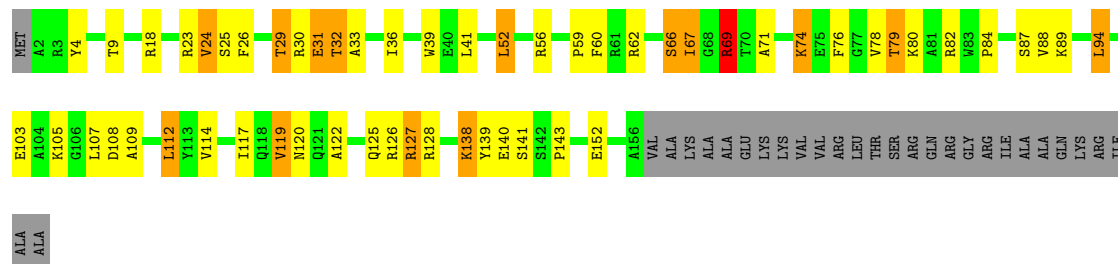
Chain O:  49% 34% 14%





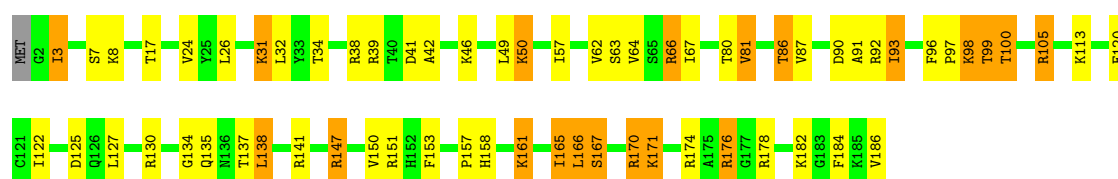
• Molecule 16: 60S RIBOSOMAL PROTEIN L17-A

Chain P: 54% 22% 8% 16%



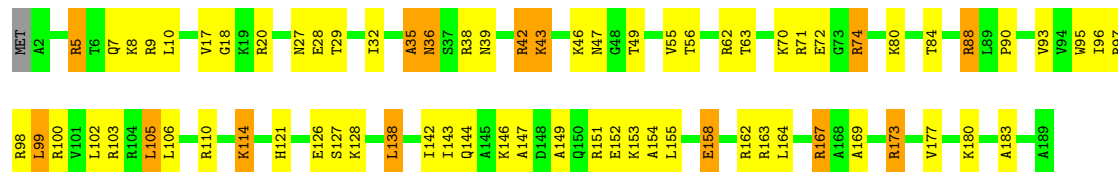
• Molecule 17: 60S RIBOSOMAL PROTEIN L18-B

Chain Q: 65% 24% 11%



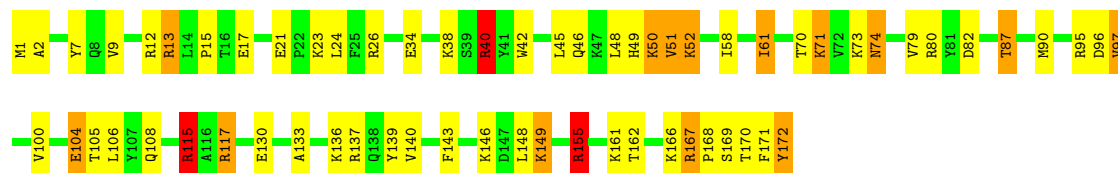
• Molecule 18: 60S RIBOSOMAL PROTEIN L19-B

Chain R: 61% 31% 7%



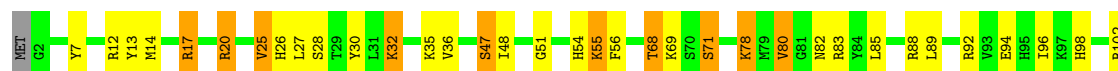
• Molecule 19: 60S RIBOSOMAL PROTEIN L20-A

Chain S: 63% 27% 8%



• Molecule 20: 60S RIBOSOMAL PROTEIN L21-A

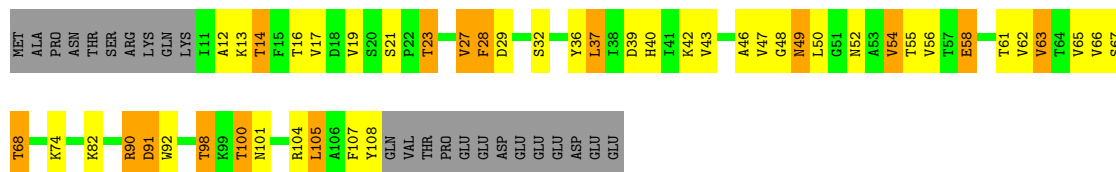
Chain T: 67% 21% 11%





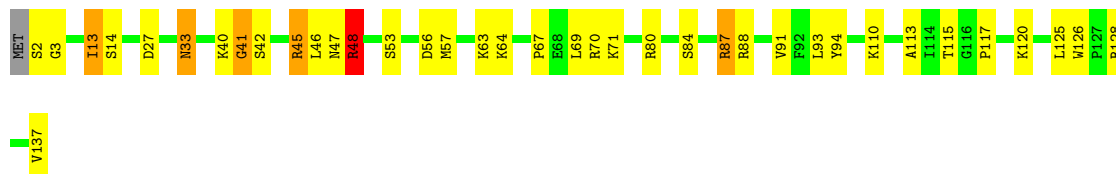
• Molecule 21: 60S RIBOSOMAL PROTEIN L22-A

Chain U: 42% 26% 12% 19%



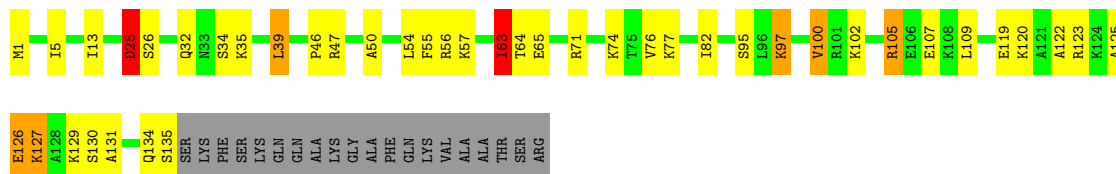
• Molecule 22: 60S RIBOSOMAL PROTEIN L23-A

Chain V: 72% 23% . . .



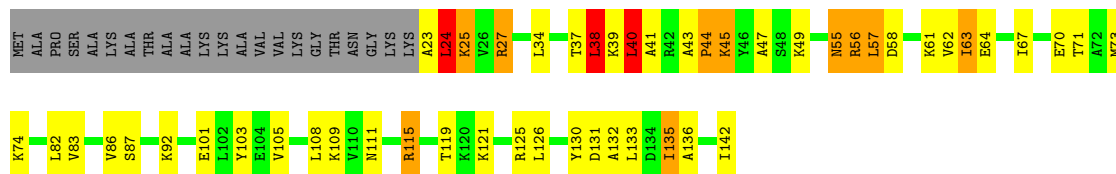
• Molecule 23: 60S RIBOSOMAL PROTEIN L24-A

Chain W: 59% 23% . . 13%



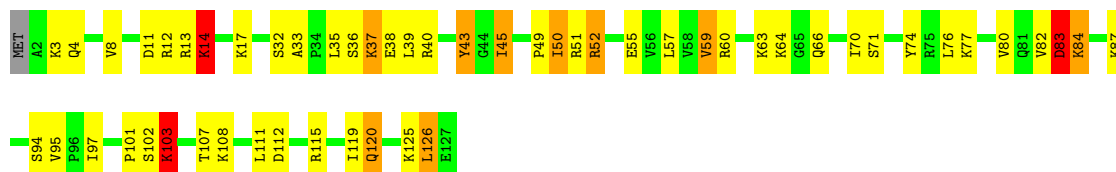
• Molecule 24: 60S RIBOSOMAL PROTEIN L25

Chain X: 49% 27% 7% . 15%



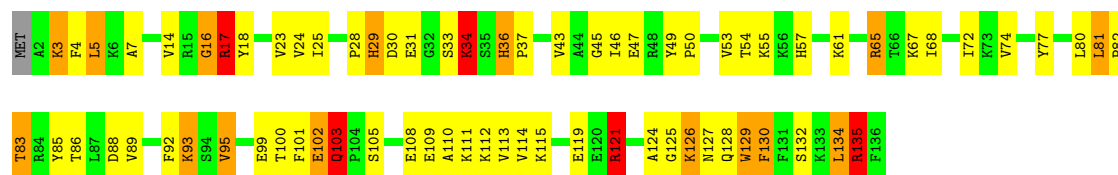
• Molecule 25: 60S RIBOSOMAL PROTEIN L26-A

Chain Y: 57% 33% 7% . .



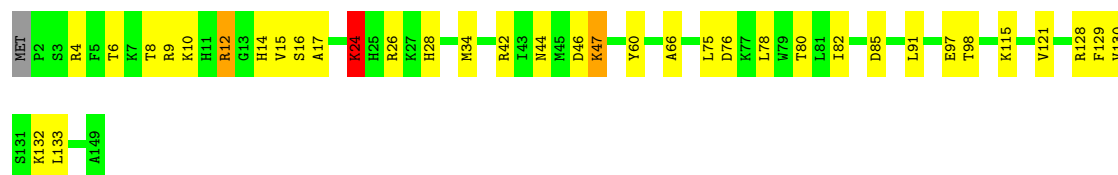
- Molecule 26: 60S RIBOSOMAL PROTEIN L27-A

Chain Z: 



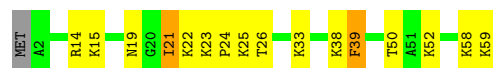
- Molecule 27: 60S RIBOSOMAL PROTEIN L28

Chain a: 




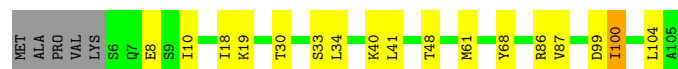
- Molecule 28: 60S RIBOSOMAL PROTEIN L29

Chain b: 



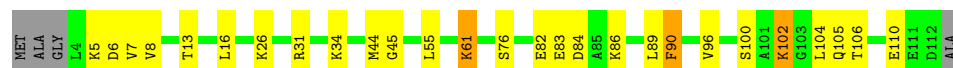
- Molecule 29: 60S RIBOSOMAL PROTEIN L32

Chain c: 



- Molecule 30: 60S RIBOSOMAL PROTEIN L31-A

Chain d: 




- Molecule 31: 60S RIBOSOMAL PROTEIN L30

Chain e: 



- Molecule 32: 60S RIBOSOMAL PROTEIN L33-A

Chain f: 



- Molecule 33: 60S RIBOSOMAL PROTEIN L34-A



- Molecule 34: 60S RIBOSOMAL PROTEIN L35-A



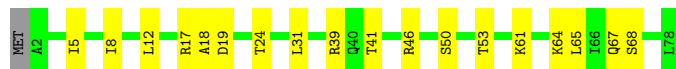
- Molecule 35: 60S RIBOSOMAL PROTEIN L36-A



- Molecule 36: 60S RIBOSOMAL PROTEIN L37-A



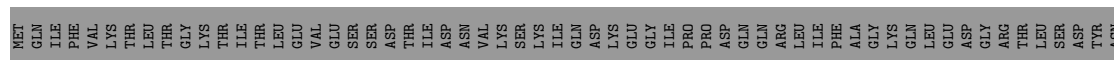
- Molecule 37: 60S RIBOSOMAL PROTEIN L38

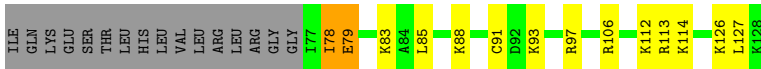


- Molecule 38: 60S RIBOSOMAL PROTEIN L39

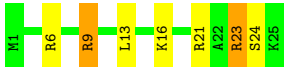


- Molecule 39: 60S RIBOSOMAL PROTEIN L40

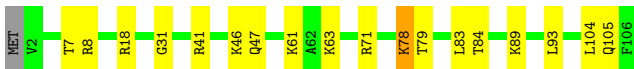
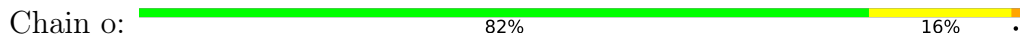




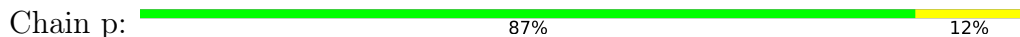
- Molecule 40: 60S RIBOSOMAL PROTEIN L41-A



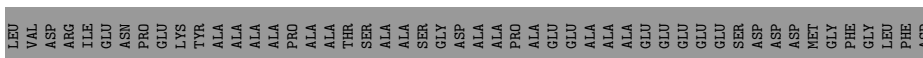
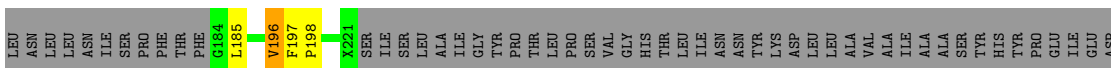
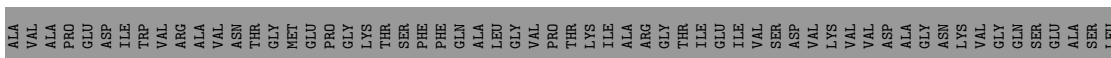
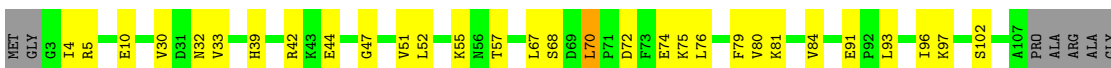
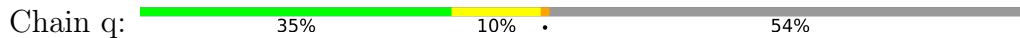
- Molecule 41: 60S RIBOSOMAL PROTEIN L42-A



- Molecule 42: 60S RIBOSOMAL PROTEIN L43-A



- Molecule 43: 60S ACIDIC RIBOSOMAL PROTEIN P0



- Molecule 44: RIBOSOMAL PROTEIN P1 ALPHA



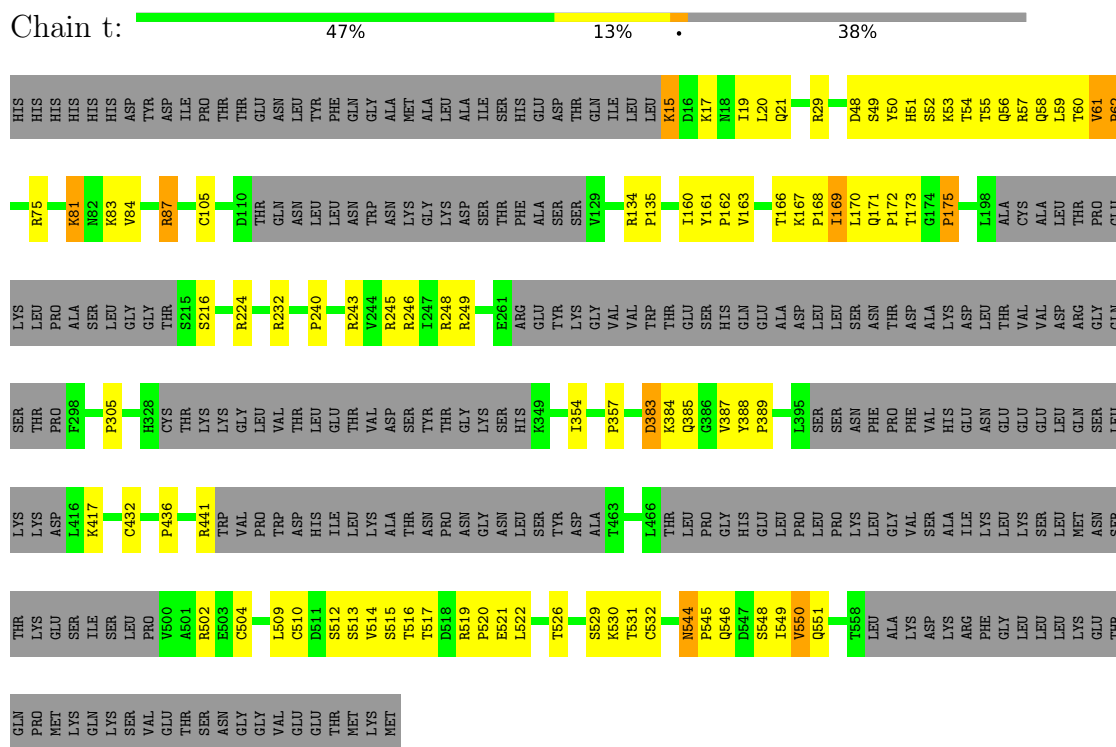
There are no outlier residues recorded for this chain.

- Molecule 45: RIBOSOMAL PROTEIN P2 BETA

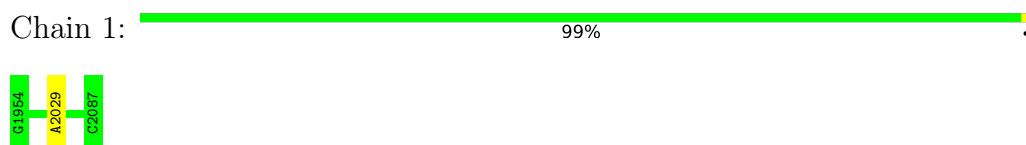


There are no outlier residues recorded for this chain.

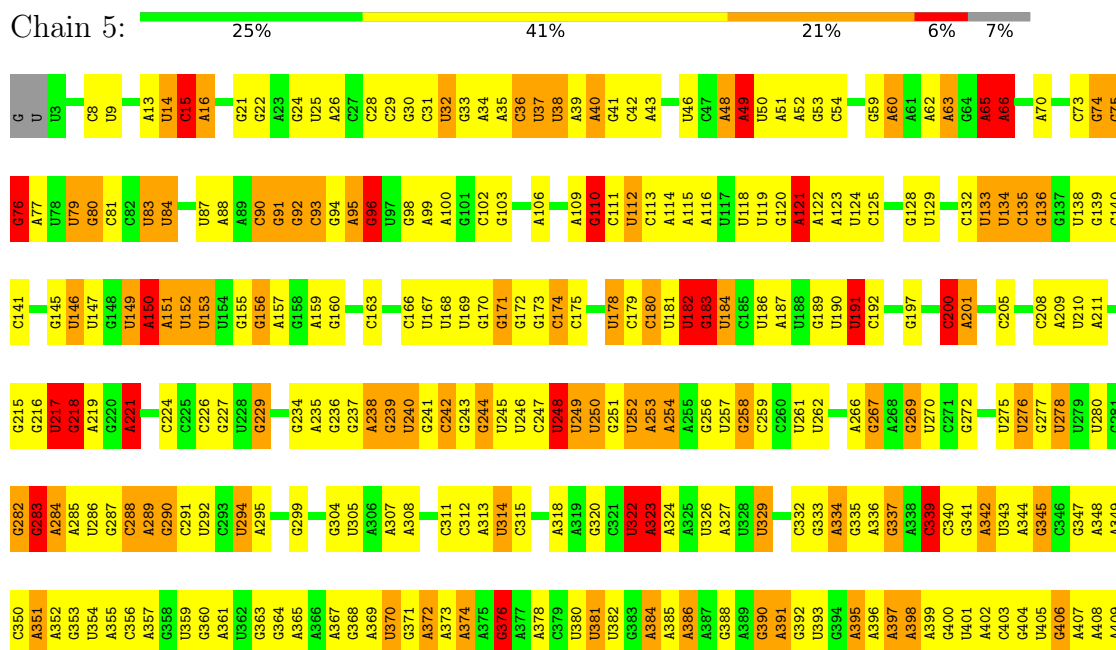
- Molecule 46: PROBABLE METALLOPROTEASE ARX1



• Molecule 47: ES27 OF THE 25S RRNA



• Molecule 48: 25S RIBOSOMAL RNA



A1407	A1408	A1409	A1410	A1411	A1412	A1413	A1414	A1415	A1416	A1417	A1418	A1419	A1420	A1421	A1422	A1423	A1424	A1425	A1426	A1427	A1428	A1429	A1430	A1431	A1432	A1433	A1434	A1435	A1436	A1437	A1438	A1439	A1440	A1441	A1442	A1443	A1444	A1445	A1446	A1447	A1448	A1449	A1450	A1451	A1452	A1453	A1454	A1455	A1456	A1457	A1458	A1459	A1460	A1461	A1462	A1463	A1464	A1465	A1466	A1467	A1468	A1469	A1470	A1471	A1472	A1473	A1474	A1475	A1476	A1477	A1478	A1479	A1480	A1481	A1482	A1483	A1484	A1485	A1486	A1487	A1488	A1489	A1490	A1491	A1492	A1493	A1494	A1495	A1496	A1497	A1498	A1499	A1500	A1501	A1502	A1503	A1504	A1505	A1506	A1507	A1508	A1509	A1510	A1511	A1512	A1513	A1514	A1515	A1516	A1517	A1518	A1519	A1520	A1521	A1522	A1523	A1524	A1525	A1526	A1527	A1528	A1529	A1530	A1531	A1532	A1533	A1534	A1535	A1536	A1537	A1538	A1539	A1540	A1541	A1542	A1543	A1544	A1545	A1546	A1547	A1548	A1549	A1550	A1551	A1552	A1553	A1554	A1555	A1556	A1557	A1558	A1559	A1560	A1561	A1562	A1563	A1564	A1565	A1566	A1567	A1568	A1569	A1570	A1571	A1572	A1573	A1574	A1575	A1576	A1577	A1578	A1579	A1580	A1581	A1582	A1583	A1584	A1585	A1586	A1587	A1588	A1589	A1590	A1591	A1592	A1593	A1594	A1595	A1596	A1597	A1598	A1599	A1600	A1601	A1602	A1603	A1604	A1605	A1606	A1607	A1608	A1609	A1610	A1611	A1612	A1613	A1614	A1615	A1616	A1617	A1618	A1619	A1620	A1621	A1622	A1623	A1624	A1625	A1626	A1627	A1628	A1629	A1630	A1631	A1632	A1633	A1634	A1635	A1636	A1637	A1638	A1639	A1640	A1641	A1642	A1643	A1644	A1645	A1646	A1647	A1648	A1649	A1650	A1651	A1652	A1653	A1654	A1655	A1656	A1657	A1658	A1659	A1660	A1661	A1662	A1663	A1664	A1665	A1666	A1667	A1668	A1669	A1670	A1671	A1672	A1673	A1674	A1675	A1676	A1677	A1678	A1679	A1680	A1681	A1682	A1683	A1684	A1685	A1686	A1687	A1688	A1689	A1690	A1691	A1692	A1693	A1694	A1695	A1696	A1697	A1698	A1699	A1700	A1701	A1702	A1703	A1704	A1705	A1706	A1707	A1708	A1709	A1710	A1711	A1712	A1713	A1714	A1715	A1716	A1717	A1718	A1719	A1720	A1721	A1722	A1723	A1724	A1725	A1726	A1727	A1728	A1729	A1730	A1731	A1732	A1733	A1734	A1735	A1736	A1737	A1738	A1739	A1740	A1741	A1742	A1743	A1744	A1745	A1746	A1747	A1748	A1749	A1750	A1751	A1752	A1753	A1754	A1755	A1756	A1757	A1758	A1759	A1760	A1761	A1762	A1763	A1764	A1765	A1766	A1767	A1768	A1769	A1770	A1771	A1772	A1773	A1774	A1775	A1776	A1777	A1778	A1779	A1780	A1781	A1782	A1783	A1784	A1785	A1786	A1787	A1788	A1789	A1790	A1791	A1792	A1793	A1794	A1795	A1796	A1797	A1798	A1799	A1800	A1801	A1802	A1803	A1804	A1805	A1806	A1807	A1808	A1809	A1810	A1811	A1812	A1813	A1814	A1815	A1816	A1817	A1818	A1819	A1820	A1821	A1822	A1823	A1824	A1825	A1826	A1827	A1828	A1829	A1830	A1831	A1832	A1833	A1834	A1835	A1836	A1837	A1838	A1839	A1840	A1841	A1842	A1843	A1844	A1845	A1846	A1847	A1848	A1849	A1850	A1851	A1852	A1853	A1854	A1855	A1856	A1857	A1858	A1859	A1860	A1861	A1862	A1863	A1864	A1865	A1866	A1867	A1868	A1869	A1870	A1871	A1872	A1873	A1874	A1875	A1876	A1877	A1878	A1879	A1880	A1881	A1882	A1883	A1884	A1885	A1886	A1887	A1888	A1889	A1890	A1891	A1892	A1893	A1894	A1895	A1896	A1897	A1898	A1899	A1900	A1901	A1902	A1903	A1904	A1905	A1906	A1907	A1908	A1909	A1910	A1911	A1912	A1913	A1914	A1915	A1916	A1917	A1918	A1919	A1920	A1921	A1922	A1923	A1924	A1925	A1926	A1927	A1928	A1929	A1930	A1931	A1932	A1933	A1934	A1935	A1936	A1937	A1938	A1939	A1940	A1941	A1942	A1943	A1944	A1945	A1946	A1947	A1948	A1949	A1950	A1951	A1952	A1953	A1954	A1955	A1956	A1957	A1958	A1959	A1960	A1961	A1962	A1963	A1964	A1965	A1966	A1967	A1968	A1969	A1970	A1971	A1972	A1973	A1974	A1975	A1976	A1977	A1978	A1979	A1980	A1981	A1982	A1983	A1984	A1985	A1986	A1987	A1988	A1989	A1990	A1991	A1992	A1993	A1994	A1995	A1996	A1997	A1998	A1999	A2000	A2001	A2002	A2003	A2004	A2005	A2006	A2007	A2008	A2009	A2010	A2011	A2012	A2013	A2014	A2015	A2016	A2017	A2018	A2019	A2020	A2021	A2022	A2023	A2024	A2025	A2026	A2027	A2028	A2029	A2030	A2031	A2032	A2033	A2034	A2035	A2036	A2037	A2038	A2039	A2040	A2041	A2042	A2043	A2044	A2045	A2046	A2047	A2048	A2049	A2050	A2051	A2052	A2053	A2054	A2055	A2056	A2057	A2058	A2059	A2060	A2061	A2062	A2063	A2064	A2065	A2066	A2067	A2068	A2069	A2070	A2071	A2072	A2073	A2074	A2075	A2076	A2077	A2078	A2079	A2080	A2081	A2082	A2083	A2084	A2085	A2086	A2087	A2088	A2089	A2090	A2091	A2092	A2093	A2094	A2095	A2096	A2097	A2098	A2099	A2100	A2101	A2102	A2103	A2104	A2105	A2106	A2107	A2108	A2109	A2110	A2111	A2112	A2113	A2114	A2115	A2116	A2117	A2118	A2119	A2120	A2121	A2122	A2123	A2124	A2125	A2126	A2127	A2128	A2129	A2130	A2131	A2132	A2133	A2134	A2135	A2136	A2137	A2138	A2139	A2140	A2141	A2142	A2143	A2144	A2145	A2146	A2147	A2148	A2149	A2150	A2151	A2152	A2153	A2154	A2155	A2156	A2157	A2158	A2159	A2160	A2161	A2162	A2163	A2164	A2165	A2166	A2167	A2168	A2169	A2170	A2171	A2172	A2173	A2174	A2175	A2176	A2177	A2178	A2179	A2180	A2181	A2182	A2183	A2184	A2185	A2186	A2187	A2188	A2189	A2190	A2191	A2192	A2193	A2194	A2195	A2196	A2197	A2198	A2199	A2200	A2201	A2202	A2203	A2204	A2205	A2206	A2207	A2208	A2209	A2210	A2211	A2212	A2213	A2214	A2215	A2216	A2217	A2218	A2219	A2220	A2221	A2222	A2223	A2224	A2225	A2226	A2227	A2228	A2229	A2230	A2231	A2232	A2233	A2234	A2235	A2236	A2237	A2238	A2239	A2240	A2241	A2242	A2243	A2244	A2245	A2246	A2247	A2248	A2249	A2250	A2251	A2252	A2253	A2254	A2255	A2256	A2257	A2258	A2259	A2260	A2261	A2262	A2263	A2264	A2265	A2266	A2267	A2268	A2269	A2270	A2271	A2272	A2273	A2274	A2275	A2276	A2277	A2278	A2279	A2280	A2281	A2282	A2283	A2284	A2285	A2286	A2287	A2288	A2289	A2290	A2291	A2292	A2293	A2294	A2295	A2296	A2297	A2298	A2299	A2300	A2301	A2302	A2303	A2304	A2305	A2306	A2307	A2308	A2309	A2310	A2311	A2312	A2313	A2314	A2315	A2316	A2317	A2318	A2319	A2320	A2321	A2322	A2323	A2324	A2325	A2326	A2327	A2328	A2329	A2330	A2331	A2332	A2333	A2334	A2335	A2336	A2337	A2338	A2339	A2340	A2341	A2342	A2343	A2344	A2345	A2346	A2347	A2348	A2349	A2350	A2351	A2352	A2353	A2354	A2355	A2356	A2357	A2358	A2359	A2360	A2361	A2362	A2363	A2364	A2365	A2366	A2367	A2368	A2369	A2370	A2371	A2372	A2373	A2374	A2375	A2376	A2377	A2378	A2379	A2380	A2381	A2382	A2383	A2384	A2385	A2386	A2387	A2388	A2389	A2390	A2391	A2392	A2393	A2394	A2395	A2396	A2397	A2398	A2399	A2400	A2401	A2402	A2403	A2404	A2405	A2406	A2407	A2408	A2409	A2410	A2411	A2412	A2413	A2414	A2415	A2416	A2417	A2418	A2419	A2420	A2421	A2422	A2423	A2424	A2425	A2426	A2427	A2428	A2429	A2430	A2431	A2432	A2433	A2434	A2435	A2436	A2437	A2438	A2439	A2440	A2441	A2442	A2443	A2444	A2445	A2446	A2447	A2448	A2449	A2450	A2451	A2452	A2453	A2454	A2455	A2456	A2457	A2458	A2459	A2460	A2461	A2462	A2463	A2464	A2465	A2466	A2467	A2468	A2469	A2470	A2471	A2472	A2473	A2474	A2475	A2476	A2477	A2478	A2479	A2480	A2481	A2482	A2483	A2484	A2485	A2486	A2487	A2488	A2489	A2490	A2491	A2492	A2493	A2494	A2495	A2496	A2497	A2498	A2499	A2500	A2501	A2502	A2503	A2504	A2505	A2506	A2507	A2508	A2509	A2510	A2511	A2512	A2513	A2514	A2515	A2516	A2517	A2518	A2519	A2520	A2521	A2522	A2523	A2524	A2525	A2526	A2527	A2528	A2529	A2530	A2531	A2532	A2533	A2534	A2535	A2536	A2537	A2538	A2539	A2540	A2541	A2542	A2543	A2544	A2545	A2546	A2547	A2548	A2549	A2550	A2551	A2552	A2553	A2554	A2555	A2556	A2557	A2558	A2559	A2560	A2561	A2562	A2563	A2564	A2565	A2566	A2567	A2568	A2569	A2570	A2571	A2572	A2573	A2574	A2575	A2576	A2577	A2578	A2579	A2580	A2581	A2582	A2583	A2584	A2585	A2586	A2587	A2588	A2589	A2590	A2591	A2592	A2593	A2594	A2595	A2596	A2597	A2598	A2599	A2600	A2601	A2602	A2603	A2604	A2605	A2606	A2607	A2608	A2609	A2610	A2611	A2612	A2613	A2614	A2615	A2616	A2617	A2618	A2619	A2620	A2621	A2622	A2623	A2624	A2625	A2626	A2627	A2628	A2629	A2630	A2631	A2632	A2633	A2634	A2635	A2636	A2637	A2638	A2639	A2640	A2641	A2642	A2643	A2644	A2645	A2646	A2647	A2648	A2649	A2650	A2651	A2652	A2653	A2654	A2655	A2656	A2657	A2658	A2659	A2660	A2661	A2662	A2663	A2664	A2665	A2666	A2667	A2668	A2669	A2670	A2671	A2672	A2673	A2674	A2675	A2676	A2677	A2678	A2679	A2680	A2681	A2682	A2683	A2684	A2685	A2686	A2687	A2688	A2689	A2690	A2691	A2692	A2693	A2694	A2695	A2696	A2697	A2698	A2699	A2700	A2701	A2702	A2703	A2704	A2705	A2706	A2707	A2708	A2709	A2710	A2711	A2712	A2713	A2714	A2715	A2716	A2717	A2718	A2719	A2720	A2721	A2722	A2723	A2724	A2725	A2726	A2727	A2728	A2729	A2730	A2731	A2732	A2733	A2734	A2735	A2736	A2737	A2738	A2739	A2740	A2741	A2742	A2743	A2744	A2745	A2746	A2747	A2748	A2749	A2750	A2751	A2752	A2753	A2754	A2755	A2756	A2757	A2758	A2759	A2760	A2761	A2762	A2763	A2764	A2765	A2766	A2767	A2768	A2769	A2770	A2771	A2772	A2773	A2774	A2775	A2776	A2777	A2778	A2779	A2780	A2781	A278
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WORLDWIDE  
**PDB**  
PROTEIN DATA BANK

 **EMDataBank**  
Unified Data Resource for 3DEM

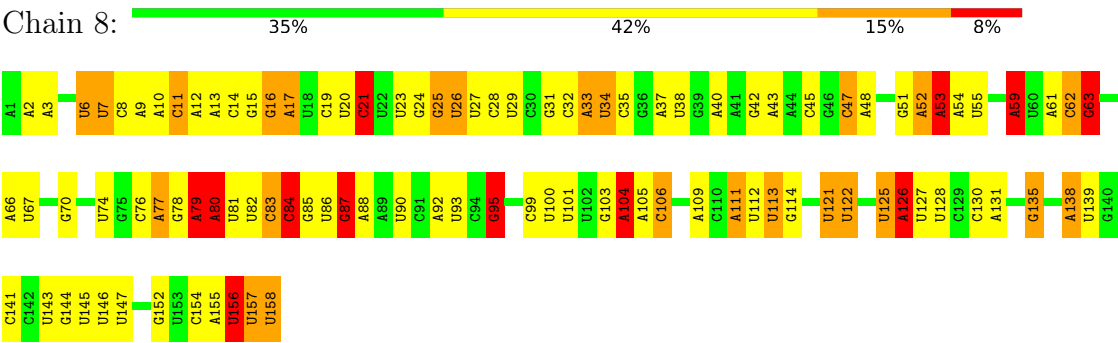
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C3277	C3278	C3279	U3280	C3281	U3282	U3283	C3284	C3285	C3286	U3287	C3288	C3289	C3290	C3291	C3292	C3293	C3294	C3295	C3296	C3297	C3298	U3301	U3302	C3303	C3304	C3305	C3306	C3307	C3308	C3309	C3310	C3311	C3312	C3313	C3314	C3315	C3316	C3317	C3318	C3319	C3320	C3321	C3322	C3323	C3324	C3325	C3326	C3327	C3328	C3329	C3330	C3331	C3332	C3333	C3334	C3335	C3336	C3337	C3338	C3339																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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• Molecule 49: 5S RIBOSOMAL RNA

Chain 7: 28% 50% 21%

G67	G68	G69	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C100	C101	C102	C103	C104	C105	C106	C107	C110	C111	C112	C113	C114	C115	C116	C120	C121	C122	C123	C124	C125	C126	C127	C128	C129	C130	C131	C132	C133	C134	C135	C136	C137	C138	C139	C140	C141	C142	C143	C144	C145	C146	C147	C148	C149	C150	C151	C152	C153	C154	C155	C156	C157	C158	C159	C160	C161	C162	C163	C164	C165	C166	C167	C168	C169	C170	C171	C172	C173	C174	C175	C176	C177	C178	C179	C180	C181	C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	C193	C194	C195	C196	C197	C198	C199	C200	C201	C202	C203	C204	C205	C206	C207	C208	C209	C210	C211	C212	C213	C214	C215	C216	C217	C218	C219	C220	C221	C222	C223	C224	C225	C226	C227	C228	C229	C230	C231	C232	C233	C234	C235	C236	C237	C238	C239	C240	C241	C242	C243	C244	C245	C246	C247	C248	C249	C250	C251	C252	C253	C254	C255	C256	C257	C258	C259	C260	C261	C262	C263	C264	C265	C266	C267	C268	C269	C270	C271	C272	C273	C274	C275	C276	C277	C278	C279	C280	C281	C282	C283	C284	C285	C286	C287	C288	C289	C290	C291	C292	C293	C294	C295	C296	C297	C298	C299	C300	C301	C302	C303	C304	C305	C306	C307	C308	C309	C310	C311	C312	C313	C314	C315	C316	C317	C318	C319	C320	C321	C322	C323	C324	C325	C326	C327	C328	C329	C330	C331	C332	C333	C334	C335	C336	C337	C338	C339	C340	C341	C342	C343	C344	C345	C346	C347	C348	C349	C350	C351	C352	C353	C354	C355	C356	C357	C358	C359	C360	C361	C362	C363	C364	C365	C366	C367	C368	C369	C370	C371	C372	C373	C374	C375	C376	C377	C378	C379	C380	C381	C382	C383	C384	C385	C386	C387	C388	C389	C390	C391	C392	C393	C394	C395	C396	C397	C398	C399	C400	C401	C402	C403	C404	C405	C406	C407	C408	C409	C410	C411	C412	C413	C414	C415	C416	C417	C418	C419	C420	C421	C422	C423	C424	C425	C426	C427	C428	C429	C430	C431	C432	C433	C434	C435	C436	C437	C438	C439	C440	C441	C442	C443	C444	C445	C446	C447	C448	C449	C450	C451	C452	C453	C454	C455	C456	C457	C458	C459	C460	C461	C462	C463	C464	C465	C466	C467	C468	C469	C470	C471	C472	C473	C474	C475	C476	C477	C478	C479	C480	C481	C482	C483	C484	C485	C486	C487	C488	C489	C490	C491	C492	C493	C494	C495	C496	C497	C498	C499	C500	C501	C502	C503	C504	C505	C506	C507	C508	C509	C510	C511	C512	C513	C514	C515	C516	C517	C518	C519	C520	C521	C522	C523	C524	C525	C526	C527	C528	C529	C530	C531	C532	C533	C534	C535	C536	C537	C538	C539	C540	C541	C542	C543	C544	C545	C546	C547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614	C615	C616	C617	C618	C619	C620	C621	C622	C623	C624	C625	C626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	C1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	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
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● Molecule 50: 5.8S RIBOSOMAL RNA



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84113	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PER FRAME	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	83000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	A	0.87	1/1946 (0.1%)	1.05	4/2614 (0.2%)
10	J	0.81	1/1374 (0.1%)	0.99	3/1842 (0.2%)
12	L	0.82	0/1573	1.04	6/2113 (0.3%)
13	M	0.95	0/1074	1.01	4/1446 (0.3%)
14	N	0.83	0/1757	1.00	6/2354 (0.3%)
15	O	0.98	11/3159 (0.3%)	1.02	25/4205 (0.6%)
16	P	1.05	1/1250 (0.1%)	1.09	5/1683 (0.3%)
17	Q	0.89	1/1465 (0.1%)	1.12	8/1965 (0.4%)
18	R	0.78	1/1538 (0.1%)	0.87	3/2050 (0.1%)
19	S	1.02	0/1481	1.09	7/1990 (0.4%)
2	B	1.02	4/3146 (0.1%)	1.11	14/4228 (0.3%)
20	T	1.01	2/1300 (0.2%)	1.01	1/1743 (0.1%)
21	U	0.56	0/794	0.77	0/1076
22	V	0.98	0/1018	1.09	4/1369 (0.3%)
23	W	0.80	0/1052	0.90	1/1398 (0.1%)
24	X	0.72	0/974	0.86	0/1314
25	Y	0.79	1/1004 (0.1%)	0.98	2/1341 (0.1%)
26	Z	0.55	0/1118	0.83	2/1497 (0.1%)
27	a	0.95	2/1204 (0.2%)	1.14	9/1612 (0.6%)
28	b	0.91	0/473	1.14	1/629 (0.2%)
29	c	0.61	0/775	0.77	0/1040
3	C	0.87	0/2800	1.07	11/3790 (0.3%)
30	d	0.94	2/897 (0.2%)	0.95	1/1205 (0.1%)
31	e	1.04	0/1041	1.27	12/1394 (0.9%)
32	f	1.12	1/868 (0.1%)	1.09	3/1168 (0.3%)
33	g	0.72	0/890	0.92	0/1189
34	h	0.67	0/974	0.79	0/1297
35	i	0.67	0/777	0.85	0/1033
36	j	0.87	0/696	1.04	3/923 (0.3%)
37	k	0.50	0/614	0.70	0/822
38	l	0.90	0/443	1.02	1/588 (0.2%)
39	m	1.08	2/423 (0.5%)	1.13	1/562 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
4	D	0.89	1/2408 (0.0%)	0.96	3/3248 (0.1%)
40	n	0.90	0/234	1.15	1/300 (0.3%)
41	o	0.83	0/860	0.88	1/1136 (0.1%)
42	p	0.86	0/701	0.98	1/934 (0.1%)
43	q	0.54	0/977	0.75	1/1313 (0.1%)
46	t	5.64	18/2985 (0.6%)	4.15	194/4053 (4.8%)
48	5	1.46	609/75414 (0.8%)	1.88	3517/117575 (3.0%)
49	7	1.38	13/2883 (0.5%)	1.80	118/4491 (2.6%)
5	E	0.90	1/1269 (0.1%)	1.00	3/1705 (0.2%)
50	8	1.16	5/3746 (0.1%)	1.70	132/5832 (2.3%)
6	F	0.99	1/1828 (0.1%)	1.04	6/2461 (0.2%)
7	G	0.64	0/1795	0.81	1/2429 (0.0%)
8	H	0.97	2/1539 (0.1%)	1.01	1/2073 (0.0%)
9	I	0.92	1/1758 (0.1%)	1.08	11/2358 (0.5%)
All	All	1.49	681/138295 (0.5%)	1.70	4127/203388 (2.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
15	O	0	2
19	S	0	1
22	V	0	1
25	Y	0	1
26	Z	0	1
27	a	0	3
28	b	0	1
3	C	0	1
4	D	0	1
46	t	0	6
48	5	0	1
5	E	0	1
6	F	0	2
All	All	0	24

The worst 5 of 681 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	168	PRO	N-CD	120.75	3.16	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	545	PRO	N-CD	120.48	3.16	1.47
46	t	162	PRO	N-CD	120.12	3.16	1.47
46	t	172	PRO	N-CD	118.10	3.13	1.47
46	t	520	PRO	N-CD	117.23	3.12	1.47

The worst 5 of 4127 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	81	LYS	O-C-N	-73.85	4.54	122.70
46	t	15	LYS	O-C-N	-50.53	41.85	122.70
46	t	544	ASN	O-C-N	-46.67	32.42	121.10
46	t	162	PRO	N-CA-CB	37.84	148.71	103.30
46	t	168	PRO	N-CA-CB	37.79	148.65	103.30

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	GLU	Peptide
1	A	211	HIS	Peptide
3	C	91	GLY	Peptide
4	D	271	LYS	Peptide
5	E	129	GLU	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1912	0	1976	86	0
2	B	3075	0	3142	116	0
3	C	2748	0	2859	99	0
4	D	2359	0	2311	85	0
5	E	1248	0	1339	33	0
6	F	1791	0	1869	47	0
7	G	1763	0	1819	72	0
8	H	1518	0	1587	66	0
9	I	1722	0	1755	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1353	0	1383	56	0
11	K	750	0	185	11	0
12	L	1548	0	1613	45	0
13	M	1059	0	1154	40	0
14	N	1720	0	1779	63	0
15	O	3119	0	3302	94	0
16	P	1227	0	1236	32	0
17	Q	1441	0	1543	39	0
18	R	1521	0	1617	38	0
19	S	1445	0	1487	49	0
20	T	1276	0	1323	51	0
21	U	778	0	791	25	0
22	V	1003	0	1048	25	0
23	W	1038	0	1071	21	0
24	X	959	0	1020	27	0
25	Y	993	0	1081	28	0
26	Z	1092	0	1155	53	0
27	a	1173	0	1215	0	0
28	b	462	0	491	0	0
29	c	767	0	816	0	0
30	d	883	0	918	0	0
31	e	1020	0	1090	0	0
32	f	850	0	880	0	0
33	g	880	0	945	0	0
34	h	965	0	1067	0	0
35	i	770	0	846	0	0
36	j	681	0	683	0	0
37	k	608	0	671	0	0
38	l	436	0	475	0	0
39	m	417	0	455	0	0
40	n	233	0	284	0	0
41	o	847	0	915	0	0
42	p	694	0	734	0	0
43	q	1077	0	1012	0	0
44	r	235	0	50	0	0
45	s	230	0	49	0	0
46	t	2938	0	2993	0	0
47	1	114	0	0	2	0
48	5	67376	0	33833	1087	0
49	7	2579	0	1303	38	0
50	8	3353	0	1695	42	0
51	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	m	1	0	0	0	0
51	o	1	0	0	0	0
51	p	1	0	0	0	0
All	All	130050	0	94865	2205	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 15.

The worst 5 of 2205 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)
17:Q:171:LYS:CE	17:Q:171:LYS:NZ	1.67	1.55
20:T:82:ASN:HD21	47:1:2029:A:P	157.50	1.52
10:J:8:PRO:CG	10:J:8:PRO:CB	1.75	1.49
20:T:82:ASN:ND2	47:1:2029:A:P	157.87	1.25
2:B:296:THR:HG22	2:B:298:PHE:H	1.18	1.06

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	213 (85%)	30 (12%)	7 (3%)	5	37
2	B	384/387 (99%)	341 (89%)	34 (9%)	9 (2%)	7	41
3	C	359/362 (99%)	306 (85%)	32 (9%)	21 (6%)	2	23
4	D	292/297 (98%)	267 (91%)	19 (6%)	6 (2%)	8	43
5	E	153/176 (87%)	134 (88%)	15 (10%)	4 (3%)	6	38
6	F	221/244 (91%)	201 (91%)	15 (7%)	5 (2%)	7	41
7	G	229/256 (90%)	181 (79%)	27 (12%)	21 (9%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	8	43
9	I	209/221 (95%)	175 (84%)	22 (10%)	12 (6%)	2	23
10	J	167/174 (96%)	135 (81%)	19 (11%)	13 (8%)	1	17
12	L	192/199 (96%)	161 (84%)	20 (10%)	11 (6%)	2	23
13	M	135/138 (98%)	124 (92%)	10 (7%)	1 (1%)	24	67
14	N	201/204 (98%)	182 (90%)	13 (6%)	6 (3%)	5	35
15	O	352/219 (161%)	324 (92%)	18 (5%)	10 (3%)	5	37
16	P	153/184 (83%)	142 (93%)	9 (6%)	2 (1%)	13	54
17	Q	183/186 (98%)	168 (92%)	9 (5%)	6 (3%)	4	33
18	R	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	11	50
19	S	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	27	70
20	T	157/160 (98%)	146 (93%)	9 (6%)	2 (1%)	13	54
21	U	96/121 (79%)	80 (83%)	13 (14%)	3 (3%)	4	35
22	V	134/137 (98%)	124 (92%)	8 (6%)	2 (2%)	11	51
23	W	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	2	22
24	X	118/142 (83%)	103 (87%)	7 (6%)	8 (7%)	1	19
25	Y	124/127 (98%)	107 (86%)	12 (10%)	5 (4%)	3	29
26	Z	133/136 (98%)	107 (80%)	13 (10%)	13 (10%)	1	12
27	a	146/149 (98%)	123 (84%)	18 (12%)	5 (3%)	4	33
28	b	56/59 (95%)	44 (79%)	7 (12%)	5 (9%)	1	14
29	c	98/105 (93%)	87 (89%)	8 (8%)	3 (3%)	4	35
30	d	107/113 (95%)	88 (82%)	13 (12%)	6 (6%)	2	24
31	e	125/130 (96%)	109 (87%)	10 (8%)	6 (5%)	2	26
32	f	104/107 (97%)	96 (92%)	5 (5%)	3 (3%)	5	36
33	g	110/121 (91%)	93 (84%)	13 (12%)	4 (4%)	4	32
34	h	117/120 (98%)	99 (85%)	14 (12%)	4 (3%)	4	33
35	i	97/100 (97%)	77 (79%)	13 (13%)	7 (7%)	1	18
36	j	85/88 (97%)	75 (88%)	8 (9%)	2 (2%)	6	40
37	k	75/78 (96%)	61 (81%)	10 (13%)	4 (5%)	2	25
38	l	48/51 (94%)	41 (85%)	6 (12%)	1 (2%)	8	43
39	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	8	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	n	23/25 (92%)	22 (96%)	0	1 (4%)	3	28
41	o	103/106 (97%)	90 (87%)	11 (11%)	2 (2%)	9	45
42	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
43	q	117/312 (38%)	93 (80%)	18 (15%)	6 (5%)	2	25
46	t	376/614 (61%)	354 (94%)	14 (4%)	8 (2%)	8	43
All	All	6846/7529 (91%)	6010 (88%)	585 (8%)	251 (4%)	6	31

5 of 251 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	LEU
2	B	129	ALA
2	B	140	ASP
2	B	347	SER
3	C	14	GLU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/196 (98%)	154 (80%)	38 (20%)	1	9
2	B	321/323 (99%)	251 (78%)	70 (22%)	1	7
3	C	288/289 (100%)	222 (77%)	66 (23%)	1	6
4	D	243/245 (99%)	196 (81%)	47 (19%)	1	10
5	E	135/153 (88%)	115 (85%)	20 (15%)	3	18
6	F	187/205 (91%)	158 (84%)	29 (16%)	3	17
7	G	177/208 (85%)	138 (78%)	39 (22%)	1	7
8	H	171/171 (100%)	132 (77%)	39 (23%)	1	6
9	I	179/187 (96%)	142 (79%)	37 (21%)	1	8
10	J	147/150 (98%)	114 (78%)	33 (22%)	1	7
12	L	154/159 (97%)	124 (80%)	30 (20%)	1	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	108/109 (99%)	84 (78%)	24 (22%)	1	7
14	N	175/176 (99%)	143 (82%)	32 (18%)	2	12
15	O	323/179 (180%)	267 (83%)	56 (17%)	2	13
16	P	125/146 (86%)	103 (82%)	22 (18%)	2	13
17	Q	150/151 (99%)	123 (82%)	27 (18%)	2	12
18	R	153/154 (99%)	121 (79%)	32 (21%)	1	8
19	S	156/156 (100%)	123 (79%)	33 (21%)	1	7
20	T	136/137 (99%)	109 (80%)	27 (20%)	1	9
21	U	85/107 (79%)	62 (73%)	23 (27%)	0	4
22	V	104/105 (99%)	96 (92%)	8 (8%)	14	44
23	W	100/129 (78%)	85 (85%)	15 (15%)	3	18
24	X	104/118 (88%)	81 (78%)	23 (22%)	1	7
25	Y	109/110 (99%)	85 (78%)	24 (22%)	1	7
26	Z	115/116 (99%)	89 (77%)	26 (23%)	1	6
27	a	118/119 (99%)	95 (80%)	23 (20%)	1	10
28	b	46/47 (98%)	35 (76%)	11 (24%)	1	5
29	c	84/88 (96%)	69 (82%)	15 (18%)	2	12
30	d	94/97 (97%)	73 (78%)	21 (22%)	1	7
31	e	109/111 (98%)	89 (82%)	20 (18%)	2	12
32	f	90/91 (99%)	79 (88%)	11 (12%)	5	24
33	g	95/103 (92%)	71 (75%)	24 (25%)	0	4
34	h	103/105 (98%)	77 (75%)	26 (25%)	0	4
35	i	80/82 (98%)	51 (64%)	29 (36%)	0	1
36	j	70/71 (99%)	53 (76%)	17 (24%)	1	5
37	k	67/69 (97%)	53 (79%)	14 (21%)	1	8
38	l	45/46 (98%)	34 (76%)	11 (24%)	1	5
39	m	47/116 (40%)	34 (72%)	13 (28%)	0	3
40	n	23/23 (100%)	16 (70%)	7 (30%)	0	2
41	o	90/91 (99%)	74 (82%)	16 (18%)	2	13
42	p	71/72 (99%)	61 (86%)	10 (14%)	4	20
43	q	105/233 (45%)	76 (72%)	29 (28%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
46	t	332/539 (62%)	330 (99%)	2 (1%)	87 93
All	All	5806/6282 (92%)	4687 (81%)	1119 (19%)	4 10

5 of 1119 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	O	12[A]	LYS
18	R	98	ARG
38	l	21	ARG
15	O	74[A]	ARG
16	P	69	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
16	P	55	GLN
20	T	49	GLN
46	t	156	HIS
17	Q	9	GLN
21	U	40	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	1	0/114	-	-
48	5	3145/3396 (92%)	731 (23%)	129 (4%)
49	7	120/121 (99%)	18 (15%)	0
50	8	157/158 (99%)	32 (20%)	3 (1%)
All	All	3422/3789 (90%)	781 (22%)	132 (3%)

5 of 781 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	5	14	U
48	5	15	C
48	5	16	A
48	5	26	A
48	5	38	U

5 of 132 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	1554	U
48	5	1842	A
48	5	3269	U
48	5	1568	U
48	5	1724	U

## 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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	K	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	52:UNK	C	54:UNK	N	3.86
1	K	23:UNK	C	28:UNK	N	3.48