



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Feb 28, 2018 – 01:00 PM EST

PDB ID : 4V8T
EMDB ID: : EMD-2169
Title : Cryo-EM Structure of the 60S Ribosomal Subunit in Complex with Arx1 and Rei1
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
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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

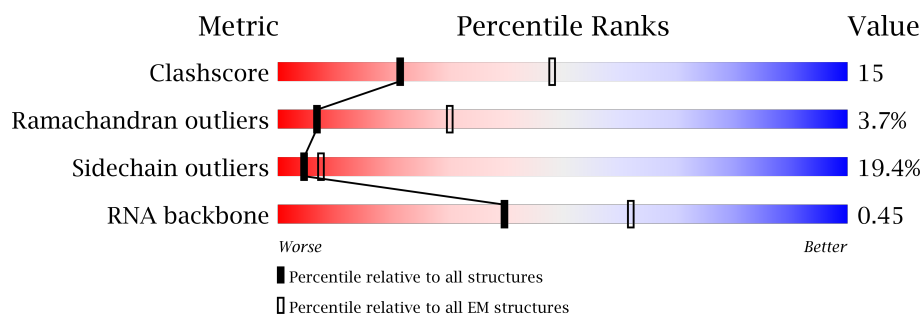
1 Overall quality at a glance

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.















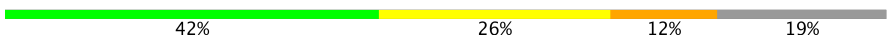












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	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% .









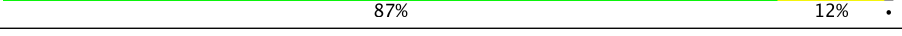

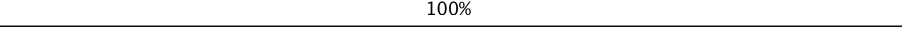
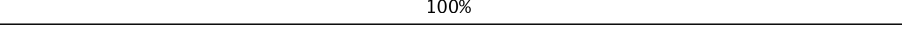
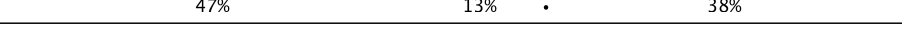
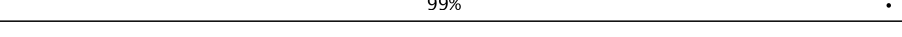

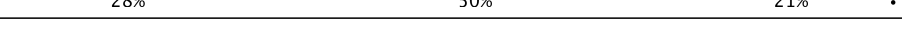

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Mol	Chain	Length	Quality of chain
9	I	221	
10	J	174	
11	K	155	
12	L	199	
13	M	138	
14	N	204	
15	O	219	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	155	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	59	
29	c	105	
30	d	113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

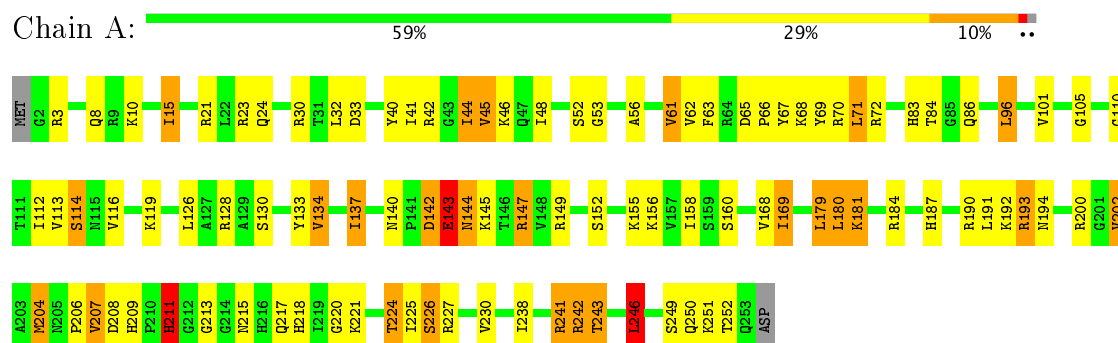
- Molecule 51 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

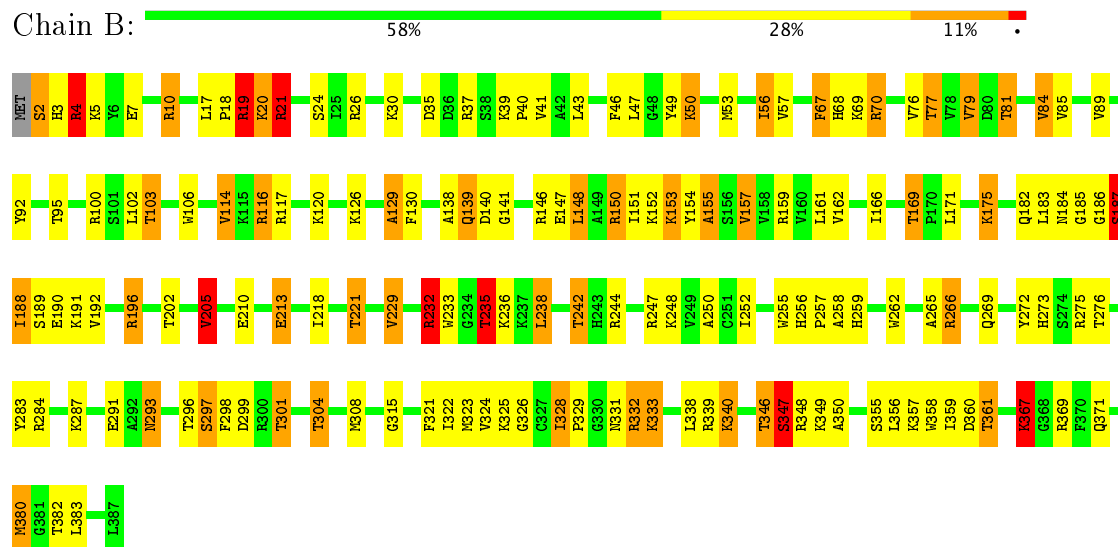
3 Residue-property plots

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.

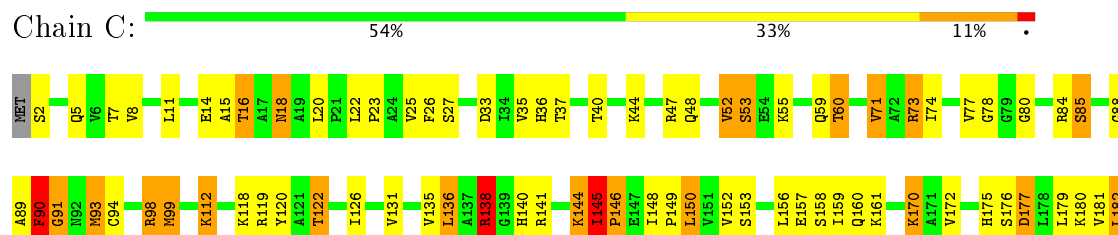
• Molecule 1: 60S RIBOSOMAL PROTEIN L2-B

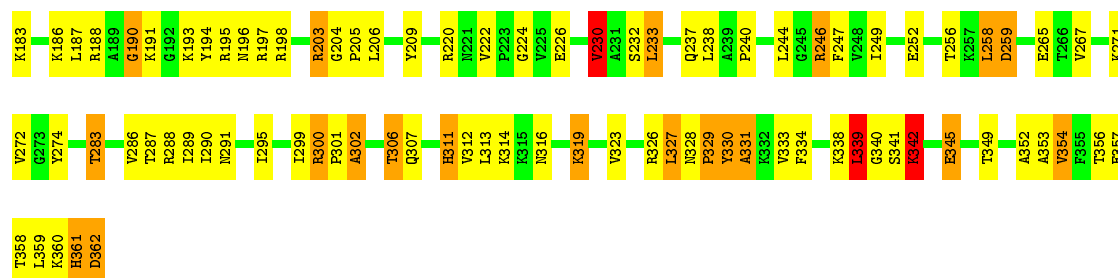


• Molecule 2: 60S RIBOSOMAL PROTEIN L3

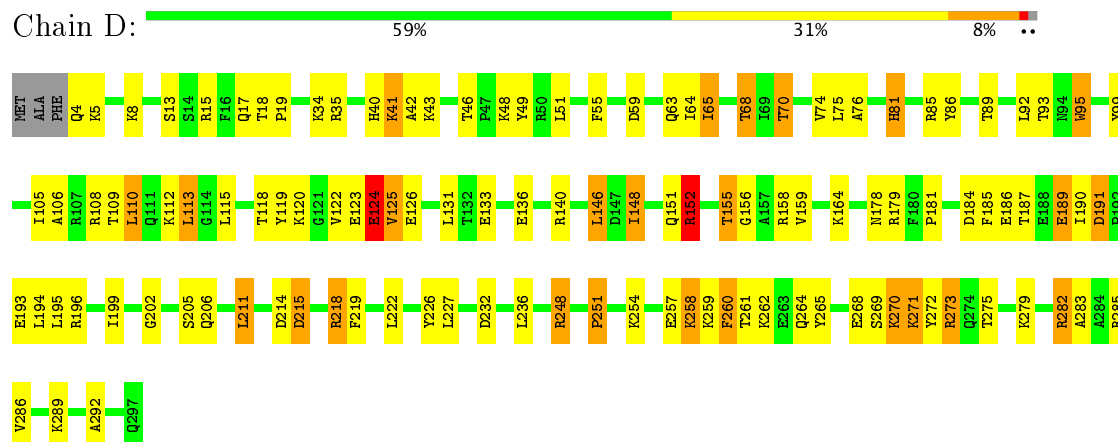


• Molecule 3: 60S RIBOSOMAL PROTEIN L4-A

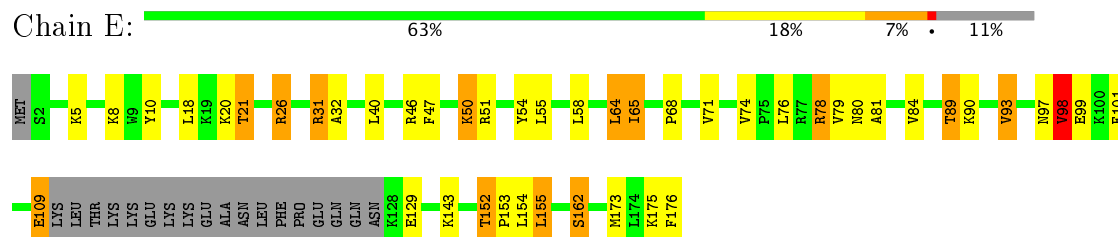




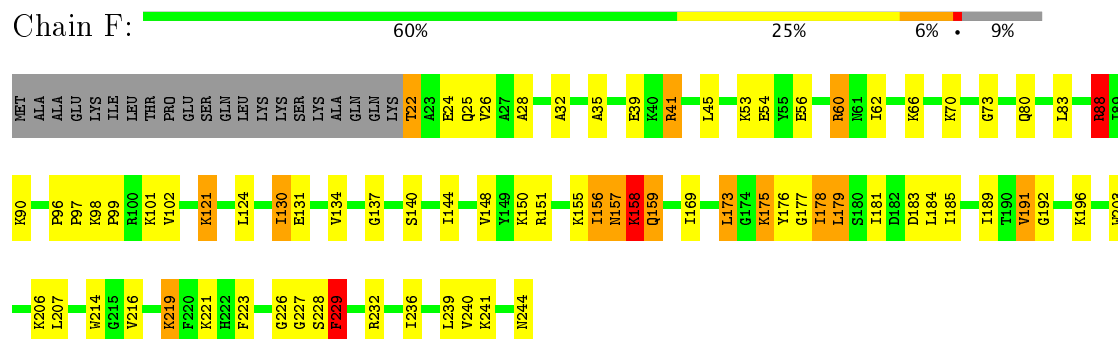
• Molecule 4: 60S RIBOSOMAL PROTEIN L5



• Molecule 5: 60S RIBOSOMAL PROTEIN L6-A

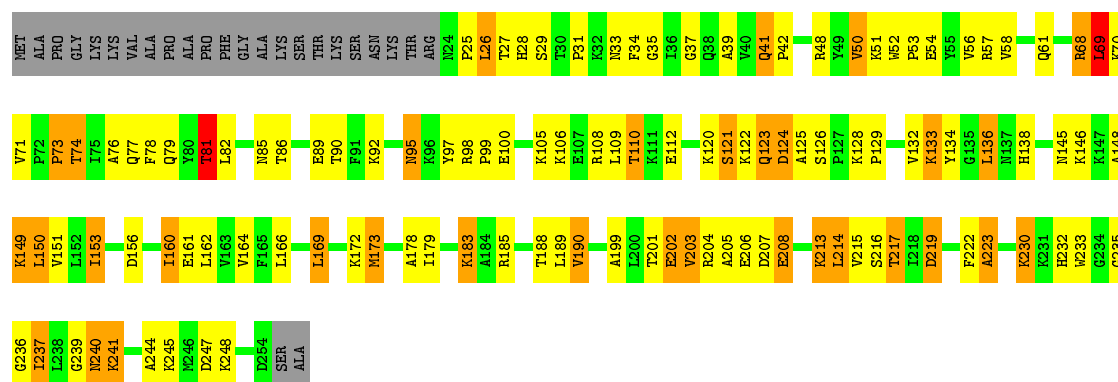


• Molecule 6: 60S RIBOSOMAL PROTEIN L7-A



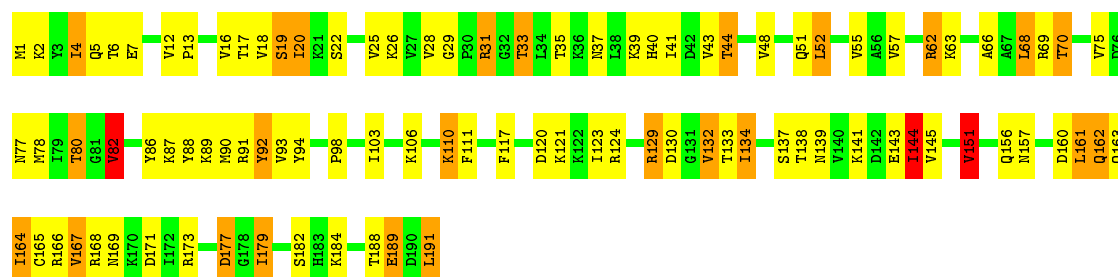
• Molecule 7: 60S RIBOSOMAL PROTEIN L8-A





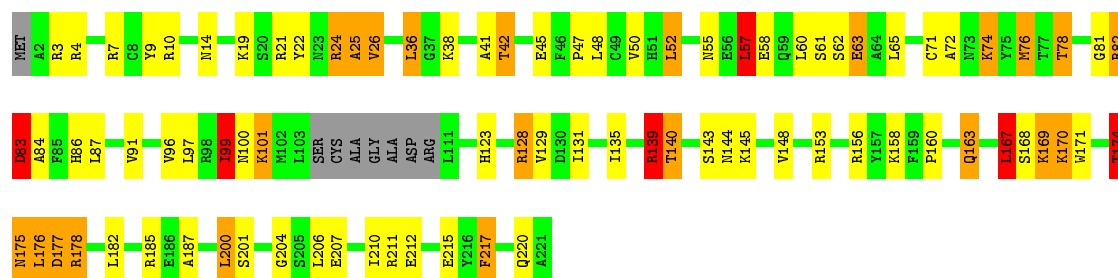
• Molecule 8: 60S RIBOSOMAL PROTEIN L9-A

Chain H: 50% 36% 13%



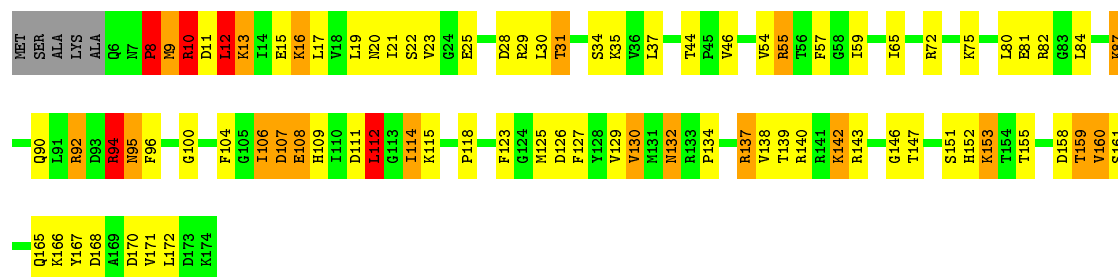
• Molecule 9: 60S RIBOSOMAL PROTEIN L10

Chain I: 57% 26% 10%




• Molecule 10: 60S RIBOSOMAL PROTEIN L11-B

Chain J: 49% 34% 11%



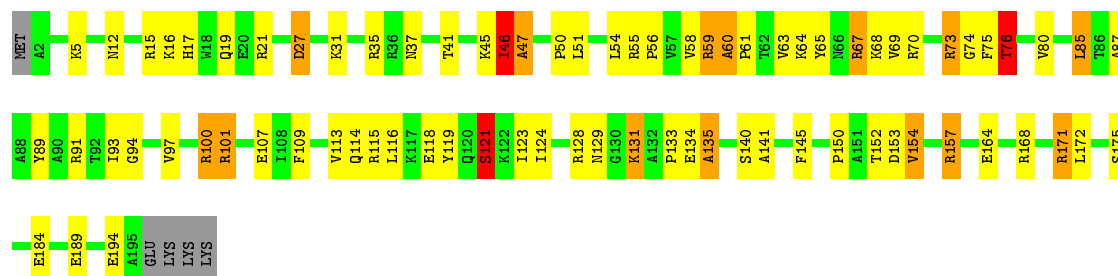
• Molecule 11: 60S RIBOSOMAL PROTEIN L12

Chain K:  85% 12%



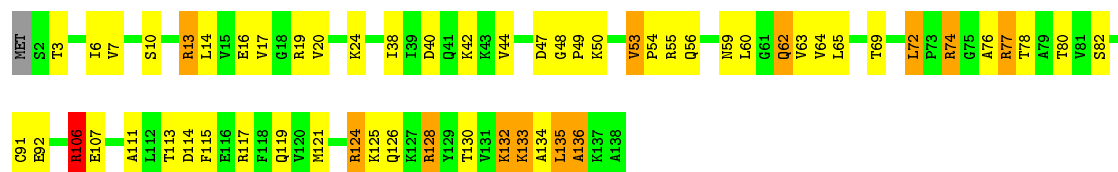
• Molecule 12: 60S RIBOSOMAL PROTEIN L13-A

Chain L:  58% 31% 7%



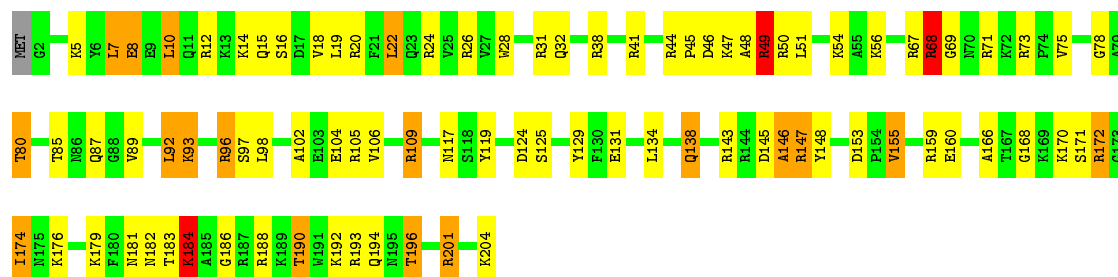
• Molecule 13: 60S RIBOSOMAL PROTEIN L14-A

Chain M:  57% 33% 9%



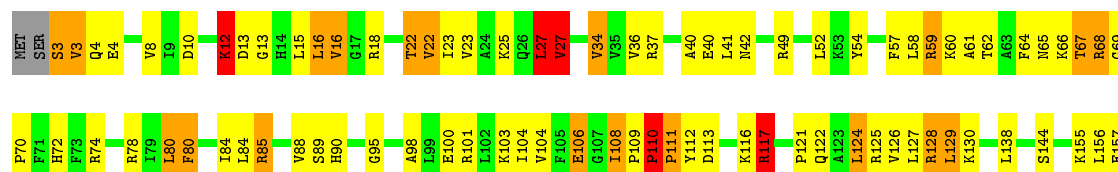
• Molecule 14: 60S RIBOSOMAL PROTEIN L15-A

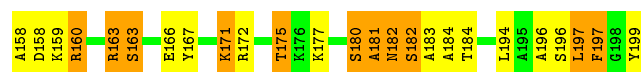
Chain N:  56% 33% 9%



• Molecule 15: 60S RIBOSOMAL PROTEIN L16-A

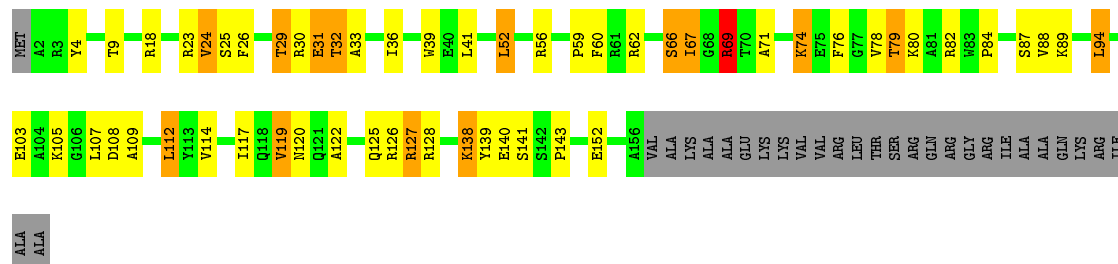
Chain O:  49% 34% 14%





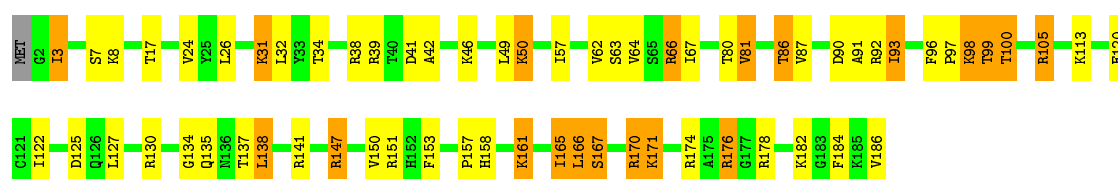
• Molecule 16: 60S RIBOSOMAL PROTEIN L17-A

Chain P: 54% 22% 8% 16%



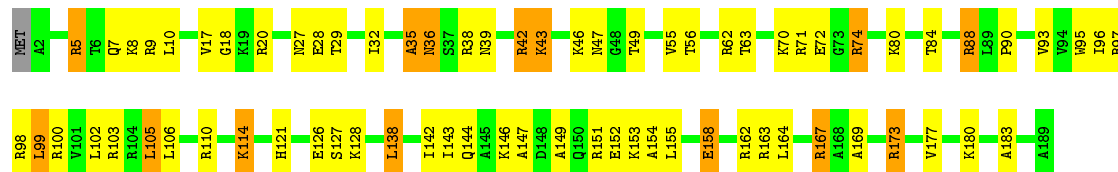
• Molecule 17: 60S RIBOSOMAL PROTEIN L18-B

Chain Q: 65% 24% 11%



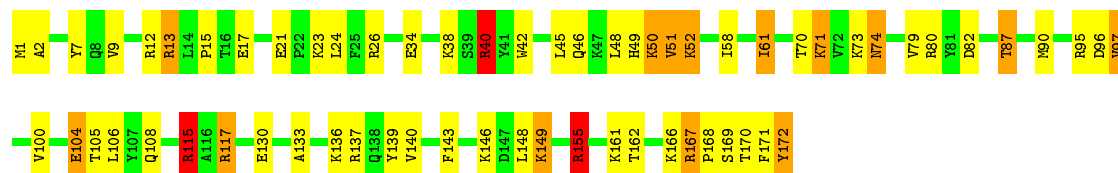
• Molecule 18: 60S RIBOSOMAL PROTEIN L19-B

Chain R: 61% 31% 7%



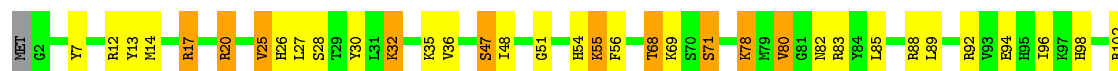
• Molecule 19: 60S RIBOSOMAL PROTEIN L20-A

Chain S: 63% 27% 8%



• Molecule 20: 60S RIBOSOMAL PROTEIN L21-A

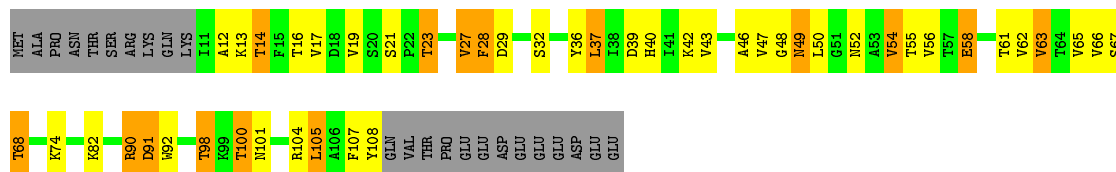
Chain T: 67% 21% 11%





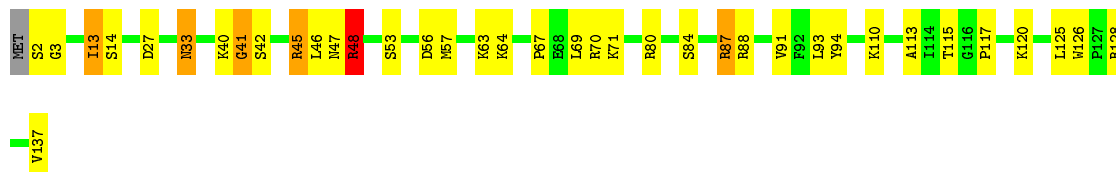
• Molecule 21: 60S RIBOSOMAL PROTEIN L22-A

Chain U: 42% 26% 12% 19%



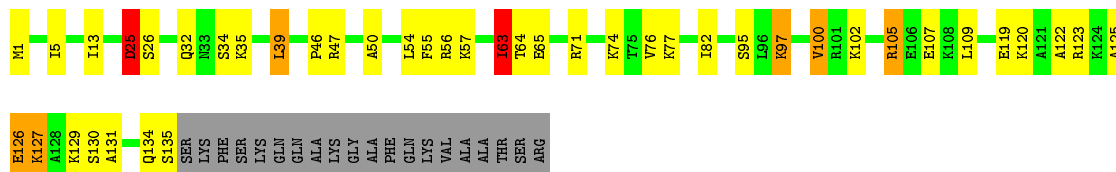
• Molecule 22: 60S RIBOSOMAL PROTEIN L23-A

Chain V: 72% 23% . .



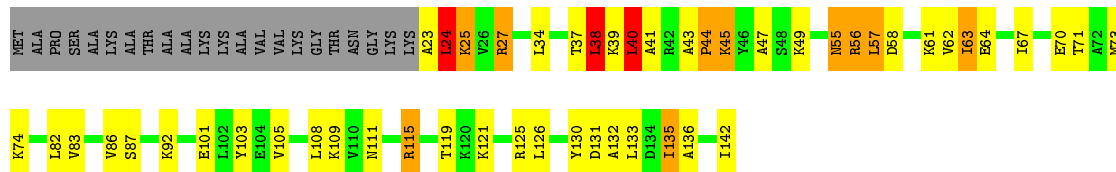
• Molecule 23: 60S RIBOSOMAL PROTEIN L24-A

Chain W: 59% 23% . . 13%



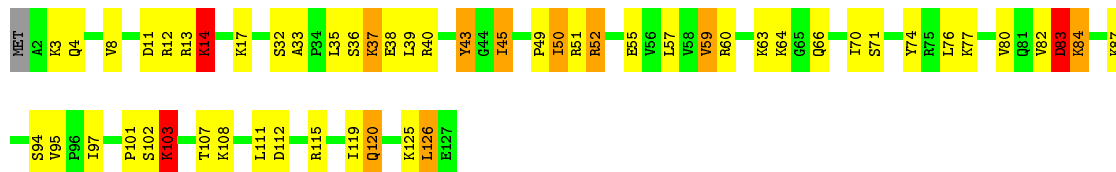
• Molecule 24: 60S RIBOSOMAL PROTEIN L25

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



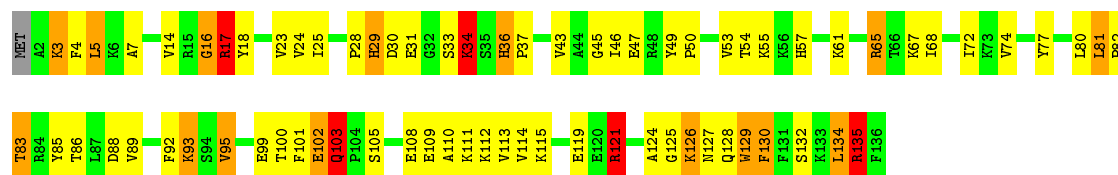
• Molecule 25: 60S RIBOSOMAL PROTEIN L26-A

Chain Y: 57% 33% 7% . .



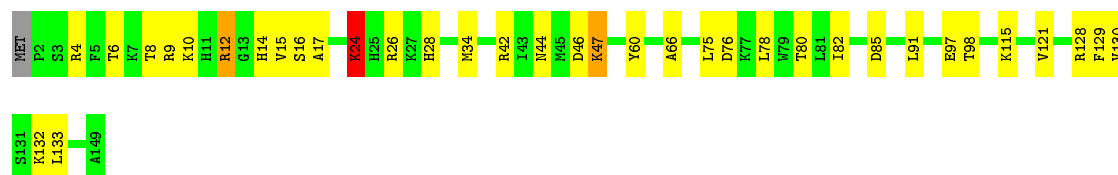
- Molecule 26: 60S RIBOSOMAL PROTEIN L27-A

Chain Z: 



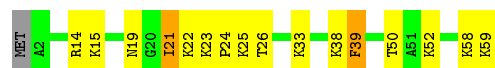
- Molecule 27: 60S RIBOSOMAL PROTEIN L28

Chain a: 




- Molecule 28: 60S RIBOSOMAL PROTEIN L29

Chain b: 



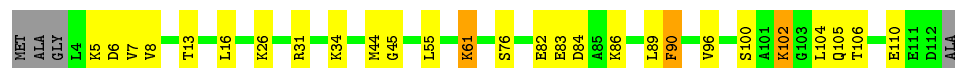
- Molecule 29: 60S RIBOSOMAL PROTEIN L32

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: 



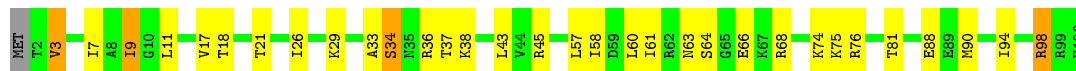
- Molecule 33: 60S RIBOSOMAL PROTEIN L34-A



- Molecule 34: 60S RIBOSOMAL PROTEIN L35-A



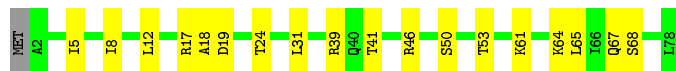
- Molecule 35: 60S RIBOSOMAL PROTEIN L36-A



- Molecule 36: 60S RIBOSOMAL PROTEIN L37-A



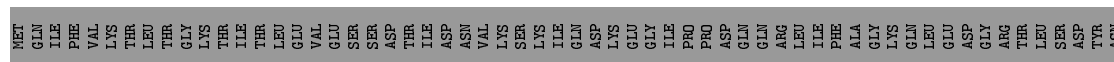
- Molecule 37: 60S RIBOSOMAL PROTEIN L38

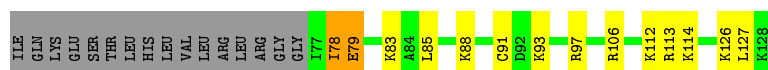


- Molecule 38: 60S RIBOSOMAL PROTEIN L39



- Molecule 39: 60S RIBOSOMAL PROTEIN L40





- Molecule 40: 60S RIBOSOMAL PROTEIN L41-A

Chain n: 72% 20% 8%



- Molecule 41: 60S RIBOSOMAL PROTEIN L42-A

Chain o: 82% 16% ..



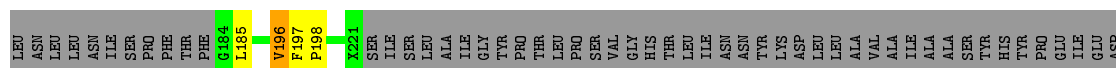
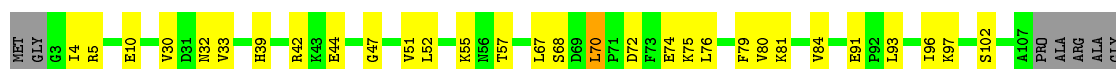
- Molecule 42: 60S RIBOSOMAL PROTEIN L43-A

Chain p: 87% 12% .



- Molecule 43: 60S ACIDIC RIBOSOMAL PROTEIN P0

Chain q: 35% 10% . 54%



- Molecule 44: RIBOSOMAL PROTEIN P1 ALPHA

Chain r: 100%

There are no outlier residues recorded for this chain.

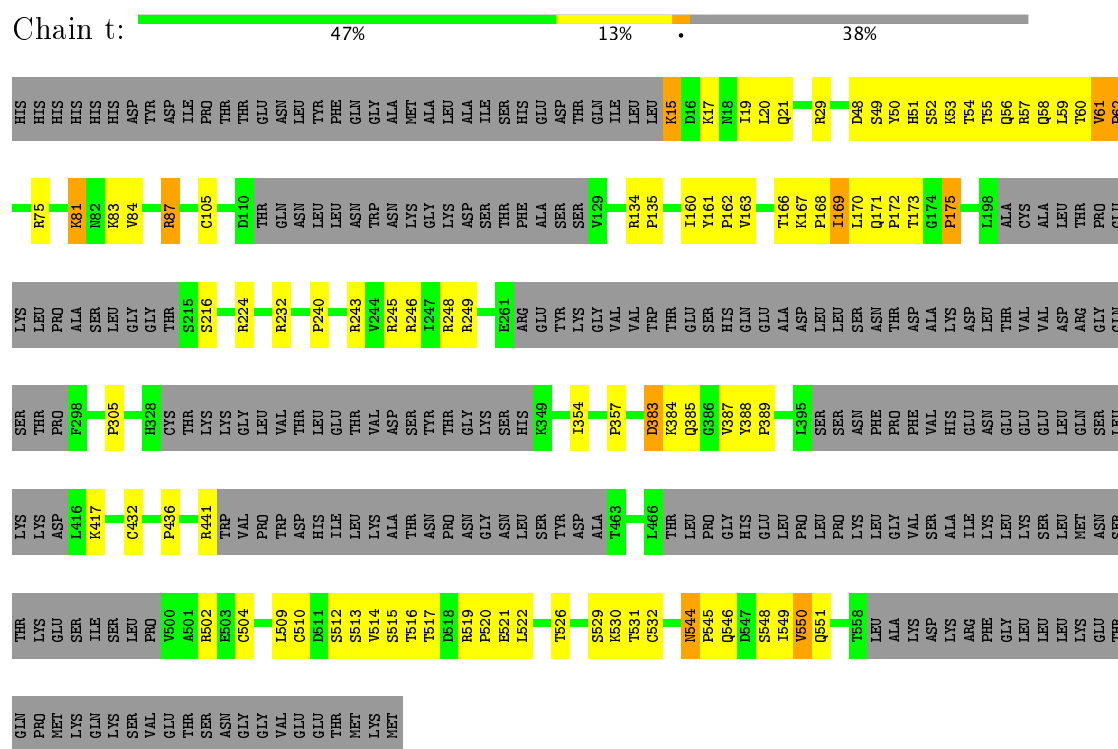
- Molecule 45: RIBOSOMAL PROTEIN P2 BETA

Chain s: 100%

There are no outlier residues recorded for this chain.

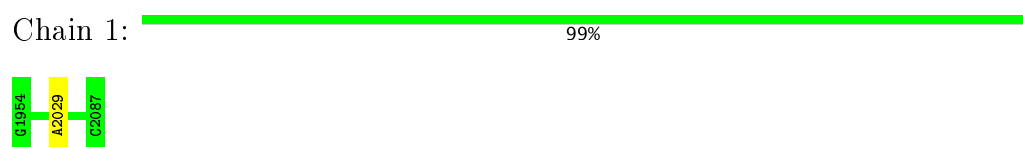
- Molecule 46: PROBABLE METALLOPROTEASE ARX1

Chain t:



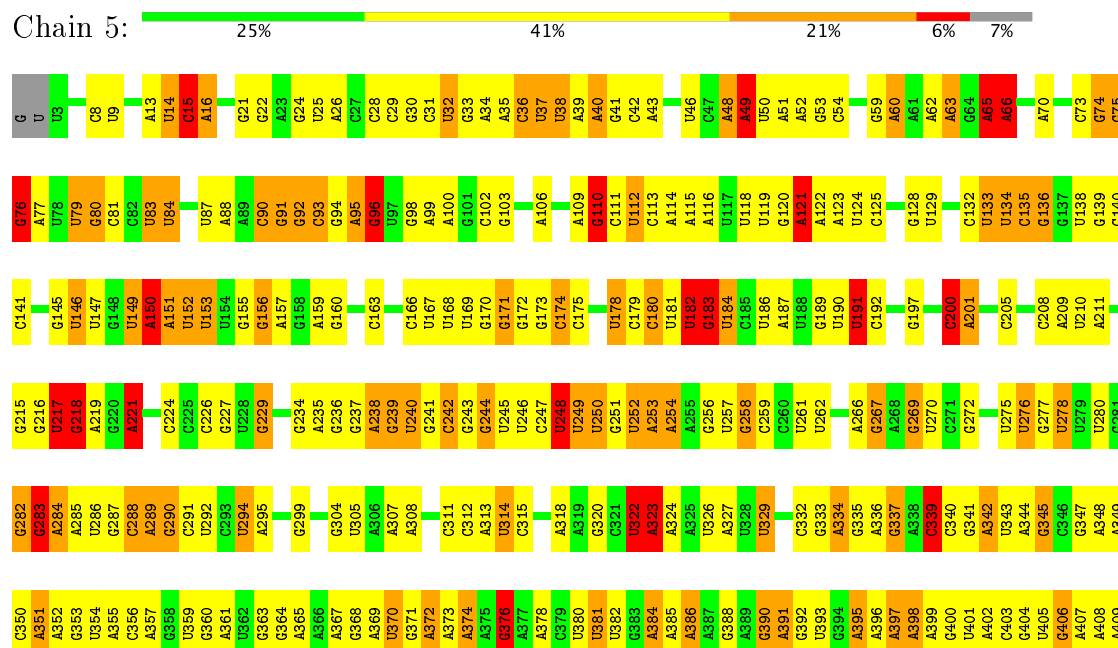
- Molecule 47: ES27 OF THE 25S RRNA

Chain 1:



- Molecule 48: 25S RIBOSOMAL RNA

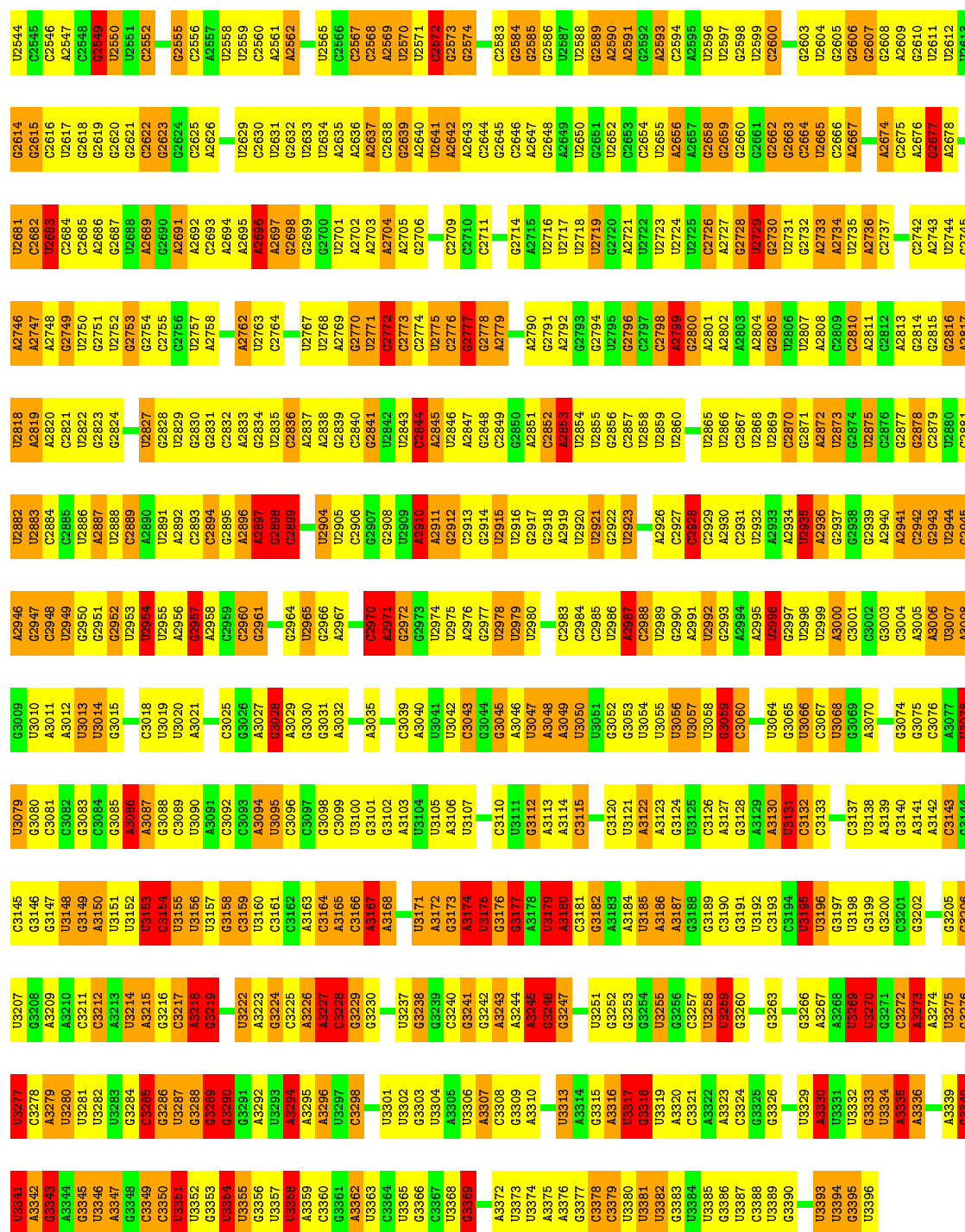
Chain 5:



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	A2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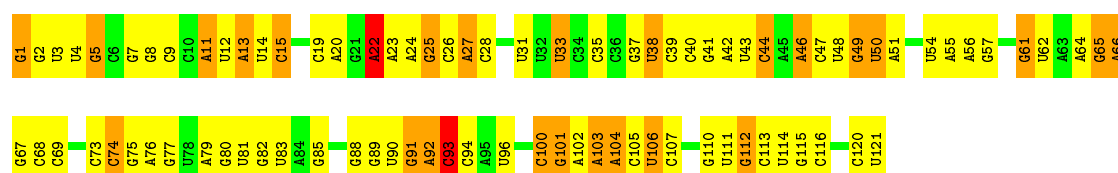
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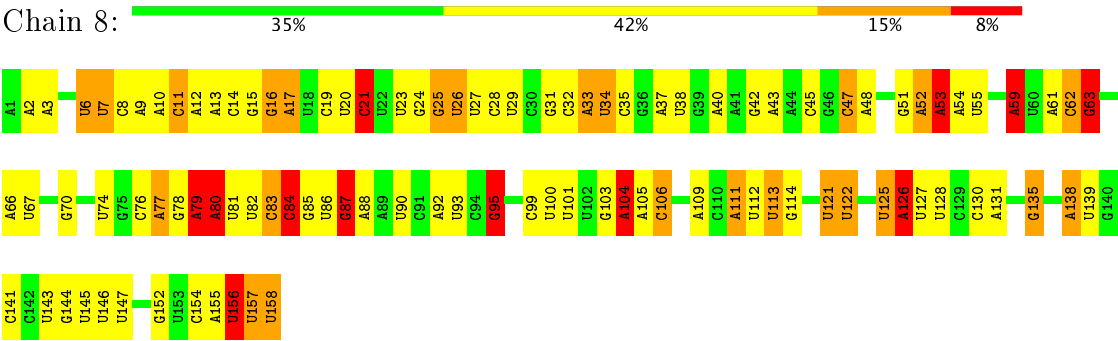


Molecule 49: 5S RIBOSOMAL RNA

Chain 7: 28% 50% 21%



● 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

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%)	6	39
2	B	384/387 (99%)	341 (89%)	34 (9%)	9 (2%)	7	43
3	C	359/362 (99%)	306 (85%)	32 (9%)	21 (6%)	2	24
4	D	292/297 (98%)	267 (91%)	19 (6%)	6 (2%)	8	45
5	E	153/176 (87%)	134 (88%)	15 (10%)	4 (3%)	6	40
6	F	221/244 (91%)	201 (91%)	15 (7%)	5 (2%)	7	43
7	G	229/256 (90%)	181 (79%)	27 (12%)	21 (9%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	8	45
9	I	209/221 (95%)	175 (84%)	22 (10%)	12 (6%)	2	24
10	J	167/174 (96%)	135 (81%)	19 (11%)	13 (8%)	1	18
12	L	192/199 (96%)	161 (84%)	20 (10%)	11 (6%)	2	24
13	M	135/138 (98%)	124 (92%)	10 (7%)	1 (1%)	25	68
14	N	201/204 (98%)	182 (90%)	13 (6%)	6 (3%)	5	37
15	O	352/219 (161%)	324 (92%)	18 (5%)	10 (3%)	6	39
16	P	153/184 (83%)	142 (93%)	9 (6%)	2 (1%)	14	56
17	Q	183/186 (98%)	168 (92%)	9 (5%)	6 (3%)	4	35
18	R	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	11	51
19	S	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	28	71
20	T	157/160 (98%)	146 (93%)	9 (6%)	2 (1%)	14	56
21	U	96/121 (79%)	80 (83%)	13 (14%)	3 (3%)	5	37
22	V	134/137 (98%)	124 (92%)	8 (6%)	2 (2%)	12	53
23	W	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	2	23
24	X	118/142 (83%)	103 (87%)	7 (6%)	8 (7%)	1	20
25	Y	124/127 (98%)	107 (86%)	12 (10%)	5 (4%)	3	31
26	Z	133/136 (98%)	107 (80%)	13 (10%)	13 (10%)	1	13
27	a	146/149 (98%)	123 (84%)	18 (12%)	5 (3%)	4	35
28	b	56/59 (95%)	44 (79%)	7 (12%)	5 (9%)	1	15
29	c	98/105 (93%)	87 (89%)	8 (8%)	3 (3%)	5	37
30	d	107/113 (95%)	88 (82%)	13 (12%)	6 (6%)	2	25
31	e	125/130 (96%)	109 (87%)	10 (8%)	6 (5%)	2	28
32	f	104/107 (97%)	96 (92%)	5 (5%)	3 (3%)	5	38
33	g	110/121 (91%)	93 (84%)	13 (12%)	4 (4%)	4	33
34	h	117/120 (98%)	99 (85%)	14 (12%)	4 (3%)	4	35
35	i	97/100 (97%)	77 (79%)	13 (13%)	7 (7%)	1	19
36	j	85/88 (97%)	75 (88%)	8 (9%)	2 (2%)	7	42
37	k	75/78 (96%)	61 (81%)	10 (13%)	4 (5%)	2	26
38	l	48/51 (94%)	41 (85%)	6 (12%)	1 (2%)	8	45
39	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	9	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	n	23/25 (92%)	22 (96%)	0	1 (4%)	3	29
41	o	103/106 (97%)	90 (87%)	11 (11%)	2 (2%)	9	47
42	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
43	q	117/312 (38%)	93 (80%)	18 (15%)	6 (5%)	2	26
46	t	376/614 (61%)	354 (94%)	14 (4%)	8 (2%)	8	45
All	All	6846/7529 (91%)	6010 (88%)	585 (8%)	251 (4%)	7	33

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	10
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	20
6	F	187/205 (91%)	158 (84%)	29 (16%)	3	19
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	14
16	P	125/146 (86%)	103 (82%)	22 (18%)	2	14
17	Q	150/151 (99%)	123 (82%)	27 (18%)	2	13
18	R	153/154 (99%)	121 (79%)	32 (21%)	1	8
19	S	156/156 (100%)	123 (79%)	33 (21%)	1	8
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%)	15	47
23	W	100/129 (78%)	85 (85%)	15 (15%)	3	20
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	7
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	13
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%)	6	26
33	g	95/103 (92%)	71 (75%)	24 (25%)	0	5
34	h	103/105 (98%)	77 (75%)	26 (25%)	0	5
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	22
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%)	89 94
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