



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:25 PM BST

PDB ID : 4V6W
EMDB ID: : EMD-5591
Title : Structure of the D. melanogaster 80S ribosome
Authors : Anger, A.M.; Armache, J.-P.; Berninghausen, O.; Habeck, M.; Subklewe, M.;
Wilson, D.N.; Beckmann, R.
Deposited on : 2013-02-27
Resolution : 6.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

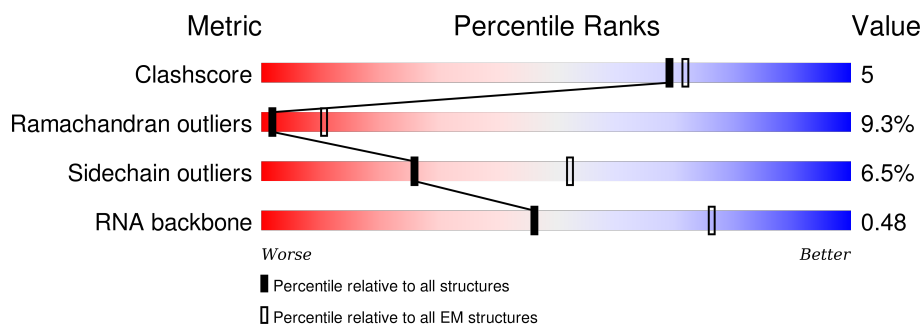
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 Å.

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















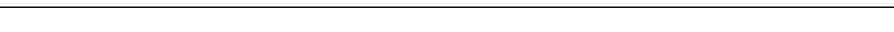

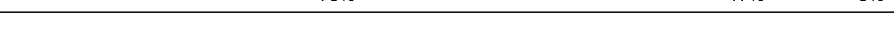

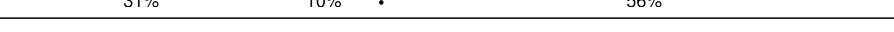








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	Az	844	70% 22% 5% ..
2	Ag	318	86% 13% .
3	AU	120	68% 15% . 15%
4	AK	163	38% 15% .. 42%
5	AO	151	64% 19% . . 11%
6	AX	143	78% 18% . .
7	AM	139	57% 19% 6% . 14%
8	AS	152	65% 18% . . 10%









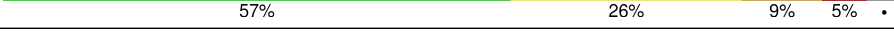

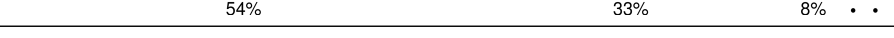
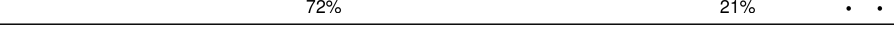

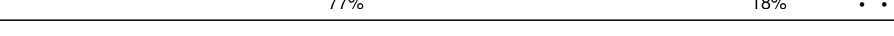


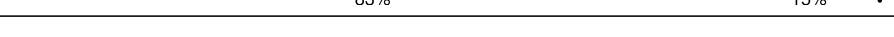

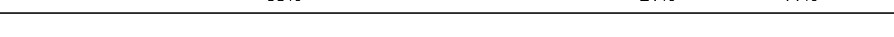






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Mol	Chain	Length	Quality of chain
9	Ad	56	
10	AN	151	
11	AL	155	
12	AR	131	
13	AP	148	
14	AT	156	
15	AB	268	
16	AA	313	
17	AV	83	
18	AY	131	
19	AZ	117	
20	Aa	114	
21	Ab	84	
22	Ac	65	
23	AD	246	
24	Ae	132	
25	Af	80	
26	AJ	195	
27	AE	261	
28	AC	267	
29	AG	248	
30	AF	228	
31	AH	194	
32	AW	130	
33	AI	208	

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Mol	Chain	Length	Quality of chain
34	AQ	148	
35	Ah	121	
36	B2	1995	
37	BC	75	
38	Cz	218	
39	Cq	223	
40	CK	165	
41	CO	205	
42	CL	218	
43	CV	140	
44	CM	166	
45	Ca	149	
46	CN	204	
47	CI	218	
48	CD	299	
49	CQ	188	
50	CR	203	
51	CA	256	
52	CS	177	
53	CT	159	
54	CP	186	
55	CU	299	
56	CX	277	
57	CY	149	
58	CW	155	

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Mol	Chain	Length	Quality of chain
59	CZ	135	
60	Cr	144	
61	Ch	123	
62	Cb	76	
63	CB	416	
64	CF	252	
65	Cc	111	
66	Cd	124	
67	Ce	134	
68	Cf	157	
69	Cg	162	
70	Ci	115	
71	Cj	93	
72	Ck	70	
73	Cl	51	
74	CC	401	
75	Cm	52	
76	Cn	25	
77	Cp	92	
78	Co	104	
79	CJ	184	
80	CH	190	
81	CE	243	
82	CG	271	
83	A5	3970	

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Mol	Chain	Length	Quality of chain
84	A9	30	<div><div></div><div>63%</div><div>23%</div><div>13%</div></div>
85	A7	120	<div><div></div><div>63%</div><div>33%</div><div></div></div>
86	A8	123	<div><div></div><div>59%</div><div>34%</div><div></div></div>

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 230721 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 Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Az	837	Total	C	N	O	S	0	0
			6574	4170	1123	1235	46		

- Molecule 2 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 3 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 4 is a protein called 40S ribosomal protein S10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AK	95	Total	C	N	O	S	0	0
			797	522	136	137	2		

- Molecule 5 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AO	134	Total	C	N	O	S	0	0
			1003	616	196	187	4		

- Molecule 6 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 7 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 8 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS	137	Total	C	N	O	S	0	0
			1128	707	220	198	3		

- Molecule 9 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 13 is a protein called 40S ribosomal protein S15, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 14 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AT	154	Total	C	N	O	S	0	0
			1203	762	230	207	4		

- Molecule 15 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

- Molecule 16 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	CONFLICT	UNP O76927
AV	8	PHE	ASN	CONFLICT	UNP O76927
AV	25	GLY	HIS	CONFLICT	UNP O76927
AV	32	ILE	VAL	CONFLICT	UNP O76927
AV	34	MET	LEU	CONFLICT	UNP O76927
AV	35	ASN	SER	CONFLICT	UNP O76927
AV	36	VAL	ILE	CONFLICT	UNP O76927
AV	58	ALA	GLU	CONFLICT	UNP O76927
AV	68	SER	CYS	CONFLICT	UNP O76927
AV	70	LEU	VAL	CONFLICT	UNP O76927
AV	75	ALA	LYS	CONFLICT	UNP O76927
AV	79	VAL	ILE	CONFLICT	UNP O76927
AV	80	SER	THR	CONFLICT	UNP O76927

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 19 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AZ	74	Total	C	N	O	S	0	0
			608	390	112	106			

- Molecule 20 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 21 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 22 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 24 is a protein called 40S ribosomal protein S30, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ae	58	Total	C	N	O	S	0	0
			469	289	105	75			

- Molecule 25 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 27 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 29 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 30 is a protein called 40S ribosomal protein S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	190	Total	C	N	O	S	0	0
			1497	934	285	269	9		

- Molecule 31 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 32 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 33 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 34 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 35 is a protein called Vig2, isoform B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ah	58	Total	C	N	O	S	0	0
			486	298	93	94	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	212	LYS	GLU	CONFLICT	UNP Q9VBX3
Ah	213	GLU	ASP	CONFLICT	UNP Q9VBX3
Ah	215	PRO	SER	CONFLICT	UNP Q9VBX3
Ah	217	GLU	GLN	CONFLICT	UNP Q9VBX3
Ah	226	ILE	LEU	CONFLICT	UNP Q9VBX3
Ah	227	GLN	ARG	CONFLICT	UNP Q9VBX3
Ah	228	ASN	ASP	CONFLICT	UNP Q9VBX3

- Molecule 36 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B2	1957	Total	C	N	O	P	0	0
			39523	17589	6780	13198	1956		

- Molecule 37 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	75	Total	C	N	O	P	0	0
			1605	717	296	518	74		

- Molecule 38 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cz	72A	SER	-	EXPRESSION TAG	UNP Q9VTP4

- Molecule 39 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cq	223	Total	C	N	O	S	0	0
			1710	1089	297	314	10		

- Molecule 40 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CK	158	Total	C	N	O	S	0	0
			1180	739	213	222	6		

- Molecule 41 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 43 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 45 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 49 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 50 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 51 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

- Molecule 52 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 53 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 54 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 55 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CU	116	Total	C	N	O	S	0	0
			961	607	167	185	2		

- Molecule 56 is a protein called 60S ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 57 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CW	130	Total	C	N	O	S	0	0
			1047	662	207	172	6		

- Molecule 59 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cr	134	Total	C	N	O	S	0	0
			1051	670	205	176			

- Molecule 61 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 63 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 64 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CF	229	Total	C	N	O	S	0	0
			1921	1234	372	312	3		

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

- Molecule 66 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	111	Total	C	N	O	S	0	0
			924	573	180	169	2		

- Molecule 67 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 68 is a protein called 60S ribosomal protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 69 is a protein called 60S ribosomal protein L34a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cg	113	Total	C	N	O	S	0	0
			926	575	193	152	6		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cj	92	Total	C	N	O	S	0	0
			737	450	160	122	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 74 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

- Molecule 75 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 78 is a protein called 60S ribosomal protein L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 79 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 80 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 81 is a protein called 60S ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 82 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 83 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A5	3806	Total	C	N	O	P	0	0
			77967	34770	13566	25827	3804		

- Molecule 84 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 85 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

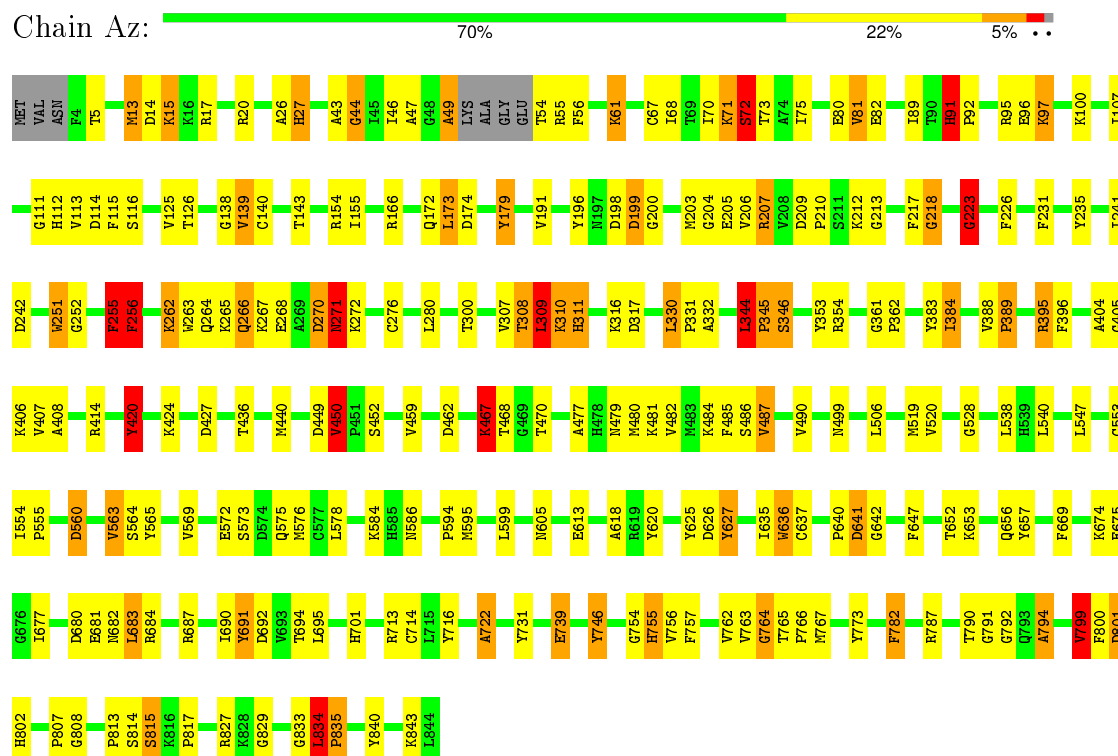
- Molecule 86 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

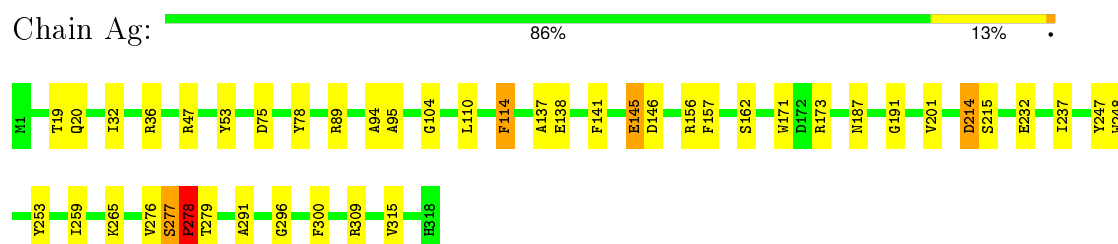
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Elongation factor 2



- Molecule 2: Guanine nucleotide-binding protein subunit beta-like protein



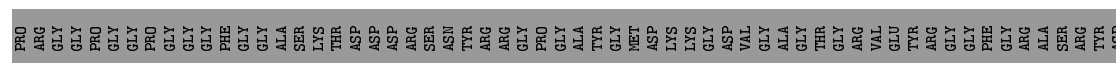
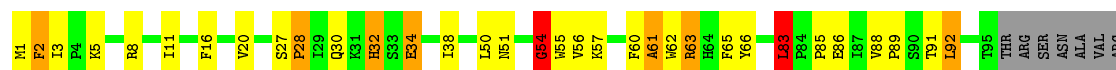
- Molecule 3: 40S ribosomal protein S20





- Molecule 4: 40S ribosomal protein S10a

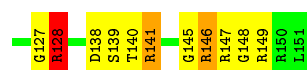
Chain AK: 38% 15% 42%



ASN

- Molecule 5: 40S ribosomal protein S14

Chain AO: 64% 19% 11%



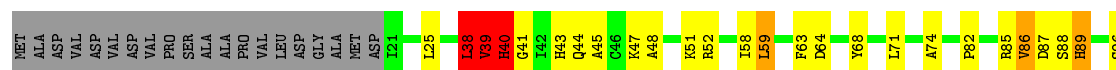
- Molecule 6: 40S ribosomal protein S23

Chain AX: 78% 18% 4%



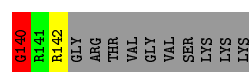
- Molecule 7: 40S ribosomal protein S12

Chain AM: 57% 19% 6% 14%

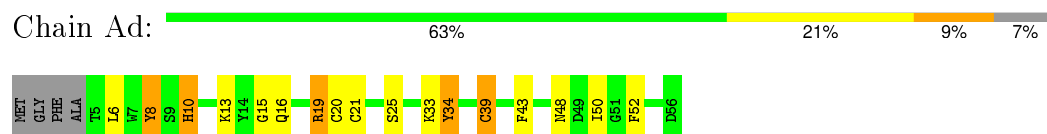


- Molecule 8: 40S ribosomal protein S18

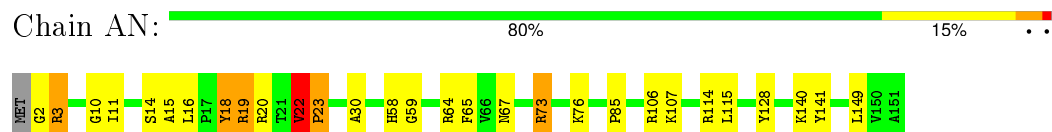
Chain AS: 65% 18% 10%



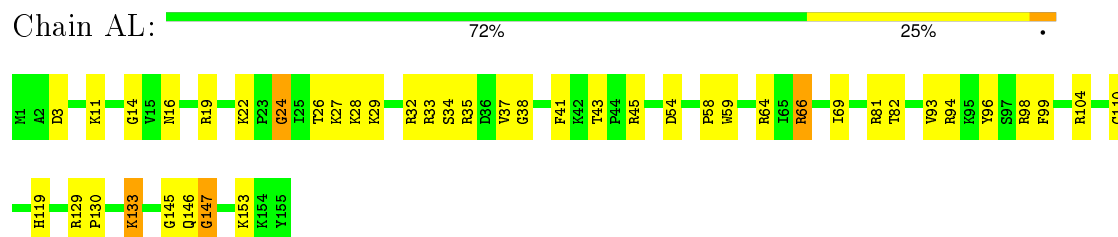
- Molecule 9: 40S ribosomal protein S29



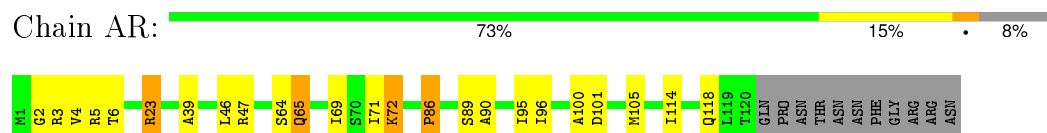
- Molecule 10: 40S ribosomal protein S13



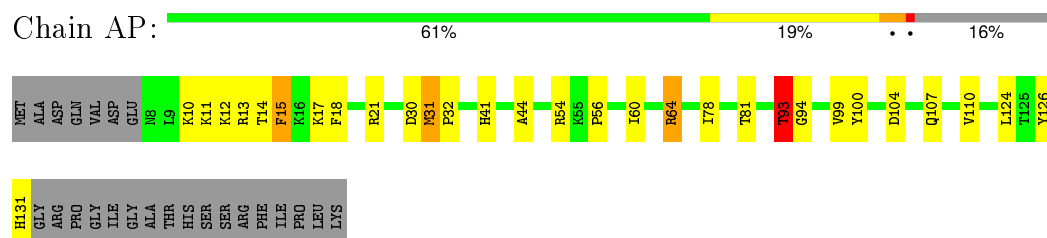
- Molecule 11: 40S ribosomal protein S11



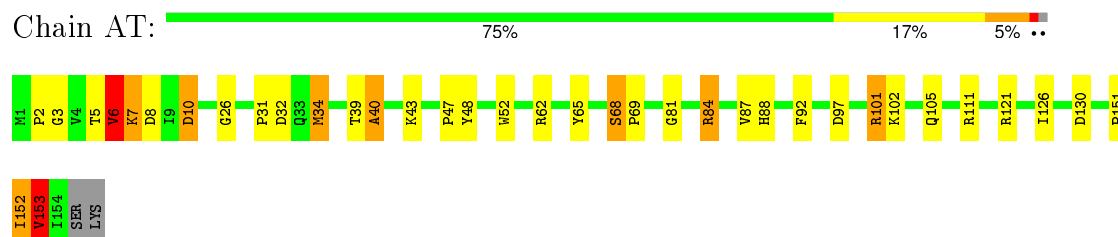
- Molecule 12: 40S ribosomal protein S17



- Molecule 13: 40S ribosomal protein S15, isoform A

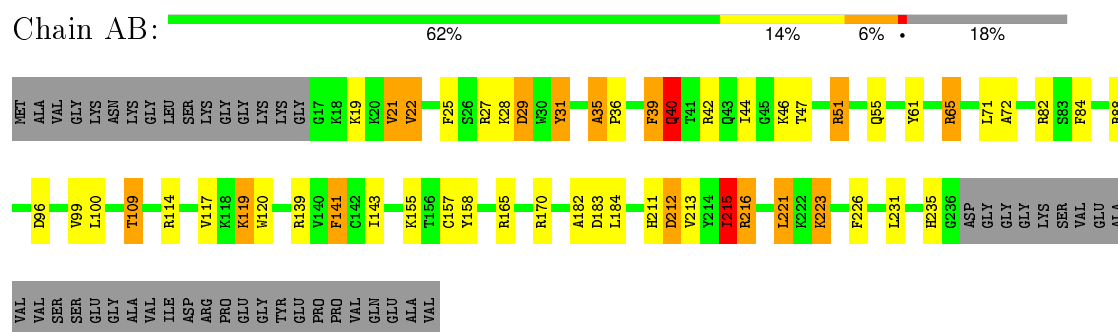


- Molecule 14: 40S ribosomal protein S19a



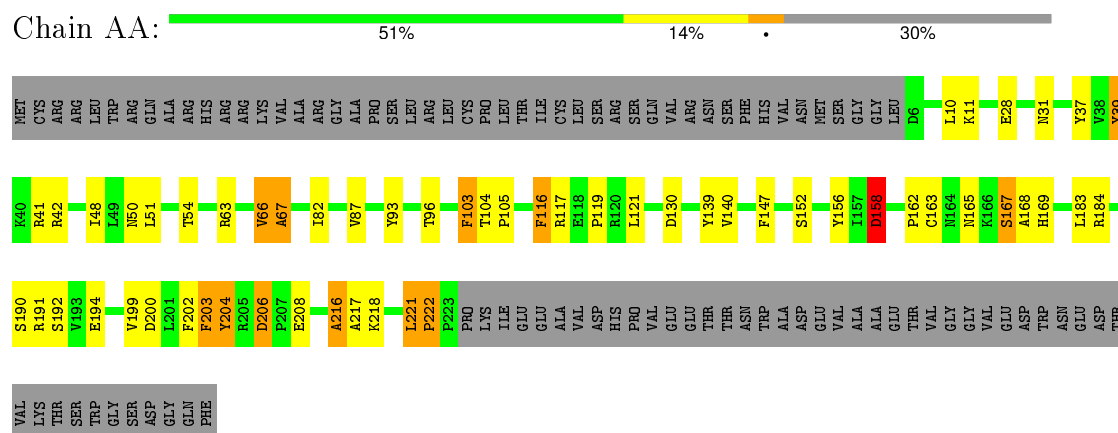
- Molecule 15: 40S ribosomal protein S3a

Chain AB:



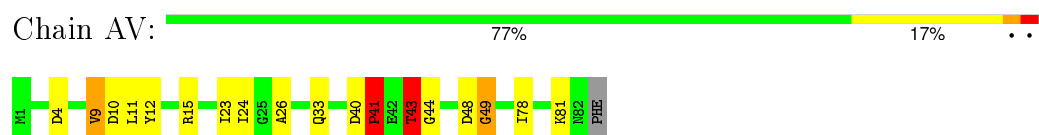
- Molecule 16: 40S ribosomal protein SA

Chain AA:



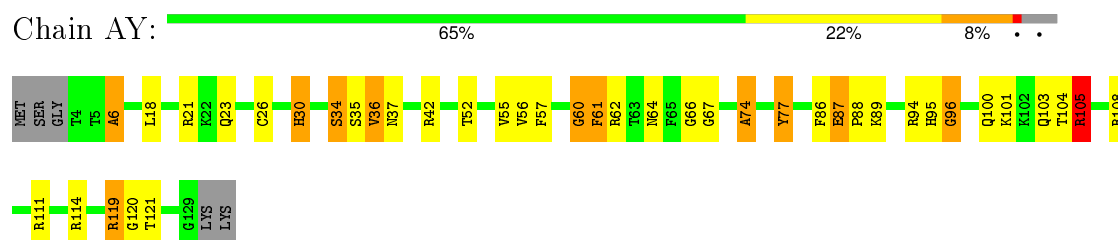
- Molecule 17: 40S ribosomal protein S21

Chain AV:



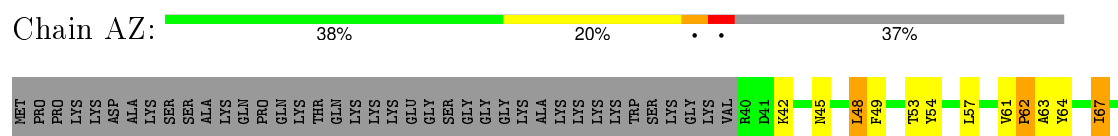
- Molecule 18: 40S ribosomal protein S24

Chain AY:



- Molecule 19: 40S ribosomal protein S25

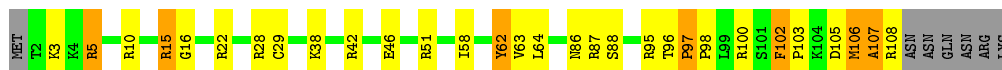
Chain AZ:





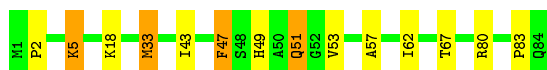
- Molecule 20: 40S ribosomal protein S26

Chain Aa: 68% 20% 6% 6%



- Molecule 21: 40S ribosomal protein S27

Chain Ab: 83% 12% 5%



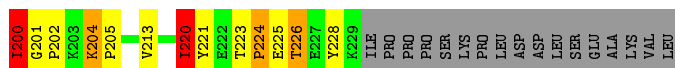
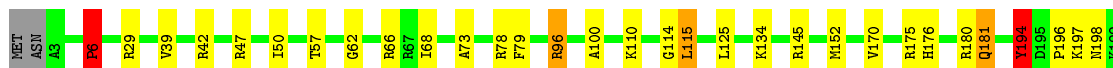
- Molecule 22: 40S ribosomal protein S28

Chain Ac: 75% 17% 5%



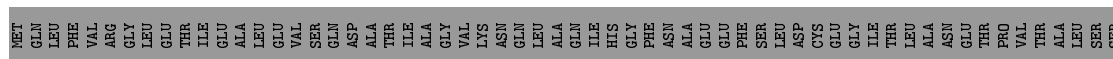
- Molecule 23: 40S ribosomal protein S3

Chain AD: 74% 14% 8%



- Molecule 24: 40S ribosomal protein S30, isoform A

Chain Ae: 31% 10% 56%



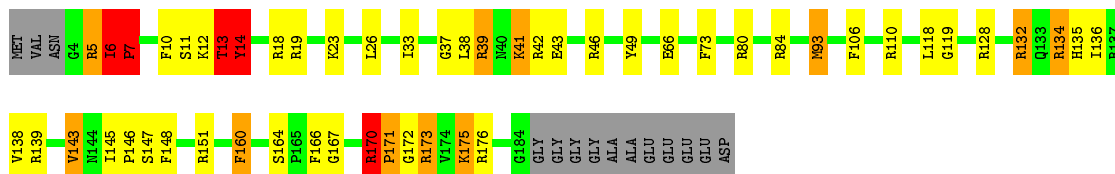
- Molecule 25: 40S ribosomal protein S27a

Chain Af: 53% 34% 11%


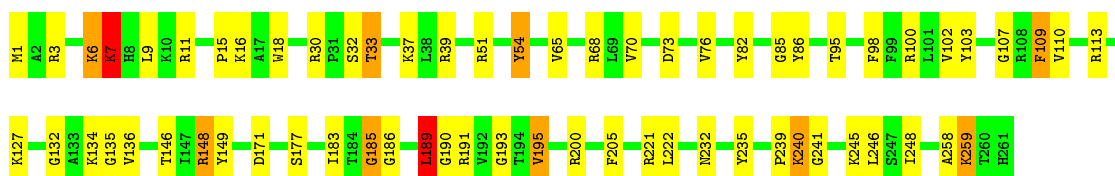


E155
K156

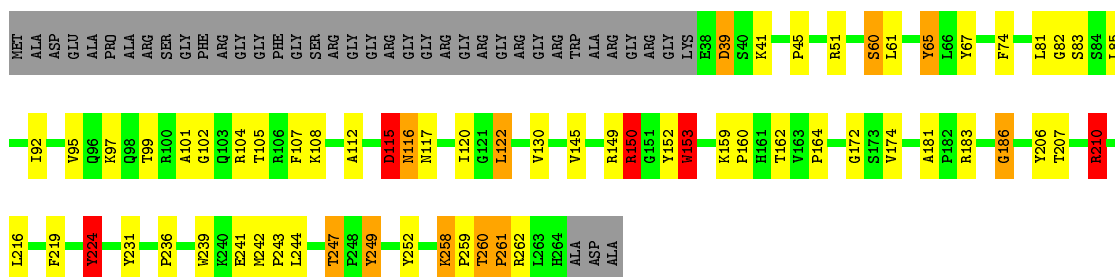
- Molecule 26: 40S ribosomal protein S9

Chain AJ:  66% 19% 6% 7%

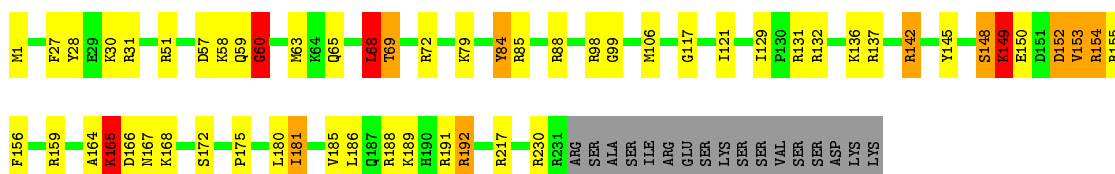
- Molecule 27: 40S ribosomal protein S4

Chain AE:  75% 21% . .

- Molecule 28: 40S ribosomal protein S2

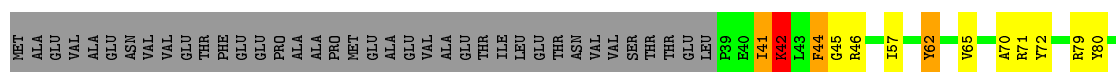
Chain AC:  61% 18% . . 15%

- Molecule 29: 40S ribosomal protein S6

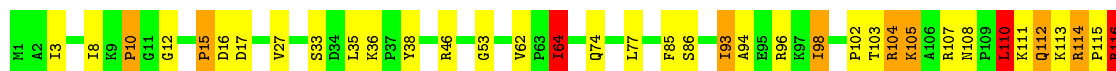
Chain AG:  70% 18% . . 7%

- Molecule 30: 40S ribosomal protein S5a

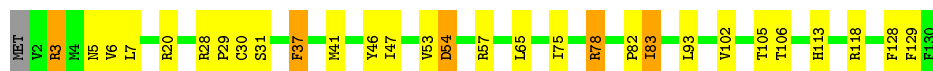
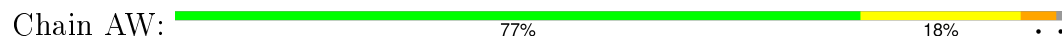
Chain AF:  64% 14% . . 17%



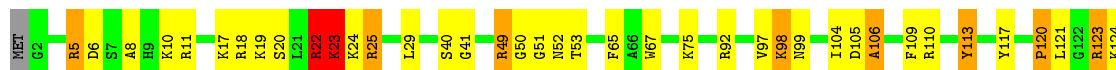
- Molecule 31: 40S ribosomal protein S7



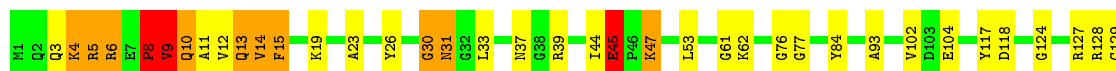
- Molecule 32: 40S ribosomal protein S15Aa



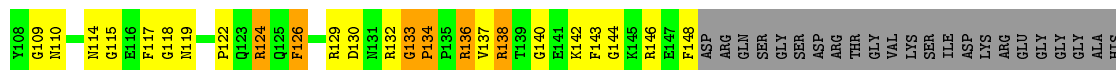
- Molecule 33: 40S ribosomal protein S8



- Molecule 34: 40S ribosomal protein S16



- Molecule 35: Vig2, isoform B



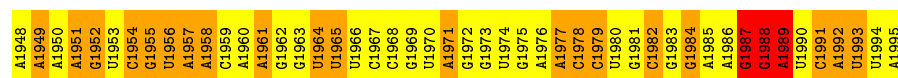
ASN	TRP	GLY	SER	PRO	LVS	GLN	ASP	ILE	ASP	ASP	LEU	LYS	THR	THR	GLU	GLU	THR	SER	PRO	GLN	ALA	ALA	ASN	GLU	SER	ALA	ASP	PRO	ALA	VAL	ALA	ALA	ALA	GLU	K212	E213	E214	P215	K216	A225	I228
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------

● Molecule 36: 18S ribosomal RNA

Chain B2: 9% 53% 29% 6%

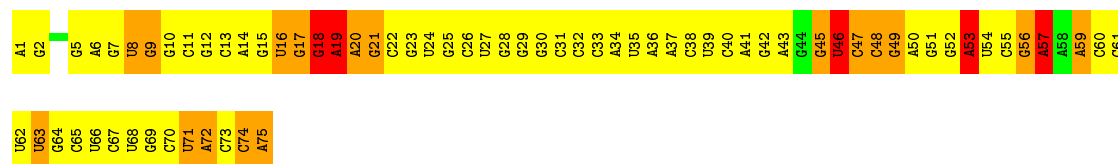
A891	U831	A	U608	G548	U487	C366	A304	U243	A183	A121	A61	A1
A892	U832	C	A609	A549	A488	C367	A305	A244	A184	A122	A62	U2
A893	U833	U	U610	C550	C489	C368	A306	U245	U185	G123	G63	U3
A894	A834	A	U611	A551	A490	G369	U307	U246	U186	U124	U64	C4
A895	U835	C	A612	A552	G491	C370	G308	G247	A187	C125	A65	U5
U886	C836	U	A613	A553	G492	C371	U309	G248	C188	G126	C66	G6
A897	A837	U	A614	U554	A493	A372	C310	U249	C189	U127	A67	G7
A898	U838	G	U615	U555	C494	U373	U311	U250	U190	C131	C68	U8
G901	A839	U	U616	G556	U495	A374	G312	G251	U191	A132	A69	U9
U902	U840	U	U617	G557	C496	A375	C313	A252	A192	G71	C70	G10
U903	U841	G	U618	A558	A497	G376	C314	A253	U193	G133	G71	A11
U904	A842	U	U619	U559	U498	G377	C315	C254	G194	U134	A72	U12
U905	G843	G	U620	U560	A499	G378	U316	U255	G195	U135	A73	C13
U906	A844	U	G621	U561	U500	U379	U317	C256	G196	U136	U74	C14
G907	U845	U	U622	C562	C501	U380	U318	U257	A197	C137	U75	U15
U908	U846	U	G623	U563	C502	A442	C319	A258	G198	U138	A76	G16
U909	G847	A	G624	A564	U503	A443	A320	G259	G199	U139	A77	C17
U910	C848	U	U625	U565	G505	U444	A321	A260	U200	G140	A78	C18
G911	U849	G	U626	U566	G506	U445	C322	U261	G201	G141	A79	A19
U912	U850	U	A627	C567	C507	U385	U323	A262	U202	A142	G80	G20
A851	U913	U	G628	U568	C508	C447	C324	A263	G203	U143	U81	U21
G914	A852	U	U629	G569	C509	C448	U325	C264	G204	A144	G82	A22
U915	U853	U	A630	U570	U510	C449	U326	A265	U205	A145	A83	G23
U916	G854	U	G631	U571	G511	A450	G327	U266	U206	C146	A84	U24
U917	C855	U	G632	U572	U512	C451	A328	G267	U207	U147	A85	U25
G918	U856	U	U633	C573	A513	U452	U329	C268	U208	G148	C86	A26
U919	U857	U	G634	C574	A514	C453	A329	A269	A209	U149	C87	U27
U920	G858	U	U635	U575	U515	C454	G331	G270	U210	G150	G88	A28
U921	C859	U	G636	G576	U516	C455	U332	A271	U211	G151	C89	U29
G922	U860	U	U637	C577	G517	A456	A333	U272	A212	U152	C90	G30
U923	U861	U	A638	U578	G518	C457	G334	C273	G213	A153	A91	C31
G924	C862	U	G639	U579	A519	U458	U335	G274	G214	A154	A92	U32
U925	U863	U	U640	C580	A520	U459	A336	U275	C215	U155	A93	U33
U926	A864	U	U641	C581	U521	C460	U337	A276	U216	G156	G94	G34
U927	G865	U	G642	U582	G522	G461	C338	U277	A217	C157	G95	U35
C928	U866	U	A643	C583	A523	G462	U339	G278	A218	U158	C96	C36
A929	G867	U	U644	U584	G524	A463	A340	G279	A219	A159	U97	U37
U930	C868	U	U645	G585	U525	G464	G341	U280	A220	G160	C98	C38
A931	U869	U	U646	U586	A526	A465	A342	C281	C221	A161	A99	A39
U932	U870	U	U647	C587	C527	U466	A343	U282	C222	G162	U100	A40
C933	G871	U	G648	A588	A528	G467	C344	U283	C223	C163	U101	A41
U934	U872	U	U649	U589	C529	U468	U345	G284	A224	U164	A102	G42
A935	U873	U	U650	U590	U530	A469	A346	U285	G225	A165	U103	A43
U936	U874	U	G651	C591	U531	G470	C347	U286	C226	A166	A104	U44
G938	A875	U	U652	C592	A532	U471	U411	C287	G227	U167	U105	U45
U939	U876	U	U653	A593	U533	G472	A349	C288	A228	A168	C106	A46
U940	U877	U	C654	C594	A534	A473	U350	G289	U229	C169	A107	A47
A941	G878	U	A855	C595	A535	C474	G351	A290	C230	A170	G108	G48
U942	U879	U	U656	U596	U536	G475	C352	C291	G231	U171	U109	C49
U943	G880	U	A857	C597	C537	A476	U416	G292	C232	G172	A110	C50
G944	U881	U	U658	C598	C538	A477	C356	C293	A233	C173	A111	A51
A945	A882	U	G659	G599	U539	U478	A357	C294	A234	A174	U112	U52
U946	C883	U	A660	U600	U540	A479	A358	A295	G235	A175	G113	G53
U947	U884	U	G661	U601	U541	A480	C359	U296	A236	U176	G114	C54
A948	U885	U	U662	A602	A542	U481	G360	U298	C237	U177	U115	A55
U949	G886	U	A863	C603	A543	A482	G361	C299	C238	A178	U116	U56
U950	U887	U	G664	C604	C544	G423	G362	U300	G239	A179	C117	G57
A951	G888	U	A665	U605	A545	G424	U363	U301	U240	A180	C118	U58
U952	U889	U	C666	U606	A546	G425	A364	C302	U241	A181	U119	C59
G953	U890	A	U667	U607	C547	A426	A365	U303	U242	C182	U120	U60

G1886	A1887	C1826	G1766	U1706	G1646	U1586	A1526	G1436	U1376	G1336	G1256	G1195	G1135	C1135	G1074	C1014	A954
A1887	A1768	A1827	G1767	A1707	G1647	U1587	G1526	A1437	U1377	U1317	U1256	G1196	G1135	G1136	U1075	U1015	A955
A1888	A1769	C1828	A1768	A1708	C1648	C1588	G1527	A1438	C1378	A1318	G1257	G1197	G1137	G1137	U1076	A1016	A956
A1889	A1770	G1830	A1769	A1709	U1649	C1589	G1528	U1439	G1379	A1319	G1258	G1198	G1137	G1137	C1077	A1017	A957
C1890	C1710	G1831	G1650	G1590	G1650	U1591	G1529	U1440	U1380	A1320	A1259	G1199	U1138	U1138	G1078	C1018	A958
	C1711	G1832	G1651	U1591	G1651	U1592	G1530	U1441	G1381	A1321	G1260	A1200	U1139	A1139	A1079	U1019	U959
G1894	G1712	A1832	A1652	C1592	A1652	C1592	G1531	U1442	G1382	C1322	C1261	A1201	G1140	G1140	A1080	U1020	U960
A1895	C1713	C1833	G1653	U1593	G1653	U1593	G1532	U1443	G1383	A1323	C1262	G1202	G1141	G1141	A1081	A1021	U961
G1896	U1714	G1834	G1654	A1594	G1654	A1594	C1533	C1444	G1384	A1324	C1263	G1203			G1082	A1022	G962
A1897	G1715	C1835	G1655	G1595	G1655	G1595	G1534	A1445	U1385	A1325	G1264	A1204	U1144	U1144	C1083	G1023	G963
G1898	A1716	G1836	G1656	C1596	G1656	C1596	U1535	G1446	U1386	U1326	C1265	G1205	U1145	U1145	G1084	C1024	G964
A1899	A1717	G1837	G1657	A1597	G1657	A1597	G1536	G1447	A1387	G1327	G1266	G1206	U1146	U1146	A1085	G1025	G965
U1900	C1718	G1838	G1658	C1598	G1658	A1598	C1537	U1448	U1388	U1328	G1267	G1207	U1147	U1147	U1086	A1026	G966
A1901	C1719	C1839	G1659	U1599	G1659	U1599	C1538	U1449	U1389	A1329	C1268	U1208	U1148	U1148	C1087	A1027	C967
G1902	A1720	A1840	U1660	A1600	U1660	A1600		U1450	U1390	U1330	U1269	U1209	A1149	A1149	A1088	A1028	A968
G1903	C1721	C1841	A1661	A1601	A1661	A1601	U1541	A1451	G1391	U1331	U1270	G1210	U1150	U1150	G1029	A1029	U969
G1904	U1722	G1842	C1662	G1602	C1662	G1602	U1542	U1452	U1392	G1332	A1271	C1211	G1151	G1151	A1090	C1030	U970
A1905	G1723	C1843	G1663	G1603	G1663	G1603	U1543	G1453	C1393	C1333	G1272	A1212	G1152	G1152	U1091	A1031	A971
U1906	U1724	C1844	A1664	A1604	A1664	A1604	G1544	G1454	U1394	U1334	U1273	A1213	C1153	C1153	A1092	U1032	G972
C1907	C1725	C1845	G1665	G1605	G1665	G1605	U1545	U1455	G1395	C1335	U1274	A1214	U1154	U1154	C1093	U1033	U973
U1908	A1726	G1846	G1666	A1606	G1666	A1606	U1546	G1456	U1396	U1336	U1275	G1215	C1155	C1155	C1094	U1034	A974
A1909	U1727	A1847	A1667	U1607	A1667	U1607	U1547	C1457	U1397	U1337	G1276	C1216	U1156	U1156	G1095	G1035	U975
U1910	G1728	C1848	A1668	G1608	A1668	G1608	G1548	U1458	U1398	U1338	A1277	U1217	C1157	C1157	C1096	C1036	U976
G1911	C1729	A1849	A1669	G1609	A1669	G1609	U1549	G1459	A1399	U1339	C1278	C1218	U1158	U1158	C1097	C1037	A977
C1912	U1730	G1850	G1670	A1610	A1670	A1610	C1550	A1460	A1400	U1340	U1279	A1219	G1159	G1159	C1098	A1038	C978
C1913	U1731	A1851	U1671	G1611	A1671	G1611	C1551	A1461	U1401	C1341	C1280	A1220	A1160	A1160	U1099	A1039	G979
A1914	G1732	A1852	A1672	C1612	A1672	C1612	C1552	G1462	U1402	G1342	A1281	A1221	G1161	G1161	A1100	A1040	A980
A1915	C1733	C1853	U1673	A1613	U1673	A1613	A1553	C1463	A1403	A1343	A1282	C1222	U1162	U1162	G1101	G1041	C981
U1916	G1734	C1854	C1674	A1614	C1674	A1614	U1554	U1464	C1404	A1344	C1283	U1223	C1163	C1163	U1102	A1042	G982
A1917	A1735	A1855	A1675	G1615	A1675	G1615	U1555	U1465	A1405	U1345	A1284	U1224	G1164	G1164	U1103	U1043	C983
G1918	U1736	U1856	A1676	A1616	A1676	A1616	U1556	A1466	A1406	C1346	C1285	A1225	C1165	C1165	C1104	G1044	G984
U1919	C1737	C1857	C1677	A1617	C1677	A1617	U1557	U1467	U1407	U1347	U1286	A1226	U1166	U1166	U1105	U1045	A985
U1920	G1738	U1858	G1678	C1618	A1678	C1618	U1558	G1468	A1408	U1348	G1287	A1227	U1167	U1167	A1106	U1046	G986
A1921	U1739	A1859	A1679	A1619	A1679	A1619	U1559	U1469	A1409	U1349	A1288	G1228	C1168	C1168	U1107	U1047	A987
G1922	G1740	G1860	G1680	G1620	U1680	G1620	G1560	A1470	C1410	G1350	A1289	G1229	C1169	C1169	C1108	U1048	G988
C1923	A1741	C1861	G1681	G1621	U1681	G1621	G1561	G1471	A1411	G1351	A1290	A1230	G1170	G1170	C1109	C1049	G989
G1924	A1742	G1862	A1682	U1622	G1682	U1622	A1562	C1472	A1412	G1352	A1291	U1231	G1171	G1171	A1050	A1050	U990
G1925	C1743	A1863	C1683	C1623	U1683	C1623	C1563	C1473	A1413	U1353	A1292	U1232	G1172	G1172	U1051	U1051	G991
A1926	U1744	G1864	U1684	U1624	U1684	U1624	A1564		C1414	G1354	C1293	U1233	A1173	A1173	U1052	U1052	A992
C1927	G1745	G1865	G1685	G1625	U1685	G1625	C1565	C1476	G1415	G1355	U1294	G1234	A1174	A1174	A1053	A1053	A993
G1928	A1746	C1866	G1686	U1626	U1686	U1626	U1566		A1416	U1356	U1295	A1235	G1175	G1175	U1054	A1054	A994
U1929	C1747	C1867	C1687	G1627	U1687	G1627	A1567	U1479	G1417	G1357	C1236	G1236	C1176	C1176	U1055	U1055	U995
U1930	A1748	U1868	A1688	A1628	U1688	A1628	G1568		A1418	U1358	G1297	G1237	C1177	C1177	C1116	C1056	U996
G1931	C1749	C1869	A1689	G1629	U1689	G1629	C1569	A1482	C1419	U1359	C1298	G1238	A1178	A1178	A1057	A1057	C997
A1932	U1750	C1870	G1690	G1630	U1690	G1630	U1570	A1493	U1420	G1360	A1299	A1239	A1179	A1179	U1118	A1058	U998
U1933	G1751	A1891	A1691	C1631	A1691	C1631	U1571	A1494	C1421	C1361	G1300	A1240	A1180	A1180	G1119	G1059	U999
G1934	U1752	C1892	C1692	C1632	U1692	C1632	C1572	A1495	A1422	A1362	G1301	G1241	C1181	C1181	C1120	A1060	G1000
A1935	U1753	C1893	C1693	C1633	U1693	C1633	U1573	U1496	A1423	U1363	U1302	G1242	C1182	C1182	C1121	A1061	G1001
U1936	C1754	G1894	G1694	U1634	U1694	U1634	U1574		A1424	G1364	C1303	G1243	U1183	U1183	A1122	C1062	A1002
G1937	A1755	C1895	A1695	U1635	U1695	U1635	A1575	U1499	U1425	G1365	G1304	C1244	U1184	U1184	G1123	G1063	C1003
U1938	C1756	C1896	G1696	A1636	U1696	A1636	A1576		A1426	C1366	A1305	A1245	U1185	U1185	C1124	A1064	C1004
A1939	G1757	A1897	G1697	G1637	U1697	G1637	U1577	U1503	A1427	C1367	A1306	C1246	U1186	U1186	U1125	A1065	G1005
G1940	A1758	C1898	A1698	A1638	U1698	A1638	U1578	G1504	A1428	G1368	C1307	C1247	U1187	U1187	A1126	A1066	U1006
A1941	U1759	G1899	G1699	U1639	U1699	U1639	U1579		A1429	U1369	A1308	A1248	G1188	G1188	G1127	G1067	C1007
G1942	C1760	C1880	U1700	G1640	U1700	G1640	U1580	U1519	U1430	U1370	C1249	G1249	G1189	G1189	C1128	U1068	G1008
G1943	A1761	A1881	A1641	U1641	U1641	U1641	A1581	A1520	A1431	C1371	C1250	C1250	G1190	G1190	A1129	U1069	U1009
A1944	C1762	C1882	C1642	C1642	U1642	C1642	U1582	U1521	A1432	U1372	A1251	A1251	C1191	C1191	A1130	A1070	A1010
G1945	C1763	A1883	C1643	U1643	U1643	U1643	A1583	U1522	A1433	U1373	G1252	G1252	U1192	U1192	U1131	A1071	A1011
U1946	G1704	C1884	A1644	U1644	U1644	U1644	A1584	U1523	A1434	A1374	G1253	G1253	C1193	C1193	U1132	A1072	G1012
U1947	U1765	A1885	G1705	U1645	U1645	G1645	A1585	A1524	A1435	G1375	U1315	A1254	C1194	C1194	G1133	G1073	A1013



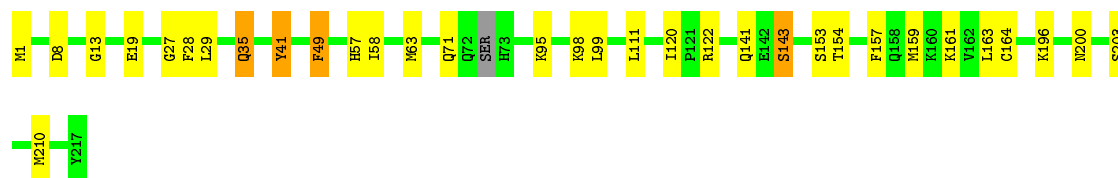
• Molecule 37: E-tRNA

Chain BC: 5% 65% 23% 7%



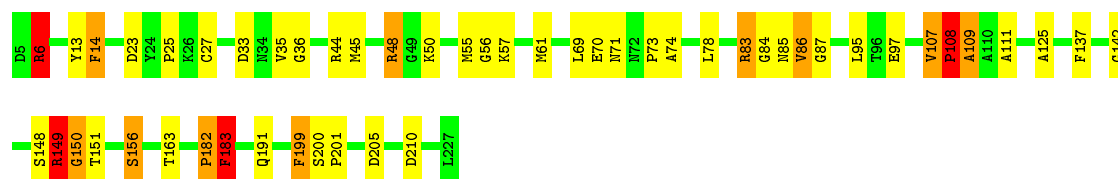
• Molecule 38: 60S ribosomal protein L10a-2

Chain Cz: 84% 13%



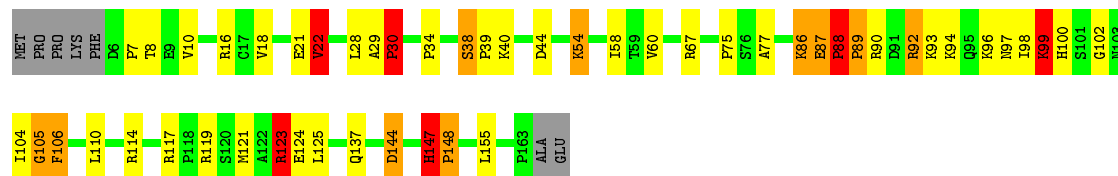
• Molecule 39: 60S acidic ribosomal protein P0

Chain Cq: 77% 17%



• Molecule 40: 60S ribosomal protein L12

Chain CK: 65% 21% 6%



• Molecule 41: 60S ribosomal protein L13a

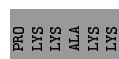
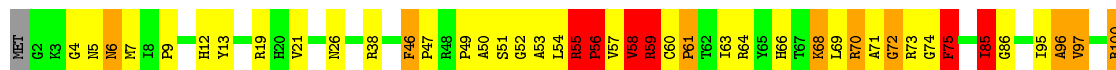
Chain CO: 78% 15% 5%





- Molecule 42: 60S ribosomal protein L13

Chain CL: 57% 26% 9% 5% .



- Molecule 43: 60S ribosomal protein L23

Chain CV: 81% 14% .



- Molecule 44: 60S ribosomal protein L14

Chain CM: 54% 33% 8% . .



- Molecule 45: 60S ribosomal protein L27a

Chain Ca: 72% 21% . .



- Molecule 46: 60S ribosomal protein L15

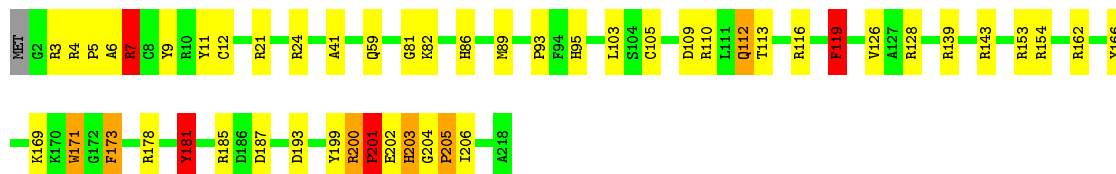
Chain CN: 72% 23% . .





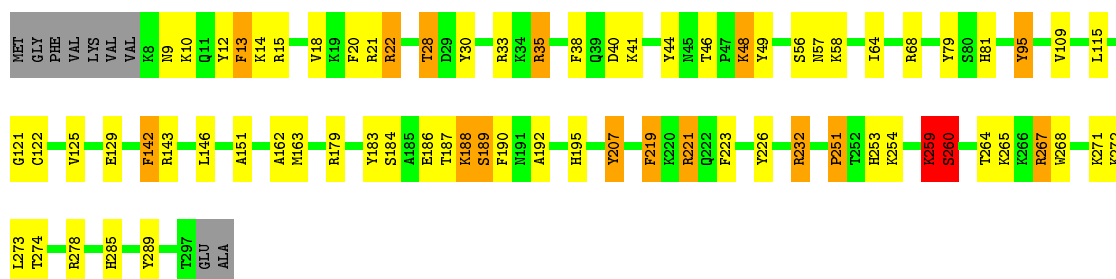
- Molecule 47: 60S ribosomal protein L10

Chain CI: 77% 18%



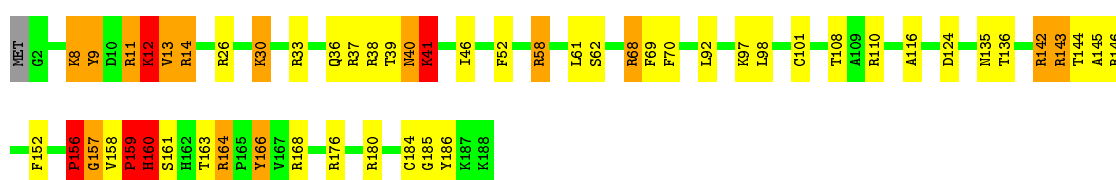
- Molecule 48: 60S ribosomal protein L5

Chain CD: 73% 19% 5%



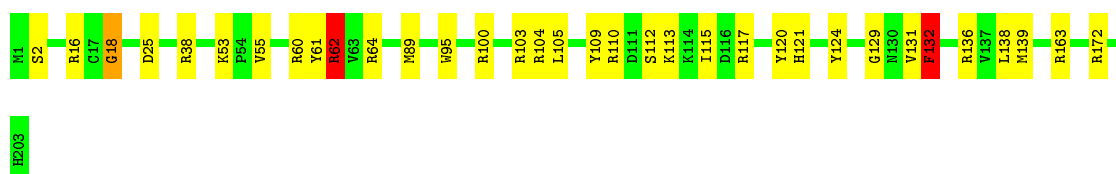
- Molecule 49: 60S ribosomal protein L18

Chain CQ: 71% 19% 7%



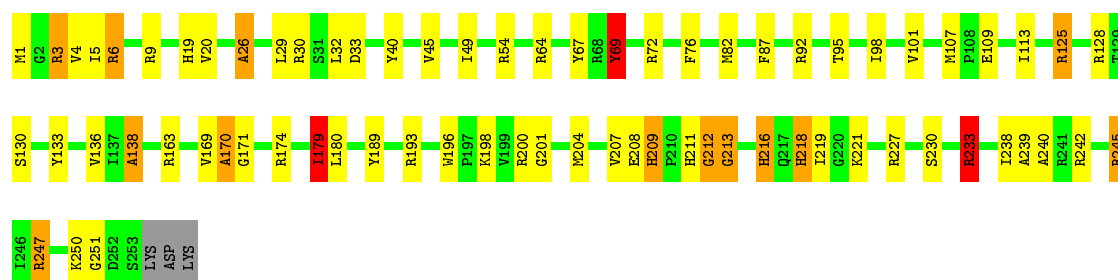
- Molecule 50: 60S ribosomal protein L19

Chain CR: 83% 15%

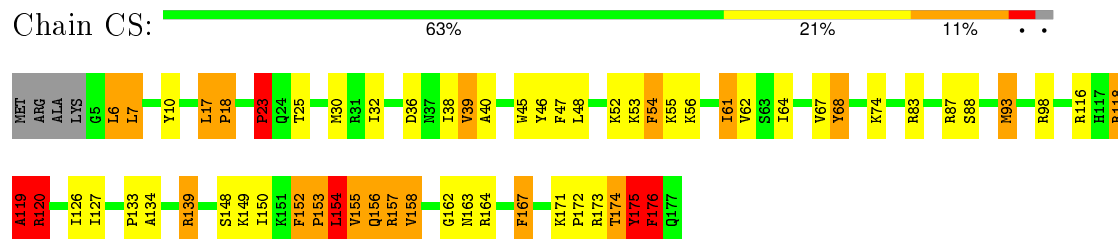


- Molecule 51: 60S ribosomal protein L8

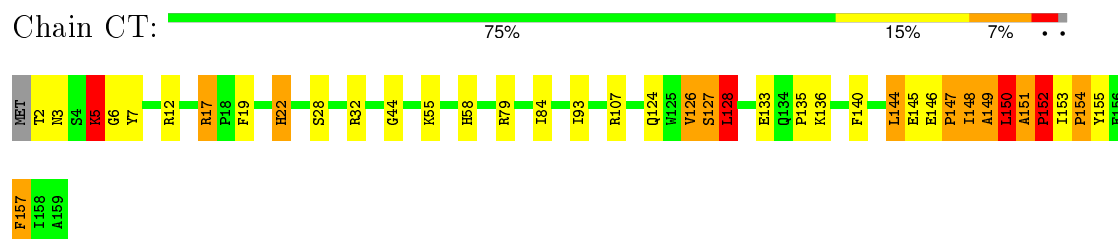
Chain CA: 71% 22% 5%



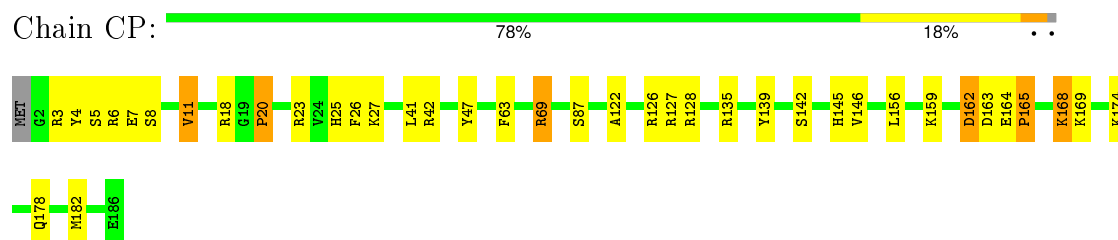
- Molecule 52: 60S ribosomal protein L18a



- Molecule 53: 60S ribosomal protein L21



- Molecule 54: 60S ribosomal protein L17



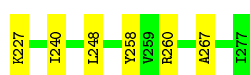
- Molecule 55: 60S ribosomal protein L22





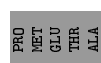
- Molecule 56: 60S ribosomal protein L23A

Chain CX: 36% 5% 57%



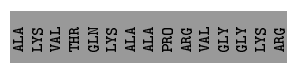
- Molecule 57: 60S ribosomal protein L26

Chain CY: 70% 15% 12%



- Molecule 58: 60S ribosomal protein L24

Chain CW: 65% 12% 5% 16%



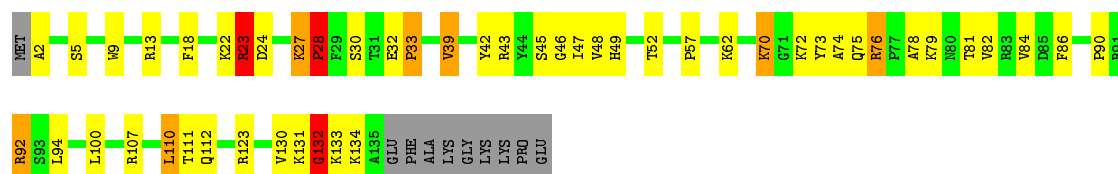
- Molecule 59: 60S ribosomal protein L27

Chain CZ: 73% 22% 5%



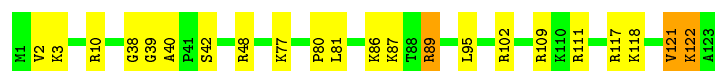
- Molecule 60: 60S ribosomal protein L28

Chain Cr: 58% 28% 5% 7%



- Molecule 61: 60S ribosomal protein L35

Chain Ch: 82% 15%



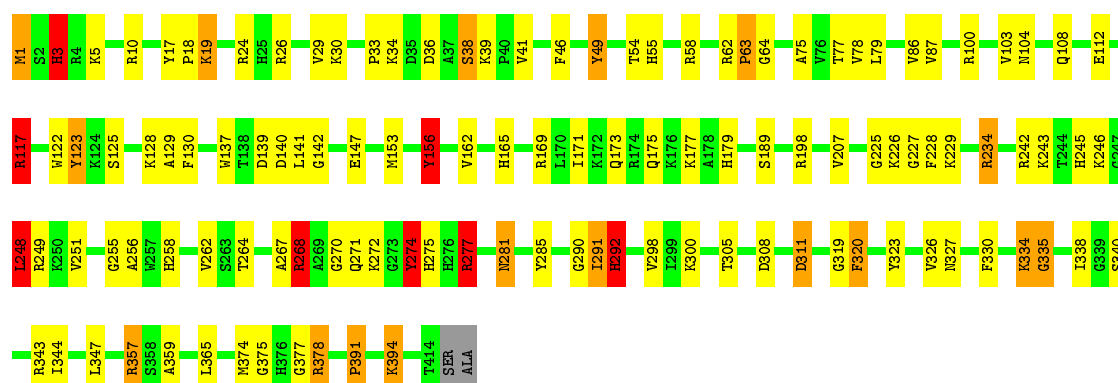
- Molecule 62: 60S ribosomal protein L29

Chain Cb: 71% 20% 5%



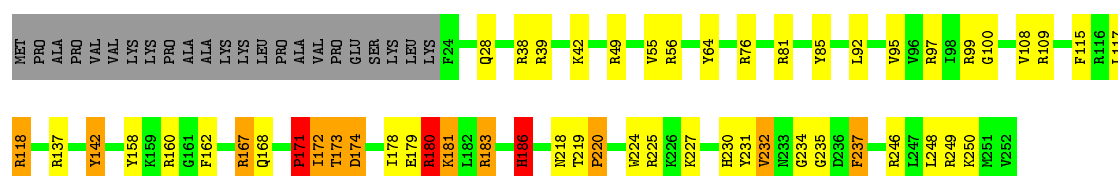
- Molecule 63: 60S ribosomal protein L3

Chain CB: 71% 23%



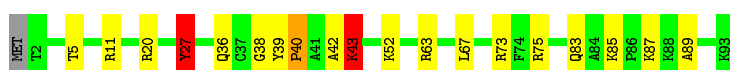
- Molecule 64: 60S ribosomal protein L7

Chain CF: 69% 16% 9%

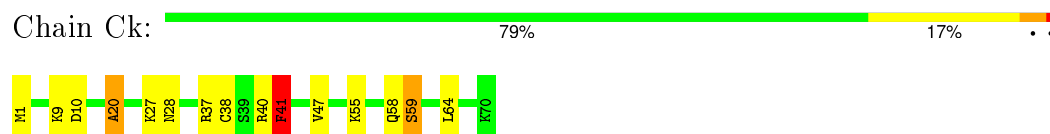


- Molecule 65: 60S ribosomal protein L30

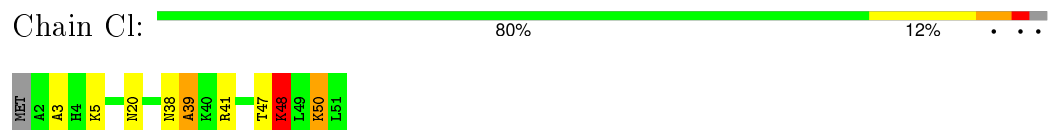
Chain Cc: 74% 13% 10%



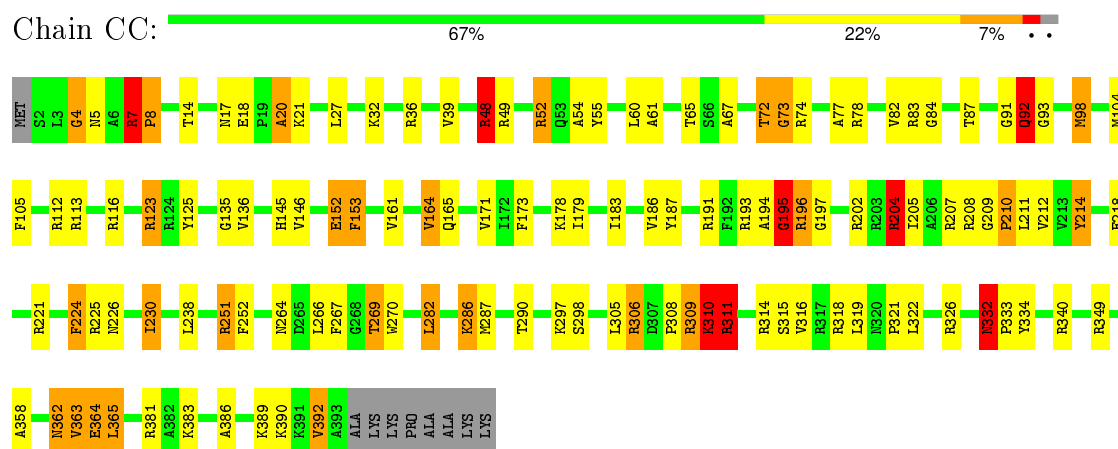
- Molecule 72: 60S ribosomal protein L38



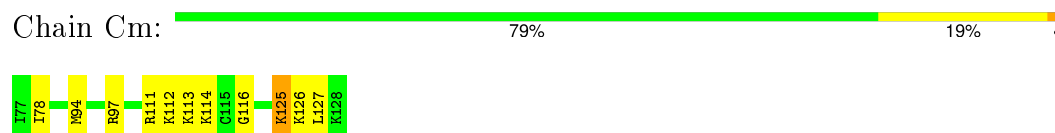
- Molecule 73: 60S ribosomal protein L39



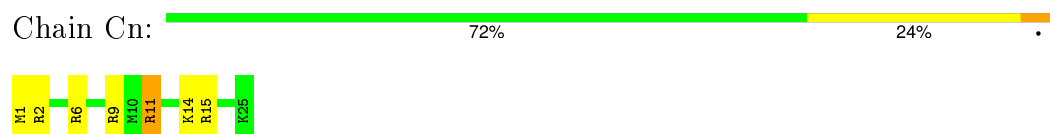
- Molecule 74: 60S ribosomal protein L4



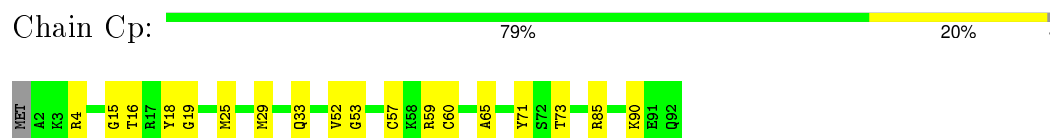
- Molecule 75: 60S ribosomal protein L40



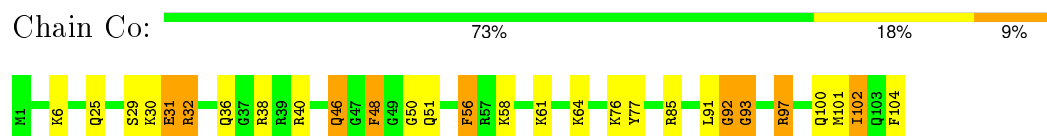
- Molecule 76: 60S ribosomal protein L41



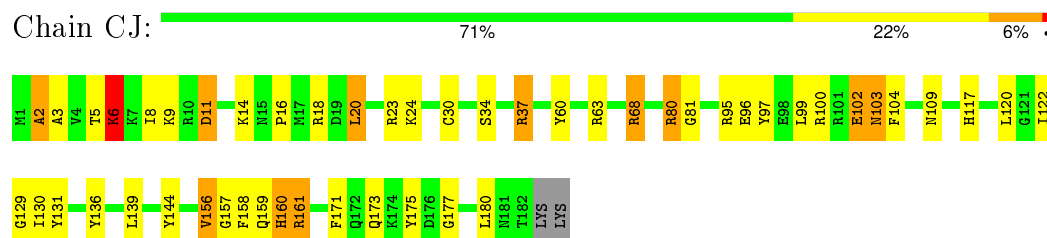
- Molecule 77: 60S ribosomal protein L37a



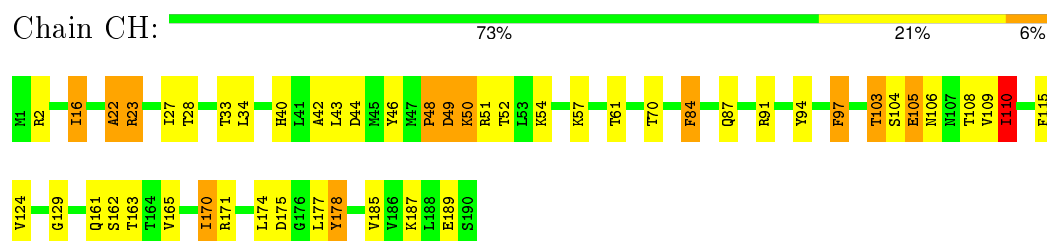
- Molecule 78: 60S ribosomal protein L36A



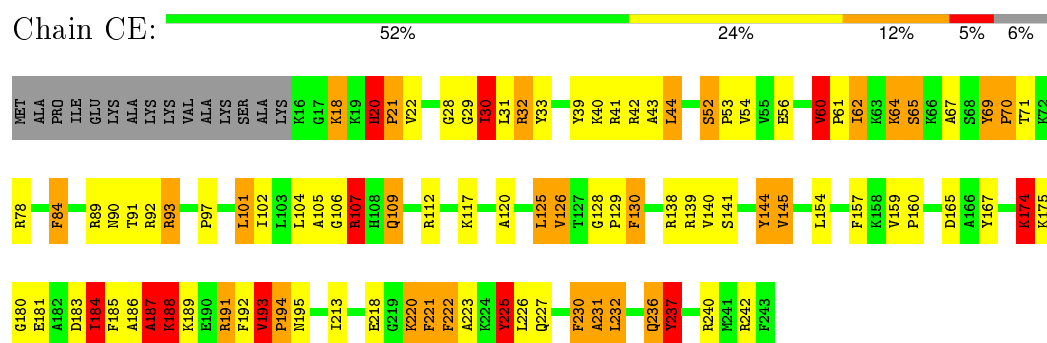
- Molecule 79: 60S ribosomal protein L11



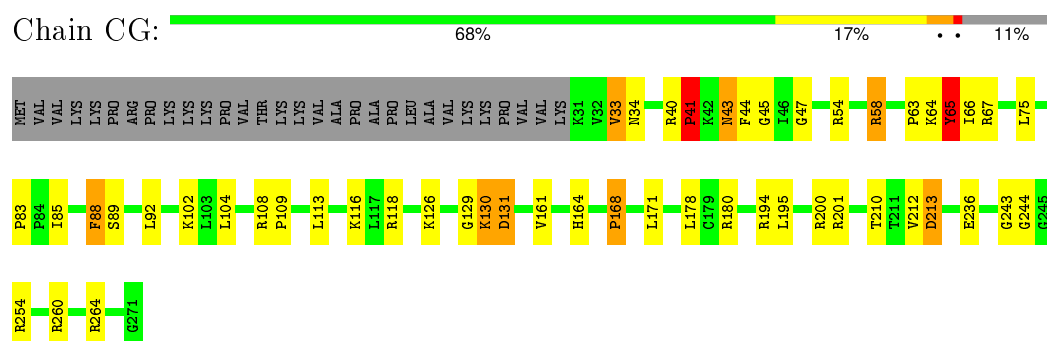
- Molecule 80: 60S ribosomal protein L9



- Molecule 81: 60S ribosomal protein L6, isoform A



- Molecule 82: 60S ribosomal protein L7a



● Molecule 83: 28S ribosomal RNA

Chain A5:  8% 51% 30% 7%

U1	A61	A121	A181	C242	A302	A362	U423	A484	U544	G610	G670	U731	C791	G851	A911
U2	G62	C122	G182	A242	G303	G363	G424	A485	U545	G611	A671	U732	U792	C852	A912
A3	G63	U123	U183	G244	U304	U364	A425	A486	G546	U612	U672	A733	U793	G853	C914
U4	A64	A184	A184	G245	G305	A365	A426	A487	U547	U613	U673	U734	G794	U854	C915
A5	A65	A125	U185	C246	C306	A366	A427	U488	A548	G614	A674	U735	A795	A855	C916
U6	A66	G126	G186	C247	A307	A367	C428	U489	A549	G615	C675	U736	A796	A856	C917
A7	A67	U127	A187	C248	G308	C368	U429	G490	U550	A616	A676	U737	A797	U857	C918
C8	A68	C128	G188	G249	C309	A369	G430	U491	C551	U617	A677	U738	C798	U858	C919
A9	A69	A129	A189	G250	A310	A370	C431	A492	U552	U618	G677	U739	A799	A859	C920
A10	A70	A130	A190	A251	C311	G371	U432	A493	A553	U619	G679	G740	C800	A860	C921
C11	A71	U131	A191	A252	U312	U372	U433	U494	U554	U620	C680	C741	C901	C861	C922
C12	A72	C72	A192	A253	A313	A373	A434	A495	U555	A621	G681	A742	G802	U862	G923
U13	U73	U133	U193	A254	A314	C374	G435	U496	A556	A622	U682	C743	A803	U863	G924
C14	A74	G134	A194	C255	G315	C375	A436	U497	G557	C623	U683	U744	C804	G864	U924
A15	A75	U135	A195	G256	U316	G376	G437	U498	C558	A624	A684	U745	C905	A865	C925
A16	C76	C136	C196	U257	G317	U377	G438	A499	A559	C625	A685	G746	A806	C866	U926
C17	A77	U137	G197	U258	G318	G378	U439	A500	U560	A626	U686	U747	A807	U867	U927
U18	A78	A138	A198	A259	G319	A379	U440	A501	A561	A627	U687	A748	G808	A868	U928
C19	G79	U139	U199	A260	U320	G380	A441	U502	U562	A628	U688	U749	G809	A869	A929
A20	G80	A140	U200	U261	G321	G381	A442	A503	A563	A629	U689	U750	A810	U870	U930
U21	A81	U141	U201	G262	G322	G382	G443	A504	A564	U630	U690	A751	G811	A871	A931
A22	A82	G142	A202	A263	U323	A383	C444	A505	C565	A631	G691	U752	U812	A872	G932
U23	U83	G143	A203	U264	U324	A384	C445	A506	A566	A632	G692	U753	C913	U873	U933
G24	U84	C144	G204	U265	A325	A385	C446	U507	A567	A633	A693	U754	U814	G874	U934
G25	U85	A145	U205	A266	A326	G386	U449	U508	A568	U634	A694	A755	A815	G875	A935
G26	C86	A146	C206	C267	C327	U387	U450	A509	U569	G635	A695	C756	A816	G876	U936
A27	U87	A147	C207	U268	U328	U388	G451	U510	U570	U636	U696	A757	C817	A877	G937
C28	U88	U148	U208	A269	C329	G389	A452	U511	A571	U637	U697	U758	A818	U878	U938
U29	A89	G149	U209	G270	A330	A390	A453	A512	A572	A638	A698	U759	U819	U879	A939
A30	G90	U150	C210	A271	C331	A391	C454	U513	A573	U639	G699	G760	A820	A880	U940
C31	U91	G151	U211	U272	U332	A392	C455	A514	C574	U640	A700	C761	U821	G881	A941
C32	A92	A152	U212	G273	C333	A393	U456	A515	A575	A641	U701	G762	G822	U882	A942
C33	G93	A153	A213	A274	U334	G394	U457	U516	U576	A642	A702	A763	U823	U883	U943
C34	C94	A154	A214	U275	A335	A395	A458	U517	A577	U643	U703	A764	G824	U884	G944
C35	G95	U155	G216	G276	A336	A396	U459	U519	A578	U644	U704	A765	C825	U885	U945
U36	G96	G156	U216	U277	A337	C397	U460	U520	A579	U645	G705	G766	A826	U886	A946
G37	C97	C157	G217	U278	A338	U398	U461	U521	A580	G646	G706	A767	U827	U887	U947
A38	G98	A158	A218	U279	C339	C399	C462	U522	U581	U647	C707	U768	G828	A888	U958
A39	A99	G159	G219	C280	U340	U400	C463	G523	A582	U648	A708	U769	U830	G889	U959
U40	G100	U160	G220	C281	A341	G401	A464	A524	A583	A649	U709	U770	U831	C890	U960
U41	C101	G161	C221	A282	A342	A402	U465	U525	A584	A650	A710	A771	U832	A891	A961
U42	G102	U162	C222	A283	A343	A403	U466	U526	A585	A651	A711	G772	U833	A892	U962
A43	A103	A163	A223	A284	U344	U404	U467	U527	C586	G652	U712	G773	U834	U893	G963
A44	A104	U164	U224	G285	A345	A405	A468	U528	C587	U653	U713	A774	G835	U894	C964
G45	A105	G165	U225	A286	U346	G406	U469	U529	U588	G654	A714	U775	G836	U895	C965
C46	A106	G166	U226	U287	A347	U409	C470	U530	A589	C655	U715	A776	U837	A896	U966
A47	G107	A167	A227	U288	A348	A410	G471	U531	U590	U656	C716	C777	U838	U897	U967
U48	G108	G168	C228	C289	C349	G410	A472	C531	A591	G657	A717	C778	U839	A898	C967
A49	A109	G169	C229	G290	C350	U411	A473	C532	G592	U658	U718	U779	U840	G899	U968
U50	A110	U170	C230	U291	A351	U412	A474	A533	U593	U659	U719	U780	U841	C900	A969
U51	A111	U171	U232	G292	U352	A413	A475	U534	U594	A660	G720	C781	A842	U901	A970
A52	C112	C172	A233	G293	U353	A414	U476	A535	U595	G661	U723	G782	U843	A902	C971
A53	A113	A173	G234	U294	G354	A415	U477	U536	A596	A662	U724	G783	C944	A903	U972
U54	G114	A174	A235	G295	G355	C416	C477	A537	U597	U663	U725	G784	C945	U904	G973
U55	U115	U175	G236	C296	A356	A417	A478	A538	U598	U664	U726	G785	C946	U905	G974
A56	U116	A176	G237	U297	C357	G418	U479	G539	A601	U665	U727	C786	C947	A906	G975
G57	C117	U177	G238	U298	C358	U419	C480	G540	A602	U666	G727	C787	U948	A907	A976
G58	A118	U178	U239	G299	G359	U420	A481	A541	U599	U667	U728	C788	C949	C908	A977
G59	C119	U179	G240	A300	A360	A421	U482	C542	U600	U668	G729	G789	U950	A909	G978
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A1887	C1887	A1767	A1707	A1647	U1587	C1527	A1466	G1406	C1346	U1286	G1226	A1162	G1102	C1040	A980
A1888	A1888	G1768	G1708	A1648	A1588	G1528	A1467	G1407	A1347	U1287	C1227	G1163	U1103	A1041	C981
A1889	A	A1769	A1709	G1649	A1589	C1529	A1468	A1408	A1348	U1288	C1228	G1164	U1104	A1042	C982
A1890	U	C1770	G1710	C1650	A1590	U1530	C1469	G1409	A1349	C1289	U1229	A1165	U1105	G1043	U983
A1891	A	G1711	C1711	C1651	U1591	U1591	C1470	A1410	A1350	U1290	U1230	U1166	A1106	G1044	U984
A1892	A	G1712	C1712	C1652	U1592	A1532	G1471	U1411	C1351	U1291	A1231	A1167	G1107	G1045	G985
C1893	A	U1773	U1713	G1653	U1593	A1533	C1472	A1412	U1352	G1292	G1232	G1168	G1108	A1046	A986
A1894	C	C1774	U1714	C1654	U1594	G1534	U1473	C1413	G1353	A1293	G1233	C1169	G1109	A1047	G987
A1895	A	G1715	C1715	A1655	G1595	A1535	A1474	C1414	G1354	U1294	G1234	U1170	G1110	A1048	C988
A1896	A	U1656	G1716	U1656	A1596	U1536	A1475	A1415	C1355	U1295	U1235	G1171	C1111	C1049	A989
A1897	A	G1657	A1717	G1657	A1597	G1537	G1476	A1416	C1356	U1296	C1236	G1172	G1112	C1050	U990
A1898	C	G1658	G1718	G1658	A1598	U1538	G1477	A1417	C1357	G1297	G1237	U1173	A1113	G1051	A991
A1899	G	A1659	G1719	A1659	C1599	A1539	A1478	A1418	U1358	A1298	G1238	G1174	A1114	U1052	U992
U1900	G	G1660	A1720	G1660	U1600	U1540	G1479	A1419	G1359	A1299	A1239	C1175	A1115	G1053	A993
G1901	A	U1781	C1721	G1661	A1601	A1541	U1480	A1420	U1360	G1300	A1240	A1176	G1116	A1054	U994
U1902	A	C1782	U1722	U1662	U1602	C1542	G1481	G1421	G1361	A1177	A1241	U1177	A1117	U1055	G995
U1903	U	A1783	G1723	G1663	A1603	C1543	U1482	G1422	G1362	U1302	U1178	U1178	C1118	G1056	C996
G1904	U	A1784	A1724	C1664	G1604	U1544	G1483	G1423	G1363	C1303	A1243	U1179	C1119	U997	U997
A1905	A	G1785	A1725	C1665	U1605	A1545	U1484	G1424	A1364	A1304	U1244	U1180	A1120	G998	G998
G1906	U	G1786	G1726	A1666	G1606	U1546	A1485	U1425	U1365	A1305	C1245	A1181	A1121	G1060	U999
U1907	A	C1787	U1727	U1667	A1607	U1547	A1486	U1426	G1366	G1306	U1246	A1182	A1122	G1061	G1000
A1908	A	G1788	G1728	U1668	G1608	C1548	C1487	G1427	A1367	G1307	U1247	A1183	C1123	C1062	A1001
U1909	U	A1789	G1729	G1669	U1609	A1549	A1488	G1428	A1368	U1308	A1248	G1124	G1124	C1063	C1002
C1910	A	A1790	A1730	G1670	A1610	U1550	A1489	A1429	C1369	U1309	A1249	A1125	A1125	G1064	C1003
C1911	C	A1791	G1731	G1671	G1611	U1551	C1490	U1430	C1370	A1310	C1250	U1190	A1126	A1065	C1004
G1912	A	A1792	A1732	A1672	G1612	A1552	U1491	G1431	A1371	U1311	C1251	A1191	C1127	A1066	G1005
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U1914	U	G1794	A1734	A1674	A1614	C1554	A1493	A1433	A1373	A1313	U1253	A1193	A1129	A1068	A1007
U1915	U	A1795	G1735	G1675	G1615	G1555	C1494	A1434	C1374	U1314	U1254	A1194	U1130	A1069	A1008
G1916	G	A1796	G1736	A1676	G1616	C1556	U1495	A1435	G1375	A1315	U1255	U1195	C1131	G1070	G1009
U1917	A	A1797	U1737	U1677	U1617	U1557	G1497	A1436	U1376	U1316	C1256	A1196	U1132	U1071	A1010
U1920	A	A1798	U1738	C1678	A1618	A1558	C1498	A1437	A1377	A1317	U1257	A1197	A1133	U1072	U1011
U1921	U1859	U1799	U1739	C1679	C1619	A1559	C1499	A1438	A1378	A1318	U1258	U1198	A1134	C1073	G1012
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A1923	U1861	U1801	G1741	G1681	A1621	G1561	A1501	A1440	G1380	U1320	A1260	U1200	A1136	G1075	U1014
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A1926	U1864	G1684	U1744	G1684	G1624	G1564	C1504	A1443	A1383	C1323	U1263	U1203	U1139	G1078	A1017
U1927	U1865	G1685	G1745	G1685	U1625	A1565	A1505	G1444	C1384	C1324	U1264	C1204	G1140	U1079	C1018
G1928	G1866	A1686	A1746	A1686	A1626	U1566	A1506	G1445	G1385	C1325	U1265	U1205	G1141	G1080	U1019
G1929	A1867	U1687	A1747	U1687	U1627	C1567	C1507	A1446	U1386	A1326	A1266	G1206	U1142	C1081	A1020
G1930	A1868	C1688	C1748	A1688	G1628	A1568	U1508	C1447	G1387	G1327	A1267	U1207	U1143	A1082	U1021
C1931	A1869	G1689	A1749	G1689	C1629	A1569	A1509	G1448	C1388	U1328	A1268	U1208	C1144	A1083	A1022
C1932	G1870	U1690	U1750	A1690	G1630	U1570	G1510	G1449	C1389	G1329	U1269	A1209	C1145	C1023	A1023
U1933	A1871	A1691	U1751	A1691	U1631	C1571	C1511	U1450	C1390	G1330	G1270	A1210	U1146	U1024	U1024
C1934	A1872	G1692	G1752	G1692	A1632	A1572	C1512	G1451	A1391	G1331	G1271	A1211	U1147	U1025	U1025
G1935	A1873	C1693	G1753	C1693	G1633	U1573	C1513	A1452	A1392	C1332	G1272	G1212	C1148	G1087	G1026
U1936	G1874	A1694	U1754	A1694	A1634	U1574	U1514	U1453	A1393	C1333	C1273	C1213	C1149	A1088	A1027
G1937	G1875	A1695	U1755	A1695	A1635	U1575	U1515	C1454	U1394	A1334	A1274	G1214	G1150	U1089	U1028
G1938	G1876	A1696	U1756	G1696	G1636	U1576	A1516	A1455	U1395	C1335	A1275	A1215	A1151	C1029	C1029
C1939	A1877	U1697	A1757	U1697	U1637	A1577	A1517	U1456	A1396	U1336	G1276	A1216	A1152	G1091	A1030
U1939	A1878	A1698	U1758	A1698	G1638	U1578	A1518	G1457	A1397	U1337	G1277	U1217	G1153	G1031	G1031
C1940	U1879	C1699	U1759	U1699	U1639	U1579	A1519	A1458	C1398	U1338	A1278	G1218	U1154	A1094	G1032
A1941	A1880	U1700	A1760	U1700	U1640	U1580	U1520	A1459	A1399	U1339	C1279	A1219	U1155	G1095	U1033
U1942	C1881	C1701	G1761	U1701	U1641	G1581	G1521	A1460	A1400	G1340	C1280	U1220	U1156	A1096	U1034
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C1944	G1883	A1703	A1763	A1703	G1643	A1583	A1523	U1462	U1402	U1342	U1282	A1222	C1158	U1098	A1036
U1945	U1884	A1704	C1764	A1704	C1644	U1584	U1524	C1463	C1403	A1343	U1283	G1223	C1159	U1099	A1037
G1946	U1885	U1705	G1765	U1705	G1645	U1585	G1525	A1464	A1404	A1344	A1284	A1224	U1160	G1100	G1038
G1947	C1886	U	U1766	G1706	U1646	A1586	G1526	A1465	U1405	G1345	C1285	G1225	C1161	A1101	U1039




U9392	C3872	A3811	C3751	A3690	C3630	C3570	U3510	G3450	U3390	C3330	G3269	G3209	U3149	U3070	U2969
G3933	A3873	C3812	G3752	A3691	C3631	C3571	U3511	A3451	U3391	A3331	G3270	A3210	G3150	U3071	U2970
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U3937	G3877	A3816	A3756	G3695	G3635	G3575	C3515	U3455	G3395	A3335	A3274	C3214	C3154	A3089	U2983
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A3940	A3880	C3819	G3759	A3698	U3638	A3578	A3518	A3458	C3398	U3338	A3277	A3217	U3157	U2986	U2986
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U3942	C3882	G3821	U3761	U3700	A3640	G3580	U3520	C3460	U3400	A3340	A3279	A3219	C3159	U3094	U2988
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G3964	G3904	C3843	A3783	C3722	G3662	C3602	C3542	G3482	A3422	G3362	G3302	G3241	G3181	C3120	U3010
A3965	A3905	U3844	C3784	A3723	U3663	C3603	A3543	G3483	U3423	G3363	C3303	A3242	U3182	A3121	C3011
U3966	U3906	A3845	A3785	U3724	A3664	G3604	G3544	U3484	U3424	C3364	U3304	C3243	G3183	A3122	A3012
U3967	G3907	U3846	U3786	U3725	U3665	A3605	C3545	U3485	G3425	G3365	U3305	U3244	U3184	G3123	C3013
C3968	U3908	U3847	A3787	U3726	C3666	G3606	A3546	U3486	U3426	G3366	U3306	U3245	C3185	G3124	G3014
G3969	A3909	U3848	C3788	A3727	C3667	C3607	U3547	A3487	G3427	A3307	A3307	G3246	C3186	A3125	A3015
A3970	A3910	A3849	U3789	A3728	G3668	G3608	U3548	G3488	A3428	C3368	A3308	A3247	C3187	C3126	G3016
	G3911	U3850	A3729	U3729	U3669	A3609	C3549	A3489	A3429	A3369	A3309	U3248	A3188	A3127	U3017
	U3912	U3851	G3730	G3730	G3670	C3610	C3550	C3490	G3430	A3370	G3310	C3249	A3189	U3128	U3018
	G3913	A3852	A3731	C3671	C3671	C3611	U3551	C3491	C3431	G3371	A3311	U3250	G3190	U3129	A3029
	G3914	C3853	U3732	U3672	U3672	A3612	G3552	G3492	A3432	C3372	G3312	G3251	G3191	G3130	A3024
	U3915	A3854	U3733	G3673	G3673	G3613	C3553	U3493	A3433	C3373	G3313	G3252	C3192	C3131	U3025
	U3916	A3855	A3734	G3674	G3674	U3614	G3554	C3494	A3434	U3374	U3314	G3253	C3193	C3132	A3026
	G3917	U3856	A3735	A3675	A3675	G3615	U3555	G3495	A3435	C3375	U3315	U3254	A3194	G3135	U3026
	A3918	C3857	C3676	C3676	C3676	G3616	A3556	U3496	U3436	C3376	G3316	G3255	G3195	U3136	U3029
	G3919	U3857	U3736	U3677	U3677	G3617	G3557	G3497	U3437	A3377	U3317	U3256	C3196	U3137	C3030
	A3921	A3861	U3737	C3678	C3678	A3618	U3558	A3498	C3438	U3378	U3318	U3257	U3197	A3137	G3031
	G3922	A3862	G3738	C3679	C3679	U3619	A3559	G3499	A3439	A3379	A3319	C3258	C3198	G3138	C3032
	C3923	U3863	U3741	A3680	A3680	G3620	C3560	A3500	C3440	G3380	C3320	A3259	A3199	G3139	A3033
	U3924	G3863	A3742	C3681	A3681	A3621	G3561	C3501	C3441	A3381	A3321	G3260	G3200	G3140	A3034
	G3925	C3864	C3743	U3682	U3682	C3622	A3562	A3502	A3442	G3382	A3322	U3261	U3201	A3141	C3035
	C3926	U3865	U3744	G3683	G3683	G3623	G3563	C3503	A3443	A3383	G3323	A3262	G3202	G3142	
	U3927	A3866	U3745	C3684	C3684	C3624	A3564	G3504	G3444	C3384	A3324	C3263	G3203	U3143	
	C3927	U3867	U3746	U3685	U3685	G3625	G3565	C3505	C3445	G3385	G3325	A3264	G3204	U3144	A3049
	A3928	G3868	A3746	A3686	A3686	A3626	G3566	U3506	G3446	U3386	G3326	C3265	G3205	U3145	A3050
	U3929	U3869	U3747	C3687	A3687	C3627	A3567	A3507	U3447	C3387	U3327	A3266	A3206	G3146	U3068
	A3930	A3870	U3748	A3688	A3688	G3628	A3568	C3508	U3448	C3388	G3328	C3267	C3207	A3147	
	C3931	U3871	A3750	U3629	U3629	U3629	C3569	U3509	G3449	C3389	U3329	A3268	A3208	C3148	U3069

- Molecule 84: 2S ribosomal RNA

Chain A9:  63% 23% 13%

U1 G2 G3 U4 U5 G6 G7 A8 C9 U10 A11 C12 A13 U14 A15 U16 G17 G18 U19 U20 G21 A22 G23 G24 G25 U26 U27 G28 U29 A30

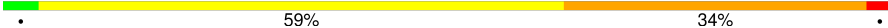
- Molecule 85: 5S ribosomal RNA

Chain A7:  63% 33%

G1 C2 C3 A4 A5 C6 G7 A8 C9 C10 G11 U12 U13 A14 C15 A16 G17 G18 C19 U20 G21 A22 A23 U24 A25 C26 A27 U28 C29 G30 G31 U32 U33 C34 U35 U36 G37 G38 C39 C40 A41 A42 U43 C44 A45 C46 G47 G48 G49 A50 A51 U52 U53 A54 A55 G56 C57 A58 U59 C60

G61 U62 C63 G64 A65 G66 G67 A68 C69 G70 G71 U72 U73 A74 G75 A76 U77 G78 U79 U80 A81 G82 A83 U84 A85 G86 G87 A88 C89 G90 G91 C92 C93 G94 U95 U96 G97 G98 G99 A100 A101 G102 A103 C104 C105 G106 G107 G108 U109 A110 G111 U112 G113 U114 U115 G116 G117 C118 G119 U120

- Molecule 86: 5.8S ribosomal RNA

Chain A8:  59% 34%

A1 A2 C3 U4 C5 U6 A7 A8 G9 C10 G11 G12 U13 G14 G15 A16 U17 C18 A19 C20 U21 C22 G23 G24 C25 U26 C27 A28 U29 U30 G31 C32 G33 U34 C35 A36 U37 G38 A39 A40 A41 G42 A43 C44 G45 C46 G47 G48 C49 A50 A51 A52 C53 U54 G55 U56 G57 C58 G59 U60

G61 A62 C63 G64 U65 G66 G67 U68 G69 A70 G71 G72 U73 G74 A75 A76 G77 G78 A79 C80 A81 C82 A83 U84 G85 A86 A87 A88 C89 U90 C91 G92 G93 A94 A95 U96 U97 U98 U99 G100 A101 A102 C103 G104 C105 A106 U107 U108 U109 C110 G111 C112 A113 G114 U115 U116 C117 A118 U119 G120

G121 U122 G123

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	134500	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	each subvolume	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	90000	Depositor
Image detector	Eagle 4k CCD	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	Az	1.21	2/6704 (0.0%)	1.68	114/9051 (1.3%)
10	AN	1.26	1/1225 (0.1%)	1.45	13/1641 (0.8%)
11	AL	1.35	2/1296 (0.2%)	1.53	12/1725 (0.7%)
12	AR	1.26	1/993 (0.1%)	1.41	6/1333 (0.5%)
13	AP	1.22	0/1036	1.44	8/1383 (0.6%)
14	AT	1.23	0/1228	1.51	12/1653 (0.7%)
15	AB	1.24	2/1825 (0.1%)	1.49	22/2448 (0.9%)
16	AA	1.25	3/1777 (0.2%)	1.63	29/2422 (1.2%)
17	AV	1.29	0/622	1.47	4/835 (0.5%)
18	AY	2.40	7/1032 (0.7%)	1.64	17/1373 (1.2%)
19	AZ	1.27	1/616 (0.2%)	1.61	10/826 (1.2%)
2	Ag	1.19	0/2574	1.46	21/3506 (0.6%)
20	Aa	1.34	2/883 (0.2%)	1.65	18/1184 (1.5%)
21	Ab	1.28	1/668 (0.1%)	1.48	4/898 (0.4%)
22	Ac	1.41	0/502	1.46	2/670 (0.3%)
23	AD	1.28	4/1808 (0.2%)	1.50	13/2427 (0.5%)
24	Ae	1.33	1/475 (0.2%)	1.53	7/625 (1.1%)
25	Af	1.30	3/672 (0.4%)	1.69	11/887 (1.2%)
26	AJ	1.34	6/1526 (0.4%)	1.65	23/2037 (1.1%)
27	AE	1.27	6/2096 (0.3%)	1.54	27/2819 (1.0%)
28	AC	1.24	3/1785 (0.2%)	1.57	26/2415 (1.1%)
29	AG	1.31	0/1891	1.61	34/2519 (1.3%)
3	AU	1.26	1/825 (0.1%)	1.52	9/1111 (0.8%)
30	AF	1.28	2/1518 (0.1%)	1.53	21/2037 (1.0%)
31	AH	1.25	2/1593 (0.1%)	1.63	19/2145 (0.9%)
32	AW	1.26	3/1046 (0.3%)	1.51	14/1402 (1.0%)
33	AI	1.31	2/1689 (0.1%)	1.62	29/2250 (1.3%)
34	AQ	1.30	1/1202 (0.1%)	1.70	25/1608 (1.6%)
35	Ah	1.37	1/495 (0.2%)	1.76	13/658 (2.0%)
36	B2	2.32	1859/44058 (4.2%)	2.09	2463/68404 (3.6%)
37	BC	2.25	72/1796 (4.0%)	1.89	84/2800 (3.0%)
38	Cz	1.18	0/1727	1.43	7/2308 (0.3%)
39	Cq	1.20	2/1736 (0.1%)	1.56	24/2342 (1.0%)
4	AK	1.20	0/819	1.52	10/1110 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	CK	1.19	1/1196 (0.1%)	1.57	13/1614 (0.8%)
41	CO	1.33	4/1700 (0.2%)	1.51	22/2277 (1.0%)
42	CL	1.35	4/1726 (0.2%)	1.76	47/2308 (2.0%)
43	CV	1.28	1/1014 (0.1%)	1.52	14/1362 (1.0%)
44	CM	1.37	1/1326 (0.1%)	1.65	20/1780 (1.1%)
45	Ca	1.28	2/1235 (0.2%)	1.66	29/1640 (1.8%)
46	CN	1.43	8/1750 (0.5%)	1.62	26/2335 (1.1%)
47	CI	1.33	2/1827 (0.1%)	1.54	14/2447 (0.6%)
48	CD	1.32	2/2379 (0.1%)	1.55	31/3196 (1.0%)
49	CQ	1.34	3/1544 (0.2%)	1.64	40/2069 (1.9%)
5	AO	1.27	1/1016 (0.1%)	1.59	17/1364 (1.2%)
50	CR	1.27	3/1703 (0.2%)	1.46	19/2255 (0.8%)
51	CA	1.33	4/1970 (0.2%)	1.61	29/2635 (1.1%)
52	CS	1.29	1/1491 (0.1%)	1.66	26/1998 (1.3%)
53	CT	1.28	3/1326 (0.2%)	1.53	13/1773 (0.7%)
54	CP	1.31	2/1529 (0.1%)	1.50	16/2042 (0.8%)
55	CU	1.21	1/974 (0.1%)	1.46	6/1302 (0.5%)
56	CX	1.27	1/1001 (0.1%)	1.58	7/1348 (0.5%)
57	CY	1.36	3/1094 (0.3%)	1.51	14/1456 (1.0%)
58	CW	1.29	1/1063 (0.1%)	1.55	9/1410 (0.6%)
59	CZ	1.28	1/1141 (0.1%)	1.56	10/1517 (0.7%)
6	AX	1.30	1/1152 (0.1%)	1.50	11/1540 (0.7%)
60	Cr	1.29	0/1069	1.70	20/1432 (1.4%)
61	Ch	1.30	0/1024	1.45	8/1353 (0.6%)
62	Cb	1.29	2/628 (0.3%)	1.67	12/832 (1.4%)
63	CB	1.24	3/3356 (0.1%)	1.61	41/4494 (0.9%)
64	CF	1.31	2/1958 (0.1%)	1.56	29/2622 (1.1%)
65	Cc	1.20	1/779 (0.1%)	1.55	9/1048 (0.9%)
66	Cd	1.28	0/939	1.54	10/1262 (0.8%)
67	Ce	1.36	1/1132 (0.1%)	1.54	13/1508 (0.9%)
68	Cf	1.33	0/1270	1.74	22/1696 (1.3%)
69	Cg	1.44	2/938 (0.2%)	1.65	19/1252 (1.5%)
7	AM	1.15	0/937	1.59	15/1260 (1.2%)
70	Ci	1.30	1/944 (0.1%)	1.62	16/1250 (1.3%)
71	Cj	1.41	1/750 (0.1%)	1.47	5/993 (0.5%)
72	Ck	1.26	0/583	1.72	10/774 (1.3%)
73	Cl	1.39	0/445	1.46	3/589 (0.5%)
74	CC	1.32	5/3163 (0.2%)	1.57	43/4253 (1.0%)
75	Cm	1.24	0/435	1.51	4/575 (0.7%)
76	Cn	1.55	0/237	1.43	3/300 (1.0%)
77	Cp	1.30	0/719	1.49	9/954 (0.9%)
78	Co	1.30	2/887 (0.2%)	1.63	15/1162 (1.3%)
79	CJ	1.30	3/1494 (0.2%)	1.53	15/2001 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	AS	1.25	1/1146 (0.1%)	1.64	19/1535 (1.2%)
80	CH	1.21	0/1519	1.54	23/2042 (1.1%)
81	CE	1.29	3/1883 (0.2%)	1.75	45/2514 (1.8%)
82	CG	1.26	7/1968 (0.4%)	1.47	21/2637 (0.8%)
83	A5	2.33	3665/87035 (4.2%)	2.12	5062/135254 (3.7%)
84	A9	2.28	39/714 (5.5%)	2.32	45/1112 (4.0%)
85	A7	2.35	134/2854 (4.7%)	2.03	160/4447 (3.6%)
86	A8	2.29	115/2932 (3.9%)	2.05	138/4568 (3.0%)
9	Ad	1.38	0/443	1.61	7/589 (1.2%)
All	All	1.95	6027/247076 (2.4%)	1.91	9425/360828 (2.6%)

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	Az	105	86
10	AN	0	6
11	AL	0	9
12	AR	0	5
13	AP	1	4
14	AT	2	11
15	AB	0	4
16	AA	0	6
17	AV	0	2
18	AY	0	11
19	AZ	1	2
2	Ag	0	4
20	Aa	1	6
21	Ab	0	4
22	Ac	0	3
23	AD	1	10
24	Ae	0	2
25	Af	0	10
26	AJ	0	7
27	AE	0	13
28	AC	0	14
29	AG	0	11
3	AU	0	3
30	AF	0	7
31	AH	2	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	AW	0	2
33	AI	0	12
34	AQ	0	12
35	Ah	0	6
36	B2	1	0
38	Cz	1	2
39	Cq	1	16
4	AK	0	8
40	CK	0	13
41	CO	0	9
42	CL	29	21
43	CV	0	4
44	CM	2	15
45	Ca	1	12
46	CN	1	13
47	CI	0	11
48	CD	1	8
49	CQ	0	7
5	AO	2	1
50	CR	0	5
51	CA	0	8
52	CS	28	22
53	CT	1	12
54	CP	1	4
55	CU	0	4
56	CX	1	4
57	CY	0	4
58	CW	0	10
59	CZ	0	6
6	AX	0	3
60	Cr	0	14
61	Ch	0	3
62	Cb	0	4
63	CB	1	24
64	CF	1	7
65	Cc	0	5
66	Cd	1	3
67	Ce	0	8
68	Cf	7	22
69	Cg	0	7
7	AM	1	7
70	Ci	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
71	Cj	0	3
72	Ck	0	2
73	Cl	0	4
74	CC	1	21
75	Cm	0	2
76	Cn	0	2
77	Cp	0	2
78	Co	0	5
79	CJ	1	10
8	AS	0	6
80	CH	1	11
81	CE	3	26
82	CG	1	7
83	A5	7	0
9	Ad	0	4
All	All	208	716

The worst 5 of 6027 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	A5	1668	U	C2'-C1'	-31.14	1.19	1.53
36	B2	1320	G	C2'-C1'	-30.14	1.20	1.53
18	AY	77	TYR	CE1-CZ	30.11	1.77	1.38
18	AY	77	TYR	CE2-CZ	28.88	1.76	1.38
18	AY	77	TYR	CG-CD1	27.53	1.75	1.39

The worst 5 of 9425 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	A5	3514	C	O4'-C1'-N1	37.72	138.37	108.20
83	A5	3368	C	O4'-C1'-N1	35.09	136.28	108.20
36	B2	1087	C	O4'-C1'-N1	32.98	134.59	108.20
83	A5	3676	C	O4'-C1'-N1	31.58	133.46	108.20
83	A5	2491	C	O4'-C1'-N1	31.03	133.03	108.20

5 of 208 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Az	4	PHE	CA
1	Az	15	LYS	CA
1	Az	49	ALA	CA
1	Az	55	ARG	CA

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Mol	Chain	Res	Type	Atom
1	Az	68	ILE	CA

5 of 716 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Az	14	ASP	Peptide
1	Az	20	ARG	Sidechain
1	Az	27	HIS	Peptide
1	Az	47	ALA	Peptide
1	Az	49	ALA	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	Az	6574	0	6616	0	0
2	Ag	2511	0	2438	0	0
3	AU	815	0	871	0	0
4	AK	797	0	817	6	0
5	AO	1003	0	1035	8	0
6	AX	1131	0	1190	4	0
7	AM	924	0	960	17	0
8	AS	1128	0	1177	13	0
9	Ad	433	0	424	0	0
10	AN	1202	0	1291	4	0
11	AL	1274	0	1351	9	0
12	AR	981	0	1038	0	0
13	AP	1016	0	1086	6	0
14	AT	1203	0	1250	7	0
15	AB	1798	0	1867	11	0
16	AA	1737	0	1750	7	0
17	AV	617	0	613	1	0
18	AY	1016	0	1073	17	0
19	AZ	608	0	658	5	0
20	Aa	867	0	920	0	0
21	Ab	653	0	680	0	0
22	Ac	498	0	525	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AD	1782	0	1862	4	0
24	Ae	469	0	503	0	0
25	Af	659	0	695	0	0
26	AJ	1503	0	1620	34	0
27	AE	2054	0	2165	10	0
28	AC	1746	0	1827	12	0
29	AG	1866	0	2028	16	0
30	AF	1497	0	1556	9	0
31	AH	1566	0	1664	9	0
32	AW	1028	0	1071	9	0
33	AI	1665	0	1746	3	0
34	AQ	1183	0	1255	10	0
35	Ah	486	0	458	0	0
36	B2	39523	0	19572	367	0
37	BC	1605	0	814	15	0
38	Cz	1702	0	1814	0	0
39	Cq	1710	0	1777	0	0
40	CK	1180	0	1246	6	0
41	CO	1668	0	1783	13	0
42	CL	1695	0	1790	21	0
43	CV	998	0	1046	2	0
44	CM	1302	0	1388	22	0
45	Ca	1204	0	1260	0	0
46	CN	1710	0	1778	10	0
47	CI	1785	0	1805	16	0
48	CD	2334	0	2354	24	0
49	CQ	1518	0	1626	10	0
50	CR	1683	0	1827	5	0
51	CA	1935	0	2037	22	0
52	CS	1454	0	1503	21	0
53	CT	1297	0	1364	5	0
54	CP	1505	0	1556	5	0
55	CU	961	0	975	2	0
56	CX	984	0	1058	4	0
57	CY	1078	0	1159	8	0
58	CW	1047	0	1140	4	0
59	CZ	1115	0	1199	7	0
60	Cr	1051	0	1148	0	0
61	Ch	1015	0	1163	0	0
62	Cb	619	0	650	0	0
63	CB	3287	0	3432	52	0
64	CF	1921	0	2039	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	Cc	770	0	802	0	0
66	Cd	924	0	942	0	0
67	Ce	1110	0	1181	0	0
68	Cf	1244	0	1316	0	0
69	Cg	926	0	1013	0	0
70	Ci	934	0	1029	0	0
71	Cj	737	0	770	0	0
72	Ck	576	0	633	0	0
73	Cl	437	0	483	0	0
74	CC	3109	0	3298	23	0
75	Cm	429	0	472	0	0
76	Cn	236	0	286	0	0
77	Cp	710	0	756	0	0
78	Co	874	0	956	0	0
79	CJ	1468	0	1507	10	0
80	CH	1499	0	1569	12	0
81	CE	1845	0	1981	27	0
82	CG	1936	0	2103	4	0
83	A5	77967	0	38740	799	0
84	A9	639	0	321	5	0
85	A7	2554	0	1296	37	0
86	A8	2621	0	1328	45	0
All	All	230721	0	173165	1591	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 5.

The worst 5 of 1591 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)
18:AY:77:TYR:CZ	18:AY:77:TYR:CE1	1.77	1.73
18:AY:77:TYR:CG	18:AY:77:TYR:CD1	1.74	1.64
18:AY:77:TYR:CE2	18:AY:77:TYR:CZ	1.76	1.63
83:A5:3843:U:C2'	83:A5:3843:U:C1'	1.74	1.47
42:CL:59:ARG:HG2	83:A5:77:A:N3	1.17	1.44

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	Az	835/844 (99%)	647 (78%)	96 (12%)	92 (11%)	0	11
2	Ag	316/318 (99%)	274 (87%)	25 (8%)	17 (5%)	2	29
3	AU	100/120 (83%)	84 (84%)	6 (6%)	10 (10%)	1	14
4	AK	93/163 (57%)	75 (81%)	7 (8%)	11 (12%)	0	9
5	AO	132/151 (87%)	104 (79%)	13 (10%)	15 (11%)	0	10
6	AX	141/143 (99%)	118 (84%)	15 (11%)	8 (6%)	2	27
7	AM	117/139 (84%)	85 (73%)	16 (14%)	16 (14%)	0	6
8	AS	135/152 (89%)	107 (79%)	16 (12%)	12 (9%)	1	17
9	Ad	50/56 (89%)	30 (60%)	10 (20%)	10 (20%)	0	3
10	AN	148/151 (98%)	136 (92%)	7 (5%)	5 (3%)	5	40
11	AL	153/155 (99%)	128 (84%)	16 (10%)	9 (6%)	2	26
12	AR	118/131 (90%)	99 (84%)	12 (10%)	7 (6%)	2	26
13	AP	122/148 (82%)	95 (78%)	13 (11%)	14 (12%)	0	9
14	AT	152/156 (97%)	125 (82%)	17 (11%)	10 (7%)	1	24
15	AB	218/268 (81%)	179 (82%)	23 (11%)	16 (7%)	1	21
16	AA	216/313 (69%)	174 (81%)	22 (10%)	20 (9%)	1	16
17	AV	80/83 (96%)	64 (80%)	6 (8%)	10 (12%)	0	8
18	AY	124/131 (95%)	96 (77%)	10 (8%)	18 (14%)	0	6
19	AZ	72/117 (62%)	49 (68%)	11 (15%)	12 (17%)	0	5
20	Aa	105/114 (92%)	75 (71%)	14 (13%)	16 (15%)	0	5
21	Ab	82/84 (98%)	64 (78%)	12 (15%)	6 (7%)	1	21
22	Ac	60/65 (92%)	53 (88%)	1 (2%)	6 (10%)	1	14
23	AD	225/246 (92%)	183 (81%)	29 (13%)	13 (6%)	2	27
24	Ae	56/132 (42%)	37 (66%)	10 (18%)	9 (16%)	0	5
25	Af	78/80 (98%)	46 (59%)	15 (19%)	17 (22%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AJ	179/195 (92%)	148 (83%)	17 (10%)	14 (8%)	1	20
27	AE	259/261 (99%)	204 (79%)	37 (14%)	18 (7%)	1	22
28	AC	225/267 (84%)	186 (83%)	17 (8%)	22 (10%)	1	14
29	AG	229/248 (92%)	196 (86%)	20 (9%)	13 (6%)	2	27
30	AF	188/228 (82%)	152 (81%)	20 (11%)	16 (8%)	1	17
31	AH	192/194 (99%)	147 (77%)	28 (15%)	17 (9%)	1	17
32	AW	127/130 (98%)	114 (90%)	10 (8%)	3 (2%)	7	47
33	AI	205/208 (99%)	164 (80%)	12 (6%)	29 (14%)	0	6
34	AQ	146/148 (99%)	114 (78%)	14 (10%)	18 (12%)	0	8
35	Ah	54/121 (45%)	31 (57%)	6 (11%)	17 (32%)	0	0
38	Cz	215/218 (99%)	186 (86%)	17 (8%)	12 (6%)	2	28
39	Cq	221/223 (99%)	183 (83%)	21 (10%)	17 (8%)	1	20
40	CK	156/165 (94%)	95 (61%)	29 (19%)	32 (20%)	0	3
41	CO	203/205 (99%)	183 (90%)	12 (6%)	8 (4%)	4	36
42	CL	208/218 (95%)	141 (68%)	28 (14%)	39 (19%)	0	3
43	CV	132/140 (94%)	116 (88%)	13 (10%)	3 (2%)	8	48
44	CM	157/166 (95%)	123 (78%)	20 (13%)	14 (9%)	1	17
45	Ca	147/149 (99%)	116 (79%)	17 (12%)	14 (10%)	1	15
46	CN	201/204 (98%)	175 (87%)	20 (10%)	6 (3%)	5	42
47	CI	215/218 (99%)	176 (82%)	19 (9%)	20 (9%)	1	16
48	CD	288/299 (96%)	242 (84%)	20 (7%)	26 (9%)	1	17
49	CQ	185/188 (98%)	153 (83%)	18 (10%)	14 (8%)	1	20
50	CR	201/203 (99%)	187 (93%)	7 (4%)	7 (4%)	4	39
51	CA	251/256 (98%)	205 (82%)	27 (11%)	19 (8%)	1	20
52	CS	171/177 (97%)	131 (77%)	18 (10%)	22 (13%)	0	7
53	CT	156/159 (98%)	122 (78%)	17 (11%)	17 (11%)	0	11
54	CP	183/186 (98%)	154 (84%)	16 (9%)	13 (7%)	1	22
55	CU	114/299 (38%)	88 (77%)	18 (16%)	8 (7%)	1	22
56	CX	118/277 (43%)	96 (81%)	15 (13%)	7 (6%)	2	26
57	CY	129/149 (87%)	113 (88%)	9 (7%)	7 (5%)	2	29
58	CW	128/155 (83%)	102 (80%)	12 (9%)	14 (11%)	0	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	CZ	132/135 (98%)	111 (84%)	15 (11%)	6 (4%)	3	33
60	Cr	132/144 (92%)	88 (67%)	22 (17%)	22 (17%)	0	5
61	Ch	121/123 (98%)	99 (82%)	10 (8%)	12 (10%)	1	14
62	Cb	73/76 (96%)	53 (73%)	11 (15%)	9 (12%)	0	8
63	CB	412/416 (99%)	325 (79%)	56 (14%)	31 (8%)	1	20
64	CF	227/252 (90%)	195 (86%)	17 (8%)	15 (7%)	1	24
65	Cc	98/111 (88%)	91 (93%)	3 (3%)	4 (4%)	3	35
66	Cd	109/124 (88%)	91 (84%)	14 (13%)	4 (4%)	4	37
67	Ce	130/134 (97%)	101 (78%)	16 (12%)	13 (10%)	1	14
68	Cf	155/157 (99%)	115 (74%)	14 (9%)	26 (17%)	0	5
69	Cg	111/162 (68%)	92 (83%)	12 (11%)	7 (6%)	2	25
70	Ci	111/115 (96%)	82 (74%)	16 (14%)	13 (12%)	0	9
71	Cj	90/93 (97%)	75 (83%)	9 (10%)	6 (7%)	1	23
72	Ck	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	3	33
73	Cl	48/51 (94%)	40 (83%)	4 (8%)	4 (8%)	1	18
74	CC	390/401 (97%)	309 (79%)	36 (9%)	45 (12%)	0	9
75	Cm	50/52 (96%)	38 (76%)	6 (12%)	6 (12%)	0	8
76	Cn	23/25 (92%)	22 (96%)	0	1 (4%)	3	34
77	Cp	89/92 (97%)	77 (86%)	8 (9%)	4 (4%)	3	33
78	Co	102/104 (98%)	79 (78%)	10 (10%)	13 (13%)	0	8
79	CJ	180/184 (98%)	139 (77%)	17 (9%)	24 (13%)	0	7
80	CH	188/190 (99%)	160 (85%)	16 (8%)	12 (6%)	2	25
81	CE	226/243 (93%)	149 (66%)	34 (15%)	43 (19%)	0	3
82	CG	239/271 (88%)	197 (82%)	22 (9%)	20 (8%)	1	18
All	All	13015/14439 (90%)	10459 (80%)	1348 (10%)	1208 (9%)	2	16

5 of 1208 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Az	5	THR
1	Az	15	LYS
1	Az	44	GLY
1	Az	54	THR
1	Az	82	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	Az	721/726 (99%)	667 (92%)	54 (8%)	17	54
2	Ag	280/280 (100%)	268 (96%)	12 (4%)	35	70
3	AU	95/108 (88%)	93 (98%)	2 (2%)	61	84
4	AK	88/132 (67%)	80 (91%)	8 (9%)	12	44
5	AO	103/118 (87%)	92 (89%)	11 (11%)	8	36
6	AX	116/116 (100%)	109 (94%)	7 (6%)	24	61
7	AM	104/119 (87%)	98 (94%)	6 (6%)	25	61
8	AS	123/136 (90%)	120 (98%)	3 (2%)	57	82
9	Ad	45/47 (96%)	43 (96%)	2 (4%)	35	69
10	AN	130/131 (99%)	122 (94%)	8 (6%)	23	60
11	AL	138/138 (100%)	130 (94%)	8 (6%)	25	61
12	AR	108/118 (92%)	98 (91%)	10 (9%)	11	43
13	AP	111/130 (85%)	105 (95%)	6 (5%)	27	64
14	AT	125/127 (98%)	113 (90%)	12 (10%)	10	41
15	AB	199/233 (85%)	182 (92%)	17 (8%)	13	48
16	AA	190/271 (70%)	178 (94%)	12 (6%)	22	59
17	AV	67/68 (98%)	61 (91%)	6 (9%)	12	44
18	AY	105/110 (96%)	103 (98%)	2 (2%)	65	86
19	AZ	67/100 (67%)	57 (85%)	10 (15%)	4	24
20	Aa	94/101 (93%)	92 (98%)	2 (2%)	61	84
21	Ab	72/72 (100%)	69 (96%)	3 (4%)	36	70
22	Ac	54/57 (95%)	50 (93%)	4 (7%)	17	54
23	AD	192/210 (91%)	179 (93%)	13 (7%)	20	57
24	Ae	47/108 (44%)	45 (96%)	2 (4%)	35	70
25	Af	70/70 (100%)	58 (83%)	12 (17%)	2	18
26	AJ	161/169 (95%)	152 (94%)	9 (6%)	26	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	AE	220/220 (100%)	209 (95%)	11 (5%)	30	66
28	AC	188/209 (90%)	178 (95%)	10 (5%)	28	64
29	AG	200/216 (93%)	185 (92%)	15 (8%)	17	54
30	AF	161/193 (83%)	156 (97%)	5 (3%)	47	77
31	AH	175/175 (100%)	157 (90%)	18 (10%)	9	37
32	AW	113/114 (99%)	107 (95%)	6 (5%)	28	64
33	AI	175/176 (99%)	167 (95%)	8 (5%)	33	68
34	AQ	122/122 (100%)	115 (94%)	7 (6%)	25	62
35	Ah	51/100 (51%)	47 (92%)	4 (8%)	16	52
38	Cz	190/191 (100%)	173 (91%)	17 (9%)	12	44
39	Cq	186/186 (100%)	170 (91%)	16 (9%)	13	47
40	CK	131/137 (96%)	126 (96%)	5 (4%)	40	73
41	CO	175/175 (100%)	158 (90%)	17 (10%)	10	40
42	CL	173/180 (96%)	157 (91%)	16 (9%)	11	43
43	CV	101/106 (95%)	100 (99%)	1 (1%)	82	92
44	CM	138/142 (97%)	124 (90%)	14 (10%)	9	38
45	Ca	122/122 (100%)	112 (92%)	10 (8%)	14	49
46	CN	174/175 (99%)	165 (95%)	9 (5%)	29	65
47	CI	187/188 (100%)	181 (97%)	6 (3%)	46	76
48	CD	241/248 (97%)	234 (97%)	7 (3%)	50	78
49	CQ	164/165 (99%)	151 (92%)	13 (8%)	15	51
50	CR	176/176 (100%)	171 (97%)	5 (3%)	51	78
51	CA	195/198 (98%)	180 (92%)	15 (8%)	16	53
52	CS	156/159 (98%)	142 (91%)	14 (9%)	12	44
53	CT	137/138 (99%)	129 (94%)	8 (6%)	25	61
54	CP	160/161 (99%)	153 (96%)	7 (4%)	35	69
55	CU	108/203 (53%)	104 (96%)	4 (4%)	41	73
56	CX	106/205 (52%)	102 (96%)	4 (4%)	40	73
57	CY	116/130 (89%)	114 (98%)	2 (2%)	68	87
58	CW	107/124 (86%)	100 (94%)	7 (6%)	21	58
59	CZ	121/122 (99%)	108 (89%)	13 (11%)	8	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	Cr	112/120 (93%)	102 (91%)	10 (9%)	12	44
61	Ch	112/112 (100%)	110 (98%)	2 (2%)	66	87
62	Cb	67/68 (98%)	62 (92%)	5 (8%)	17	54
63	CB	349/350 (100%)	335 (96%)	14 (4%)	38	71
64	CF	203/222 (91%)	194 (96%)	9 (4%)	35	69
65	Cc	84/93 (90%)	78 (93%)	6 (7%)	18	55
66	Cd	103/114 (90%)	96 (93%)	7 (7%)	20	57
67	Ce	120/122 (98%)	108 (90%)	12 (10%)	9	38
68	Cf	123/123 (100%)	111 (90%)	12 (10%)	10	40
69	Cg	104/137 (76%)	97 (93%)	7 (7%)	20	57
70	Ci	100/101 (99%)	89 (89%)	11 (11%)	8	34
71	Cj	77/78 (99%)	67 (87%)	10 (13%)	5	28
72	Ck	65/65 (100%)	59 (91%)	6 (9%)	11	43
73	Cl	45/46 (98%)	43 (96%)	2 (4%)	35	69
74	CC	323/329 (98%)	294 (91%)	29 (9%)	12	44
75	Cm	48/48 (100%)	47 (98%)	1 (2%)	61	84
76	Cn	23/23 (100%)	21 (91%)	2 (9%)	13	45
77	Cp	74/75 (99%)	71 (96%)	3 (4%)	37	71
78	Co	94/94 (100%)	89 (95%)	5 (5%)	28	64
79	CJ	155/157 (99%)	148 (96%)	7 (4%)	34	69
80	CH	169/169 (100%)	156 (92%)	13 (8%)	16	53
81	CE	197/208 (95%)	177 (90%)	20 (10%)	9	37
82	CG	210/237 (89%)	196 (93%)	14 (7%)	20	57
All	All	11331/12242 (93%)	10589 (94%)	742 (6%)	26	58

5 of 742 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Cz	157	PHE
45	Ca	73	GLU
78	Co	64	LYS
39	Cq	48	ARG
41	CO	182	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
42	CL	11	GLN
48	CD	285	HIS
78	Co	3	ASN
42	CL	14	HIS
45	Ca	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	B2	1794/1995 (89%)	501 (27%)	117 (6%)
37	BC	74/75 (98%)	12 (16%)	3 (4%)
83	A5	3568/3970 (89%)	947 (26%)	263 (7%)
84	A9	29/30 (96%)	7 (24%)	2 (6%)
85	A7	119/120 (99%)	23 (19%)	5 (4%)
86	A8	122/123 (99%)	18 (14%)	4 (3%)
All	All	5706/6313 (90%)	1508 (26%)	394 (6%)

5 of 1508 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	B2	2	U
36	B2	3	U
36	B2	4	C
36	B2	8	U
36	B2	16	G

5 of 394 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	A5	641	A
83	A5	1293	A
83	A5	3808	A
83	A5	675	C
83	A5	1016	A

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.