

Sequence	Helices		Helix Classes		Features		H:HC		HC:F		H:F	
	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev
V1	118.8	5.7	50.7	3.1	6.5	0.7	2.4	0.2	7.9	1.2	<b>18.5</b>	2.7
V2	177.1	7.9	81.5	4.9	6.6	0.6	2.2	0.1	<b>12.4</b>	1.4	<b>26.9</b>	2.6
V3	<b>158.3</b>	8.1	<b>68.5</b>	4.2	8.1	0.7	2.3	0.1	8.6	1.1	19.8	2.2
T1	133.7	6.5	59.0	3.9	10.4	0.8	2.3	0.1	5.7	0.6	12.9	1.4
T2	98.4	8.0	43.4	5.1	6.8	0.4	2.3	0.1	6.3	0.7	14.4	1.2
T3	102.7	6.0	49.8	4.3	<b>5.0</b>	0.2	2.1	0.1	9.9	0.9	20.4	1.3
S1	238.4	10.1	129.2	8.2	11.2	0.5	<b>1.8</b>	0.1	11.6	1.0	21.4	1.4
S2	106.4	5.9	47.2	4.6	13.0	0.2	2.3	0.2	3.6	0.4	8.2	0.5
S3	<b>64.6</b>	7.0	<b>23.0</b>	2.5	10.3	0.5	<b>2.8</b>	0.2	<b>2.2</b>	0.3	<b>6.3</b>	0.7
H1	211.8	10.0	108.2	6.6	9.0	0.000	2.0	0.1	12.0	0.7	23.5	1.1
H2	220.2	6.4	79.0	4.7	<b>9.5</b>	0.5	2.8	0.1	<b>8.3</b>	0.6	23.3	1.4
H3	189.1	7.1	79.3	4.7	11.3	0.5	2.4	0.1	7.0	0.5	16.8	0.9
P1	<b>309.7</b>	10.0	<b>163.2</b>	7.1	<b>13.9</b>	0.3	1.9	0.1	11.8	0.5	22.3	0.9
P2	172.1	9.7	86.6	5.6	9.8	0.8	2.0	0.1	8.9	1.0	17.7	2.0
P3	94.8	6.3	41.7	3.7	8.0	0.2	<b>2.3</b>	0.1	5.2	0.5	11.8	0.9

Table 1: Data for Fig. 6a: the average and standard deviation in number of helices, helix classes and features, with amplification ratios calculated as average number of helices to helix classes, helix classes to features, and helices to features. Median, minimum and maximum values for averages are bolded.

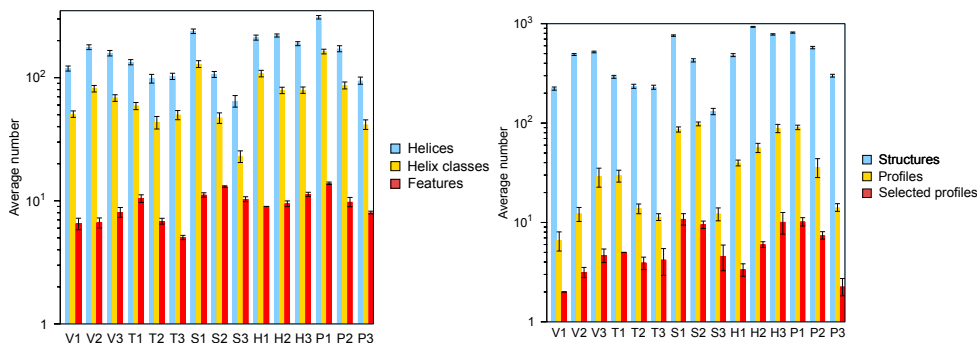


Figure 1: The average number of (left) helices, helix classes and features across 25 samples, and (right) structures, profiles and selected profiles across 25 samples, with bars indicating standard deviation. Log scale is used for additional clarity.

Sequence	Structures		Profiles		S. Profiles		S:P		P:SP		S:SP	
	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev	Ave	Stdev
V1	222.5	8.3	<b>6.6</b>	1.4	<b>2.0</b>	0.0	35.9	10.3	3.3	0.7	111.2	4.1
V2	489.8	10.9	12.2	2.0	3.2	0.4	<b>41.2</b>	6.7	3.9	0.5	<b>156.7</b>	15.0
V3	519.5	10.1	28.9	6.3	<b>4.7</b>	0.7	18.9	4.4	<b>6.3</b>	1.8	114.1	20.0
T1	292.1	9.8	<b>29.5</b>	4.0	5.0	0.0	10.1	1.5	5.9	0.8	58.4	2.0
T2	234.7	11.1	13.8	1.5	3.9	0.6	17.2	2.0	3.6	0.7	61.0	8.6
T3	229.7	10.8	11.4	0.9	4.2	1.3	20.3	1.7	3.1	1.3	61.8	24.8
S1	759.1	12.9	86.4	5.1	<b>10.8</b>	1.4	8.8	0.5	8.1	1.1	71.3	9.8
S2	427.9	16.1	<b>98.2</b>	4.3	9.5	0.8	<b>4.4</b>	0.2	10.4	1.1	45.3	4.8
S3	<b>131.0</b>	9.6	12.2	1.8	4.6	1.3	11.0	1.8	<b>3.0</b>	1.3	<b>32.0</b>	13.8
H1	<b>483.2</b>	16.5	39.8	2.7	3.4	0.5	12.2	1.0	<b>12.1</b>	2.0	146.4	18.9
H2	<b>929.6</b>	9.4	56.5	6.0	6.0	0.4	<b>16.6</b>	1.8	9.5	1.3	155.7	10.9
H3	780.3	12.1	88.6	8.5	10.1	2.5	8.9	0.8	9.2	1.9	81.6	18.7
P1	813.9	11.3	90.6	4.7	10.2	1.0	9.0	0.4	9.0	1.0	<b>80.5</b>	7.9
P2	575.1	15.9	36.1	7.8	7.4	0.6	16.7	3.7	4.9	1.2	77.8	6.4
P3	300.0	9.6	14.2	1.3	2.3	0.4	21.3	2.0	6.4	1.1	136.0	22.8

Table 2: Data for Fig. 6b: the average and standard deviation in the number of collections of structures, profiles and selected profiles, with amplification ratio calculated as average number of structures to profiles, profiles to selected profiles, and structures to selected profiles. Median, minimum and maximum values for averages are bolded.

Sequence	By Features		By Selected Profiles	
	Ave	Stdev	Ave	Stdev
V1	95.8	0.6	94.2	1.5
V2	90.3	1.0	89.5	1.9
V3	<b>89.5</b>	1.0	80.8	5.5
T1	83.7	2.9	<b>82.6</b>	2.7
T2	94.8	0.6	92.9	2.0
T3	92.8	0.5	<b>97.3</b>	1.7
S1	82.7	1.1	65.0	3.7
S2	95.4	0.3	73.5	2.1
S3	<b>99.4</b>	0.1	97.0	2.2
H1	88.8	0.9	74.6	2.7
H2	88.5	1.1	72.7	2.6
H3	87.2	0.9	62.1	4.9
P1	78.6	0.8	<b>50.5</b>	2.9
P2	<b>76.7</b>	2.1	82.7	8.2
P3	96.7	0.3	89.0	2.5

Table 3: Average (with standard deviation) percent coverage across 25 runs of helices by features, and structures by selected profiles. Median, minimum and maximum values for averages are bolded.

Sequence	Features		Selected profiles	
	Ave	Stdev	Ave	Stdev
V1	0.938	0.032	<b>1.000</b>	0.000
V2	0.944	0.055	0.809	0.066
V3	0.952	0.038	0.895	0.075
T1	0.957	0.011	0.805	0.098
T2	<b>0.981</b>	0.008	0.854	0.081
T3	0.994	0.031	<b>0.839</b>	0.098
S1	0.983	0.027	0.827	0.062
S2	0.997	0.013	0.958	0.027
S3	0.980	0.029	0.789	0.088
H1	<b>1.000</b>	0.000	0.942	0.077
H2	0.975	0.026	0.965	0.044
H3	0.983	0.027	0.825	0.129
P1	0.992	0.003	0.826	0.060
P2	<b>0.933</b>	0.051	<b>0.753</b>	0.048
P3	0.996	0.021	0.933	0.108

Table 4: Average reproducibility across 25 runs with standard deviation. Median, minimum and maximum values for averages are bolded.

<b>Qrr</b>			
Helix class	V1	V2	V3
1	(1,16,6)	(1,25,8)	(59,88,10)
2	(38,56,7)	(77,102,10)	(2,14,5)
3	(64,88,10)	(47,64,7)	(37,53,7)
4	(31,63,6)	(32,43,4)	(22,33,4)
5	(19,28,3)	(27,47,5)	(54,93,4)
6	(21,30,1)	(51,75,7)	(1,16,1)
7	(23,28,1)	(29,71,3)	(70,77,1)
8	(23,34,4)	(48,77,3)	(59,89,3)
9			(17,37,3)

Table 5: Potential features for Qrr sequences found across 25 runs, in (i,j,k) notation for associated maximal helix.

<b>tRNA</b>			<b>5S ribosomal RNA</b>				
Helix class	T1	T2	T3	Helix class	S1	S2	S3
1	(1,13,4)	(1,71,7)	(1,72,7)	1	(1,119,10)	(1,118,9)	(3,133,9)
2	(15,70,6)	(23,47,3)	(49,65,5)	2	(33,88,10)	(25,63,7)	(12,123,6)
3	(48,64,5)	(27,43,5)	(26,44,6)	3	(95,104,3)	(66,109,7)	(22,73,8)
4	(36,47,4)	(48,64,5)	(9,26,5)	4	(20,31,4)	(84,93,3)	(75,117,10)
5	(23,34,3)	(7,22,6)	(31,40,3)	5	(61,77,5)	(78,99,5)	(86,106,8)
6	(26,42,5)	(31,40,3)	(52,61,3)	6	(91,107,3)	(31,44,4)	(37,57,4)
7	(29,54,5)	(19,51,3)		7	(48,57,3)	(22,53,3)	(43,51,3)
8	(25,59,6)			8	(89,108,4)	(28,48,2)	(32,62,3)
9	(21,47,2)			9	(46,55,3)	(14,65,2)	(93,100,2)
10	(24,44,1)			10	(10,22,5)	(76,100,1)	(29,67,3)
11	(14,72,5)			11	(60,69,3)	(75,102,2)	(35,61,2)
				12	(25,108,4)	(29,48,4)	
				13		(73,103,2)	
				14		(35,42,2)	

Table 6: Potential features for tRNA and for 5S ribosomal RNA sequences found across 25 runs, in (i,j,k) notation for associated maximal helix.

<b>THF riboswitch</b>			<b>TPP riboswitch</b>				
Helix class	H1	H2	H3	Helix class	P1	P2	P3
1	(1,99,5)	(10,88,6)	(10,79,10)	1	(16,31,6)	(1,86,4)	(6,88,5)
2	(72,89,7)	(28,54,8)	(1,91,5)	2	(37,50,5)	(56,67,4)	(62,75,4)
3	(10,30,8)	(59,75,7)	(28,52,7)	3	(68,81,4)	(6,81,5)	(16,27,4)
4	(57,62,1)	(34,49,6)	(35,46,4)	4	(12,57,5)	(49,74,4)	(32,44,5)
5	(49,73,5)	(1,101,5)	(58,66,2)	5	(1,81,7)	(13,43,5)	(56,81,4)
6	(38,94,5)	(16,83,4)	(26,55,3)	6	(61,73,5)	(19,37,4)	(11,51,5)
7	(54,64,2)	(20,78,3)	(22,62,5)	7	(10,58,6)	(23,30,2)	(11,50,4)
8	(40,93,4)	(5,94,4)	(25,54,2)	8	(62,88,3)	(10,47,3)	(56,82,3)
9	(55,67,2)	(17,84,7)	(16,70,6)	9	(30,37,2)	(71,80,3)	(60,78,2)
10		(35,45,3)	(19,69,3)	10	(19,48,5)	(9,69,5)	
11			(7,85,1)	11	(26,41,3)	(20,59,10)	
12			(54,69,2)	12	(54,69,2)	(5,96,6)	(53,71,3)
				13		(10,59,1)	
				14	(62,87,3)		

Table 7: Potential features for THF riboswitch and for TPP riboswitch sequences found across 25 runs, in (i,j,k) notation for associated maximal helix.

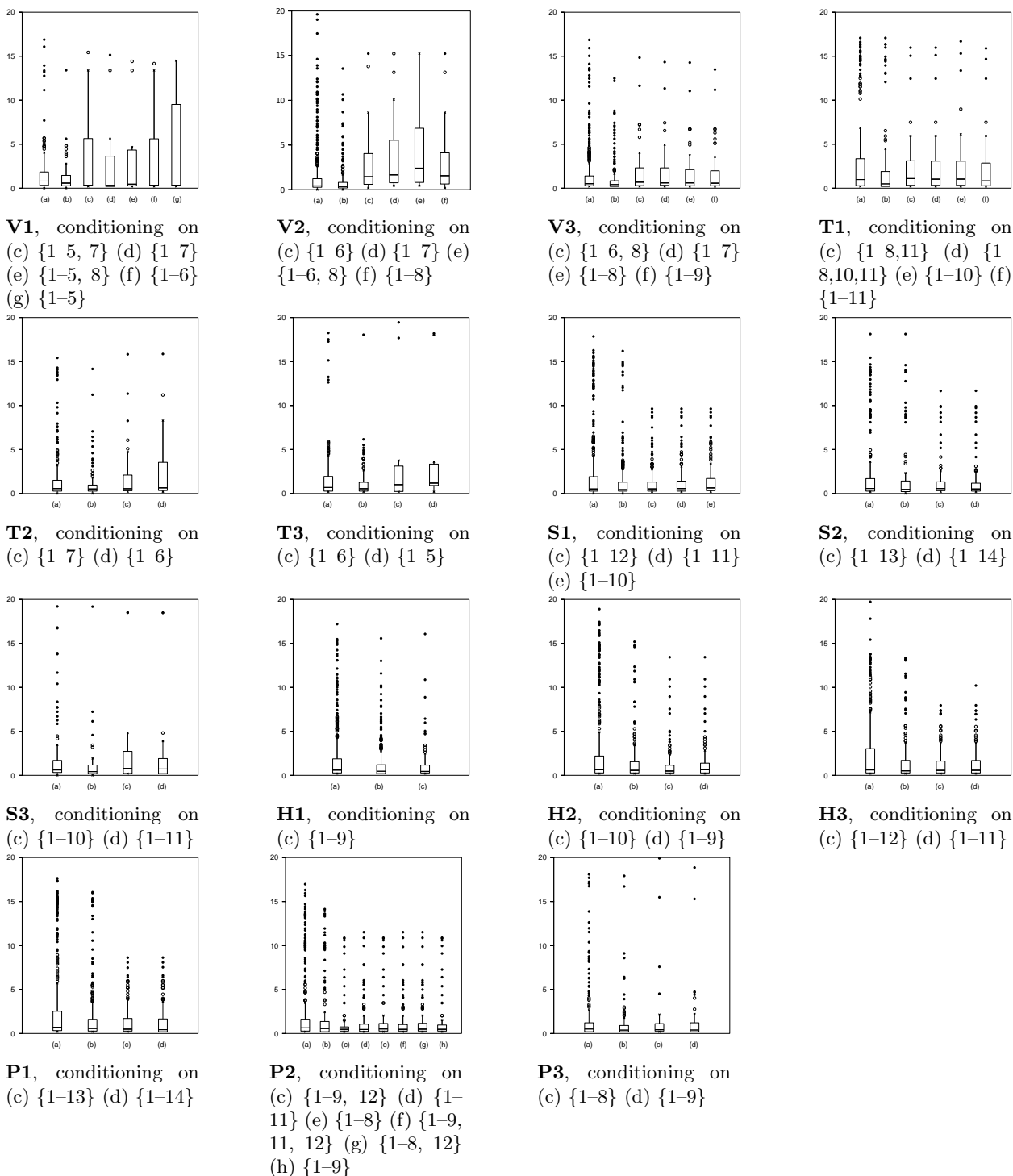


Figure 2: Columns from left to right indicate respectively standard deviations in frequency for base pairs, helix classes, and profiles conditioned on feature sets encountered in 25 samples for a given sequence. Helix classes specific to each sequence are listed by maximal helices in Tables 5, 6, and 7. Using standard deviations in base pair frequencies as a benchmark (leftmost boxplot), we observe that all the other boxplots to the right of leftmost exhibit behavior comparable to or less variable than the benchmark, regardless of conditioning.