

Supplementary Information

An RNA-binding peptide consisting of four types of amino acid

by *in vitro* selection using cDNA display

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Supplementary Table

Table 1. Selected DNA sequences of eXact tag and GNC random region. eXact tag region

Ref.	20	40	60	80	100
Ref.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
1.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
2.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
3.	TTTCTAGTGGTTTACCTTATGGCCGAAACGACCGGANNCTGAGAGCTCACTGAGGTAAGCGGTTAATGTAAGGCAACAACACACCAACCCGCCTCTC				
4.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
5.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
6.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
7.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
8.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
9.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
10.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
11.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
12.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
13.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
14.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
15.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
16.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
17.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
18.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
19.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
20.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
21.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
22.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
23.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
24.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
25.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
26.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
27.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
28.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
29.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
30.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
31.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
32.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
33.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
34.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
35.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
36.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
37.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
38.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
39.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
40.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
41.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
42.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
43.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
44.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
45.	GGAGGGAAATCAAACGGGGAAAA	GAAATATATTGTCGGGTTCAAACAGGGCTTTAAGAGCTGCGCTAAGAAGGAGG			
46.	AAAAAAAAAATTTGAAATTTTCGGNNNNNTTANNTTCAACGTTTCAGATTTTSCNNNTAAATGTNNGTATSCACNGAAGGGCANAGAGTGATGTTTC				

	120	140	160	180	200								
Ref.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
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2.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
3.	CGCGNTG	CGCGGATTCATTA	AGNNGGCAG	CACGCGTTCCNGG	TTTGGAAAGCG	CAATGTAGCGCAAAAGCACTAA	CGTCTT	GCTC					
4.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
5.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
6.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
7.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
8.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
9.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
10.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
11.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
12.	AGGGAT	CTCATTTCTGAAAAA	GGCGGGAGACTC	CAAAAAGTCTTC	CAATATGTAG	AGCTAGCGCTACATTAAACGAAAAA	AGCTGTAA	CAAT					
13.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
14.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
15.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
16.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
17.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
18.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
19.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
20.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
21.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
22.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
23.	TA	GGGAGAGCTCC	CGATTTGGATG	ATAGCTT	CTATACTATA	GTGTACT	TAATAGCTTGG	GTAAATCATGGTCATAGCTG	TTCTG	TGTGTA			
24.	GGAGAT	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG									
25.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
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27.	GCGACG	GGCCCAATTTG	CGCTTAA	AGTCCGTATACT	-----	ATTA AACGAAAAAG							
28.	GCCTGGAG	ATA	BCTTGATATTC	TATAGTGT	CACTAAATAGCT	TGGCGTAA	TCATG	CTATAGCTGTTCC	TGTGT	GAATTTGTT	ATCCGCTCA	AAA	
29.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
30.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
31.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
32.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
33.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
34.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
35.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
36.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
37.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
38.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
39.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
40.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
41.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
42.	TTTCAC	CTCTCC	CGGATCA	CTG	CTCGTCTG	GA	CA	CGA	CA	CGA	CA	CGA	CA
43.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
44.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
45.	TGTCATTT	CTGAAAAA	GGCGGGAAAC	TCCAAAAGTGCTTCAAATATGTAGACGCAGCTAGCGCTAC	-----	ATTA AACGAAAAAG							
46.	GGNGGTT	GGCNGATGAT	NAA	TNNTT	TATTA	TATTA	TATTA	TATTA	TATTA	TATTA	TATTA	TATTA	TATTA

	220	240	260	280	300
Ref.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
1.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
2.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
3.	ATTCTAGAGCACCACGCTCTNCACACTTTACGCTTCAGGCTTGATGTTGTGTGGANTGGTGAAGTGGATAGCAGTTTCCCACAGGAAACAGCTATGACC	-----	-----	-----	-----
4.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
5.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
→ 6.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
7.	ATTCTAGAGCACCACGCTCTNCACACTTTACGCTTCAGGCTTGATGTTGTGTGGANTGGTGAAGTGGATAGCAGTTTCCCACAGGAAACAGCTATGACC	-----	-----	-----	-----
8.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
9.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
10.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
→ 11.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
12.	TGAAATTAAGATCCGACCGCTCGCGTACGTAGAAGAGACAAGCTCTTCAAAGCTTTGGACGGCTCGTCCGCGTAGAAGAGACAAGCTCTTCAAAGCTTT	-----	-----	-----	-----
13.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
14.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
15.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
16.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
17.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
→ 18.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
19.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
20.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
21.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
22.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
23.	AAATTTCTATCCGCTCTTAATTTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT	-----	-----	-----	-----
24.	AGAAGATTAAGCTCTTCAAAGCTTTGGCCGTCGCGTCCCGACGGGGGAGATGGAGGTGATAGGACGGGGGGCGCGGGGAAAAATCGAATTCCTC	-----	-----	-----	-----
25.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
→ 26.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
27.	-----	-----	-----	-----	-----
28.	TTCCATTCATCACCTGCGGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGCTTT	-----	-----	-----	-----
→ 29.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
30.	GCTGTAGAGAGATTTCAAAAAAGATCCGAGCGTCCGCTACGTAGAAGAGACAAGCTCTTCAAAGCTTTGGTTCGTCGACGTCGCCGCGTCCGCGACG	-----	-----	-----	-----
31.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
32.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
33.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
34.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
35.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
36.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
37.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
38.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
39.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
40.	AAAAGCTAATTCCTAAGCTTACAACAATTACCAACAACAACAACAACAACAACAATTACATTTTACATTTCTACAACCTACAGCCACCATGGGAG	-----	-----	-----	-----
41.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
42.	GACGGCTAATTCCTAAGCTTACAACAATTACCAACAACAACAACAACAACAACAATTACATTTTACATTTCTACAACCTACAGCCACCATGGGAG	-----	-----	-----	-----
→ 43.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
44.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
45.	CTGTAGAAGAATTGAAAAA	-----	-----	-----	-----
46.	TTCCGATTTCTCTGATTTCTCAGCTATGCTTCTGTTTTATGTTGTGTGGAGAGGGTAGGGGTGAACAATTTACAGACAGGAAATCGTAATGACAAT	-----	-----	-----	-----

Ref.	Sequence
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2.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
3.	ATGATTACGCGAAGGTATTTAGGTGAAAGSATACTCGAACTACTCAGCTCAGCAT
4.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
5.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
→ 6.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
7.	CGCGCGTCTCAGGAGATGGAGGTGATGAGCGGSGGGGGCGGSGAAAA
8.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
9.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
10.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
→ 11.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
12.	GGGCGACGCGCTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
13.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
14.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
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16.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
17.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
→ 18.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
19.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
20.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
21.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
22.	AAAAAGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
23.	TGCGTCAATGTCGCTTTTCCATCGGSAATCTGTCTGACAGCTGCATTAA
24.	GCGGCGCGCATGCGCGCGGAGCATGCGCGTCGGGCGCAATTCGCGCTATA
25.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
→ 26.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
27.	-----
28.	CCAGTCGGGAAATGTCTGTGCTAGCTGCATTATGATCGGCFAATGCGCG
→ 29.	AGATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
30.	TCCAGCGGTGAGCGCGATGAGGTAGGACGSGGGGGCGGSGAAAA
31.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
32.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
33.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
34.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
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37.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
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39.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
40.	GGAAATTAAACGSAAGSGGGAGATGGAGGTGATAGSAAGGGGGGCGGCG
41.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
42.	GCGTCTACATATTTAAAGCACTTTGAGATTTTCCGCTTTTCAAGAAATGAC
→ 43.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
44.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
45.	GATCCGAGCGTCGCGTACGTAGAAGAAGACAAGCTCTTCAAAGCTTTG
46.	GGTACGTCAGTATAATTTATATTTTCGCTATGATGAGCAATCTAAGSATA

GADV random region

	20	40	60	80
Ref.	GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC - GNC GNC GNC GNC GNC GNC GNC GNC GNC GNC			
1.	G.T.A.A.C.T.A.C.A.T.A.T.T.G.A.A.T.A.-A.T.A.T.A.T.A.A.C.*C.C			
2.	AC.G.T.T.T.C.T.A.*****_*****			
3.	CCAAAGCGTTGG.AGCTGTC.CATATG.T.A.CTGCAG.GG.C.GGAATTC AATAGTGATGG.AG.GAAATCAACCGCCGAAAAGAAA			
4.	T.T.G.T.T.T.C.T.T.T.A.T.T.*****_*****			
5.	T.G.T.T.*.T.A.G.T.C.*****_*****			
→ 6.	G.T.T.T.T.T.T.T.T.C.C.T.C.A.T.A.G.A.C.T.-T.T.A.T.G.A.T.A.T.T.T			
7.	AT.ACTAGT.AATT.C.C.TG.AGGTCGAC.ATATGG.AGAG.TC.CAACG.GTTG.AT.CATAGCTT.AGTATTCTATA.TGTCA			
8.	C.A.A.G.T.A.C.T.T.T.T.T.T.A.A.A.A.C.A.-T.T.G.T.T.C.T.*.T.T.C.			
9.	G.T.A.A.A.C.C.*****_*****			
10.	A.*T.T.A.T.G.T.T.T.T.G.T.T.T.AT.T.A.-A.A.A.C.G.T*.A.T.*****			
→ 11.	T.T.G.T.T.C.T.A.T.T.A.A.C.T.T.T.-A.G.T.T.*****			
12.	CG.CG.GGAAAATCGAATTC.C.C.ATG.CG.C.GGAG.ATGCGACGTC.GGCC.AATTCGCC.TATAGT.AGTCGTATACA			
13.	T.A.A.*****_*****			
14.	A.T.T.A.A.*C.T.TGTG.CC.T.A.T.*****_*****			
15.	G.A.A.C.C.T.T.*****_*****			
16.	AG.G.T.T.A.T.*.C.T.*****_*****			
17.	T.T.C*.T.A.T.T.T.*****_*****			
→ 18.	C.T.T.A.T.T.T.C.T.A.T.G.A.T.G.A.T.T.A.-T.*****			
19.	T.T.G.A.T.A.T.T.T.A.T.T.T.A.T.T.AT.T.C.A.G.G.A.T.T.A.T.C.A.*T.			
20.	AG.T.T.C.A.T.A.A.C.T.A.G.T.T.T.A*.C.A.T.-A.C.A.G.T.C.A.C.A*.A.A.			
21.	G.G.T.A.G.T.A.C.T.*A.T.A.T.C.A.T.T.G.T.-T.A.A.A.G.T.T.T.C.T.T.			
22.	C.T.T.T.*****_*****			
23.	TGAAT.G.CAACG.CG.GGAGA.G.GTTTGC GTATT.GGCG.TCTTC.CTTC.TCG.TCACTGACTCG.TG.CTCGTCGTT.G			
24.	TGAGTCGTATAC*****			
25.	T.C.T.T.A.C.T.T.T.T.T.C.T.T.A.C.A.G.TT-T.T.T.G.T.A.G.C*.A.A.T			
→ 26.	T.G.T.A.C.T.T.A.T.A.T.G.G.A.T.T.A.T.A.-A.T.TT.C.G.T.T.G.T.T.T			
27.	a*****			
28.	GA.AG.CG.TTTG.TATTG.G.CTCTCCGCTTCCTCG.TCACTGACTCG.TG.GCT.GTCGTTCG.CT.CG.CGAG.GTAT.AG			
→ 29.	T.A.C.T.T.G.T.G.A.A.T.T.T.T.C.G.T.G.-C.*****			
30.	AATCGAATTC.C.C.ATG.CG.C.GGAG.ATGCGACGTCGG.C.CAATT.GCC.TATAGT.AGTCGTATA*****			
31.	T.C.A.C.T.C.T.T.T.C.T.A.T.T.G*A.T.T.T.-T.T.A.G.T.G.*.T.T.T.A			
32.	T.A.T.G.T.C*.T.T.T.A.T.T.T.T.T.T*.G.C.*T.T.G.G.T.T.T.T.A.T.T			
33.	T.T.A.T.T.T.T.AT.*****_*****			
34.	A.T.A.T.T.T.*****_*****			
35.	G.T.C.T.T.T.A.T.G*.T.GG*T.A.A.T.G.A.A*.A.-C.T*.T.T.*C.T.G.A.C.C.T			
36.	G.T.C.T.T.T.A.T.G*.T.GG*T.A.A.T.G.A.A*.A.-C.T*.T.T.*C.T.G.A.C.C.T			
37.	*T.T.C.T.T.T.T.A.A.T.A.G.G.T.T.A.TT.T.T.-G.A.T.T.C.A.C.T.A.T.***			
38.	AT.T.A.G.T.A.G.A.G.T.A.T.T.C.G.T.T.T.A.-T.G.T.*T.G.T.C.T.T.T			
39.	A.T.T.A.T.T.G.T.G.*A.A.G.T.T.C.T.T.T.-C.A.T.G.T.C.A.A.T.*****			
40.	GAAAAT.AATT.CCGCGCCG CCGCATGGCGCCG.GA.CATG.A.T.GGCC.AATTCG.CCTATA.TGAGTCGTATAC			
41.	C.C.T.T.A.T.T.T.G.T.T.T.A.T.A.T.A.T.T.-G.A.*A.C.T.A.G.T.T.*****			
42.	A.AT.CT.CTCTTAG.CA.CTCTTAAA.C.CTGTTC.AACC.A.AATATGTTCTTTTC.CCGTTT.ATTT.CCTCCAACT.ACTAGT			
→ 43.	C.T.T.C.G.T.T.A.C.T.T.T.T.T.T.A.AT-A.A.C.T.A.A.T.C.G.C.***			
44.	T.T.A.A.T.T.T.T.*.A.A.T.T.*.TGCG.C.A.C*.G.-*T.T.G.T.C.T.*T.G.C.A.***			
45.	C.G.T.*A.T.T.A.T.*.T.A.A.T*.T.T.T.G.T.T.-T.C.T.T.T.C*.T.T.A.T.T			
46.	TTGCAATGG.AGTT.TGATTTATNN.AACTTG.AGGTGGCCGTGAATTC AATAT.TAT.AGAGAAATCAAACG.GGAAAAGAAATATNTTG			

Arrows indicate the selected peptides that consisted of four types of amino acid. The sequences 6, 11, 18, 26, 29, and 43 correspond to GADV1, GADV4, GADV6, GADV2, GADV5, and GADV3, respectively.

Supplementary Figures

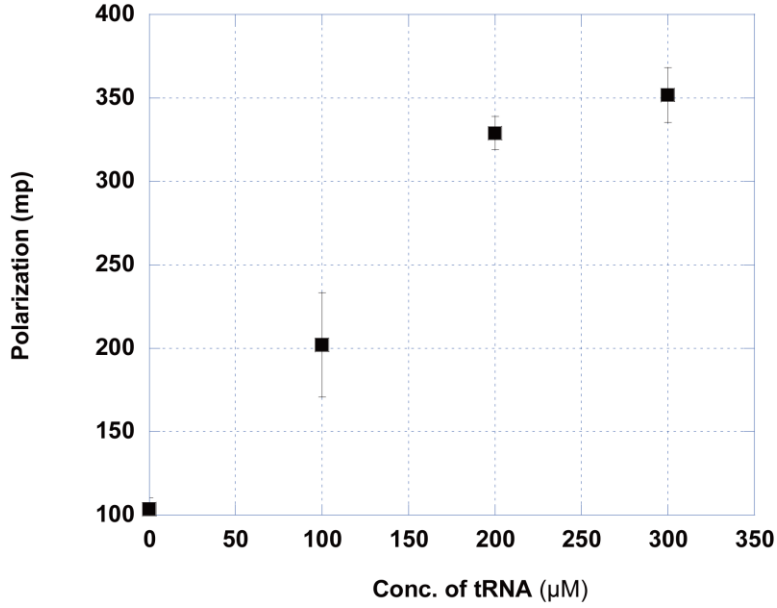


Figure S1. Fluorescent depolarization analysis of the interaction between GADV1 and tRNA. The GADV1 peptide (100 nM) and the tRNA (each conc.) were incubated at 25 °C for 1 h in 100 μL of the selection buffer. The polarization of those solutions was measured using a Beacon 2000 (Invitrogen). The polarization is shown by:

$$mp = \frac{[\text{Strength of parallelism}] - [\text{strength of verticalism}]}{[\text{Strength of parallelism}] + [\text{strength of verticalism}]} \propto \frac{3\eta V}{RT}, \quad (1)$$

where η denotes viscosity, V the size of the molecules, R the gas constant and T the absolute temperature. The GADV1 peptide-tRNA complex has a higher mp-value than the peptide only, because the peptide-tRNA complex has a larger rotational relaxation time than the peptide. Higher mp value was observed as the concentration of tRNA was increased, indicating that GADV1 peptide interacted with tRNA and/or the viscosity was increased.

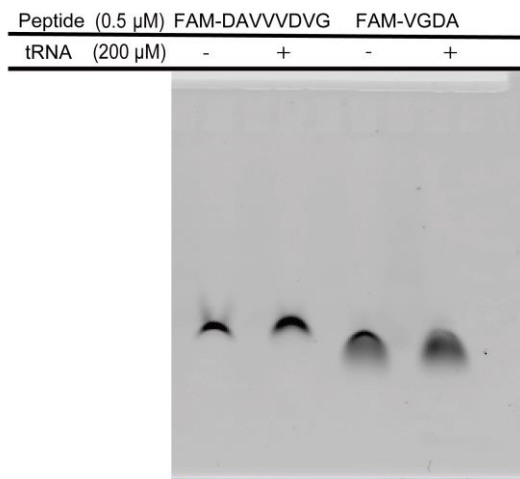
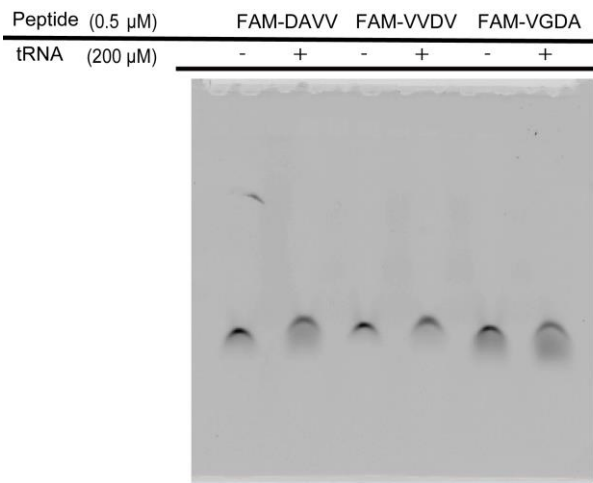


Figure S2. Binding assay of the short consensus peptide sequences against tRNA by an electrophoretic mobility shift assay (EMSA). The peptides were incubated with 200 μ M of tRNA at 25 $^{\circ}$ C for 1 h in the selection buffer (50 mM Tris-HCl, pH 7.0, 467 mM NaCl, 57 mM MgCl₂, 13 mM CaCl₂, 9 mM KCl, 0.2% Tween20) and loaded onto a 4% native PAGE after performing pre-electrophoresis at 100 V for 1 h. The BPB was loaded to confirm alternate lanes. The electrophoresis was performed at 100 V for 90 min at 4 $^{\circ}$ C and visualized with a fluorescence image analyzer.

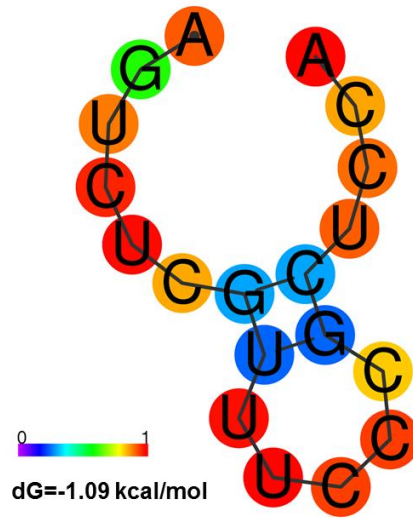


Figure S3. The possible secondary structure of the single strand RNA. The RNA secondary structure was predicted by CentroidFold.¹ The dG at 25°C was predicted by mfold.²⁻⁴ The base paired regions consist of only two or three base pairs, and therefore are unlikely to be stable.

Prey molecule GADV 1 : FAM -GVVVVVVAAVADVGDGDAVVVDVGDVDVWVGGD

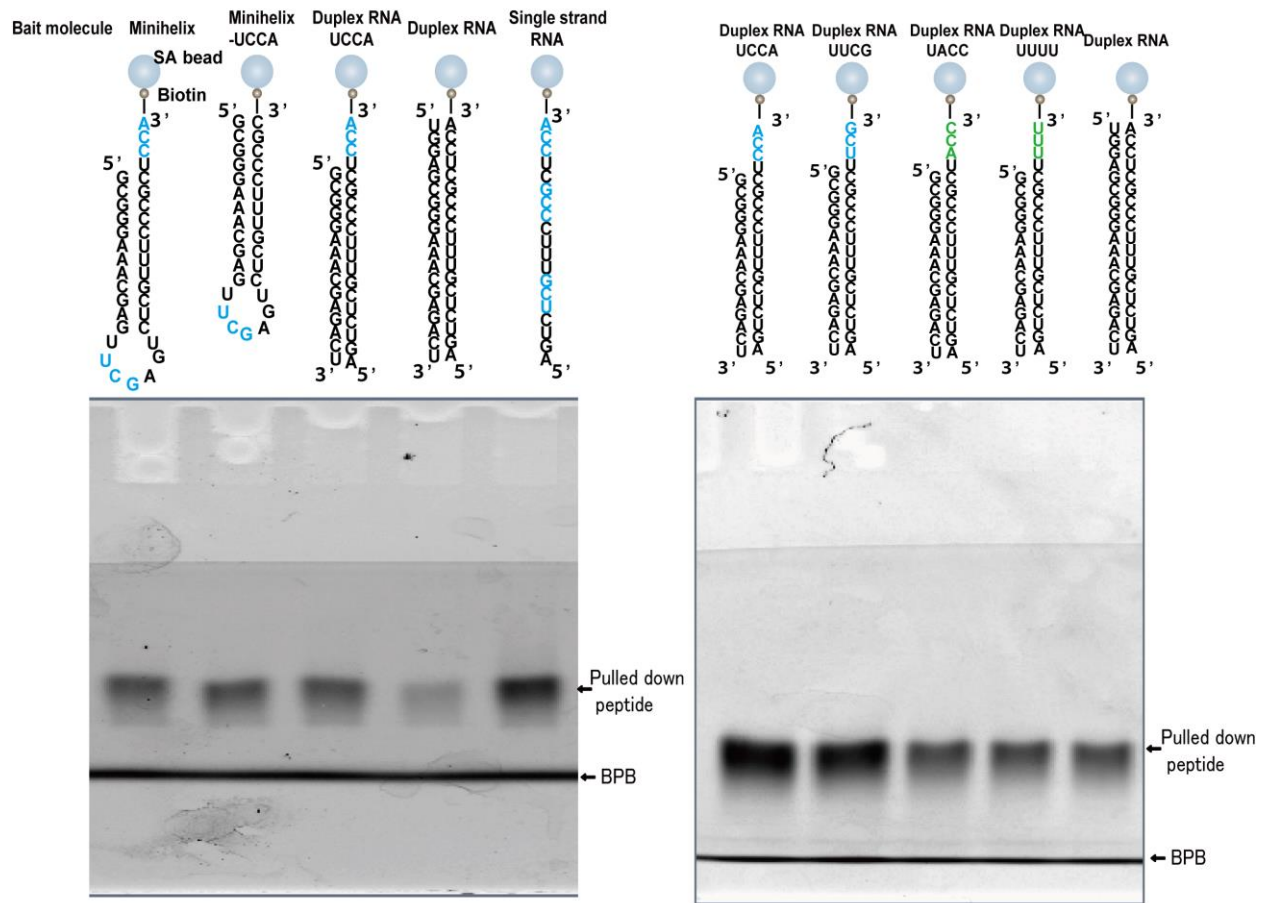


Figure S4 Full gel images for main text figures. The full gels are provided for main text Figure 2a and

2b.

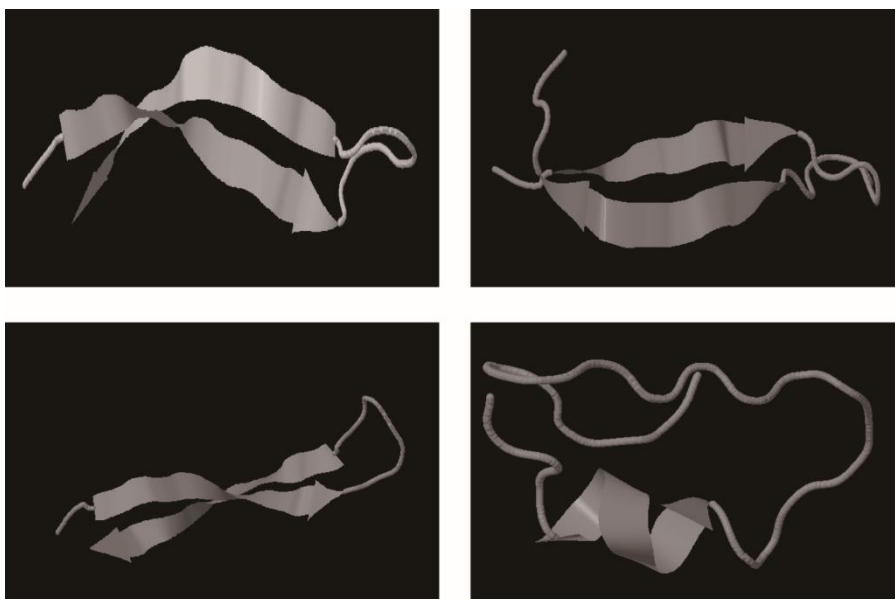


Figure S5. Four possible conformations of the GADV1 peptide obtained by PEP-FOLD.⁵⁻⁷ Cartoon models are depicted using Jmol software. The peptide was predicted to form both β -sheet and α -helix secondary structures.

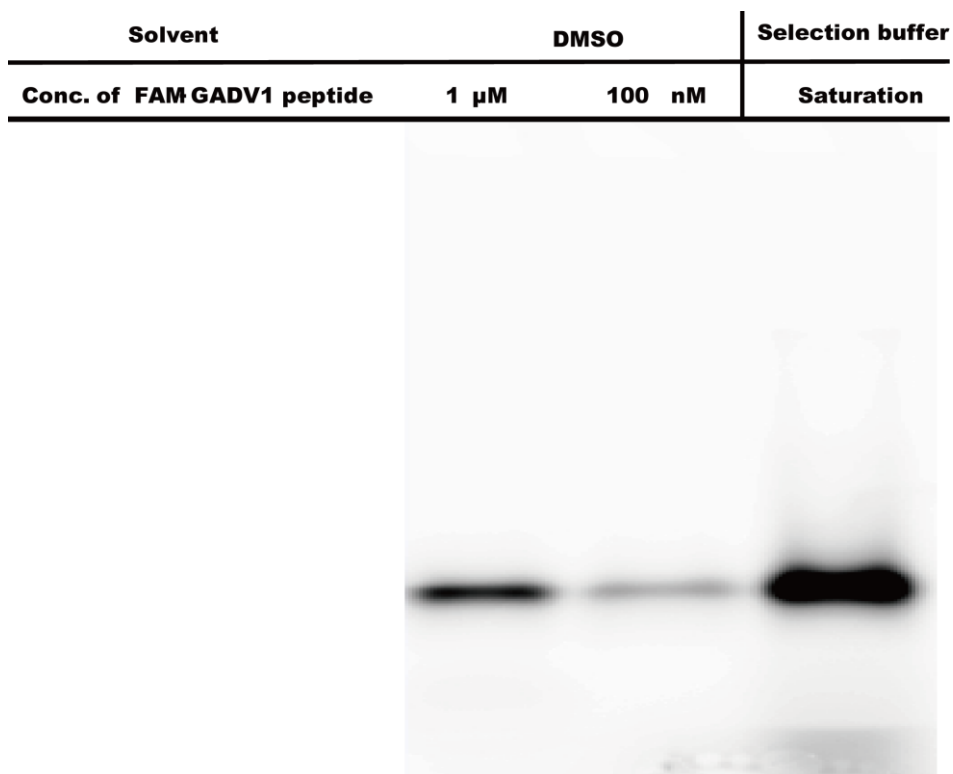


Figure S6. Tricine SDS-PAGE analysis of the GADV1 peptide for the estimation of peptide concentration. The GADV1 peptide was shaken at room temperature for 30 min in DMSO (1 μ M and 100 nM) or the selection buffer at saturating concentration. The precipitate of GADV1 peptide formed in the selection buffer was removed by centrifugation and the supernatant was used for Tricine SDS-PAGE. Each GADV1 peptide in the solution at different concentrations was subjected to Tricine SDS-PAGE and visualized with a fluorescence image analyzer. The single bands were detected and the concentration of the GADV1 peptide in the saturated selection buffer solution was estimated to be 3–4 μ M based on the band intensity.

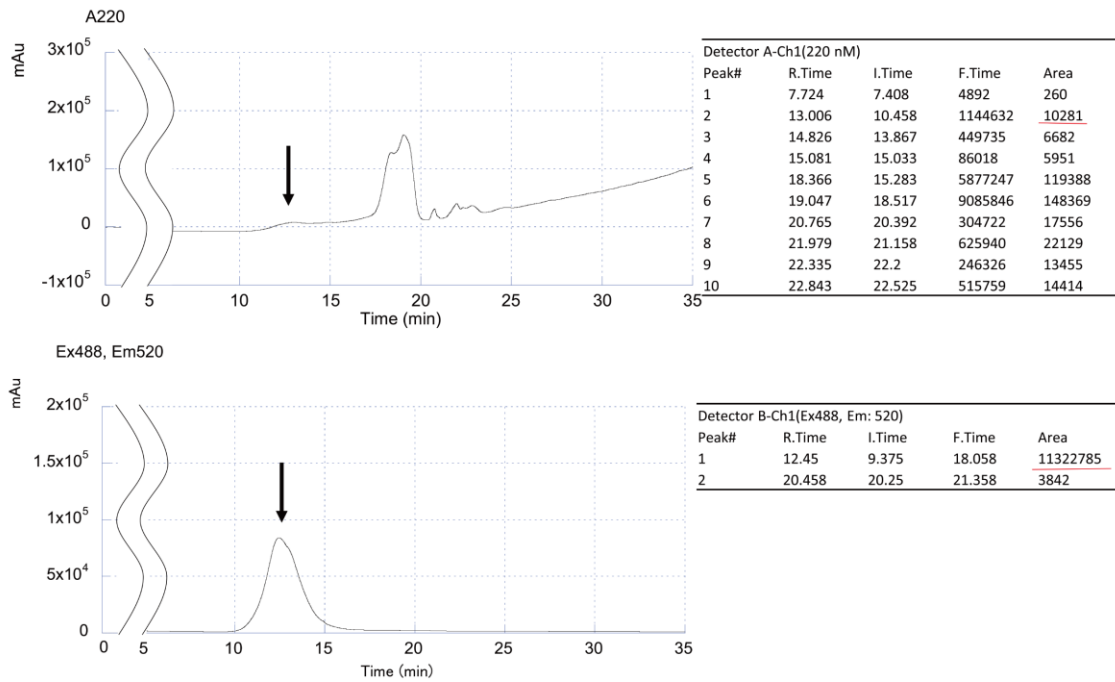


Figure S7. Reversed-phase HPLC analysis of the GADV1 peptide. The fraction corresponding to the peak having absorbance at 220 nm and emission at 520 nm at the same time was defined as the FAM-GADV1 peptide (arrow). The area of FAM-GADV1 peptide (monitored at 220 nm absorbance) represents 3% of the total peptides. If the other 97% was defined as GADV1 without FAM, the total concentration of GADV1 ([FAM-GADV1] + [GADV1]) was estimated to be 17 μ M in binding assay of GADV1 against tRNA by EMSA. Even so, the apparent concentration of the concentration of tRNA at which 50% of the peptide is bound (66 μ M) was determined to be higher than that of GADV1 (17 μ M).

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