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# An *in silico* Investigation of Anticancer Peptide Candidates in Fermented Food Microbiomes

**Muzaffer Arikan** [1,2]

[1]Research Institute for Health Science and Technologies (SABITA), Istanbul Medipol University, İstanbul, Turkiye
[2]Department of Medical Biology, Faculty of Medicine, Istanbul Medipol University, İstanbul, Turkiye

ORCID ID: M.A.0000-0001-5162-2000

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## ABSTRACT

**Objective:** Cancer is a leading cause of death worldwide, requires development of new effective, specific, and safe strategies that do not carry the disadvantages of traditional cancer treatment approaches. Hence, this study aimed to identify anticancer peptide candidates in fermented food microbiomes through an in *silico* investigation.

**Materials and Methods:** One hundred eight shotgun metagenomic sequencing samples from six studies on fermented food microbiomes were downloaded from the NCBI and ENA databases and included in the study. Bioinformatic analyses including quality control of raw data, *de novo* assembly, prediction of protein sequences, anticancer peptide predictions by an integrated use of four different prediction tools, toxicity predictions and database comparisons were performed.

**Results:** One hundred forty-two novel anticancer peptide candidates were identified. Liquor, coffee, kefir fermentation samples contained the greatest numbers of anticancer peptide candidates while sugar, dairy, coconut kefir and brine-type fermentations were dominant sources according to the substrate type.

**Conclusion:** This study indicates the potential of fermented food microbiomes as a useful source for candidate anticancer peptide detection. *In vitro and in vivo* validations of detected peptides may lead to development of new candidate molecules for cancer therapy in the future.

**Keywords:** Fermented food, microbiome, bioinformatics, metagenomics, anticancer peptide

## INTRODUCTION

Cancer is a leading cause of death worldwide and responsible for an estimated 9.6 million deaths each year (1). According to the Global Cancer Observatory, the most common types of cancer are lung, breast and colorectal cancer (2). Traditional approaches to cancer management, such as radiotherapy, chemotherapy, surgery, can have significant negative effects (3,4). Considering the disadvantages of current treatment approaches such as medical complexities, adverse effects and high treatment costs, the development of effective, specific and safe new strategies is of paramount importance in terms of public health and economic benefits (5).

The focus on peptides as potential anticancer agents gained momentum after studies reporting antimicrobial peptides with varying levels of activity against tumor cells (6). Anticancer peptides show their cytotoxic activities in a similar way to antimicrobial peptides. Many anticancer peptides destroy cancer cells via apoptosis and necrosis by membrane lysis or pore formation (7). Anticancer peptides

**Corresponding Author:** Muzaffer Arıkan **E-mail:** muzafferarikan@gmail.com
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have many advantages such as crossing biological barriers more easily, broad target range, less side effects, less accumulation in tissues and lower toxicity which make them stand out as potential anticancer agents when compared to currently used chemotherapy drugs (8). Peptides with anticancer properties and desirable properties such as specificity, solubility, tumor penetration and safety are among the new alternatives suitable for cancer therapy (9).

Fermented foods have been part of the human diet for several millennia and are consumed in a variety of ways around the world. Fermented foods have been associated with alleviating various health problems in humans (10), and these properties have been attributed to bioactive compounds formed as a result of microbial fermentation (11). In recent years, there has been a growing number of reports on the anticancer effects of fermented foods (12). Anticancer peptides derived from fermented foods have the potential of being used as suitable alternatives to traditional cancer management approaches (5), many computational methods for anti-cancer peptide identification have been developed in the last decade (13). However, considering the massive amount of data produced by high throughput genomics technologies for fermented foods, there is a strong need for efficient strategies for the prediction and testing of anticancer peptide candidates in fermented food microbiomes.

In this study, shotgun metagenomics based fermented food microbiome samples reported by different studies were analyzed to conduct an *in silico* investigation of anticancer peptide candidates encoded within the genomes of the microbiome members using a bioinformatics workflow including metagenome assembly, combined use of anticancer peptide prediction tools, toxicity and novelty analyses.

## MATERIALS AND METHODS

One hundred eight shotgun metagenomic sequencing samples from six studies focusing on fermented food microbiomes were downloaded from the National Center for Biotechnology Information (NCBI), and the European Nucleotide Archive (ENA) databases and included in the study. The overall analysis strategy of the study is presented in Figure 1. Quality control of the data was first performed to clean raw sequences. Using trimmomatic, the adapter sequences were removed, the low-quality ends of the sequences were trimmed from the position with the quality score value below 20, and the sequences with a length shorter than 30 bases were eliminated. Quality controlled and filtered clean sequences were used for metagenome assembly analysis which was performed using the default parameters of the metaSPAdes (v3.15.0) (14) and contig sequences were obtained. Protein-coding sequences (CDS) for each of these contigs were predicted and annotated using Prokka (v1.4.0) with option –metagenome (15). Thereafter, CDS with the length between 15 amino acids and 50 amino acids were determined using SeqKit (v2.3.0) (16) and used for downstream analyses. The anticancer activity potentials of these peptides were estimated by four different anticancer peptide prediction tools, AntiCP2 (v2.0) (17), mACPred (v1.0) (18), ACP-MHCNN (v1.0) (19), ACPred (v1.0) (20) using default options for each tool. By combining the results obtained from these tools, the anticancer peptides predicted commonly by all four prediction tools were determined and considered as a reliable set. Next, ToxinPred (v1.0) (21) was used to carry out an *in silico* toxicity analysis. Finally, CancerPPD (v1.0) (22), a manually curated database of experimentally validated anticancer peptides, was used to check the novelty of anticancer peptide, candidates with minimum similarity threshold of 100% and the peptides with the highest anticancer property score and the lowest toxicity were determined.

## RESULTS

One hundred eight shotgun metagenomics samples from six studies focusing on fermented food microbiomes were included in this study. Fermented food samples represented five main substrate types, namely brine, coconut kefir, dairy, soy, and sugar (Figure 2). Anticancer peptides candidates were recovered in samples from a total of 13 countries (Cote d'Ivoire, Saudi Arabia, Ecuador, Egypt, Benin, Russia, United Kingdom, Germany, Mexico, China, Ireland, Japan, and Turkiye) across five continents (Asia, Africa, Europe, North America, South America)

**Table 1.** General characteristics of sequencing data at different steps of bioinformatics analysis.

| Study ID | Raw | QC Filtered* | Contigs | CDS* | CDS (15<n<50) | Reference** |
|---|---|---|---|---|---|---|
| PRJEB19968 | 2,287,242 | 1,824,414 | 48,044 | 36,241 | 3,348 | - |
| PRJEB21086 | 26,002,221 | 22,511,121 | 86,532 | 34,884 | 3,550 | - |
| PRJEB22200 | 2,275,543,745 | 1,991,566,237 | 608,723 | 308,949 | 43,830 | (29) |
| PRJEB24129 | 56,774,402 | 46,729,715 | 3,669,361 | 1,349,589 | 183,550 | (30) |
| PRJEB35321 | 347,841,507 | 263,627,918 | 7,102,933 | 2,076,255 | 305,492 | (23) |
| PRJNA260163 | 1,683,868,773 | 1,425,472,508 | 12,142,357 | 7,586,687 | 444,668 | - |
| **Total** | 4,392,317,890 | 3,751,731,913 | 23,657,950 | 11,392,605 | 984,438 | |

*QC: Quality Control Filtered, CDS: Protein Coding Sequence, **3 studies did not have any associated publication in the NCBI and ENA databases

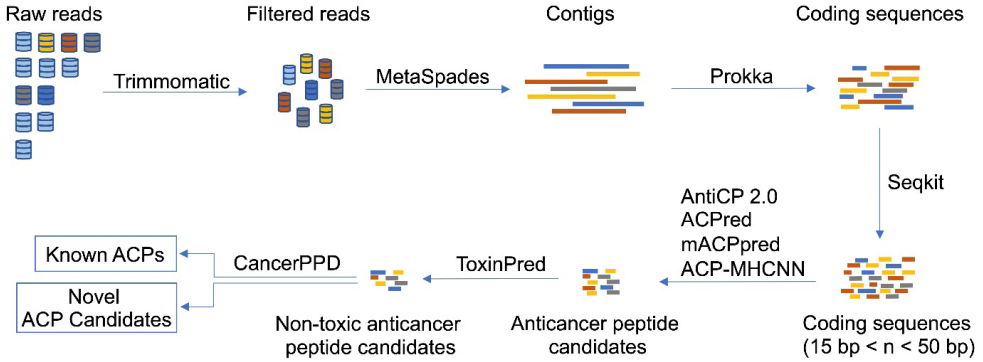


**Figure 1.** Overall analysis strategy.

(Figure 2). The majority of samples were collected in China (n=24), Ireland (n=24) and Turkiye (12).

To predict anticancer peptide candidates in fermented food microbiomes, a total of 4.4 billion reads were analyzed (Table 1). Metagenome assemblies yielded 23.6 million contigs. Then, CDS for each of these contigs were predicted and a combined set of 11.4 million CDS were obtained among which 984,438 short CDS (between 15 amino acids and 50 amino acids in length) were used for prediction of anticancer peptide candidates.

Anticancer peptide predictions were performed by combining four different anticancer peptide prediction tools, namely AntiCP2, mACPred, ACP-MHCNN and ACPred. ACPred predicted the highest number of anticancer peptide candidates (n=80,646) while AntiCP2 predicted the lowest number of anticancer peptide candidates (n=7,570; Figure 3). Since the correct identification of anticancer peptide candidates vary between different methods, only 168 anticancer peptide candidates predicted by all tools were considered as reliable and used for downstream analyses. The overlap between all four prediction tools was approximately 0.001% (168 anticancer peptide candidates in 133,263 anticancer peptide candidates predicted in total).

One hundred sixty-eight anticancer peptide candidates commonly predicted by all prediction tools were further analyzed to assess their anticancer activity potential. These anticancer peptides were first tracked back to the studies and samples they originated from. The results showed liquor, coffee, and kefir fermentation samples as main sources of these anticancer peptides while sugar and brine type fermentations were main substrate types (Figure 4). Next, the potential toxicity and novelty of 168 anticancer peptide candidates were examined which resulted in 142 anticancer peptide candidates predicted as non-toxin and have not been reported to date (Supplementary File 1).

## DISCUSSION

Microorganisms involved in the fermentation process play an important role in the formation of health associated properties of fermented foods (23). It is known that the bioactive molecules produced by these microorganisms could have anti-inflammatory, antifungal, antibiotic, or anticancer properties (12). Thus, examination of microbial genomes can lead to the discovery of new biological agents used in treatment of a variety of diseases, or facilitating biotechnological process. Considering the increasing number of reports on the anticancer effects of fermented food (12), the genomes of microorganisms participating in the fermentation process may be a potential reservoir for novel anticancer peptides. Thanks to the growing

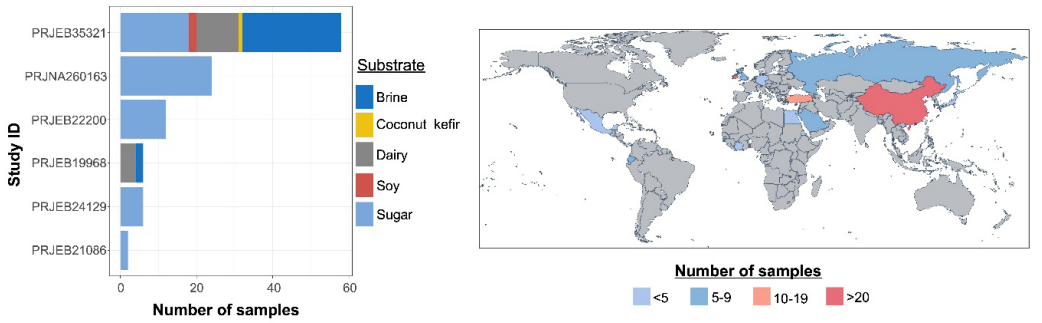


**Figure 2.** Number of samples for each study used to predict anticancer peptide candidates, colored according to fermented-food substrates. Geographic distribution of the number of samples retrieved per country.

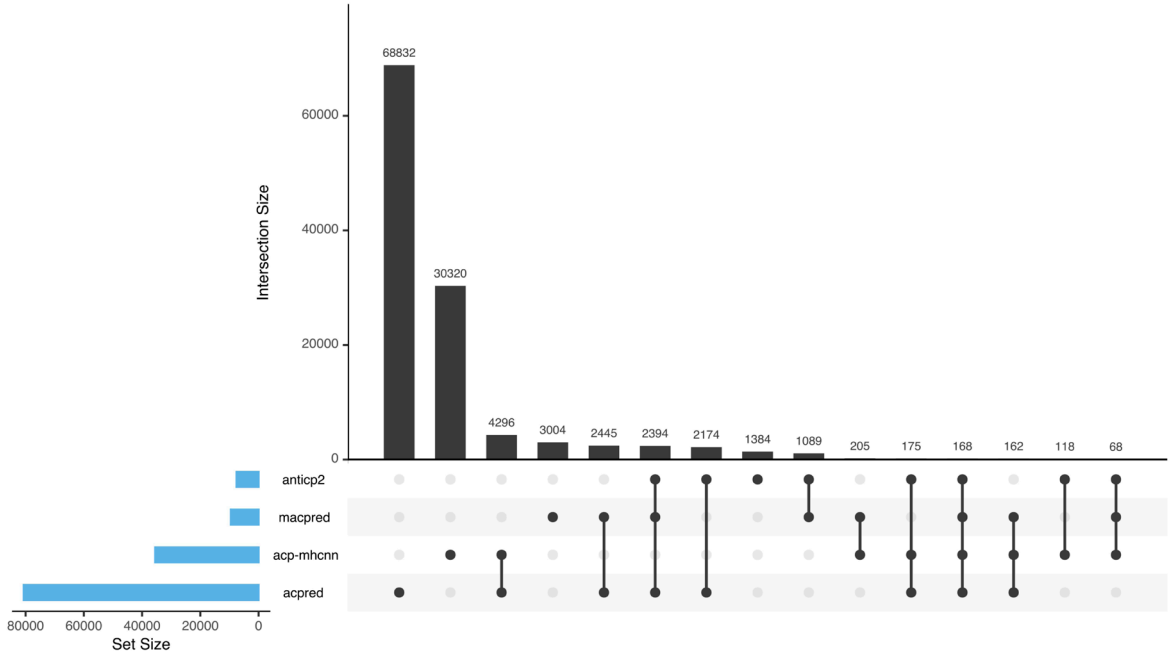


**Figure 3.** Number of predicted anticancer peptide candidates across anticancer peptide prediction tools. Vertical bars represent the number of predicted anticancer peptide candidates shared between the specific tools highlighted with connected dots in the lower panel. Horizontal bars in the lower panel indicate the total number of anticancer peptide candidates predicted by each prediction tool.

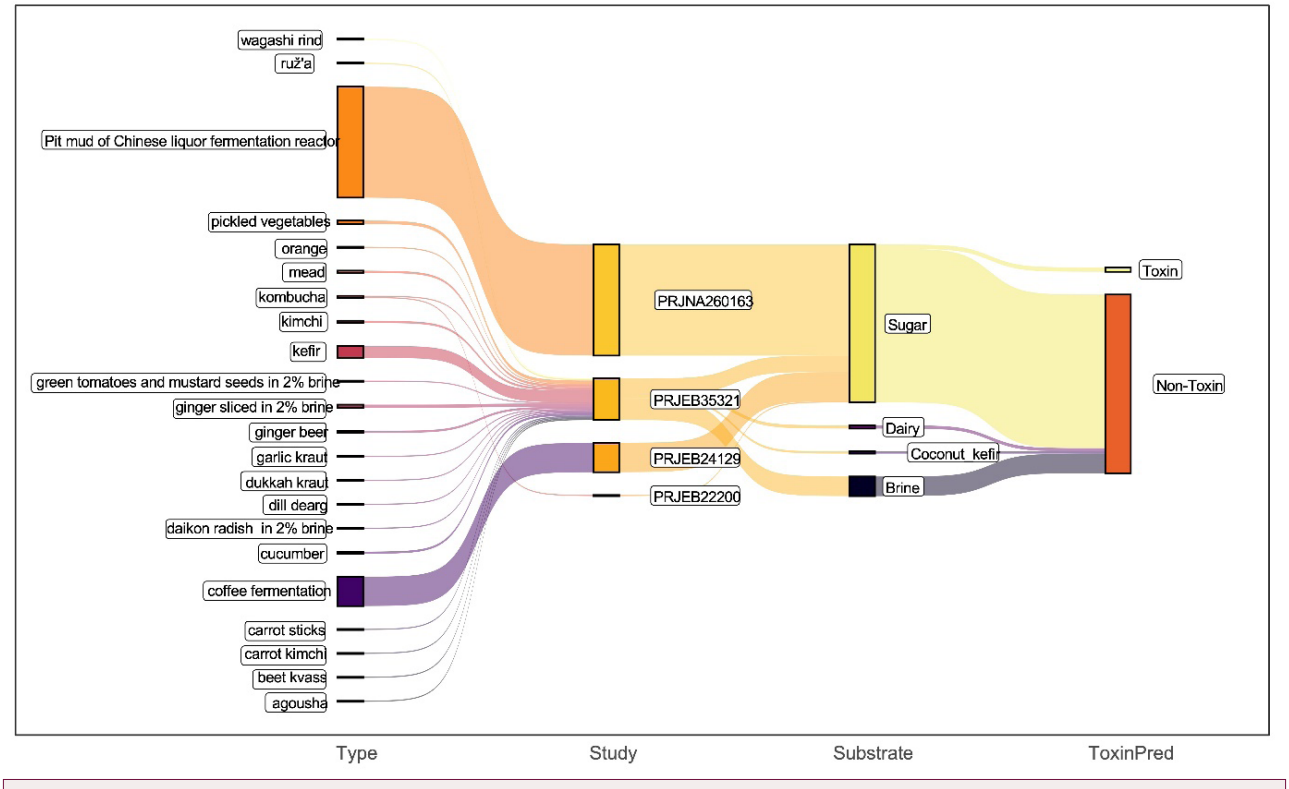


**Figure 4.** Sankey plot displaying distribution of 168 anticancer peptide candidates across fermented food, study, substrate type and predicted toxicity categories.

use of the next generation sequencing technologies and development of bioinformatics tools, the microbial genomes can be screened for anticancer peptide candidates through much more comprehensive approaches (13).

In this study, microbiomes of many fermented food types originating from different countries were analyzed together to detect anticancer peptide candidates. Starting with billions of DNA sequencing reads, 142 novel anticancer peptide candidates have been predicted and reported. One of the findings of the study was the high-level inconsistency between different anticancer peptide prediction tools which suggests that caution is needed when using a single anticancer peptide prediction tool. Thus, a consensus approach based on multiple anticancer peptide prediction tools -as applied in this study- can be used to alleviate this issue and ensure robust predictions. Moreover, the size distribution after length-based filtering of CDS yielded peptide sequences with lengths ranging from 30 amino acids to 50 amino acids and potentially caused missing shorter anticancer peptide candidates. As this is a known limitation related to software used for CDS prediction and annotations, new tools for small open reading frames would serve as valuable tools to overcome this limitation in the future (24).

The detected anticancer peptide candidates mainly originated from liquor, coffee and kefir fermentations which are classified as sugar, dairy and brine type fermentations. Among these fermented foods, interestingly, kefir has been reported to have anticancer effects by several studies (25–28). This distribution could be partly attributed to the number of raw reads obtained from the samples; however, interestingly, there was very low number of anticancer peptide candidates detected in other samples sequenced with very high coverage such as kombucha samples. It should also be noted that the microbial diversity in the samples potentially have significant effects on the number of the predicted anticancer peptides. The toxicity analysis and comparison with the previously characterized anticancer peptides revealed that most of the predicted anticancer peptide candidates have not been reported before. Considering the high throughput characteristics of the approach applied in this study, comprehensive high throughput wet laboratory testing, and characterization methods will be strongly needed in the future.

Fermented food microbiomes were found to be a useful source for candidate anticancer peptide discovery. *In vitro* and *in vivo* validations of the identified peptides may lead to development of new candidate molecules that can be used in cancer therapy.

**Ethics Committee Approval:** Ethics committee approval is not required because of no material or experimental animal that would require permission.

**Peer-review:** Externally peer-reviewed.

**Conflicts of Interest:** The author declare no conflict of interest.

**Financial Disclosure:** The author declare that this study has received no financial support.

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## SUPPLEMENTARY INFORMATION

**Supplementary File 1.** The sequences of 142 novel anticancer peptide candidates determined in the study.

>acp1
MNWGKRWWRRGGKREEKKIKKGDKKKEKLAGTINARAGNGGVGGDGGQ
>acp2
MLHLIPNMSHHLFLGKLKLLPHASEKHISK
>acp3
MFLNIVKCVFFKILKFFEIIVVKVVKNLVGEKLDKKLIC
>acp4
MKLWKVKNEISKWKEEGGVKKIGPAGYSIGS
>acp5
MGSVIKKRRKRMSKKKHRKMLRRTRVQRRKLGK
>acp6
MLRQALMAKKLYGKRVTKWQKQQDDKKAADKKAAKKAQKA
>acp7
MLCRGGFSKQTIGCHQAGCHAIVQRHGKRRGRCRAVGIRHRIREGVG
>acp8
MKWMKWLKFGMGVYIVWFAVVLIIIGLAVYVYFHPFWLFG
>acp9
MKILKKFCYAKQNLWIVDLLEFGLKKQSIKKKKYLKRIFLKENILKRCT
>acp10
MAFIIGLGVVLKNVKVRKEKKNSKGFQKS
>acp11
MKPNAKKKVWYLVKPFKLGSSGVNKALFKAIVDKEVGQTALAG
>acp12
MKKKKKRWGAKKKNKNMEHYWIKRENKFLKMKVIIV
>acp13
MVKLLSKVVVKIAKYLCNKKLLSARDAKI
>acp14
MKKKKEKRKEGKRKNKKGGVALVKTRKGTKVGFLMKGEIGMK
>acp15
MILSYFRHYLGKCFNLKKKAKLKRFAVLVAFPEIGILHFQNVALKFAKR
>acp16
MMMMIKMKKQMKKKMKKKTHIKIMTLGKAIKKKKHIKIMTLGKAIK
>acp17
MFGAILVLLLLPSLDRSIIRGNAFKPFSKFLF
>acp18
MRLLRKGIAVKINTYIKKHANYVGWLLLIGAVVNAVIGLMIK
>acp19
MSSKKKKKPDKKVLIAKYVAIGAWAVPATSLVDLIKTLIKHFLR
>acp20
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>acp21
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>acp22
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>acp23
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>acp26
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>acp27
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>acp28
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>acp30
MGSVVKKRRKRMAKKKHRKLLRKTRHQRRNKK
>acp31
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>acp32
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>acp33
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>acp34
MFRKVNIGFNQVIVILIGFKIGGDGGLFIVA
>acp35
MVIVIKINKKFKKNFNNNLFAVFLSVLKLVSVTYAF
>acp36
MLPKQLKMLIKCKKMGKGILLSMENLKKKLLMVIKNWLSVDILQVLLWVL
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>acp38
MKLYAIGLGKKEKMLLGLVTILLCLFKKKKSMII
>acp39
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>acp40
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>acp41
MGSVIKKRRKRMSKKKHRKLLRKTRHQRK
>acp42
MVKKYLIKIFLNKLLKIIFKTQCYGNKHFGVLLVVLLLVVL
>acp43
MFKKKFLSNGWCILYTLIPIVFIVGTMIAIKV
>acp44
MAKTKTTKNKTQKTNAKAAKTASKTATTKKKVVKKPVTKTKTAK
>acp45
MGGKKRICKQTNKKKKLNVVNLASRNFQQVALQVFFLKIRKASKK
>acp46
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>acp47
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>acp70
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>acp71
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>acp72
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>acp73
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>acp74
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>acp75
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>acp79
MKKTFKKSVTRACAKVFNTAANAAAQTPCWGPHYQPKTPKKLRK
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MDCVKNVEIFFFMFVLKGKKLKACETKTC
>acp81
MKVVVVKSPKVVGGILRKIFGIKKKNYIEP
>acp82
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>acp83
MILKRFSNAKIINTKSLFKDSLRKKFKDTA
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