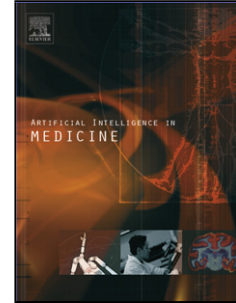


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# **iACP-GAEnsC: Evolutionary genetic Algorithm based Ensemble Classification of Anticancer Peptides by utilizing Hybrid Feature space**

**Shahid Akbar, Maqsood Hayat\*, Muhammad Iqbal, Mian Ahmad Jan**

Department of Computer Science, Abdul Wali Khan University Mardan, KP 23200, Pakistan

## **Authors' e-mail addresses**

Shahid Akbar: [Shahid.akbar@awkum.edu.pk](mailto:Shahid.akbar@awkum.edu.pk)

Dr. Maqsood Hayat: [m.hayat@awkum.edu.pk](mailto:m.hayat@awkum.edu.pk)

Muhammad Iqbal: [mdiqbalpk@gmail.com](mailto:mdiqbalpk@gmail.com)

Dr. Mian Ahmad Jan: [mianjan@awkum.edu.pk](mailto:mianjan@awkum.edu.pk)

\*Corresponding authors

[m.hayat@awkum.edu.pk](mailto:m.hayat@awkum.edu.pk)

## **Highlights**

- Computational model is developed for Anti-cancer peptides.
- Three discrete feature extraction methods are used.
- Ensemble feature space is formed
- Simple majority and GA based majority are used
- Obtained quite promising results than existing methods.

## **Abstract**

Cancer is a fatal disease, responsible for one-quarter of all deaths in developed countries. Traditional anticancer therapies such as, chemotherapy and radiation, are highly expensive, susceptible to errors and ineffective techniques. These conventional techniques induce severe side-effects on human cells. Due to perilous impact of cancer, the development of an accurate and highly efficient intelligent computational model is desirable for identification of anticancer peptides. In this paper, evolutionary intelligent genetic algorithm-based ensemble model, 'iACP-GAEnsC', is proposed for the identification of anticancer peptides. In this model, the protein

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