

عنوان مقاله:

Bioinformatic Analysis of L-Asparaginase II from Citrobacter Freundii 1101, Erwinia Chrysanthemi DSM F510, E. coli BLY1 and Klebsiella Pneumoniae ATCC 100 P1

محل انتشار:

مجله بين المللي أزمايشگاه يزشكي, دوره 4, شماره 2 (سال: 1396)

تعداد صفحات اصل مقاله: 12

نویسندگان: Khosrow Aghaiypour - Gene-Bank Department, Razi Vaccine and Serum Research Institute (RVSRI), Karaj, Iran

.Elham Bahreini - Department of Biochemistry, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran

.Shiva Jafari - Gene-Bank Department, Razi Vaccine and Serum Research Institute (RVSRI), Karaj, Iran

خلاصه مقاله:

Backgroung and Aims: L-Asparaginase II is a cornerstone of treatment protocols for acute lymphoblastic leukemia. Only asparaginase II obtained from E. coli Kır and Erwinia chrysanthemi have been used in human as therapeutic drug. The therapeutic effects of asparaginase II from E. coli K\u00a7 and Erwinia chrysanthemi is accompanied by side effects. It is desirable to search for other asparaginase II sources with novel properties that could be therapeutic and produce an enzyme with less adverse effects. Materials and Methods: Previously, we performed the in vitro studies, including cloning, sequencing and expression of L-asparaginase II genes (ansB) from Citrobacter freundii 11-1, Erwinia chrysanthemi DSM F510, E. coli BLY1 and Klebsiella pneumoniae ATCC 100P1. In this article, the obtained results were compared bioinformatically. The nucleotide and amino acid sequence alignments were carried out by ClustalWY. Protein localization and signal peptides were predicted by PSORT and SIG-Pred softwares, respectively. Percentages of hydrophobic and hydrophilic residues were calculated by Genscript software. The physicochemical parameters were computed using Expasy's ProtParam prediction server. The secondary and PD structures were predicted by SOPMA and the online server Phyrer, respectively. The antigenicity of the asparaginase IIs was predicted using Semiempirical method. Results: E. coli BLY1 and Citrobacter freundii 11-1 had the most similarity in physicochemical parameters and antigenicity with E. coli KIY. Also, Erwinia chrysanthemi DSM F510 had the most similarity in physicochemical parameters and antigenicity with Erwinia chrysanthemi. Conclusions: In spite of these similarities with drug types, the potentiality of other low-similar asparaginase IIs should also be determined and compared with .drug types

كلمات كليدى:

Asparaginase, Bioinformatic, Citrobacter freundii, E. coli, Erwinia chrysanthemi, Klebsiella pneumoniae

لینک ثابت مقاله در پایگاه سیویلیکا:

https://civilica.com/doc/1713350

