

***In silico* analysis for the construction of multiple sequence alignment and phylogenetic evaluation for the CEAL1, BCRA3 and BCRA3 related mRNA and proteins**

Niket Bhargava\*  
Tiratha Raj Singh\*\*\*

Amit Sugandhi\*\*  
Manish Manoria

\*nikresearch@rediffmail.com  
\*\*sugandhi\_amit@yahoo.com  
\*\*\*trajsingh@rediffmail.com

**Abstract**

An evolutionary study on the mRNA and related proteins for the CEAL1, BRCA3 and related biological sequences has been performed. MSA has been generated through the alignment of DNA and protein sequences through Clustal W and verified through other MSA building tool, T-Coffee. Phylogenetic tree has been reconstructed using Phylip. Tree was also reconstructed through Treeview from the Newick format data generated through Clustal W. Studies support the positions of sequences in tree for mammals as well as for some rodents. Our analysis supports the view to use rodents as model organisms for the study about some cancers in humans and other mammals.