

In silico structural and functional prediction of African swine fever virus protein-B263R reveals features of a TATA-binding protein

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ABSTRACT

African swine fever virus (ASFV) is the etiological agent of ASF, a fatal hemorrhagic fever that affects domestic pigs. There is currently no vaccine against ASFV, making it a significant threat to the pork industry. The ASFV genome sequence has been published; however, about half of ASFV open reading frames have not been characterized in terms of their structure and function despite being essential for our understanding of ASFV pathogenicity. The present study reports the three-dimensional structure and function of uncharacterized protein, pB263R (NP_042780.1), an open reading frame found in all ASFV strains. Sequence-based profiling and hidden Markov model search methods were used to identify remote pB263R homologs. Iterative Threading Assembly Refinement (I-TASSER) was used to model the three-dimensional structure of pB263R. The posterior probability of fold family assignment was calculated using TM-fold, and biological function was assigned using TM-site, RaptorXBinding, Gene Ontology, and TM-align. Our results suggests that pB263R has the features of a TATA-binding protein and is thus likely to be involved in viral gene transcription.

Subjects

Biochemistry, Bioinformatics, Biotechnology, Computational Biology

Keywords

African swine fever virus, TATA-binding protein, BA71V pB263R, In silico characterization, I-TASSER, Sequence homology search, African swine fever transcription factor

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