# Construction of mutant heparinase I with significantly increased specific activity. 

Anna Kalinina ${ }^{1}$, Larisa Borshchevskaya ${ }^{1}$, Elena Patrusheva ${ }^{1}$, Tatiana Gordeeva ${ }^{2}$, and Sergey Sineoky ${ }^{1}$<br>${ }^{1}$ NRC "Kurchatov Institute"<br>${ }^{2}$ NRC "Kurchatov Institute" - GosNIIgenetika, Genomic Center

April 28, 2020


#### Abstract

The cleavage of heparin by heparin lyases showed great potential as a cost-effective and innoxious method for producing heparin with low molecular weight (LMWH). One of the most studied and sought heparin lyase is heparinase I (HepI). However, the industrial use of HepI was largely hampered by its low specific activity and thermal stability. In this article we describe increasing in specific heparinase I activity by stepwise site-directed mutagenesis. Thus after two cycles of mutagenesis, we obtained mutant heparinase I Flavobacterium heparinum with significantly increased specific activity ( $25 \%$ ).


## Hosted file

article+.doc available at https://authorea.com/users/313756/articles/444202-construction-of-mutant-heparinase-i-with-significantly-increased-specific-activity

|  | ■ |  |
| :---: | :---: | :---: |
| FH | MKKQILYLIVLQQLFICSAYAQQKKSGNIPYRVNVQADSAKKKAIIDNKWVAVGINKEY | 60 |
| BT | -----MLTAQTKNTQTLMPLTERVNVQADSARINQI IDGCWVAVGTNKPHA | 46 |
| FH | LGYDDKLRENGKPSYRFELKAEDNSLEGYA AEETKGRTELSYSYATTNDEKKFEPSVYQN | 120 |
| BT | RDFTNLEDGKPSYREELKTEDNTLEGYAKGETKGRAEDSYCYATSDDERGLPADVYCK | 106 |
| FH | AOKLKTVYHYGKGICEOGSSRSYTFSVYIPSSFPD AATTIFAOWHCAESRTLVATPEGEI | 180 |
| BT | AOITKTVYHHGKGACPQSSSDYEESVYIPSSLDSEVSTIFAQWHGMEDRTLVQTPQGEV | 166 |
|  | - ${ }^{\text {a }}$ |  |
| FH |  | 232 |
| BT | KKLTVDEEVELEKTTREKKNVGHEKVARLDKQGNPVKDKNGKPVYKAGKPNGWLVEQGGY | 226 |
| FH | LAFGESKGY EYIKANSDEQWLTDKADFNNANPENSEVMKEYSSEYKTSTIAYKMPFAQ | 292 |
| BT | LAFGESGGLEY IKANSDRKWLTDKDDFCNANEGKTPVMKELTSEYKASTIAYKLPEAD | 286 |
| FH | FPKDCWITEDVAIDWTKYGKEANTILKPGKLDVM TYTKNKKPQKAHIVNQQEILIGRND | 352 |
| BT | FPKDCWITERVHIDWTVYGKEAETIVKPGMLDVRMDYQEQGKKVSKHIVDNEKILIGRND | 346 |
| FH | DDGYYFKFGIYRVGNSTVPVTYNLSGYSETAR | 384 |
| BT | EDGYYFKFGIYRVGDSTVPVCYNLAGYSER-- | 376 |

MKKQILYLIVLQQLFLCSAYAQQKKSGNIPYRVNVQADSAKQSEIIDNKWVAVGINKPY ALQYDDKLRFNGKPSYRFELKAEDNSLEGYAAGETKGRIELSYSYATTNDFKKFPPSVY QNAQKLKTVYHYGKGICEQGSSRSYTFSVYIPSSFPDNATTIFAQWHGAPSRTLVATPEG EIKTLSIEEFLALYDRMIFKKNIAHDKVEKKDKDGKITYVAGKPNGWKVEQGGYPPLAF GFSKGYFYIKANSDRQWLTDKADRNNANPENSEVMKPYSSEYKTSTIAYKMPFAQFPK DCWITFDVAIDWTKYGKEANTILKPGKLDVMMTYTKNKKPQKAHIVNQQEILIGRNDD DGYYFKFGIYRVGNSTVPVTYNLSGYSETAR





