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discussion forum and
information source for
next generation

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sequencing.

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SEQanswers was founded to be an information resource and user-driven community focused on all aspects of next-generation genomics. We hope to become the central location for next generation sequencing technology discussion and education.

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SEQanswers is a discussion forum and information source for next generation sequencing.

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(Review)

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9,060 daily visitors and
has the potential to
earn up to 1,087 USD
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The difference is not in
the focus as I think
both cover very similar

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topics but in the way the sites approach content management. Seqanswers is a traditional web forum where each post follows the other by creation date. There are no restrictions/recommendations on what each post may contain.

Biostar Vs. Seqanswers: What Is The Difference?

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a,genomics,high,through
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For those that follow both biostar and seqanswers, I think it would be great if Biostar Related Questions would show similar content posted in seqanswers. If

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there's been a question already answered in seqanswers, it would help us all having it pop up at Related Questions when typing it in biostar.

Showing Seqanswers.Com Content In Biostar Related Questions?

seqanswers.com is 1 decade 2 years old. It has a global traffic rank of #145,207 in the world. It is a domain

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This website is
estimated worth of \$
82,800.00 and have a
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If you would like to know more about SEQanswers, take a look at the two

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“official” publications!
About the forum and community:
SEQanswers: an open access community for collaboratively decoding genomes. Li et al. 2012. About the SEQanswers wiki for NGS tools: The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis.

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Omixon | NGS for HLA

An alignment I was running of 150 bp paired-end data took a lot of time (more than a week) to run. As the stage that took it too much time in the log file was "reporting output tracks" , I thought to limit the output of tophat via "-g 1" (--max-multihits), thinking this is the reporting of all combinations of all

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paired reads that takes time.. However, the alignment results are different ...

Tophat alignment and -g parameter

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