

1. What is BioGyan?  
BioGyan is a comprehensive search tool specially designed for biologists, enabling search, annotation and ranking of scientific literature from public databases using proprietary text-mining algorithms. It shows PubMed abstracts, biological pathways and 3D-structures of proteins.
2. What is the relevance of Biological score?  
Biological score provides information about the biological relevance of the abstract. Certain terms (e.g. gene symbols) can be either biological or chemical entities. BioGyan parses the abstract to identify if the search term is used in the abstract in a biological context and assigns a score.
3. What is the relevance of Process score?  
Process score is the sum of the occurrence of queried gene + Interaction terms + queried process or queried gene + process or only process in the same sentence. Process score provides information about relationship between the gene and process search terms. In our experience, we found a score  $\geq 2$  as relevant. Thus, any abstract that has process score  $\geq 2$  is called as relevant.
4. What abstracts are grouped in miscellaneous?  
The abstract which do not contain any searched process terms, falls under miscellaneous.
5. Can I add/edit processes to be searched against?  
Yes. In order to add a process, go to settings and select "Add/Edit Process". This will bring up the process list file, which is an editable text file.
6. Can I add/edit connection terms?  
Yes. In order to add a connection terms, go to settings and select "Add/Edit Connection Terms". This will bring up the connection list file, which is an editable text file.
7. Can I export the references in EndNote compatible format?  
Yes. In order to export the references in EndNote compatible format, click on the "export" icon in the Results/Literature table. Select the "EndNote" option from "Export as citation".
8. What is the difference between PubMed search and BioGyan search?  
Performing a PubMed keyword search in the application will bring up the abstracts with the specified key terms highlighted in the abstract, but the biological score and process scores are not calculated. Additionally, the abstracts are not marked as relevant/irrelevant. BioGyan search allows searching on the basis of genes, cell type and processes. A BioGyan search will bring up abstracts with the searched genes, processes and sentences containing both gene(s) and process(es) highlighted in the abstract.

Further, the abstracts will be marked as relevant/irrelevant. BioGyan search provides valuable information about relevance of the abstract to your search terms.

9. How does BioGyan uses the Organism information in the search?  
The organism specified is used for searching annotation databases (e.g. NCBI Gene), and not for searching PubMed abstracts.
10. How can I add/remove Organism?  
In order to add Organism, go to “Add / Remove” button placed next to the Organism dropdown.
11. How do I use the mark valid/invalid functionality?  
BioGyan assigns a relevant/irrelevant tag to abstracts; however user may want to curate the abstracts manually to mark only those that they think are valid based on their expertise and area of research interest. Marking abstracts as valid/invalid also helps in selectively exporting the abstracts.
12. Which Pathway(s) and Structure(s) are present in the result?  
BioGyan fetches Pathway from the NCBI Gene page and Structure from the UniProt, for queried gene.
13. How do I access my previous search results?  
BioGyan saves all searches. In order to get previous search results, go to “History” at the top right corner.
14. How can I conserve my Processes and Interaction terms while updating/reinstalling BioGyan?  
Before uninstalling/reinstalling BioGyan, please save the *data* directory from installation directory of the application to other location, update/reinstall BioGyan, and replace the new *data* directory with the one you saved.
15. How can I check the java version on my machine?  
Open command prompt and type *java -version*. This will show the currently installed version of Java.
16. How to install Java 1.6?  
Go to <http://www.java.com>, and download Java 1.6 and install.
17. Is there any limit to the number of abstracts I can fetch from BioGyan?  
BioGyan is tested for 1200 abstracts on a Windows 7 32-bit machine with 4 GB RAM. The fetch limit will vary depending on the available RAM on your machine.
18. Are there any known issues?  
BioGyan has following known issues:

- Java Heap Exception may occur when there are too many results. The actual number depends on the internal memory of your computer. This exception may lead to crashing/freezing of the application.
- Premature EOF Exception may occur when the internet speed or server response is very slow.
- If a gene has been replaced/modified in NCBI database, the application will not be able to fetch the annotation.