More stories at [WordBlanks.com](https://www.wordblanks.com)

RNAseq Analysis

1. Adjective __________
2. Verb - Base Form __________
3. Noun __________
4. Adjective __________
5. Noun __________
6. Adjective __________
7. Verb - Base Form __________
8. Noun __________
9. Noun __________
10. Noun - Plural __________
11. Noun __________
12. Adverb __________
13. Noun __________
14. Verb - Base Form __________
15. Verb - Present Ends In Ing __________
16. Noun - Plural __________
17. Noun __________
18. Adjective __________
19. Noun __________
20. Verb - Base Form __________
21. Noun - Plural __________
22. Noun __________
23. Verb - Base Form __________

24. Adjective ______________________________

RNAseq Analysis

Anthony Hall already gave an ______Adjective______ introduction to RNA-seq, so I will only ______Verb - Base Form______ a brief review. RNA-seq refers to the ______Noun______ of using ______Adjective______ parallel sequencing to obtain global information on an RNA component from an ______Noun______. This could be poly(A) RNA (representing mRNA), total RNA, ______Adjective______ RNA, or some other fraction. Here we ______Verb - Base Form______ on analysis of poly(A) RNA.

There are many questions that can be answered from RNA-seq data. RNA-seq data can be used to:

Determine which ______Noun______ of a genome are expressed

Annotate a ______Noun______

Find splice or alternative splice sites

Examine ______Noun - Plural______ in expressed genes

Use de novo assembly in organisms with no ______Noun______ to assemble a set of cDNAs.

Find genes that are ______Adverb______ expressed between treatments, ______Noun______, timepoints, etc.

This lab will ______Verb - Base Form______ on differential expression and on polymorphism discovery.

______Verb - Present ends in ING______ RNA-seq data is an evolving field and there are no truly plug-and-play ______Noun - Plural______. The basic steps are to:

Perform a quality control analysis of the ______Noun______

Filter reads to remove:

o Reads of ______Adjective______ quality

o Adapter contamination

o rRNA or other ______Noun______

______Verb - Base Form______ reads to a reference genome or cDNA set.

Normalize read counts between ______Noun - Plural______

Fit a statistical ______Noun______ to ______Verb - Base Form______ for genes that are significantly ______Adjective______

expressed.