

**Q1 - Please indicate your familiarity with these terms and concepts.**

Sorted by Very Familiar

<b>Question</b>	<b>Not at all Familiar</b>	<b>Have Heard of It</b>	<b>Somewhat Familiar</b>	<b>Very Familiar</b>
<b>BLAST</b>	0%	9%	17%	74%
<b>Genomic Sequence</b>	0%	9%	22%	70%
<b>Gene ID</b>	0%	0%	35%	65%
<b>FASTA</b>	0%	0%	35%	65%
<b>SNP</b>	4%	4%	30%	61%
<b>Transcript</b>	0%	14%	27%	59%
<b>ORF</b>	0%	13%	30%	57%
<b>Annotation</b>	0%	9%	39%	52%
<b>RNA-Seq</b>	4%	13%	30%	52%
<b>Alignment</b>	0%	9%	39%	52%
<b>Parasite Isolate</b>	4%	13%	35%	48%
<b>Non-synonymous</b>	4%	30%	17%	48%
<b>Allele Frequency</b>	4%	22%	26%	48%
<b>CDS</b>	17%	22%	13%	48%
<b>Metabolic Pathway</b>	4%	13%	35%	48%
<b>Transmembrane Domains</b>	4%	17%	35%	43%
<b>Epitope</b>	9%	17%	30%	43%
<b>Ortholog</b>	4%	26%	30%	39%
<b>Signal Peptide</b>	0%	22%	39%	39%
<b>UTR</b>	13%	13%	35%	39%
<b>Protein Data Bank</b>	9%	17%	35%	39%
<b>Motif</b>	0%	13%	52%	35%
<b>Mapping</b>	4%	22%	39%	35%
<b>Substrate</b>	13%	9%	43%	35%
<b>Genomic Segment</b>	13%	22%	35%	30%
<b>Proteomics</b>	0%	9%	61%	30%
<b>Expression Value</b>	17%	22%	30%	30%
<b>Genome Browser</b>	22%	22%	26%	30%
<b>Mass Spec Peptide</b>	9%	23%	41%	27%
<b>EST</b>	22%	22%	30%	26%
<b>Microarray</b>	4%	26%	43%	26%
<b>Histone modification</b>	9%	43%	26%	22%
<b>GFF</b>	57%	13%	9%	22%
<b>Metabolomics</b>	4%	26%	48%	22%
<b>ncRNA</b>	39%	17%	22%	22%
<b>WGA, whole genome analysis</b>	13%	30%	35%	22%
<b>CNV, copy number variation</b>	30%	22%	26%	22%
<b>Contig and Scaffold</b>	26%	17%	39%	17%

<b>GO Terms/Numbers</b>	30%	17%	35%	17%
<b>GO Term Enrichment</b>	43%	13%	26%	17%
<b>Bonferroni adjusted P-value</b>	35%	30%	17%	17%
<b>word cloud</b>	48%	22%	13%	17%
<b>PFAM</b>	39%	26%	17%	17%
<b>BAM</b>	43%	22%	17%	17%
<b>Paralog</b>	4%	48%	30%	17%
<b>ChIP-Seq</b>	18%	41%	27%	14%
<b>Synten</b>	18%	41%	27%	14%
<b>PubMed Compound</b>	41%	23%	23%	14%
<b>InterPro</b>	43%	17%	26%	13%
<b>KEGG Pathway</b>	39%	30%	17%	13%
<b>Ontology</b>	26%	39%	22%	13%
<b>reference based sequence mapping</b>	30%	35%	22%	13%
<b>Nucleosome Mapping</b>	22%	48%	22%	9%
<b>Benjamini-Hochberg FDR</b>	57%	26%	9%	9%
<b>EC Number</b>	43%	30%	17%	9%
<b>Splice Site Junction</b>	17%	22%	52%	9%
<b>OrthoMCL</b>	43%	22%	26%	9%
<b>ChIP-chip</b>	35%	39%	17%	9%
<b>Protein Microarray</b>	22%	43%	26%	9%
<b>Antibody Microarray</b>	26%	39%	26%	9%
<b>Metadata</b>	39%	30%	22%	9%
<b>SRA</b>	70%	13%	9%	9%
<b>eQTL</b>	36%	41%	18%	5%
<b>background genes</b>	57%	26%	13%	4%
<b>Polysomal Profiling</b>	52%	39%	4%	4%
<b>Galaxy workflow analysis platform</b>	39%	43%	13%	4%
<b>GATK Tools</b>	74%	17%	4%	4%
<b>VCF</b>	65%	17%	13%	4%
<b>Genomic colocation</b>	26%	48%	26%	0%
<b>Globus</b>	83%	17%	0%	0%
<b>PECALLER</b>	87%	13%	0%	0%

Sorted by Not at all Familiar

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<b>PECALLER</b>	87%	13%	0%	0%
<b>Globus</b>	83%	17%	0%	0%
<b>GATK Tools</b>	74%	17%	4%	4%
<b>SRA</b>	70%	13%	9%	9%
<b>VCF</b>	65%	17%	13%	4%

<b>GFF</b>	57%	13%	9%	22%
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<b>background genes</b>	57%	26%	13%	4%
<b>Polysomal Profiling</b>	52%	39%	4%	4%
<b>word cloud</b>	48%	22%	13%	17%
<b>GO Term Enrichment</b>	43%	13%	26%	17%
<b>BAM</b>	43%	22%	17%	17%
<b>InterPro</b>	43%	17%	26%	13%
<b>EC Number</b>	43%	30%	17%	9%
<b>OrthoMCL</b>	43%	22%	26%	9%
<b>PubMed Compound</b>	41%	23%	23%	14%
<b>ncRNA</b>	39%	17%	22%	22%
<b>PFAM</b>	39%	26%	17%	17%
<b>KEGG Pathway</b>	39%	30%	17%	13%
<b>Metadata</b>	39%	30%	22%	9%
<b>Galaxy workflow analysis platform</b>	39%	43%	13%	4%
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<b>Bonferroni adjusted P-value</b>	35%	30%	17%	17%
<b>ChIP-chip</b>	35%	39%	17%	9%
<b>CNV, copy number variation</b>	30%	22%	26%	22%
<b>GO Terms/Numbers</b>	30%	17%	35%	17%
<b>reference based sequence mapping</b>	30%	35%	22%	13%
<b>Contig and Scaffold</b>	26%	17%	39%	17%
<b>Ontology</b>	26%	39%	22%	13%
<b>Antibody Microarray</b>	26%	39%	26%	9%
<b>Genomic colocation</b>	26%	48%	26%	0%
<b>Genome Browser</b>	22%	22%	26%	30%
<b>EST</b>	22%	22%	30%	26%
<b>Nucleosome Mapping</b>	22%	48%	22%	9%
<b>Protein Microarray</b>	22%	43%	26%	9%
<b>ChIP-Seq</b>	18%	41%	27%	14%
<b>Synteny</b>	18%	41%	27%	14%
<b>CDS</b>	17%	22%	13%	48%
<b>Expression Value</b>	17%	22%	30%	30%
<b>Splice Site Junction</b>	17%	22%	52%	9%
<b>UTR</b>	13%	13%	35%	39%
<b>Substrate</b>	13%	9%	43%	35%
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