Q1 Please select the choice that best describes your level of familiarity with each term.

Answered: 31   Skipped: 0

	Not at all familar	Have heard of it	Slightly familiar	Very familiar	Total	Average Rating
Gene ID	0.00% 0	12.90% 4	25.81% 8	61.29% 19	31	3.48
Annotation	0.00% 0	25.81% 8	35.48% 11	38.71% 12	31	3.13
Parasite isolate	9.68% 3	25.81% 8	22.58% 7	41.94% 13	31	2.97
Genomic segment	9.68% 3	25.81% 8	41.94% 13	22.58% 7	31	2.77
Motif	0.00% 0	16.13% 5	38.71% 12	45.16% 14	31	3.29
Genomic sequence	0.00% 0	0.00% 0	25.81% 8	74.19% 23	31	3.74
EST	16.13% 5	29.03% 9	35.48% 11	19.35% 6	31	2.58
ORF	0.00% 0	3.23% 1	32.26% 10	64.52% 20	31	3.61
SNP	0.00% 0	12.90% 4	35.48% 11	51.61% 16	31	3.39
Non-synonymous	19.35% 6	22.58% 7	25.81% 8	32.26% 10	31	2.71
Allele frequency	3.23% 1	35.48% 11	25.81% 8	35.48% 11	31	2.94
Proteomics	0.00% 0	9.68% 3	48.39% 15	41.94% 13	31	3.32
Mass spec peptide	9.68% 3	22.58% 7	41.94% 13	25.81% 8	31	2.84
Microarray	0.00% 0	25.81% 8	38.71% 12	35.48% 11	31	3.10
Expression level/value	3.23% 1	25.81% 8	38.71% 12	32.26% 10	31	3.00
RNA-Seq	0.00% 0	32.26% 10	41.94% 13	25.81% 8	31	2.94
Alignment	0.00% 0	0.00% 0	22.58% 7	77.42% 24	31	3.77
eQTL	67.74% 21	22.58% 7	9.68% 3	0.00% 0	31	1.42
ChIP-Seq	41.94% 13	35.48% 11	12.90% 4	9.68% 3	31	1.90
Histone H3	19.35% 6	32.26% 10	25.81% 8	22.58% 7	31	2.52

Q2 Please select the choice that best describes your level of familiarity with each term.

Answered: 31   Skipped: 0

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Total	Average Rating
Nucleosome mapping	56.67% 17	33.33% 10	6.67% 2	3.33% 1	30	1.57
Synteny	12.90% 4	22.58% 7	32.26% 10	32.26% 10	31	2.84
Ortholog	0.00% 0	16.13% 5	32.26% 10	51.61% 16	31	3.35
Contig and Scaffold	6.67% 2	26.67% 8	43.33% 13	23.33% 7	30	2.83
GO Terms/Numbers	9.68% 3	29.03% 9	25.81% 8	35.48% 11	31	2.87
GO Term Enrichment	22.58% 7	41.94% 13	22.58% 7	12.90% 4	31	2.26
EC Number	32.26% 10	25.81% 8	19.35% 6	22.58% 7	31	2.32
Signal Peptide	3.23% 1	12.90% 4	29.03% 9	54.84% 17	31	3.35
BLAST	0.00% 0	3.23% 1	22.58% 7	74.19% 23	31	3.71
Low complexity region	22.58% 7	25.81% 8	29.03% 9	22.58% 7	31	2.52
Genomic colocation	16.13% 5	54.84% 17	9.68% 3	19.35% 6	31	2.32
Mapping	3.33% 1	36.67% 11	33.33% 10	26.67% 8	30	2.83
Transcript	0.00% 0	13.33% 4	16.67% 5	70.00% 21	30	3.57
Protein Data Bank	0.00% 0	12.90% 4	35.48% 11	51.61% 16	31	3.39
Transmemebrane domains	0.00% 0	16.13% 5	29.03% 9	54.84% 17	31	3.39
Protein export domains	12.90% 4	25.81% 8	25.81% 8	35.48% 11	31	2.84
Epitope	3.23% 1	29.03% 9	35.48% 11	32.26% 10	31	2.97
Splice site junction	9.68% 3	38.71% 12	35.48% 11	16.13% 5	31	2.58
Comparative genomic hybridization	35.48% 11	41.94% 13	16.13% 5	6.45% 2	31	1.94
FASTA	0.00% 0	0.00% 0	22.58% 7	77.42% 24	31	3.77
GFF	67.74%	6.45%	16.13%	9.68%		

GFT	**37.74%** 21	**3.45%** 2	**16.13%** 5	**9.68%** 3	31	1.68
BAM	**61.29%** 19	**12.90%** 4	**12.90%** 4	**12.90%** 4	31	1.77
Genome Browser	**12.90%** 4	**19.35%** 6	**29.03%** 9	**38.71%** 12	31	2.94
OrthoMCL	**61.29%** 19	**22.58%** 7	**6.45%** 2	**9.68%** 3	31	1.65
CDS	**25.81%** 8	**12.90%** 4	**19.35%** 6	**41.94%** 13	31	2.77

Q3 Please select the choice that best describes your level of familiarity with each item.

Answered: 31   Skipped: 0

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Total	Average Rating
PubMed Compound	25.81% 8	45.16% 14	9.68% 3	19.35% 6	31	2.23
Metabolic Pathway	0.00% 0	16.13% 5	45.16% 14	38.71% 12	31	3.23
Metabolomics	6.45% 2	35.48% 11	41.94% 13	16.13% 5	31	2.68
Substrate	3.23% 1	25.81% 8	22.58% 7	48.39% 15	31	3.16
KEGG Pathway	38.71% 12	19.35% 6	25.81% 8	16.13% 5	31	2.19
ChIP-Chip	19.35% 6	61.29% 19	12.90% 4	6.45% 2	31	2.06
Protein Microarray	22.58% 7	54.84% 17	12.90% 4	9.68% 3	31	2.10
Antibody Microarray	25.81% 8	51.61% 16	16.13% 5	6.45% 2	31	2.03
Metadata	25.81% 8	48.39% 15	9.68% 3	16.13% 5	31	2.16
Ontology	6.45% 2	41.94% 13	32.26% 10	19.35% 6	31	2.65
GO Term Enrichment	25.81% 8	38.71% 12	22.58% 7	12.90% 4	31	2.23