

Q1 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
Histone H3	0% 0	0% 0	0% 0	0% 0	0	0.00
Gene ID	0% 0	9.68% 3	22.58% 7	67.74% 21	31	3.58
Annotation	3.23% 1	0% 0	25.81% 8	70.97% 22	31	3.65
Parasite isolate	0% 0	25.81% 8	25.81% 8	48.39% 15	31	3.23
Genomic segment	6.45% 2	12.90% 4	38.71% 12	41.94% 13	31	3.16
Motif	0% 0	16.13% 5	16.13% 5	67.74% 21	31	3.52
Genomic sequence	0% 0	3.23% 1	16.13% 5	80.65% 25	31	3.77
EST	9.68% 3	25.81% 8	22.58% 7	41.94% 13	31	2.97
ORF	0% 0	9.68% 3	19.35% 6	70.97% 22	31	3.61
SNP	0% 0	12.90% 4	29.03% 9	58.06% 18	31	3.45
Non-synonymous	9.68% 3	25.81% 8	12.90% 4	51.61% 16	31	3.06
Allele frequency	3.23% 1	35.48% 11	25.81% 8	35.48% 11	31	2.94
Proteomics	0% 0	16.13% 5	25.81% 8	58.06% 18	31	3.42
Mass spec peptide	6.45% 2	16.13% 5	35.48% 11	41.94% 13	31	3.13
Microarray	0% 0	9.68% 3	32.26% 10	58.06% 18	31	3.48
Expression level/value	6.45% 2	19.35% 6	38.71% 12	35.48% 11	31	3.03
RNA-Seq	3.23% 1	35.48% 11	35.48% 11	25.81% 8	31	2.84
Alignment	0% 0	6.45% 2	12.90% 4	80.65% 25	31	3.74
eQTL	54.84% 17	29.03% 9	12.90% 4	3.23% 1	31	1.65
ChIP-Seq	22.58% 7	38.71% 12	32.26% 10	6.45% 2	31	2.23
Histone H3	22.58% 7	45.16% 14	29.03% 9	3.23% 1	31	2.13

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

Answered: 29 Skipped: 2

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Total	Average Rating
Nucleosome mapping	41.38% 12	44.83% 13	13.79% 4	0% 0	29	1.72
Syntenly	6.90% 2	48.28% 14	13.79% 4	31.03% 9	29	2.69
Ortholog	0% 0	13.79% 4	20.69% 6	65.52% 19	29	3.52
Contig	0% 0	27.59% 8	34.48% 10	37.93% 11	29	3.10
GO Terms/Numbers	17.24% 5	24.14% 7	34.48% 10	24.14% 7	29	2.66
EC Number	37.93% 11	27.59% 8	10.34% 3	24.14% 7	29	2.21
Signal Peptide	6.90% 2	17.24% 5	37.93% 11	37.93% 11	29	3.07
BLAST	0% 0	3.45% 1	13.79% 4	82.76% 24	29	3.79
Low complexity region	17.24% 5	27.59% 8	27.59% 8	27.59% 8	29	2.66
Genomic colocation	24.14% 7	37.93% 11	24.14% 7	13.79% 4	29	2.28
Mapping	3.45% 1	34.48% 10	37.93% 11	24.14% 7	29	2.83
Transcript	0% 0	3.45% 1	20.69% 6	75.86% 22	29	3.72
Protein Data Bank	6.90% 2	13.79% 4	31.03% 9	48.28% 14	29	3.21
Transmembrane domains	10.34% 3	3.45% 1	27.59% 8	58.62% 17	29	3.34
Protein export domains	10.34% 3	24.14% 7	27.59% 8	37.93% 11	29	2.93
Epitope	6.90% 2	13.79% 4	27.59% 8	51.72% 15	29	3.24
Splice site junction	10.34% 3	37.93% 11	31.03% 9	20.69% 6	29	2.62
Comparative genomic hybridization	41.38% 12	27.59% 8	24.14% 7	6.90% 2	29	1.97
FASTA	0% 0	24.14% 7	10.34% 3	65.52% 19	29	3.41
GFF	67.86% 19	17.86% 5	0% 0	14.29% 4	28	1.61
BAM	62.07% 18	27.59% 8	0% 0	10.34% 3	29	1.59
Genome Browser	3.45% 1	20.69% 6	31.03% 9	44.83% 13	29	3.17
BLASTX	3.45% 1	34.48% 10	20.69% 6	41.38% 12	29	3.00

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OrthoMCL	58.62% 17	20.69% 6	10.34% 3	10.34% 3	29	1.72
CDS	24.14% 7	17.24% 5	13.79% 4	44.83% 13	29	2.79

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

Answered: 30 Skipped: 1

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Total	Average Rating
PubMed Compound	46.67% 14	20% 6	23.33% 7	10% 3	30	1.97
Metabolic Pathway	0% 0	23.33% 7	30% 9	46.67% 14	30	3.23
Metabolomics	13.33% 4	16.67% 5	40% 12	30% 9	30	2.87
Substrate	3.33% 1	6.67% 2	50% 15	40% 12	30	3.27
KEGG Pathway	26.67% 8	33.33% 10	26.67% 8	13.33% 4	30	2.27
Chip-Chip	26.67% 8	50% 15	23.33% 7	0% 0	30	1.97