

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
BLAST	0.0% (0)	0.0% (0)	20.7% (6)	79.3% (23)	3.79	29
BLAST X	3.4% (1)	10.3% (3)	27.6% (8)	58.6% (17)	3.41	29
BLASTP	0.0% (0)	17.2% (5)	24.1% (7)	58.6% (17)	3.41	29
OrthoMCL	51.7% (15)	34.5% (10)	13.8% (4)	0.0% (0)	1.62	29
KEGG Map	41.4% (12)	20.7% (6)	17.2% (5)	20.7% (6)	2.17	29
PROSITE motif	34.5% (10)	20.7% (6)	27.6% (8)	17.2% (5)	2.28	29
PFAM domain	17.2% (5)	13.8% (4)	44.8% (13)	24.1% (7)	2.76	29
Signal peptide	0.0% (0)	20.7% (6)	24.1% (7)	55.2% (16)	3.34	29
GPI anchor	10.3% (3)	17.2% (5)	27.6% (8)	44.8% (13)	3.07	29
HMM	34.5% (10)	10.3% (3)	27.6% (8)	27.6% (8)	2.48	29
Transmembrane domain	0.0% (0)	6.9% (2)	27.6% (8)	65.5% (19)	3.59	29
Gene	0.0% (0)	0.0% (0)	3.4% (1)	96.6% (28)	3.97	29
Contig	0.0% (0)	10.3% (3)	13.8% (4)	75.9% (22)	3.66	29
Scaffold	3.4% (1)	17.2% (5)	34.5% (10)	44.8% (13)	3.21	29
Chromosome	0.0% (0)	3.4% (1)	6.9% (2)	89.7% (26)	3.86	29
Next generation sequencing	6.9% (2)	17.2% (5)	31.0% (9)	44.8% (13)	3.14	29
RNA-sequence	3.4% (1)	6.9% (2)	24.1% (7)	65.5% (19)	3.52	29
454 sequencing	24.1% (7)	13.8% (4)	31.0% (9)	31.0% (9)	2.69	29
Illumina sequencing	10.3% (3)	31.0% (9)	24.1% (7)	34.5% (10)	2.83	29
Solexa sequencing	17.2% (5)	34.5% (10)	31.0% (9)	17.2% (5)	2.48	29
answered question						29

skipped question

0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
ChIP	24.1% (7)	24.1% (7)	31.0% (9)	20.7% (6)	2.48	29
ChIP-chip	27.6% (8)	24.1% (7)	34.5% (10)	13.8% (4)	2.34	29
ChIP-sequence	24.1% (7)	31.0% (9)	34.5% (10)	10.3% (3)	2.31	29
Daltons	10.3% (3)	0.0% (0)	13.8% (4)	75.9% (22)	3.55	29
Annotated	3.4% (1)	6.9% (2)	17.2% (5)	72.4% (21)	3.59	29
Curated annotation	13.8% (4)	13.8% (4)	17.2% (5)	55.2% (16)	3.14	29
Automated annotation	13.8% (4)	17.2% (5)	24.1% (7)	44.8% (13)	3.00	29
Syntenic/Syteny	10.3% (3)	17.2% (5)	24.1% (7)	48.3% (14)	3.10	29
EST	3.4% (1)	10.3% (3)	37.9% (11)	48.3% (14)	3.31	29
EST Clusters	10.3% (3)	31.0% (9)	24.1% (7)	34.5% (10)	2.83	29
EC numbers	10.3% (3)	27.6% (8)	20.7% (6)	41.4% (12)	2.93	29
GO term	13.8% (4)	17.2% (5)	20.7% (6)	48.3% (14)	3.03	29
CDS	6.9% (2)	13.8% (4)	17.2% (5)	62.1% (18)	3.34	29
Translation	3.4% (1)	0.0% (0)	6.9% (2)	89.7% (26)	3.83	29
Attributes	17.2% (5)	20.7% (6)	31.0% (9)	31.0% (9)	2.76	29
Metabolic Pathway	3.4% (1)	3.4% (1)	24.1% (7)	69.0% (20)	3.59	29
Genbank Protein Record	3.4% (1)	13.8% (4)	24.1% (7)	58.6% (17)	3.38	29
Genomic context	10.3% (3)	6.9% (2)	37.9% (11)	44.8% (13)	3.17	29
answered question						29
skipped question						0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
GO process	34.5% (10)	17.2% (5)	24.1% (7)	24.1% (7)	2.38	29
GO component	34.5% (10)	17.2% (5)	24.1% (7)	24.1% (7)	2.38	29
GO function	31.0% (9)	17.2% (5)	24.1% (7)	27.6% (8)	2.48	29
GeneDB	0.0% (0)	3.4% (1)	34.5% (10)	62.1% (18)	3.59	29
RefSeqs	13.8% (4)	27.6% (8)	27.6% (8)	31.0% (9)	2.76	29
CYC Metabolic pathways	69.0% (20)	20.7% (6)	6.9% (2)	3.4% (1)	1.45	29
SAGE Tags	41.4% (12)	41.4% (12)	17.2% (5)	0.0% (0)	1.76	29
PDB structures	27.6% (8)	27.6% (8)	20.7% (6)	24.1% (7)	2.41	29
SignalP	24.1% (7)	17.2% (5)	20.7% (6)	37.9% (11)	2.72	29
PlasmoAP	51.7% (15)	27.6% (8)	13.8% (4)	6.9% (2)	1.76	29
Mass spec data	6.9% (2)	20.7% (6)	41.4% (12)	31.0% (9)	2.97	29
Metabolomics	10.3% (3)	20.7% (6)	37.9% (11)	31.0% (9)	2.90	29
Microarray	3.4% (1)	6.9% (2)	55.2% (16)	34.5% (10)	3.21	29
Affymetrix probes	27.6% (8)	34.5% (10)	20.7% (6)	17.2% (5)	2.28	29
Affymetrix Genotyped SNP probes	34.5% (10)	31.0% (9)	13.8% (4)	20.7% (6)	2.21	29
cDNA microarray	3.4% (1)	24.1% (7)	34.5% (10)	37.9% (11)	3.07	29
Oligonucleotide microarray	6.9% (2)	31.0% (9)	34.5% (10)	27.6% (8)	2.83	29
Pearson Correlation	51.7% (15)	17.2% (5)	17.2% (5)	13.8% (4)	1.93	29
Gametocyte	10.3% (3)	0.0% (0)	37.9% (11)	51.7% (15)	3.31	29
Non-Redundant Protein DB (NRDB)	31.0% (9)	20.7% (6)	24.1% (7)	24.1% (7)	2.41	29
Hydropathy	31.0% (9)	13.8% (4)	24.1% (7)	31.0% (9)	2.55	29
answered question						29
skipped question						0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
Helix	0.0% (0)	13.8% (4)	10.3% (3)	75.9% (22)	3.62	29
Coil	3.4% (1)	10.3% (3)	17.2% (5)	69.0% (20)	3.52	29
AA sequence	3.4% (1)	6.9% (2)	3.4% (1)	86.2% (25)	3.72	29
Promoter	0.0% (0)	6.9% (2)	6.9% (2)	86.2% (25)	3.79	29
Centromere	3.4% (1)	3.4% (1)	20.7% (6)	72.4% (21)	3.62	29
Oligo	3.4% (1)	0.0% (0)	10.3% (3)	86.2% (25)	3.79	29
Sequence Similarity	0.0% (0)	3.4% (1)	10.3% (3)	86.2% (25)	3.83	29
cDNA	0.0% (0)	3.4% (1)	17.2% (5)	79.3% (23)	3.76	29
ePCR	34.5% (10)	20.7% (6)	20.7% (6)	24.1% (7)	2.34	29
Peptide Mass Fingerprinting	31.0% (9)	17.2% (5)	24.1% (7)	27.6% (8)	2.48	29
Motif Search	3.4% (1)	10.3% (3)	51.7% (15)	34.5% (10)	3.17	29
Mitochondrion	3.4% (1)	10.3% (3)	13.8% (4)	72.4% (21)	3.55	29
Apicoplast	13.8% (4)	24.1% (7)	10.3% (3)	51.7% (15)	3.00	29
ProDom	51.7% (15)	27.6% (8)	13.8% (4)	6.9% (2)	1.76	29
Phylogeny	3.4% (1)	10.3% (3)	20.7% (6)	65.5% (19)	3.48	29
Protein coding	0.0% (0)	10.3% (3)	6.9% (2)	82.8% (24)	3.72	29
Pseudogene	0.0% (0)	13.8% (4)	24.1% (7)	62.1% (18)	3.48	29
snRNA	13.8% (4)	13.8% (4)	37.9% (11)	34.5% (10)	2.93	29
Telomere	0.0% (0)	6.9% (2)	20.7% (6)	72.4% (21)	3.66	29
rRNA	0.0% (0)	6.9% (2)	20.7% (6)	72.4% (21)	3.66	29
PDB structures	27.6% (8)	17.2% (5)	13.8% (4)	41.4% (12)	2.69	29
SignalP	20.7% (6)	20.7% (6)	13.8% (4)	44.8% (13)	2.83	29

PlasmoAP	55.2% (16)	17.2% (5)	17.2% (5)	10.3% (3)	1.83	29
Mass spec data	3.4% (1)	31.0% (9)	27.6% (8)	37.9% (11)	3.00	29
Metabolomics	13.8% (4)	17.2% (5)	34.5% (10)	34.5% (10)	2.90	29
Microarray	3.4% (1)	13.8% (4)	41.4% (12)	41.4% (12)	3.21	29
Affymetrix probes	31.0% (9)	37.9% (11)	10.3% (3)	20.7% (6)	2.21	29
Affymetrix Genotyped SNP probes	34.5% (10)	27.6% (8)	17.2% (5)	20.7% (6)	2.24	29
cDNA microarray	6.9% (2)	17.2% (5)	34.5% (10)	41.4% (12)	3.10	29
Oligonucleotide microarray	6.9% (2)	27.6% (8)	31.0% (9)	34.5% (10)	2.93	29
Pearson Correlation	44.8% (13)	24.1% (7)	6.9% (2)	24.1% (7)	2.10	29
Gametocyte	10.3% (3)	10.3% (3)	24.1% (7)	55.2% (16)	3.24	29
Non-Redundant Protein DB (NRDB)	31.0% (9)	17.2% (5)	24.1% (7)	27.6% (8)	2.48	29
Hydropathy	24.1% (7)	24.1% (7)	20.7% (6)	31.0% (9)	2.59	29
answered question						29
skipped question						0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
low complexity	10.3% (3)	27.6% (8)	24.1% (7)	37.9% (11)	2.90	29
SNPs	0.0% (0)	13.8% (4)	24.1% (7)	62.1% (18)	3.48	29
RefSeq protein	13.8% (4)	20.7% (6)	31.0% (9)	34.5% (10)	2.86	29
GenPept protein	34.5% (10)	24.1% (7)	17.2% (5)	24.1% (7)	2.31	29
Expression timing	20.7% (6)	20.7% (6)	44.8% (13)	13.8% (4)	2.52	29
Expression profile	0.0% (0)	27.6% (8)	37.9% (11)	34.5% (10)	3.07	29
Expression level	0.0% (0)	20.7% (6)	44.8% (13)	34.5% (10)	3.14	29
Expression profiles correlation	24.1% (7)	31.0% (9)	34.5% (10)	10.3% (3)	2.31	29
ncRNA	37.9% (11)	17.2% (5)	27.6% (8)	17.2% (5)	2.24	29
Proteomics	3.4% (1)	3.4% (1)	27.6% (8)	65.5% (19)	3.55	29
Intergenic region	3.4% (1)	3.4% (1)	24.1% (7)	69.0% (20)	3.59	29
UTR	0.0% (0)	24.1% (7)	13.8% (4)	62.1% (18)	3.38	29
Ortholog	3.4% (1)	0.0% (0)	27.6% (8)	69.0% (20)	3.62	29
Homolog	3.4% (1)	0.0% (0)	27.6% (8)	69.0% (20)	3.62	29
Paralog	3.4% (1)	17.2% (5)	17.2% (5)	62.1% (18)	3.38	29
Xenolog	41.4% (12)	20.7% (6)	20.7% (6)	17.2% (5)	2.14	29
Ortholog Group	3.4% (1)	17.2% (5)	44.8% (13)	34.5% (10)	3.10	29
Orthology-based Phylogenetic profile	13.8% (4)	24.1% (7)	37.9% (11)	24.1% (7)	2.72	29
PDB structure	24.1% (7)	17.2% (5)	27.6% (8)	31.0% (9)	2.66	29
answered question						29
skipped question						0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
Pubcrawler	65.5% (19)	13.8% (4)	13.8% (4)	6.9% (2)	1.62	29
Query	6.9% (2)	20.7% (6)	13.8% (4)	58.6% (17)	3.24	29
Boolean	37.9% (11)	10.3% (3)	20.7% (6)	31.0% (9)	2.45	29
Set operation	55.2% (16)	20.7% (6)	6.9% (2)	17.2% (5)	1.86	29
Join (as in set theory)	37.9% (11)	17.2% (5)	13.8% (4)	31.0% (9)	2.38	29
Intersect (as in set theory)	37.9% (11)	17.2% (5)	13.8% (4)	31.0% (9)	2.38	29
Subtract (as in set theory)	37.9% (11)	17.2% (5)	13.8% (4)	31.0% (9)	2.38	29
Locus	3.4% (1)	6.9% (2)	10.3% (3)	79.3% (23)	3.66	29
Wildcard character	41.4% (12)	6.9% (2)	20.7% (6)	31.0% (9)	2.41	29
tRNA	0.0% (0)	10.3% (3)	17.2% (5)	72.4% (21)	3.62	29
Scaffolds	13.8% (4)	24.1% (7)	27.6% (8)	34.5% (10)	2.83	29
SNP density	13.8% (4)	17.2% (5)	34.5% (10)	34.5% (10)	2.90	29
Genetic Markers	10.3% (3)	0.0% (0)	20.7% (6)	69.0% (20)	3.48	29
Annotation Density	31.0% (9)	27.6% (8)	10.3% (3)	31.0% (9)	2.41	29
EST Alignments	17.2% (5)	24.1% (7)	17.2% (5)	41.4% (12)	2.83	29
TIGR	24.1% (7)	24.1% (7)	20.7% (6)	31.0% (9)	2.59	29
Unigene	41.4% (12)	27.6% (8)	13.8% (4)	17.2% (5)	2.07	29
NCBI	0.0% (0)	0.0% (0)	3.4% (1)	96.6% (28)	3.97	29
GLEAN Gene	72.4% (21)	13.8% (4)	6.9% (2)	6.9% (2)	1.48	29
TigrScan Gene	72.4% (21)	17.2% (5)	3.4% (1)	6.9% (2)	1.45	29
TwinScan Gene Models	75.9% (22)	13.8% (4)	6.9% (2)	3.4% (1)	1.38	29
answered question						29
skipped question						0

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

	Not at all familiar	Have heard of it	Slightly familiar	Very familiar	Rating Average	Response Count
Repeat Regions	0.0% (0)	10.3% (3)	27.6% (8)	62.1% (18)	3.52	29
3 -frame translation (reverse)	6.9% (2)	6.9% (2)	17.2% (5)	69.0% (20)	3.48	29
3 -frame translation (forward)	6.9% (2)	6.9% (2)	17.2% (5)	69.0% (20)	3.48	29
DNA/GC Content	0.0% (0)	0.0% (0)	17.2% (5)	82.8% (24)	3.83	29
Genotyped SNPs	6.9% (2)	34.5% (10)	20.7% (6)	37.9% (11)	2.90	29
Microsatellite	0.0% (0)	27.6% (8)	31.0% (9)	41.4% (12)	3.14	29
Microsatellite map	6.9% (2)	34.5% (10)	31.0% (9)	27.6% (8)	2.79	29
GBrowse	55.2% (16)	24.1% (7)	3.4% (1)	17.2% (5)	1.83	29
GBrowse track	58.6% (17)	24.1% (7)	6.9% (2)	10.3% (3)	1.69	29
Parasite strain	3.4% (1)	0.0% (0)	6.9% (2)	89.7% (26)	3.83	29
Parasite isolate	3.4% (1)	6.9% (2)	6.9% (2)	82.8% (24)	3.69	29
Allele	0.0% (0)	6.9% (2)	6.9% (2)	86.2% (25)	3.79	29
Allele frequency	0.0% (0)	6.9% (2)	17.2% (5)	75.9% (22)	3.69	29
Major Allele	0.0% (0)	17.2% (5)	31.0% (9)	51.7% (15)	3.34	29
Minor Allele	0.0% (0)	17.2% (5)	31.0% (9)	51.7% (15)	3.34	29
Synonymous	0.0% (0)	17.2% (5)	17.2% (5)	65.5% (19)	3.48	29
Nonsynonymous	0.0% (0)	17.2% (5)	17.2% (5)	65.5% (19)	3.48	29
Nonsense	3.4% (1)	13.8% (4)	17.2% (5)	65.5% (19)	3.45	29
Dn/Ds	55.2% (16)	17.2% (5)	10.3% (3)	17.2% (5)	1.90	29
Interpro	37.9% (11)	24.1% (7)	17.2% (5)	20.7% (6)	2.21	29
Epitope	0.0% (0)	6.9% (2)	20.7% (6)	72.4% (21)	3.66	29
Isoelectric	6.9% (2)	13.8% (4)	17.2% (5)	62.1% (18)	3.34	29

Spectra	10.3% (3)	24.1% (7)	17.2% (5)	48.3% (14)	3.03	29
ORF	0.0% (0)	0.0% (0)	10.3% (3)	89.7% (26)	3.90	29
answered question						29
skipped question						0