*Research question: what is the content of contemporary scientific research?*

**Field of studies**

|  |  |
| --- | --- |
| neuroscience | 226 |
| molecular biology | 166 |
| immunology | 154 |
| cell biology | 124 |
| physiology | 97 |
| oncology | 96 |
| evolutionary biology | 94 |
| ecology | 92 |
| microbiology | 90 |
| genetics | 87 |
| biochemistry | 78 |
| developmental biology | 65 |
| biophysics | 60 |
| plant biology | 58 |
| computational biology | 50 |
| medical biology | 52 |
| virology | 41 |
| pharmacology | 41 |
| epidemiology | 28 |
| paleontology | 21 |
| clinical biology | 21 |
| zoology | 17 |
| behavioral biology | 16 |
| endocrinology | 14 |
| population biology | 12 |
| anthropology | 9 |
| agricultural biology | 8 |
| archaeology | 7 |
| environmental science | 6 |
| mathematical biology | 6 |
| biogeography | 4 |
| marine biology | 3 |
| structural biology | 2 |
| nanotechnology | 1 |

**Organisational levels**

|  |  |
| --- | --- |
| cellular | 913 |
| organism | 846 |
| organ | 540 |
| molecular | 438 |
| population | 247 |
| tissue | 181 |
| organ system | 133 |
| ecosystem | 84 |
| community | 73 |
| ecosphere | 2 |
| biome | 1 |

**Research methods**

|  |  |
| --- | --- |
| 1. Lab-based | 1029 |
| 3. Computational / data-driven | 692 |
| 2. Fieldwork | 257 |
| 5. Clinical | 127 |
| 4. Mathematical / logic | 114 |
| 6. Questionnaires / interviews | 20 |

|  |  |
| --- | --- |
| 1. Lab-based | 1029 |
| 2. Fieldwork | 257 |
| 3. Computational / data-driven | 692 |
| 4. Mathematical / logic | 114 |
| 5. Clinical | 127 |
| 6. Questionnaires / interviews | 20 |

**Model organisms**

|  |  |
| --- | --- |
| **Model** | **Count** |
| Human cells | 311 |
| Bacteria | 270 |
| Mice | 229 |
| Human cancer cells | 193 |
| Humans | 193 |
| Plants | 183 |
| Transgenic / KI / KO / mutant mice | 119 |
| Mammals | 102 |
| Mouse cells | 93 |
| Insects | 87 |
| Proteins | 79 |
| Algae | 54 |
| Fish | 47 |
| Human tissue | 47 |
| Primates | 46 |
| Rats | 45 |
| Virus | 44 |
| Cells | 43 |
| Mouse cancer cells | 40 |
| Birds | 39 |
| Mammalian cells | 31 |
| Marine organisms | 31 |
| Extinct species | 28 |
| Insect cells | 28 |
| Fungi | 26 |
| Mollusca | 24 |
| Reptiles | 23 |
| Nematodes | 20 |
| In silico models | 19 |
| Amphibians | 18 |
| Human liquids | 15 |
| DNA / RNA | 13 |
| Human organoids | 13 |
| Other | 13 |
| Protists | 13 |
| Primate cells | 12 |
| Membranes | 11 |
| Mouse tissue | 11 |
| Community | 10 |
| Animals | 9 |
| Molecules | 9 |
| Vesicles | 8 |
| Protozoa | 7 |
| Rat cells | 7 |
| Tissue | 6 |
| Omics | 5 |
| Robotics | 5 |
| Animal tissue | 4 |
| Eukaryota | 4 |
| Human population | 4 |
| Human organs | 3 |
| Mammalian tissue | 3 |
| Cancer cells | 2 |
| Phytoplankton | 2 |
| Plant organelles | 2 |
| Plasmids | 2 |
| Animal organ | 1 |
| Archaea | 1 |
| Insect tissue | 1 |
| Mammalian liquids | 1 |
| Mouse organ | 1 |
| Pests | 1 |
| Plant cells | 1 |
| Rat tissue | 1 |

Molecular & Cellular = 885

* Cells: 526
* Cancer cells: 235
* Molecules: 124

Tissue level = 107

* Tissue: 73
* Organs: 18
* Liquids: 16

Organisms = 1636

* Rodents: 393
* Microbes: 322
* Primates: 239
* Plants: 183
* Aquatic: 78
* Other: 421

Population / community = 43

* Extinct species
* Communities: 10
* Human population 4
* Pests: 1

Other = 42

* In silico models: 19
* Various: 13
* Omics: 5
* Robotics; 5

**Analysis methods**

|  |  |  |  |
| --- | --- | --- | --- |
| Statistical | 4220 | General | 967 |
| Statistical tests | 2178 |
| Correlation | 228 |
| Linear models | 376 |
| Effect size | 106 |
| Survival analysis | 140 |
| Models | 41 |
| Bayesian | 184 |
| Molecular / genetic | 2698 | Image processing | 214 |
| Molecular visualisation (2D/3D/4D) | 489 |
| Lab methods | 1396 |
| Bioinformatics | 599 |
| Computational | 1354 | Machine learning | 123 |
| Software | 828 |
| Algorithms | 403 |
| Mathematical | 1202 | Various | 699 |
| Dimensionality reduction | 228 |
| Distributions | 275 |
| Various | 129 | Species diversity | 31 |
| Phylogenetic trees | 55 |
| Other | 43 |

Statistical

*General* (967)

* Means = 256
* Variance = 251
* Mean ± standard deviation = 25
* SEm (Standard Error of the Mean) = 105
* Confidence intervals = 105
* P-value = 222
* E-value = 3

*Statistical tests* (2178)

Means / counts (1236)

* ANOVA = 516
* T-test = 499
* Z-test = 39
* Geisser-Greenhouse correction = 11
* Bartlett's test = 5
* Wald's Test = 18
* Permutation test = 42
* Fisher's Exact test = 71
* Chi-squared = 34
* Barnard exact test = 1

Non-parametric (499)

* MWU = 147
* Wilcoxon signed-rank test = 60
* Kruskal-Wallis = 93
* Friedman = 10
* Kolmogorov-Smirnov = 42
* Rank-sum test = 66
* Levene's = 9
* Shapiro-Wilk = 64
* D’Agostino & Pearson omnibus normality test = 8

Post-hoc (433)

* Tukey = 186
* Bonferroni = 86
* Dunnett = 53
* Dunn's = 51
* Sidak = 34
* Holm = 15
* LSD = 12
* Duncan = 6

*Correlation* (228)

* Pearson = 140
* Spearman = 82
* Kendall = 6

*Linear models*

* Linear = 100
* Multiple = 25
* GLM = 150
* Mixed effect models = 90
* LASSO = 11

*Effect size* (106)

* Cohen's D = 14
* R-squared = 88
* Standardized mean difference = 3
* Cohen's F = 1

*Survival analysis* (140)

* Cox PH model = 43
* Kaplan-Meier Estimator = 45
* Random Survival Forests = 1
* Logrank / Mantel-Cox = 51

*Models* (41)

* AIC = 32
* SEM = 9

*Bayesian* (184)

* Bayesian statistics = 108
* Likelihood = 72
* Bayesian = 4

Molecular / genetic

*Lab methods* (1396)

* Microscopy = 173
* Immublotting = 78
* Gel electrophorese = 107
* RNA seq = 132
* DNA seq = 65
* Mass spectrometry = 136
* Cyro = 50
* PCR = 170
* Sanger sequencing = 11
* Spectroscopy = 39
* Flow cytometry = 86
* ELISA = 39
* Staining methods = 82
* Immunoprecipitation = 32
* X-ray techniques = 20
* Luciferase essay = 18
* ATAC-seq = 17
* Nanodrop = 11
* Chromatography = 95
* BLAST = 35

*Bioinformatics* (559)

* FlowJo = 48
* Cytoscape = 23
* DESeq2 = 76
* Bedtools = 20
* GSEA = 41
* SAMtools = 28
* deepTools = 10
* STAR = 18
* Seurat = 66
* Pipeline = 52
* burrows wheeler aligner = 22
* limma = 23
* KEGG = 20
* MAFFT = 18
* IGV (Integrative Genomics Viewer) = 19
* Gene-ontology = 33
* edgeR = 30
* featurecounts = 25
* bowtie2 = 27

*Molecular visualization (2D/3D/4D)* (489)

* Chimera = 119
* PyMOL = 53
* PHENIX = 78
* COOT = 64
* Imaris = 27
* RELION = 45
* Cryosparc = 42
* MolProbity = 31
* Motioncor2 = 30

*Image processing* (214)

* ImageJ = 153
* Fiji = 61

Computational

*Machine learning / AI* (123)

* Neural networks = 56
* Alphafold = 45
* Random forest = 22

*Software* (828)

* R = 250
* GraphPad Prism = 222
* R packages = 223
* SPSS = 18
* Python = 42
* MatLab = 73

*Algorithms* (403)

* Hierarchical clustering = 88
* Algorithm = 284
* Markov chain Monte Carlo = 31

Mathematical

*Various* (699)

* ROC = 60
* AUC = 60
* FDR = 91
* Fourier shell correlation = 36
* Benjamini-Hochberg correction = 55
* RMSD = 40
* 2-ΔΔCt method = 32
* IC50 = 24
* Volcano plot = 22
* Hill equation = 14
* Euclidean distance = 31
* Michaelis-Menten kinetics = 15
* Logarithm = 155
* Fold change = 60

*Dimensionality reduction* (228)

* PCA = 130
* Linear discriminant analysis = 25
* T-SNE (t-distributed Stochastic Neighbor Embedding) = 18
* UMAP (Uniform Manifold Approximation and Projection) = 55

*Distributions* (275)

* Normal / Gaussian = 52
* Binomial = 13
* LOESS smoothing = 14
* Kernel density estimate = 18
* Bootstrap = 47
* Data transformation = 131

**Various**

*Species diversity* (31)

* Bray-Curtis dissimilarity = 13
* Shannon alpha diversity= 12
* Simpson beta diversity = 6

*Phylogeny* (55)

* Phylogenetic trees = 50
* Maximum parsimony (MP) = 5

*Other* (43)

* ggplot = 41
* Cohen’s kappa = 2

**Terminology**

|  |  |  |
| --- | --- | --- |
| **Field of studies** | **# distinct words / word groups** | **# words (total count)** |
| Clinical / medical biology | 18340 | 33212 |
| Biochemistry / molecular biology | 16494 | 27733 |
| Cell biology | 9292 | 19395 |
| Genetics | 9134 | 18827 |
| Physiology | 5064 | 8117 |
| Biophysics | 5032 | 7757 |
| Pharmacology | 4854 | 7790 |
| Mathematical biology | 4507 | 8212 |
| Microbiology | 3130 | 5285 |
| Immunology | 3029 | 6672 |
| Epidemiology | 3012 | 4749 |
| Environmental science | 2888 | 5081 |
| Plant biology | 2881 | 4232 |
| Oncology | 2820 | 5398 |
| Neuroscience | 2792 | 4852 |
| Computational biology | 2615 | 4753 |
| Evolutionary biology | 2395 | 4569 |
| Zoology | 2142 | 3328 |
| Biogeography | 1762 | 2824 |
| Ecology | 1699 | 2590 |
| Agricultural biology | 1462 | 2035 |
| Marine biology | 1410 | 1834 |
| Developmental biology | 1351 | 2015 |
| Virology | 1287 | 2131 |
| Population biology | 1256 | 2176 |
| Anthropology | 933 | 1416 |
| Behavioral biology | 923 | 1165 |
| Archaeology | 525 | 727 |
| Palaeontology | 408 | 587 |
| Endocrinology | 407 | 669 |

Field of studies

Word combinations top 10 per field of studies

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Physiology** | **Plant biology** | **Population** | **Virology** | **Zoology** |
| Reactive oxygen species (ROS) | Ecosystem function | Abundance | Pathogenesis | Morphology |
| Antibody | Photosynthesis | Genetic drift | SARS-CoV | Species |
| Neural circuit | Cell wall | Growth rate | Viral particles | Abundance |
| Mutation rate | Nitrocellulose membrane | Effective population size | Lentivirus | Taxonomy |
| Metabolism | Stem cell | Population structure | Pathogen | Vertebrate |
| Monoclonal antibody | Chloroplast | Population dynamics | Sequence read archive | Habitat |
| Substrate | Immune system | Mortality | Infection | Migration |
| Blood-brain barrier | Germination | Immigration | Replicating viruses | Mammal |
| Substrate specificity | Model system | Gene flow | Adenoassociated viral vectors | Diversity |
| Lipid metabolism | Seedling | Extinction | Multiplicities of infection (MOI) | Turnover |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Microbiology** | **Neuroscience** | **Oncology** | **Palaeontology** | **Pharmacology** |
| Plasmid | Neurons | Mutation | Fossil record | Binding affinity |
| Genome | Astrocytes | Phylogenetic | Stratigraphy | Protease inhibitor |
| E.coli | Synaptic plasticity | Apoptosis | Extinction | GAPDH |
| Pathogenesis | Central nervous system (CNS) | T cell proliferation | Palaeocene | Enzyme |
| Cell culture | Hippocampus | Tumour micro-environment | Anaerobic chamber | Plasma membrane |
| Whole genome sequencing | Microglia | Cytotoxicity | Extinction coefficient | Metabolism |
| Lentivirus | Neuronal activity | Mutation rate | Fossil calibration | Protein Data Bank (PDB) |
| Ribosome | Neurogenesis | Angiogenesis | Taphonomy | Cytotoxicity |
| Lipopolysaccharide | Neuroimaging | DNA repair | Local extinction | Metabolite |
| Pathogen | Prefrontal cortex | Immunotherapy | Extinction rate | Binding site |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Evolutionary** | **Genetics** | **Immunology** | **Marine** | **Mathematical** |
| Phylogeny | Gene expression | Cytokines | Salinity | Statistical significance |
| Mutations | RNA sequence | Immuno-fluorescence | Zebrafish | Statistical analysis |
| Allele frequency | Transcription factor | Immuno-histochemistry | Seasonality | Statistical power |
| Mutation rate | Mutation | Antibody | Phytoplankton | Simulation |
| Positive selection | cDNA | Macrophage | Biodiversity | Logistic regression |
| Fitness coefficient of variation | Gene ontology | Immune response | Mammals | Biostatistics |
| Natural selection | mRNA | CD3+ T cells | Zooplankton | Statistical model |
| Genetic drift | Genotype | Immunoblotting | Invertebrates | Computational mode. |
| Genetic variation | Phylogenetic tree | Immunopreci-pitation | Plankton | Deep learning |
| Positive selection | Transcription | Immunostaining | Sea surface temperature (SST) | Neural network |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Developmental** | **Ecology** | **Endocrinology** | **Environmental** | **Epidemiology** |
| Differentiation | Species richness | Oestrogen receptor | Species richness | False discovery rate |
| Lineage | Biodiversity | Insulin | Agrobiodiversity | Pathogenesis |
| Segmentation | Climate change | Hypothalamus | Climate change | Mutation rate |
| Morphogenesis | Ecosystem services | Androgen receptor | Species | Transmission electron microscope |
| Cell fate | Population structure | Leptin | Ecosystem function | Mortality |
| Stem cells | Effective population size | Progesterone receptor | Environmental stress | Substrate |
| Embryogenesis | Population dynamics | Insulin signalling | Plant species distribution | Expression vector |
| Neurodevelopment | Population genetics | Testosterone | Environmental conditions | Growth rate |
| Neuronal differentiation | Conservation | Sex steroid hormone | Ammonium bicarbonate | Prevalence |
| Hematopoietic stem cells | Species diversity | Pancreas | Ecosystem | Vector |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Biogeography** | **Biophysics** | **Cell biology** | **Clinical / medic** | **Computational** |
| Biodiversity | Mass spectrometry | Transcription factor | Gene expression | Bioinformatics |
| Climate change | Electron microscopy | RNA sequence | Mutation | Sequence alignment |
| Ecosystem | Cryoelectron microscopy | Flow cytometer | Biological replicates | Machine learning |
| Species distribution | Molecular dynamics | Cytokine | cDNA | Protein structure |
| Environmental stress | Electron density | cDNA | Cytokines | Simulation |
| Spatial distribution | Neural circuits | mRNA | Gene ontology | Pipeline |
| Environmental conditions | Transmission electron microscopy | Transcription | RNA sequencing | Transcriptomics |
| Ecological niche | Plasma | cDNA | mRNA | Genomics |
| Ecology | Electron density map | Posttranslational modifications | Immune response | Computational modelling |
| Habitat | Electron transport chain | HEK293 cells | Phylogenetic tree | Convolutional neural network |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Agricultural** | **Anthropology** | **Archaeology** | **Behavioral** | **Biochemistry** |
| Photosynthesis | Evolution | Fossil record | Dispersal | Western blot |
| Chloroplast | Evolutionary history | Radiocarbon dating | Reproductive success | Mass spectrometry |
| Germination | Lineage | Artifacts | Behavioral performance | Immuno-histochemistry |
| Leaf height | Convergent evolution | Stratigraphy | Reproductive isolation | Macrophage |
| Necropsy | Fossil record | Digestion | Foraging | Phosphorylating |
| Seedlings | Migration | Digital caliper | Reproductive traits | Phylogenetic tree |
| Micropipette | Adaptation | Motion artifacts | Competition | Alphafold |
| Plant biomass | Culture | Biostratigraphy | Dispersal limitation | Hydrogen bond |
| Seed dispersal | Tools | Droplet digital PCR | Mate choice | Phosphate buff-ered saline (PBS) |
| Soil moisture | Evolutionary conservation | Fossil calibrations | Sexual selection | Site-directed mutagenesis |

Single words top 10 per field of studies

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Physiology** | **Plant biology** | **Population** | **Virology** | **Zoology** |
| Antibody | Tree | Abundance | Virus | Species |
| Neural | Plant | Migration | Infected | Behavior |
| Temperature | Stem | Mortality | Pathogen | Morphology |
| Blood | Root | Extinction | SARS-CoV | Migration |
| Substrate | Vascular | Dispersal | Vaccine | Habitat |
| Metabolic | Ecosystem | Genetic | Vector | Mammal |
| Motor | Leaf | Species | Pathogenesis | Vertebral |
| Body | Seed | History | Lentiviral | Richness |
| Muscle | Pollen | Dynamic | Particle | Reproduction |
| Pressure | (Cell) Wall | Subpopulation | Antiviral | Insects |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Microbiology** | **Neuroscience** | **Oncology** | **Palaeontology** | **Pharmacology** |
| Genome | Neuron | Mutation | Fossil | Binding |
| Viral | Cortex | Genetic | Extinct | Receptor |
| Plasmid | Brain | Tumor | Sediment | Enzyme |
| Infected | Synaptic | Cancer | Record | Inhibitor |
| Pathogen | Axon | Epigenetic | Calibrated | Kinase |
| Culture | Activity | Apoptosis | Stratigraphy | Metabolic |
| Bacterial | Synapse | Proliferation | Rate | Protein |
| Cell | Astrocyte | Checkpoint | Cretaceous | Dose |
| Colony | Postsynaptic | Cytotoxic | Taphonomy | Drug |
| Antibiotic | Plasticity | Rate | Reconstruction | Molecule |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Evolutionary** | **Genetics** | **Immunology** | **Marine** | **Mathematical** |
| Mutation | Gene | Antibody | Fish | Model |
| Phylogenetic | RNA | Immunity | Season | Statistics |
| Selection | DNA | T cell | Ocean | Network |
| Allele | Mutated | Antigen | Sea | Pattern |
| Variation | Genome | Cytokine | Downstream | Quantitative |
| Fitness | Transcription | Macrophage | Plankton | Algorithm |
| Adaptive | Expression | Response | Reef | Computational |
| Divergent | Sequence | B cell | Seahorse | Simulation |
| Frequency | Phylogenetic | Immunofluorescent | Upstream | Probability |
| Homology | Translation | CD4(+ T cell) | Phytoplankton | Bayesian |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Developmental** | **Ecology** | **Endocrinology** | **Environmental** | **Epidemiology** |
| Cell | Population | Insulin | Species | Rate |
| Differentiation | Conservation | Hormone | Ecology | Vector |
| Stem (cell) | Community | Receptor | Carbon | Substrate |
| Embryo | Niche | Signal | Water | Infection |
| Progenitor | Habitat | Gonad | Climate | Pathogen |
| Segmental | Biodiversity | Resistance | Soil | Transmission |
| Induction | Species | Androgen | Conserved | Strategy |
| Pattern | Competition | Oestrogen | Emission | Exposure |
| Morphogenesis | Climate | Growth | Habitat | Risk |
| Stage | (Species) richness | Estrogen | Marine | Health |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Biogeography** | **Biophysics** | **Cell biology** | **Clinical / medic** | **Computational** |
| Distribution | Mass | Cell | Cell | Software |
| Environmental | Electron | Transcription | Protein | Model |
| Climate | Dynamic | RNA | Gene | Predicted |
| Ecosystem | Energy | DNA | DNA | Bioinformatic |
| Landscape | Nuclear | Membrane | RNA | Algorithm |
| Niche | Light | T cell | Mutation | Simulation |
| Migration | Microscopy | Mitochondria | Receptor | Database |
| Habitat | Field | Translation | Expression | Computer |
| Biodiversity | Frequency | Cytokine | Immunity | Network |
| Species | Force | Sequence | Antibody | Neural |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Agricultural** | **Anthropology** | **Archaeology** | **Behavioral** | **Biochemistry** |
| Plant | Evolutionary | Digest | Reproduction | Acid |
| Root | Lineage | Fossil | Social | Buffer |
| Soil | Social | Artifact | Competition | Base |
| Leaf | Fossil | Paradigm | Dispersal | Enzyme |
| Seed | Tools | Skeleton | Community | Phase |
| Crop | Culture | Radiocarbon | Mate | Phenotype |
| Yield | Migration | Record | Predator | Phylogenetic |
| Chloroplast | Agriculture | Dated | Foraging | Amino |
| Photosynthesis | Artifact | Calibrated | Dominant | Reaction |
| Seedling | History | Data | Success | Phosphate |

All terminology

Word combinations and single words top 100

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Word combination** | **Counts** |  | **Single words** | **Counts** |
| gene expression | 259 |  | cell | 5358 |
| statistical significance | 213 |  | protein | 3522 |
| flow cytometry | 201 |  | gene | 2953 |
| standard deviation | 199 |  | sequence | 2398 |
| bioinformatics | 186 |  | model | 2313 |
| RNAseq | 159 |  | analysis | 2220 |
| PCR | 148 |  | activity | 1868 |
| ANOVA | 145 |  | test | 1737 |
| mutation | 144 |  | expression | 1733 |
| ImageJ | 139 |  | signal | 1613 |
| Western blot | 138 |  | structure | 1579 |
| GraphPad Prism | 136 |  | function | 1572 |
| mass spectrometry | 135 |  | fluorescence | 1536 |
| confidence interval | 129 |  | data | 1489 |
| DAPI | 125 |  | genome | 1445 |
| ELISA | 125 |  | s | 1436 |
| NaCl | 120 |  | dna | 1406 |
| biological replicates | 117 |  | rna | 1391 |
| immunofluorescence | 116 |  | mutation | 1377 |
| apoptosis | 115 |  | transcription | 1361 |
| immunohistochemistry | 110 |  | acid | 1300 |
| EDTA | 108 |  | binding | 1267 |
| PBS | 106 |  | domain | 1186 |
| CRISPR/Cas9 | 102 |  | assay | 1177 |
| p-value | 100 |  | system | 1164 |
| sequence alignment | 100 |  | t | 1152 |
| centrifugation | 97 |  | neuron | 1114 |
| qPCR | 95 |  | response | 1103 |
| phosphorylation | 94 |  | imaging | 1045 |
| statistical analysis | 91 |  | rate | 1041 |
| Triton X-100 | 91 |  | interactions | 1040 |
| SDS/PAGE | 90 |  | molecular | 1040 |
| cDNA | 89 |  | antibody | 1035 |
| confocal microscopy | 89 |  | specific | 1033 |
| cytokines | 88 |  | receptor | 1033 |
| oxidative stress | 88 |  | site | 1021 |
| signal transduction | 86 |  | factor | 1016 |
| transcription factor | 86 |  | species | 1002 |
| in vitro | 84 |  | buffer | 973 |
| electron microscopy | 82 |  | statistical | 965 |
| transfection | 81 |  | immune | 943 |
| gene ontology | 79 |  | membrane | 932 |
| RNA sequencing | 79 |  | biological | 924 |
| fluorescence intensity | 78 |  | based | 910 |
| fluorescence microscopy | 77 |  | genetic | 865 |
| one-way ANOVA | 77 |  | sample | 854 |
| in vivo | 76 |  | time | 853 |
| paraformaldehyde | 74 |  | standard | 824 |
| HEPES | 73 |  | mean | 792 |
| UMAP | 72 |  | region | 785 |
| mRNA | 71 |  | complex | 767 |
| macrophages | 70 |  | anti | 758 |
| plasmid | 70 |  | pathway | 750 |
| DESeq2 | 69 |  | effect | 747 |
| fluorescence | 69 |  | microscopy | 739 |
| Sanger sequencing | 69 |  | distribution | 733 |
| cryoEM | 68 |  | value | 720 |
| immune response | 68 |  | control | 718 |
| Western blotting | 68 |  | density | 715 |
| phylogenetic tree | 67 |  | mass | 712 |
| glycerol | 65 |  | map | 709 |
| site-directed mutagenesis | 65 |  | state | 706 |
| transcription | 65 |  | type | 697 |
| Tris-HCl | 65 |  | level | 676 |
| machine learning | 63 |  | tissue | 674 |
| phosphate-buffered saline | 63 |  | metabolic | 674 |
| RT-qPCR | 63 |  | electron | 670 |
| transcription factors | 63 |  | processing | 669 |
| cytokine | 62 |  | clustering | 666 |
| fold change | 62 |  | neural | 652 |
| binding affinity | 61 |  | positive | 648 |
| genome | 61 |  | selection | 635 |
| immunoblotting | 61 |  | pcr | 632 |
| Seurat | 61 |  | change | 631 |
| chromatin | 60 |  | size | 630 |
| fetal bovine serum | 60 |  | single | 625 |
| GFP | 60 |  | c | 610 |
| principal component analysis | 60 |  | normalized | 610 |
| confocal microscope | 59 |  | dynamics | 600 |
| Coot | 59 |  | differentiation | 599 |
| DMEM | 59 |  | dependent | 587 |
| protein expression | 59 |  | correlation | 585 |
| confidence intervals | 58 |  | score | 579 |
| FBS | 58 |  | mechanism | 577 |
| ATP | 57 |  | enzyme | 576 |
| Il6 | 57 |  | disease | 568 |
| linear regression | 57 |  | replication | 566 |
| optical density | 57 |  | phase | 559 |
| Fisher’s exact test | 56 |  | network | 557 |
| immunoprecipitation | 56 |  | tumor | 557 |
| transcriptome | 56 |  | ratio | 555 |
| genotype | 55 |  | staining | 555 |
| immunostaining | 55 |  | inhibitor | 545 |
| mCherry | 55 |  | surface | 544 |
| PHENIX | 55 |  | variant | 536 |
| Protein Data Bank | 55 |  | spatial | 532 |
| PyMOL | 55 |  | high | 528 |
| reactive oxygen species | 55 |  | marker | 522 |
| cryoelectron microscopy | 54 |  | residues | 521 |

Single words top 100