# MATHBIO EVALUATION

# Background

- Program aims to encourage collaboration by bringing mathematical scientists into research areas of biological and biomedical interest.

- The goal of this collaboration has been to focus sophisticated mathematical formalisms and statistical models on understanding basic biomedical research problems relevant to the mission of both MPS/DMS and NIGMS.

- For each of the last 12 years, NIGMS has set aside $3m (partnered with $2m from NSF) and funded approximately 10 new proposals annually (124 total over the period 2002-2014).

# Evaluation Questions

As part of the process to reissue the FOA for the MathBio program, this evaluation is being conducted to assess the outcomes of the program in four areas:

1. Do the methodologies used and scientific areas covered by the research produced under the MathBio program reflect increased use of statistics and mathematics relative to its R01 counterparts?

2. Does the MathBio program fund a greater proportion of investigators with no prior NIH research funding relative to NIH-originated R01s in quantitative study sections?

3. Do NIGMS-funded MathBio PIs remain in the NIH system?

4. Has the research conducted by these PIs had an impact on the scientific community?

# Establishing a Comparator Group

- Similarly quantitative R01's that do not come to NIGMS through the MathBio program
  - Quantitative study sections: MABS and BDMA
  - Same time period as MathBio program (2002-2014)
  - Type 2 awards have data from 2002-2014 (presented in appendix)
  - Type 1 awards only have data from 2006-2014

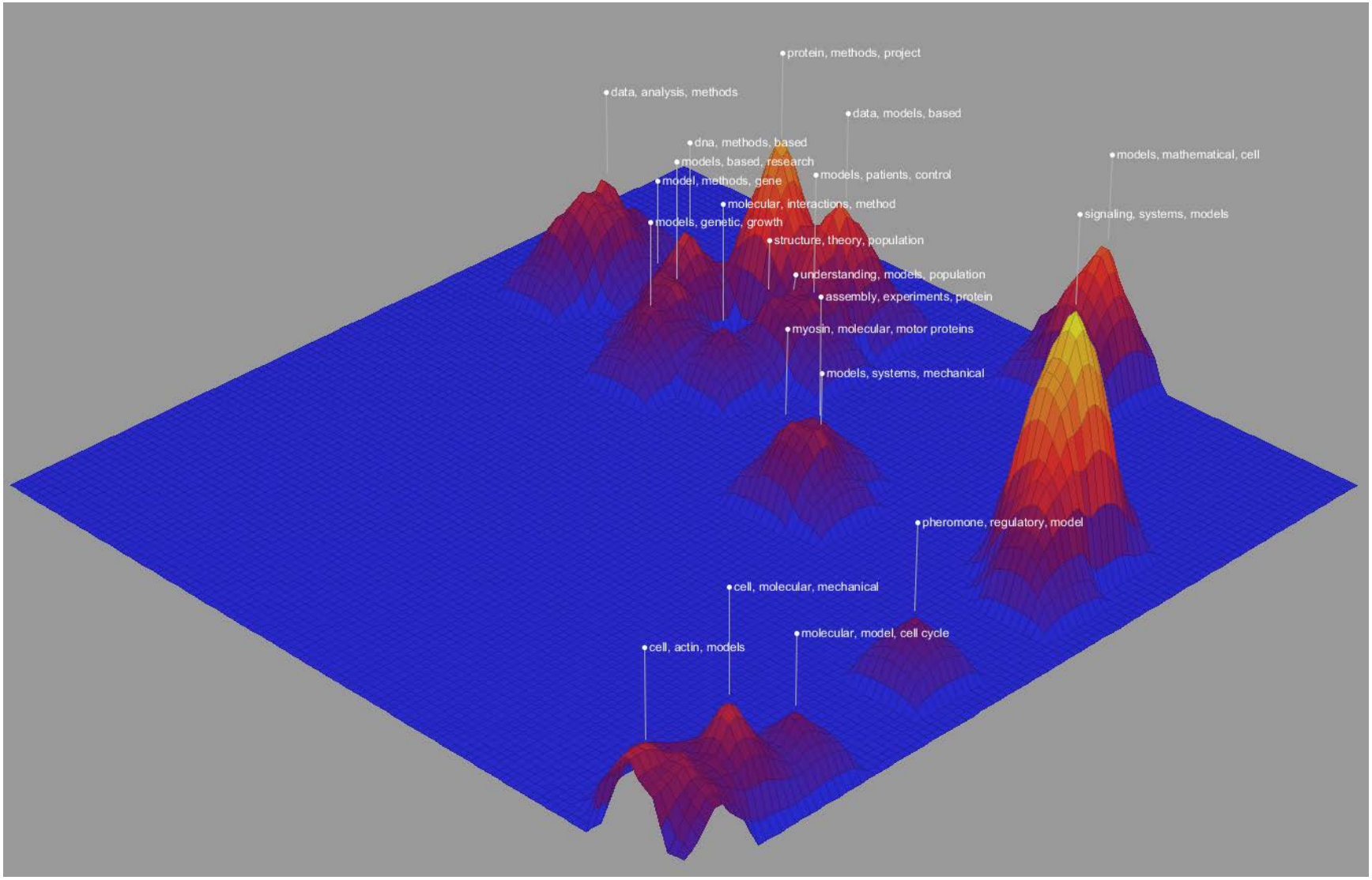
# No significant difference in themes of grants

## Type 1's Only

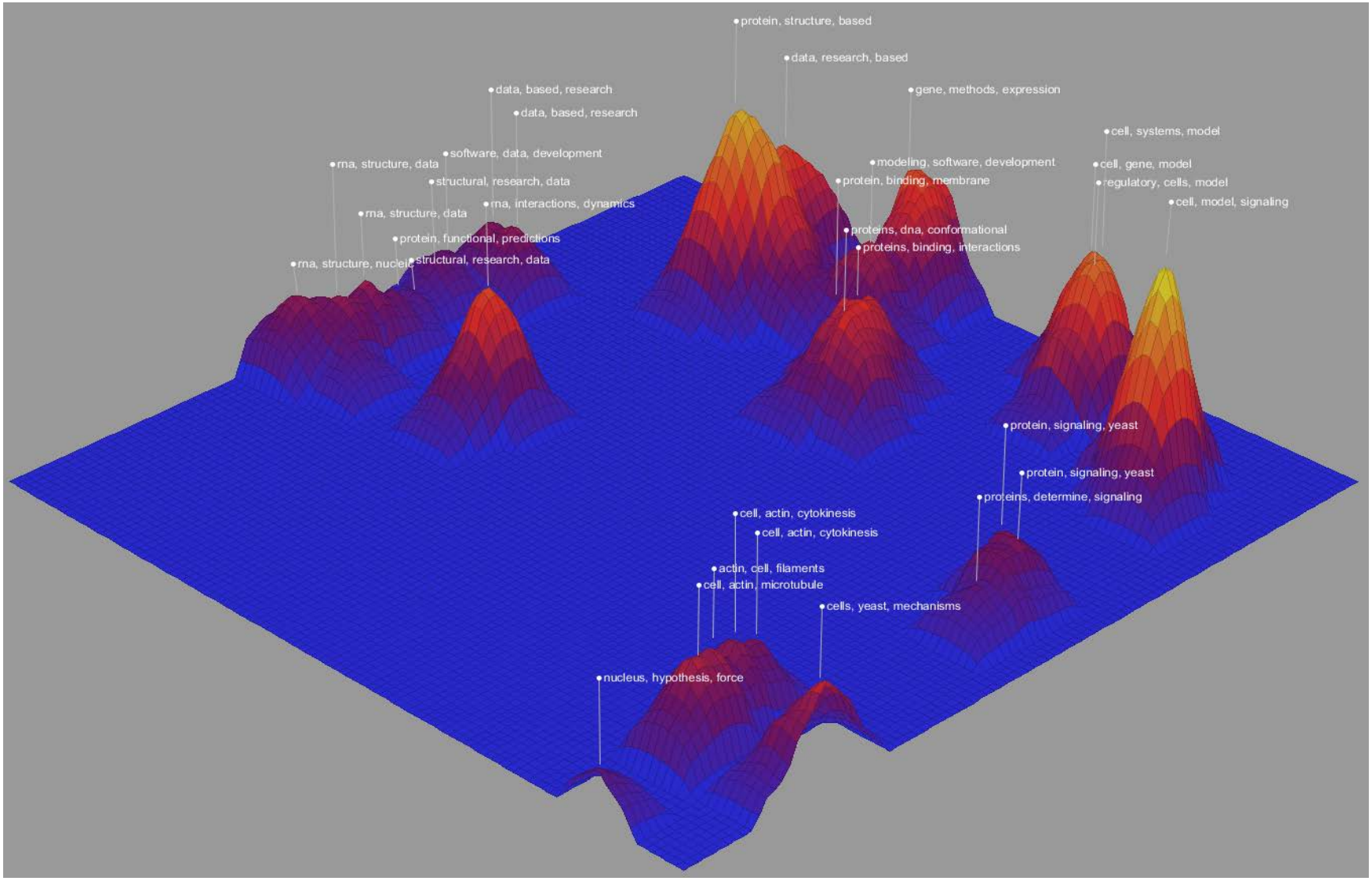
**Top 25 Themes from Grant Abstracts, Titles, and Specific Aims**

| MathBio | Comparator |
|---|---|
| develop, data | models, develop |
| methods, models | data, model |
| proteins, mechanisms | structure, users |
| computational methods, computational scientists | network, coli |
| provided | signaling pathways, computational model |
| proposed research, collaborative research | computational methods, develop computational methods |
| biofilm, biofilms | software packages, research community |
| statistical models, dna sequences | computational modeling, mechanical forces |
| eukaryotic cells, complex genome rearrangements | data sets, gene expression data |
| experimental data | regulatory network, regulatory networks |
| systems biology, biological responses | develop algorithms, nucleic acids |
| measures, infection | rna, rna molecules |
| noise, stochastic fluctuations | cell division, cell cycle |
| model predictions, acute inflammatory response | experimental data |
| gene networks, cellular differentiation | target genes, transcription factors |
| loop, synthetic networks | cell types, cell motility |
| motions, motion | mathematical model, model predictions |
| major challenge, dimensional structure | cell signaling, signaling network |
| protein structure, art methods | signaling proteins, target protein |
| effective data analysis, human diseases | biological systems, ms |
| actin cytoskeleton, actin polymerization | annotation, structural genomics |
| deterministic models, single yeast cells | gene ontology, ontology development |
| gene regulation, ccc data | computational models, cell fates |
| ions, molecular recognition | living cells, mitotic spindle |
| recombination, immune system | scoring, protein flexibility |

# Scientific Areas – MathBio PI's Type 1's

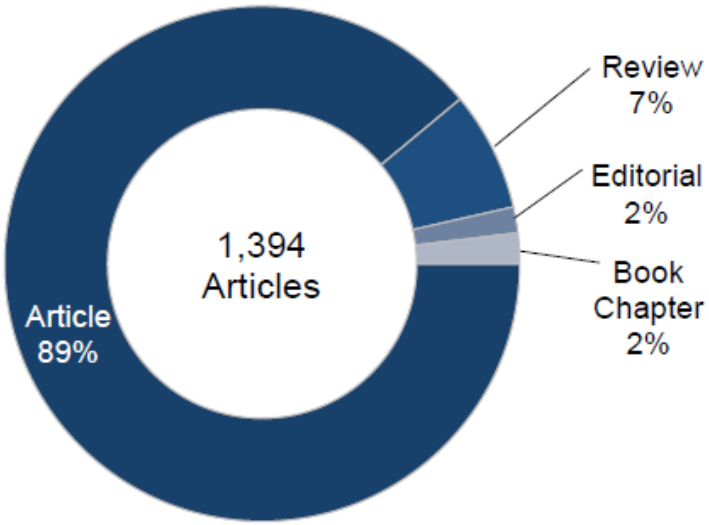


# Scientific Areas – Comparator PI's Type 1's

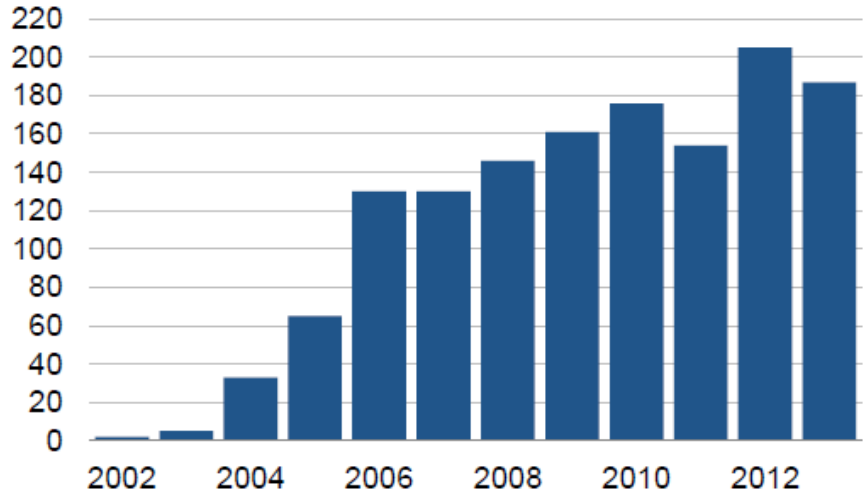


# Productivity: Mathematical Biology Program

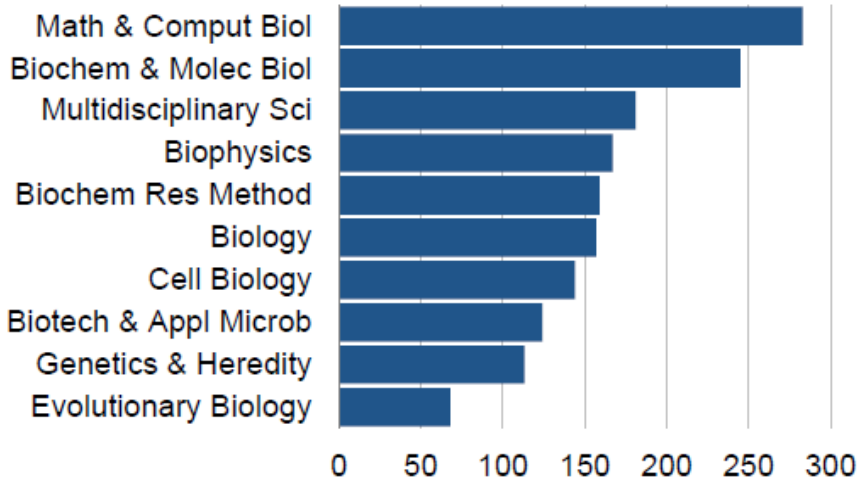
**Article Type Distribution**[1]



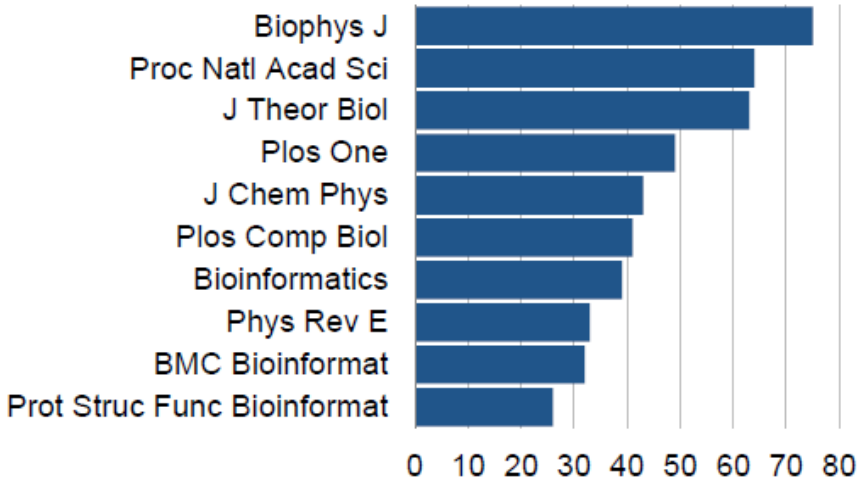

**Articles per Year**




**Articles per WOS Subject Category**[2]

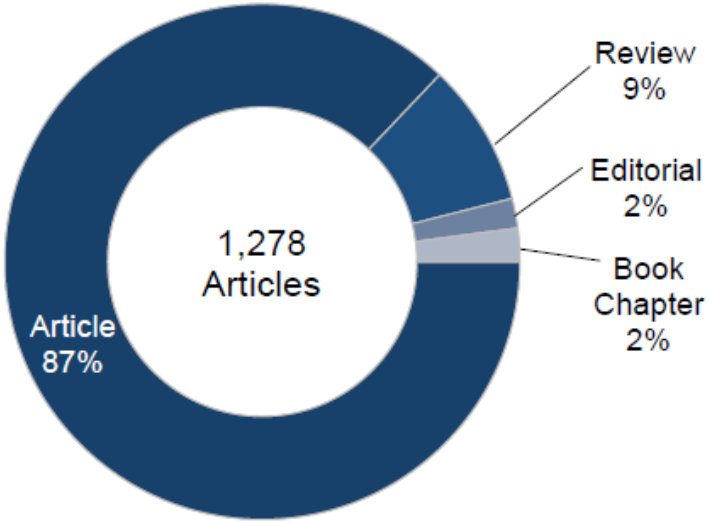



**Articles per Journal**[3]

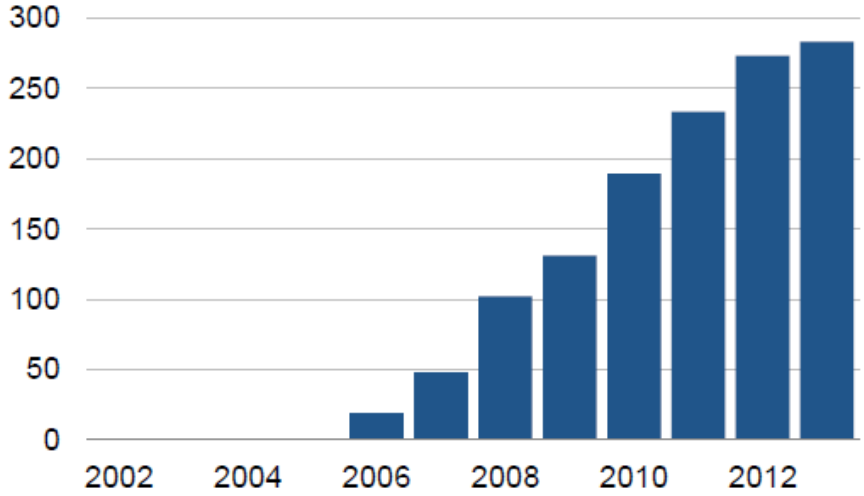


# Productivity: Comparator Program

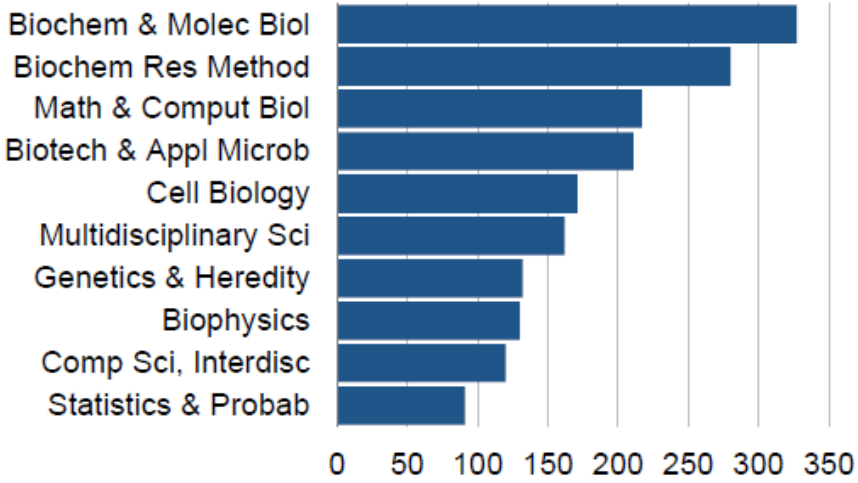
**Article Type Distribution**[1]



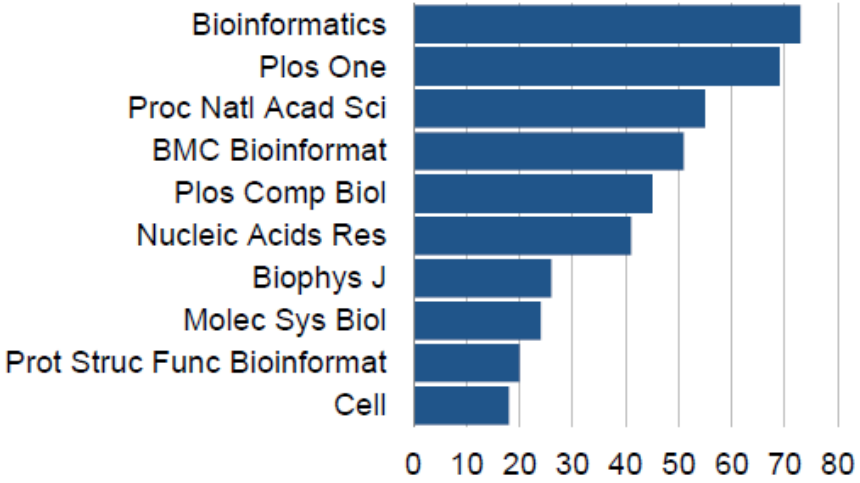

**Articles per Year**




**Articles per WOS Subject Category**[2]

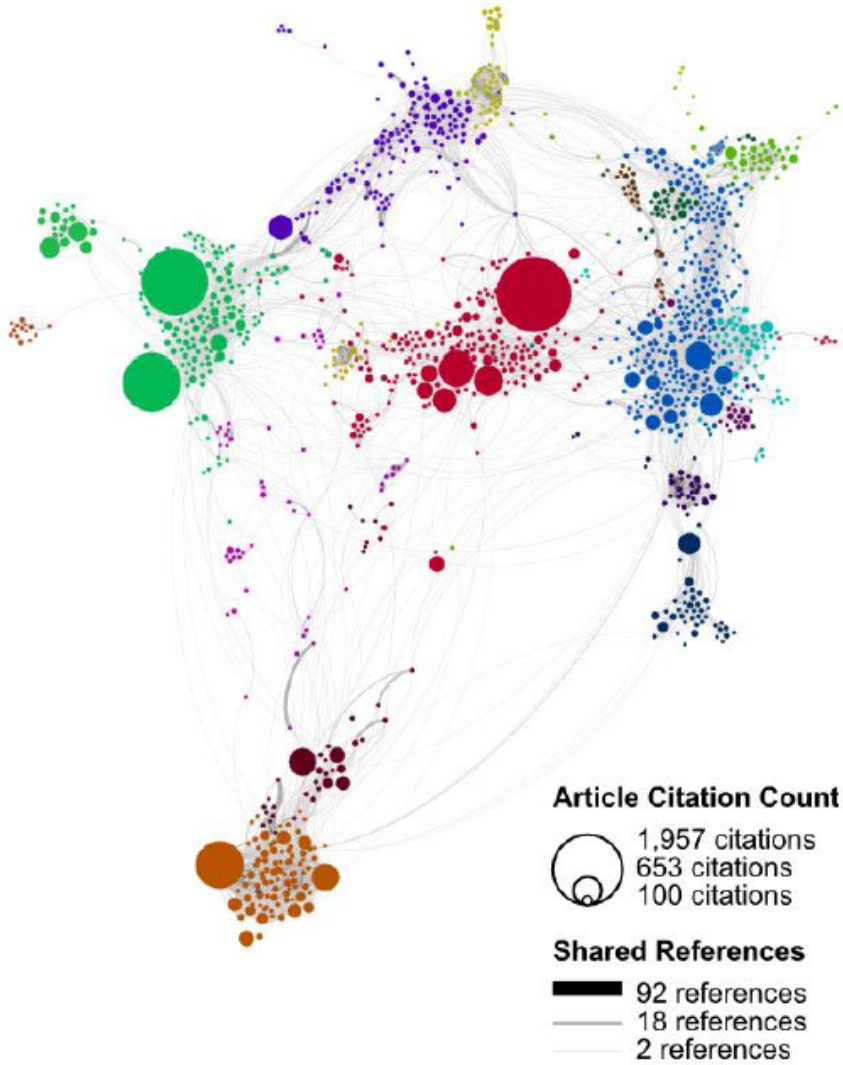



**Articles per Journal**[3]

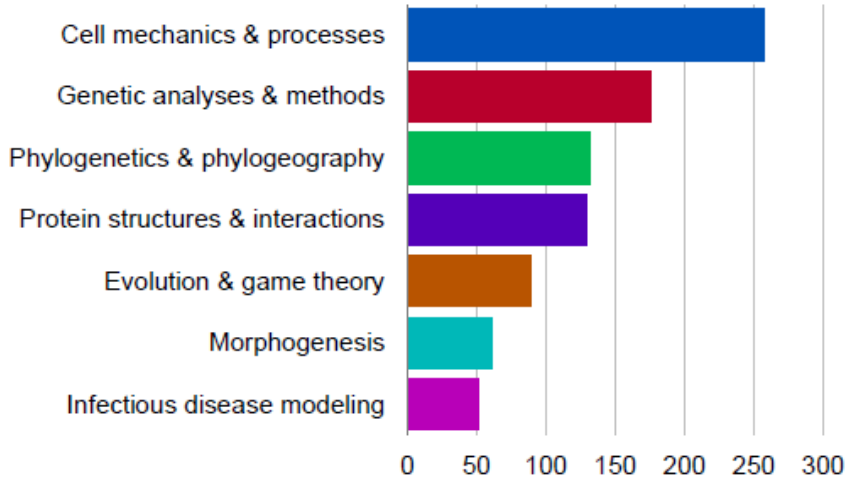


# Research Topics: Mathematical Biology Program

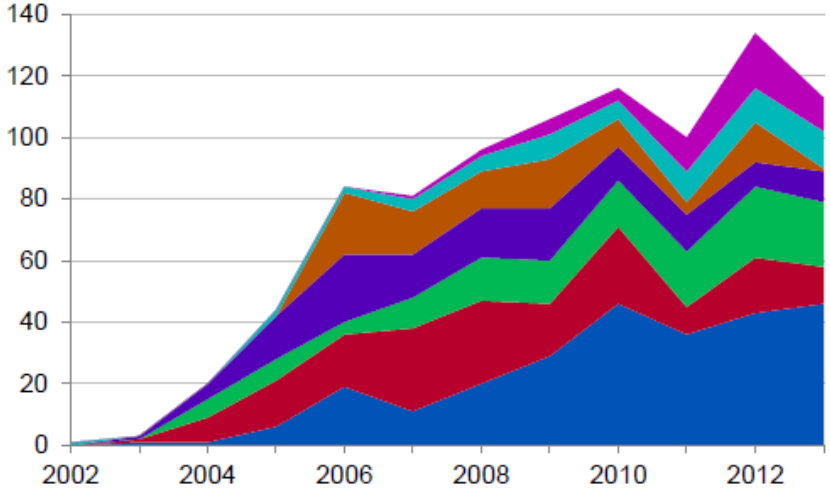
**Article Topic Map**[4]




**Articles per Topic**[5]

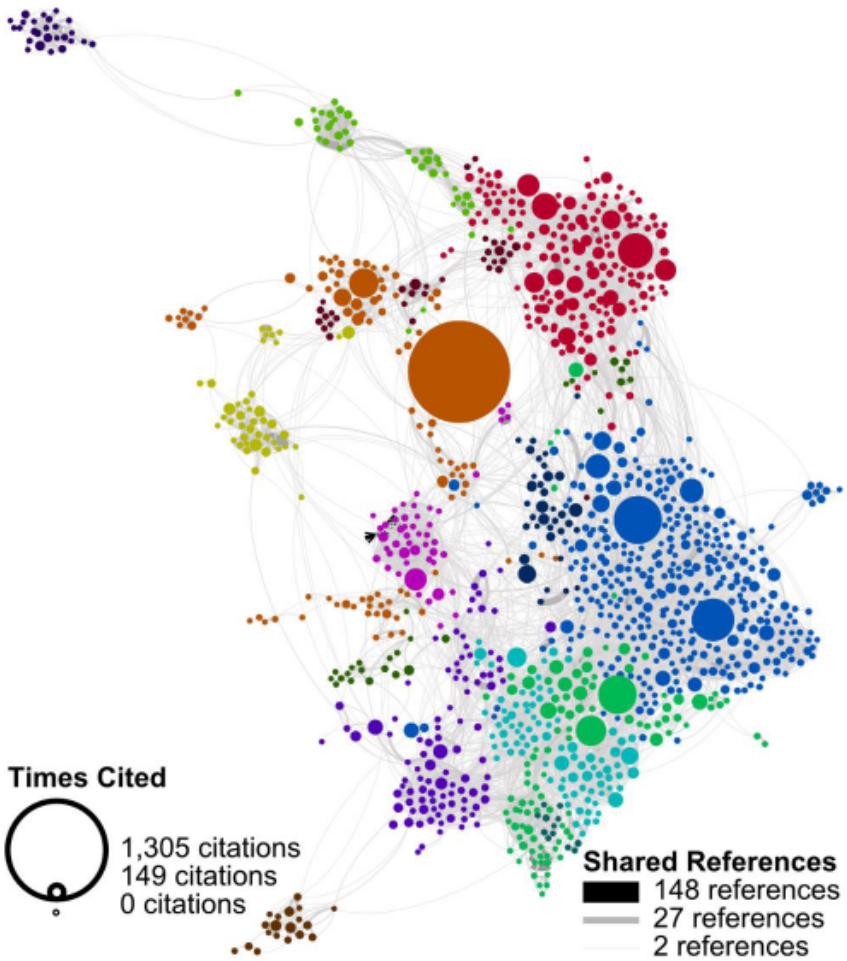



**Articles per Topic per Year**[6]

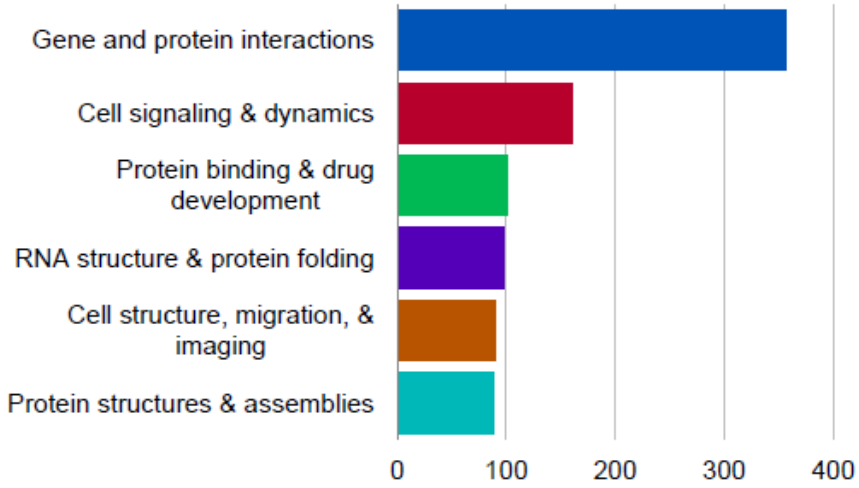


# Research Topics: Comparator Program

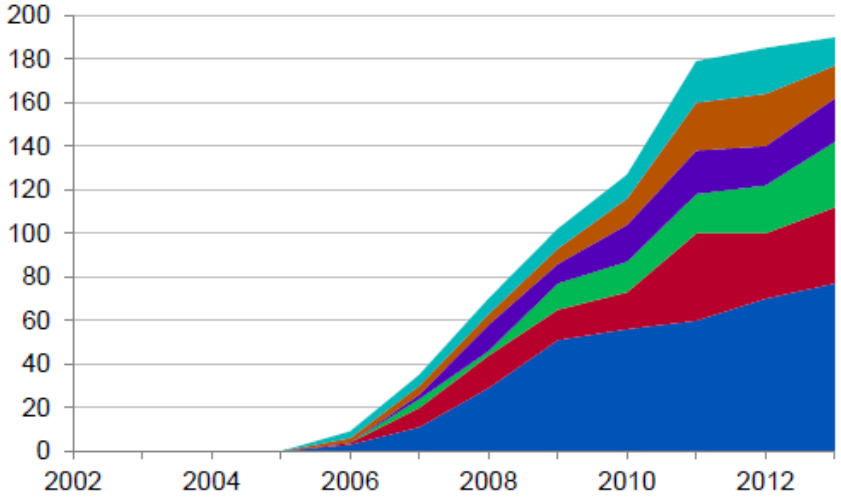
## Article Topic Map[4]



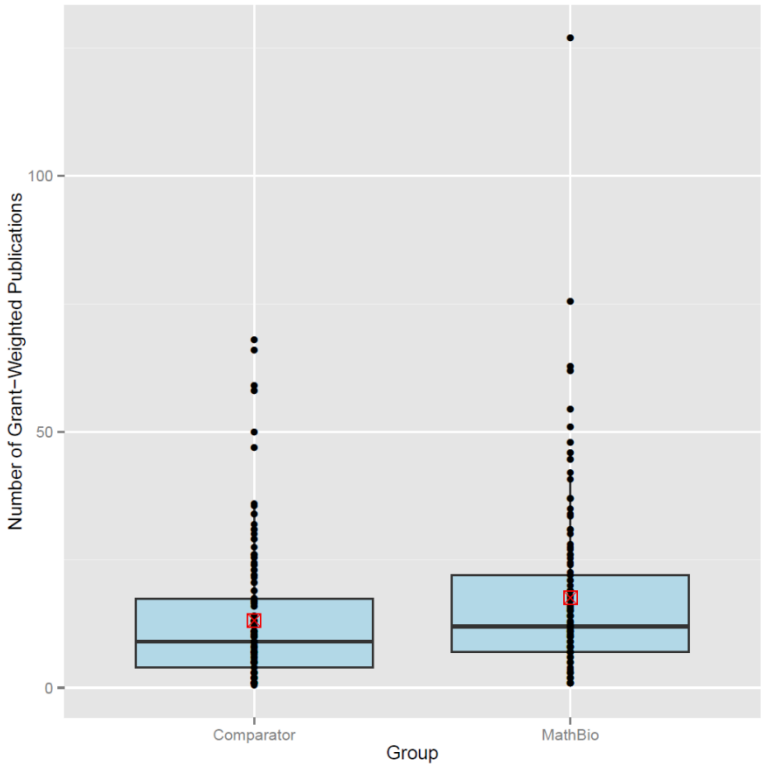

## Articles per Topic[5]

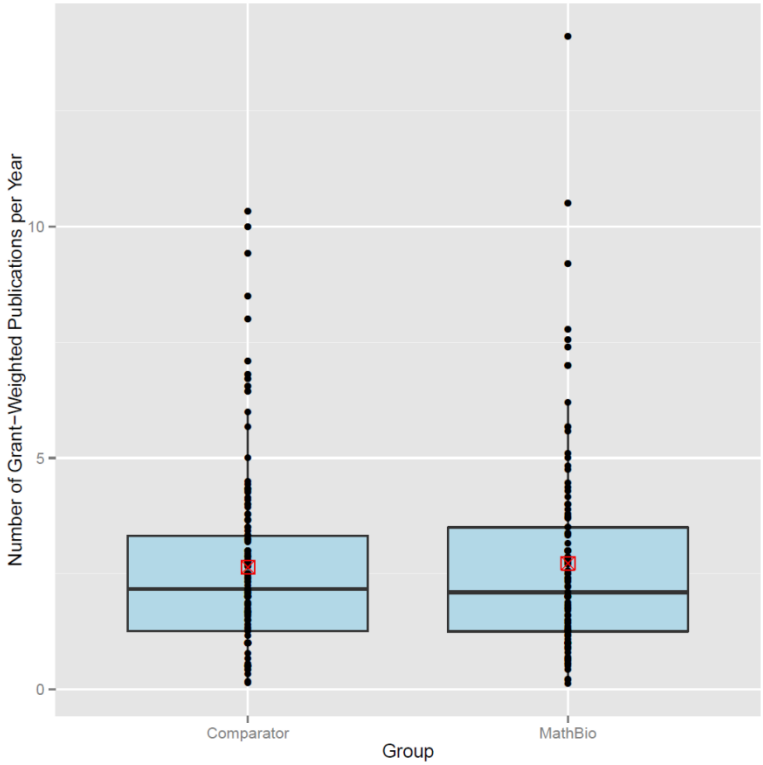



## Articles per Topic per Year[6]



# Publications



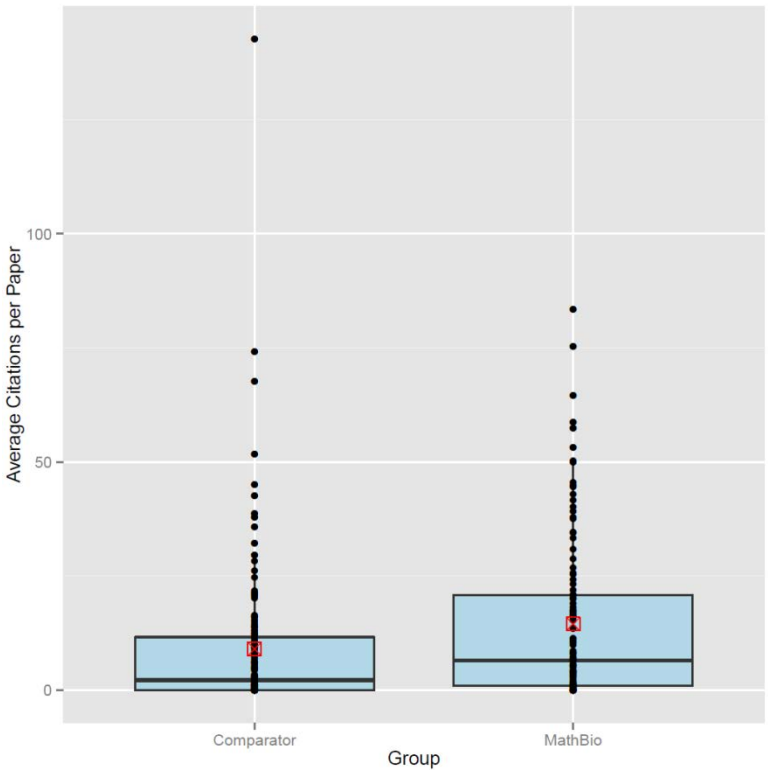



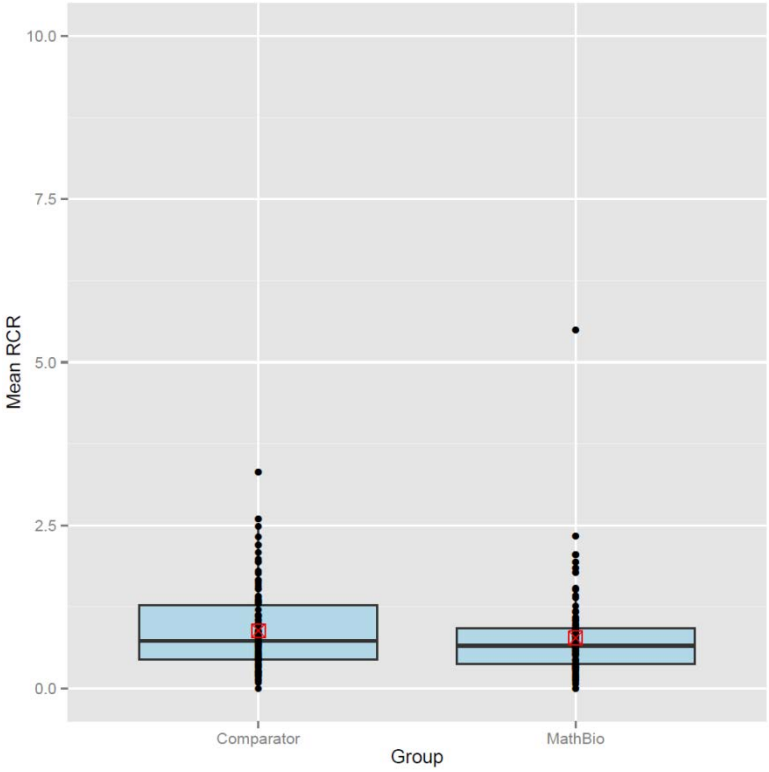

MathBio projects produce, on average, one additional grant-weighted publication over comparable quantitative R01's.

- While statistically significant, this difference is very small.

There is no statistically significant difference between the two groups in terms of grant-weighted publications per year.

# Citations and RCR



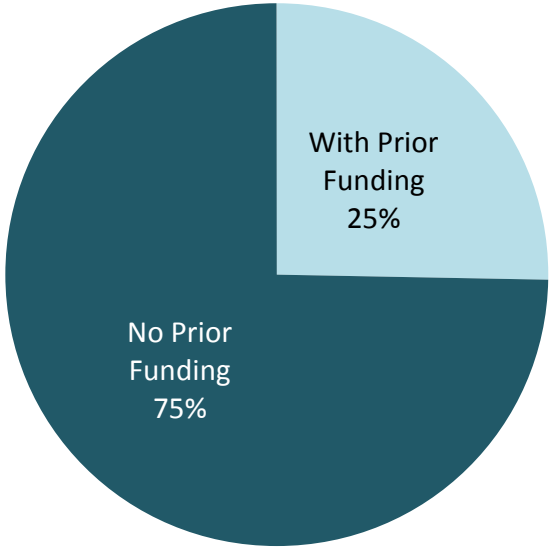

MathBio projects receive, on average, one additional citation per paper over comparable quantitative R01's.

- While statistically significant, this difference is very small.

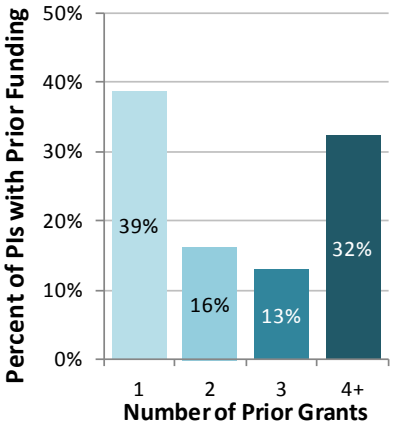
There is no statistically significant difference between the two groups in terms of Relative Citation Ratio (RCR).

# Prior NIH Funding

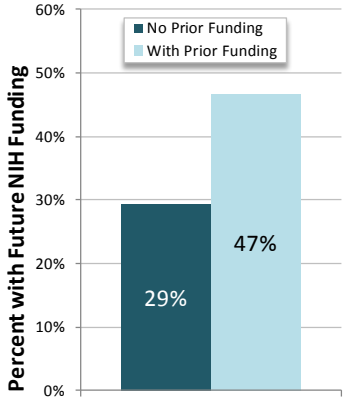
## MathBio PI's Prior NIH Funding




## Prior RPGs/Centers



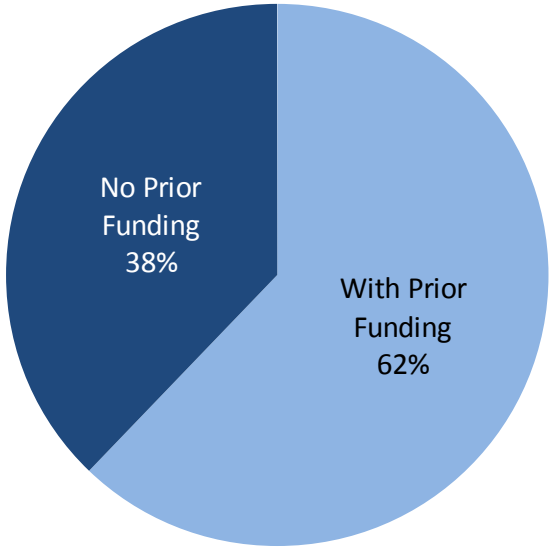

## Future NIH Funding Attainment Rates



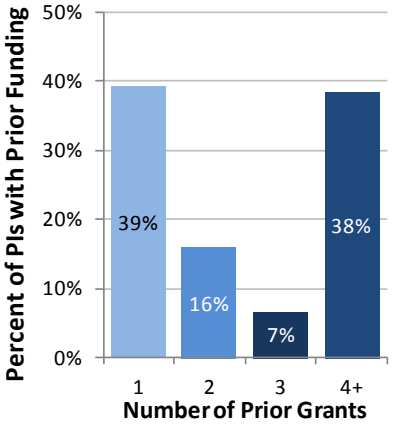

**25%** of MathBio PI's had received an NIH RPG/Center grant prior to beginning the MathBio program compared to **62%** of PI's over the same period for NIH-initiated Type 1 R01's reviewed in quantitative study sections.

% of MathBio PI's with prior funding receive future NIH funding compared with % of PI's who did not have NIH funding prior to the MathBio program.

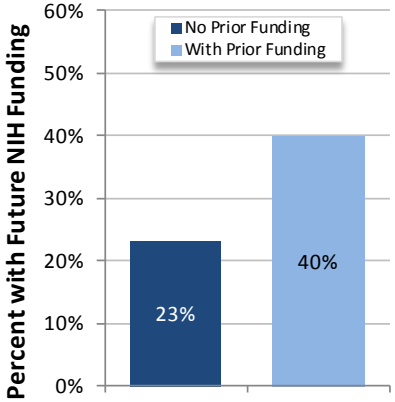
## Comparator PI's Prior NIH Funding




## Prior RPGs/Centers

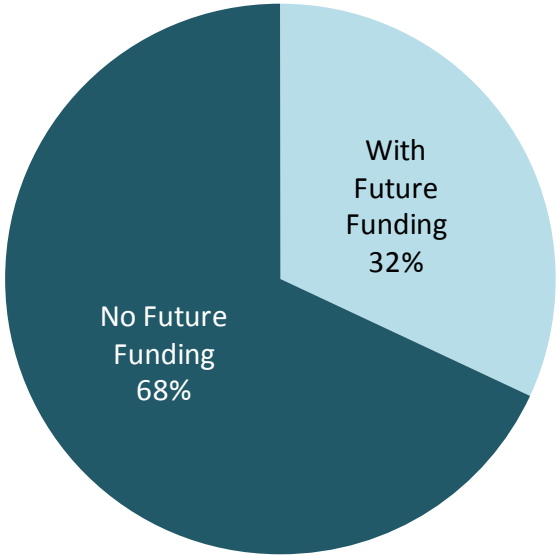



## Future NIH Funding Attainment Rates

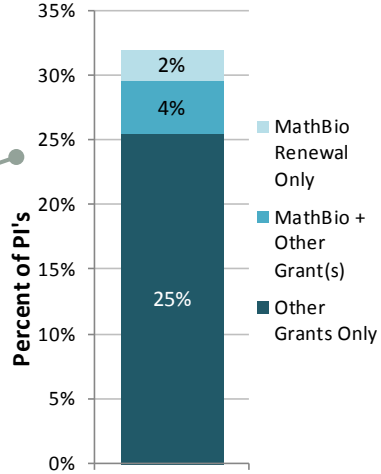


# Future NIH Funding – MathBio PI's

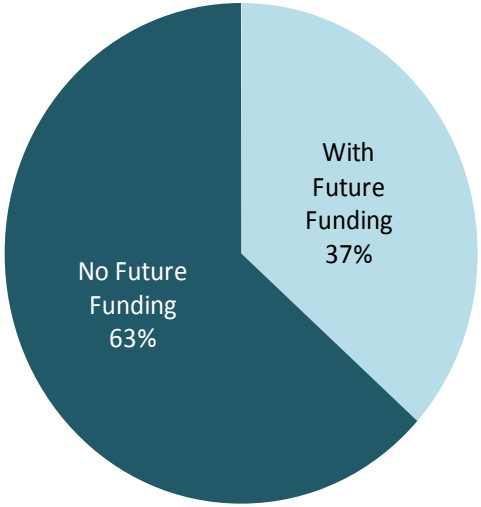
## MathBio PI's Future NIH Funding




## Future Funding

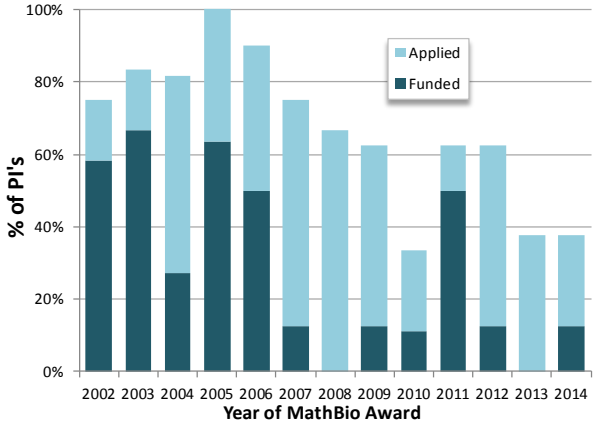



## Only PI's Eligible for Renewal

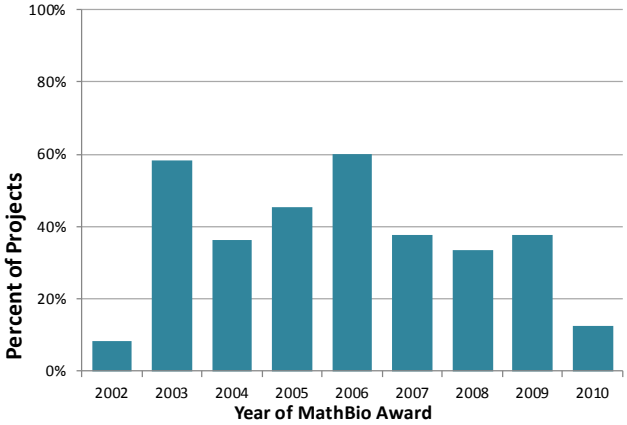



- **69%** of MathBio PI's apply for additional grants (any mechanism) after they begin the MathBio program.
- **32%** of MathBio PI's receive future NIH funding (any mechanism).
- **18%** of MathBio PI's receive a funded R01.

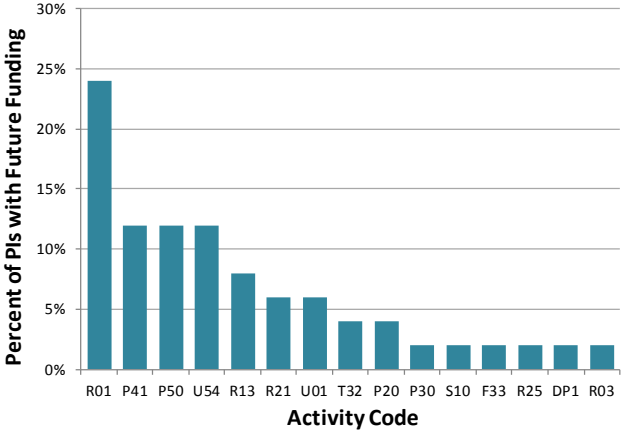
## Later Applications - All Mechanisms




## MathBio Projects Applying for Renewal

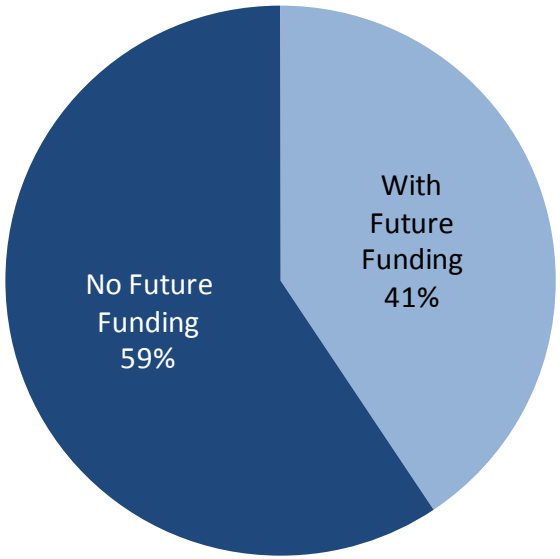



## Future Funding by Activity Code

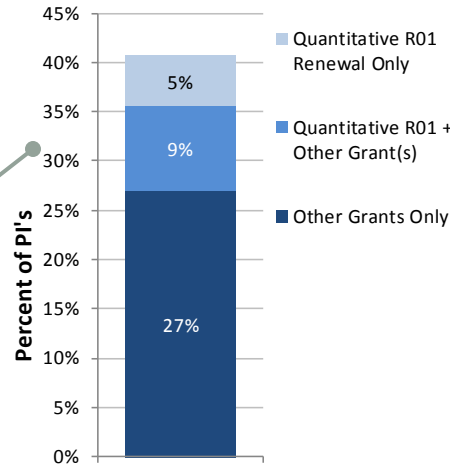


# Future NIH Funding – Comparator PI's

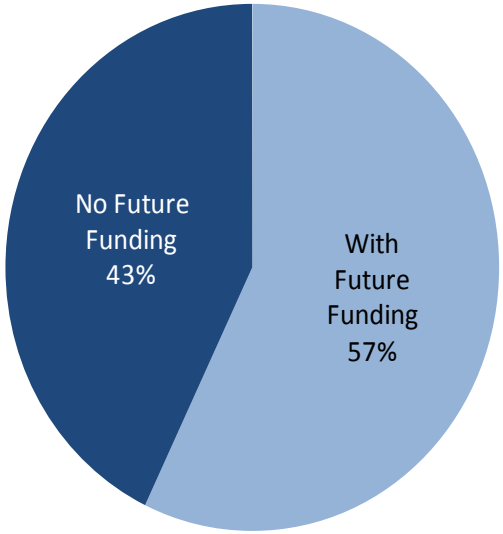
## Comparator PI's Future NIH Funding




## Future Funding

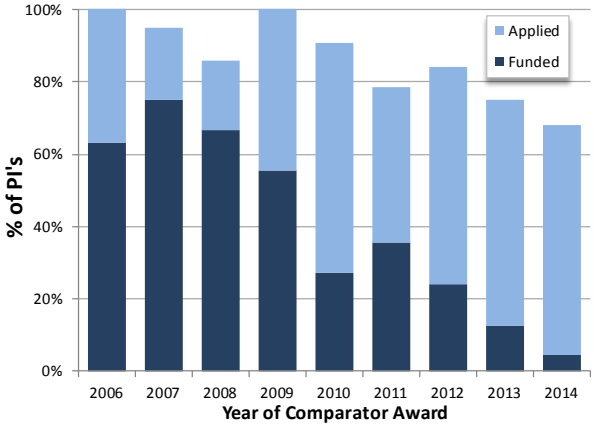



## Only PI's Eligible for Renewal

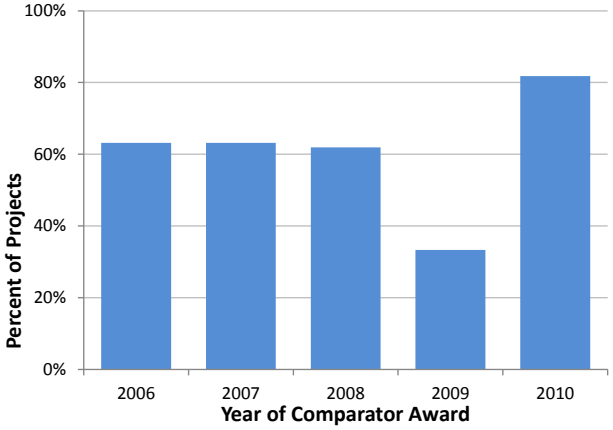



- **86%** of Comparator PI's apply for additional grants (any mechanism) after the initial comparator grant.
- **41%** of Comparator PI's receive future NIH funding (any mechanism).
- **26%** of Comparator PI's receive a funded R01.

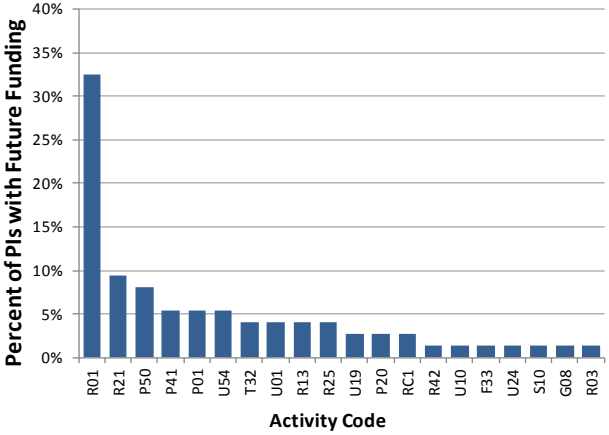
## Later Applications - All Mechanisms




## Comparator Projects Applying for Renewal



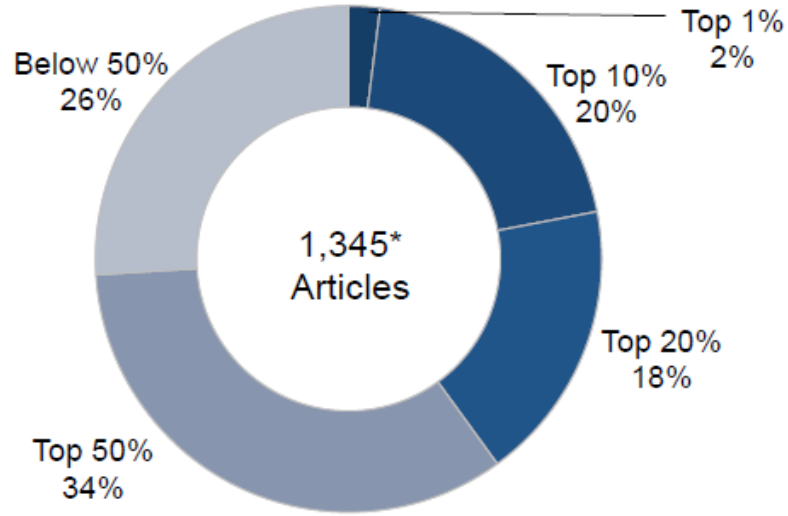

## Future Funding by Activity Code



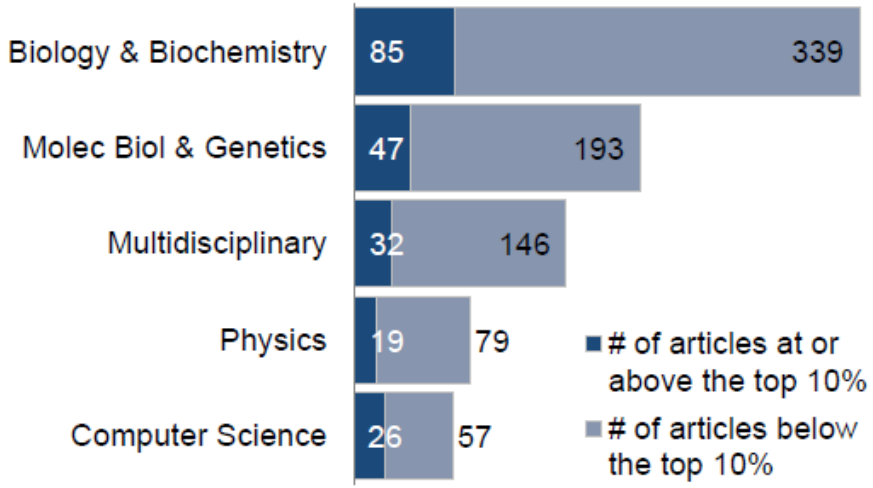
# Citation Impact: Mathematical Biology Program

| Bibliometric Indicator[7] | Value |
|---|---|
| Number of articles | 1,394 |
| Number of citations | 56,838 |
| Mean citation count | 40.8 |
| Median citation count | 16 |
| Self-citation rate | 3.7% |
| Program H-Index | 100 |
| # of articles in the top 10% for citations | 298 |
| % of articles in the top10% for citations | 22% |

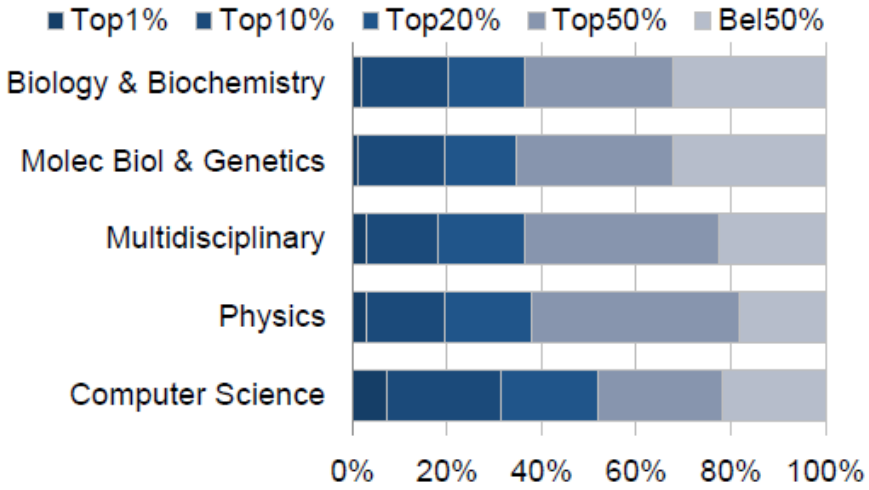
**% of Articles per Citation Percentile Rank[8]**




**Distribution of Articles per ESI Subject Category[9]**




**% Distribution of Articles per ESI Subject Category[10]**

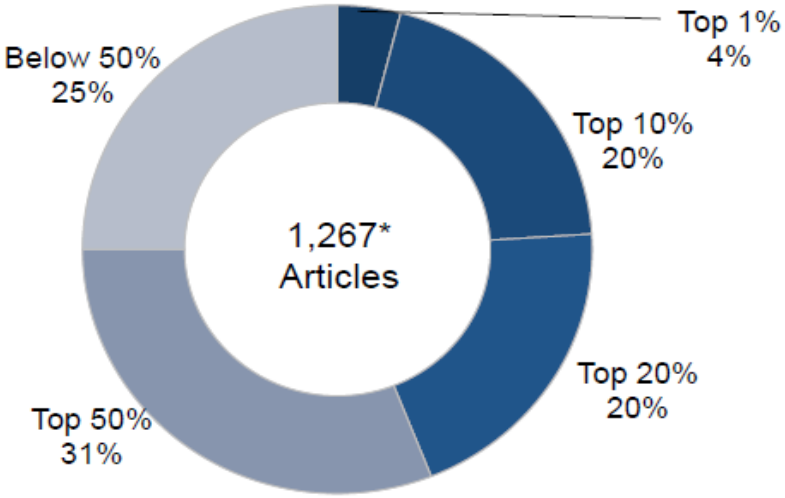



***Note:** 49 articles could not be assigned to an ESI subject category, so I excluded them from these analyses.

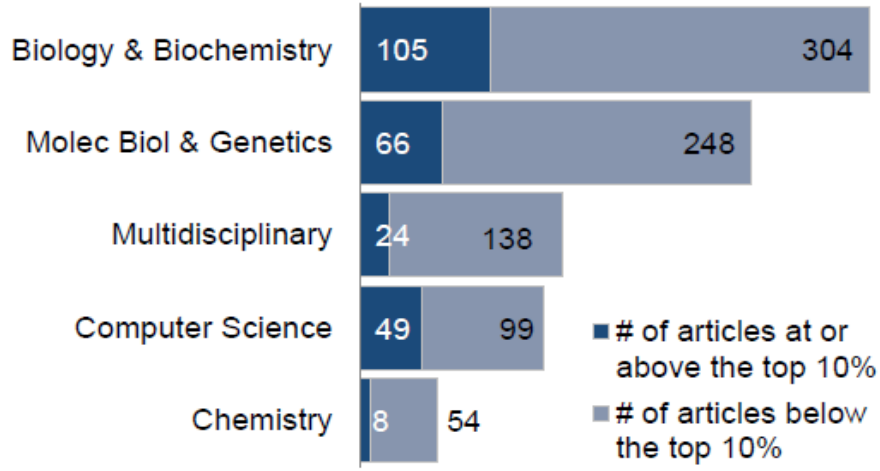
# Citation Impact: Comparator Program

| Bibliometric Indicator[7] | Value |
|---|---|
| Number of articles | 1,278 |
| Number of citations | 35,572 |
| Mean citation count | 27.8 |
| Median citation count | 13 |
| Self-citation rate | 4.8% |
| Program H-Index | 80 |
| # of articles in the top 10% for citations | 304 |
| % of articles in the top10% for citations | 24% |

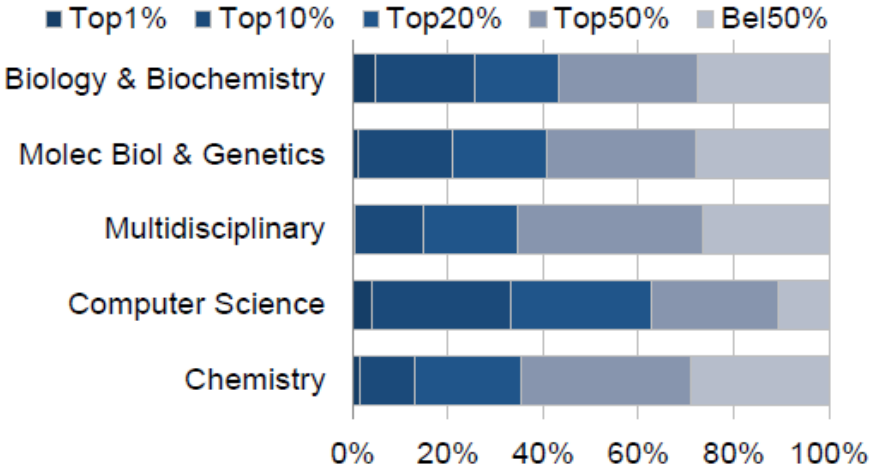
**% of Articles per Citation Percentile Rank[8]**




**Distribution of Articles per ESI Subject Category[9]**



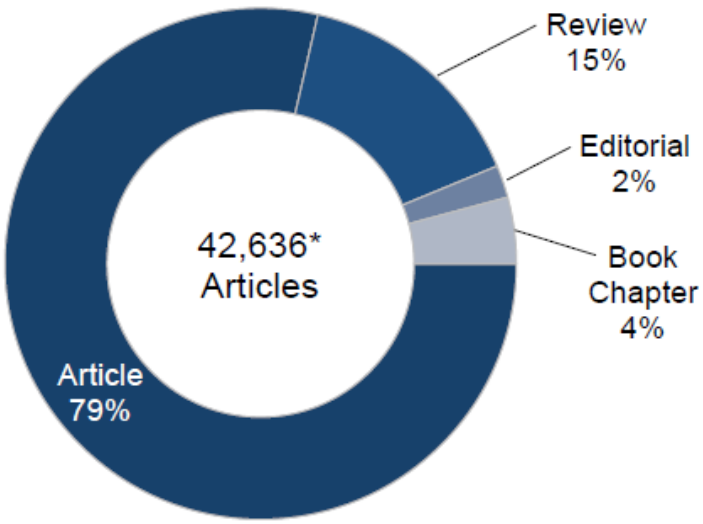

**% Distribution of Articles per ESI Subject Category[10]**



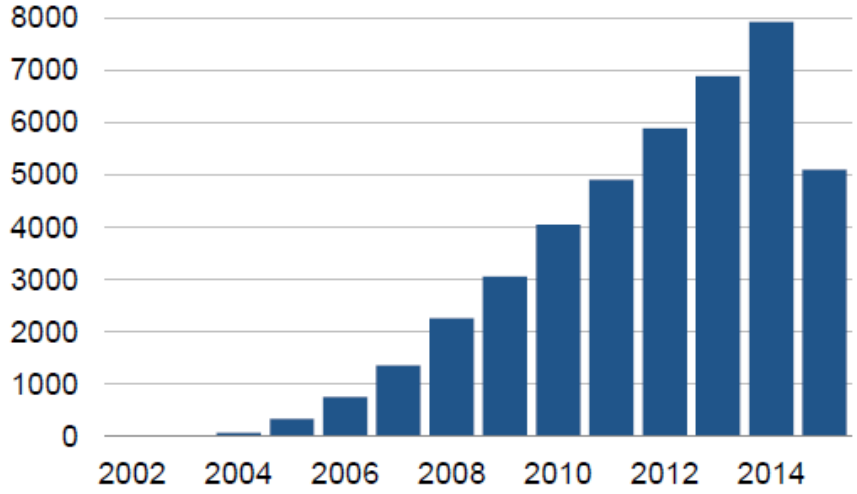

***Note:** 11 articles could not be assigned to an ESI subject category, so I excluded them from these analyses.

# Articles Citing the Mathematical Biology Program

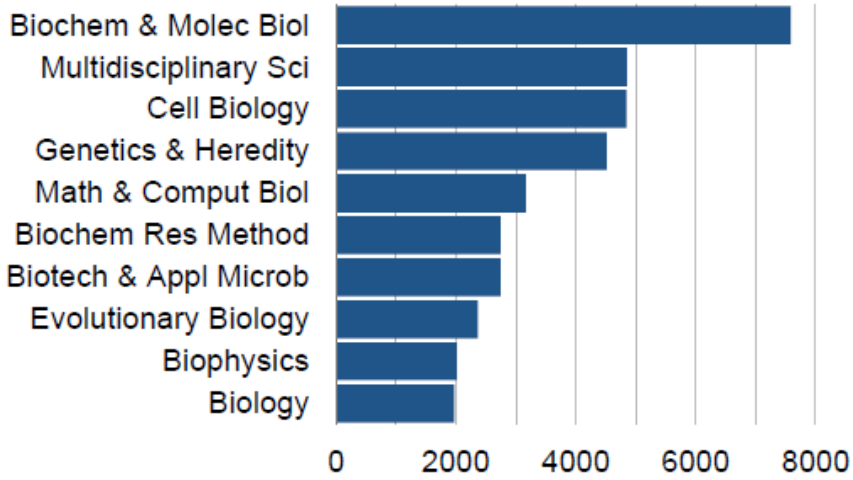
### Citing Article Type Distribution[1]



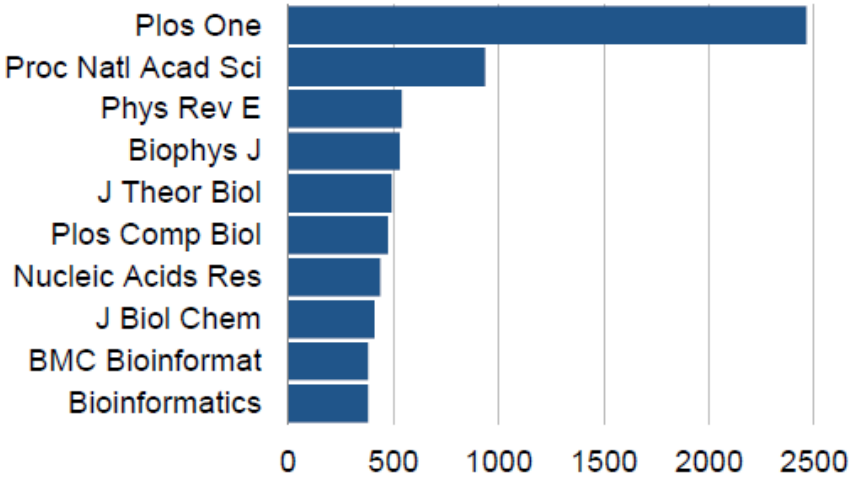

### Citing Articles per Year




### Citing Articles per WOS Subject Category[2]



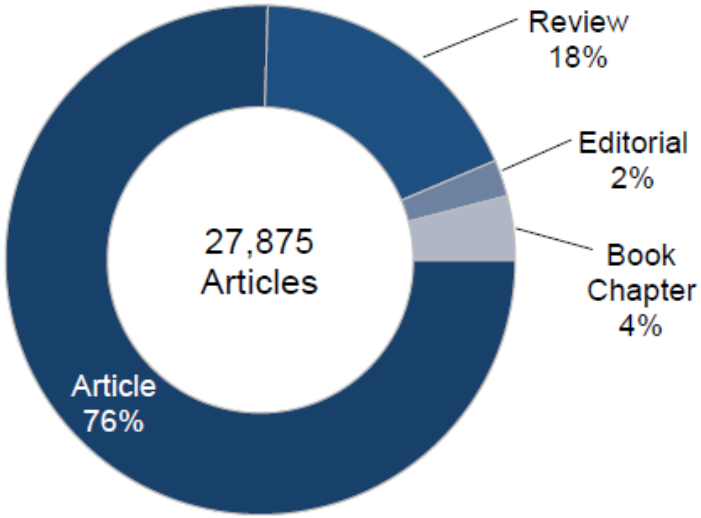

### Citing Articles per Journal[3]



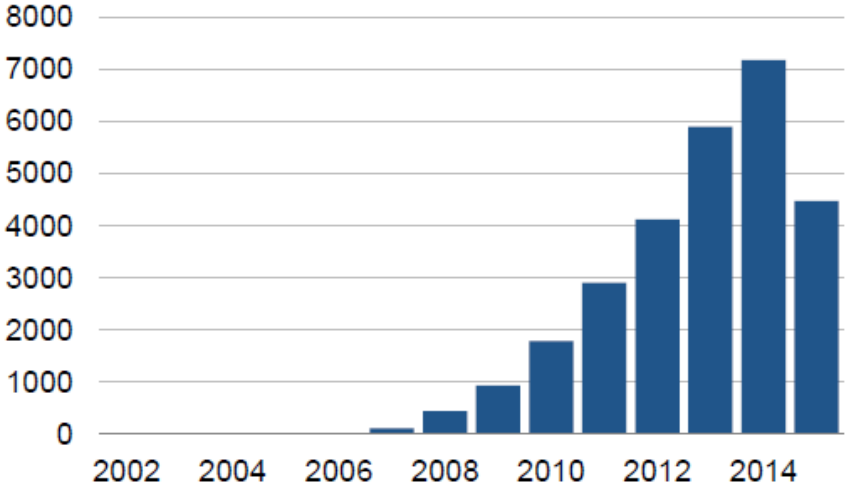

***Note:** Citing article counts are based on WOS databases to which we have access, whereas times cited counts are based on all WOS databases

# Articles Citing the Comparator Program

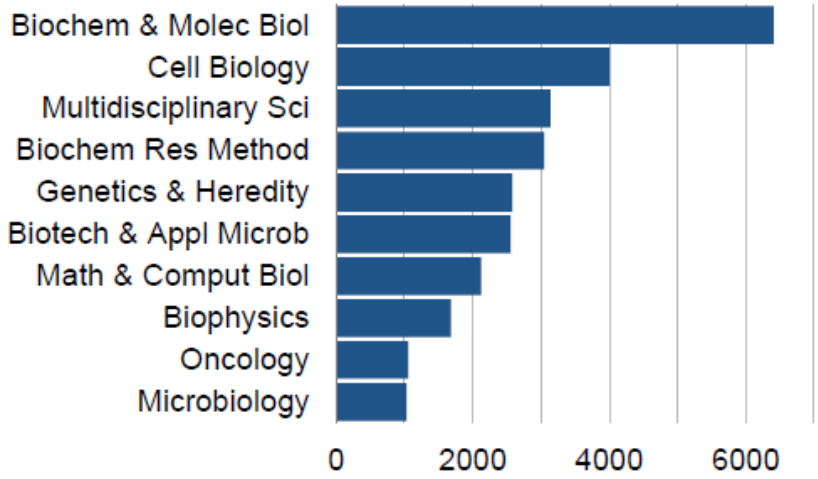
### Citing Article Type Distribution[1]



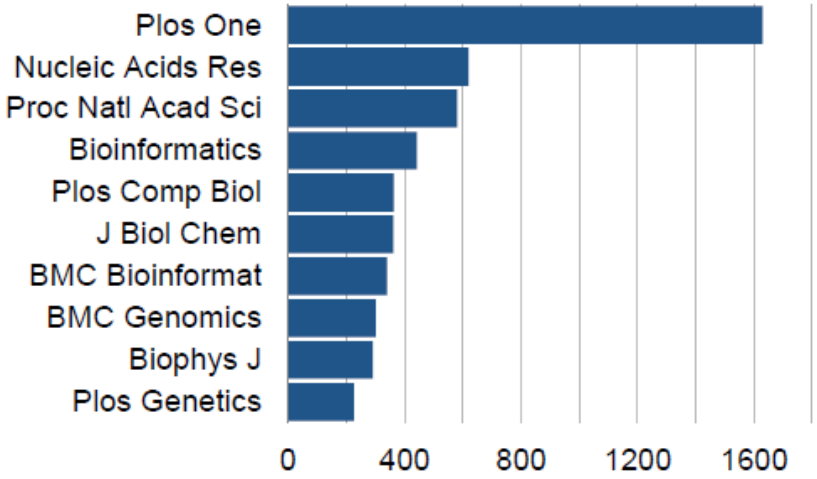

### Citing Articles per Year




### Citing Articles per WOS Subject Category[2]




### Citing Articles per Journal[3]




*Note: Citing article counts are based on WOS databases to which we have access, whereas times cited counts are based on all WOS databases

# Impact on Scientific Community

- MathBio PI's are at least as influential as the comparator group.
  - Lower self-citation rate for MathBio PI's
  - A greater number of articles cite the MathBio publications
  - MathBio PI's have more high-impact papers as measured by citation count than comparator group

# APPENDIX

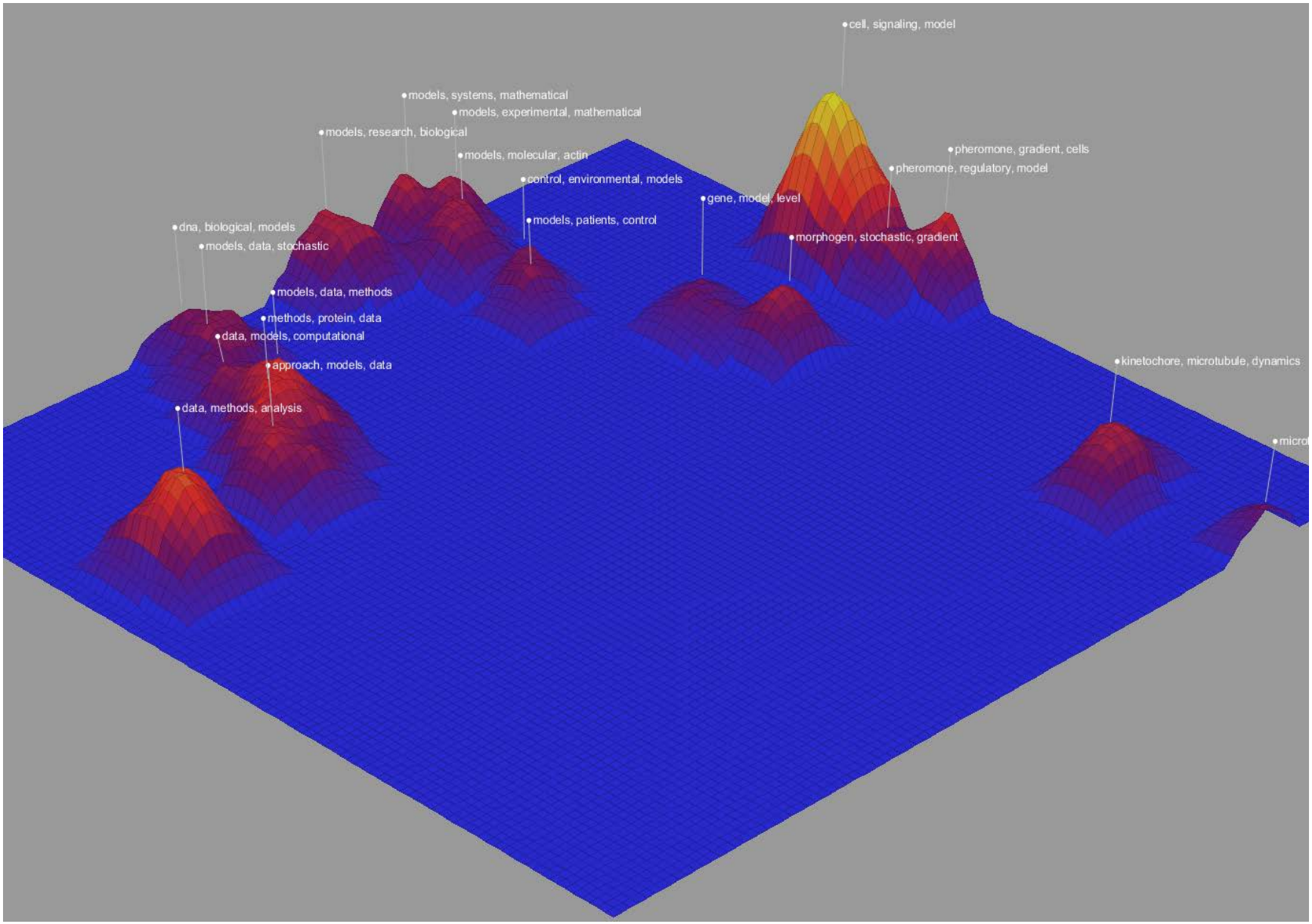
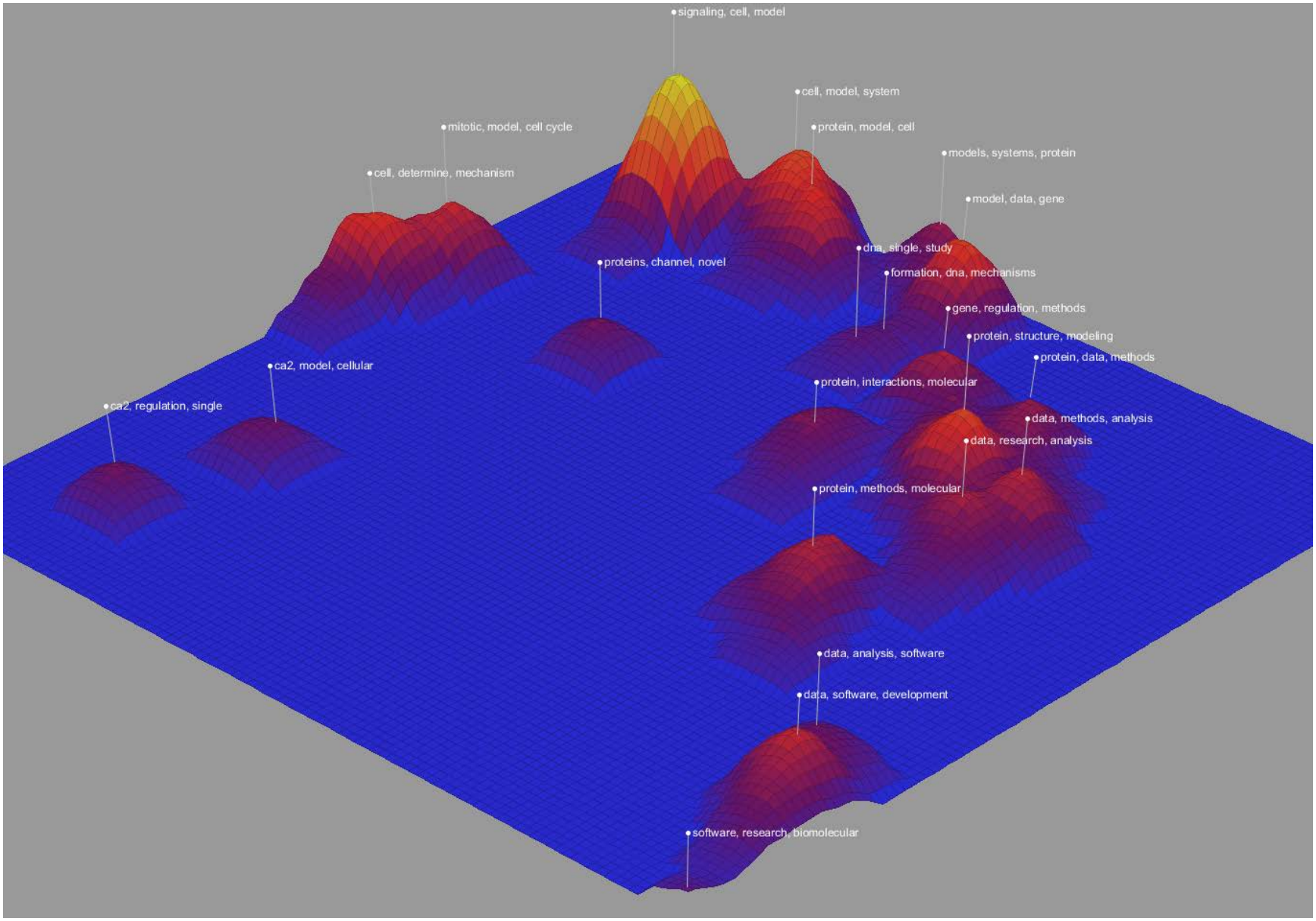
# No significant difference in themes of grants

## All Grants

**Top 25 Themes from Grant Abstracts, Titles, and Specific Aims**

| MathBio | Comparator |
|---|---|
| models, cells | data, software |
| develop, gene expression | cell, cells |
| methods, proteins | proteins, structure |
| data, yeast | yeast, cell division |
| mathematical models, mathematical modeling | computational methods, experimental data |
| signaling pathways, gradient | signaling pathways, computational analysis |
| stochastic effects, noise | research community, software package |
| computational methods, computational scientists | computational models, computational modeling |
| signal transduction, mapk | regulatory network, regulatory networks |
| provided, statistical modeling | signaling network, signaling molecules |
| experimental data, biofilm | rna, rna sequences |
| bacteria, bacterial species | cancer cells, mammalian cells |
| protein structure, loop | cell motility, cell polarization |
| cell shape, actin | gene ontology, ontology development |
| stochastic fluctuations, stochastic model | molecular interactions, computational approaches |
| statistical analysis, dimensional data | protein folding, folding |
| budding yeast, single yeast cells | develop computational methods, genomic data |
| statistical models, dna sequences | transcription factors, transcriptional regulation |
| spindle, microtubule | human cells, cell biology |
| systems biology, biological responses | ms, protein identification |
| macromolecular complexes, mathematical methods | cell types, cell types to regulate functions |
| ring, polymerization | human genome, apollo |
| motility, flagella | silico model, metabolic networks |
| cell variability, morphogen gradients | candidate genes, genetic basis |
| dimensional structures, dimensional structure | quantitative understanding, quantitative analysis |

# Scientific Areas – MathBio PI's



# Scientific Areas – Comparator PI's