

# Smadar Ben-tabou De-leon

## List of Publications by Year in descending order

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29  
papers

916  
citations

566801

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500791

28  
g-index

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docs citations

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times ranked

900  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The Evolution of Biomineralization through the Co-Option of Organic Scaffold Forming Networks. <i>Cells</i> , 2022, 11, 595.  | 1.8 | 14        |
| 2  | Distinct regulatory states control the elongation of individual skeletal rods in the sea urchin embryo. <i>Developmental Dynamics</i> , 2022, 251, 1322-1339.   | 0.8 | 9         |
| 3  | Calcium-vesicles perform active diffusion in the sea urchin embryo during larval biomineralization. <i>PLoS Computational Biology</i> , 2021, 17, e1008780.   | 1.5 | 11        |
| 4  | The tolerance to hypoxia is defined by a time-sensitive response of the gene regulatory network in sea urchin embryos. <i>Development (Cambridge)</i> , 2021, 148, .  | 1.2 | 7         |
| 5  | VEGF signaling activates the matrix metalloproteinases, MmpL7 and MmpL5 at the sites of active skeletal growth and MmpL7 regulates skeletal elongation. <i>Developmental Biology</i> , 2021, 473, 80-89.              | 0.9 | 18        |
| 6  | The biological regulation of sea urchin larval skeletogenesis – From genes to biomineralized tissue. <i>Journal of Structural Biology</i> , 2021, 213, 107797.  | 1.3 | 12        |
| 7  | Possible cooption of a VEGF-driven tubulogenesis program for biomineralization in echinoderms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12353-12362.       | 3.3 | 49        |
| 8  | Developmental transcriptomes of the sea star, <i>Patiria miniata</i> , illuminate how gene expression changes with evolutionary distance. <i>Scientific Reports</i> , 2019, 9, 16201.                                 | 1.6 | 15        |
| 9  | Parallel embryonic transcriptional programs evolve under distinct constraints and may enable morphological conservation amidst adaptation. <i>Developmental Biology</i> , 2017, 430, 202-213.                         | 0.9 | 21        |
| 10 | The network remains. <i>History and Philosophy of the Life Sciences</i> , 2017, 39, 32.   | 0.6 | 0         |
| 11 | Regulatory heterochronies and loose temporal scaling between sea star and sea urchin regulatory circuits. <i>International Journal of Developmental Biology</i> , 2017, 61, 347-356.                                  | 0.3 | 8         |
| 12 | Robustness and Accuracy in Sea Urchin Developmental Gene Regulatory Networks. <i>Frontiers in Genetics</i> , 2016, 7, 16.   | 1.1 | 4         |
| 13 | Mature maternal mRNAs are longer than zygotic ones and have complex degradation kinetics in sea urchin. <i>Developmental Biology</i> , 2016, 414, 121-131.  | 0.9 | 8         |
| 14 | Quantitative developmental transcriptomes of the Mediterranean sea urchin <i>Paracentrotus lividus</i> . <i>Marine Genomics</i> , 2016, 25, 89-94.  | 0.4 | 23        |
| 15 | Comparative Study of Regulatory Circuits in Two Sea Urchin Species Reveals Tight Control of Timing and High Conservation of Expression Dynamics. <i>PLoS Genetics</i> , 2015, 11, e1005435.                           | 1.5 | 44        |
| 16 | Gene regulatory control in the sea urchin aboral ectoderm: Spatial initiation, signaling inputs, and cell fate lockdown. <i>Developmental Biology</i> , 2013, 374, 245-254.   | 0.9 | 61        |
| 17 | The conserved role and divergent regulation of <i>foxa</i> , a pan-eumetazoan developmental regulatory gene. <i>Developmental Biology</i> , 2011, 357, 21-26.   | 0.9 | 18        |
| 18 | Information processing at the <i>foxa</i> node of the sea urchin endomesoderm specification network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10103-10108. | 3.3 | 55        |

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|----|--|------|-----------|
| 19 | Perturbation analysis analyzedâ€”mathematical modeling of intact and perturbed gene regulatory circuits for animal development. <i>Developmental Biology</i> , 2010, 344, 1110-1118.                         | 0.9  | 4         |
| 20 | Experimentally based sea urchin gene regulatory network and the causal explanation of developmental phenomenology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 237-246.  | 6.6  | 20        |
| 21 | Modeling the dynamics of transcriptional gene regulatory networks for animal development. <i>Developmental Biology</i> , 2009, 325, 317-328.   | 0.9  | 84        |
| 22 | The regulatory genome and the computer. <i>Developmental Biology</i> , 2007, 310, 187-195.   | 0.9  | 76        |
| 23 | Gene Regulation: Gene Control Network in Development. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007, 36, 191-212.   | 18.3 | 145       |
| 24 | Deciphering the Underlying Mechanism of Specification and Differentiation: The Sea Urchin Gene Regulatory Network. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2006, 2006, pe47-pe47. | 4.1  | 22        |
| 25 | Neurons culturing and biophotonic sensing using porous silicon. <i>Applied Physics Letters</i> , 2004, 84, 4361-4363.  | 1.5  | 49        |
| 26 | The spin structure of quasiâ€”two-dimensional biexcitons in quantum wells. <i>Europhysics Letters</i> , 2002, 59, 728-734.   | 0.7  | 9         |
| 27 | Exciton-exciton interactions in quantum wells: Optical properties and energy and spin relaxation. <i>Physical Review B</i> , 2001, 63, .   | 1.1  | 94        |
| 28 | InAs/GaSb interfaces; the problem of boundary conditions. <i>Journal of Physics Condensed Matter</i> , 1998, 10, 8715-8729.  | 0.7  | 12        |
| 29 | Energy spectrum of heterostructures. <i>Solid State Communications</i> , 1997, 104, 257-262.   | 0.9  | 20        |