

# HervÃ© Seligmann

## List of Publications by Year in descending order

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Version: 2024-02-01

113  
papers

3,634  
citations

101496

36  
h-index

182361

51  
g-index

115  
all docs

115  
docs citations

115  
times ranked

1560  
citing authors

#	ARTICLE	IF	CITATIONS
1	Codon assignment evolvability in theoretical minimal RNA rings. <i>Gene</i> , 2021, 769, 145208.	1.0	4
2	Negative CG dinucleotide bias: An explanation based on feedback loops between Arginine codon assignments and theoretical minimal RNA rings. <i>BioEssays</i> , 2021, 43, 2000071.	1.2	3
3	Balanced evaluation of preliminary data on a candidate COVID-19 hydroxychloroquine treatment. <i>International Journal of Antimicrobial Agents</i> , 2021, 57, 106292.	1.1	1
4	Unpredictable, Counter-Intuitive Geoclimatic and Demographic Correlations of COVID-19 Spread Rates. <i>Biology</i> , 2021, 10, 623.	1.3	7
5	Combinatorial Fusion Rules to Describe Codon Assignment in the Standard Genetic Code. <i>Life</i> , 2021, 11, 4.	1.1	11
6	Estimation of Daily Reproduction Numbers during the COVID-19 Outbreak. <i>Computation</i> , 2021, 9, 109.	1.0	14
7	Pentamers with Non-redundant Frames: Bias for Natural Circular Code Codons. <i>Journal of Molecular Evolution</i> , 2020, 88, 194-201.	0.8	14
8	Identification of Noncanonical Transcripts Produced by Systematic Nucleotide Exchanges in HIV-Associated Centroblastic Lymphoma. <i>DNA and Cell Biology</i> , 2020, 39, 1444-1448.	0.9	4
9	Accretion history of large ribosomal subunits deduced from theoretical minimal RNA rings is congruent with histories derived from phylogenetic and structural methods. <i>Gene</i> , 2020, 738, 144436.	1.0	12
10	Inverted Covariate Effects for First versus Mutated Second Wave Covid-19: High Temperature Spread Biased for Young. <i>Biology</i> , 2020, 9, 226.	1.3	25
11	Comparisons between small ribosomal RNA and theoretical minimal RNA ring secondary structures confirm phylogenetic and structural accretion histories. <i>Scientific Reports</i> , 2020, 10, 7693.	1.6	17
12	First arrived, first served: competition between codons for codon-amino acid stereochemical interactions determined early genetic code assignments. <i>Die Naturwissenschaften</i> , 2020, 107, 20.	0.6	6
13	Temperature Decreases Spread Parameters of the New Covid-19 Case Dynamics. <i>Biology</i> , 2020, 9, 94.	1.3	113
14	Natural pyrrolysine-biased translation of stop codons in mitochondrial peptides entirely coded by expanded codons. <i>BioSystems</i> , 2020, 196, 104180.	0.9	3
15	Why Is AUG the Start Codon?. <i>BioEssays</i> , 2020, 42, 1900201.	1.2	10
16	Systematic Nucleotide Exchange Analysis of ESTs From the Human Cancer Genome Project Report: Origins of 347 Unknown ESTs Indicate Putative Transcription of Non-Coding Genomic Regions. <i>Frontiers in Genetics</i> , 2020, 11, 42.	1.1	2
17	Deamination gradients within codons after 1<sup>st</sup>2 position swap predict amino acid hydrophobicity and parallel $\beta$ -sheet conformational preference. <i>BioSystems</i> , 2020, 191-192, 104116.	0.9	4
18	The primordial tRNA acceptor stem code from theoretical minimal RNA ring clusters. <i>BMC Genetics</i> , 2020, 21, 7.	2.7	14

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19	RNA Rings Strengthen Hairpin Accretion Hypotheses for tRNA Evolution: A Reply to Commentaries by Z.F. Burton and M. Di Giulio. <i>Journal of Molecular Evolution</i> , 2020, 88, 243-252.	0.8	17
20	Codon Directional Asymmetry Suggests Swapped Prebiotic 1st and 2nd Codon Positions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 347.	1.8	8
21	SARS-CoV-2 and miRNA-like inhibition power. <i>Medical Hypotheses</i> , 2020, 144, 110245.	0.8	20
22	Theoretical minimal RNA rings mimick molecular evolution before tRNA-mediated translation: codon-amino acid affinities increase from early to late RNA rings. , 2020, 343, 111-122.		7
23	The Uroboros Theory of Life's Origin: 22-Nucleotide Theoretical Minimal RNA Rings Reflect Evolution of Genetic Code and tRNA-rRNA Translation Machineries. <i>Acta Biotheoretica</i> , 2019, 67, 273-297.	0.7	25
24	Theoretical minimal RNA rings designed according to coding constraints mimic deamination gradients. <i>Die Naturwissenschaften</i> , 2019, 106, 44.	0.6	19
25	Syntenies Between Cohosted Mitochondrial, Chloroplast, and Phycodnavirus Genomes: Functional Mimicry and/or Common Ancestry?. <i>DNA and Cell Biology</i> , 2019, 38, 1257-1268.	0.9	5
26	Chimeric Translation for Mitochondrial Peptides: Regular and Expanded Codons. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1195-1202.	1.9	9
27	Evolution of tRNA into rRNA secondary structures. <i>Gene Reports</i> , 2019, 17, 100483.	0.4	14
28	Bias for 3'â€²-Dominant Codon Directional Asymmetry in Theoretical Minimal RNA Rings. <i>Journal of Computational Biology</i> , 2019, 26, 1003-1012.	0.8	19
29	Transcripts with systematic nucleotide deletion of 1-12 nucleotide in human mitochondrion suggest potential non-canonical transcription. <i>PLoS ONE</i> , 2019, 14, e0217356.	1.1	12
30	Localized Context-Dependent Effects of the 'Ambush' Hypothesis: More Off-Frame Stop Codons Downstream of Shifty Codons. <i>DNA and Cell Biology</i> , 2019, 38, 786-795.	0.9	15
31	Giant viruses: spore-like missing links between Rickettsia and mitochondria?. <i>Annals of the New York Academy of Sciences</i> , 2019, 1447, 69-79.	1.8	11
32	Theoretical minimal RNA rings recapitulate the order of the genetic code's codon-amino acid assignments. <i>Journal of Theoretical Biology</i> , 2019, 471, 108-116.	0.8	25
33	More Pieces of Ancient than Recent Theoretical Minimal Proto-tRNA-Like RNA Rings in Genes Coding for tRNA Synthetases. <i>Journal of Molecular Evolution</i> , 2019, 87, 152-174.	0.8	27
34	Spontaneous evolution of circular codes in theoretical minimal RNA rings. <i>Gene</i> , 2019, 705, 95-102.	1.0	33
35	Tailed giant Tupanvirus possesses the most complete translational apparatus of the known virosphere. <i>Nature Communications</i> , 2018, 9, 749.	5.8	247
36	Alignment-based and alignment-free methods converge with experimental data on amino acids coded by stop codons at split between nuclear and mitochondrial genetic codes. <i>BioSystems</i> , 2018, 167, 33-46.	0.9	27

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37	Bijjective codon transformations show genetic code symmetries centered on cytosineâ€™s coding properties. <i>Theory in Biosciences</i> , 2018, 137, 17-31.	0.6	14
38	Swinger RNAs in the Human Mitochondrial Transcriptome. , 2018, , .		6
39	Directed Mutations Recode Mitochondrial Genes: From Regular to Stopless Genetic Codes. , 2018, , .		9
40	Protein Sequences Recapitulate Genetic Code Evolution. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 177-189.	1.9	25
41	Stem-Loop RNA Hairpins in Giant Viruses: Invading rRNA-Like Repeats and a Template Free RNA. <i>Frontiers in Microbiology</i> , 2018, 9, 101.	1.5	34
42	Giant viruses as protein-coated amoeban mitochondria?. <i>Virus Research</i> , 2018, 253, 77-86.	1.1	17
43	Natural mitochondrial proteolysis confirms transcription systematically exchanging/deleting nucleotides, peptides coded by expanded codons. <i>Journal of Theoretical Biology</i> , 2017, 414, 76-90.	0.8	28
44	Genetic Code Optimization for Cotranslational Protein Folding: Codon Directional Asymmetry Correlates with Antiparallel Betasheets, tRNA Synthetase Classes. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 412-424.	1.9	38
45	Reviewing evidence for systematic transcriptional deletions, nucleotide exchanges, and expanded codons, and peptide clusters in human mitochondria. <i>BioSystems</i> , 2017, 160, 10-24.	0.9	21
46	Evolution of Nucleotide Punctuation Marks: From Structural to Linear Signals. <i>Frontiers in Genetics</i> , 2017, 8, 36.	1.1	30
47	Swinger RNA self-hybridization and mitochondrial non-canonical swinger transcription, transcription systematically exchanging nucleotides. <i>Journal of Theoretical Biology</i> , 2016, 399, 84-91.	0.8	32
48	Systematically frameshifting by deletion of every 4th or 4th and 5th nucleotides during mitochondrial transcription: RNA self-hybridization regulates delRNA expression. <i>BioSystems</i> , 2016, 142-143, 43-51.	0.9	24
49	Cryptic tRNAs in chaetognath mitochondrial genomes. <i>Computational Biology and Chemistry</i> , 2016, 62, 119-132.	1.1	41
50	Chimeric mitochondrial peptides from contiguous regular and swinger RNA. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 283-297.	1.9	30
51	Unbiased Mitoproteome Analyses Confirm Non-canonical RNA, Expanded Codon Translations. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 391-403.	1.9	23
52	Natural chymotrypsin-like-cleaved human mitochondrial peptides confirm tetra-, pentacodon, non-canonical RNA translations. <i>BioSystems</i> , 2016, 147, 78-93.	0.9	27
53	Translation of mitochondrial swinger RNAs according to tri-, tetra- and pentacodons. <i>BioSystems</i> , 2016, 140, 38-48.	0.9	34
54	Unifying view of stemâ€™loop hairpin RNA as origin of current and ancient parasitic and non-parasitic RNAs, including in giant viruses. <i>Current Opinion in Microbiology</i> , 2016, 31, 1-8.	2.3	55

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55	Sharp switches between regular and swinger mitochondrial replication: 16S rDNA systematically exchanging nucleotides A<math>\leftrightarrow</math>T+C<math>\leftrightarrow</math>G in the mitogenome of <i>Kamimuria wangi</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2440-2446.	0.7	24
56	Phylogeny of genetic codes and punctuation codes within genetic codes. BioSystems, 2015, 129, 36-43.	0.9	38
57	Swinger RNAs with sharp switches between regular transcription and transcription systematically exchanging ribonucleotides: Case studies. BioSystems, 2015, 135, 1-8.	0.9	26
58	Codon expansion and systematic transcriptional deletions produce tetra-, pentacoded mitochondrial peptides. Journal of Theoretical Biology, 2015, 387, 154-165.	0.8	40
59	Systematic exchanges between nucleotides: Genomic swinger repeats and swinger transcription in human mitochondria. Journal of Theoretical Biology, 2015, 384, 70-77.	0.8	20
60	Species radiation by DNA replication that systematically exchanges nucleotides?. Journal of Theoretical Biology, 2014, 363, 216-222.	0.8	31
61	The relation between hairpin formation by mitochondrial WANCY tRNAs and the occurrence of the light strand replication origin in Lepidosauria. Gene, 2014, 542, 248-257.	1.0	32
62	Bijjective transformation circular codes and nucleotide exchanging RNA transcription. BioSystems, 2014, 118, 39-50.	0.9	57
63	Mitochondrial swinger replication: DNA replication systematically exchanging nucleotides and short 16S ribosomal DNA swinger inserts. BioSystems, 2014, 125, 22-31.	0.9	30
64	Putative anticodons in mitochondrial tRNA sidearm loops: Pocketknife tRNAs?. Journal of Theoretical Biology, 2014, 340, 155-163.	0.8	46
65	Pocketknife tRNA hypothesis: Anticodons in mammal mitochondrial tRNA side-arm loops translate proteins?. BioSystems, 2013, 113, 165-176.	0.9	42
66	Tetracoding increases with body temperature in Lepidosauria. BioSystems, 2013, 114, 155-163.	0.9	37
67	Polymerization of non-complementary RNA: Systematic symmetric nucleotide exchanges mainly involving uracil produce mitochondrial RNA transcripts coding for cryptic overlapping genes. BioSystems, 2013, 111, 156-174.	0.9	40
68	Systematic asymmetric nucleotide exchanges produce human mitochondrial RNAs cryptically encoding for overlapping protein coding genes. Journal of Theoretical Biology, 2013, 324, 1-20.	0.8	42
69	Triplex DNA:RNA, 3' to 5' Inverted RNA and Protein Coding in Mitochondrial Genomes. Journal of Computational Biology, 2013, 20, 660-671.	0.8	37
70	Coding Constraints Modulate Chemically Spontaneous Mutational Replication Gradients in Mitochondrial Genomes. Current Genomics, 2012, 13, 37-54.	0.7	59
71	Overlapping genes coded in the 3' to 5' direction in mitochondrial genes and 3' to 5' polymerization of non-complementary RNA by an "invertase"™. Journal of Theoretical Biology, 2012, 315, 38-52.	0.8	45
72	Putative mitochondrial polypeptides coded by expanded quadruplet codons, decoded by antisense tRNAs with unusual anticodons. BioSystems, 2012, 110, 84-106.	0.9	41

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73	Overlapping genetic codes for overlapping frameshifted genes in Testudines, and Lepidochelys olivacea as special case. Computational Biology and Chemistry, 2012, 41, 18-34.	1.1	46
74	An overlapping genetic code for frameshifted overlapping genes in Drosophila mitochondria: Antisense antitermination tRNAs UAR insert serine. Journal of Theoretical Biology, 2012, 298, 51-76.	0.8	49
75	Positive and Negative Cognate Amino Acid Bias Affects Compositions of Aminoacyl-tRNA Synthetases and Reflects Functional Constraints on Protein Structure. Bio, 2012, 2, 11-26.	0.6	14
76	Probable presence of an ubiquitous cryptic mitochondrial gene on the antisense strand of the cytochrome oxidase I gene. Biology Direct, 2011, 6, 56.	1.9	69
77	Two genetic codes, one genome: Frameshifted primate mitochondrial genes code for additional proteins in presence of antisense antitermination tRNAs. BioSystems, 2011, 105, 271-285.	0.9	53
78	Error compensation of tRNA misacylation by codon-anticodon mismatch prevents translational amino acid misinsertion. Computational Biology and Chemistry, 2011, 35, 81-95.	1.1	37
79	Pathogenic mutations in antisense mitochondrial tRNAs. Journal of Theoretical Biology, 2011, 269, 287-296.	0.8	37
80	Positive correlations between molecular and morphological rates of evolution. Journal of Theoretical Biology, 2010, 264, 799-807.	0.8	34
81	The ambush hypothesis at the whole-organism level: Off frame, "hidden" stops in vertebrate mitochondrial genes increase developmental stability. Computational Biology and Chemistry, 2010, 34, 80-85.	1.1	45
82	Mitochondrial tRNAs as light strand replication origins: Similarity between anticodon loops and the loop of the light strand replication origin predicts initiation of DNA replication. BioSystems, 2010, 99, 85-93.	0.9	64
83	Avoidance of antisense, antiterminator tRNA anticodons in vertebrate mitochondria. BioSystems, 2010, 101, 42-50.	0.9	45
84	Do anticodons of misacylated tRNAs preferentially mismatch codons coding for the misloaded amino acid?. BMC Molecular Biology, 2010, 11, 41.	3.0	27
85	Undetected antisense tRNAs in mitochondrial genomes?. Biology Direct, 2010, 5, 39.	1.9	53
86	Evolution of the third eye: a phylogenetic comparative study of parietal-eye size as an ecophysiological adaptation in Liolaemus lizards. Biological Journal of the Linnean Society, 2010, 101, 870-883.	0.7	10
87	Morphological, functional and evolutionary aspects of tail autotomy and regeneration in the "living fossil" Sphenodon (Reptilia: Rhynchocephalia). Biological Journal of the Linnean Society, 2008, 93, 721-743.	0.7	34
88	Relationship between mRNA secondary structure and sequence variability in Chloroplast genes: possible life history implications. BMC Genomics, 2008, 9, 48.	1.2	14
89	Hybridization between mitochondrial heavy strand tDNA and expressed light strand tRNA modulates the function of heavy strand tDNA as light strand replication origin. Journal of Molecular Biology, 2008, 379, 188-199.	2.0	53
90	Analysis of the locomotor activity of a nocturnal desert lizard (Reptilia: Gekkonidae: Teratoscincus) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.6	25

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91	Cost minimization of ribosomal frameshifts. <i>Journal of Theoretical Biology</i> , 2007, 249, 162-167.	0.8	46
92	Mitochondrial tRNA sequences as unusual replication origins: Pathogenic implications for Homo sapiens. <i>Journal of Theoretical Biology</i> , 2006, 243, 375-385.	0.8	44
93	Possible multiple origins of replication in primate mitochondria: Alternative role of tRNA sequences. <i>Journal of Theoretical Biology</i> , 2006, 241, 321-332.	0.8	72
94	Error propagation across levels of organization: From chemical stability of ribosomal RNA to developmental stability. <i>Journal of Theoretical Biology</i> , 2006, 242, 69-80.	0.8	27
95	Mitochondrial replication origin stability and propensity of adjacent tRNA genes to form putative replication origins increase developmental stability in Lizards. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006, 306B, 433-449.	0.6	51
96	Evolution of base-substitution gradients in primate mitochondrial genomes. <i>Genome Research</i> , 2005, 15, 665-673.	2.4	53
97	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. <i>DNA and Cell Biology</i> , 2004, 23, 707-714.	0.9	67
98	Ancestral Sequence Reconstruction in Primate Mitochondrial DNA: Compositional Bias and Effect on Functional Inference. <i>Molecular Biology and Evolution</i> , 2004, 21, 1871-1883.	3.5	66
99	The Ambush Hypothesis: Hidden Stop Codons Prevent Off-Frame Gene Reading. <i>DNA and Cell Biology</i> , 2004, 23, 701-705.	0.9	119
100	Cost-Minimization of Amino Acid Usage. <i>Journal of Molecular Evolution</i> , 2003, 56, 151-161.	0.8	144
101	More injuries in left-footed individual lizards and <i>Sphenodon</i> . <i>Journal of Zoology</i> , 2003, 260, 129-144.	0.8	23
102	Avoiding injury and surviving injury: two coexisting evolutionary strategies in lizards. <i>Biological Journal of the Linnean Society</i> , 2003, 78, 307-324.	0.7	16
103	Behavioural and morphological asymmetries in hindlimbs of <i>Hoplodactylus duvaucelii</i> (Lacertilia: Tj ETQq1 1 0.784314 rgBT /Overlock 0.5 19		
104	Chemical interactions between amino acid and RNA: multiplicity of the levels of specificity explains origin of the genetic code. <i>Die Naturwissenschaften</i> , 2002, 89, 542-551.	0.6	42
105	Evolution and ecology of developmental processes and of the resulting morphology: directional asymmetry in hindlimbs of Agamidae and Lacertidae (Reptilia: Lacertilia). <i>Biological Journal of the Linnean Society</i> , 2000, 69, 461-481.	0.7	28
106	Resource partition history and evolutionary specialization of subunits in complex systems. <i>BioSystems</i> , 1999, 51, 31-39.	0.9	15
107	Systematics and distribution of the <i>Acanthodactylus pardalis</i> group (Lacertidae) in Egypt and Israel. <i>Zoology in the Middle East</i> , 1999, 17, 21-50.	0.2	18
108	Evidence that minor directional asymmetry is functional in lizard hindlimbs. <i>Journal of Zoology</i> , 1998, 245, 205-208.	0.8	31

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109	Effect of environmental complexity on salt-adaptation in Sorghum bicolor. BioSystems, 1998, 45, 213-220.	0.9	7
110	Leaf malformation during early development in Sorghum. Evidence for an embryonic developmental window. Physiologia Plantarum, 1997, 99, 470-476.	2.6	9
111	Transmission of acquired adjustments to salinity in Sorghum bicolor. BioSystems, 1997, 40, 257-261.	0.9	6
112	Mutation Patterns Due to Converging Mitochondrial Replication and Transcription Increase Lifespan, and Cause Growth Rate-Longevity Tradeoffs. , 0, , .		18
113	Replicational Mutation Gradients, Dipole Moments, Nearest Neighbour Effects and DNA Polymerase Gamma Fidelity in Human Mitochondrial Genomes. , 0, , .		9