

# HervÃ© Seligmann

## List of Publications by Year in descending order

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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	Tailed giant Tupanvirus possesses the most complete translational apparatus of the known virosphere. <i>Nature Communications</i> , 2018, 9, 749.	5.8	247
2	Cost-Minimization of Amino Acid Usage. <i>Journal of Molecular Evolution</i> , 2003, 56, 151-161.	0.8	144
3	The Ambush Hypothesis: Hidden Stop Codons Prevent Off-Frame Gene Reading. <i>DNA and Cell Biology</i> , 2004, 23, 701-705.	0.9	119
4	Temperature Decreases Spread Parameters of the New Covid-19 Case Dynamics. <i>Biology</i> , 2020, 9, 94.	1.3	113
5	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
6	Probable presence of an ubiquitous cryptic mitochondrial gene on the antisense strand of the cytochrome oxidase I gene. <i>Biology Direct</i> , 2011, 6, 56.	1.9	69
7	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. <i>DNA and Cell Biology</i> , 2004, 23, 707-714.	0.9	67
8	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
9	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. <i>BioSystems</i> , 2010, 99, 85-93.	0.9	64
10	Coding Constraints Modulate Chemically Spontaneous Mutational Replication Gradients in Mitochondrial Genomes. <i>Current Genomics</i> , 2012, 13, 37-54.	0.7	59
11	Bijjective transformation circular codes and nucleotide exchanging RNA transcription. <i>BioSystems</i> , 2014, 118, 39-50.	0.9	57
12	Unifying view of stem-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
13	Evolution of base-substitution gradients in primate mitochondrial genomes. <i>Genome Research</i> , 2005, 15, 665-673.	2.4	53
14	Hybridization between mitochondrial heavy strand tDNA and expressed light strand tRNA modulates the function of heavy strand tDNA as light strand replication origin. <i>Journal of Molecular Biology</i> , 2008, 379, 188-199.	2.0	53
15	Undetected antisense tRNAs in mitochondrial genomes?. <i>Biology Direct</i> , 2010, 5, 39.	1.9	53
16	Two genetic codes, one genome: Frameshifted primate mitochondrial genes code for additional proteins in presence of antisense antitermination tRNAs. <i>BioSystems</i> , 2011, 105, 271-285.	0.9	53
17	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
18	An overlapping genetic code for frameshifted overlapping genes in <i>Drosophila</i> mitochondria: Antisense antitermination tRNAs UAR insert serine. <i>Journal of Theoretical Biology</i> , 2012, 298, 51-76.	0.8	49

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19	Cost minimization of ribosomal frameshifts. <i>Journal of Theoretical Biology</i> , 2007, 249, 162-167.	0.8	46
20	Overlapping genetic codes for overlapping frameshifted genes in Testudines, and <i>Lepidochelys olivacea</i> as special case. <i>Computational Biology and Chemistry</i> , 2012, 41, 18-34.	1.1	46
21	Putative anticodons in mitochondrial tRNA sidearm loops: Pocketknife tRNAs?. <i>Journal of Theoretical Biology</i> , 2014, 340, 155-163.	0.8	46
22	The ambush hypothesis at the whole-organism level: Off frame, "hidden" stops in vertebrate mitochondrial genes increase developmental stability. <i>Computational Biology and Chemistry</i> , 2010, 34, 80-85.	1.1	45
23	Avoidance of antisense, antiterminator tRNA anticodons in vertebrate mitochondria. <i>BioSystems</i> , 2010, 101, 42-50.	0.9	45
24	Overlapping genes coded in the 3' to 5' direction in mitochondrial genes and 3' to 5' polymerization of non-complementary RNA by an "invertase". <i>Journal of Theoretical Biology</i> , 2012, 315, 38-52.	0.8	45
25	Mitochondrial tRNA sequences as unusual replication origins: Pathogenic implications for <i>Homo sapiens</i> . <i>Journal of Theoretical Biology</i> , 2006, 243, 375-385.	0.8	44
26	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
27	Pocketknife tRNA hypothesis: Anticodons in mammal mitochondrial tRNA side-arm loops translate proteins?. <i>BioSystems</i> , 2013, 113, 165-176.	0.9	42
28	Systematic asymmetric nucleotide exchanges produce human mitochondrial RNAs cryptically encoding for overlapping protein coding genes. <i>Journal of Theoretical Biology</i> , 2013, 324, 1-20.	0.8	42
29	Putative mitochondrial polypeptides coded by expanded quadruplet codons, decoded by antisense tRNAs with unusual anticodons. <i>BioSystems</i> , 2012, 110, 84-106.	0.9	41
30	Cryptic tRNAs in chaetognath mitochondrial genomes. <i>Computational Biology and Chemistry</i> , 2016, 62, 119-132.	1.1	41
31	Polymerization of non-complementary RNA: Systematic symmetric nucleotide exchanges mainly involving uracil produce mitochondrial RNA transcripts coding for cryptic overlapping genes. <i>BioSystems</i> , 2013, 111, 156-174.	0.9	40
32	Codon expansion and systematic transcriptional deletions produce tetra-, pentacoded mitochondrial peptides. <i>Journal of Theoretical Biology</i> , 2015, 387, 154-165.	0.8	40
33	Phylogeny of genetic codes and punctuation codes within genetic codes. <i>BioSystems</i> , 2015, 129, 36-43.	0.9	38
34	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
35	Error compensation of tRNA misacylation by codon-anticodon mismatch prevents translational amino acid misinsertion. <i>Computational Biology and Chemistry</i> , 2011, 35, 81-95.	1.1	37
36	Pathogenic mutations in antisense mitochondrial tRNAs. <i>Journal of Theoretical Biology</i> , 2011, 269, 287-296.	0.8	37

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37	Tetracoding increases with body temperature in Lepidosauria. <i>BioSystems</i> , 2013, 114, 155-163.	0.9	37
38	Triplex DNA:RNA, 3â€™-to-5â€™ Inverted RNA and Protein Coding in Mitochondrial Genomes. <i>Journal of Computational Biology</i> , 2013, 20, 660-671.	0.8	37
39	Morphological, functional and evolutionary aspects of tail autotomy and regeneration in the "living fossil" <i>Sphenodon</i> (Reptilia: Rhynchocephalia). <i>Biological Journal of the Linnean Society</i> , 2008, 93, 721-743.	0.7	34
40	Positive correlations between molecular and morphological rates of evolution. <i>Journal of Theoretical Biology</i> , 2010, 264, 799-807.	0.8	34
41	Translation of mitochondrial swinger RNAs according to tri-, tetra- and pentacodons. <i>BioSystems</i> , 2016, 140, 38-48.	0.9	34
42	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
43	Spontaneous evolution of circular codes in theoretical minimal RNA rings. <i>Gene</i> , 2019, 705, 95-102.	1.0	33
44	The relation between hairpin formation by mitochondrial WANCY tRNAs and the occurrence of the light strand replication origin in Lepidosauria. <i>Gene</i> , 2014, 542, 248-257.	1.0	32
45	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
46	Evidence that minor directional asymmetry is functional in lizard hindlimbs. <i>Journal of Zoology</i> , 1998, 245, 205-208.	0.8	31
47	Species radiation by DNA replication that systematically exchanges nucleotides?. <i>Journal of Theoretical Biology</i> , 2014, 363, 216-222.	0.8	31
48	Mitochondrial swinger replication: DNA replication systematically exchanging nucleotides and short 16S ribosomal DNA swinger inserts. <i>BioSystems</i> , 2014, 125, 22-31.	0.9	30
49	Chimeric mitochondrial peptides from contiguous regular and swinger RNA. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 283-297.	1.9	30
50	Evolution of Nucleotide Punctuation Marks: From Structural to Linear Signals. <i>Frontiers in Genetics</i> , 2017, 8, 36.	1.1	30
51	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
52	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
53	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
54	Do anticodons of misacylated tRNAs preferentially mismatch codons coding for the misloaded amino acid?. <i>BMC Molecular Biology</i> , 2010, 11, 41.	3.0	27

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55	Natural chymotrypsin-like-cleaved human mitochondrial peptides confirm tetra-, pentacodon, non-canonical RNA translations. <i>BioSystems</i> , 2016, 147, 78-93.	0.9	27
56	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
57	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
58	Swinger RNAs with sharp switches between regular transcription and transcription systematically exchanging ribonucleotides: Case studies. <i>BioSystems</i> , 2015, 135, 1-8.	0.9	26
59	Analysis of the locomotor activity of a nocturnal desert lizard (Reptilia: Gekkonidae: Teratoscincus) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	25
60	Protein Sequences Recapitulate Genetic Code Evolution. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 177-189.	1.9	25
61	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
62	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
63	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
64	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
65	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> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2440-2446.	0.7	24
66	More injuries in left-footed individual lizards and Sphenodon. <i>Journal of Zoology</i> , 2003, 260, 129-144.	0.8	23
67	Unbiased Mitoproteome Analyses Confirm Non-canonical RNA, Expanded Codon Translations. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 391-403.	1.9	23
68	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
69	Systematic exchanges between nucleotides: Genomic swinger repeats and swinger transcription in human mitochondria. <i>Journal of Theoretical Biology</i> , 2015, 384, 70-77.	0.8	20
70	SARS-CoV-2 and miRNA-like inhibition power. <i>Medical Hypotheses</i> , 2020, 144, 110245.	0.8	20
71	Behavioural and morphological asymmetries in hindlimbs of <i>Hoplodactylus duvaucelii</i> (Lacertilia:) Tj ETQq1 1 0.784314 rgBT /Overlock	0.5	19
72	Theoretical minimal RNA rings designed according to coding constraints mimic deamination gradients. <i>Die Naturwissenschaften</i> , 2019, 106, 44.	0.6	19

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73	Bias for 3â€²-Dominant Codon Directional Asymmetry in Theoretical Minimal RNA Rings. <i>Journal of Computational Biology</i> , 2019, 26, 1003-1012.	0.8	19
74	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
75	Mutation Patterns Due to Converging Mitochondrial Replication and Transcription Increase Lifespan, and Cause Growth Rate-Longevity Tradeoffs. , 0, , .		18
76	Giant viruses as protein-coated amoeban mitochondria?. <i>Virus Research</i> , 2018, 253, 77-86.	1.1	17
77	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
78	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
79	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
80	Resource partition history and evolutionary specialization of subunits in complex systems. <i>BioSystems</i> , 1999, 51, 31-39.	0.9	15
81	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
82	Relationship between mRNA secondary structure and sequence variability in Chloroplast genes: possible life history implications. <i>BMC Genomics</i> , 2008, 9, 48.	1.2	14
83	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
84	Evolution of tRNA into rRNA secondary structures. <i>Gene Reports</i> , 2019, 17, 100483.	0.4	14
85	Pentamers with Non-redundant Frames: Bias for Natural Circular Code Codons. <i>Journal of Molecular Evolution</i> , 2020, 88, 194-201.	0.8	14
86	The primordial tRNA acceptor stem code from theoretical minimal RNA ring clusters. <i>BMC Genetics</i> , 2020, 21, 7.	2.7	14
87	Positive and Negative Cognate Amino Acid Bias Affects Compositions of Aminoacyl-tRNA Synthetases and Reflects Functional Constraints on Protein Structure. <i>Bio</i> , 2012, 2, 11-26.	0.6	14
88	Estimation of Daily Reproduction Numbers during the COVID-19 Outbreak. <i>Computation</i> , 2021, 9, 109.	1.0	14
89	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
90	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

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91	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
92	Combinatorial Fusion Rules to Describe Codon Assignment in the Standard Genetic Code. <i>Life</i> , 2021, 11, 4.	1.1	11
93	Evolution of the third eye: a phylogenetic comparative study of parietal-eye size as an ecophysiological adaptation in <i>Liolaemus</i> lizards. <i>Biological Journal of the Linnean Society</i> , 2010, 101, 870-883.	0.7	10
94	Why Is AUG the Start Codon?. <i>BioEssays</i> , 2020, 42, 1900201.	1.2	10
95	Leaf malformation during early development in <i>Sorghum</i> . Evidence for an embryonic developmental window. <i>Physiologia Plantarum</i> , 1997, 99, 470-476.	2.6	9
96	Directed Mutations Recode Mitochondrial Genes: From Regular to Stopless Genetic Codes. , 2018, , .		9
97	Chimeric Translation for Mitochondrial Peptides: Regular and Expanded Codons. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1195-1202.	1.9	9
98	Replicational Mutation Gradients, Dipole Moments, Nearest Neighbour Effects and DNA Polymerase Gamma Fidelity in Human Mitochondrial Genomes. , 0, , .		9
99	Codon Directional Asymmetry Suggests Swapped Prebiotic 1st and 2nd Codon Positions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 347.	1.8	8
100	Effect of environmental complexity on salt-adaptation in <i>Sorghum bicolor</i> . <i>BioSystems</i> , 1998, 45, 213-220.	0.9	7
101	Unpredictable, Counter-Intuitive Geoclimatic and Demographic Correlations of COVID-19 Spread Rates. <i>Biology</i> , 2021, 10, 623.	1.3	7
102	Theoretical minimal RNA rings mimic molecular evolution before tRNA-mediated translation: codon-amino acid affinities increase from early to late RNA rings. , 2020, 343, 111-122.		7
103	Transmission of acquired adjustments to salinity in <i>Sorghum bicolor</i> . <i>BioSystems</i> , 1997, 40, 257-261.	0.9	6
104	Swinger RNAs in the Human Mitochondrial Transcriptome. , 2018, , .		6
105	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
106	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
107	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
108	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

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109	Codon assignment evolvability in theoretical minimal RNA rings. <i>Gene</i> , 2021, 769, 145208.	1.0	4
110	Natural pyrrolysine-biased translation of stop codons in mitochondrial peptides entirely coded by expanded codons. <i>BioSystems</i> , 2020, 196, 104180.	0.9	3
111	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
112	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
113	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