

Toni Gabaldón

Publication list (as of January 2016)

Peer-reviewed publications (& indicates corresponding author, C=number of citations as of January 2016 (ISI), other remarks such as Faculty of 1000 recommendations or editor's choice are indicated).

Total citations : **4,124** (30,2 cit/article) h-index=**36** (h-index papers with citations in red).& indicates correspondence

Publications in international peer-reviewed journals

1. **Gabaldón, T.** and Huynen, MA. (2003) Reconstruction of the protomitochondrial metabolism. *Science* 1;301(5633):609. **C=111, recommended in Faculty of 1000.**
2. **Gabaldón, T.** and Huynen, MA. (2004) Prediction of protein function and pathways in the genome era. *Cell. Mol. Life Sci.* 61;(7-8):930-44. **C=59**
3. **Gabaldón T[&].** & Huynen MA. (2004) Shaping the mitochondrial proteome. *BBA– Bioenergetics*. Vol 1659/2-3 pp 212-220. **C=76. Among the top-5 most downloaded paper in that journal in 2005**
4. **Gabaldón T,** Rainey D and Huynen, MA. (2005) Tracing the evolution of a large protein complex in the eukaryotes, NADH:ubiquinone oxidoreductase (Complex I) . *J. Mol. Biol.*. 13;348(4):857-70. **C=130. featured in Science Editor's choice**
5. **Gabaldón T.** and Huynen MA. (2005) Lineage-specific gene loss following mitochondrial endosymbiosis and its applications for function prediction in the eukaryotes. *Bioinformatics* 21 S2:ii144-ii150. C=20
6. **Gabaldón T.** (2005) Evolution of proteins and proteomes: a phylogenetics approach. *Evolutionary Bioinformatics Online*. 2005:1 51-61. C=12
7. Boxma B, Graaf RM, van der Staay GW, van Alen TA, Ricard G, **Gabaldón T,** van Hoek AHAM, Moon-van der Staay SY, Koopman WJH, van Hellemond JJ, Tielens AGM, Friedrich T, Veenhuis M, Huynen MA, Hackstein JHP (2005) An anaerobic mitochondrion that produces hydrogen. *Nature*. 3;434(7029):74-9. **C=122. Recommended in Faculty of 1000**
8. Huynen, MA., Spronk C.A.E.M., **Gabaldón, T.** and Snel B (2005) Combining data from genomes, Y2H and 3D data indicates that BolA is a reductase interacting with a glutaredoxin. *FEBS-Letters* 579(3):591-596 **C=46**
9. Huynen MA., **Gabaldón T** and Snel B. (2005) Variation and evolution of biomolecular systems: searching for functional relevance. *FEBS-Letters* 579(8):1839-1845. C=12
10. **Gabaldón, T.** Snel, B. van Zimmeren, F. Hemrika, W. Tabak, H. and Huynen, MA. (2006) Origin and evolution of the peroxisomal proteome. *Biology Direct* 2006 1:8. **C=96. recommended in Faculty of 1000**
11. **Gabaldón, T[&].** (2006) Computational approaches for the prediction of protein function in the mitochondrion. *Am J Physiol Cell Physiol*. 291:1121-1128. C=6
12. **Gabaldón, T,** Peretó J.,Montero F., Gil, R., Latorre A. and Moya A (2007). Structural analysis of a hypothetical minimal metabolism. *Philos Trans R Soc Lond B Biol Sci*. 362(1486):1751-62. C=20
13. Huerta-Cepas J., Dopazo H, Dopazo J and **Gabaldón, T[&].** (2007). The human phylome. *Genome Biology* 2007, 8:R109. **C=87.**
14. **Gabaldón T[&].** and Huynen MA. (2007). From endosymbiont to host-controlled organelle: the hijacking of the mitochondrial protein synthesis and metabolism. *PLoS Comp Biol* 3(11):e219. **C=57**
15. Schluter A, Fourcade S, Domenech-Estevéz E, **Gabaldón T,** Huerta-Cepas J, Berthommier G, Ripp

- R, Wanders RJ, Poch O, and Pujol A. (2007) PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. *Nucl Acids Res.* 35(Database issue):D815-22. C=32
16. Tarraga J, Medina I, Arbiza L, Huerta-Cepas J, **Gabaldón, T.**, Dopazo J and Dopazo H. (2007) Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. *Nucleic Acids Res.* 35(Web Server issue):W38-42. **C=37**
 17. Huerta-Cepas J., Bueno A, Dopazo J and **Gabaldón, T[&]**. (2008). PhylomeDB: a database for genome-wide collections of gene phylogenies. *Nucleic Acids Res* 36:D491-6. **C=57**
 18. **Gabaldón T[&]**. (2008). Large-scale assignment of orthology: back to phylogenetics?. *Genome Biology* 2008. 9:235. **C=75.**
 19. Marcet-Houben M and **Gabaldón T[&]**. (2009) The tree versus the forest: the fungal tree of life and the topological diversity within the yeast phylome. *PLoS ONE.* 2009;4(2):e4357. **C=44.**
 20. Capella-Gutiérrez S, Silla-Martínez JM and **Gabaldón T[&]**. (2009) trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25(15):1972-3. **C=433.**
 21. Marcet-Houben M. Marcedu G, and **Gabaldón T[&]**. (2009). Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. *BMC Evol. Biology.* 9:295. C=21
 22. Gil-Borlado MC, González-Hoyuela M, Blázquez A., García-Silva MT, **Gabaldón T**, Manzanares J, Vara J, Martín MA, Seneca S, Arenas J and Ugalde C. (2009) Pathogenic mutations in the 5' untranslated region of BCS1L mRNA in mitochondrial complex III deficiency. *Mitochondrion.* 9(5):299-305. C=15
 23. **Gabaldón T[&]**, Dessimoz C, Huxley-Jones J, Vilella AJ, Sonnhammer EL, Lewis S. (2009) Joining forces in the quest for orthologs. *Genome Biol.* 10(9):403. C=35
 24. Schlüter A, Real-Chicharro A, **Gabaldón T**, Sanchez-Jimenez F and Pujol A. (2009) PeroxisomeDB 2.0: an integrative view of the global peroxisomal metabolism. *Nucl Acids Res.* 8(Database issue):D800-5. C=35.
 25. **Gabaldón T[&]**. (2010). Peroxisome diversity and evolution. *Philos Trans R Soc Lond B Biol Sci.* 365(1541):765-73. **C=63.**
 26. Marcet-Houben M. and **Gabaldón T[&]**. (2010). Acquisition of prokaryotic genes by fungal genomes. *Trends in Genetics.* 26(1):5-8. **C=85.**
 27. Mihailovitch M, Militti C, **Gabaldón T** and Gebauer F. (2010). Eukaryotic cold-shock domain proteins: highly versatile regulators of gene expression. *Bioessays* 32(2):109-18. **C=49.**
 28. Huerta-Cepas J, Dopazo J. and **Gabaldón T[&]**. (2010). ETE: A python environment for tree exploration. *BMC Bioinformatics.* 11(1):24. **C=113.**
 29. Gómez-Baldó L, Schmidt S, Maxwell CA, Bonifaci N, **Gabaldón T**, Vidalain PO, Senapedis W, Kletke A, Rosing M, Barnekow A, Rottapel R, Capellá G, Vidal M, Astrinidis A, Piekorz RP, Pujana MA. (2010) TACC3-TSC2 maintains nuclear envelope structure and controls cell division. *Cell Cycle.* 18;9(6). C=25
 30. International Aphid Genomics Consortium (Including **Gabaldón T** as analysis leader). (2010) Genome sequence of the pea aphid *Acyrtosiphon pisum*. *PLoS Biol.* 8(2):e1000313. **C=295.**
 31. Ahmadinejad N, Dagan T, Gruenheit N, Martin W, **Gabaldón T[&]**. (2010) Evolution of spliceosomal introns following endosymbiotic gene transfer. *BMC Evol Biol.* 10:57. C=14
 32. Gerardo NM, Altincicek B, Anselme C, Atamian H, Barribeau SM, de Vos M, Duncan, E, Evans JD, Gabaldon T, Ghanim M, Heddi A, Kaloshian I, Latorre A, Moya A, Nakabachi A, Parker BJ, Perez-Brocail V, Pignatelli M, Rhabé Y, Ramsey JS, Spragg, C, Tamames J, Tamarit D, Tamborindeguy C, Vincent-Monegat C, Vilcinskas A. (2010) Immunity and other defenses in pea aphids, *Acyrtosiphon pisum*. *Genome Biol.* 11(2):R21. **C=116.**
 33. Peña A, Teeling H, Huerta-Cepas J, Santos F, Yarza P, Brito-Echeverría J, Lucio M, Schmitt-Kopplin P, Meseguer I, Schenowitz C, Dossat C, Barbe V, Dopazo J, Rosselló-Mora R, Schüler M, Glöckner

- FO, Amann R, **Gabaldón T**, Antón J. (2010) Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting *Salinibacter ruber* strains. *ISME Journal*. 4(7):882-95. **C=37**
34. Milinkovitch MC, Helaers R, Depiereux E, Tzika AC, **Gabaldón T**. (2010) 2x genomes -depth does matter. *Genome Biol*. 11(2):R16. **C=38**.
 35. Huerta-Cepas J, Marcet-Houben M, Pignatelli M, Moya A and **Gabaldón T**[&]. (2010). The pea aphid phylome: a complete catalogue of evolutionary histories and arthropod orthology and paralogy relationships for *Acyrtosiphon pisum* genes. *Insect Molecular Biology*. 19(2):13-21. C=23
 36. Diez J, Walter. D, Muñoz-Pinedo C and **Gabaldón T**. (2010) DeathBase: a database on structure, evolution and function of proteins involved in apoptosis and other forms of cell death. *Cell Death and Differentiation* 17(5):735-6 . C=13
 37. **Gabaldón T**[&]. and Capella-Gutiérrez S. (2010) Lack of phylogenetic support for a supposed actinobacterial origin of peroxisomes. *Gene* 465(1-2):61-5. C=5
 38. Benítez-Páez A, Villarroya M, Douthwaite S, **Gabaldón T**[&], Armengod ME. (2010) YibK is the 2'-O-methyltransferase TrmL that modifies the wobble nucleotide in *Escherichia coli* tRNA(Leu) isoacceptors. *RNA*. 16(11):2131-43. C=21
 39. Gil Borlado MC, Moreno Lastres D, Gonzalez Hoyuela M, Moran M, Blazquez A, Pello R, Marin Buera L, **Gabaldón T**, Garcia Peñas JJ, Martín MA, Arenas J, Ugalde C. (2010) Impact of the mitochondrial genetic background in complex III deficiency. *PLoS One*. 17;5(9). C=7
 40. Lingner T, Mühlhausen S, **Gabaldón T**, Notredame C, Meinicke P. (2010). Predicting phenotypic traits of prokaryotes from protein domain frequencies. *BMC Bioinformatics*. 11:481. C=3
 41. Prysycz LP, Huerta-Cepas J, **Gabaldón T**[&]. (2011) MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. *Nucleic Acid Res*. 39(5):e32. **C=36**
 42. Huerta-Cepas J, Capella-Gutiérrez S, Prysycz LP, Denisov I, Kormes D, Marcet-Houben M, **Gabaldón T**[&]. (2011) PhylomeDB v3.0: An expanding repository of genome-wide collections of phylogenies, alignments and orthology and paralogy predictions. *Nucleic Acid Res*. 39(Database issue):D556-60. **Featured article by NAR's editors. C=74**.
 43. Huerta-Cepas J, **Gabaldón T**[&]. (2011) Assigning duplications to relative temporal scales in genome-wide studies. *Bioinformatics* 27(1):38-45. C=19.
 44. Roetzer A, **Gabaldón T**, Schüller C. (2011) From *Saccharomyces cerevisiae* to *Candida glabrata* in a few easy steps: important adaptations for an opportunistic pathogen. *FEMS Microbiol Lett*. 314(1):1-9. **C=45**
 45. Roetzer A, Klopff E, Gratz N, Marcet-Houben M, Hiller E, Rupp S, **Gabaldón T**, Kovarik P, Schüller C. (2011). Regulation of *Candida glabrata* oxidative stress resistance is adapted to host environment. *FEBS Lett*. 585(2):319-27 **C=97**.
 46. Marcet-Houben M, **Gabaldón T**[&] (2011) TreeKO: A duplication-aware algorithm for the comparison of phylogenetic trees. *Nucleic Acid Res*. 39(10):e66 C=9
 47. Neurohr G, Naegeli A, Titos I, Theler D, Greber B, Diez J, **Gabaldón T**, Mendoza M, Barral Y. (2011) A Midzone-Based Ruler Adjusts Chromosome Compaction to Anaphase Spindle Length. *Science*. 332(6028):465-8. C=28
 48. Vellozo AF, Véron AS, Baa-Puyoulet P, Huerta-Cepas J, Cottret L, Febvay G, Calevro F, Rahbé Y, Douglas AE, **Gabaldón T**, Sagot MF, Charles H, Colella S. (2011) CycADS: an annotation database system to ease the development and update of BioCyc databases. *Database 2011:bar008*. C=5
 49. Huerta-Cepas J, Dopazo J, Huynen MA, **Gabaldón T**[&]. (2011) Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. *Brief Bioinform*. 12(5)442-8. C=16
 50. Sánchez R, Serra F, Tárraga J, Medina I, Carbonell J, Pulido L, de María A, Capella-Gutiérrez S, Huerta-Cepas J, **Gabaldón T**, Dopazo J, Dopazo H. (2011) Phylemon 2.0: a suite of web-tools for

- molecular evolution, phylogenetics, phylogenomics and hypotheses testing. *Nucleic Acids. Res.* 39(Webserver Issue):W470-4. **C=45.**
51. Faria R, Pinheiro A, **Gabaldón T**, Weiss S, Alexandrino P. (2011). Molecular tools for species discrimination and detection of hybridization between two closely related Clupeid fishes *Alosa alosa* and *A. fallax*. *J Appl. Ichtyil.* 27(supl.3):16-20. C=2
 52. Lopes-Silva L, Marcet-Houben M, Zerlotini A, **Gabaldón T**, Oliveira G, Alves-Nahum L (2011). Evolutionary histories of expanded peptidases families in *Schistosoma mansoni*. *Mem. Inst. Oswaldo Cruz* 106(7):846-77. C=4
 53. Ollivier M, **Gabaldón T**, Poulain J, Gavory F, Leterme N, Gauthier JP, Legeai F, Tagu D, Simon JC, Rispe C. (2012) Comparison of gene repertoires and patterns of evolutionary rates in eight aphid species that differ by reproductive mode. *Genome Biol Evo* 4(2):155-67. C=8
 54. Bohle MH[&]. **Gabaldón T[&]**. (2012) Selection of marker genes using whole-genome DNA polymorphism analysis. *Evol. Bioinf.* 2012(8):161-169. C=1
 55. Dessimoz C, **Gabaldón T**, Roos DS, Sonnhammer EL, Herrero J, and the Quest for Orthologs Consortium (2012) Toward Community Standards in the Quest for Orthologs. *Bioinformatics* 28(6):900-904. C=33
 56. Lee JH, Wan KL, Mohd-Adnan A[&], **Gabaldón T[&]**. (2012) Evolution of the ferritin family in vertebrates. *Trends in Evol. Biol.* 4:e3 C=2
 57. Capella-Gutiérrez S, Marcet-Houben M, **Gabaldón T[&]** (2012) Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. *BMC Biology.* 10(1):47. (**Highly accessed**). **C=53**
 58. Piškur J, Ling Z, Marcet-Houben M, Ishchuk OP, Aerts A, Labutti K, Copeland A, Lindquist E, Barry K, Compagno C, Bisson L, Grigoriev IV, **Gabaldón T**, Phister T. (2012). The genome of wine yeast *Dekkera bruxellensis* provides a tool to explore its food-related properties. *Int J Food Microbiol.* 157(2):202-9. C=33
 59. Garcia-Mas J, Benjak A, Sanseverino W, Bourgeois M, Mir G, González VM, Hénaff E, Câmara F, Cozzuto L, Lowy E, Alioto T, Capella-Gutiérrez S, Blanca J, Cañizares J, Ziarsolo P, Gonzalez-Ibeas D, Rodríguez-Moreno L, Droege M, Du L, Alvarez-Tejado M, Lorente-Galdos B, Melé M, Yang L, Weng Y, Navarro A, Marques-Bonet T, Aranda MA, Nuez F, Picó B, **Gabaldón T**, Roma G, Guigó R, Casacuberta JM, Arús P, Puigdomènech P. (2012) The genome of melon (*Cucumis melo* L.). *PNAS* 109(29):11872-11877. **C=238.**
 60. Miranda-Saavedra D, **Gabaldón T**, Barton GJ, Langsley G, Doering C. (2012) The kinomes of apicomplexan parasites. *Microbes and Infection* 14(10):796-810. C=14
 61. Valach M, Prysycz LP, Tomaska L, Gacser A, **Gabaldón T**, Nosek J.(2012) Mitochondrial genome variability within the *Candida parapsilosis* species complex. *Mitochondrion.* 12(5):514-519 C=6
 62. Silva LL, Marcet-Houben M, Nahum LA, Zerlotini A, **Gabaldón T**, Oliveira G. (2012) The *Schistosoma mansoni* phylome: using evolutionary genomics to gain insight into a parasite's biology. *BMC Genomics.* 13:617. (**Highly accessed**) C=11
 63. Marcet-Houben M, Ballester AR, de la Fuente B, Harries E, Marcos JF, González-Candelas L[&], **Gabaldón T[&]**. (2012) Genome sequence of the necrotrophic fungus *Penicillium digitatum*, the main postharvest pathogen of citrus. *BMC Genomics.* 13:646. (**Highly accessed**) **C=42**
 64. Mohd-Padil H, Mohd-Adnan A[&], **Gabaldón T[&]**. (2013) Phylogenetic Analyses Uncover a Novel Clade of Transferrin in Nonmammalian Vertebrates. *Mol Biol Evol.* 30(4):894-905. C=3
 65. Jiménez-Guri E, Huerta-Cepas J, Cozzuto L, Wotton KR, Kang H, Himmelbauer H, Roma G, **Gabaldón T[&]**, Jaeger J[&]. (2013) Comparative transcriptomics of early dipteran development. *BMC Genomics.* 14(1):123 (**Highly accessed**) C=21
 66. Ferreira PG, Patalano S, Chauhan R, Ffrench-Constant R, **Gabaldón T**, Guigo R, Sumner S. (2013) Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. *Genome Biol.* 14(2):R20. (**Highly accessed**) **C=36**
 67. Capella-Gutiérrez S, **Gabaldón T[&]** (2013) Measuring guide-tree dependency of inferred gaps in

- progressive aligners. *Bioinformatics* 29(8):1011-7 C=6
68. Collén J, Porcel B, Carré W, Ball SG, Chaparro C, Tonon T, Barbeyron T, Michel G, Noel B, Valentin K, Elias M, Artiguenave F, Arun A, Aury JM, Barbosa-Neto JF, Bothwell JH, Bouget FY, Brillet L, Cabello-Hurtado F, Capella-Gutiérrez S, Charrier B, Cladière L, Cock JM, Coelho SM, Colleoni C, Czjzek M, Da Silva C, Delage L, Denoeud F, Deschamps P, Dittami SM, **Gabaldón T**, Gachon CM, Groisillier A, Hervé C, Jabbari K, Katinka M, Kloareg B, Kowalczyk N, Labadie K, Leblanc C, Lopez PJ, McLachlan DH, Meslet-Cladiere L, Moustafa A, Nehr Z, Nyvall Collén P, Panaud O, Partensky F, Poulain J, Rensing SA, Rousvoal S, Samson G, Symeonidi A, Weissenbach J, Zambounis A, Wincker P, Boyen C. (2013). Genome structure and metabolic features in the red seaweed *Chondrus crispus* shed light on evolution of the Archaeplastida. *PNAS*. 110(13):5247-52. **C=64.**
 69. **Gabaldón T**[&], Koonin EV[&]. (2013) Functional and evolutionary implications of gene orthology. (2013) *Nat Rev Genet*. 14(5):360-6 **C=55.**
 70. Lavín JL, Marcet-Houben M, Gutiérrez-Vázquez RL, Ramírez L, Pisabarro AG, **Gabaldón T**, Oguiza JA. (2013) FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. *Mitochondrion*. 13(4):357-9.
 71. Hatzihristidis T, Liu S, Prysycz L, Hutchins AP, **Gabaldón T**, Tremblay ML, Miranda-Saavedra D. (2013). PTP-central: A comprehensive resource of protein tyrosine phosphatases in eukaryotic genomes. *Methods*. S1046-2023(13)00280-6. C=2
 72. i5K Consortium. (2013) The i5K Initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. *J Hered*. 104(5):595-600. C=26
 73. Hagen F, Ceresini PC, Polacheck I, Ma H, van Nieuwerburgh F, **Gabaldón T**, Kagan S, Pursall ER, Hoogveld HL, van Iersel LJ, Klau GW, Kelk SM, Stougie L, Bartlett KH, Voelz K, Prysycz LP, Castañeda E, Lazera M, Meyer W, Deforce D, Meis JF, May RC, Klaassen CH, Boekhout T. (2013) Ancient dispersal of the human fungal pathogen *Cryptococcus gattii* from the Amazon rainforest. *PLoS One*. 8(8):e71148. C=35
 74. **Gabaldón T**[&], Martin T, Marcet-Houben M, Durrens P, Bolotin-Fukuhara M, Lespinet O, Arnaise S, Boisnard S, Aguilera G, Atanasova R, Bouchier C, Couloux A, Creno S, Almeida Cruz J, Devillers H, Enache-Angoulvant A, Guitard J, Jaouen L, Ma L, Marck C, Neuvéglise C, Pelletier E, Pinard A, Poulain J, Recoquillay J, Westhof E, Wincker P, Dujon B, Hennequin C, Fairhead C[&]. (2013) Comparative genomics of emerging pathogens in the *Candida glabrata* clade. *BMC Genomics*. 14:623 (**Highly accessed**) C=22
 75. Traeger S, Altegoer F, Freitag M, **Gabaldón T**, Kempken F, Kumar A, Marcet-Houben M, Pöggeler S, Stajich JE, Nowrousian M. (2013) The genome and development-dependent transcriptomes of *Pyronema confluens*: a window into fungal evolution. *PLoS Genet*. 9(9):e1003820. C=13
 76. Prysycz LP, Németh T, Gácsér A[&], **Gabaldón T**[&]. (2013) Unexpected Genomic Variability in Clinical and Environmental Strains of the Pathogenic Yeast *Candida parapsilosis*. *Genome Biol Evol*. 5(12):2382-92. C=8
 77. Morales L, Noel B, Porcel B, Marcet-Houben M, Hullo MF, Sacerdot C, Tekaiia F, Leh-Louis V, Despons L, Khanna V, Aury JM, Barbe V, Couloux A, Labadie K, Pelletier E, Souciet JL, Boekhout T, **Gabaldón T**, Wincker P, Dujon B. (2013). Complete DNA Sequence of *Kuraishia capsulata* Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). *Genome Biol Evol*. 5(12):2524-39. C=8
 78. Huerta-Cepas J, Capella-Gutiérrez S, Prysycz LP, Marcet-Houben M, **Gabaldón T**[&]. (2014) PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. *Nucleic Acids Res*. 42(1):D897-902. C=24

79. Powell S, Forslund K, Szklarczyk D, Trachana K, Roth A, Huerta-Cepas J, **Gabaldón T**, Rattei T, Creevey C, Kuhn M, Jensen LJ, von Mering C, Bork P. (2014) eggNOG v4.0: nested orthology inference across 3686 organisms. *Nucleic Acids Res.* 42(1):D231-9 **C=59**
80. Hinojosa-Alvarez S, Díaz-Jaimes P, Marcet-Houben M, **Gabaldón T**. (2014) The complete mitochondrial genome of the Giant Manta ray, *Manta birostris*. *Mitochondrial DNA (in press)*.
81. **Gabaldón T**&. (2014) A metabolic scenario for the evolutionary origin of peroxisomes from the endomembranous system. *Cell Mol Life Sci.* 71(13):2373-6. **C=7**
82. Dohm JC, Minoche AE, Holtgräwe D, Capella-Gutiérrez S, Zakrzewski F, Tafer H, Rupp O, Sörensen TR, Stracke R, Reinhardt R, Goesmann A, Kraft T, Schulz B, Stadler PF, Schmidt T, **Gabaldón T**, Lehrach H, Weisshaar B, Himmelbauer H. (2014). The genome of the recently domesticated crop plant sugar beet (*Beta vulgaris*). *Nature* 505(7484):546-9. **C=51**
83. Aguilera G, de Vienne DM, Ross ON, Hood ME, Giraud T, Petit E, **Gabaldón T**&. (2014) High Variability of Mitochondrial Gene Order among Fungi. *Genome Biol Evol.* 6(2):451-65. **C=4**
84. Krisko A, Copi T, **Gabaldón T**, Lehner B, Supek F. (2014) Inferring gene function from evolutionary change in signatures of translation efficiency. *Genome Biol.* 3;15(3):R44 **C=5**
85. Capella-Gutierrez S, Kauff F, **Gabaldón T**&. (2014) A phylogenomics approach for selecting robust sets of phylogenetic markers. *Nucleic Acids Res.* 42(7):e54. **C=5**
86. Supek F, Miñana, Valcarcel J, Gabaldón T, Lehner B. (2014) Synonymous mutations frequently act as driver mutations in human cancer. *Cell* 156(6):1324-35 **C=40**
87. Pruszcz LP, Németh T, Gácsér A, **Gabaldón T**&. (2014) Genome comparison of *Candida orthopsilosis* clinical strains reveals the existence of hybrids between two distinct subspecies. *Genome Biol Evol.* 6(5):1069-78 **C=9**
88. Kunze G, Gaillardin C, Czernicka M, Durrens P, Martin T, Böer E, **Gabaldón T**, Cruz JA, Talla E, Marck C, Goffeau A, Barbe V, Baret P, Baronian K, Beier S, Bleykasten C, Bode R, Casaregola S, Despons L, Fairhead C, Giersberg M, Gierski PP, Hähnel U, Hartmann A, Jankowska D, Jubin C, Jung P, Lafontaine I, Leh-Louis V, Lemaire M, Marcet-Houben M, Mascher M, Morel G, Richard GF, Riechen J, Sacerdot C, Sarkar A, Savel G, Schacherer J, Sherman DJ, Stein N, Straub ML, Thierry A, Trautwein-Schult A, Vacherie B, Westhof E, Worch S, Dujon B, Souciet JL, Wincker P, Scholz U, Neuvéglise C. (2014) The complete genome of *Blastobotrys (Arxula) adenivorans* LS3 - a yeast of biotechnological interest. *Biotechnol Biofuels.* 24;7:66. **C=6**
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