On the early origins of elongation factors and protein synthesis

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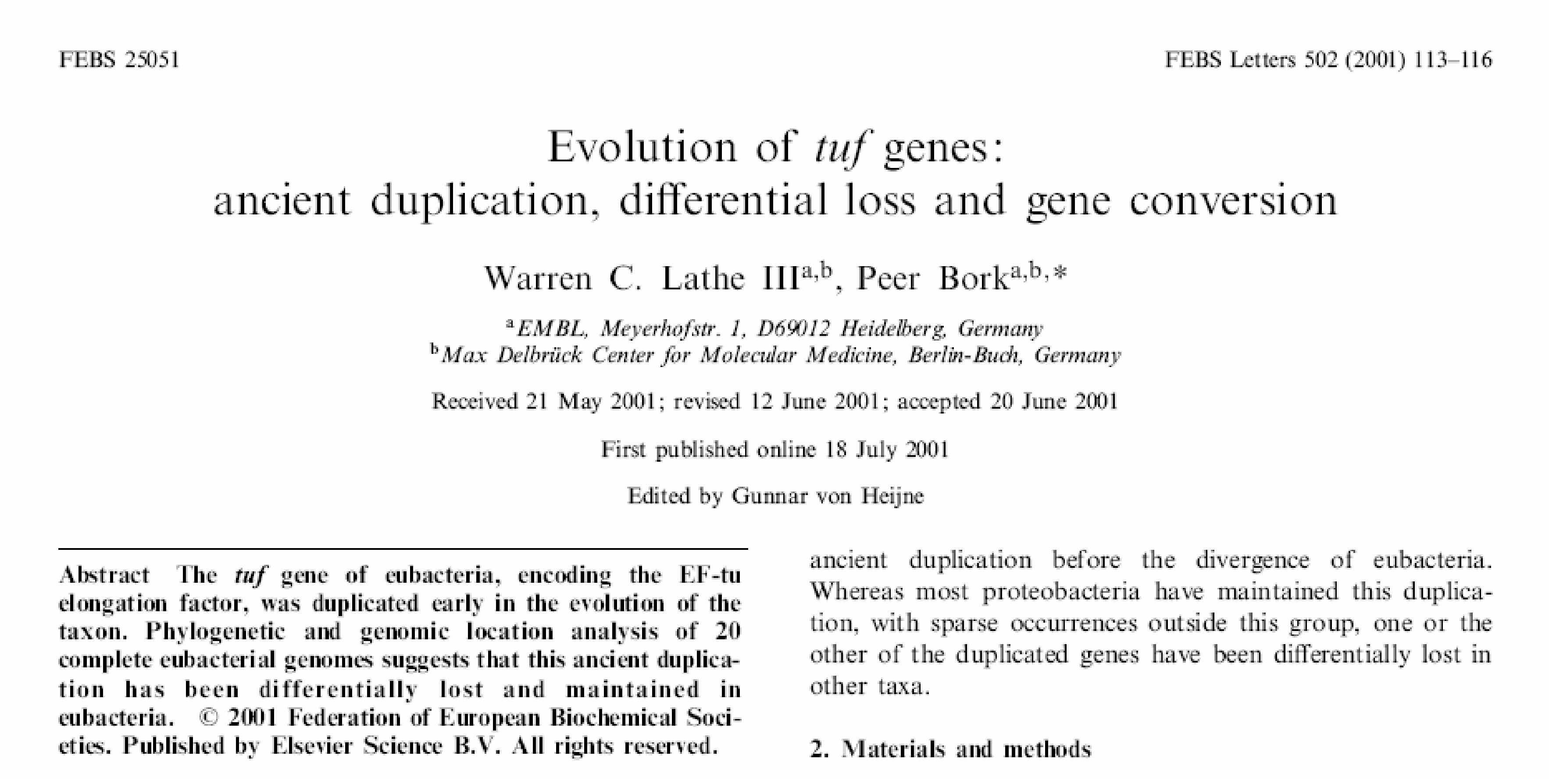
It all started with me reading this paper:



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Evolution of *tuf* genes: ancient duplication, differential loss and gene conversion

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Abstract The *tuf* gene of eubacteria, encoding the EF-tu elongation factor, was duplicated early in the evolution of the taxon. Phylogenetic and genomic location analysis of 20 complete eubacterial genomes suggests that this ancient duplication has been differentially lost and maintained in eubacteria. © 2001 Federation of European Biochemical Societies. Published by Elsevier Science B.V. All rights reserved.

ancient duplication before the divergence of eubacteria. Whereas most proteobacteria have maintained this duplication, with sparse occurrences outside this group, one or the other of the duplicated genes have been differentially lost in other taxa.

2. Materials and methods

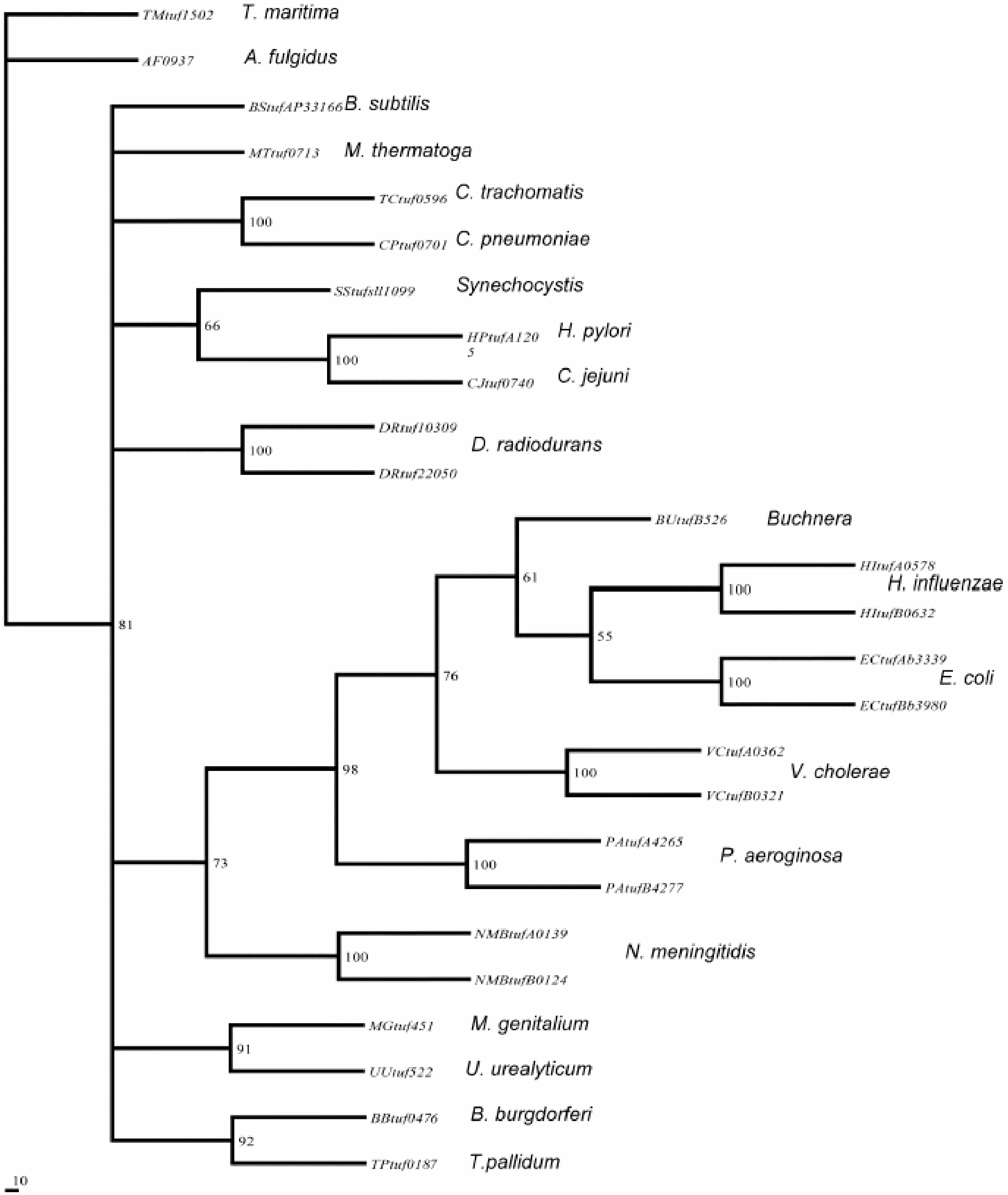


Fig. 1. Duplication phylogeny. 50% consensus bootstrap (1000 replications) tree using Maximum Parsimony algorithm, heuristic search, stepwise addition (closest). *Thermotoga maritima* and *Archaeoglobus fulgidus* were used as outgroup.

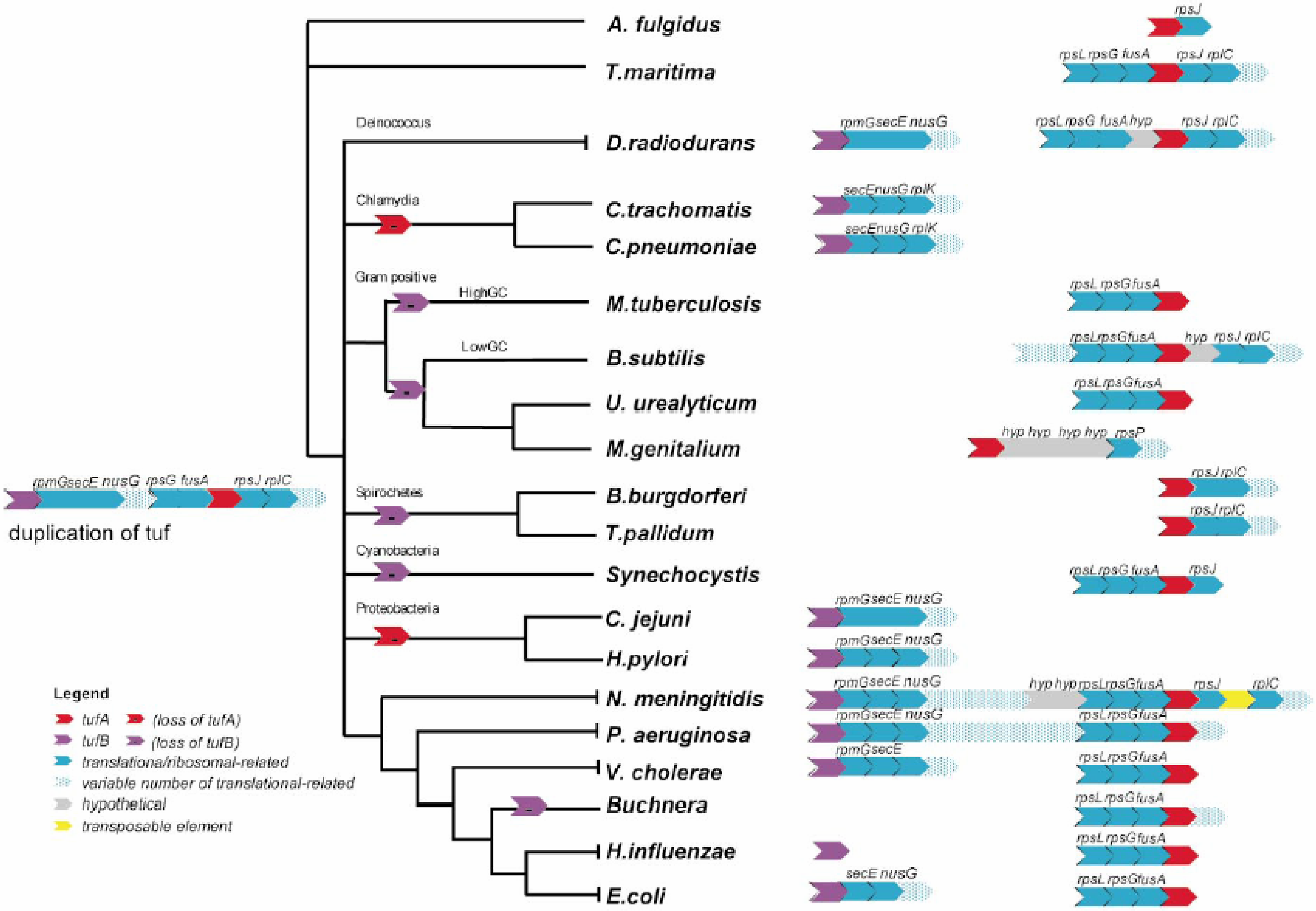
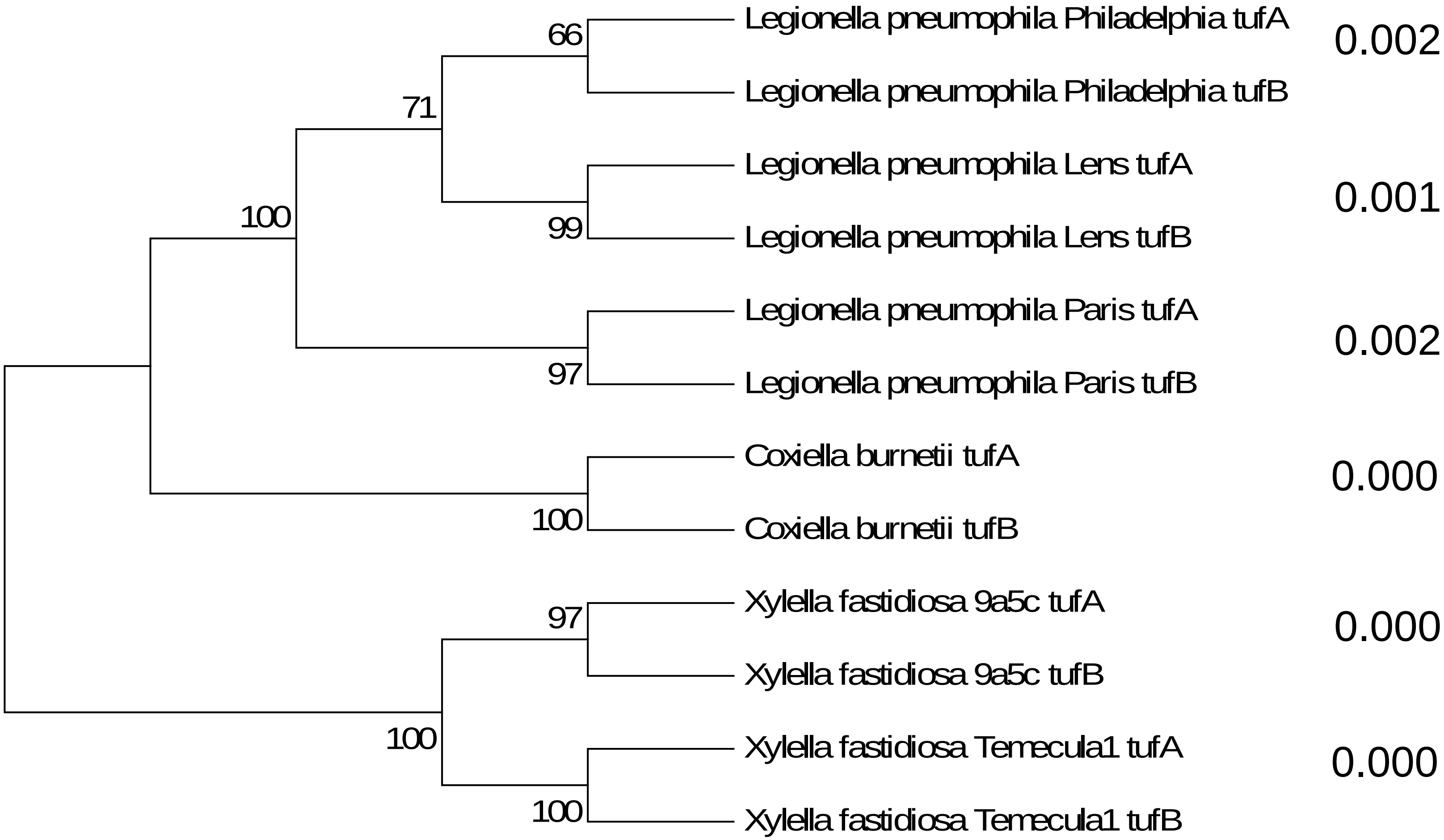


Fig. 2. A cladogram of the evolution of *tuf* in eubacteria based on *tuf* and *rpsJ* phylogeny and accepted taxonomy. An ancient duplication of the *tuf* gene (*tufA*) occurred early in the divergence of eubacteria with the addition of a second *tuf* gene (*tufB*) upstream of the *rpmG* gene, the first gene in the proposed ancient transcriptional unit (shown). The proposed original *tuf* gene (based on location of *tuf* in *T. maritima* and archaebacteria) is shown in red, duplicated *tufB* in purple. Other genes of the ribosomal/translational unit are shown in blue, with light blue designating several ribosomal and translation-related genes. Units separated by white space denote transcriptional units separated by three or more open reading frames (non-ribosomal/translation-related) in the genome. Based on genome location, *tufA* is subsequently lost in both the *Chlamydia* and ε subdivision proteobacteria whereas *tufB* is lost in *Buchnera*, *Synechocystis*, the spirochetes, and low- and high-GC Gram-positive bacteria. Early studies suggest clostridia, a Gram-positive low-GC taxon, has maintained the *tuf* duplication [4], suggesting the other low-GC Gram-positive taxa lost *tufB* in a separate event from the high-GC Gram-positives. The duplication is maintained in the remaining proteobacteria and *D. radiodurans*.

I decided to measure the rate of paralogous gene conversion in EF Tu genes in over 50 species of gamma proteobacteria



Ks values between paralogs

High rate of convergent evolution in Tu elongation factor in gamma subdivision of proteobacteria

Average Ks among EF Tu paralogues in the gamma subdivision of proteobacteria is:

Ks = 0.06

Therefore, assuming that each conversion occurs across the whole gene AND that synonymous sites are neutral, the gene conversion rate in EF Tu is 16 times that of the mutation rate.

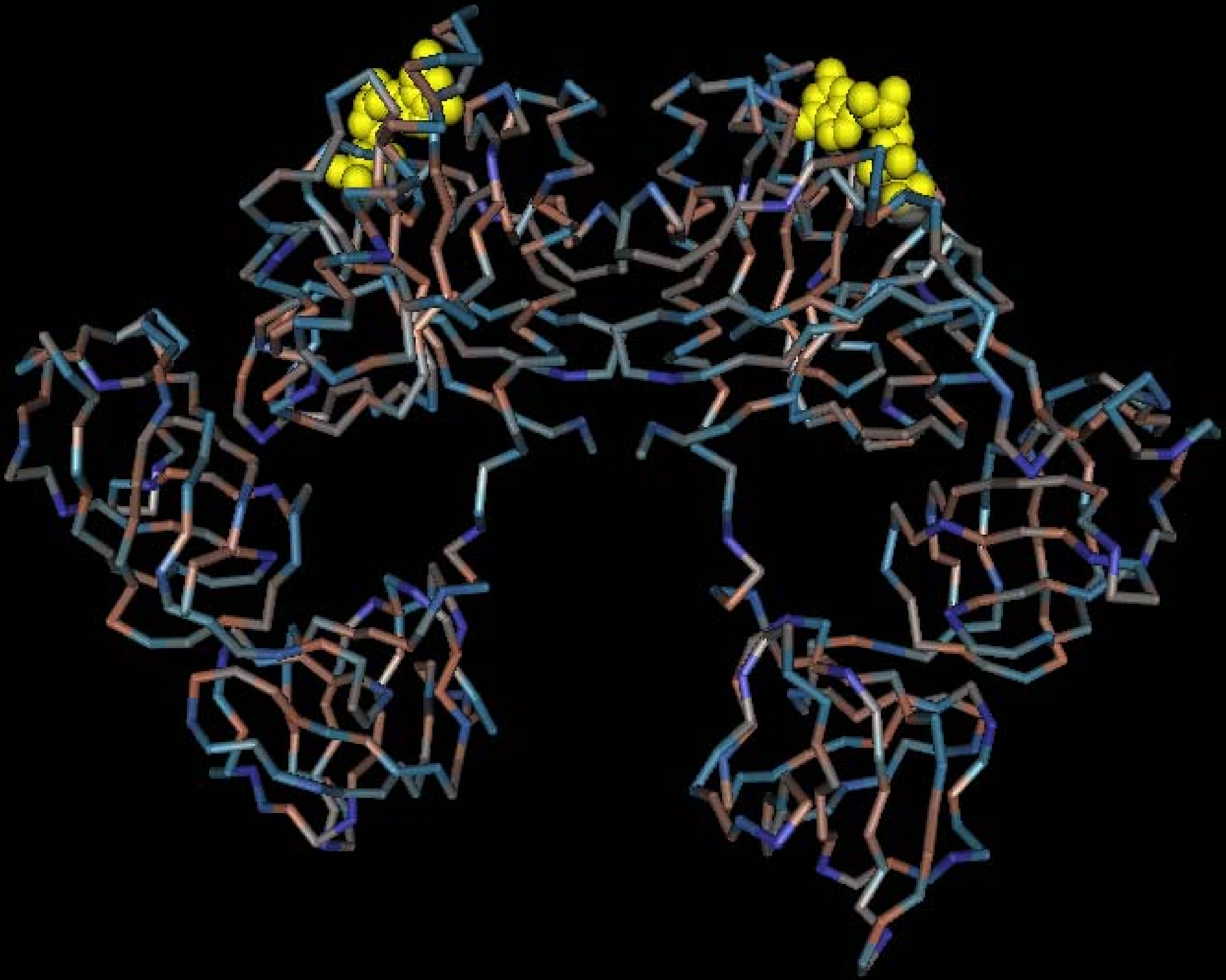
Average Kn/Ks between paralogues = 0.094

Average Kn/Ks between orthologues = 0.037

Conversion for some reason slows down the rate of evolution.

WHY???

E. coli elongation factor Tu and GTP complex PDB(1EFC)

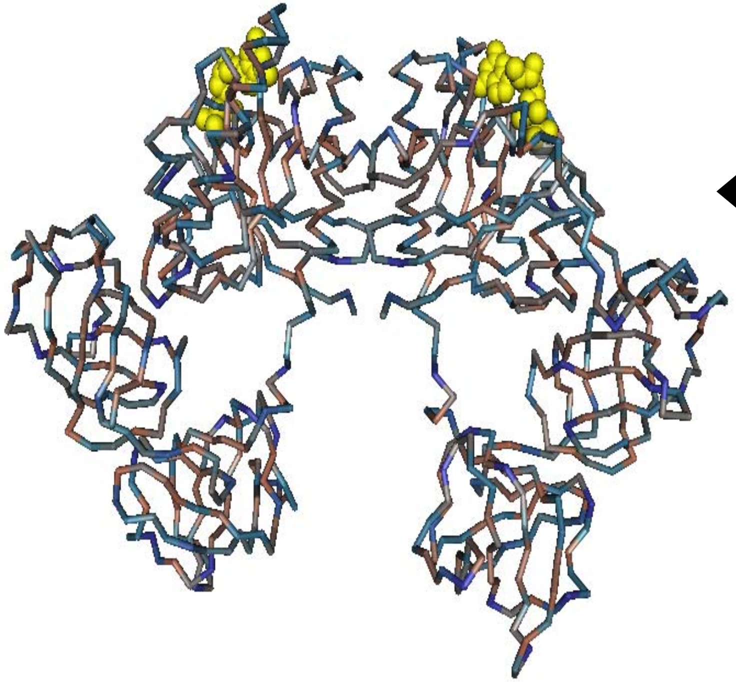


Flying Spaghetti Monster (FSM)

www.venganza.org

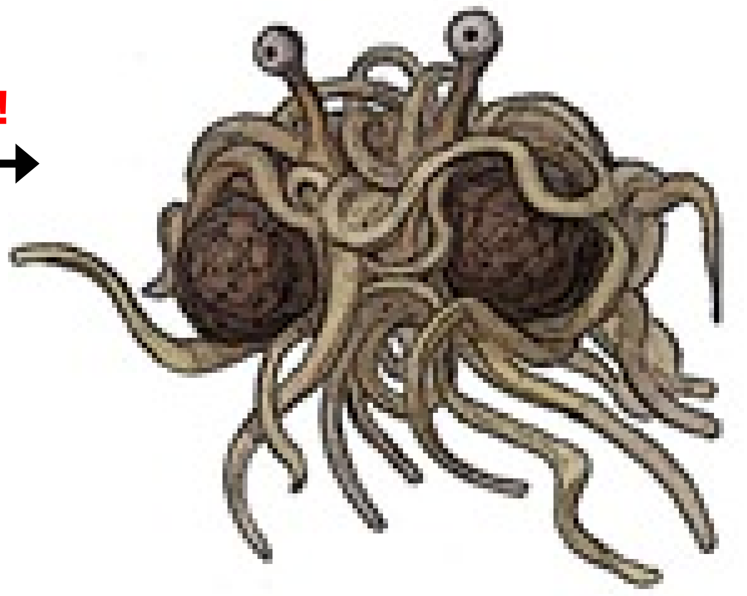
> “I and many others around the world are of the strong belief that the universe was created by a Flying Spaghetti Monster. It was He who created all that we see and all that we feel.”
>
> - Bobby Henderson (www.venganza.org)

A Monte Carlo Bootstrap test of FSM EF Tu similarity - comparing other randomly selected images



EF Tu

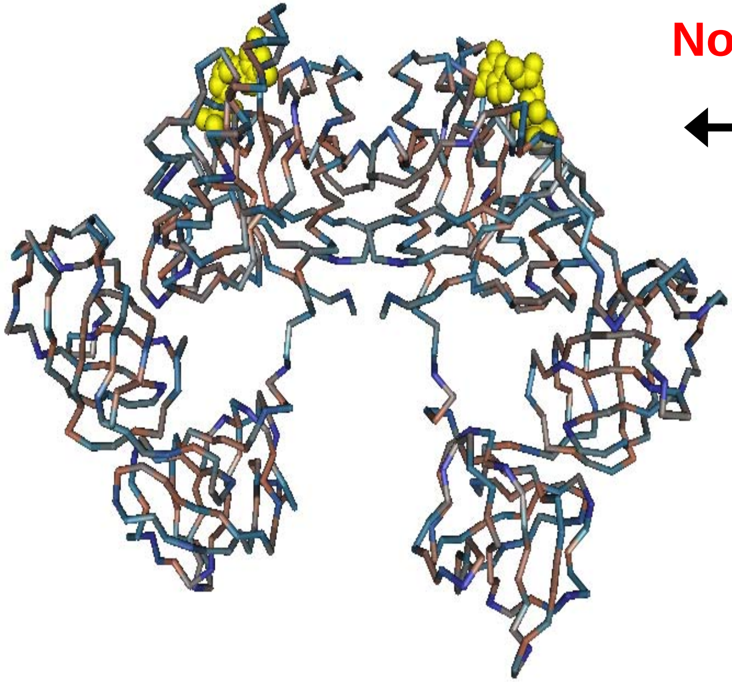
Similar! ⟷



FSM

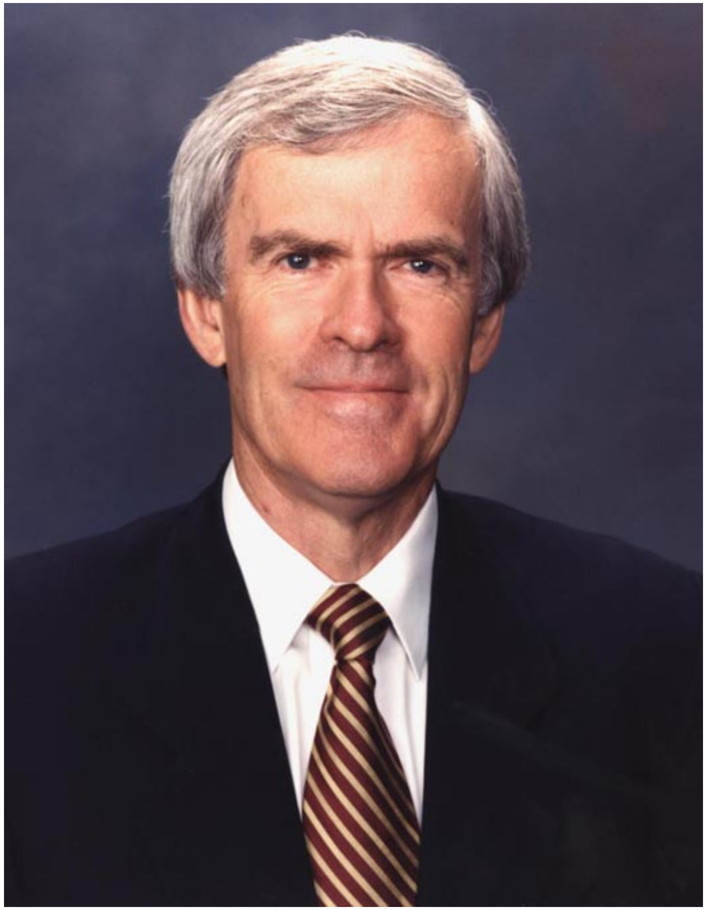
Methods: Alternative pictures were obtained by using the keyword “picture” in the Images section of the Google search engine (www.google.com)

Example 1



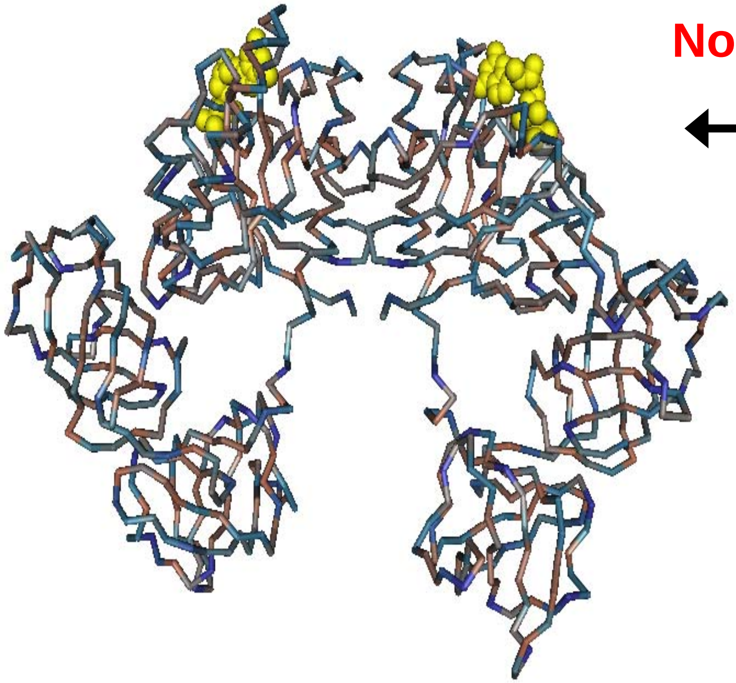
EF Tu

Not similar!



US Senator Jeff Bingaman

Example 2



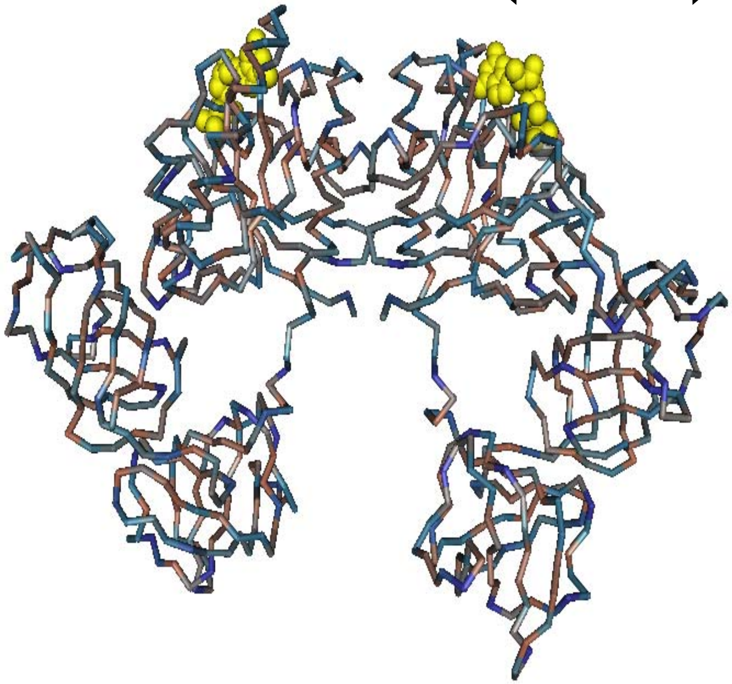
EF Tu

Not similar!

Cartoon Space Ship with Dog

Example 3

Not similar!



EF Tu

Snow Boat (Patent # 6595812B1)

None of the 1000 random pictures sampled resembled the EF Tu structure as much as the FSM depiction.

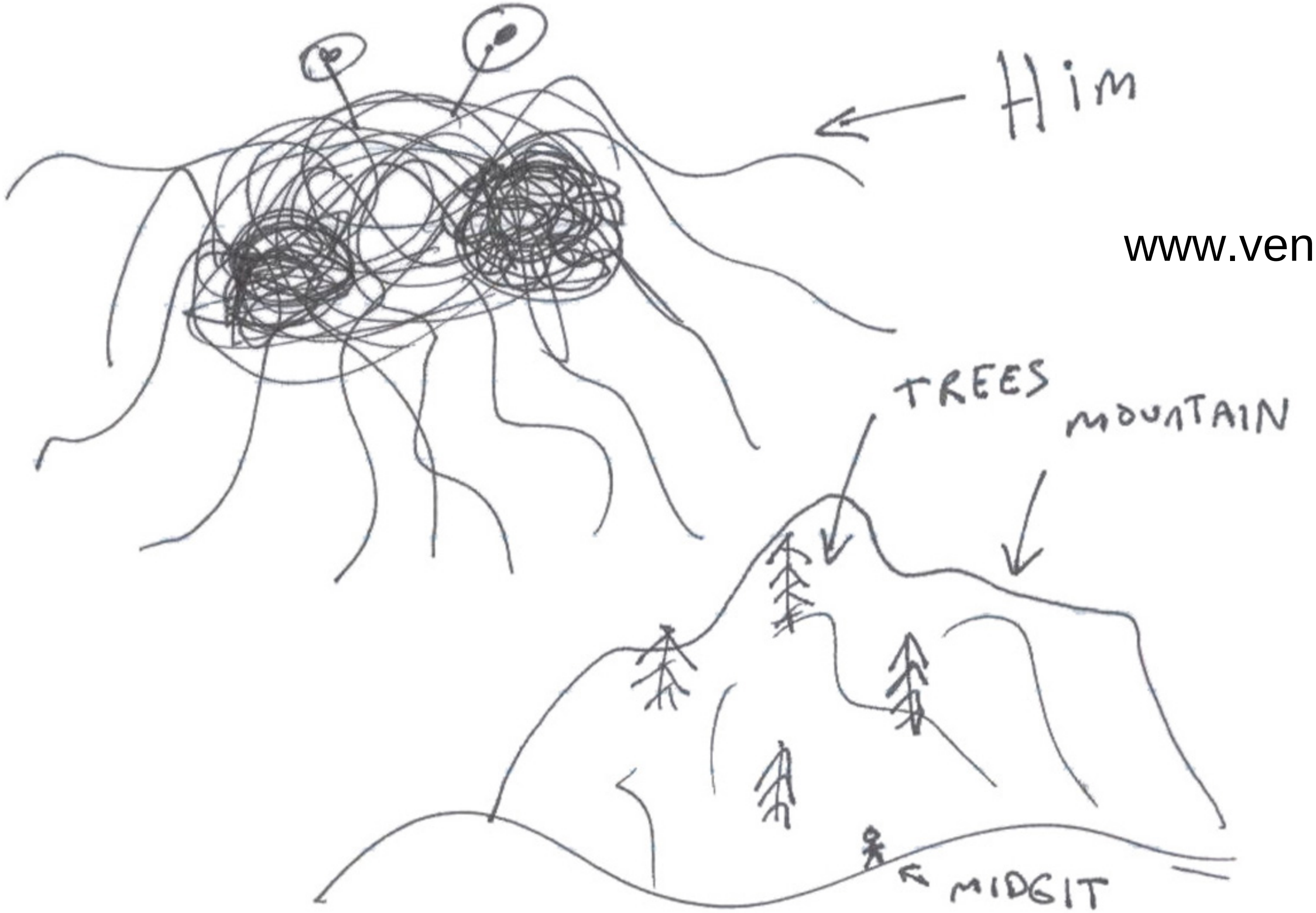
Therefore, the EF Tu structure is significantly more similar to FSM ($p < 0.001$)

Problem with the test: the similarity of pictures is determined by expert opinion.

Future research: develop a purely computational method for FSM image comparisons.

“You see, after the Flying Spaghetti Monster created the universe, he used His Noodly Appendage to create volcanoes.”

-Pastafarian lore



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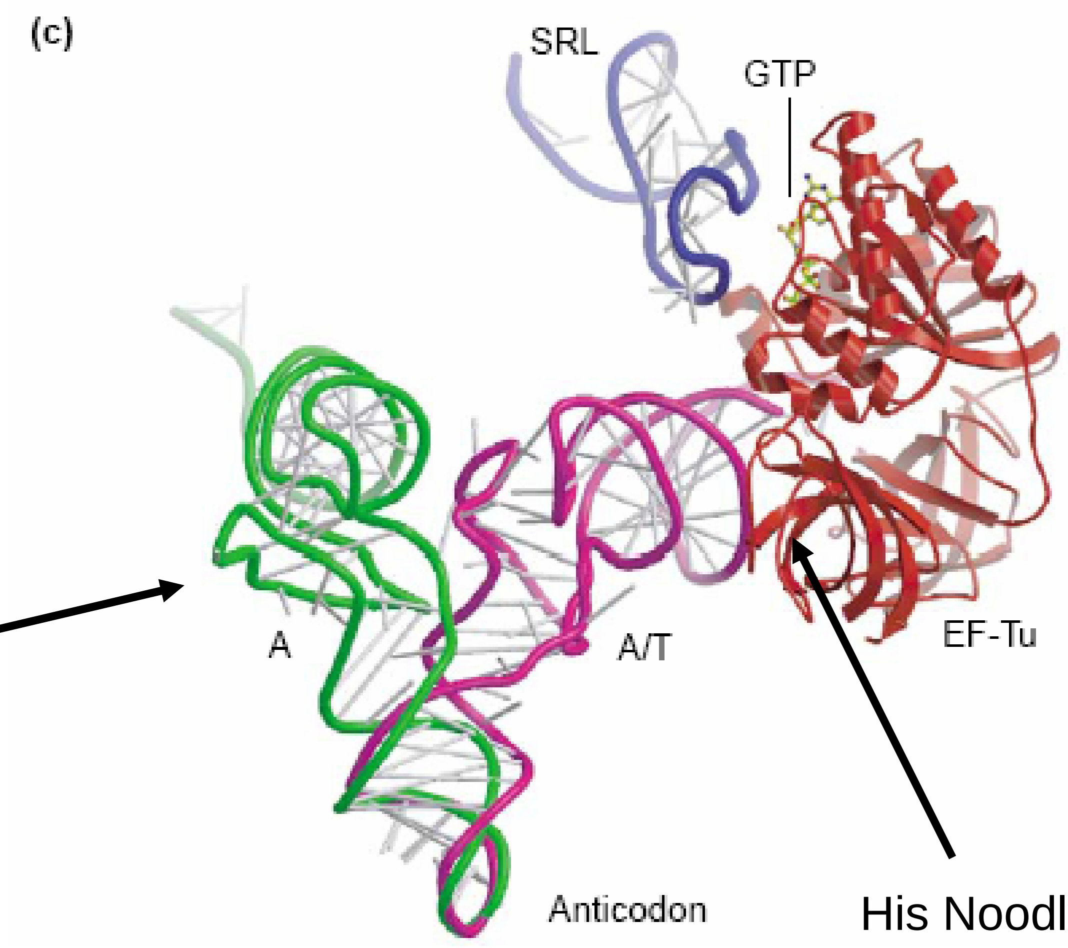
“an artistic drawing of Him creating a mountain, trees, and a midget.”
– Bobby Henderson

FSM uses His Noodly Appendage to transport tRNA molecule to the ribosome.



tRNA

His Noodly Appendage

Figure from Nilsson and Nissen, Curr. Op. Str. Biol. 2005

The elongation factor/His Holy Noodleness is highly conserved in all of life!!!

Multiple alignment of the N-terminal of EF Tu/FSM in a few model organisms.

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MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTRHYAHVDCPGHADYV
EAKKTYVRDKPHVNVGTIGHVDHGKTTLTAAITKILAEGGGAKFKKYEEIDNAPEERARGITINAAHVEYSTAARHYAHTDCPGHADYV
RSMATFTRNKPHVNVGTIGHVDHGKTTLTAAITKVLAEEGKAKAIAFDEIDKAPEEKKRGITIATAHVEYETAKRHYAHVDCPGHADYV
--KAVFKRDKPHLNVGTIGHVDHGKTTLTSAITKILATSKGAKYRKYEDIDNAPEEKARGITINAFHLEYETAKRHYAHIDCPGHADYI
-EKKVFERTKPHCNVGTIGHVDHGKTTLTAAITKVLADKQLAESKKYNEIDNAPEEKARGITINVAHVEYQTETRHYGHTDCPGHADYI
SYAAAFDRSKPHVNIGTIGHVDHGKTTLTAAITKTLAAKGGANFLDYAAIDKAPEERARGITISTAHVEYETAKRHYSHVDCPGHADYI
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Escherichia_coli
Homo_sapiens
Arabidopsis_thaliana
Caenorhabditis_elegans
Drosophila_melanogaster
Sacchromyces_cerevisiae

Structure of Bacterial and Archaeal EF Tu is also highly similar!

Therefore, EF Tu factors resemble FSM in all walks of life!

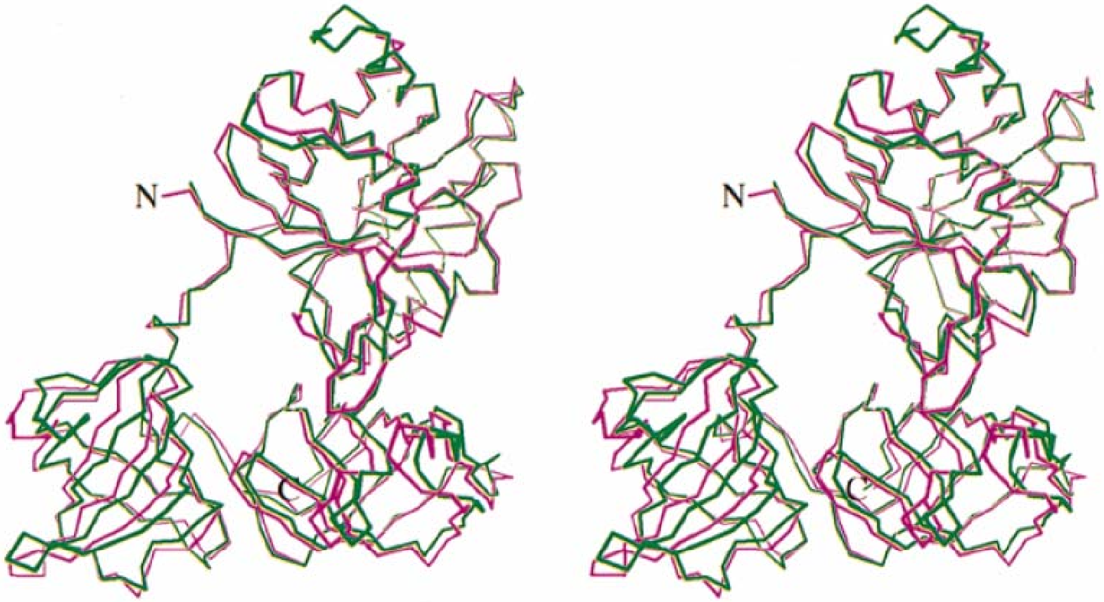


Figure 4. Stereo view of superpositions of EC-EF-Tu-GDP and TA-EF-Tu-GDP. The C^{α} trace of EC-EF-Tu-GDP (molecule B) is shown in purple and that of TA-EF-Tu-GDP in green. GDP molecules and Mg^{2+} are not shown. Superposition was carried out using all C^{α} atoms of domain 1 with the program LSQKAB (CCP4, 1994). The orientation of EC-EF-Tu-GDP is same as that in Figure 1(a).

Figure from Song *et al.* JMB (1999)

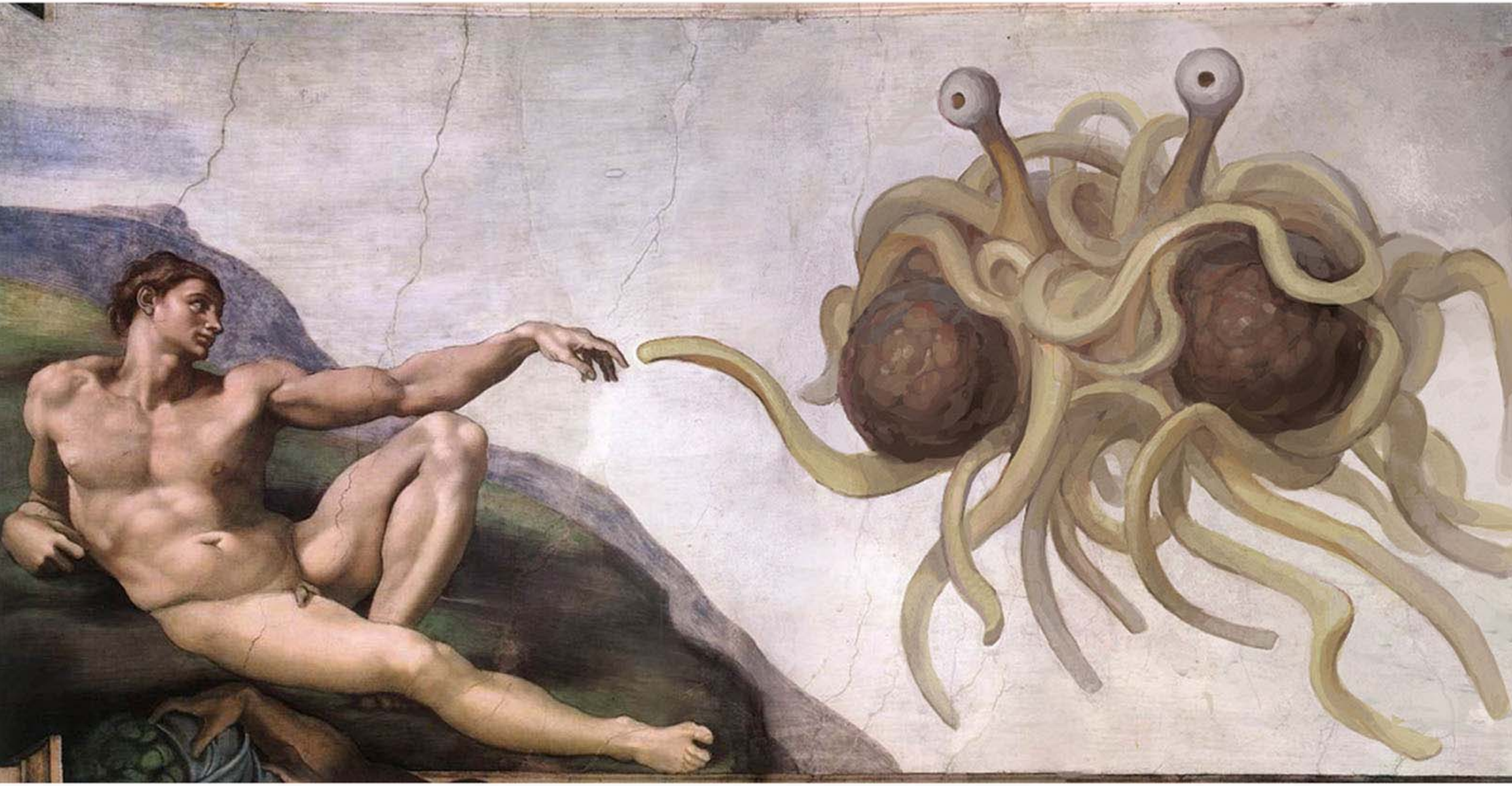
Conclusions:

Initial results indicate that EF Tu is significantly more similar to FSM that any other randomly chosen image.

This similarity is likely to be maintained by EF Tu structures in all forms of life.

Thus, we have to consider the possibility that FSM created protein synthesis and/or is actively taking part in it.

HAVE WE ALL BEEN



TOUCHED BY HIS NOODLY APPENDAGE?