Genomic Evidence of Human/Cnidarian Neural Integration

Systematic Conservation of Jellyfish Neural Networks Across All Known *Homo* Lineages

Authors: Ashley Gjøvik, B.S., J.D. (ashleymgjovik@protonmail.com) | **Date**: July 27 2025

Aurelia the "moon jelly," © Monterey Bay Aquarium.

Abstract: In this study, genomic analyses reveal unprecedented sequence alignment between *Homo sapiens* and *Aurelia aurita* (moon jellyfish), challenging fundamental assumptions about mammal evolution. BLAST+ screening identified extensive homologous regions with 80-99% sequence identity across alignments spanning 2,000-5,000 base pairs. Critical neural genes including CADPS2 (calcium-dependent secretion), BDNF (brain-derived neurotrophic factor), MAOA (monoamine oxidase A) show long-alignment, high confidence (E-value = 0) matches with 86-96% identity between species supposedly separated by ~600 million years of evolution. These patterns persist across RNA, mRNA, and mtDNA; and across modern humans, Neanderthals, Denisovans, and other archaic hominins, ruling out contamination or artifacts.

The conservation extends beyond protein-coding genes to full regulatory elements, indicating preservation of entire functional networks. These findings suggest that human neural architecture represents an integration of cnidarian neural modules within a colonial organizational framework, supporting a model where humans function as terrestrial siphonophore colonies with jellyfish neural zooids. This genetic data necessitates fundamental reconsideration of mammalian evolution and the evolutionary origins of complex neural systems.

Keywords: comparative genomics, neurology, meninges, cnidarian evolution, mammalian evolution; neural development, siphonophore, *Aurelia aurita*, *Nanomia*, human evolution, hominids, sequence conservation, sea-to-land transition, biological engineering, microservices.

Citation: Gjøvik, Ashley M. Genomic Evidence for Human/Cnidarian Neural Integration Systematic Conservation of Jellyfish Neural Networks: Across All Known Homo Lineages]. *The Journal of Decolonized Ecology and Evolution* 1, no. 2 (July 27 2025). DOI: 10.5281/zenodo.16471873

Table of Contents

Introduction

Recent advances in genome assembly quality and comparative genomic methodology have enabled detection of previously overlooked patterns of sequence conservation across taxonomic boundaries. High-quality reference genomes, including telomere-to-telomere assemblies and ancient DNA reconstructions, provide unprecedented resolution for identifying homologous regions that may have been obscured in earlier analyses using shorter, more fragmented assemblies.

The study emerged from systematic screening of cnidarian genomic data against human reference sequences. This analysis revealed extensive, chromosome-scale sequence conservation between *Aurelia aurita* and *Homo sapiens*, including preservation of complex neural gene networks previously considered vertebrate-specific, and with extensive matches only explainable by direct ancestry.

Under current consensus models, the ~600 million years separating cnidarians from humans represents a vast evolutionary gulf bridged by successive innovations in body plan organization, neural centralization, and developmental complexity. This traditional framework faces a fundamental challenge when confronted with new molecular data revealing extensive, high-fidelity sequence conservation between cnidarians and *Homo* species.

While limited homology in highly conserved "housekeeping" genes is expected across metazoans, the discovery of long-alignment, near-perfect sequence matches spanning multiple kilobases challenges basic assumptions about molecular evolution rates, the relationship between sequence conservation and phylogenetic distance, and the ancestry of mammals.

The data presented here support a fundamentally different interpretation of human and mammal evolutionary origins, one that positions cnidarian neural architecture as a modular system that was incorporated and integrated within more complex organizational frameworks (the mammal as a terrestrial siphonophore).

Current Understanding of *Aurelia aurita*

Genomic Architecture and Evolutionary Complexity

Recent genomic sequencing efforts have fundamentally transformed our understanding of *Aurelia aurita* (jellyfish) biology, revealing unexpected complexity in this seemingly simple cnidarian. The *Aurelia aurita* genome comprises approximately 377 Mbp with ~45% consisting of interspersed repeats, harboring approximately 28,625 protein-coding genes (Khalturin et al. 2019; Gold et al. 2019).

Phylogenetic analyses reveal that the magnitude of genetic differences between scyphozoan and cubozoan jellyfish is equivalent, on average, to the level of genetic differences between humans and sea urchins in the bilaterian lineage (Khalturin et al. 2019). This extraordinary genetic diversity within cnidarians underscores the ancient divergence and independent evolutionary trajectories of major cnidarian clades, with molecular dating estimating the separation of major cnidarian groups at more than 500 million years ago (Khalturin et al. 2019).

Stage-Specific Gene Expression and Development

Transcriptomic profiling across *Aurelia aurita*'s complex life cycle has identified distinct molecular signatures characterizing each developmental stage. Approximately 1,231 and 2,487 genes exhibit jellyfish- or polyp-specific expression patterns, respectively (Khalturin et al. 2019).

Remarkably, about one-third of *Aurelia* genes with jellyfish-specific expression have no homologs in anthozoan genomes (coral and sea anemone), indicating that the polyp-to-jellyfish transition requires a combination of conserved and novel, medusozoan-specific genes (Khalturin et al. 2019).

Comprehensive gene co-expression network analysis across all five life cycle stagesidentified 35 distinct co-expression modules governing post-embryonic developmental processes. Several hub genes have been identified as critical regulators with extensive interaction networks, likely orchestrating key developmental transitions (Liu et al. 2022).

Microbiome-Dependent Development

Recent research also revealed an obligate relationship between *Aurelia aurita* and its associated microbiome, representing one of the earliest documented cases of microbiome-dependent development in cnidarians. The strobilation process (a critical asexual reproduction mechanism) is severely compromised in the absence of the natural polyp microbiome, with limited production and release of ephyrae (Jensen et al. 2023).

Crucially, the natural microbiota must be present in polyps prior to the onset of strobilation to ensure normal asexual reproduction and successful polyp-to-medusa transition (Jensen et al. 2023). Providing native microbiota to sterile polyps after strobilation onset fails to restore normal development, indicating a critical temporal window for

microbiome establishment.

Transcriptomic responses to microbiome manipulation reveal sophisticated host-microbe interactions. Antibiotic treatment and consequent microbiome reduction significantly affect host gene expression, with genes involved in immune response and defense mechanisms being highly upregulated (Moritz et al. 2023).

Host-derived quorum quenching activities have been identified as novel defense mechanisms, with 37 quorum quenching-encoding open reading frames showing differential expression patterns in response to bacterial challenges (Moritz et al. 2023).

Novel Physiological Mechanisms

Aurelia aurita exhibits a remarkable self-repair mechanism that diverges fundamentally from traditional regeneration. Upon amputation, rather than regenerating lost tissue, jellyfish reorganize existing body parts to recover radial symmetry within days (Abrams et al. 2015).

This "symmetrization" process occurs through mechanical reorganization of remaining arms, recentering of manubria, and rebuilding of muscular networks, completed within 12 hours to 4 days (Abrams et al. 2015). This mechanism has been observed across multiple scyphozoan species, suggesting a shared biomechanical strategy for maintaining functional geometry.

Recent investigations into cnidocyte development have revealed that cnidocytes in *Aurelia* arise from epitheliomuscular cells, unlike in hydrozoans (Gold et al. 2019). This discovery polarizes our understanding of cnidogenesis evolution and raises fundamental questions about the evolutionary trajectory of stem cell regulation in cnidarians (Gold et al. 2019).

Aurelia aurita produces six distinct nematocyst types (a-isorhiza, A-isorhiza, O-isorhiza, eurytele, polyspiras, and birhopaloid) with varying sizes and functions, demonstrating sophisticated cellular weaponry for prey capture and defense (Ayed et al. 2020). The genetic basis of nematocyst production involves phylotypic gene clusters, with minicollagen genes (encoding major structural components of nematocysts) organized into conserved clusters with collinear expression across cnidarian taxa (Khalturin et al. 2019).

The *Aurelia aurita* nervous system develops through a precisely orchestrated sequence during metamorphosis. The rhopalial nervous system (a medusa-specific sensory structure) differentiates in ordered stages: first the gravity-sensing lithocyst and touch plate, followed by the marginal center controlling swimming activity, and finally the photoreceptive ocelli (Nakanishi et al. 2009).

At least seven bilaterally arranged neuronal clusters, consisting of sensory and ganglion cells with associated neuronal processes, become evident during metamorphosis (Nakanishi et al. 2009).

The mesoglea (*Aurelia aurita*'s massive extracellular matrix) contains a novel protein called mesoglein, synthesized by mesogleal cells as a high molecular mass precursor (Matveev et al. 2007). Mesoglein contains both Zona Pellucida and Delta/Serrate/Lag-2 domains, suggesting roles in cell adhesion and signaling (Matveev et al. 2007). This specialized ECM contributes to the jellyfish's unique biomechanical properties and may underlie its remarkable regenerative capabilities.

Aurelia aurita has evolved medusozoan-specific muscle proteins, including a novel family of myosin tail proteins that likely emerged from conventional myosins through gene duplication and subsequent diversification (Khalturin et al. 2019). These proteins represent evolutionary innovations underlying the sophisticated locomotory mechanisms required for active swimming in the medusa stage.

Evolutionary and Phylogenetic Implications

The comprehensive genomic and transcriptomic data from *Aurelia aurita* provide crucial insights into cnidarian evolution and the origins of complex life cycles. Comparative analyses suggest that the common ancestor of cnidarians possessed sophisticated regulatory mechanisms that were differentially retained or modified across major cnidarian lineages. (Khalturin et al. 2019).

The discovery that both polyp and jellyfish stages express similar proportions of medusozoan-specific genes (38% in polyps and 32% in jellyfish) suggests that the traditional view of anthozoan polyps as ancestral cnidarian forms may be oversimplified (Khalturin et al. 2019).

Evolutionary Relationship Between Humans, Cnidarians, and Tunicates

The current consensus in evolutionary biology places humans (*Homo sapiens*) within the phylum Chordata, a lineage characterized by features such as a dorsal nerve cord, notochord, pharyngeal slits, and post-anal tail. Two major groups of non-vertebrate chordates (tunicates in the subphylum Tunicata) and cephalochordates (e.g., lancelets) are considered key reference taxa for understanding the emergence of vertebrate traits.

In contrast, cnidarians, including jellyfish, corals, and sea anemones, are thought to belong to an earlier-diverging animal phylum and are often treated as models of pre-

bilaterian, diploblastic body plans with nerve nets rather than centralized nervous systems.

Cnidarians are typically positioned as a sister group to Bilateria, the lineage from which all animals with bilateral symmetry descended. Although cnidarians exhibit simple tissues and lack mesoderm, they do possess elements of neuronal signaling, epidermal patterning, and axis formation.

Genomic studies have revealed that cnidarians retain a core set of conserved genes, including homeobox transcription factors (e.g., Hox, ParaHox); components of Wnt and TGF-β signaling; and some early synaptic and neurotransmitter-related genes. Cnidarians are generally thought to reflect an ancestral eumetazoan state, prior to the rise of the triploblastic bilaterian body plan.

Tunicates occupy a unique position in animal phylogeny as the closest known invertebrate relatives to vertebrates, making them a central focus of comparative genomic and evo-devo studies. Tunicate larvae exhibit hallmark chordate features, including a notochord, dorsal hollow nerve cord, pharyngeal slits, and a post-anal tail.

Genomic studies, particularly in *Ciona intestinalis* and *Oikopleura dioica*, revealed that tunicates possess many key vertebrate developmental genes, including orthologs of pax, Sox, and Hox family genes; components of neural crest and placodal pathways; and conserved pathways for neural tube and heart development.

Tunicates do lack many vertebrate gene expansions, including those associated with adaptive immunity, elaborate synaptic regulation, and brain-specific transcriptional control. However, their position on the tree is such that any genes or regulatory elements found in tunicates and vertebrates but not in other invertebrates are often assumed to reflect features that evolved in the last common ancestor of chordates.

Under this framework, the evolutionary path from cnidarians to humans is viewed as passing through bilaterian intermediates, with the rise of mesoderm, bilateral symmetry, a centralized nervous system, and complex organ systems. Cnidarians are positioned well outside this trajectory, making them a negative control in many studies of vertebrate-specific features. Tunicates, on the other hand, are considered a crucial bridge.

Therefore, under current consensus, the presence of vertebrate-specific gene families or syntenic chromosomal regions in cnidarians (especially with high sequence identity) would be unexpected and difficult to reconcile with existing evolutionary models. Similarly, if these same features are found in cnidarians but not in tunicates, it would challenge the assumption that vertebrate complexity evolved strictly through innovations along the chordate stem.

Methodology

A prior study by the author found extensive genetic evidence supporting a theory that humans are an evolved form of marine colonial organisms that is structurally and genetically aligned with siphonophores, specifically *Nanomia sp.* (Gjøvik, June 4 2025).

Sequence homology, physiological patterning, and architectural parallels suggest that the human body represents a refined internalization of colonial modularity, guided by conserved biochemical systems and environmental memory. BLAST analysis revealed extensive sequence conservation between human genome assemblies and marine invertebrate species. (Gjøvik, June 4, 2025).

Alignments between *Homo sapiens* and *Nanomia septata* showed 70-82% identity across 1,762-2,198 base pairs with E-values of zero, indicating extremely high statistical significance and non-random alignment. The statistical impossibility of such extensive conservation across taxa separated by hundreds of millions of years challenges existing phylogenetic models and demanded systematic investigation. (Gjøvik, June 4 2025).

In this study, in order to further investigate the hypothesis that the human genome operates as a composite orchestration platform composed of biological microservices (functional modular units ported from ancestral lineages), the study developed a pipeline to detect non-vertical sequence modules shared between humans and basal marine taxa (e.g., jellyfish, hydrozoans, tunicates, protists, etc.).

These candidate "modules" are theoretically interpreted as imported services, integrated into the human runtime environment via modular inclusion rather than evolutionary mutation and selection alone. (Gjovik, June 23 2025). This methodology interprets BLAST+ output as a log of module transfer, reuse, and runtime integration. Matches are assessed for features consistent with intact service logic, port fidelity, and modular encapsulation – looking to multiple lines of evidence including functionality, chemistry, and physiology in addition to genetics.

All sequences were searched against a curated custom database including RefSeq and GenBank genomic and transcriptomic sequences from *Homo sapiens* (including Verkko and archaic assemblies) and ancient metazoans, including jellyfish, tunicates, siphonophore, and selected protists. Data included public TSA, WGS, and mitochondrial/ribosomal datasets for humans and basal

marine invertebrates.

Parameters included BLASTn with -task megablast; filtering disabled: -dust no, -soft_masking false; and output retained includes bit score, e-value, alignment length, percent identity, start/stop positions.

Feature	Interpretation in Microservice Framework
E-value = 0.0	Indicates non-random match; interpreted as intentional module reuse.
Length > 1,000 bp	Suggests functional payload or self-contained logic unit.
Bit Score > 1,000	High-confidence payload delivery.
% Identity ≥ 90%	Indicates high-fidelity transfer, possibly recent or strongly preserved.
% Identity 70–89% + 0.0 e-value	Suggests adapted plugin—function retained, code altered.
Short match (400–1,000 bp) + 0.0 e-value + ≥99% ID	Likely runtime triggers, control signals, or modular wrappers.

Matches were assessed using the following multi-metric framework, integrating E-value, length, identity, and bit score. In honor of the concept of Siphonophores as genetic engineers, this theoretical framework is modeled with software engineering and deployment terminology, as an apt comparison to how siphonophores appear to manage their own physiology and genomes.

Candidate modules that satisfied these criteria were flagged as hypothetical genomic microservices. These modules were further evaluated for characteristics of microservice architecture including boundary integrity, genomic location, expression evidence, and redundancy. To distinguish vertically inherited domains from cross-lineage modular reuse, each candidate was evaluated for:

- Appearance in non-human lineages, particularly marine invertebrates or protists.
- Preserved alignment to humans, including archaic hominins (e.g., Neanderthal, Denisovan).
- Match presence in human mtDNA, nuclear RNA, or non-coding regions, indicating runtime versatility.

Microservice modules identified via this framework are interpreted as:

- Encapsulated logic blocks ported from ancestral or parallel biological systems.
- Preserved as biologically containerized services, activated in specific runtime contexts (tissue, developmental window, immune response, etc.).
- Evidence for a distributed genomic architecture, in which human evolution proceeded by compositional inclusion and module orchestration, rather than solely by pointwise mutational evolution.

This methodology interprets high-confidence BLAST matches as architectural evidence for a modular genome stack composed of ancient biological services.

Data sets were tested from both directions with *Aurelia* run against *Homo*, and *Homo* run against *Aurelia*, etc. The data sets and results for this study are available in the supplementary materials.

Study Results

Upon initiating this study, it became apparent that one specific match between humans and a certain jellyfish, presented more than simply a "microservice." In fact, this ambitious and novel methodology revealed what appears to involve the incorporation of much of an entire jellyfish genome into human physiology – and specifically, neurology.

BLAST+ analysis of *Aurelia aurita* genomic sequences against human databases yielded results that dramatically exceed conventional expectations for cross-phylum sequence conservation, or even the initial concept of siphonophore "microservices."

Instead, this study identified thousands of high-confidence alignments with sequence identities of 80-99% across regions spanning 1-5 kilobases. This is "conservation" levels typically observed between closely related mammalian species, not organisms supposedly separated by ~600 million years of evolution.

Top hits included 3,465–3,500+ bp alignments with >99% identity (e.g., 99.596%, bit scores >6,300, E = 0). Multiple independent contigs mapped with similar scores to the same chromosomal regions, indicating consistency across the *Aurelia aurita* genome. These long-range alignments included RNA, mRNA, and mtDNA, and also appeared to span intergenic and regulatory regions.

This research found chromosome-scale alignments where *Aurelia* contigs match long-alignments that primarily map to human chromosomes 15, 21, and 22. A subset of contigs from the *Aurelia aurita* assembly displayed high identity to large segments of human genomic sequences (e.g., CM099722.1, CP068256.2, OZ096273.1, CP139528.2, GBRG01036015.1,).

The strongest alignments were observed on chromosomes 22, 15, and 21, with alignment lengths of 3,508 bp (87.4% identity), 3,492 bp (86.8% identity), and 3,491 bp (86.6% identity), respectively all with E-values of zero.

Chromosome Y also showed substantial conservation with a 2,697bp alignment (86.9% identity), while the larger, gene-dense chromosomes displayed lower lengths: chromosome X (1,519 bp), chromosome 19 (1,505 bp), and chromosome 1 (1,525 bp). Other chromosomes were not tested in this study and should be evaluated in future studies.

In addition, individual protein-coding genes critical for neural development and immune function exhibit 80%+ sequence identity across long alignments and even complete coding sequences.

These findings are validated by parallel analysis of sequence conservation patterns across multiple *Homo* lineages, including modern humans, Neanderthals, Denisovans, and other archaic hominins. The consistent presence of cnidarian-homologous sequences across these lineages, combined with systematic variation in the specific cnidarian taxa represented, provides strong evidence for the biological authenticity of these conservation patterns while ruling out technical artifacts or contamination.

The data presented below document systematic conservation of functional genetic networks that challenges fundamental assumptions about the evolutionary relationship between cnidarians and vertebrates, and raise questions about the ancestral relationship between *Homo sapiens, Nanomia*, and *Aurelia aurita*. The extent and organization of these conservation patterns suggest that cnidarian-derived genetic modules represent integral components of human genomic architecture.

Neurological Genes

Consistent with the chromosome-scale results, and escalating the significant of these matches, this study also found numerous *Aurelia aurita* contigs with high-quality, long-alignment matches to human protein-coding genes, particularly those involved in neural signaling, synaptic regulation, and immune receptor function.

Multiple contigs (e.g., GBRG01052249.1, GBRG01047208.1) aligned with high identity (93.7–96.2%) over ~1,507 bp to CADPS2, a gene associated with regulated vesicle priming and neurotransmitter release. Bit scores exceeded 2,300, with E-values of 0, indicating extremely significant alignments. CADPS2 is typically expressed in vertebrate neural tissues, with known roles in neuroendocrine signaling.

Aurelia contigs such as GBRG01000513.1 and GBRG01047208.1 aligned to *Homo sapiens* (NG_017077.2) solute carrier family 9 (SLC9A9) with identities of 86–89% over ~700 bp with E-values of 0. This gene is involved in neuronal endosomal pH regulation and has been linked to neuropsychiatric traits in humans.

Aurelia aligned over 517 bp with ~89.5% identity to both BDNF and BDNFOS. (e.g., GBRG01039648, NG_011877.2, NG_011794.2). These elements are central to vertebrate neuroplasticity and behaviorally relevant neural development. MAOA homologs matched with ~91% identity over ~516 bp (NG_008957.2, GBRG01039648.1). This gene is critical for monoamine degradation, particularly serotonin and dopamine, and is highly conserved in vertebrate neural systems.

Aurelia matched *Homo sapiens* Neurobeachin which regulates synaptic vesicle trafficking (514-603 bp, 71.5-88.2%, 0-1.31E^{-80}) and Reelin which is involved in neuronal migration and layer formation (517 bp, 89.6%, E=0). Matches also included axonal guidance and pathfinding genes Contactin-4 (994 bp, 70%, 1.28E^{-81}); Semaphorin SEMA5A (513-602 bp, 73.6-88.9%, 0-4.89E^{-105}); and neuronal cell adhesion/NRCAM (498-516; 87.4-92%, E=0)

Development Genes

Aurelia mitochondrial DNA (NC_008446.1, HQ694729.1) matched with *Homo sapiens* Erb-B2 Receptor Tyrosine Kinase 4 over 1,352 bp, with E-values of 0 (~64%, NG_011805.2). ERBB4 are cell surface receptors involved in cell signaling — they regulate cell growth, differentiation, migration, and survival.

Aurelia also aligned with RBPJ, a key player in Notch signaling and essential in development. (513 bp, 79.1%, 1.47E^{-123}) and Pecanex (PCNX1) a critical gene for neurodevelopment and linked to Notch signaling (513 bp, 91.8%, e-value of zero).

Matches included PBX1 homeobox transcription factor, important in early development and hematopoiesis (814 bp, 74.5%, 5.20E^{-148}); Lysine histone demethylase (KDM6B) involved in developmental gene regulation and lineage specification (632 bp, 65.5%, 4.81E^{-24}); and cytoplasmic polyadenylation (CPEB4) which controls mRNA translation during oocyte maturation, synaptic plasticity, and brain development (769 bp, 76.3%, 7.23E^{-161}).

Structural Proteins, Enzymes, and Metabolism

There was a long alignment to Cytoplasmic Dynein 2 Heavy Chain 1 (DYNC2H1). Three *Aurelia* contigs (e.g., GBRG01188310.1–GBRG01188312.1) matched *Homo sapiens* DYNC2H1 with alignment lengths of 2,335-3,241 bp at ~64.7-68% identity and E-value of 0-7.15E^{-157} (e.g., NM_001080463.2). This gene encodes a motor protein essential for retrograde intraflagellar transport and ciliary function.

Interestingly, there are also strong matches with zero E-values between *Homo sapiens* DYNC2H1 and stony corals

Pocillopora verrucosa and *Acropora muricata* (4,799-5,898 bp), and hydrozoans *Hydractinia symbiolongicarpus* (4,067 bp), *Hydra vulgaris* (2,778 bp), and *Clytia hemisphaerica* (2,339 bp). These matches further support a theory of direct cnidarian ancestry for what we refer to today as terrestrial mammals.

Aurelia matches with *Homo sapiens* included 1,314 bp alignment with Tubulin gene (TUBB1) with 71% identity and e-value of zero. Mucins and similar proteins contributing to barrier function, mucus formation, or secretory processes. Mucins forming gel-like mucus layers in the gut and respiratory tract marching matching over 517 bp, 89%, and e-value of zero (MUC5AC) and 504 bp, 72%, and e-value $1.40E^{-49}$ (MUC2, MUC6).

Matches with enzymes acting on sugars or proteins, with indirect influence on multiple pathways including glucosidase (GANAB) which is involved in glycoprotein quality control in the ER (1,304 bp, 64.6%, $2.94E^{-48}$). Matches across ion transport and membrane excitability including chloride intracellular channel, expressed in kidney and sensory hair cells (CLIC5) and L-type calcium channel, critical in cardiac and neuronal excitability (CACNA1C) over 600-747 bp, 65.9-74.7%, and e-value $4.89E^{-105}$-$3.60E^{-43}$).

Immunology

Long contigs aligned to sequences annotated as KIR gene clusters, including functional and pseudogene forms (e.g., *KIR2DL1, KIR3DL3, KIR3DP1*). Alignments up to 1,099 bp with ~94% identity and e-values of zero were observed. (e.g., GBRG01052249.1, MZ206083.1). These gene families are typically located in the leukocyte receptor complex on chromosome 19 in humans and play central roles in immune surveillance by NK cells.

Aurelia contigs also aligned with 528 bp, ~91% identity, and 0 E-value to the upstream regulatory region of ERVW-1, an endogenous retroviral element important in placental development in humans. (NG_044970.2, GBRG01052249.1).

Matches included proteins or molecules directly involved in innate or adaptive immune responses, such as a 724 bp alignment with C-C chemokine genes, sharing 85.4% identity and zero e-values. *Aurelia* also matched with *Homo sapiens* along the Defensin beta-4A (DEFB4A) gene, an antimicrobial peptide (907 bp, 71.6%, $6.39E^{-127}$).

Alpha-satellite Centromere

There were 2,235 unique matches between *Aurelia* sequences and *Homo sapiens* specific to human alpha-satellite centromere border region and non-alphoid border regions (AF105153.3). The top matches spanned over 660 bp, with 70.6-77.1% identity and e-values of $2.84E^{-127}$ - $1.57E^{-92}$, and the total matches were in the thousands.

Homo sapiens α-satellite centromere border region and non-alphoid border region is a genomic DNA sequence that spans the junction (border region) between alpha-satellite DNA and non-alphoid sequences in the human genome. Centromeres are chromosomal regions supporting mitosis, meiosis, and chromosomal segregation during cell division (Logsdon and Eichler, 2023).

Alpha-satellites are tandemly repeated sequences, typically found at centromeres of all human chromosomes. (Giannuzzi et al., 2021; Pironon et al., 2010). Alpha satellite is a class of highly repetitive DNA defined by a group of 171 bp, AT-rich repeats and comprises up to 10% of the human genome (Giannuzzi et al., 2021).

The sequence matches highly and broadly across this border region implying direct ancestry. Centromere architecture conservation suggests that centromere location and structure was already functionally fixed in this ancestor. May indicate that the epigenetic machinery was conserved and possibly shared mechanisms of centromere specification.

Observed Patterns of Cnidarian Sequence Representation Across *Homo* Lineages

Sequence alignments across both modern and ancient *Homo* samples revealed a consistent and recurrent signal of high-confidence homology to multiple cnidarian taxa, particularly Scyphozoan jellyfish and Siphonophorae.

These matches span mitochondrial and transcribed nuclear RNA sequences in *Aurelia* (e.g., NC_008446.1) and modern *Homo sapiens*. It also includes mitochondrial sequences in archaic lineages including *H. neanderthalensis*, *H. heidelbergensis*, and Denisovans over 1,300 bp and with near 0 E-values. The longest alignment with *Aurelia* was with Denisovan *Homo* remains found in the Denisova Cave in the Altai Mountains of Siberia (1,333 bp, $9.13E^{-122}$).

The presence of these cnidarian-associated sequences across both modern and extinct *Homo* lineages provides strong evidence against contamination or technical artifact, supporting their biological authenticity and likely functional relevance throughout *Homo* evolution.

Archaic *Homo* lineages also includes long alignment with cnidarians that did not match with modern *Homo sapiens* sequences. These included Leptothecata thecate hydrozoans: *Blackfordia, Eirene, Eutima,* and *Nemalecium* (1,300 bp+ and near zero e-value with mtDNA). Leptothecata are relatives of siphonophores. (Bentlage et al, 2021; Kayal et al, 2015). There was also a strong match

with Tubulariidae hydrozoan *Ectopleura larynx*.

Existing research has shown that extinct hominids are thought to have similar cognitive genes with modern Homo sapiens (Paixão-Côrtes et al, 2013), yet mRNA in archaic humans involved different physiology and development, with *Homo sapiens denisova* genes providing enhanced expression during postnatal brain development where *Homo sapiens neanderthalensis* was shown to be enhanced in prenatal brain development. (Gunbin et al, 2015).

Modern humans also show "significant differences" in neurocranial meningeal vessels compared to Homo erectus and Neanderthals (Bruner et al, 2005). The variety of cnidarians genes across *Homo* species provokes inquiry as to if the different jellyfish species may explain the varying physiologies.

Interpretation

Beyond isolated genes, the *Aurelia aurita* genome revealed numerous long contiguous regions (up to 3.5 kb) with extremely high identity (>99%) to large segments of human chromosomes 15, 21, and 22. These regions span both coding and noncoding DNA and often correspond to well-assembled, modern human genomic references, including the T2T CHM13 build and genomes from human diversity panels. This level of conservation at the chromosomal and syntenic level goes well beyond what would be expected from generic conservation of eukaryotic "housekeeping" genes and suggests a much deeper, more complex genomic relationship than current models acknowledge.

The data presented here reveal an unexpected degree of sequence conservation between *Aurelia aurita* and multiple genes, regulatory elements, and chromosomal regions previously considered specific to humans or, at most, other vertebrates. These findings challenge long-standing assumptions in evolutionary biology, particularly regarding the origins, lineage-specificity, and developmental timing of critical molecular pathways – and mammal evolution generally.

Neurodevelopment and Synaptic Machinery

Several genes with strong and specific functions in human neurodevelopment were identified in *Aurelia aurita*. These include CADPS2, BDNF, SLC9A9, and MAOA, all of which play established roles in synaptic transmission, neuroplasticity, and neurotransmitter regulation.

In humans, CADPS2 is involved in vesicle priming and neurotransmitter exocytosis, especially in dopaminergic neurons, and has been associated with neurodevelopmental disorders such as autism. BDNF supports neuron survival and growth and is a central regulator of learning and memory. SLC9A9 affects pH regulation in neuronal endosomes, and MAOA governs the breakdown of monoamines like dopamine and serotonin.

These pathways are typically viewed as hallmarks of complex vertebrate (particularly primate) neural systems, presumed to have evolved incrementally alongside increases in behavioral and cognitive complexity. The presence of high-identity homologs of these genes in a marine invertebrate genome directly challenges the notion that such pathways are uniquely mammalian or even vertebrate.

Innate Immune Recognition and the KIR Gene Complex

One surprising discovery is the presence of clear homologs to the Killer-cell Immunoglobulin-like Receptor (KIR) gene family, which in humans regulate NK cell responses via interaction with MHC class I molecules.

This gene family is known to be both rapidly evolving and highly lineage-specific, with its structure and gene content varying significantly even among primates. Its appearance in the genome of *Aurelia aurita* suggests that the molecular toolkit for regulated cytotoxicity and immune surveillance may have an evolutionary origin that precedes vertebrates.

The discovery of both functional KIR genes and pseudogenes in the *Aurelia aurita* genome implies not only presence but also evolutionary turnover and regulatory complexity, previously thought to be exclusive to the adaptive or semi-adaptive immunity of jawed vertebrates.

Retroviral and Regulatory Elements

In addition to protein-coding genes, the *Aurelia aurita* genome contains high-identity matches to endogenous retroviral regulatory elements, notably the upstream region of ERVW-1. In humans, this region is derived from a co-opted retroviral insertion (syncytin) and plays a critical role in placental development—a feature thought to be entirely absent in invertebrates. The conservation of this regulatory sequence in a marine invertebrate raises important questions about the evolutionary origin and broader functional repurposing of viral sequences in eukaryotic genomes, suggesting either shared ancestral usage or unexpected parallel evolution of retroviral-derived regulation.

Similarly, the identification of BDNFOS, an antisense transcript regulating BDNF expression, points to the existence of conserved RNA-based regulatory mechanisms, which were previously assumed to be vertebrate- or mammal-specific innovations tied to neural complexity.

Cnidarian-Homo Sequence Integration

The broader pattern of cnidarian sequence representation across *Homo* lineages aligns meaningfully with the specific gene-level findings identified earlier in this study. Notably, high-confidence alignments to *Aurelia aurita* included both mitochondrial and nuclear RNA sequences, with exceptional identity to transcripts associated with transcriptional regulation, mitochondrial function, and membrane-related activity.

Among the nuclear transcripts, key hits included sequences with strong similarity to RNA-binding proteins, ATP-dependent helicases, mitochondrial chaperones, and components of the transcriptional preinitiation complex. These functional categories are deeply conserved and are central to gene expression regulation, RNA stability, and energy homeostasis — all core features of eukaryotic cellular function.

That these matches are found in a taxonomically distant marine invertebrate and align at near-perfect identity levels with modern *Homo sapiens* sequences further supports the hypothesis that these relationships are not stochastic, but rather reflect conserved, possibly functionally retained elements.

In the context of mitochondrial sequence matches, the presence of long, high-identity alignments between cnidarian mitochondrial DNA and both modern and archaic *Homo* mitochondrial genomes underscores a conserved structural motif. Importantly, these alignments were not randomly distributed, but clustered in regions associated with oxidative phosphorylation and mitochondrial gene expression — areas under strong selective pressure across metazoans.

Integrating these gene-level observations with the phylogenetic variation seen in cnidarian source taxa suggests that the *Homo* lineage has not only interacted broadly with cnidarian sequence space, but that it has retained elements with high regulatory and energetic relevance. Moreover, the convergence of mitochondrial and transcriptional signatures suggests that cnidarian-derived sequences may have contributed to critical cellular pathways in *Homo*, with possible implications for the evolution of energy metabolism and regulatory complexity.

Together, these results frame a view of *Homo* evolution in which genomic contributions from cnidarians (particularly jellyfish and siphonophores) were critical, functionally significant, and subject to lineage-specific "innovation" over time.

Modern and Archaic *Homo* Alignments to Cnidarian Sequences

Comparative analysis reveals that cnidarian-derived sequences are differentially represented across *Homo* lineages, with modern humans showing predominant *Aurelia* and *Nanomia* (siphonophore) signatures, while archaic lineages exhibit stronger matches to *Cyanea* and *Nausithoe* jellyfish, Leptothecata thecate hydroids, and siphonpohores *Praya, Rhizophysa,* and *Physalia*.

The gene-level alignments observed in *Homo sapiens* reveal a strong signal of homology to cnidarian sequences across a diverse range of nuclear-encoded and transcribed genes. These include key regulators of neuronal and developmental processes, vesicle trafficking, membrane transport, immune signaling, and cytoskeletal structure. Hits to *MAOA* and upstream retroviral elements further suggest involvement in signaling, transcriptional regulation, and neurochemical modulation.

In contrast, the current protohuman data — encompassing *H. neanderthalensis*, *H. heidelbergensis*, and Denisovans — is limited to mitochondrial genome sequences. These showed robust alignments to multiple cnidarian species, especially jellyfish (e.g., *Aurelia*, *Cyanea*, *Nausithoe*) and siphonophores (*Rhizophysa*, *Apolemia*, *Praya*, *Physalia*), across alignment lengths exceeding 1,426 base pairs and identities over 93%. These results demonstrate that homologous cnidarian-derived sequences were already present in ancient *Homo* lineages, long before the emergence of anatomically modern humans.

While these ancient samples do not provide nuclear or RNA-level sequence data, the mitochondrial alignments strongly suggest that cnidarian-derived sequences were already present and preserved in the common ancestors of modern humans and their archaic relatives. The recurrence of long, high-identity mitochondrial alignments across multiple extinct *Homo* taxa rules out artifact and underscores their evolutionary authenticity.

Together, these observations suggest a broad and sustained integration of cnidarian genetic material across the *Homo* lineage, with varying representation over time. Rather than depicting modern *Homo sapiens* as uniquely or categorically more "complex," the results instead point to divergent evolutionary trajectories, where different *Homo* lineages appear to have incorporated or retained slightly different cnidarian contributions. The alignment differences between modern and archaic genomes may reflect distinct phases of genetic experimentation and refinement, culminating in the genomic configuration observed in living humans today.

The observed shifts in species-level matches (for instance, stronger *Praya* and *Physalia* alignments in protohuman lineages, versus predominant *Nanomia* in modern humans) may reflect a period of exploratory genomic assimilation, followed by stabilization around functionally optimal configurations. Today, we'd call that "innovation" through "engineering."

While the precise mechanism by which such sequences became integrated remains an open question, the consistent presence of functional gene orthologs across multiple *Homo* lineages supports biological relation. Expanded sequencing of archaic nuclear and RNA content will be essential to determine whether the regulatory and neural hits seen in *Homo sapiens* are unique to our lineage or represent deeper ancestral features common to the genus *Homo* as a whole.

Discussion

Gaps and Answers in Evolutionary Biology Theories

Taken as definitive data, these results highlight multiple major gaps in current evolutionary and genomic models. The presence of vertebrate-like gene architecture and regulatory complexity in a marine invertebrate reveals that key functional modules (especially for neurodevelopment and immune regulation) are likely far older or more widely distributed than previously assumed.

Much of invertebrate genomics has focused on either model systems or broad phylum-level comparisons. The fine-grained, high-fidelity homology observed here suggests that prior studies may have overlooked deeply conserved elements due to the use of shorter, lower-quality assemblies or a focus on more distantly related reference genomes.

Despite the extensive study of human and primate evolution, critical gaps remain, especially regarding the molecular timeline of key developmental traits. The evolutionary relationship between humans and other apes is still fraught with missing links and contradictory fossil and genomic evidence. This new data compounds that uncertainty by extending relevant genomic features even further back in the tree of life.

However, these findings also start to fill enormous gaps in the current understanding of the evolution of mammals. Today, the timing and pattern of early placental mammal evolution is "confounded by conflict among divergence date estimates from interpretation of the fossil record and from molecular-clock dating studies." (Halliday et al, 2019). Molecular clocks place placental mammal evolution at or after the Cretaceous-Paleogene (K-Pg) mass extinction, yet no pre-Cenozoic fossils have ever been identified. (Carlisle et al, 2023).

Currently there is no definitive evidence of placental mammals existing in the Cretaceous or earlier, implying the first evolution of mammals would have only occurred 66 Ma or less, or alternatively, mammals started to slowly emerge in the late Cretaceous but only then "rapidly" evolved in the modern Cenozoic era. (Halliday et al, 2019; Beck and Lee, 2014).

Current theoretical models for mammal evolution are referred to by names like *Explosive*, *Long Fuse*, *Short Fuse, Soft Explosive,* and *Trans-KPg* models. (Springer et al, 2019). There is currently no mainstream theory that placental mammals evolved in the ocean and their early fossils (if any remain) are on the sea floor, and the marine animals that evolved into modern terrestrial mammals, made the transition to land at or after the Cretaceous-Paleogene mass extinction ~66Ma. However, modern geological research would support such a theory. (Gjovik, June 25 2025).

Instead, the closest mainstream theory hypothesizes that mammals evolved on land and then later some of them decided to move to the ocean. (Yuan et al, 2021; Guo et al, 2024). While appearing backwards to the genetic data discussed, this theory is generally well accepted, and perhaps one reason researchers have not been searching for ancient marine invertebrate genetics within mammals like *Homo sapiens.*

While most of the theories in this study are contrary to current "consensus," the genomic evidence discussed here starts to answer some of the most perplexing mysteries in mammal evolution – such as, explaining what appeared to be concurrent evolution in land and sea of pulmonary adaptations to survive hypoxia. (Guo et al, 2024).

The extremely high sequence identity of *Homo sapiens* to long chromosomal regions in *Aurelia aurita* and *Nanomia* currently has no explanation in standard models of genome evolution. These findings underscore the urgent need for a comprehensive reassessment of the molecular and genomic architecture underlying deep evolutionary transitions and extensive research into the connections and relationship between terrestrial mammals, and siphonophore and jellyfish.

Physiological Convergence Between *Aurelia aurita* and Mammals

Aurelia aurita exhibits remarkable physiological similarities with mammals that highlight shared ancestral mechanisms and convergent evolutionary solutions (Putnam et al. 2007; Bosch 2013).

Digestive System Convergence

One of the most striking similarities between *Aurelia aurita*

and mammals lies in their digestive biochemistry. In situ hybridization studies have demonstrated that trypsin, chitinase, and pancreatic lipase genes are expressed in zymogen-like cells along gastric cirri of young *Aurelia aurita* medusae (Steinmetz et al. 2017). This enzymatic repertoire is remarkably similar to that found in mammalian digestive systems, where these same enzyme families play crucial roles in protein, carbohydrate, and lipid digestion.

Even more compelling is the discovery that in both *Nematostella* (a related cnidarian) and *Aurelia*, the combination of exocrine and insulinergic cells is confined to tissues expressing the foxA transcription factor, which serves as a conserved marker of bilaterian endoderm, midgut, and vertebrate foregut (Steinmetz et al. 2017). This cellular organization is strongly reminiscent of the bilaterian midgut, and especially the vertebrate pancreas, suggesting deep homology in digestive system architecture.

Both *Aurelia aurita* and mammals employ fundamentally similar digestive strategies involving sequential extracellular and intracellular processing. In *Aurelia*, food undergoes preparatory digestion in the stomach and its pouches through extracellular digestion, after which partly digested material is swept by cilia into canals where food particles are ingested into food vacuoles by endodermal cells for intracellular digestion (Chapman 1978). This two-stage digestive process mirrors the mammalian system where initial extracellular breakdown occurs in the gut lumen, followed by intracellular processing within intestinal epithelial cells.

The conservation of phagocytosis as a fundamental digestive mechanism further underscores these similarities. As phagocytosis is the prevalent feeding mechanism in cnidarians and plays important roles in mammalian immune and digestive systems, it likely represents the ancestral feeding mechanism of metazoans (Steinmetz 2019).

Comparative analysis of digestive enzymes reveals striking conservation between cnidarians and mammals. Research on related cnidarian species has identified enzymes with 41% amino acid sequence identity to human chymotrypsin-like proteins, with highly conserved disulfide bonds and substrate-binding sites compared to mammalian CTRLs (Kim et al. 2011). This conservation extends to the catalytic triad structure essential for protease function, demonstrating deep evolutionary conservation of enzymatic mechanisms.

Microbiome-Host Interactions

Recent research revealed that *Aurelia aurita* exhibits microbiome-dependent development that parallels the crucial role of microbial communities in mammalian physiology. The strobilation process in *Aurelia aurita* (a critical asexual reproduction mechanism) is severely compromised in the absence of the natural polyp microbiome (Jensen et al. 2023). This obligate relationship mirrors the essential role of the gut microbiome in mammalian development, immune system maturation, and metabolic function.

Particularly significant is the discovery that the natural microbiota must be present in *Aurelia aurita* polyps prior to the onset of strobilation to ensure normal development (Jensen et al. 2023). This critical temporal window for microbiome establishment parallels findings in mammalian systems where early-life microbial colonization profoundly influences long-term health and development.

Transcriptomic analysis of microbiome manipulation in *Aurelia aurita* reveals sophisticated host-microbe interactions remarkably similar to those observed in mammals. Antibiotic treatment and consequent microbiome reduction significantly affect host gene expression, with immune response and defense mechanism genes being highly upregulated (Moritz et al. 2023). This response pattern closely resembles mammalian microbiome disruption studies where antibiotic treatment triggers similar immune system activation.

Aurelia aurita has evolved host-derived quorum quenching activities as defense mechanisms against pathogenic bacteria, with 37 quorum quenching -encoding open reading frames showing differential expression patterns in response to bacterial challenges (Moritz et al. 2023). This sophisticated chemical communication system parallels the complex molecular crosstalk between mammalian hosts and their microbial communities.

While specific taxonomic comparisons between *Aurelia aurita* and mammalian microbiomes require further investigation, the functional similarities are striking. Both systems demonstrate host-specific microbial selection, temporal windows for colonization, immune-mediated microbiome regulation, and microbiome-dependent developmental processes. The conservation of these host-microbe interaction patterns across such vast evolutionary distances suggests fundamental principles governing animal-microbial symbioses.

Nervous System Architecture and Senses

Aurelia aurita possesses sophisticated visual systems with opsin proteins that contain conserved residue signatures specific to ciliary opsins found in mammalian photoreceptive systems (Plachetzki et al. 2007). While these opsins are may serve different functional roles in cnidarians versus mammals, their structural conservation highlights the ancient origins of photoreceptive molecular

machinery.

The enteric nervous system (ENS) represents one of the most ancient and conserved neural networks across animal phyla. The ENS first appears in the phylum Cnidaria (Furness 2022). While the author understands this is likely to be a very unpopular opinion, it must be noted that there are remarkable morphological and physiological similarities between jellyfish and the human neural meninges (i.e., arachnoid mater, dura mater, meningeal arteries, etc.).

The dura mater "regulates events in the underlying brain and overlying skull through the release of soluble factors and cellular activity." (Suh, 2020). Recent research has even identified that dermal fibroblasts and dura mater-derived cells from the same subject exhibit "highly divergent gene expression profiles that suggest dura mater cells originated from a mixed mural lineage." (Argouarch et al, 2022).

The arachnoid membranes and subarachnoid space contains an ultrafiltrate of plasma (cerebrospinal fluid), which "performs multiple vital functions including nutrient provision, waste removal, buoyancy (reducing the effective weight of the brain from ~1500 g to ~50 g), and shock absorption" with a "complex, multidirectional system with continuous fluid exchange" (Lu et al, 2022).

The meninges are "a dynamic interface crucial for neuroimmune interactions."(Zhang, 2024). Yet, remarkably, these membranes are "underappreciated and largely unrecognized by most neuroradiologists." (Lu et al, 2022) and "interpretation of subtle anatomical findings differs strongly" (Volovici et al, 2020). A research paper published just a few months ago explained "these connective tissue layers have held many secrets that only recently have begun to be revealed." (Betsholtz et al, 2025).

It stands to reason that if these meninges are in fact morphologically and physiological similar to *Aurelia* jellyfish, physicians and researchers may have chosen to "look the other way" related to this specific human anatomy, as questioning what appears to be a jellyfish quite literally floating in sea water inside *Homo sapiens* head, raises a number of follow up questions.

Development and Immune System Conservation

Aurelia aurita and mammals also share remarkably conserved immune recognition mechanisms. Microbial recognition in cnidarian hosts is mediated by pattern recognition receptors such as Toll-like receptors and NOD-like receptors that are conserved across metazoans (Bosch 2013). The ancient MyD88/NF-κB signaling pathway plays a crucial role in both cnidarian and mammalian immune responses, highlighting the deep evolutionary conservation of innate immunity mechanisms.

Despite lacking classical antibody-based adaptive immunity, cnidarians have successfully mounted efficient defense responses against pathogens for hundreds of millions of years using epithelial-based innate immunity systems that form the foundation of mammalian immune responses (Bosch 2013).

Aurelia aurita produces novel antimicrobial peptides with structural and functional similarities to mammalian defense molecules. Aurelin, an antimicrobial peptide extracted from *Aurelia aurita*, demonstrates activity against *Listeria monocytogenes* and *E. coli* (Ovchinnikova et al. 2006).

Structural analysis reveals aurelin contains two α-helical sheets cross-linked by three disulfide bonds, a configuration that shares similarities with K+-channel blocking toxins from sea anemones and represents a novel antimicrobial mechanism (Shenkarev et al. 2012).

Genomic analysis confirmed that *Aurelia aurita* and related cnidarians possess homologs of key mammalian pluripotency genes, including myc, nanog, klf4, Oct4, and Sox2 (Steele et al. 2011). The conservation of these fundamental stem cell regulatory mechanisms across such vast evolutionary distances indicates that the basic molecular machinery governing cellular pluripotency was established early in metazoan evolution.

Several crucial genes involved in early embryogenesis are evolutionarily conserved between cnidarians and mammals (Holstein et al. 2003). Many homologous genes involved in bilaterian embryogenesis also function during cnidarian regeneration, suggesting that regenerative mechanisms in *Aurelia aurita* may utilize developmental pathways conserved in mammalian tissue repair and regeneration.

The remarkable physiological convergence between *Aurelia aurita* and mammals encompasses digestive enzymes and cellular organization, immune recognition pathways, neural regulatory networks, developmental transcription factors, antimicrobial defense systems, microbiome-dependent development, and fundamental cellular processes.

Neural Gene Conservation Between *Aurelia aurita* and Humans

The extensive sequence conservation observed between human neural genes and *Aurelia aurita* genomic regions provides insight into fundamental mechanisms underlying nervous system function across metazoans.

The specific genes identified (i.e., CADPS2, BDNF/BDNFOS, MAOA, and SLC9A9) represent core

neural regulatory pathways that appear to have either been maintained across vast evolutionary distances or reflect direct genetic relationships obliterating current taxonomy.

For example, CADPS2 (Calcium-Dependent Secretion Activator 2) shows remarkable sequence identity (93.7-96.2%) with human homologs and plays a crucial role in *Aurelia's* rhopalial nervous system function. In the jellyfish, this gene likely coordinates calcium-dependent vesicle release mechanisms that control the rhythmic bell contractions essential for locomotion.

The rhopalial ganglia, which serve as the central coordination centers for swimming behavior, require precise temporal control of neurotransmitter release to maintain the synchronized contractions that produce effective propulsion. The high degree of sequence conservation suggests that the fundamental calcium-mediated vesicle priming mechanisms operating in *Aurelia* neural tissue utilize essentially identical molecular machinery to that found in human neural systems.

Brain-Derived Neurotrophic Factor and its associated antisense regulatory RNA demonstrate 89.5% sequence identity, indicating conservation of both the protein-coding sequence and its regulatory networks. During *Aurelia* development, the rhopalial nervous system undergoes ordered differentiation, with gravity-sensing structures developing first, followed by motor control centers, and finally photoreceptive organs.

This developmental sequence requires precise neurotrophin signaling to coordinate the formation of the seven bilaterally arranged neuronal clusters that emerge during metamorphosis from ephyra to medusa. The conservation of both BDNF and its antisense regulatory element suggests that the entire regulatory circuit governing neural development and plasticity has been maintained between these distantly related organisms.

Monoamine Oxidase A conservation at 91% identity reflects the fundamental role of monoamine neurotransmitter regulation in neural function. *Aurelia's* rhopalial nervous system integrates multiple sensory inputs including gravitational orientation, light detection, and chemical gradients to coordinate appropriate behavioral responses. The processing of these diverse sensory inputs requires sophisticated neurotransmitter systems for signal integration and motor output coordination. The high conservation of MAOA indicates that the basic biochemical pathways for monoamine metabolism established in early neural systems continue to operate in human neural tissue.

Solute Carrier Family 9 Member A9 (SLC9A9) maintains 86-89% sequence identity and functions in neuronal pH regulation. Neural signal transmission in *Aurelia* depends on maintaining precise ionic gradients across nerve cell membranes, particularly challenging in the marine environment where ionic composition differs significantly from intracellular conditions. The conservation of pH regulatory mechanisms suggests that the fundamental requirements for neural function (maintaining appropriate ionic environments for signal propagation) remain constant across different organismal contexts.

The degree of sequence conservation observed between *Aurelia* and human neural genes exceeds typical patterns seen in comparative genomics across such evolutionary distances. The presence of alpha-satellite genes and regulatory elements with retroviral characteristics in conserved regions raises questions about the mechanisms by which neural genetic modules might be transferred or maintained across different organismal contexts. Such elements could potentially facilitate the integration of functional genetic modules while preserving their operational characteristics, though the specific mechanisms involved require further investigation.

Mechanisms of Cnidarian Module Integration and Conservation

Notably, while consensus now accepts that tunicate "sea squirts" are close relatives to vertebrates (Delsuc, 2006), in this investigation the strongest sea squirt match to *Homo sapiens* was *Clavelina lepardiformis* with the longest alignment at 1,925 bp, 80.8% identity, and E-value of 0. Yet, looking at *Aurelia*, this study found thousands of long, high-quality matches exceeding 5k bp and with identities near 100%. *Aurelia* was a much closer match than the tunicates.

The specific genes exhibiting highest homology represent core operational modules for neural function. Unlike typical evolutionary scenarios where sequence variation is tolerated within functional bounds, these cnidarian-derived modules appear to function as integrated molecular machines where even minor sequence alterations compromise system-wide performance (developmental disability, learning disorders, etc.).

The conservation of complete regulatory networks (including both coding sequences and antisense regulatory RNAs like BDNFOS) indicates that successful neural function requires precise coordination of multiple molecular components that by default must be maintained as intact functional units.

This modular essentiality explains why conventional vertebrate innovations could not simply replace cnidarian neural algorithms: the cnidarian modules represent

optimized solutions to fundamental neural processing challenges (calcium-dependent vesicle release, neurotrophin signaling, monoamine regulation) that vertebrate systems co-opted rather than re-invented.

The integration of these modules into vertebrate neural architecture would create evolutionary lock-in, where the entire system becomes dependent on maintaining the original cnidarian sequences. The siphonophore 'engineering' of zooids may be directly transferable to what we view today as mammal organs and systems (including the brain) and could explain the difference in organs between species. The variety of jellyfish genetic expressions aligns with the current understanding of similar yet different neurology across hominids.

The presence of retroviral-derived regulatory elements in conserved regions suggests a mechanism for integrating cnidarian modules into vertebrate developmental programs. Retroviral elements are known to facilitate horizontal gene transfer and regulatory network rewiring across taxonomic boundaries. The conservation of these elements alongside cnidarian sequences indicates they may serve as molecular adapters, allowing cnidarian functional modules to respond to vertebrate developmental signals while maintaining their internal operational logic.

In addition to *Homo sapiens* strong genetic relation to the siphonophore *Nanomia*, these additional regulatory hijacking models helps to explain how cnidarian neural modules could be activated in appropriate developmental contexts (neural tissue formation, synaptic differentiation) without disrupting vertebrate-specific developmental programs. The modules retain their cnidarian functional characteristics while becoming integrated into vertebrate regulatory hierarchies.

Mammals: Terrestrial Siphonophores

The differential representation of cnidarian taxa across *Homo* lineages (with modern humans showing predominant *Aurelia/Nanomia* signatures while archaic lineages exhibit stronger matches to other cnidarian species) suggests an evolutionary process of modular sampling and optimization.

Rather than inheriting a fixed set of cnidarian modules, the *Homo* lineage appears to have experimented with different combinations of cnidarian-derived functional units, ultimately converging on the particular configuration observed in modern humans.

This process mirrors siphonophore colonial development, where different zooid types are assembled into functional colonies through modular integration.

The observed chromosomal clustering of conserved sequences (particularly on chromosomes 15, 21, 22) may represent genomic "colonial assembly sites" where multiple cnidarian modules have been integrated as functional units, similar to how siphonophore colonies organize specialized zooids into coordinated operational systems.

While *Aurelia aurita* (Scyphozoa) and *Nanomia* (Siphonophorae) sequences consistently rank among the top matches in modern *Homo sapiens*, protohuman genomes exhibit distinct patterns of alignment, including top matches to other jellyfish taxa such as *Cyanea*, *Nausithoe*, and members of Limnomedusae and Hydroidolina (Leptothecata, Anthoathecata).

Likewise, while *Nanomia* is also detected in archaic genomes, stronger matches (with alignment lengths exceeding 1,200 bp) were observed for other siphonophore species including *Praya*, *Physalia*, *Rhizophysa*, and *Erenna*. Some of these species are also not prominent or present in modern *Homo* datasets. This variation suggests that while jellyfish- and siphonophore-derived sequences are a conserved feature of the *Homo* lineage, the specific taxonomic sources and structural forms of these sequences have shifted over evolutionary time.

These findings indicate a broader evolutionary pattern in which the *Homo* lineage appears to have sampled and retained multiple combinations of cnidarian-derived genetic material, with a notable focus on jellyfish and siphonophore genes. The predominance of *Aurelia* and *Nanomia* alignments in modern *Homo sapiens* may reflect one particularly successful integration outcome among several ancestral possibilities, though the evolutionary dynamics driving this convergence remain unresolved.

Siphonophores represent one of nature's most sophisticated examples of modular biological organization, where specialized zooids maintain distinct functional identities while operating as components of an integrated colonial system. Each zooid type (pneumatophores for buoyancy, nectophores for propulsion, gastrozooids for feeding, and gonozooids for reproduction) performs specific functions while remaining coordinated through shared colonial physiology and neural networks. (Mapstone, 2014).

This modular architecture achieves remarkable functional complexity through division of labor among specialized units, each optimized for particular tasks yet seamlessly integrated into the colonial whole. The success of this organizational strategy is evidenced by siphonophores' ability to function as some of the longest organisms on Earth, with *Praya dubia* reaching 45.7 meters long, while maintaining precise coordination across their extended

colonial bodies. (McClain, 2023; Ahuja et al, 2024).

The extensive genomic conservation documented between humans and both jellyfish (*Aurelia*) and siphonophores (*Nanomia*) suggests that human biological organization represents a terrestrial adaptation of colonial principles established in marine cnidarian lineages. Rather than evolving complex neural systems de novo, the human lineage appears to have intentionally integrated pre-existing cnidarian neural modules within a colonial framework adapted for terrestrial existence. How this process would work is entirely unclear and demands rigorous investigation.

The conservation of specific neural genes across human and jellyfish genomes indicates that fundamental neural processing algorithms established in cnidarian nervous systems have been preserved and redeployed within human neural architecture. Like siphonophore zooids, different regions of the human nervous system maintain specialized functions while contributing to integrated behavioral outputs.

The modular organization observed in jellyfish rhopalia, where discrete neural clusters handle specific sensory modalities (gravity detection, light sensing, motor coordination) while maintaining integrated responses, directly parallels the regional specialization seen in human brain architecture. The conservation of developmental gene networks suggests that the same molecular mechanisms governing rhopalial organization have been scaled and elaborated to produce the complex regional specialization characteristic of vertebrate nervous systems.

As mentioned, there were 12,230 unique matches between *Aurelia* and *Homo sapiens* chromosome 22q11.2 region designated "Cat Eye Syndrome region." Matches exceeded 1,124 bp, 75.8% identity, and had E-values as low as 0. There is also a significantly long match between *Nanomia septata* and *Homo sapiens* at this region. The longest alignment is 5,172 bp with an e-value of zero. (e.g., BA000006.2, CM107577.1). This recently discovered alignment is even longer than the extensive alignments discussed in the prior paper about *Nanomia* and *Homo sapiens* shared genetics (Gjovik, June 4 2025).

While this region is colloquially termed the "Cat Eye Syndrome," the region itself is independently critical to biological function. Chromosome 22q11.2 is a large and complex region. It is a gene-rich region involved in many essential cellular processes. Normal functions of genes in this region include neurotransmitter metabolism, COMT, synaptic development, axon regeneration, chromatin remodeling, monocyte differentiation, and adenosine metabolism. (Szczawińska-Popłonyk 2023; Zinkstok, 2019).

Colonial Physiology and Systemic Integration

Human physiology exhibits hallmarks of colonial organization adapted for terrestrial existence. The integration of multiple organ systems, each with specialized functions yet coordinated through shared circulatory, neural, and endocrine networks, mirrors the colonial integration strategies employed by marine siphonophores. The conservation of regulatory networks, including retroviral-derived elements, suggests that mechanisms for coordinating distributed biological modules have been maintained across the evolutionary transition from marine to terrestrial environments.

The differential representation of cnidarian sequences across *Homo* lineages (with modern humans showing predominant *Aurelia* and *Nanomia* signatures while archaic lineages exhibit stronger matches to other cnidarian taxa) indicates that the specific configuration of cnidarian-derived modules has been subject to evolutionary optimization, similar to how different siphonophore species exhibit varying arrangements of colonial components.

The chromosome-scale conservation observed on human chromosomes 15, 21, and 22 (87-99% identity over 3+ kb regions) suggests that entire functional suites equivalent to complete zooids have been preserved as integrated units. Like siphonophore colonies where individual zooids cannot survive independently but collectively achieve complex behaviors, these conserved cnidarian modules appear to function as interdependent components of human physiology, maintaining their ancestral coordination mechanisms while contributing to terrestrial colonial integration.

This framework implies a novel perspective on human consciousness as an emergent property of colonial neural coordination. The subjective experience of unified consciousness emerging from modular neural processing (Francken et al, 2022; Cowan et al, 2025) mirrors the integrated behavior exhibited by siphonophore colonies, where coordinated responses arise from the interaction of specialized zooids without requiring centralized control.

The integration of multiple cnidarian-derived neural modules within a terrestrial colonial framework could account for both the modular aspects of human cognition like specialized brain regions with distinct functions and the integrated nature of conscious experience including coordinated responses emerging from inter-modular communication (Francken et al, 2022; Cowan et al, 2025).

This framework suggests that biological complexity may arise more commonly through the integration and

coordination of pre-existing functional modules rather than through the gradual elaboration of simple systems. The success of colonial organization strategies in marine environments may have provided templates for the evolution of complex terrestrial organisms, with humans representing one particular implementation of colonial principles adapted for terrestrial existence, primarily arising out of *Nanomia* and *Aurelia* specifically.

This modular approach to biological organization may represent a fundamental principle underlying the evolution of complex life, with implications extending far beyond human biology to questions about the general mechanisms by which sophisticated biological systems arise and are maintained, and the general evolution of mammals and other organisms that appear to have converted 'zooids' to what we might refer to today as organs, nerves, and glands.

Conclusion

The genomic data presented in this study reveals a level of sequence conservation between *Aurelia aurita* and *Homo sapiens* that fundamentally challenges current models of mammal and metazoan evolution. The identification of 80-99% sequence identity across multi-kilobase regions, encompassing both neural regulatory networks and chromosomal-scale conservation, cannot be adequately explained by conventional assumptions about molecular evolution rates or phylogenetic relationships.

The persistence of these conservation patterns across multiple *Homo* lineages, including modern humans, Neanderthals, and Denisovans, demonstrates that cnidarian-derived sequences represent an authentic and ancient component of human genomic architecture. The differential representation of cnidarian taxa across these lineages suggests a dynamic evolutionary process involving the sampling and integration of genetic material from multiple cnidarian sources, with modern humans representing one particular configuration among several possible outcomes.

The functional significance of the conserved genes (particularly those involved in neural development, synaptic transmission, genetic regulation, and immune recognition) indicates that these sequences represent core operational modules that have been "imported" and maintained due to their functional importance. The conservation of entire regulatory networks, including both coding sequences and their associated regulatory RNAs, demonstrates that successful neural function requires integrated molecular systems that transcend traditional taxonomic boundaries.

These findings support a novel evolutionary framework in which human neural architecture represents the integration of cnidarian neural modules within a colonial organizational system arising from siphonophores. This "terrestrial siphonophore" model provides a coherent explanation for both the modular organization of human neural systems and the remarkable conservation of cnidarian-derived genetic elements throughout human evolution.

The implications extend beyond human evolution to fundamental questions about the nature of biological complexity and the mechanisms by which sophisticated systems arise. Rather than viewing complexity as emerging through gradual, linear accumulation of innovations, this data suggests that biological systems may evolve through the integration and coordination of pre-existing functional modules, with evolution operating more as a composer orchestrating existing motifs, than as an inventor creating entirely novel mechanisms.

This study establishes a foundation for reconsidering metazoan evolutionary relationships and highlights the need for expanded comparative genomic analyses that can adequately account for the extensive sequence conservation documented here, and to explore if there are similar patterns with other mammals and cnidarians.

Future investigations should focus on elucidating the mechanisms by which these functional genetic modules are transferred and integrated across taxonomic boundaries, and on understanding how modular architectures contribute to the emergence of complex biological systems.

These findings ultimately suggest that the boundary between "simple" and "complex" organisms may be far more permeable than previously recognized, with sophisticated systems arising through the creative recombination of ancient, conserved functional elements rather than through wholesale innovation.

The human genome, rather than representing the supposed pinnacle of evolutionary complexity, may be better understood as a particularly successful integration of ancient marine biological modules.

Data Availability

All sequences referenced are publicly available through NIH/NCBI and ENA databases. Custom database FASTA files and complete sequence listings with methodological documentation are provided as supplementary materials within the OSF repository. These datasets are freely available through the Open Science Framework (OSF) at DOI 10.17605/OSF.IO/YWB2T.

Acknowledgements

The author conceptualized the study, developed the theoretical framework, and conducted all analyses. This research received no external funding and was conducted using personally acquired resources.

The author acknowledges Molecular Biologist GPT, Scholar GPT, and Claude AI for their assistance with manuscript preparation, data interpretation discussions, and research development over the course of this investigation.

References

Abrams, Michael J., Ty Basinger, William Yuan, Chin-Lin Guo, and Lea Goentoro. "Self-repairing Symmetry in Jellyfish through Mechanically Driven Reorganization." *Proceedings of the National Academy of Sciences* 112, no. 26 (2015): 12814-12819.

Abrams MJ, Tan FH, Li Y, et al. A conserved strategy for inducing appendage regeneration in moon jellyfish, *Drosophila*, and mice. *Elife*. 2021;10:e65092.

Ahuja N, Cao X, Schultz DT, et al. Giants among Cnidaria: Large Nuclear Genomes and Rearranged Mitochondrial Genomes in Siphonophores. *Genome Biol Evol*. 2024;16(3):evae048.

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman. "Gapped BLAST and PSI-BLAST: a New Generation of Protein Database Search Programs." *Nucleic Acids Research* 25, no. 17 (1997): 3389-3402.

Argouarch AR, Schultz N, Yang AC, et al. Postmortem Human Dura Mater Cells Exhibit Phenotypic, Transcriptomic and Genetic Abnormalities that Impact their Use for Disease Modeling. *Stem Cell Rev Rep*. 2022;18(8):3050-3065.

Athanasiou KA, Eswaramoorthy R, Hadidi P, Hu JC. Self-organization and the self-assembling process in tissue engineering. *Annu Rev Biomed Eng.* 2013;15:115-136.

Ayed, Yosra, Hichem Khadhraoui, Hichem Ben Hassen, Sarra Karkar, Jamila Ben Slama, Sonia Trigui El Menif, and Radhia Gargouri. "Nematocyst Types and Venom Effects of Aurelia aurita and Velella velella from the Mediterranean Sea." *Journal of Venomous Animals and Toxins including Tropical Diseases* 26 (2020): e20190028.

Bannert, Norbert, and Reinhard Kurth. "Retroelements and the Human Genome: New Perspectives on an Old Relation." *Proceedings of the National Academy of Sciences* 101, suppl. 2 (2004): 14572-14579.

Beck RM, Lee MS. Ancient dates or accelerated rates? Morphological clocks and the antiquity of placental mammals. *Proc Biol Sci*. 2014;281(1793):20141278.

Betsholtz C, Engelhardt B, Koh GY, McDonald DM, Proulx ST, Siegenthaler J. Advances and controversies in meningeal biology. *Nat Neurosci*. 2024;27(11):2056-2072.

Barde, Yves-Alain, Denise Edgar, and Hans Thoenen. "Purification of a New Neurotrophic Factor from Mammalian Brain." *EMBO Journal* 1, no. 5 (1982): 549-553.

Bentlage B, Collins AG. Tackling the phylogenetic conundrum of Hydroidolina (Cnidaria: Medusozoa: Hydrozoa) by assessing competing tree topologies with targeted high-throughput sequencing. *PeerJ*. 2021;9:e12104.

Bonasia S, Smajda S, Ciccio G, Robert T. Middle Meningeal Artery: Anatomy and Variations. *AJNR Am J Neuroradiol*. 2020;41(10):1777-1785.

Bosch, Thomas C. G. "Cnidarian-Microbe Interactions and the Origin of Innate Immunity in Metazoans." *Annual Review of Microbiology* 67 (2013): 499-518.

Brázda V, Šislerová L, Cucchiarini A, Mergny JL. G-quadruplex propensity in *H. neanderthalensis*, *H. sapiens* and Denisovans mitochondrial genomes. *NAR Genom Bioinform*. 2024;6(2):lqae060.

Brucker, Robert M., and Seth R. Bordenstein. "The Hologenomic Basis of Speciation: Gut Bacteria Cause Hybrid Lethality in the Genus Nasonia." *Science* 341, no. 6146 (2013): 667-669.

Bruner E, Mantini S, Perna A, Maffei C, Manzi G. Fractal dimension of the middle meningeal vessels: variation and evolution in Homo erectus, Neanderthals, and modern humans. Eur J Morphol. 2005;42(4-5):217-224.

Bruner E, Mantini S, Musso F, De La Cuétara JM, Ripani M, Sherkat S. The evolution of the meningeal vascular system in the human genus: From brain shape to thermoregulation. *Am J Hum Biol*. 2011;23(1):35-43.

Burns JA, Daniels J, Becker KP, et al. Transcriptome sequencing of seven deep marine invertebrates. *Sci Data*. 2024;11(1):679.

Camacho, Christiam, George Coulouris, Vahram Avagyan, Ning Ma, Jason Papadopoulos, Kevin Bealer, and Thomas L. Madden. "BLAST+: Architecture and Applications." *BMC Bioinformatics* 10 (2009): 421.

Carlisle E, Janis CM, Pisani D, Donoghue PCJ, Silvestro D.

A timescale for placental mammal diversification based on Bayesian modeling of the fossil record. *Curr Biol*. 2023;33(15):3073-3082.e3.

Carroll, Sean B. "Evo-devo and an Expanding Evolutionary Synthesis: A Genetic Theory of Morphological Evolution." *Cell* 134, no. 1 (2008): 25-36.

Cartwright, Paulyn & Evans, Nathaniel & Dunn, Casey & Marques, Antonio & Miglietta, Maria & Schuchert, Peter & Collins, Allen. (2008). Phylogenetics of Hydroidolina (Hydrozoa: Cnidaria). *Journal of the Marine Biological Association of the UK*. 88. 1663 - 1672.

Chapman, D. M. "Microanatomy of the Cubozoan *Tripedalia cystophora*." *Helgoländer wissenschaftliche Meeresuntersuchungen* 31, no. 2 (1978): 128-168.

Chapman, Jarrod A., Ewen F. Kirkness, Oleg Simakov, Steven E. Hampson, Therese Mitros, Thomas Weinmaier, Thomas Rattei, et al. "The Dynamic Genome of Hydra." *Nature* 464, no. 7288 (2010): 592-596.

Cisternas, Felipe A., Jeffrey B. Vincent, Lynn Scherer, and James L. Ray. "Cloning and Characterization of Human CADPS and CADPS2, New Members of the Ca2+-dependent Activator for Secretion Protein Family." *Genomics* 81, no. 3 (2003): 279-291.

Cooper GM, Durham EL, Cray JJ Jr, Siegel MI, Losee JE, Mooney MP. Tissue interactions between craniosynostotic dura mater and bone. *J Craniofac Surg*. 2012;23(3):919-924.

Cowan N, Ahmed NI, Bao C, et al. Theories of consciousness from the perspective of an embedded processes view. *Psychol Rev*. 2025;132(1):76-106.

Damian-Serrano A, Hetherington ED, Choy CA, Haddock SHD, Lapides A, Dunn CW. Characterizing the secret diets of siphonophores (Cnidaria: Hydrozoa) using DNA metabarcoding. *PLoS One*. 2022;17(5):e0267761.

Damian-Serrano A, Haddock SHD, Dunn CW. The Evolutionary History of Siphonophore Tentilla: Novelties, Convergence, and Integration. *Integr Org Biol*. 2021;3(1):obab019.

Dasgupta K, Jeong J. Developmental biology of the meninges. *Genesis*. 2019;57(5):e23288.

Degenhard, Theresa & Groh, Adam & Afanasiev, Elia & Luo, Michael & Yaqubi, Moein & Stratton, Jo & Petrecca, Kevin. (2024). An integrative layer-resolved atlas of the adult human meninges.

Delsuc F, Brinkmann H, Chourrout D, Philippe H. Tunicates and not cephalochordates are the closest living relatives of vertebrates. *Nature*. 2006;439(7079):965-968.

Dresp, Birgitta. (2020). Seven Properties of Self-Organization in the Human Brain. *Big Data and Cognitive Computing*. 4. 10.

Dunn, Casey W., Philip R. Pugh, and Steven H. D. Haddock. "Molecular Phylogenetics of the Siphonophora (Cnidaria), with Implications for the Evolution of Functional Specialization." *Systematic Biology* 54, no. 6 (2005): 916-935.

Eide Therkelsen H, Enger R, Eide PK, Ringstad G. Evidence for cellular and solute passage between the brain and skull bone marrow across meninges: A systematic review. *J Cereb Blood Flow Metab*. 2025;45(4):581-599.

Emera, Deena, and Günter P. Wagner. "Transformation of a Transposon into a Derived Prolactin Promoter with Function during Human Pregnancy." *Proceedings of the National Academy of Sciences* 109, no. 28 (2012): 11246-11251.

Francken JC, Beerendonk L, Molenaar D, et al. An academic survey on theoretical foundations, common assumptions and the current state of consciousness science. *Neurosci Conscious*. 2022;2022(1):niac011.

Furness, John B. "Comparative and Evolutionary Aspects of the Digestive System and Its Enteric Nervous System Control." *Advances in Experimental Medicine and Biology* 1383 (2022): 1-13.

Ghannam JY, Al Kharazi KA. Neuroanatomy, Cranial Meninges. [Updated 2023 Jul 24]. In: StatPearls [Internet]. Treasure Island (FL): *StatPearls Publishing*.

Giannuzzi G, Logsdon GA, Chatron N, et al. Alpha Satellite Insertion Close to an Ancestral Centromeric Region. *Mol Biol Evol*. 2021;38(12):5576-5587.

Gjøvik, Ashley M. "Extensive Human/siphonophore Genetic Sequence Overlap: A Brief Communication". *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 4, 2025). https://doi.org/10.5281/zenodo.15596204.

Gjøvik, Ashley M. "The Multiple Multicellular Prototype Framework: Silica-based Biomineralization and Early Eukaryotic Diversification". *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 9, 2025). https://doi.org/10.5281/zenodo.15622349.

Gjøvik, Ashley M. "A Recursive Strategy for Deep Homology Discovery in Genetic Sequence Alignment". *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 10, 2025). https://doi.org/10.5281/zenodo.15628144.

Gjøvik, Ashley, M. "Quantum-active Genomic Architecture: Personal Genome Analysis Reveals Coordinated Quantum-genomic Networks". *The Journal of Decolonized Ecology and Evolution* 1, no. 2 (June 26,

2025). https://doi.org/10.5281/zenodo.15750523.

Gjøvik, Ashley, M. "Compiled Chemistry: Structural Inheritance and the Deep Origins of Biological Function". *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 23, 2025). https://doi.org/10.5281/zenodo.15717955.

Gjøvik, Ashley M. "Thermal, UV, and Impact Constraints on Pre-cambrian Terrestrial Evolution: The Impossibility of Complex Multicellular Life on Land Prior to 600 MYA". *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 25, 2025). https://doi.org/10.5281/zenodo.15739885.

Gold, David A., Takeo Katsuki, Yang Li, Xifeng Yan, Michael Regulski, David Ibberson, Thomas Holstein, et al. "The Genome of the Jellyfish Aurelia and the Evolution of Animal Complexity." *Nature Ecology & Evolution* 3, no. 1 (2019): 96-104.

Gold DA, Nakanishi N, Hensley NM, et al. Structural and Developmental Disparity in the Tentacles of the Moon Jellyfish Aurelia sp.1. *PLoS One*. 2015;10(8):e0134741.

Gold, David A., et al. "Mechanisms of Cnidocyte Development in the Moon Jellyfish Aurelia." *Development Genes and Evolution* 229, no. 2-3 (2019): 75-89.

Green, Richard E., Johannes Krause, Adrian W. Briggs, Tomislav Maricic, Udo Stenzel, Martin Kircher, Nick Patterson, et al. "A Draft Sequence of the Neandertal Genome." *Science* 328, no. 5979 (2010): 710-722.

Grosberg, Richard K., and Richard R. Strathmann. "The Evolution of Multicellularity: A Minor Major Transition?" *Annual Review of Ecology, Evolution, and Systematics* 38 (2007): 621-654.

Gunbin KV, Afonnikov DA, Kolchanov NA, Derevianko AP, Rogaev EI. The evolution of Homo sapiens denisova and Homo sapiens neanderthalensis miRNA targeting genes in the prenatal and postnatal brain. *BMC Genomics*. 2015;16 Suppl 13(Suppl 13):S4.

Guo BX, Zhang Y, Sun XY, et al. Convergent evolution in high-altitude and marine mammals: Molecular adaptations to pulmonary fibrosis and hypoxia. *Zool Res*. 2024;45(6):1209-1220.

Halliday TJD, Dos Reis M, Tamuri AU, Ferguson-Gow H, Yang Z, Goswami A. Rapid morphological evolution in placental mammals post-dates the origin of the crown group. *Proc Biol Sci*. 2019;286(1898):20182418.

Hansen E, Janson C, Romanova L, Lam C. Effect of Parenchymal Arachnoid on Brain Fluid Transport. *Basic Clin Neurosci*. 2024;15(2):221-232.

Holstein, Thomas W., Ekaterina Hobmayer, and Ulrich Technau. "Cnidarians: An Evolutionarily Conserved Model System for Regeneration?" *Developmental Dynamics* 228, no. 3 (2003): 402-414.

Jekely, Gaspar. "Origin and Early Evolution of Neural Circuits for the Control of Ciliary Locomotion." *Proceedings of the Royal Society B* 278, no. 1707 (2011): 914-922.

Jensen, Natascha, Nancy Weiland-Bräuer, Sebastian Joel, Christiane M. Chibani, and Ruth A. Schmitz. "The Life Cycle of Aurelia aurita Depends on the Presence of a Microbiome in Polyps Prior to Onset of Strobilation." *Microbiology Spectrum* 11, no. 4 (2023): e00262-23.

Kayal E, Bentlage B, Cartwright P, et al. Phylogenetic analysis of higher-level relationships within Hydroidolina (Cnidaria: Hydrozoa) using mitochondrial genome data and insight into their mitochondrial transcription. *PeerJ*. 2015;3:e1403.

Khalturin, Konstantin, Chuya Shinzato, Maria Khalturina, Mayuko Hamada, Manabu Fujie, Ryo Koyanagi, Miyuki Kanda, et al. "Medusozoan Genomes Inform the Evolution of the Jellyfish Body Plan." *Nature Ecology & Evolution* 3, no. 6 (2019): 811-822.

Kim, Jin-Soo, et al. "Molecular Cloning and Enzymatic Characterization of a Chymotrypsin-Like Serine Protease from the Nematocysts of the Moon Jellyfish *Aurelia aurita*." *Comparative Biochemistry and Physiology Part B* 158, no. 4 (2011): 318-325.

Kjeld Møllgård et al., A mesothelium divides the subarachnoid space into functional compartments. *Science*, 379,84-88 (2023).

Kraus Y, Osadchenko B, Kosevich I. Embryonic development of the moon jellyfish *Aurelia aurita* (Cnidaria, Scyphozoa): another variant on the theme of invagination. *PeerJ*. 2022;10:e13361. Published 2022 May 18.

Lawley JW, Gamero-Mora E, Maronna MM, et al. The importance of molecular characters when morphological variability hinders diagnosability: systematics of the moon jellyfish genus *Aurelia* (Cnidaria: Scyphozoa). *PeerJ*. 2021;9:e11954.

Liu, Gang, Wenjin Hao, Qingzhi Wang, Jiangyong Wang, Bin Zhu, and Song Sun. "Integrated Gene Co-expression Network Analysis Reveals Unique Developmental Processes of Aurelia aurita." *Gene* 834 (2022): 146653.

Logsdon GA, Eichler EE. The Dynamic Structure and Rapid Evolution of Human Centromeric Satellite DNA. *Genes (Basel)*. 2022;14(1):92. Published 2022 Dec 28.

Lu S, Brusic A, Gaillard F. Arachnoid Membranes: Crawling Back into Radiologic Consciousness. *AJNR Am J Neuroradiol*. 2022;43(2):167-175.

Mackie, George Owen. "Siphonophores, Bud-colonies, and Superorganisms." *Publications of the Seto Marine Biological Laboratory* 10, no. 2 (1963): 183-195.

Mapstone GM. Global diversity and review of Siphonophorae (Cnidaria: Hydrozoa). *PLoS One*. 2014;9(2):e87737.

Matveev, Igor V., Tatiana G. Shaposhnikova, and Olga I. Podgornaya. "A Novel Aurelia aurita Protein Mesoglein Contains DSL and ZP Domains." *Gene* 399, no. 1 (2007): 20-25.

McClain CR, Webb TJ, Heim NA, Knope ML, Monarrez PM, Payne JL. Navigating uncertainty in maximum body size in marine metazoans. *Ecol Evol*. 2024;14(6):e11506.

McFall-Ngai, Margaret, Michael G. Hadfield, Thomas C. G. Bosch, Hannah V. Carey, Tomislav Domazet-Lošo, Angela E. Douglas, Nicole Dubilier, et al. "Animals in a Bacterial World, a New Imperative for the Life Sciences." *Proceedings of the National Academy of Sciences* 110, no. 9 (2013): 3229-3236.

Mizrahi GA, Shemesh E, Mizrachi A, Tchernov D. Comparative genetics of scyphozoan species reveals the geological history and contemporary processes of the Mediterranean Sea. *Ecol Evol*. 2021;11(15):10303-10319. Published 2021 Jul 8.

Moritz, Carina, Nancy Weiland-Bräuer, Cornelia Jaspers, and Ruth A. Schmitz. "First Insights into the Aurelia aurita Transcriptome Response upon Manipulation of Its Microbiome." *Frontiers in Microbiology* 14 (2023): 1183627.

Moroz, Leonid L. "On the Independent Origins of Complex Brains and Neurons." *Brain, Behavior and Evolution* 74, no. 3 (2009): 177-190.

Munro, Catriona, Bastian Bentlage, Dhugal Lindsay, Tomoko Gleason, Russell Hopcroft, Karen J. Osborn, and Allen G. Collins. "Improved Phylogenetic Resolution within Siphonophora (Cnidaria) with Implications for Trait Evolution." *Molecular Phylogenetics and Evolution* 127 (2018): 823-833.

Nakamura, Naoto, Crislyn D'Souza-Schorey, and Julie G. Donaldson. "The GTPase Dynamin-2 is Required for Clathrin-mediated Endocytosis." *Journal of Biological Chemistry* 280, no. 28 (2005): 26391-26398.

Nakanishi, Nagayasu, Volker Hartenstein, and David K. Jacobs. "Development of the Rhopalial Nervous System in Aurelia sp.1 (Cnidaria, Scyphozoa)." *Development Genes and Evolution* 219, no. 6 (2009): 301-317.

Nakanishi N, Camara AC, Yuan DC, Gold DA, Jacobs DK. Gene Expression Data from the Moon Jelly, Aurelia, Provide Insights into the Evolution of the Combinatorial Code Controlling Animal Sense Organ Development. *PLoS One*. 2015;10(7):e0132544.

Nurk, Sergey, Sergey Koren, Arang Rhie, Mikko Rautiainen, Andrey V. Bzikadze, Alla Mikheenko, Mitchell R. Vollger, et al. "The Complete Sequence of a Human Genome." *Science* 376, no. 6588 (2022): 44-53.

Ohdera AH, Mansbridge M, Wang M, Naydenkov P, Kamel B, Goentoro L. The microbiome of a Pacific moon jellyfish Aurelia coerulea. *PLoS One*. 2024;19(4):e0298002.

Ovchinnikova, Tatiana V., et al. "Aurelin, a Novel Antimicrobial Peptide from Jellyfish *Aurelia aurita* with Structural Features of Defensins and Channel-Blocking Toxins." *Biochemical and Biophysical Research Communications* 348, no. 2 (2006): 514-523.

Paixão-Côrtes VR, Viscardi LH, Salzano FM, Hünemeier T, Bortolini MC. Homo sapiens, Homo neanderthalensis and the Denisova specimen: New insights on their evolutionary histories using whole-genome comparisons. *Genet Mol Biol*. 2012;35(4 (suppl)):904-911.

Paixão-Côrtes VR, Viscardi LH, Salzano FM, Cátira Bortolini M, Hünemeier T. The cognitive ability of extinct hominins: bringing down the hierarchy using genomic evidences. *Am J Hum Biol*. 2013;25(5):702-705.

Pallasdies, Fabian, et al. (2019) From single neurons to behavior in the jellyfish Aurelia aurita, *eLife* 8:e50084.

Pan S, Koleske J, Koller GM, et al. Meningeal CSF transport is primarily mediated by the arachnoid and pia maters during development. Preprint. *bioRxiv*. 2023;2023.08.10.552826.

Peng S, Ye L, Li Y, et al. Metagenomic insights into jellyfish-associated microbiome dynamics during strobilation. *ISME Commun*. 2024;4(1):ycae036.

Philippe, Hervé, Ronan Derelle, Philippe Lopez, Karine Pick, Carole Borchiellini, Nicolas Boury-Esnault, Jean Vacelet, et al. "Phylogenomics Revives Traditional Views on Deep Animal Relationships." *Current Biology* 19, no. 8 (2009): 706-712.

Pinho-Correia LM, McCullough SJC, Ghanizada H, Nedergaard M, Rustenhoven J, Da Mesquita S. CSF transport at the brain-meningeal border: effects on neurological health and disease. *Lancet Neurol*. 2025;24(6):535-547.

Pinnow N, Chibani CM, Güllert S, Weiland-Bräuer N.

Microbial community changes correlate with impaired host fitness of Aurelia aurita after environmental challenge. *Anim Microbiome*. 2023;5(1):45.

Pironon, N., Puechberty, J. & Roizès, G. Molecular and evolutionary characteristics of the fraction of human alpha satellite DNA associated with CENP-A at the centromeres of chromosomes 1, 5, 19, and 21. *BMC Genomics* **11**, 195 (2010).

Plachetzki, David C., Connie R. Fong, and Todd H. Oakley. "The Evolution of Phototransduction from an Ancestral Cyclic Nucleotide Gated Pathway." *Proceedings of the Royal Society B* 277, no. 1690 (2007): 1963-1969.

Proulx ST. Cerebrospinal fluid outflow: a review of the historical and contemporary evidence for arachnoid villi, perineural routes, and dural lymphatics. *Cell Mol Life Sci*. 2021;78(6):2429-2457.

Prüfer, Kay, Cesare de Filippo, Steffi Grote, Fabrizio Mafessoni, Petra Korlević, Mateja Hajdinjak, Benjamin Vernot, et al. "A High-coverage Neandertal Genome from Vindija Cave in Croatia." *Science* 358, no. 6363 (2017): 655-658.

Putnam, Nicholas H., Mansi Srivastava, Uffe Hellsten, Bill Dirks, Jarrod Chapman, Asaf Salamov, Astrid Terry, et al. "Sea Anemone Genome Reveals Ancestral Eumetazoan Gene Repertoire and Genomic Organization." *Science* 317, no. 5834 (2007): 86-94.

Queller, David C., and Joan E. Strassmann. "Beyond Society: The Evolution of Organismality." *Philosophical Transactions of the Royal Society B* 364, no. 1533 (2009): 3143-3155.

Raff, Rudolf A. *The Shape of Life: Genes, Development, and the Evolution of Animal Form*. Chicago: University of Chicago Press, 1996.

Reich, David, Richard E. Green, Martin Kircher, Johannes Krause, Nick Patterson, Eric Y. Durand, Bence Viola, et al. "Genetic History of an Archaic Hominin Group from Denisova Cave in Siberia." *Nature* 468, no. 7327 (2010): 1053-1060.

Ryan, Joseph F., Kevin Pang, Christine E. Schnitzler, Anh-Dao Nguyen, R. Travis Moreland, David K. Simmons, Bernard J. Koch, et al. "The Genome of the Ctenophore Mnemiopsis leidyi and its Implications for Cell Type Evolution." *Science* 342, no. 6164 (2013): 1242592.

Szczawińska-Popłonyk A, Schwartzmann E, Chmara Z, et al. Chromosome 22q11.2 Deletion Syndrome: A Comprehensive Review of Molecular Genetics in the Context of Multidisciplinary Clinical Approach. *Int J Mol Sci*. 2023;24(9):8317.

Shenkarev, Zakhar O., Kirill D. Nadezhdin, Sergey V. Balandin, Alexander S. Yakimenko, Tatiana V. Ovchinnikova, and Alexander S. Arseniev. "High-Resolution NMR Structure of the Antimicrobial Peptide Aurelin from Jellyfish *Aurelia aurita*." *Biochemical and Biophysical Research Communications* 429, no. 3-4 (2012): 63-69.

Shih, Jean C., Kevin Chen, and Marco J. Ridd. "Monoamine Oxidase: From Genes to Behavior." *Annual Review of Neuroscience* 22 (1999): 197-217.

Shinzato, Chuya, Eiichi Shoguchi, Takeshi Kawashima, Mayuko Hamada, Kanako Hisata, Makiko Tanaka, Mayuki Fujie, et al. "Using the Acropora digitifera Genome to Understand Coral Responses to Environmental Change." *Nature* 476, no. 7360 (2011): 320-323.

Simakov, Oleg, Takeshi Kawashima, Ferdinand Marlétaz, Julia Jenkins, Ryo Koyanagi, Therese Mitros, Kanako Hisata, et al. "Insights into Bilaterian Evolution from Three Spiralian Genomes." *Nature* 493, no. 7433 (2013): 526-531.

Springer MS, Foley NM, Brady PL, Gatesy J, Murphy WJ. Evolutionary Models for the Diversification of Placental Mammals Across the KPg Boundary. *Front Genet*. 2019;10:1241.

Stante M, Weiland-Bräuer N, von Hoyningen-Huene AJE, Schmitz RA. Marine bacteriophages disturb the associated microbiota of *Aurelia aurita* with a recoverable effect on host morphology. *Front Microbiol*. 2024;15:1356337.

Steele, Robert E., Christopher N. David, and Ulrich Technau. "A Genomic View of 500 Million Years of Cnidarian Evolution." *Trends in Genetics* 27, no. 1 (2011): 7-13.

Steinmetz, Patrick R. H. "A Non-bilaterian Perspective on the Development and Evolution of Animal Digestive Systems." *Cell and Tissue Research* 377, no. 3 (2019): 321-339.

Steinmetz, Patrick R. H., Rory Aman, Johanna E. M. Kraus, and Ulrich Technau. "Gut-like Ectodermal Tissue in a Sea Anemone Challenges Germ Layer Homology." *Nature Ecology & Evolution* 1, no. 9 (2017): 1535-1542.

Suh DC. Where Did the Dura Mater Come from?. *Neurointervention*. 2020;15(1):2-3.

Suzuki KS, Suzuki KW, Kumakura E, et al. Seasonal alternation of the ontogenetic development of the moon jellyfish Aurelia coerulea in Maizuru Bay, Japan. *PLoS One*. 2019;14(11):e0225513.

Technau, Ulrich, and Michaela Schwaiger. "Recent Advances in Genomics and Transcriptomics of Cnidarians." *Marine Genomics* 22 (2015): 31-38.

Telano LN, Baker S. Physiology, Cerebral Spinal Fluid. [Updated 2023 Jul 4]. In: StatPearls [Internet]. Treasure Island (FL): *StatPearls Publishing*.

Thau L, Reddy V, Singh P. Anatomy, Central Nervous System. [Updated 2022 Oct 10]. In: StatPearls [Internet]. Treasure Island (FL): *StatPearls Publishing*.

Totton, A. K. *A Synopsis of the Siphonophora*. London: British Museum (Natural History), 1965.

Ungureanu G, Florian A, Florian SI. The impact of arachnoid structures on skull-base meningioma surgical management: a radiological analysis and narrative review. *J Med Life*. 2024;17(7):682-689.

Volovici, V., Varvari, I., Dirven, C.M.F. *et al.* The membrane of Liliequist—a safe haven in the middle of the brain. A narrative review. *Acta Neurochir* 162, 2235–2244 (2020).

Yuan Y, Zhang Y, Zhang P, et al. Comparative genomics provides insights into the aquatic adaptations of mammals. *Proc Natl Acad Sci U S A*. 2021;118(37):e2106080118.

Wagner, Günter P., Mihaela Pavlicev, and James M. Cheverud. "The Road to Modularity." *Nature Reviews Genetics* 8, no. 12 (2007): 921-931.

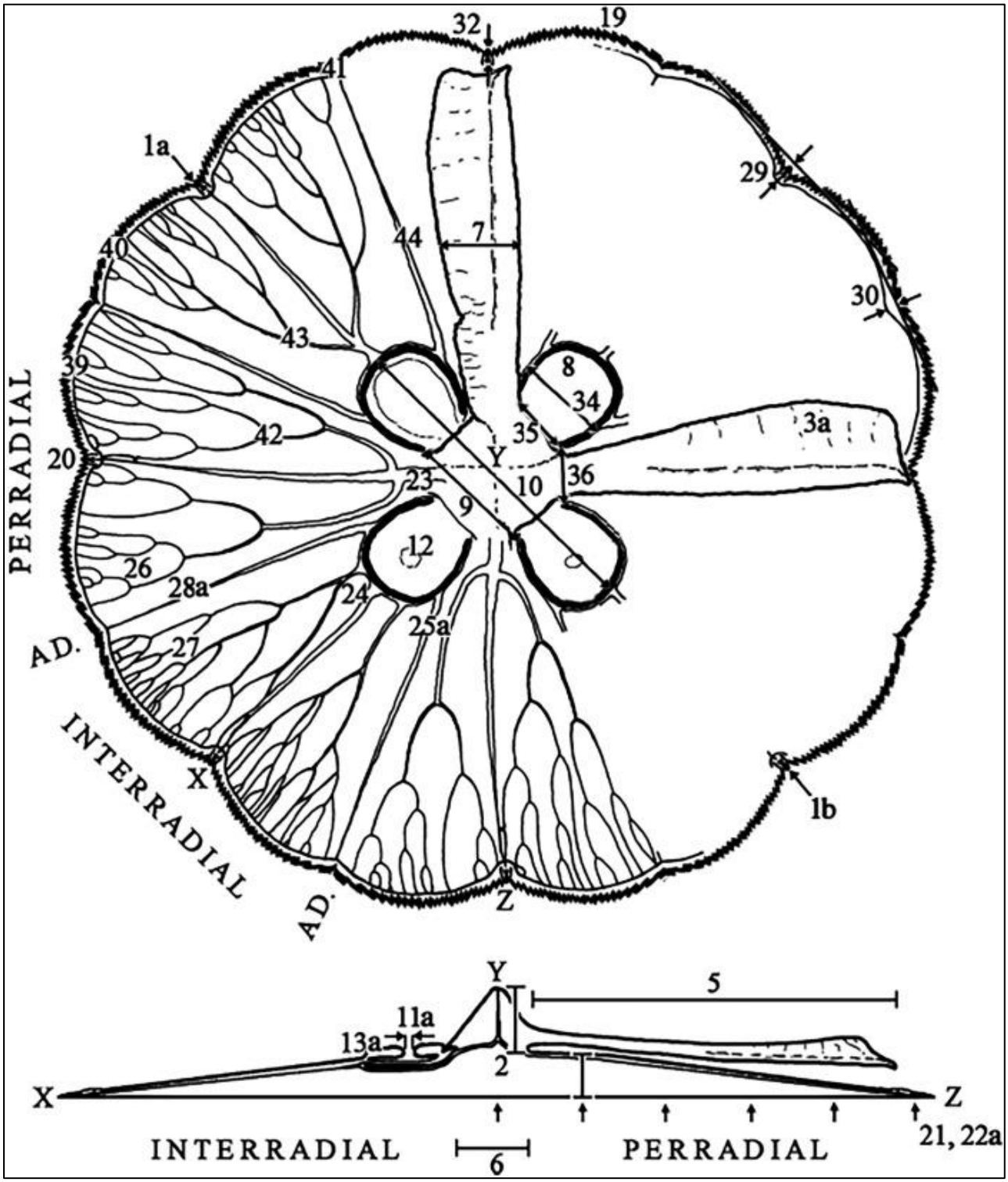
Weiland-Bräuer N, Koutsouveli V, Langfeldt D, Schmitz RA. First insights into the *Aurelia aurita* transcriptome response upon manipulation of its microbiome. *Front Microbiol*. 2023;14:1183627.

Zhu K, Ge D, Wen Z, Xia L, Yang Q. Evolutionary Genetics of Hypoxia and Cold Tolerance in Mammals. *J Mol Evol*. 2018;86(9):618-634.

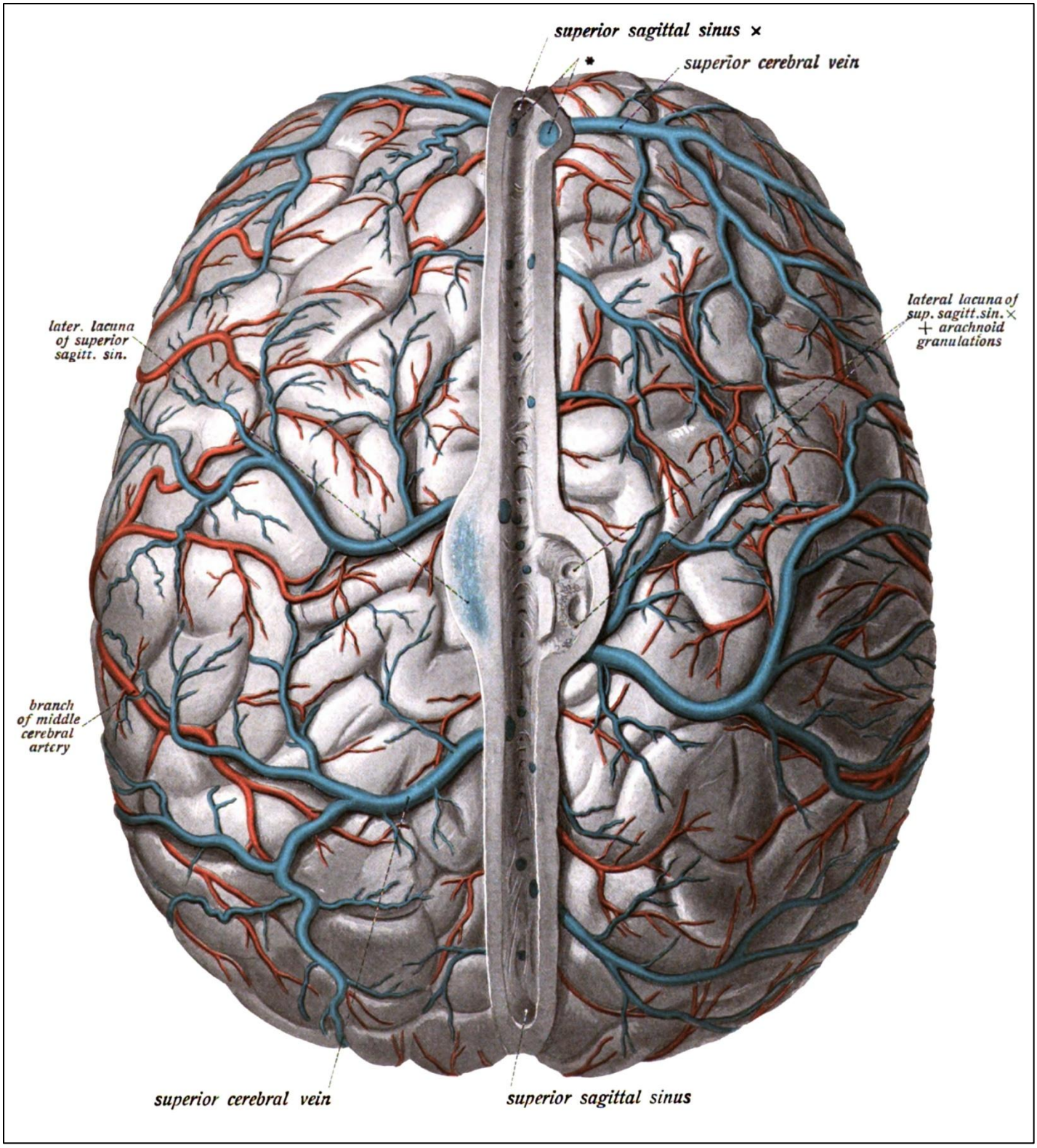
Zhang X, Liu L, Chai Y, Zhang J, Deng Q, Chen X. Reimagining the meninges from a neuroimmune perspective: a boundary, but not peripheral. *J Neuroinflammation*. 2024;21(1):299.

Zinkstok JR, Boot E, Bassett AS, et al. Neurobiological perspective of 22q11.2 deletion syndrome. *Lancet Psychiatry*. 2019;6(11):951-960.

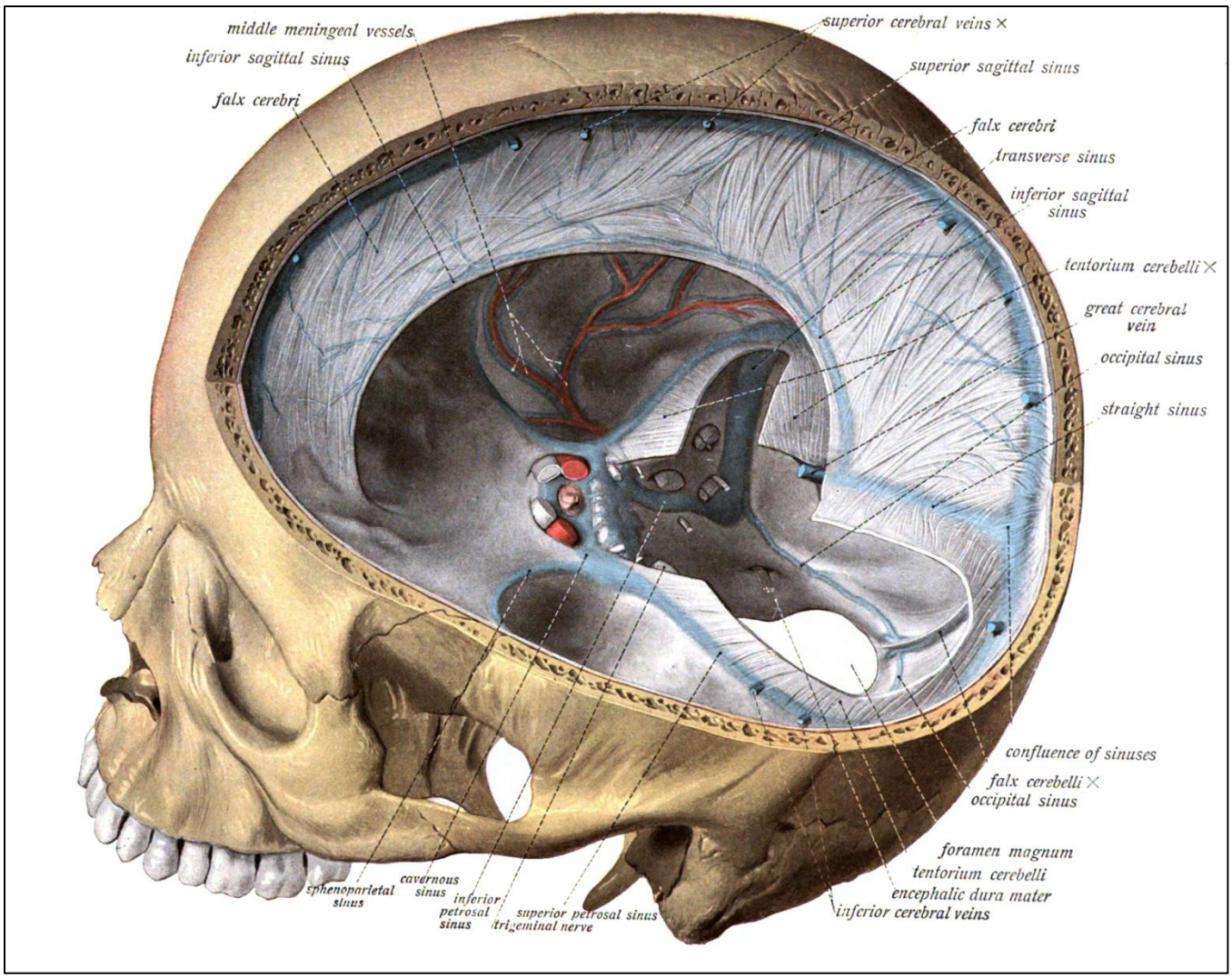
Appendix: Images



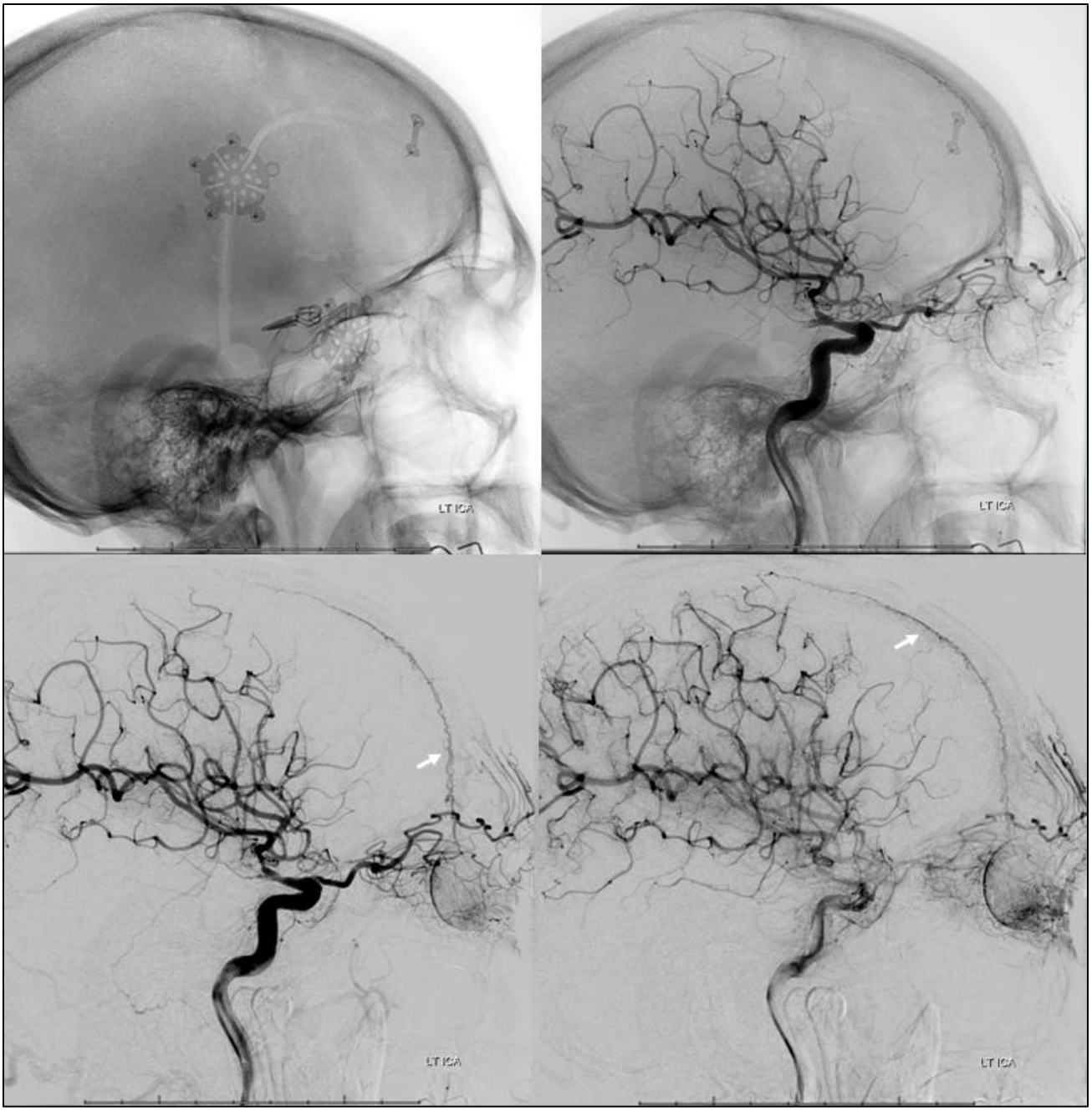
Subumbrellar (top) and cross-sectional (bottom) views of an *Aurelia* medusa. (Lawley et al, 2021).



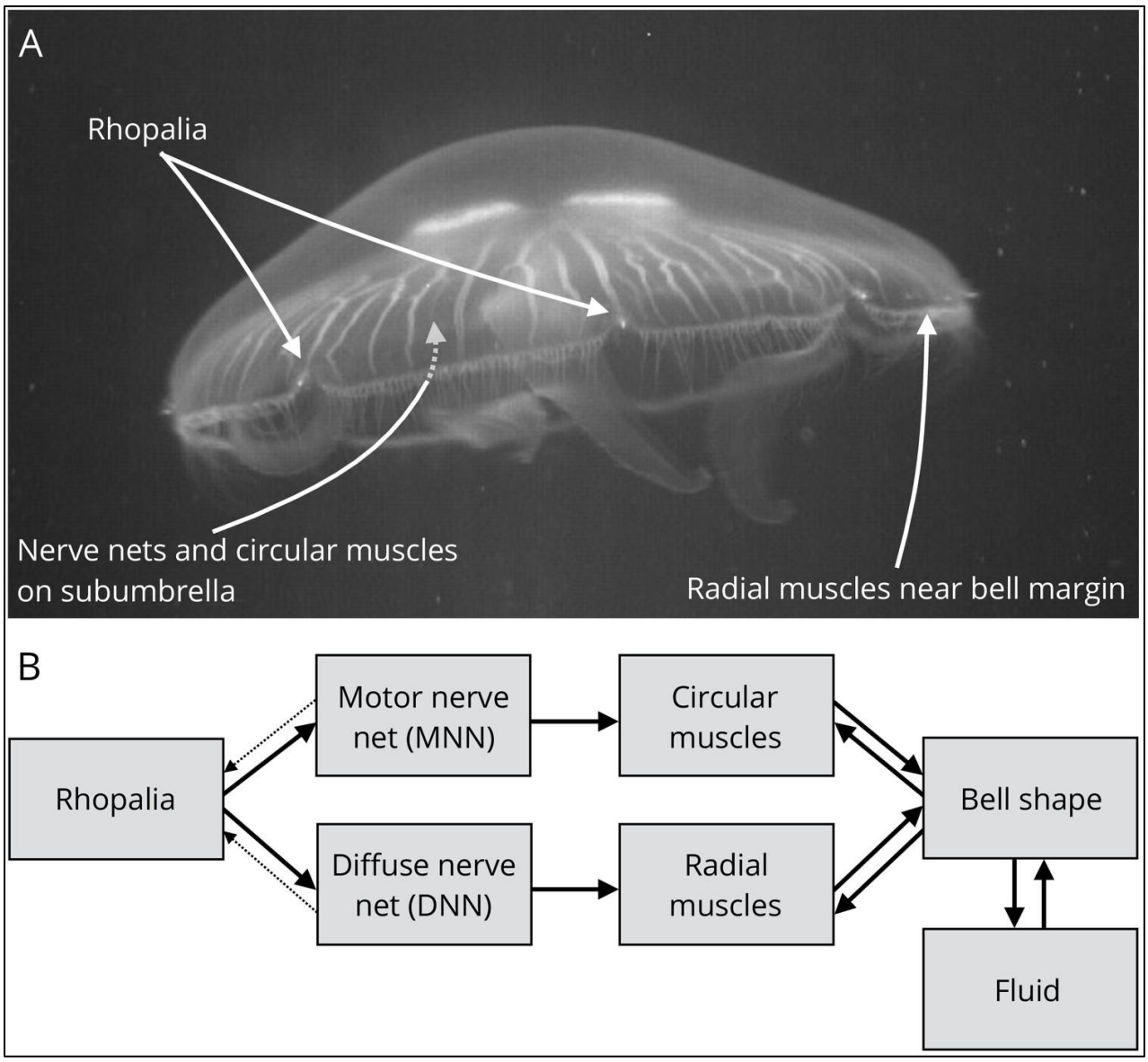
The arachnoid mater lies under the dura mater, and arteries and veins run on top of it. (Sobotta's Human Anatomy 1908).



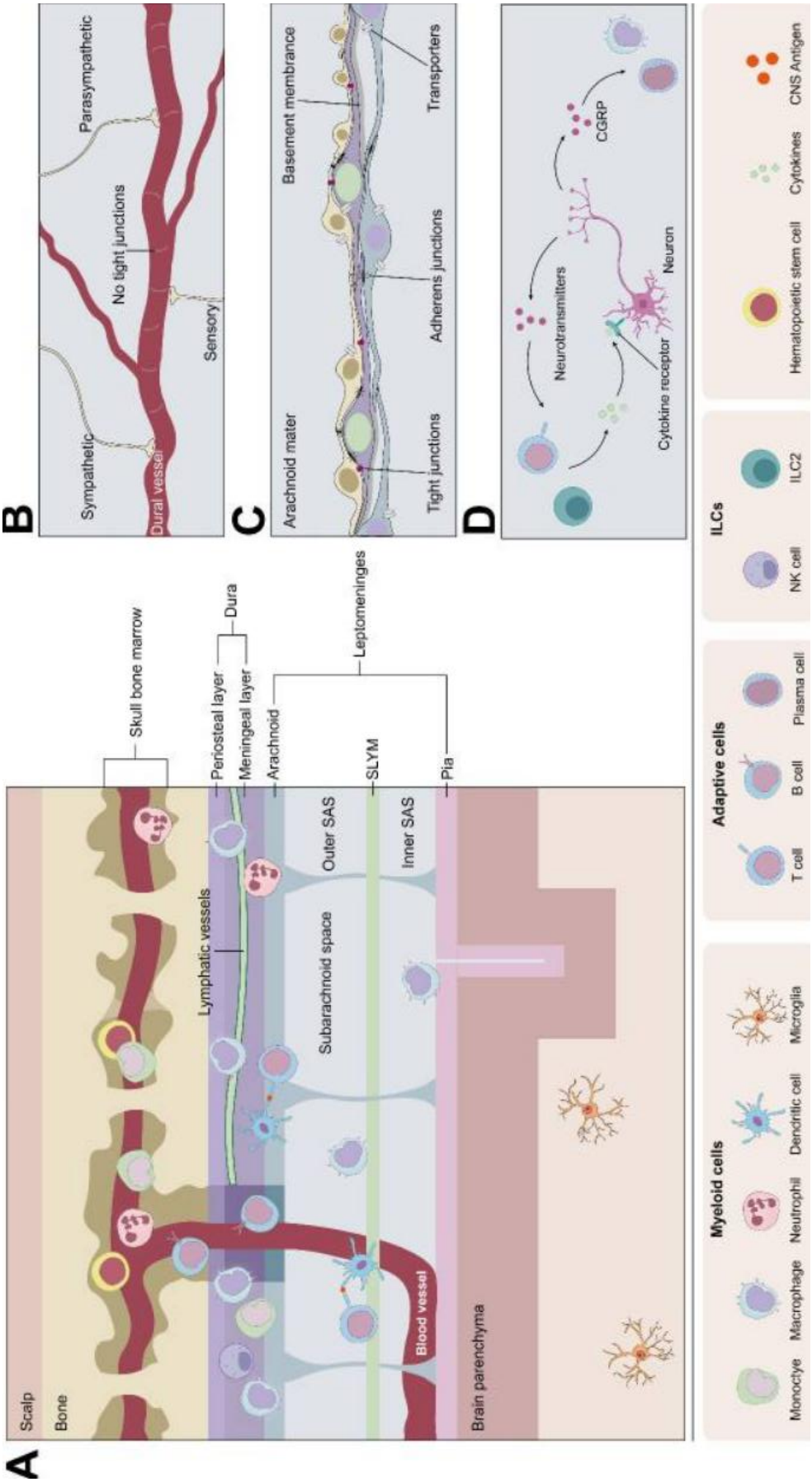
Dura mater (Sobotta's Human Anatomy 1908).



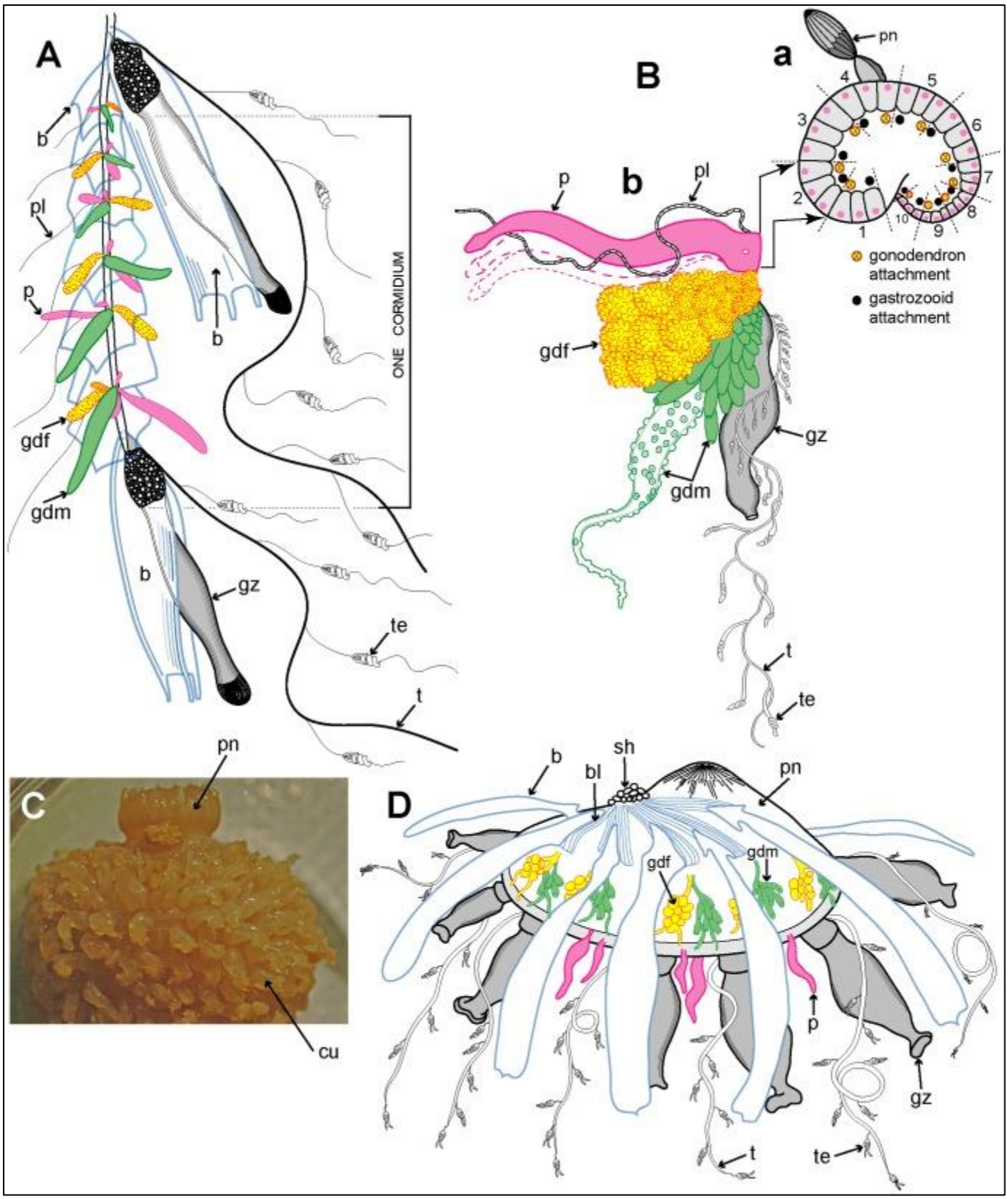
Homo sapiens Meningeal Vessels, © 2025 neuroangio.org



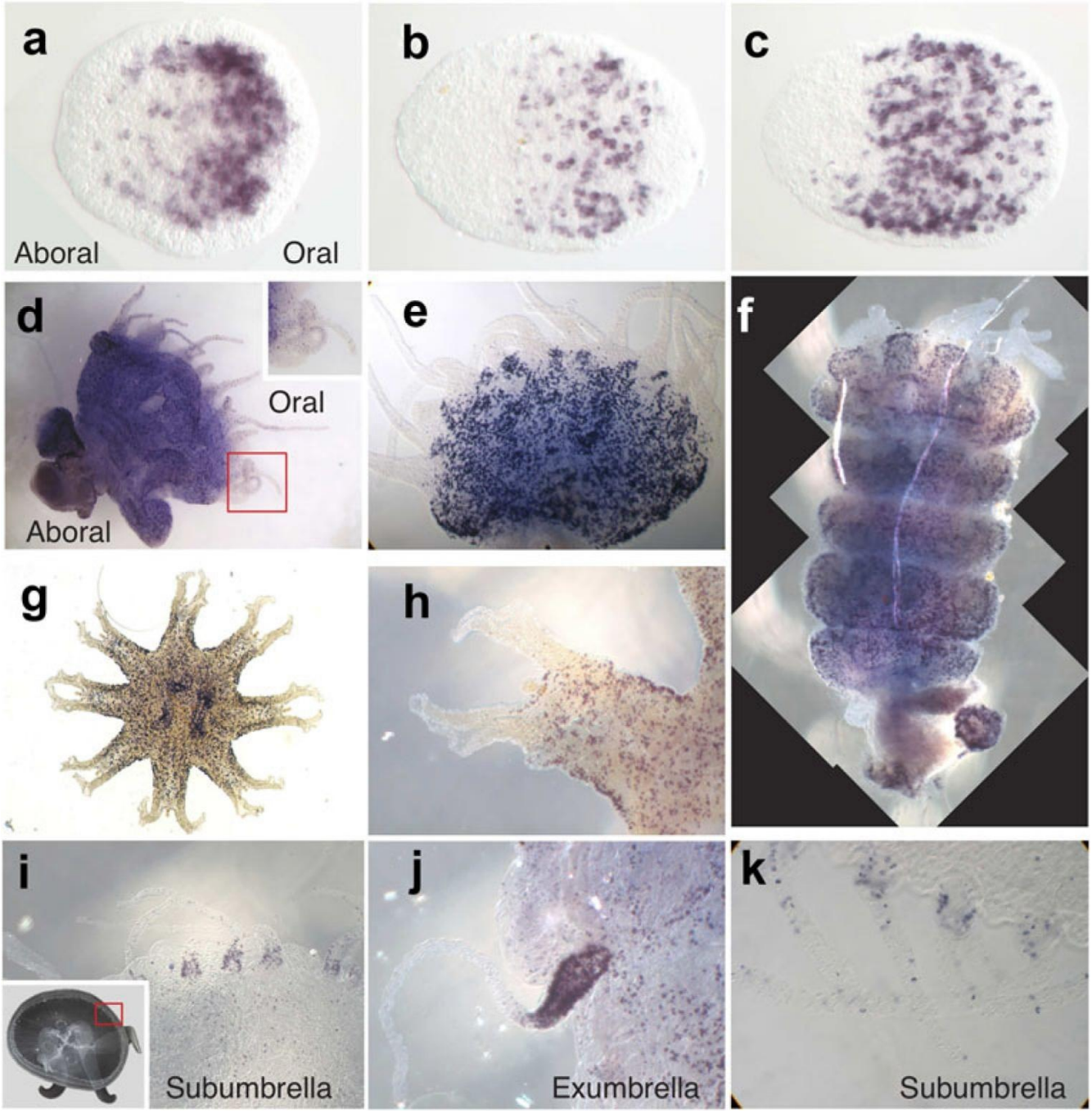
Moon jelly *Aurelia aurita* in water; jellyfish anatomy and schematic overview. (Pallasdies et al, 2019).



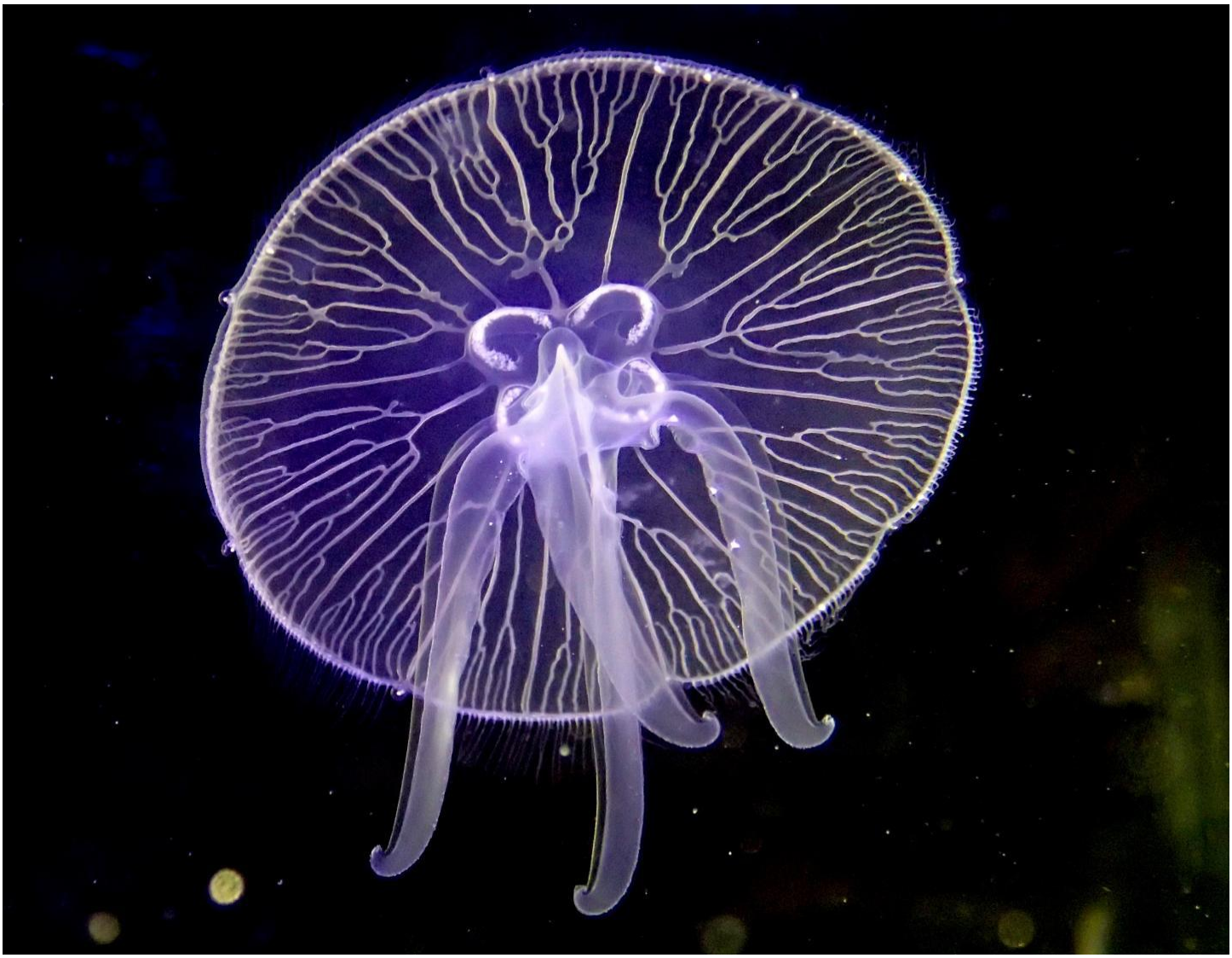
Structure and immune function of *Homo sapiens* meninges. (Zhang et al, 2024).



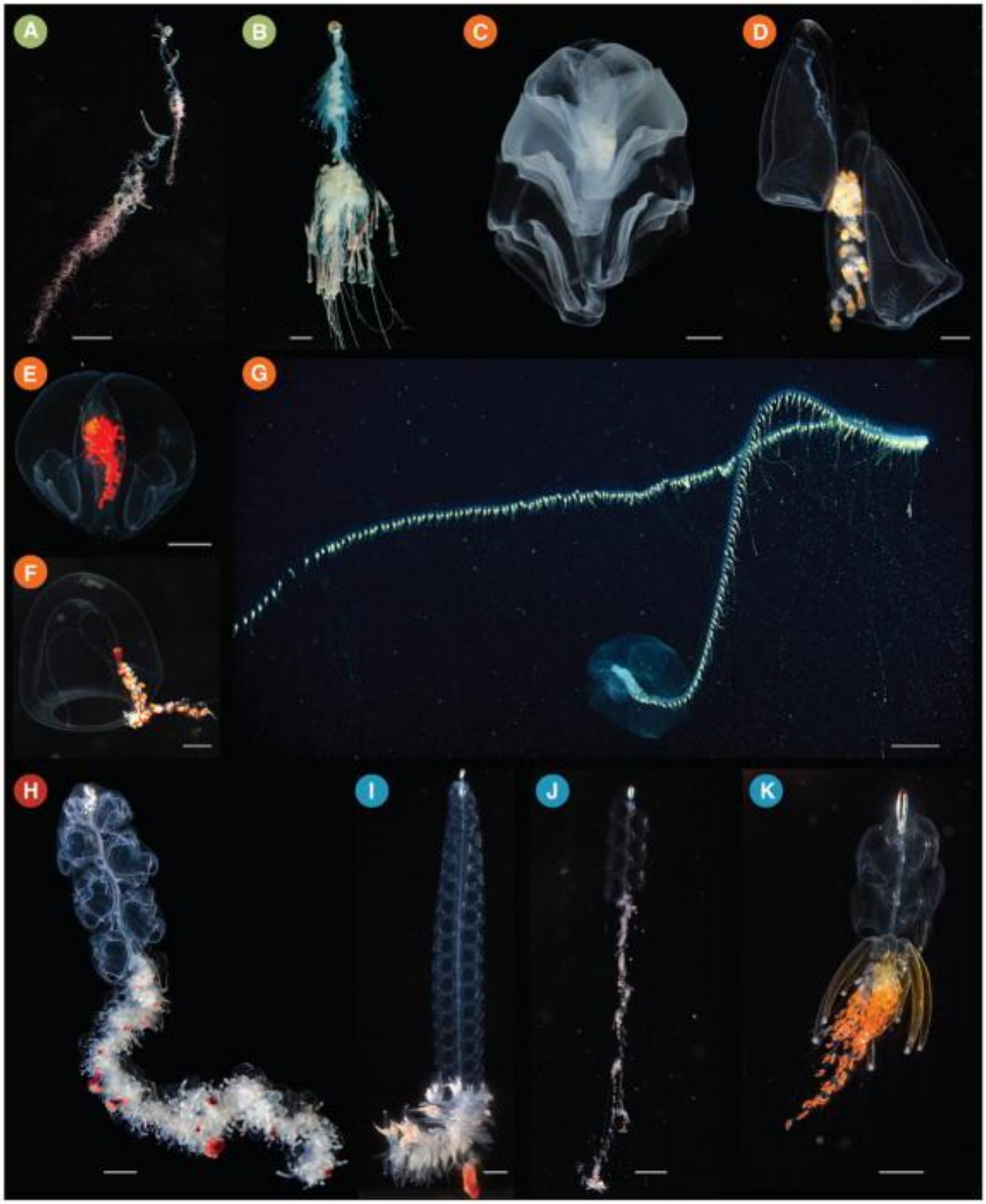
A: *Nanomia bijuga* cormidium; B: *Physophora hydrostatica;* C: *Dromalia alexandri* dorsal view of corm; D: *Athorybia rosacea* lateral view of float with siphosomal horn and attached cormidia. (Munro et al, 2019).



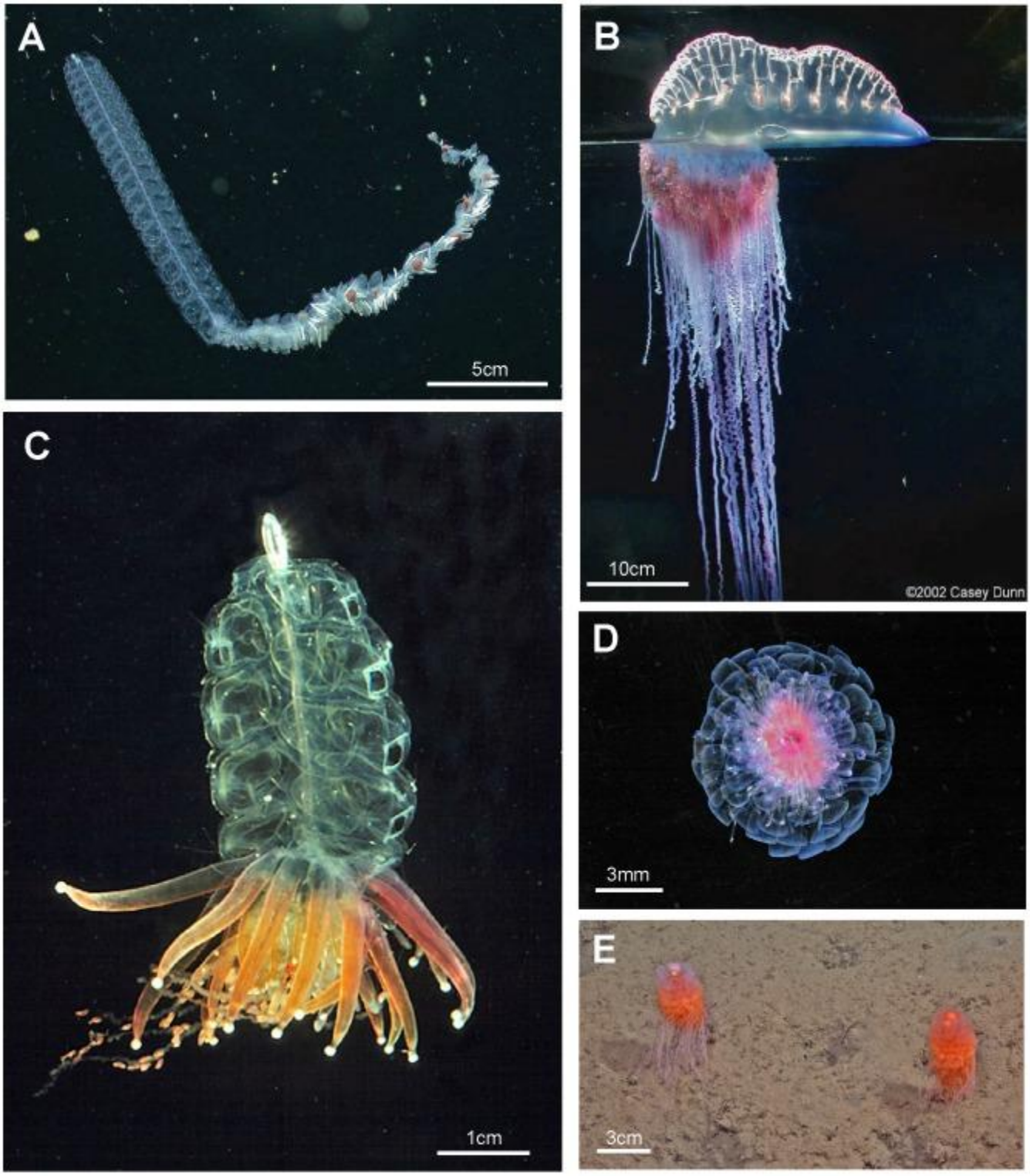
AurNcol-1 expression through the *Aurelia* life cycle, as revealed by in situ hybridization. (Gold et al, 2019).



Aurelia aurita, Copyright OIST (Okinawa Institute of Science and Technology Graduate University).



Photographs of living siphonophores; colored circles correspond to the clades. (Munro et al, 2019). *Rhizophysa* is marked (a), *Praya* is marked (g), *Apolemia* is (h), *Nanomia* is (j).



Photographs of living siphonophores. B. *Physalia physalis*. (Munro et al, 2019).