



Bases de données

- 1 - Titre
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The screenshot shows the 'Modifier Base de donnée' (Edit Database) page for 'GIGATON'. The interface includes a sidebar with navigation options like 'Tableau de bord', 'Articles', 'Médias', 'Pages', 'Commentaires', 'Bases de données', 'Evénements', 'Formations', 'Membres Mersea', 'Offres d'emploi / stages', 'Projets', 'Concours / Salonniers', 'Formations', 'Membres Mersea', 'Offres d'emploi / stages', 'Projets', 'Croniques', 'Rank Math SEO', 'Eleveur', 'Modèles', 'Éléments', 'Apparence', 'Extensions', 'Comptes', 'Outils', 'Log Elementor Kit', 'Réglages', 'AC3', 'Mon Laboratoire', 'UpdraftPlus', 'Langues', and 'Réduire le menu'. The main content area is titled 'Modifier Base de donnée' and includes a 'Ajouter une base de données' button. The database name is 'GIGATON'. The URL is 'https://mersea.unicaen.fr/bases-de-donnees/gigaton/'. The description is 'Banque de données publiques décrivant les transcriptomes de l'huître *Crossostrea gigas* (contigs de référence et niveau d'expression des transcrits dans 114 conditions : stades de développement, tissu adultes et en condition de stress). The Pacific oyster, *Crossostrea gigas*, is one of the most important aquaculture shellfish resources worldwide. Important efforts have been undertaken towards a better knowledge of its genome and transcriptome, which makes now *C. gigas* becoming a model organism among bivalve molluscs, the under-described sister clade of edyssozoans within protostomes. These massive sequencing efforts offer the opportunity to assemble gene expression data and make such resource accessible and exploitable for the scientific community. Therefore, we undertook this assembly into an up-to-date publicly available transcriptome database: the **GigaTON (Gigas TranscriptOme pipeline)** database. Description: We assembled 2204 million sequences obtained from 114 publicly available RNA-seq libraries that were realized using all embryo-larval development stages, adult organs, different environmental stressors including heavy metals, temperature, salinity and exposure to air, which were mostly performed as part of the *Crossostrea gigas* genome project. This data was analyzed *in silico* and resulted into 56621 newly assembled contigs that were deposited into a publicly available database, the GigaTON database. This database also provides powerful and user-friendly request tools to browse and retrieve information about annotation, expression level, UTRs, splice and polymorphism, and gene ontology associated to all the contigs into each, and between all libraries. Responsable scientifique : **Guillaume Rivière**, maître de conférences, Université de Caen, UMR BOREA, guillaume.riviere@unicaen.fr. The form includes fields for 'Nom contact' (Guillaume RIVIERE), 'Page du contact' (Guillaume RIVIERE), 'Lien' (<http://gigaton.unicaen.org/>), 'Image' (Ajouter image), and 'Rank Math SEO'. The sidebar on the right includes 'Monsternights', 'Publier', 'Stat : Publié Modifier', 'Visibilité : Publique Modifier', 'Publié le : 10 septembre 2024 à 15h 15 min Modifier', 'Duplicer cela', 'Lock Modified Date', 'SEO: 15 / 100', 'Mettre à la corbeille', 'Mettre à jour', 'Image mise en avant', 'Cliquez sur l'image pour la modifier ou la mettre à jour.', and 'Supprimer l'image mise en avant'.

The screenshot shows the 'GIGATON' database landing page. The header includes the 'MERSEA' logo and 'Marine Ecosystems and Organisms reSEARCH Lab'. The navigation bar includes 'LE LABORATOIRE', 'RECHERCHE', 'RÉALISATIONS', and 'NOUS REJOINDRE'. The main content area is titled 'GIGATON' and includes a 'CONTACT' button. The description is 'Banque de données publiques décrivant les transcriptomes de l'huître *Crossostrea gigas* (contigs de référence et niveau d'expression des transcrits dans 114 conditions : stades de développement, tissu adultes et en condition de stress). The Pacific oyster, *Crossostrea gigas*, is one of the most important aquaculture shellfish resources worldwide. Important efforts have been undertaken towards a better knowledge of its genome and transcriptome, which makes now *C. gigas* becoming a model organism among bivalve molluscs, the under-described sister clade of edyssozoans within protostomes. These massive sequencing efforts offer the opportunity to assemble gene expression data and make such resource accessible and exploitable for the scientific community. Therefore, we undertook this assembly into an up-to-date publicly available transcriptome database: the **GigaTON (Gigas TranscriptOme pipeline)** database. Description: We assembled 2204 million sequences obtained from 114 publicly available RNA-seq libraries that were realized using all embryo-larval development stages, adult organs, different environmental stressors including heavy metals, temperature, salinity and exposure to air, which were mostly performed as part of the *Crossostrea gigas* genome project. This data was analyzed *in silico* and resulted into 56621 newly assembled contigs that were deposited into a publicly available database, the GigaTON database. This database also provides powerful and user-friendly request tools to browse and retrieve information about annotation, expression level, UTRs, splice and polymorphism, and gene ontology associated to all the contigs into each, and between all libraries. Responsable scientifique : **Guillaume Rivière**, maître de conférences, Université de Caen, UMR BOREA, guillaume.riviere@unicaen.fr. The page includes a 'CONTACT' button, a 'LIEN EXTERNE' button, and an 'En savoir plus' button. The footer includes the 'MERSEA' logo, the 'UNICAEN' logo, and the text 'Marine Ecosystems and Organisms reSEARCH'.