

## GENOME SEQUENCING

# The Draft Genome Sequences of 50 Salamander species (Caudata, Amphibia)

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## Biodiversity Genomes

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We present partial genome sequences of 50 salamander species (Urodela) from 10 genera and 4 families. These span nearly the entire range of genome sizes in salamanders, from ~14–130GB, the latter of which is among the largest of all animal genomes. Only three salamander genomes were available to this point, from Ambystomatidae (one species) and Salamandridae (two species from two genera), to which we have added Amphiumidae (one species), Plethodontidae (45 species from 6 genera), Proteidae (one species), and Sirenidae (three species from two genera). These span ~140 million years of evolutionary divergence, leaving only Cryptobranchidae, Hynobiidae, and Rhyacotritonidae as salamander families without genome assemblies. These data should facilitate additional future work on speciation and genome evolution, both within Urodela and across Animalia.

## Methods

Tissues from single, wild-collected individuals were used for this study. Specimens were collected with relevant ethical approvals and state permits, and physical specimen vouchers were accessioned in registered natural history collections at accredited museums (Buckner et al. 2021). Notably, these include the holotypes of *Desmognathus anicetus* Pyron and Beamer 2023 and *D. valtos* Pyron and Beamer 2022a, and paratypes of *D. adatsihi* Pyron and Beamer 2022c; *D. bairdi* Pyron and Beamer 2023; *D. balsameus* Pyron and Beamer 2022c; *D. campi* Pyron and Beamer 2023; *D. cataboula* Pyron and Beamer 2023; *D. cheaha* Pyron et al. 2023; *D. kanawha* Pyron and Beamer 2022b; *D. lycos* Pyron and Beamer 2023; *D. mavrokoilius* Pyron and Beamer 2022b; *D. pascagoula* Pyron et al. 2022; and *D. tilleyi* Pyron and Beamer 2023.

DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

## Results and Data Availability

All raw read data and assembled genomes are available on Genbank:

<i>Amphiuma means</i>	JAWWEG000000000	GSU 27311
<i>Aneides aeneus</i>	JAWWEJ000000000	AMNH A-194066
<i>Desmognathus abditus</i>	JASCRC000000000	BMNH 2021.7562
<i>Desmognathus adatsihi</i>	JAUEJF000000000	NCSM 108356 (paratype)
<i>Desmognathus aeneus</i>	JASCRE000000000	BMNH 2021.7563
<i>Desmognathus amphileucus</i>	JAUCMQ000000000	MNHN-RA 2021.0156
<i>Desmognathus anicetus</i>	JAVSBX000000000	USNM 596929 (holotype)
<i>Desmognathus apalachicola</i>	JASBJ000000000	MNHN-RA 2021.0145
<i>Desmognathus aureatus</i>	JAUEJG000000000	MNHN-RA 2021.0144
<i>Desmognathus auriculatus</i>	JASBQM000000000	MNHN-RA 2021.0155
<i>Desmognathus bairdi</i>	JAVKLH000000000	MNHN-RA 2021.0132 (paratype)
<i>Desmognathus balsameus</i>	JAUBNR000000000	BMNH 2021.7526 (paratype)
<i>Desmognathus campi</i>	JAVSBW000000000	MNHN-RA 2021.0154 (paratype)
<i>Desmognathus carolinensis</i>	JASAFM000000000	MNHN-RA 2021.0126
<i>Desmognathus catahoula</i>	JAVHNH000000000	LSUMZ 129465 (paratype)
<i>Desmognathus cheaha</i>	JAUBNS000000000	AUM 45531 (paratype)
<i>Desmognathus conanti</i>	JASCRB000000000	BMNH 2021.7572
<i>Desmognathus fuscus</i>	JAUCNN000000000	AMNH A-194084
<i>Desmognathus gvnigeusgwotli</i>	JAUBNT000000000	NCSM 108359
<i>Desmognathus intermedius</i>	JAUEJH000000000	BMNH 2021.7548
<i>Desmognathus kanawha</i>	JAUBNU000000000	AMNH A-193878 (paratype)
<i>Desmognathus lycos</i>	JAWWMH000000000	NCSM 109134 (paratype)
<i>Desmognathus marmoratus</i>	JASANK000000000	MNHN-RA 2021.0120
<i>Desmognathus mavrokoilius</i>	JAUBNV000000000	AMNH A-193883 (paratype)
<i>Desmognathus monticola</i>	JASANL000000000	GMNH 52968
<i>Desmognathus ocoee</i>	JASBQK000000000	BMNH 2021.7529
<i>Desmognathus orestes</i>	JASBQG000000000	BMNH 2021.7532
<i>Desmognathus organi</i>	JASDQV000000000	MNHN-RA 2021.0124
<i>Desmognathus pascagoula</i>	JASBQL000000000	MMNS 19997 (paratype)
<i>Desmognathus perlapsus</i>	JAUEJI000000000	MNHN-RA 2021.0118
<i>Desmognathus santeetlah</i>	JASANM000000000	MNHN-RA 2021.0130
<i>Desmognathus tilleyi</i>	JAWLIA000000000	NCSM 109130 (paratype)
<i>Desmognathus valentini</i>	JASBQI000000000	MMNS 19990
<i>Desmognathus valtos</i>	JAUBNW000000000	MNHN-RA 2021.0131 (holotype)
<i>Desmognathus welteri</i>	JASCRD000000000	MNHN-RA 2021.0139
<i>Desmognathus wrighti</i>	JASBQO00000000	BMNH 2021.7561
<i>Eurycea bislineata</i>	JBCATW000000000	AMNH A-194067
<i>Eurycea cirrigera</i>	JAWWEH000000000	GSU 27312
<i>Eurycea guttolineata</i>	JAXCLM000000000	GSU 27313
<i>Eurycea paludicola</i>	JAXIUV000000000	GSU 27314
<i>Eurycea quadridigitata</i>	JAWWME000000000	GSU 27315
<i>Necturus beyeri</i>	JAWWEL000000000	GSU 27321
<i>Plethodon glutinosus</i>	JAWWVG000000000	GSU 27323
<i>Plethodon ventralis</i>	JAWWEK000000000	GSU 27322
<i>Pseudobranchius striatus</i>	JAWWMD000000000	GSU 27324
<i>Pseudotriton montanus</i>	JAXIUS000000000	GSU 27316
<i>Pseudotriton ruber</i>	JAWWEI000000000	GSU 27317
<i>Siren reticulata</i>	JAWWEF000000000	GSU 27318
<i>Siren sphagnicola</i>	JAWWMF000000000	GSU 27319
<i>Stereochilus marginatus</i>	JAVXUN000000000	GSU 27320

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