

# 1 **Genome Warehouse: A Public Repository Housing**

## 2 **Genome-scale Data**

3

4 Meili Chen<sup>1,2,#</sup>, Yingke Ma<sup>1,2,#</sup>, Song Wu<sup>1,2,3</sup>, Xinchang Zheng<sup>1,2</sup>, Hongen Kang<sup>1,2,3</sup>,  
5 Jian Sang<sup>1,2,3,†</sup>, Xingjian Xu<sup>1,2,3,††</sup>, Lili Hao<sup>1,2</sup>, Zhaohua Li<sup>1,2,3</sup>, Zheng Gong<sup>1,2,3</sup>, Jingfa  
6 Xiao<sup>1,2,3</sup>, Zhang Zhang<sup>1,2,3</sup>, Wenming Zhao<sup>1,2,3</sup>, Yiming Bao<sup>1,2,3,\*</sup>

7 <sup>1</sup> *National Genomics Data Center, Beijing Institute of Genomics, Chinese Academy of*  
8 *Sciences / China National Center for Bioinformation, Beijing 100101, China*

9 <sup>2</sup> *CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of*  
10 *Genomics, Chinese Academy of Sciences, Beijing 100101, China*

11 <sup>3</sup> *University of Chinese Academy of Sciences, Beijing 100049, China*

12

13 # Equal contribution.

14 \* Corresponding author.

15 E-mail: [baoym@big.ac.cn](mailto:baoym@big.ac.cn) (Bao Y).

16 † *Current address: Division of Cancer Epidemiology and Genetics, National Cancer*  
17 *Institute, National Institutes of Health, Bethesda, Maryland 20892, USA*

18 †† *Current address: College of Computer Science Technology, Inner Mongolia*  
19 *Normal University, Hohhot, Inner Mongolia 010010, China*

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## 36 **Abstract**

37 The Genome Warehouse (GWH) is a public repository housing genome assembly data  
38 for a wide range of species and delivering a series of web services for genome data  
39 submission, storage, release, and sharing. As one of the core resources in the National  
40 Genomics Data Center (NGDC), part of the China National Center for Bioinformation  
41 (CNCB, <https://bigd.big.ac.cn/>), GWH accepts both full genome and partial genome  
42 (chloroplast, mitochondrion, and plasmid) sequences with different assembly levels,  
43 as well as an update of existing genome assemblies. For each assembly, GWH collects  
44 detailed genome-related metadata including biological project and sample, and  
45 genome assembly information, in addition to genome sequence and annotation. To  
46 archive high-quality genome sequences and annotations, GWH is equipped with a  
47 uniform and standardized procedure for quality control. Besides basic browse and  
48 search functionalities, all released genome sequences and annotations can be  
49 visualized with JBrowse. By December 2020, GWH has received 17,264 direct  
50 submissions covering a diversity of 949 species, and has released 3370 of them.  
51 Collectively, GWH serves as an important resource for genome-scale data  
52 management and provides free and publicly accessible data to support research  
53 activities throughout the world. GWH is publicly accessible at  
54 <https://bigd.big.ac.cn/gwh/>.

55

56 **KEYWORDS:** Genome submission; Genome sequence; Genome annotation;  
57 Genome warehouse; Quality control

58

## 59 **Introduction**

60 Genome sequences and annotations are fundamental information for a wide range of  
61 genome-related studies, including various omics data analysis such as genome [1],  
62 transcriptome [2], epigenome [3,4], and genome variation [5,6]. China, as one of the  
63 most biodiverse countries in the world, harbors more than 10% of the world's known  
64 species [7]. In the past decades, a large number of genome assemblies of featured and  
65 important animals and crops in China have been sequenced [1, 8–11], most of which  
66 were submitted to International Nucleotide Sequence Database Collaboration (INSDC)  
67 members (National Center for Biotechnology Information (NCBI), European  
68 Bioinformatics Institute (EBI), and DNA Data Bank of Japan (DDBJ)) [12]. With the  
69 rapid growth of genome assembly data, in China for example, large genome data size,  
70 slow data transfer rate due to limited international network transfer bandwidth, and  
71 language barrier for communication of technical issues have obstructed researchers  
72 from efficiently submitting their data to INSDC members. All these call for a  
73 centralized genomic data repository within China to complement the INSDC.

74 Here, we report the Genome Warehouse (GWH, <https://bigd.big.ac.cn/gwh/>), a  
75 centralized resource housing genome assembly data and delivering a series of genome  
76 data services. As one of the core resources in the National Genomics Data Center  
77 (NGDC), part of the China National Center for Bioinformation (CNCB,  
78 <https://bigd.big.ac.cn/>) [13], the aim of GWH is to accept data submissions worldwide  
79 and provide an important resource for genome data quality control, data archive, rapid  
80 release, and public sharing (*e.g.*, with INSDC) in support of research activities from  
81 all over the world. To date, GWH has received a total of 12,366 genome submissions  
82 (including 14 international submissions), demonstrating its increasingly important role  
83 in global genome data management and sharing.

## 84 **Data model**

85 Designed for compatibility with the INSDC data model, each genome assembly in  
86 GWH is linked to a BioProject (<https://bigd.big.ac.cn/bioproject>) and a BioSample  
87 (<https://bigd.big.ac.cn/biosample>), which are two fundamental resources for metadata

88 description in CNCB-NGDC. Full or partial (chloroplast, mitochondrion, and plasmid)  
89 genome assemblies with different assembly levels (complete, draft in chromosome,  
90 scaffold, and contig) are all acceptable and existing genome assemblies are allowed to  
91 be updated. Accession numbers are assigned with the following rules (**Figure 1**): (1)  
92 each genome assembly has an accession number prefixed with "GWH", followed by  
93 four capital letters and eight zeros (*e.g.*, GWHAAAA00000000); (2) genome  
94 sequences have the same accession number format as their corresponding genome  
95 assembly, with the exception that the eight digits start from 00000001 and increase in  
96 order (*e.g.*, GWHAAAA00000001); (3) genes have similar accession pattern as those  
97 of genome sequences, with the addition of letter "G" between the GWH prefix and the  
98 four capital letters, and there are six digits at the end instead of eight (*e.g.*,  
99 GWHGAAAA000001); (4) transcripts use the letter "T" to replace "G" in accession  
100 numbers for genes (*e.g.*, GWHTAAAA000001); (5) proteins use the letter "P" to  
101 replace "G" in accession numbers for genes (*e.g.*, GWHPAAAA000001); (6) if the  
102 submission is an update of existing submission in GWH, it will be assigned a dot and  
103 an incremental number to represent the version (*e.g.*, GWHAAAA00000000.1).

## 104 **Database components**

105 GWH is a centralized resource housing genome-scale data, with the purpose to  
106 archive high-quality genome sequences and annotation information. GWH is  
107 equipped with a series of web services for genome data submission, release, and  
108 sharing, accordingly involving three major components, namely, data submission,  
109 quality control, and archive and release (Figure 2).

## 110 **Data submission**

111 GWH not only accepts genome assembly associated data through an on-line  
112 submission system but also allows off-line batch submissions. Users need to register  
113 first and then to provide complete description on submitted genome sequences.  
114 Biological project and sample information should be provided (through BioProject  
115 and BioSample, respectively) together with genome assembly sequence, annotation,  
116 and associated metadata. Metadata mainly consist of a variety of information about

117 submitter, general assembly, file(s), sequence assignment, and publication (if  
118 available). After submission, GWH runs an automated quality control pipeline to  
119 check the validity and consistency of submitted genome sequence and genome  
120 annotation files. Accession numbers are assigned to assemblies and sequences upon  
121 the pass of quality control. The updated assembly data can also be submitted to GWH.  
122 It should be noted that compatible with the INSDC members (*e.g.*, NCBI GenBank), it  
123 is the responsibility of the submitters to ensure the data quality, completeness, and  
124 consistency and GWH does not warrant or assume any legal liability or responsibility  
125 for the data accuracy.

### 126 **Quality control**

127 After metadata and file(s) are received, GWH automatically runs standardized quality  
128 control (QC) to check 45 different types of errors in submitted genome sequences and  
129 annotations, and to scan for contaminated genome sequences (see details at  
130 <https://bigd.big.ac.cn/gwh/documents>) if needed (Figure 2), which roughly falls into 5  
131 QC steps: (1) The component will check the consistency of file(s) according to  
132 filename and md5 code. (2) For genome sequences, the component will check the  
133 legality of genome sequence ID and sequence content, *e.g.*, unique sequence ID,  
134 sequence composition (A/T/C/G or degenerate base), sequence length ( $\geq 200$  bp). (3)  
135 For genome annotations, the component will check gene structure completeness and  
136 consistency, *e.g.*, unique ID, a exon/CDS/UTR coordinate falling within the  
137 corresponding gene coordinate, strand consistency for all features (including  
138 gene/transcript/exon/CDS/UTR), codon validity (*e.g.*, valid start/stop codon, no  
139 internal stop codon). (4) Finally, it will check the internal consistency of genome  
140 sequence and annotation, *e.g.*, sequence ID in genome annotation must match genome  
141 sequence ID, a feature coordinate falling within the range of the corresponding  
142 genome sequence. (5) Genome sequences will also be scanned to check vectors,  
143 adaptors, primers, and indices (collected from UniVec database,  
144 <ftp://ftp.ncbi.nlm.nih.gov/pub/UniVec/>) using NCBI's VecScreen  
145 (<https://www.ncbi.nlm.nih.gov/tools/vecscreen/>). If there is an error, a report will be

146 automatically sent to the submitter by email. To finish a successful submission, the  
147 submitter needs to fix all errors and resubmit files until they pass the QC process.

#### 148 **Archive and release**

149 GWH will assign a unique accession number to the submitted genome assembly upon  
150 the pass of quality control, allot accession numbers for each genome sequence, gene,  
151 transcript, and protein, generate and backup downloadable files of genome sequence  
152 and annotation in FASTA, GFF3, and TSV formats. Data generation is performed  
153 with in-house-writing scripts based on submitted genome sequence and annotation  
154 files. In order to ensure the security of submitted data, a copy of backup data is stored  
155 on a physically separate disk. GWH will release sequence data on a user-specified  
156 date, unless a paper citing the sequence or accession number is published prior to the  
157 specified release date, in which case the sequence will be released immediately. For  
158 the released data, GWH will generate web pages containing two primary tables:  
159 genome and assembly. The former shows species taxonomy information and genome  
160 assemblies, and the latter contains general information of the assembly (including  
161 external links to other related resources), statistics of genome assembly and its  
162 corresponding annotation. All released data are publicly available at GWH FTP site  
163 (<ftp://download.big.ac.cn/gwh/>). GWH provides data visualization for both genome  
164 sequence and genome annotation using JBrowse [14]. It offers statistics and charts in  
165 light of total holdings, assembly levels, genome representations, citing articles,  
166 submitting organizations, sequencing platforms, assembly methods, and downloads.  
167 GWH provides user-friendly web interfaces for data browse and query using BIG  
168 Search [13], in order to help users find any released data of interest. For a released  
169 genome assembly, GWH also provides machine-readable APIs (Application  
170 Programming Interfaces) for publicly sharing and automatically obtaining information  
171 on its associated BioProject, BioSample, genome, and assembly metadata and file  
172 paths.

## 173 **Global sharing of SARS-CoV-2 and coronavirus genomes**

174 During the COVID-19 outbreak, GWH, in support of the 2019 Novel Coronavirus  
175 Resource (2019nCoV) [15, 16] has received worldwide submissions of more than a  
176 thousand SARS-CoV-2 genome assemblies with standardized genome annotations  
177 [17], and has released 134 of them. To expand the international influence of data, 62  
178 of the released sequences have been shared, with the submitters' permission, in  
179 GenBank [18] through a data exchange mechanism established with NCBI. In this  
180 model, GWH accessions are represented as secondary accessions in NCBI GenBank  
181 records, which are retrievable by the NCBI Entrez system. This model sets a good  
182 example for data sharing among different data centers.

183 In addition, GWH offers sequences of the Coronaviridae family to facilitate  
184 researchers to reach the data conveniently and thus to study the relationship between  
185 SARS-CoV-2 and other coronaviruses. To promote the data sharing and make all  
186 relevant information of the Coronaviridae readily available, GWH integrates genomic  
187 and proteomic sequences as well as their metadata information from NCBI [19],  
188 China National GeneBank Database (CNCBdb) [20], National Microbiology Data  
189 Center (NMDC) [21] and CNCB-NGDC. Duplicated records from different sources  
190 are identified and removed to gain a non-redundant dataset. As of December 31, 2020,  
191 the dataset has 83,095 nucleotide and 575,438 protein sequences of the Coronaviridae.  
192 Filters are implemented to narrow down the required Coronaviridae sequences using  
193 multiple conditions, including country/region, host, isolation source, length, and  
194 collection date. Both the metadata and sequences of the filtered results can be selected  
195 and downloaded as a separate file. The daily updated sequences and all sequences can  
196 also be downloaded from FTP  
197 (<ftp://download.big.ac.cn/Genome/Viruses/Coronaviridae/>).

## 198 **Data statistics**

199 By December, 2020, GWH has received 17,264 direct submissions covering a broad  
200 diversity of species (**Table 1**) with different assembly levels (Figure 3). These  
201 genome assemblies link to 301 BioProjects and 16,538 BioSamples, and are



202 submitted by 231 submitters from 61 institutions (including 5 international submitters  
203 from 2 countries). There are a total of 3370 released submissions, which were  
204 reported in 83 articles from 44 journals. GWH has over 135,000 visits from 153  
205 countries/regions, with ~891,000 downloads. The amount of data, visits, and  
206 downloads in the GWH has been on the dramatic increase over the past years, clearly  
207 showing its great utility in genome-scale data management.

## 208 **Summary and future directions**

209 Collectively, GWH is a user-friendly portal for genome data submission, release, and  
210 sharing associated with a matched series of services. The rapid growth of genome  
211 assembly submissions demonstrates the great potential of GWH as an important  
212 resource for accelerating the worldwide genomic research. With the aim to fully  
213 realize the findability, accessibility, interoperability, and reusability (FAIR) of  
214 genome data [22], GWH has made ongoing efforts, including but not limited to,  
215 improvement of web interfaces for data submission, presentation, and visualization,  
216 continuous integration of newly sequenced genomes, and development of useful  
217 online tools to help users analyse genome data (such as BLAST [23]). Therefore, we  
218 will put in more efforts to provide genome annotation services, especially for bacteria  
219 and archaea genomes, with the particular consideration that uniform standardized  
220 annotation determines the accuracy of downstream data analysis. Besides, we will  
221 expand the Coronaviridae dataset to other important pathogens to improve the ability  
222 of public health emergency response. Finally, we plan to share and exchange all  
223 public genome assembly data with the INSDC members to provide comprehensive  
224 data for researchers globally.

## 225 **CRedit author statement**

226 **Meili Chen:** Methodology, Software, Investigation, Data Curation, Writing - Original  
227 Draft, Project administration. **Yingke Ma:** Software, Writing - Original Draft. **Song**  
228 **Wu:** Software, Data Curation. **Xinchang Zheng:** Data Curation. **Hongen Kang:**  
229 Software. **Jian Sang:** Investigation, Data Curation. **Xingjian Xu:** Software. **Lili Hao:**  
230 Investigation. **Zhaohua Li:** Data Curation. **Zheng Gong:** Data Curation. **Jingfa Xiao:**

231 Writing - Review & Editing. **Zhang Zhang:** Writing - Review & Editing. **Wenming**  
232 **Zhao:** Writing - Review & Editing. **Yiming Bao:** Conceptualization, Writing -  
233 Review & Editing, Supervision.

### 234 **Competing interests**

235 The authors have declared no competing interests.

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253 Chinese Academy of Sciences [153F11KYSB20160008 to ZZ].

### 254 **ORCID**

255 ORCID: 0000-0003-0102-0292 (Chen Meili)

256 ORCID: 0000-0002-9460-4117 (Ma Yingke)

257 ORCID: 0000-0002-0923-639X (Wu Song)

258 ORCID: 0000-0001-5739-861X (Zheng Xinchang)

259 ORCID: 0000-0002-9581-1329 (Kang Hongen)

- 260 ORCID: 0000-0003-4953-3417 (Sang Jian)
- 261 ORCID: 0000-0002-4466-3821 (Xu Xingjian)
- 262 ORCID: 0000-0003-3432-7151 (Hao Lili)
- 263 ORCID: 0000-0002-2673-0103 (Li Zhaohua)
- 264 ORCID: 0000-0001-7285-2630 (Gong Zheng)
- 265 ORCID: 0000-0002-2835-4340 (Xiao Jingfa)
- 266 ORCID: 0000-0001-6603-5060 (Zhang Zhang)
- 267 ORCID: 0000-0002-4396-8287 (Zhao Wenming)
- 268 ORCID: 0000-0002-9922-9723 (Bao Yiming)
- 269
- 270

## 271 **References**

- 272 [1] Liu Y, Du H, Li P, Shen Y, Peng H, Liu S, et al. Pan-genome of wild and  
273 cultivated soybeans. *Cell* 2020;182:162-76.e13.
- 274 [2] Guan Y, Chen M, Ma Y, Du Z, Yuan N, Li Y, et al. Whole-genome and  
275 time-course dual RNA-Seq analyses reveal chronic pathogenicity-related gene  
276 dynamics in the ginseng rusty root rot pathogen *Ilyonectria robusta*. *Sci Rep*  
277 2020;10:1586.
- 278 [3] Li R, Liang F, Li M, Zou D, Sun S, Zhao Y, et al. MethBank 3.0: a database of  
279 DNA methylomes across a variety of species. *Nucleic Acids Res* 2018;46:D288–D95.
- 280 [4] Xiong Z, Li M, Yang F, Ma Y, Sang J, Li R, et al. EWAS Data Hub: a resource of  
281 DNA methylation array data and metadata. *Nucleic Acids Res* 2020;48:D890–D5.
- 282 [5] Song S, Tian D, Li C, Tang B, Dong L, Xiao J, et al. Genome Variation Map: a  
283 data repository of genome variations in BIG Data Center. *Nucleic Acids Res*  
284 2018;46:D944–D9.
- 285 [6] Tang B, Zhou Q, Dong L, Li W, Zhang X, Lan L, et al. iDog: an integrated  
286 resource for domestic dogs and wild canids. *Nucleic Acids Res* 2019;47:D793–D800.
- 287 [7] McBeath J, McBeath JH. Biodiversity conservation in China: policies and practice.  
288 *Journal of International Wildlife Law & Policy* 2006;9:293–317.
- 289 [8] Fan H, Wu Q, Wei F, Yang F, Ng BL, Hu Y. Chromosome-level genome  
290 assembly for giant panda provides novel insights into Carnivora chromosome  
291 evolution. *Genome Biol* 2019;20:267.
- 292 [9] Xia Q, Zhou Z, Lu C, Cheng D, Dai F, Li B, et al. A draft sequence for the  
293 genome of the domesticated silkworm (*Bombyx mori*). *Science* 2004;306:1937–40.
- 294 [10] Lin T, Xu X, Ruan J, Liu SZ, Wu SG, Shao XJ, et al. Genome analysis of  
295 *Taraxacum kok-saghyz* Rodin provides new insights into rubber biosynthesis. *Natl Sci*  
296 *Rev* 2018;5:78–87.
- 297 [11] Li C, Song W, Luo Y, Gao S, Zhang R, Shi Z, et al. The HuangZaoSi maize  
298 genome provides insights into genomic variation and improvement history of maize.  
299 *Mol Plant* 2019;12:402–9.
- 300 [12] Arita M, Karsch-Mizrachi I, Cochrane G. The international nucleotide sequence  
301 database collaboration. *Nucleic Acids Res* 2021;49:D121–D4.
- 302 [13] Members C-N, Partners. Database resources of the National Genomics Data  
303 Center, China National Center for Bioinformatics in 2021. *Nucleic Acids Res*  
304 2021;49:D18–D28.
- 305 [14] Buels R, Yao E, Diesh CM, Hayes RD, Munoz-Torres M, Helt G, et al. JBrowse:  
306 a dynamic web platform for genome visualization and analysis. *Genome Biol*  
307 2016;17:66.
- 308 [15] Zhao WM, Song SH, Chen ML, Zou D, Ma LN, Ma YK, et al. The 2019 novel  
309 coronavirus resource. *Yi Chuan* 2020;42:212–21.
- 310 [16] Song S, Ma L, Zou D, Tian D, Li C, Zhu J, et al. The global landscape of  
311 SARS-CoV-2 genomes, variants, and haplotypes in 2019nCoV. *Genomics,*  
312 *Proteomics & Bioinformatics* 2020. [DOI: <https://doi.org/10.1016/j.gpb.2020.09.001>]

- 313 [17] Shean RC, Makhsous N, Stoddard GD, Lin MJ, Greninger AL. VAPiD: a  
314 lightweight cross-platform viral annotation pipeline and identification tool to facilitate  
315 virus genome submissions to NCBI GenBank. *BMC Bioinformatics* 2019;20:48.
- 316 [18] Sayers EW, Cavanaugh M, Clark K, Ostell J, Pruitt KD, Karsch-Mizrachi I.  
317 GenBank. *Nucleic Acids Res* 2020;48:D84–D6.
- 318 [19] Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, et al. Database  
319 resources of the National Center for Biotechnology Information. *Nucleic Acids Res*  
320 2021;49:D10–D7.
- 321 [20] Chen FZ, You LJ, Yang F, Wang LN, Guo XQ, Gao F, et al. CNGBdb: China  
322 National GeneBank DataBase. *Yi Chuan* 2020;42:799–809.
- 323 [21] Wu L, Sun Q, Desmeth P, Sugawara H, Xu Z, McCluskey K, et al. World data  
324 centre for microorganisms: an information infrastructure to explore and utilize  
325 preserved microbial strains worldwide. *Nucleic Acids Res* 2017;45:D611–D8.
- 326 [22] Zhang Z, Song S, Yu J, Zhao W, Xiao J, Bao Y. The elements of data sharing.  
327 *Genomics Proteomics Bioinformatics* 2020;18:1–4.
- 328 [23] Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, et al.  
329 Gapped BLAST and PSI-BLAST: a new generation of protein database search  
330 programs. *Nucleic Acids Res* 1997;25:3389–402.
- 331

332 **Figure legends**

333 **Figure 1 Data model in GWH**

334 Genome assembly accession number is prefixed with "GWH", followed by four  
335 capital letters (represented by XXXX) and 8 zeros. For genome sequence accessions,  
336 eight digits increase in order. For gene sequence, transcript sequence, and protein  
337 sequence accessions, G, T, and P are followed by the GWH prefix, respectively, with  
338 six digits at the end that increase in order.

339 **Figure 2 Major components in GWH data processing workflow**

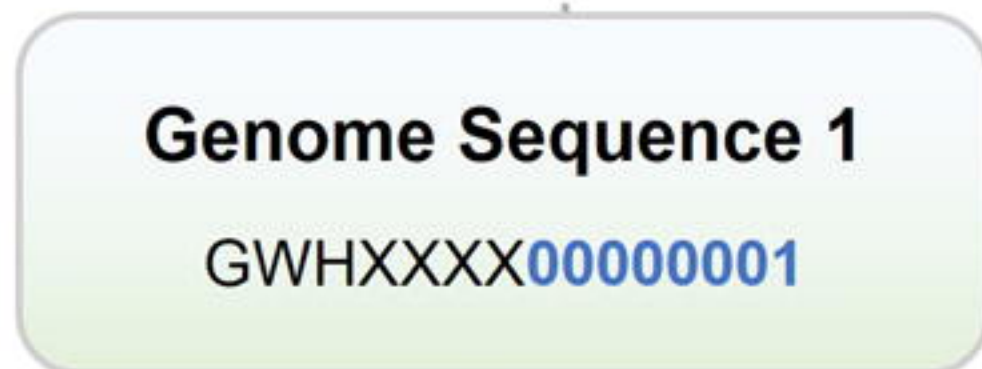
340 **Figure 3 Statistics of genome assembly in GWH (as of December 31, 2020)**

341 **Tables**

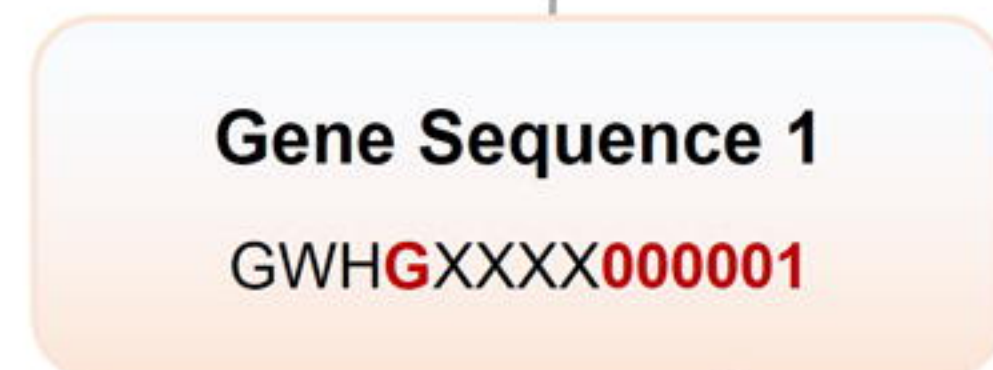
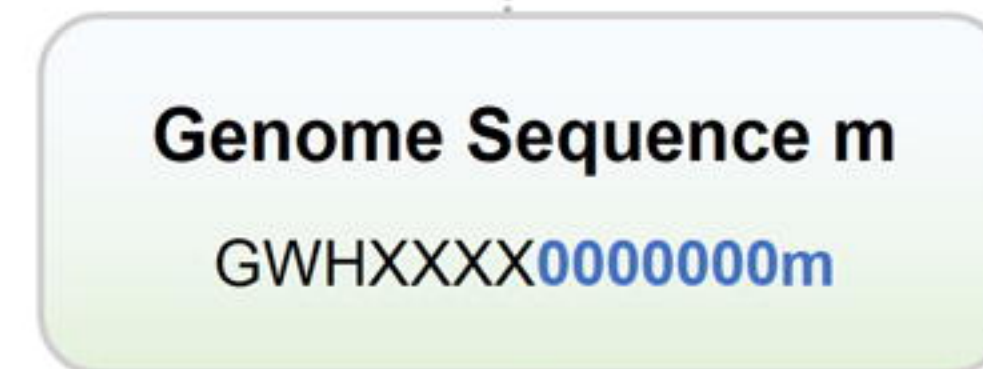
342 **Table 1 Total data holdings in GWH**

Status	Type	Animals	Plants	Fungi	Bacteria	Archaea	Viruses	Metagenomes	Others	Total
<b>Released</b>	Assembly	187 (5.55%)	210 (6.23%)	13 (0.39%)	220 (6.53%)	73 (2.17%)	701 (20.80%)	1957 (58.07%)	9 (0.27%)	3370
	Species	72 (19.41%)	139 (37.47%)	12 (3.23%)	106 (28.57%)	11 (2.96%)	19 (5.12%)	3 (0.81%)	9 (2.43%)	371
<b>Unpublic</b>	Assembly	6783 (48.82%)	926 (6.66%)	5 (0.04%)	68 (0.49%)	13 (0.09%)	939 (6.76%)	4702 (33.84%)	458 (3.30%)	13,894
	Species	22 (3.67%)	549 (91.50%)	5 (0.83%)	7 (1.17%)	2 (0.33%)	6 (1.00%)	5 (0.83%)	4 (0.67%)	600
<b>Total</b>	Assembly	6970 (40.37%)	1136 (6.58%)	18 (0.10%)	288 (1.67%)	86 (0.50%)	1640 (9.50%)	6659 (38.57%)	467 (2.71%)	17,264
	Species	92 (9.69%)	675 (71.13%)	16 (1.69%)	110 (11.59%)	13 (1.37%)	24 (2.53%)	7 (0.74%)	12 (1.26%)	949

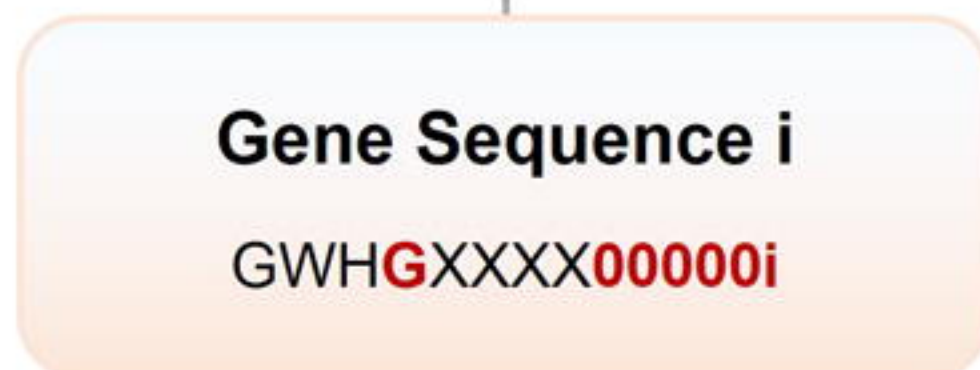
343



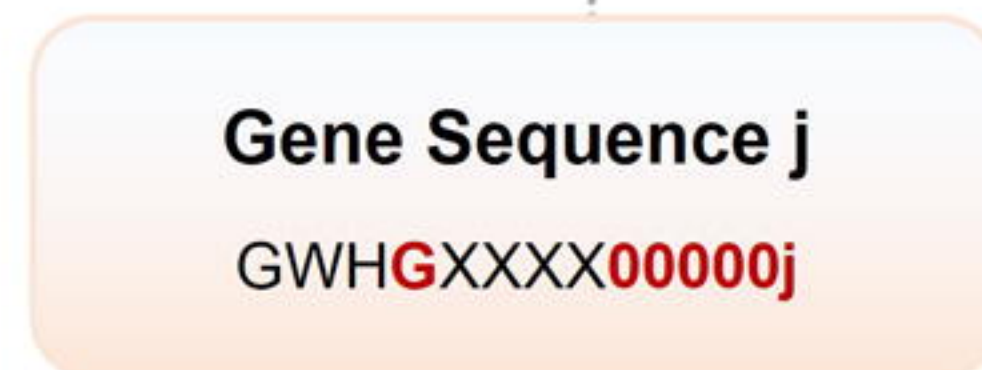
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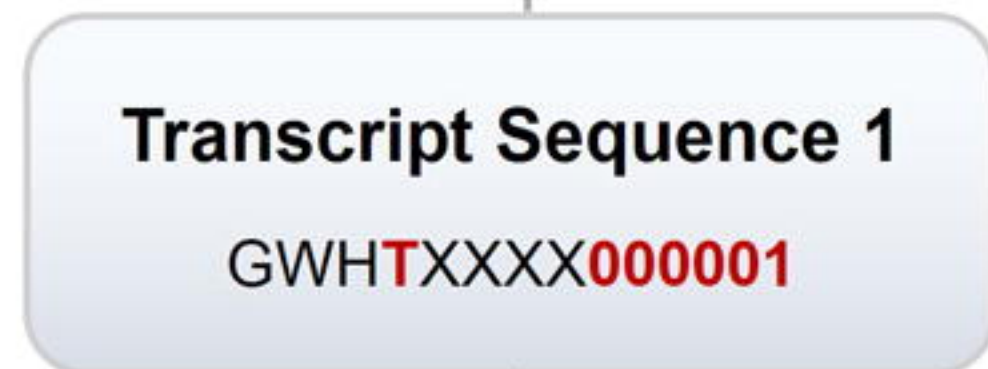
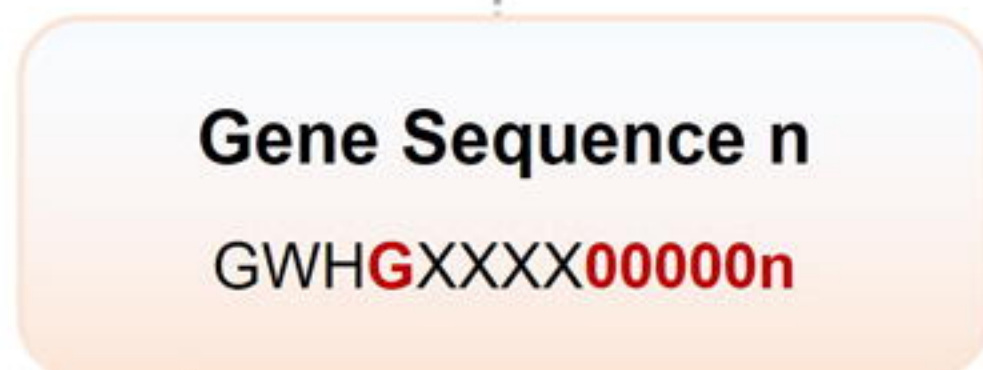
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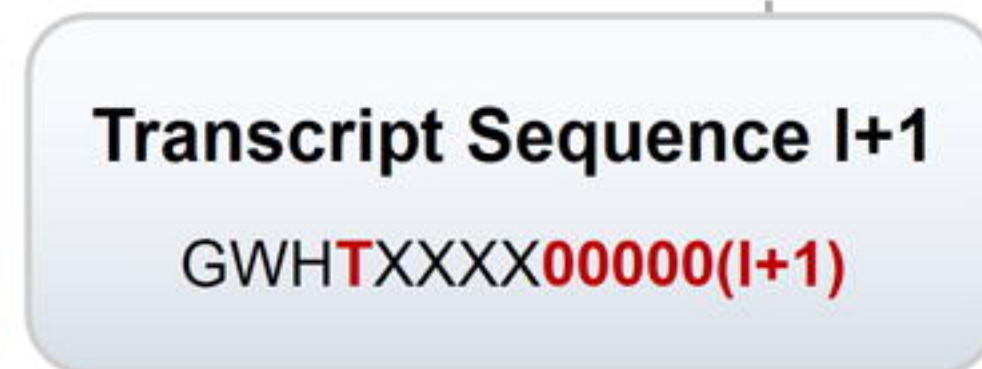
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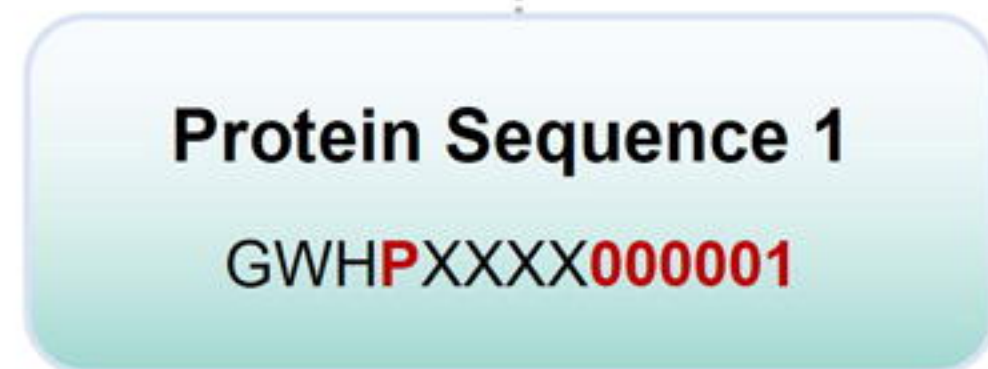
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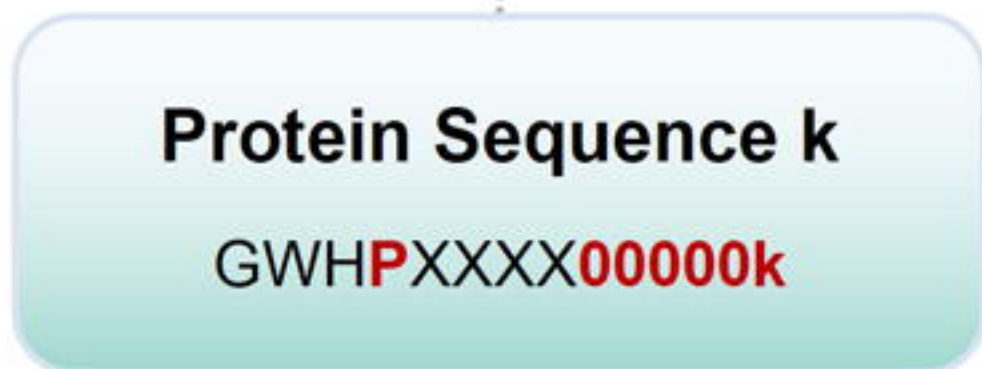
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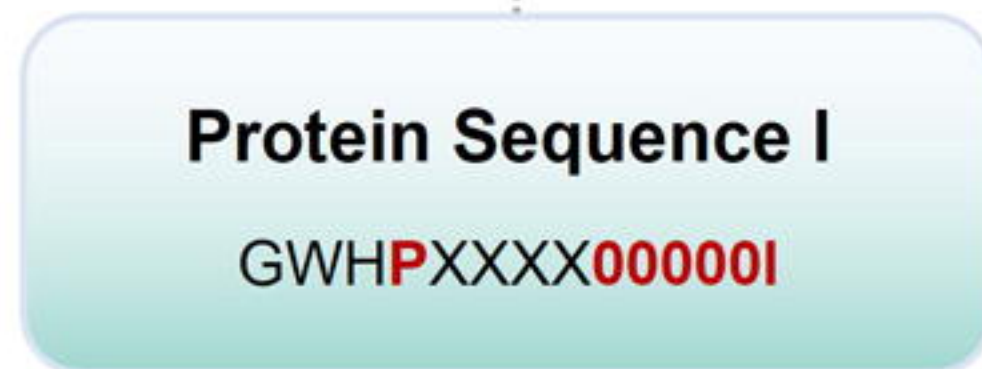
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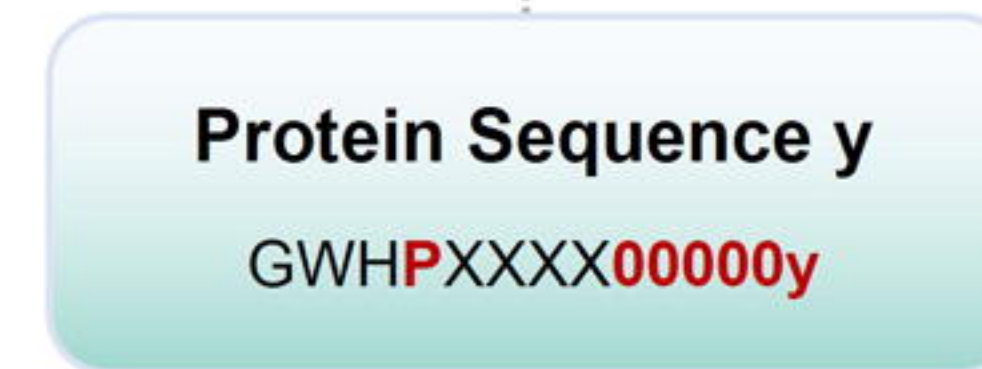
...



...



...





## Data Submission

Register account

Register BioProject

Register BioSample

Create a submission

Fill meta-data

Upload files

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## Quality Control

Filename & md5 code

Genome sequence

- Sequence ID
- Sequence content

Genome annotation

- Gene structure completeness
- Gene structure consistency

Data internal consistency

Sequence contamination  
(optional)

## Archive & Release

Accession assignment

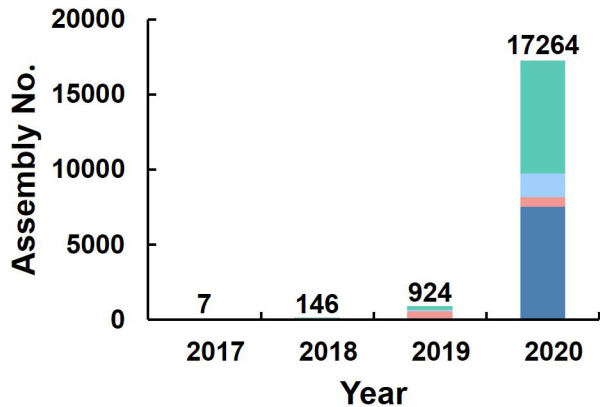
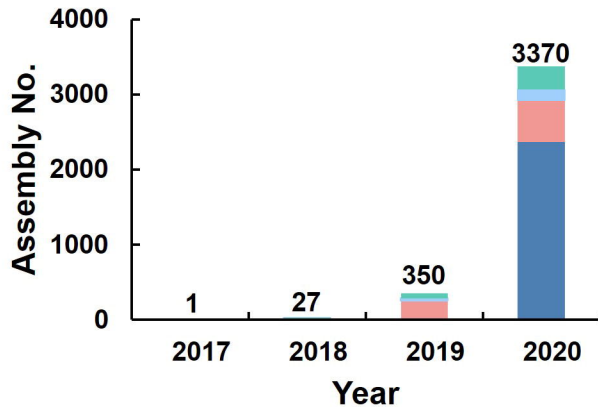
- Genome assembly
- Genome sequence
- Gene
- Transcript
- Protein

Generation of downloadable  
files & backup

- Genome sequence
- Genome annotation
- Gene feature
- RNA sequence
- CDS sequence
- Protein sequence

Release & sharing

- Genome
- Assembly
- Download files
- Genome browser
- BIG Search

**A****Total Assembly****B****Released Assembly**

Assembly level: ■ Contig ■ Scaffold ■ Chromosome ■ Complete