

How to use KAIKObase Version 3.1.0

KAIKObase
SILKWORM GENOME RESEARCH PROGRAM

HOME What's New About SGP **KAIKObase** Sequences Analysis Tools Public Data References Link

KAIKObase
KAIKObase is an integrated silkworm genome browser with 4 map browsers, 1 gene viewer, and 2 independent databases. [more...](#)

[Chromosome Overview](#) [Keyword and Position Search](#) [Scaffold Sequence Search](#)

Chromosome Overview
Two choices are available for the genome maps the PMap can be accessed by clicking the chromosome number after clicking PMap (colored pink) and the UnifiedMap by clicking the chromosome number after clicking UnifiedMap (colored green).

PMap:
physical map and genetic linkage map for each chromosome.

UnifiedMap:
PMap involving genome contigs, BAC-ends, fosmid-ends, and Fingerprint Contigs (FPC).

Remarks:
As the size of gap between adjacent scaffolds is unknown, we set an uniform space of 500 kbps between scaffolds. The direction of a scaffold containing plural markers is defined, while the direction of a scaffold having only one marker cannot be determined and the original direction is used.

[How to use KAIKObase](#)

We would like to ask for your patience not to submit papers using unpublished full-length cDNA is used for Silkworm Genome Annotation until the publication of full-length cDNA paper or annotation paper. If you have any question regarding this regulation, please contact: kmita@nias.affrc.go.jp

KAIKObase is an integrated silkworm genome database and data mining tool with 3 map browsers, 1 gene viewer, and 5 independent databases. [more...](#)

[Chromosome Overview](#) [Keyword and Position Search](#) [Scaffold Sequence Search](#)

Keyword and Position Search
- enter a keyword, position and choose from several parameters to delimit the search.

Keyword:
 Search Field

Position:
☐ Chromosome Position -
☐ Scaffold Position -

Data Set:
☐ scaffold ☐ contig ☐ FPC(Finger Print Contig)
☐ SNP marker ☐ trait marker
☐ Locus ☐ FLcDNA ☐ Complete mRNA
☒ Gene model ☐ EST
☐ BAC_end ☐ fosmid_end ☐ BAC ☐ fosmid

Graphical View:

Keyword Search Result
[Link to Top Page](#)

of 8

ID	Data Type	Position	Description	Link
ID: I00701	gene	Chromosome Position chr1: 10876713-10879032 (+) Scaffold Position Bm_scaf8: 5278759-5281078 (+)	IPR011614/Catalase, N-terminal, IPR002226/Catalase	KAIKObase Link Gene Viewer View Other Site Link KAIK02D08 View
ID: I012691	gene	Chromosome Position chr22: 3937990-3939776 (-) Scaffold Position Bm_scaf69: 151468-153254 (+)	IPR002226/Catalase, IPR011614/Catalase, N-terminal	KAIKObase Link Gene Viewer View Other Site Link KAIK02D08 View
local ID BGIBMGA011431	gene	Chromosome Position chr23: 13458483-13460431 (-) Scaffold Position Bm_scaf22: 4754065-4756013 (-)	IPR002226/Catalase, IPR006061/Bacterial extracellular solute-binding family 1, IPR011614/Catalase, N-terminal	KAIKObase Link Gene Viewer View Other Site Link KAIK02D08 View
local ID BGIBMGA011430	gene	Chromosome Position chr23: 13463890-13465404 (-)	IPR002226/Catalase, IPR011614/Catalase, N-terminal	KAIKObase Link Gene Viewer View

<http://sgp2010.dna.affrc.go.jp/KAIKObase/>

Outline

1. System overview
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3. Browsers, viewer, and external databases
 - 3.1 Pgmap
 - 3.2 UnifiedMap
 - 3.3 Gbrowse
 - 3.4 GeneViewer
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 - 3.6 Proteome database (KAIKO2DDB)
 - 3.7 KAIKOGAAS (An integrated database and automated annotation system)
 - 3.8 Full-length cDNA Database
 - 3.9 EST Database
4. Keyword and position search, and sequence search
 - 4.1 Example of keyword and position search
 - 4.2 Example of sequence search

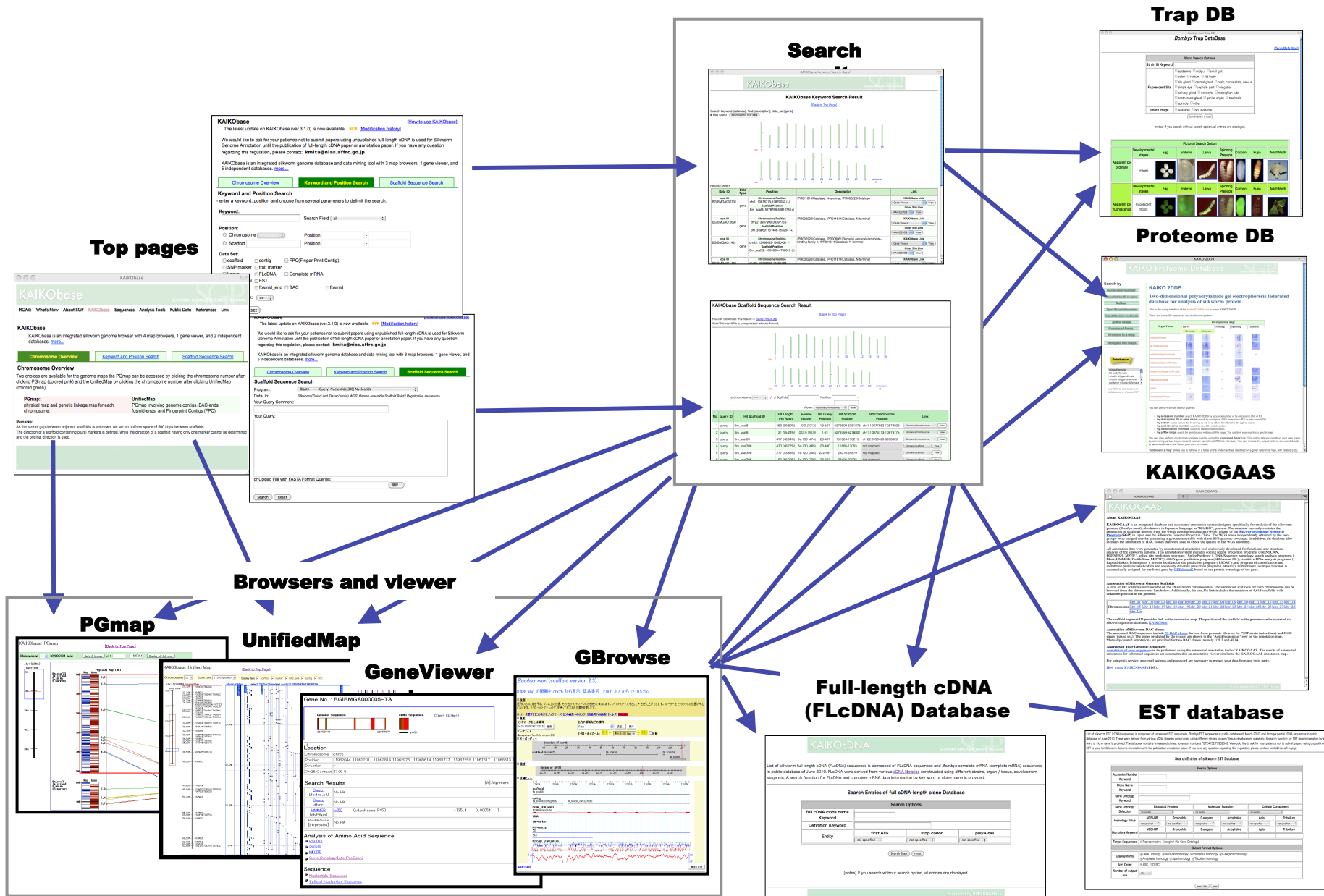
1. System overview

KAIKObase is an integrated silkworm genome browser with 3 map browsers, 1 gene viewer, and 5 independent databases.

- * PGmap : physical map and genetic linkage map for each chromosome.
- * UnifiedMap : PGmap containing genome contigs, BAC-ends, fosmid-ends, and Fingerprint Contigs (FPC).
- * GBrowse : genome annotation viewer based on GBrowse developed by GMOD.
- * GeneViewer : gene information viewer based on the gene viewer of KAIKOGAAS.
- * *Bombyx* Trap DataBase : *Bombyx* gene function database by transgenic works using GAL4 system.
- * KAIKO 2DDB : proteomic data of various developmental stages and tissues of silkworm.
- * KAIKOGAAS : An integrated database and automated annotation system.
- * Full-length cDNA (FLcDNA) Database
- * EST Database

KAIKObase provides three data mining approaches:

- (1) Narrowing the range of data sets using PGmap or UnifiedMap in Chromosome Overview
- (2) Keyword and position search
- (3) Sequence search using BLAST.



2. Top page

The top page provides access to silkworm genome information.

1) **Chromosome select:** Two choices are available for the genome maps – the PGmap can be accessed by clicking the chromosome number after clicking PGmap (colored pink) and the UnifiedMap by clicking the chromosome number after clicking UnifiedMap (colored green).

2) **Keyword and Position Search:** Input a keyword and choose data set from “Search Field”, “Search Chromosome and/or Position” or “Scaffold name and/or Position”, and “Search Data Set” delimit the area and the region of the search. The data sets include genes, scaffolds, contig within scaffolds, markers, fingerprint contigs (FPC), BAC ends, fosmid ends, BAC clones, Locus, FLcDNAs, complete mRNAs, gene models, and ESTs. As long as “Graphic View ON”, search results are shown in chromosome image as well as in Excel table.

KAIKObase
The latest update on KAIKObase (ver.3.1.0) is now available. [NEW](#) [\[Modification history\]](#) [\[How to use KAIKObase\]](#)

We would like to ask for your patience not to submit papers using unpublished full-length cDNA is used for Silkworm Genome Annotation until the publication of full-length cDNA paper or annotation paper. If you have any question regarding this regulation, please contact: kmita@nias.affrc.go.jp

KAIKObase is an integrated silkworm genome database and data mining tool with 3 map browsers, 1 gene viewer, and 5 independent databases. [more...](#)

[Chromosome Overview](#) [Keyword and Position Search](#) [Scaffold Sequence Search](#)

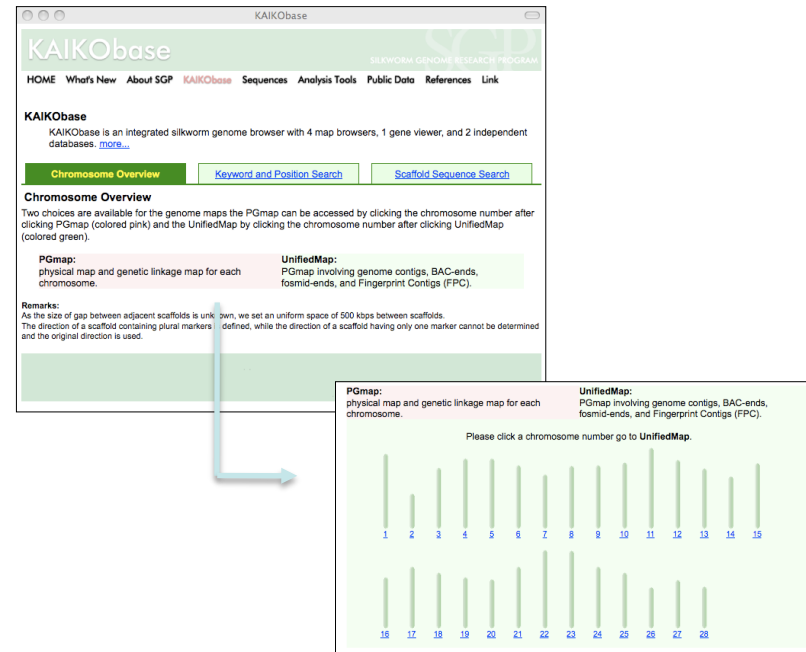
Keyword and Position Search
- enter a keyword, position and choose from several parameters to delimit the search.

Keyword: Search Field:

Position:
☐ Chromosome Position -
☐ Scaffold Position -

Data Set:
☐ scaffold ☐ contig ☐ FPC(Finger Print Contig)
☐ SNP marker ☐ trait marker
☐ Locus ☐ FLcDNA ☐ Complete mRNA
☒ Gene model ☐ EST
☐ BAC_end ☐ fosmid_end ☐ BAC ☐ fosmid

Graphical View: ☒ on ☐ off



3) **Sequence Search:** Nucleotide or amino acid sequence can be used as a query. Search results are shown in chromosome images.

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The latest update on KAIKObase (ver.3.1.0) is now available. [NEW](#) [\[Modification history\]](#) [\[How to use KAIKObase\]](#)

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[Chromosome Overview](#) [Keyword and Position Search](#) [Scaffold Sequence Search](#)

Scaffold Sequence Search
Program: (Query) Nucleotide (DB) Nucleotide
DataLib: Silkworm (Dazao' and Dazao' strain) WGS, Ramen assemble Scaffold Bulk2 Registration sequences
Your Query Comment:

Your Query:

or Upload File with FASTA Format Queries:

3. Browsers, viewer, and external database

3.1 PGmap

3.2 UnifiedMap

3.3 GBrowse

3.4 GeneViewer

3.5 *Bombyx* Trap DataBase

3.6 Proteome Database (KAIKO2DDB)

**3.7 KAIKOGAAS (An integrated database and
automated annotation system)**

3.8 Full-length cDNA (FLcDNA) database

3.9 EST database

3.1 PGmap

[Features]

- Position of markers in the linkage map and physical map at the chromosome level.

[Link]

- Choose designated region and link to GBrowse.
- Choose designated region and link to view sequence.

The screenshot shows the KAIKObase PGmap interface. It includes a 'Physical-Genetic map' window with several panels: 'Chromosome' (showing chr1(22Mb) overview), 'trait info' (showing Bm_scaf8(+) and Bm_scaf8(-)), 'scaffold map', 'physical scale', 'chromosome position', 'genetic scale', and 'marker info'. Annotations 1-7 point to specific features: 1. Select a chromosome (pointing to the chromosome dropdown), 2. Specify the desired region in the chromosome by moving the blue frame (pointing to the blue frame on the chromosome overview), 3. Click display on/off to highlight the area for GBrowse link (pointing to the 'Display-off link-area' button), 4. Specify the region for GBrowse viewing or sequence viewing by moving the red frame (pointing to the red frame on the scaffold map), 5. Click 'Go to GBrowse' button to view link (pointing to the 'Go to GBrowse' button), 6. Click 'View sequence' button to view link (pointing to the 'View Sequence' button), 7. Alternatively, enter the exact position within the chromosome and click 'Go to GBrowse' button to view link or click 'View sequence' button to view link (pointing to the 'Go to GBrowse' button and the 'View Sequence' button). A green callout box states: 'Bombyx trap DB trait information is shown by placing the indicator'. Another green callout box states: 'Region highlighted in GBrowse. The top and bottom lines can be moved to the desired region.' A third green callout box states: 'Linkage map information is shown by placing the indicator.'

As the size of gap between adjacent scaffolds is unknown, we set an uniform space of 500 kbps between scaffolds. The direction of a scaffold containing plural markers is defined, while the direction of a scaffold having only one marker cannot be determined and the original direction is used.

3.2 UnifiedMap

[Features]

- Pgmmap is integrated with the information of scaffolds and contigs of Build2, BAC ends, Fosmid ends, FPC, SNP markers and Trait markers.

[Link]

- Choose designated region on the physical map and link to GBrowse or get to sequence.
- Choose designated region on the linkage map. A red arrow appears on right side if marker information is available.

1. Select a chromosome

2. Specify the zooming level.

3. Check the desired items for display.

Specify the region in the linkage map by moving the red frame.

Specify the region in the physical map by moving the blue frame.



3.3 GBrowse

[Features]

- Genome annotation viewer with a graphical representation of a section of a chromosome.

[Link]

- Click designated region on “Details” and sequence and ID are displayed in another page.
- Click gene model on “Details” for link to GeneViewer and KAIKO2DDB (proteome database).
- Click trait marker on “Details” for link to *Bombyx* Trap DataBase.

Landmark or region can be search.

Data set can be selected.

Click desired position of Overview, then a display will change to information of the region.

After clicking gene model, jump to URLs is shown.

Check display items that you want to see in the display, then, press “Redraw” to present the desired items on the display.

Bombyx mori (chromosome, version 2.3): chr7:6929610..7029609

Search
 Landmark or Region: Search
 Data Source: Bombyx mori (chromosome, version 2.3)

Reports & Analysis:
 Annotate Restriction Sites
 Scroll/Zoom: Show 100 kbp

Overview
 chr7
 scaffold
 Bm_scaf170
 Bm_scaf45
 Bm_scaf179
 Bm_scaf15
 Bm_scaf407
 Bm_scaf90
 Bm_scaf136

Region
 chr7
 6.5M 6.6M 7.1M 7.2M 7.3M 7.4M

Details
 6930k 6940k 6950k 6960k 6970k 6980k 6990k 7000k 7010k 7020k
 scaffold
 Bm_scaf15
 contig
 Bm_scaf15_contig11439
 China gene model
 KAIKO2DDB
 6-frame translation
 DNA/GC Content
 43% GC
 0% GC

jump to ...
 • GBrowse_details
 • GeneViewer
 • KAIKO2DDB(Scaffold segment ID)

Tracks
☒ Overview ☐ All on ☐ All off
☒ scaffold
☐ Analysis ☐ All on ☐ All off
☐ Restriction Sites
☐ FPC ☐ All on ☐ All off
☐ FPC-Contig
☐ General ☐ All on ☐ All off
☒ 6-frame translation ☒ DNA/GC Content
☐ Assembly ☐ All on ☐ All off
☒ contig ☒ scaffold
☐ CDNA ☐ All on ☐ All off
☐ EST ☐ Transcriptional Profile

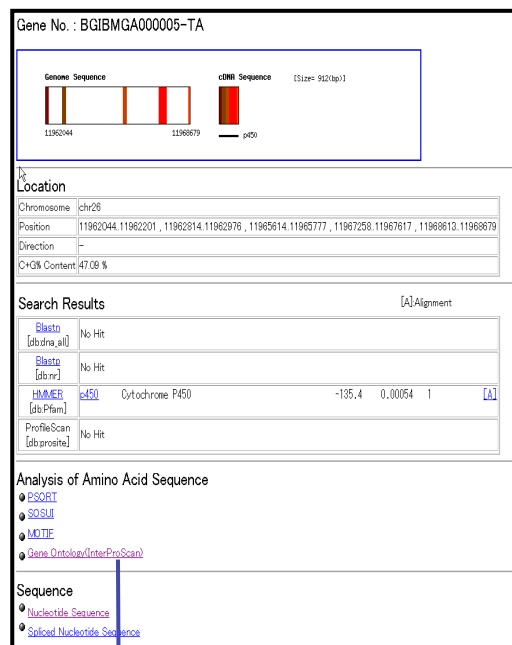
3.4 GeneViewer

[Features

- Gene information viewer, showing the detailed information of the gene model.

[Link]

- “Search Results” links to results of homology search by BLASTn, BLASTp, HMMER and ProfileScan with alignments of the sequence.
- “Analysis of amino acid sequences” links to PSORT, SOSUI, MOTIF and Gene ontology (InterProScan).
- “Sequence” provides the nucleotide sequence, spliced nucleotide sequence and translated protein sequence of the predicted gene.



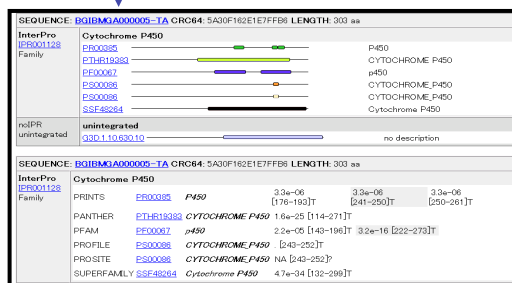
 Result of domain search in Pfam database.

➡ Detailed information of the predicted gene including chromosome number, positions of exons and GC content.

➡ Results of homology search using BLASTn (top 3 ESTs), BLASTp (top 10 proteins), HMMER and ProfileScan with the alignments of the sequence.

➡ Display the results of amino acid analysis in PSORT, SOSUI, MOTIF and Gene ontology (InterProScan).

 Links to the nucleotide sequence, spliced nucleotide sequence and translated protein sequence of the predicted gene.



➡ Graphical representation of InterProScan results

➡ Character representation of InterProScan results

3.5 Bombyx Trap DataBase

[Features]

- Information on reporter expressions and positions of transposon vectors (mutators) in transposon insertion lines (enhancer trap strains, or gene trap strains) is presented with this database.

For more details, please refer to the document, http://sgp.dna.affrc.go.jp/ETDB/howto/how_to_use_Bombyx_Trap_DB.pdf

[Link]

This database is linked from Keyword search result page of KAIKObase.

Bombyx Trap DataBase top page

Bombyx Trap DataBase

[\[How to use Bombyx Trap DataBase\]](#)
[\[Term Definition\]](#)

Word Search Options

Strain ID:

Keyword:

Search Position: Chromosome: Position:
 Scaffold: Position:

Fluorescent Site: ☐ epidermis ☐ midgut ☐ small gut
☐ colon ☐ rectum ☐ fat body
☐ silk gland ☐ dermal gland ☐ brain, corpa allata, nervus
☐ salivary gland ☐ oenocyte ☐ malpighian tube
☐ prothoracic gland ☐ genital organ ☐ tracheole
☐ spiracle ☐ other

Photo Image: ☐ Availability

[Notes] If you search without search option, all entries are displayed.

Pictorial Search Option

	Developmental stages	Egg	Larva	Spinning Prepupa	Cocoon	Pupa	Adult Moth
Apparent by ordinary	Images						
Apparent by fluorescence	Fluorescent region						
Organ/Tissue by fluorescence	Fluorescent region						

3.6 Proteome database (KAIKO2DDB)

[Features]

- Database for silkworm proteome analysis using two-dimensional polyacrylamide gel electrophoresis images of various developmental stages and tissues.
- For more details, please refer to the document, <http://au.expasy.org/ch2d/manch2d.html>

[Link]

- This database is linked from Keyword search result page or GBrowse of KAIKObase.

Proteome database (KAIKO2DDB) top page

KAIKO 2DDB
Two-dimensional polyacrylamide gel electrophoresis federated database for analysis of silkworm protein.

There are some 2D databases about silkworm protein:

Organ/Tissue	Developmental stage				
	Larva	Molting	Spinning	Pupation	
midgut/female	4th-instar	5th-instar	---	---	
fat body/female	---	---	---	---	
middle silk gland/male	---	---	---	---	
middle silk gland/female	---	---	---	---	
posterior silk gland/female	---	---	---	---	
malpighian tube	---	---	---	---	
ovary	---	---	---	---	
hemolymph/male	---	---	---	---	

Search by
You can perform simple search queries:

- by accession number: search KAIKO 2DDB by accession number or by entry name (AC or ID)
- by description, ID or gene name: search by description (DE), entry name (ID), gene name (GN) or UniProtKB/Swiss-Prot keywords (KW)
- by author: search authors list by giving an AC or an ID, or list all entries for a given author
- by spot id / serial number: search by spot ID / serial numbers
- by identification methods: search by identification methods
- by pI/Mw range: search for spots located within a pI/Mw range. You can limit your search to a specific map

You can also perform much more complex queries using the 'combined fields' link. This option lets you construct your own query by combining various keywords and boolean operators (SRS-like interface). You can choose the output fields to show and decide to save results as a text file on your own computer.

Maps
Several actions can be performed for the maps:

3.7 KAIKOGAAS

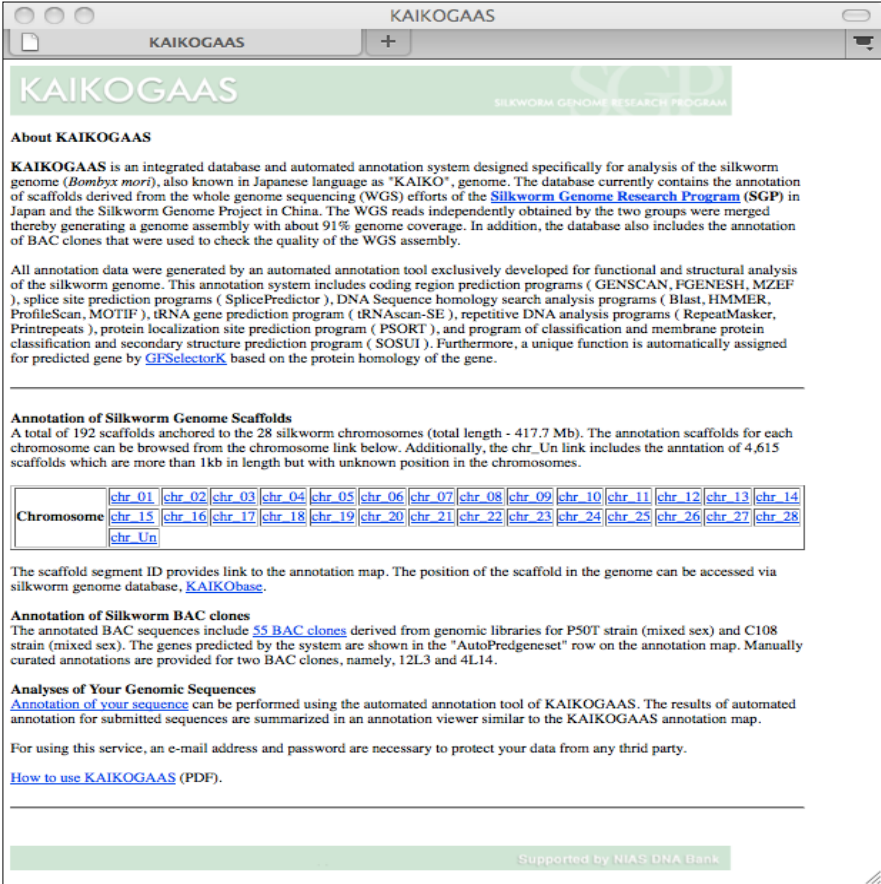
[Features]

- Database of detailed annotation of a total of 192 scaffolds anchored to the 28 silkworm chromosomes.
- For more details, please refer to the KAIKOGAAS document, <http://kaikogaas.dna.affrc.go.jp/howtokaikogaas.pdf>

[Link]

- This database is linked from GBrowse of KAIKObase.

KAIKOGAAS top page



The screenshot shows the KAIKOGAAS website interface. At the top, there's a header with the KAIKOGAAS logo and the text 'SILKWORM GENOME RESEARCH PROGRAM'. Below the header, there's a section titled 'About KAIKOGAAS' which describes the database and its purpose. This is followed by a detailed paragraph about the annotation system and the tools used. Then, there's a section titled 'Annotation of Silkworm Genome Scaffolds' which explains the total number of scaffolds and how they are anchored to chromosomes. Below this, there's a table of links for each chromosome (chr_01 to chr_28) and a link for chr_Un. The table has a 'Chromosome' label on the left and the chromosome names as links in the cells. After the table, there's a paragraph about the scaffold segment ID and a link to the KAIKObase. This is followed by a section titled 'Annotation of Silkworm BAC clones' which describes the BAC clones and the genes predicted by the system. Then, there's a section titled 'Analyses of Your Genomic Sequences' which describes the automated annotation tool. Finally, there's a paragraph about the service requirements and a link to the 'How to use KAIKOGAAS' PDF. At the bottom, there's a footer that says 'Supported by NIAS DNA Bank'.

KAIKOGAAS
SILKWORM GENOME RESEARCH PROGRAM

About KAIKOGAAS

KAIKOGAAS is an integrated database and automated annotation system designed specifically for analysis of the silkworm genome (*Bombyx mori*), also known in Japanese language as "KAIKO", genome. The database currently contains the annotation of scaffolds derived from the whole genome sequencing (WGS) efforts of the [Silkworm Genome Research Program \(SGP\)](#) in Japan and the Silkworm Genome Project in China. The WGS reads independently obtained by the two groups were merged thereby generating a genome assembly with about 91% genome coverage. In addition, the database also includes the annotation of BAC clones that were used to check the quality of the WGS assembly.

All annotation data were generated by an automated annotation tool exclusively developed for functional and structural analysis of the silkworm genome. This annotation system includes coding region prediction programs (GENSCAN, FGENESH, MZEF), splice site prediction programs (SplicePredictor), DNA Sequence homology search analysis programs (Blast, HMMER, ProfileScan, MOTIF), tRNA gene prediction program (tRNAscan-SE), repetitive DNA analysis programs (RepeatMasker, Printrepeats), protein localization site prediction program (PSORT), and program of classification and membrane protein classification and secondary structure prediction program (SOSUI). Furthermore, a unique function is automatically assigned for predicted gene by [GFPSelectorK](#) based on the protein homology of the gene.

Annotation of Silkworm Genome Scaffolds

A total of 192 scaffolds anchored to the 28 silkworm chromosomes (total length - 417.7 Mb). The annotation scaffolds for each chromosome can be browsed from the chromosome link below. Additionally, the chr_Un link includes the annotation of 4,615 scaffolds which are more than 1kb in length but with unknown position in the chromosomes.

Chromosome	chr_01	chr_02	chr_03	chr_04	chr_05	chr_06	chr_07	chr_08	chr_09	chr_10	chr_11	chr_12	chr_13	chr_14	chr_15	chr_16	chr_17	chr_18	chr_19	chr_20	chr_21	chr_22	chr_23	chr_24	chr_25	chr_26	chr_27	chr_28	chr_Un
-------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------	------------------------

The scaffold segment ID provides link to the annotation map. The position of the scaffold in the genome can be accessed via silkworm genome database, [KAIKObase](#).

Annotation of Silkworm BAC clones

The annotated BAC sequences include [55 BAC clones](#) derived from genomic libraries for P50T strain (mixed sex) and C108 strain (mixed sex). The genes predicted by the system are shown in the "AutoPredgeneset" row on the annotation map. Manually curated annotations are provided for two BAC clones, namely, 12L3 and 4L14.

Analyses of Your Genomic Sequences

[Annotation of your sequence](#) can be performed using the automated annotation tool of KAIKOGAAS. The results of automated annotation for submitted sequences are summarized in an annotation viewer similar to the KAIKOGAAS annotation map.

For using this service, an e-mail address and password are necessary to protect your data from any third party.

[How to use KAIKOGAAS](#) (PDF).

Supported by NIAS DNA Bank

3.8 Full-length cDNA (FLcDNA) Database

[Features]

- 10165 full-length cDNAs (FLcDNAs) and 2,627 complete mRNAs in public database are included in the Full-length cDNA (FLcDNA) Database.
- Keyword search provides a list of BLAST top hit annotation using the NCBI NR database.

[Link]

- 9,146 FLcDNAs of 10,165 FLcDNAs and 2,555 complete mRNAs of 2,627 complete mRNA are mapped on scaffold and linked from Gbrowse of KAIKObase.
- 10,165 FLcDNAs and 2,627 complete mRNAs are linked from keyword search result page of KAIKObase

Full-length cDNA (FLcDNA) top page

KAIKOcDNA

SILKWORM GENOME RESEARCH PROGRAM

List of silkworm full-length cDNA (FLcDNA) sequences is composed of FLcDNA sequences and *Bombyx* complete mRNA (complete mRNA) sequences in public database of June 2010. FLcDNA were derived from various [cDNA libraries](#) constructed using different strains, organ / tissue, development stage etc. A search function for FLcDNA and complete mRNA data information by key word or clone name is provided.

Search Entries of full cDNA-length clone Database

Search Options			
full cDNA clone name Keyword			
Definition Keyword			
Entity	first ATG	stop codon	polyA-tail
	not specified	not specified	not specified

[notes] If you search without search option, all entries are displayed.

Supported by NIAS DNA Bank

3.9 EST database

[Features]

- A total of 463,607 ESTs correspond to unreleased EST sequences, *Bombyx* EST sequences in public database as of March 2010, and *Bombyx* partial cDNA sequences in public database as of June 2010.
- Keyword search provides a list of Top hit annotation of InterProSacr and BLAST using database of NCBI NR, Drosophila, C.elegans, Anopheles, Apis, and Tribolium.

[Link]

- 399,510 ESTs of 463,607 ESTs are mapped on scaffold and linked from Gbrowse of KAIKObase.
- 463,607 ESTs are linked from keyword search result page of KAIKObase.

EST database top page

List of silkworm EST (cDNA) sequences is composed of unreleased EST sequences, *Bombyx* EST sequences in public database of March 2010, and *Bombyx* partial cDNA sequences in public database of June 2010. These were derived from various cDNA libraries constructed using different strains, organ / tissue, development stage etc. A search function for EST data information by keyword or clone name is provided. The database contains unreleased clones, accession numbers FS724152-FS939542. We would like to ask for your patience not to submit papers using unpublished EST is used for Silkworm Genome Annotation until the publication annotation paper. If you have any question regarding this regulation, please contact: kmita@nias.affrc.go.jp.

Search Entries of silkworm EST Database

Search Options						
Accession Number						
Keyword						
Clone Name						
Keyword						
Gene Ontology						
Keyword						
Gene Ontology Selection	Biological Process		Molecular Function		Cellular Component	
	not specified		not specified		not specified	
Homology Value	NCBI-NR	Drosophila	C.elegans	Anopheles	Apis	Tribolium
	not specified	not specified	not specified	not specified	not specified	not specified
Homology Keyword	NCBI-NR	Drosophila	C.elegans	Anopheles	Apis	Tribolium
Target Sequences	☒ Representative ☐ original (No Gene Ontology)					
Output Format Options						
Display items	☒ Gene Ontology ☒ NCBI-NR homology ☒ drosophila homology ☒ C.elegans homology ☒ Anopheles homology ☒ Apis homology ☒ Tribolium homology					
Sort Order	☒ ASC ☐ DESC					
Number of output line	10					

4. Keyword and Position search, and Sequence search

4.1 Example of keyword and position search

4.2 Example of sequence search

4.1 Example of keyword and position search

Search for “catalase” in gene data set on whole chromosome.

Enter “catalase” in query box

Do not click if all scaffolds would be scanned.

Click “Gene model”

Choose “on” from pull-down menu.

Click “Search” button.

Keyword and Position Search
- enter a keyword, position and choose from several parameters to delimit the search.

Keyword: Search Field (all)

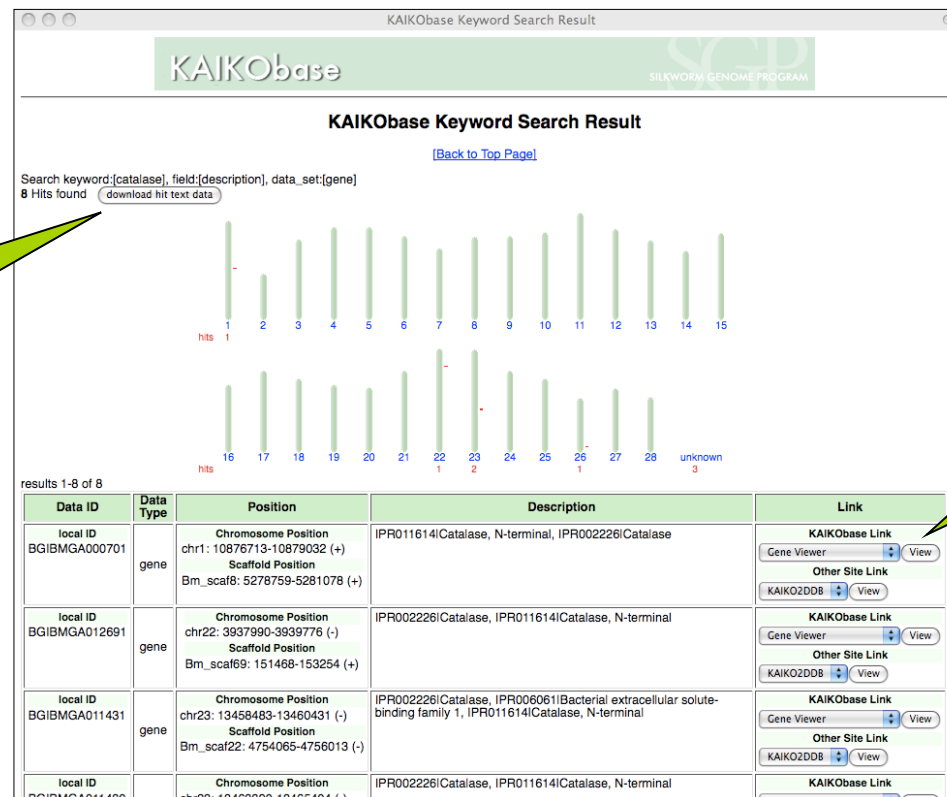
Position:
☐ Chromosome Position -
☐ Scaffold Position -

Data Set:
☐ scaffold ☐ contig ☐ FPC(Finger Print Contig)
☐ SNP marker ☐ trait marker
☐ Locus ☐ FLcDNA ☐ Complete mRNA
☒ Gene model ☐ EST
☐ BAC_end ☐ fosmid_end ☐ BAC ☐ fosmid

Graphical View: on

Choose “description” from pull-down menu

Search result is downloaded by clicking “download hit text data” button.



Click any button to view link.

Result of keyword search

4.2 Example of sequence search

Example of search for location of a specified amino acid sequence on scaffold build2.

Choose tBLASTn

Enter sequence

Set parameters

Click "Search" button

Chromosome Overview Keyword and Position Search Scaffold Sequence Search

Scaffold Sequence Search

Program: (Query) Protein [DB] Nucleotide

DataLib: SilkWorm (Dazoi and Dazoi strain) WGS, Ramen assemble Scaffold build2 Registration sequences

Your Query Comment:

Your Query:

```

MASRDPATDQ LINYKTLKDSGPGFITTSGAPVGTATQVGNKGPALL
QDQNFDEMSSFORERIPERVHAGAGAGGYFEVTHDTKYSAAKVES
IGKRTPIAVFSTVGGESGADTVRPRGFAVKEYTDDGVNOLVGNTP
FFEDPTLPFSTVGGESGADTVRPRGFAVKEYTDDGVNOLVGNTP
RGIPOGYRBM NGYSHITFKL VNSQGVGW KHYKTNQGI KNLVOKAGE
LASTDPTSTI ROLYNSIANG DYPSTPTTQ WTMQAQESC KPNFOLTKI
WPAETVPLP VGLVLDNP KNTFADEQZ AFSPALVNG IEPIDNMLQ
GRLFAYSDTH RHILGANYLQ IPACPKYKVA VSTYQDGRQ AZINQDCFN
YFNFSGGPRQ ECPRAHLQ RYNGGDOR YSGQTEFN SQATLYKQV
FDDAKORATITVH LKDAAFIDERAITFSQWHP ELGNKVAGLAPY
KKYHANL
    
```

or Upload File with FASTA Format Queries:

Search Reset

Parameters:

Expect: Match: Mismatch:

WordSize: Gap Open: Gap Extend:

Filter: DropOff: Extend Hit:

GI:

Gap Align:

Descriptions:

Alignments:

Thanks!

Now your search request is accepted.

Program: tblastn
 Datalib: SW-BUILD2-SCAFFOLD-0083
 Filter: T
 Gap Align: T
 Descriptions: 100
 Alignments: 100
 Open: 11
 Extend: 1

Begin

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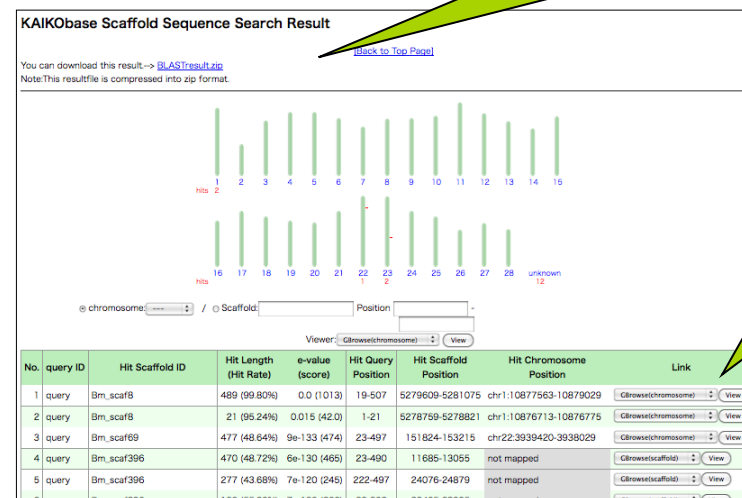
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FFEDPTLPFSTVGGESGADTVRPRGFAVKEYTDDGVNOLVGNTP
RGIPOGYRBM NGYSHITFKL VNSQGVGW KHYKTNQGI KNLVOKAGE
LASTDPTSTI ROLYNSIANG DYPSTPTTQ WTMQAQESC KPNFOLTKI
WPAETVPLP VGLVLDNP KNTFADEQZ AFSPALVNG IEPIDNMLQ
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FDDAKORATITVH LKDAAFIDERAITFSQWHP ELGNKVAGLAPY
KKYHANL
    
```

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This URL allows the user to redisplay the results for a limited period.

BLAST result is downloaded through this anchor.



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Result of sequence search