

How to use “KAIKOOGAAS” on the web

KAIKOOGAAS consists of 5 main pages: the top page, Scaffold-Chromosome (scaffold) table page, BAC table page, On-line users page and the Annotation Map page. The top page contains links to scaffold annotation table, BAC clone annotation table, and submission page for on-line users. Annotation of 192 scaffolds mapped on the 28 chromosomes could be accessed by clicking the corresponding chromosome number. Additionally, annotation of 4,615 unmapped scaffolds are available in chr_Un. The annotation of BAC clones could be accessed through the BAC clone Table link. The results of on-line submission can be viewed through links from the on-line analysis page. The Annotation Results page shows an annotation map with the automatically predicted gene sets.

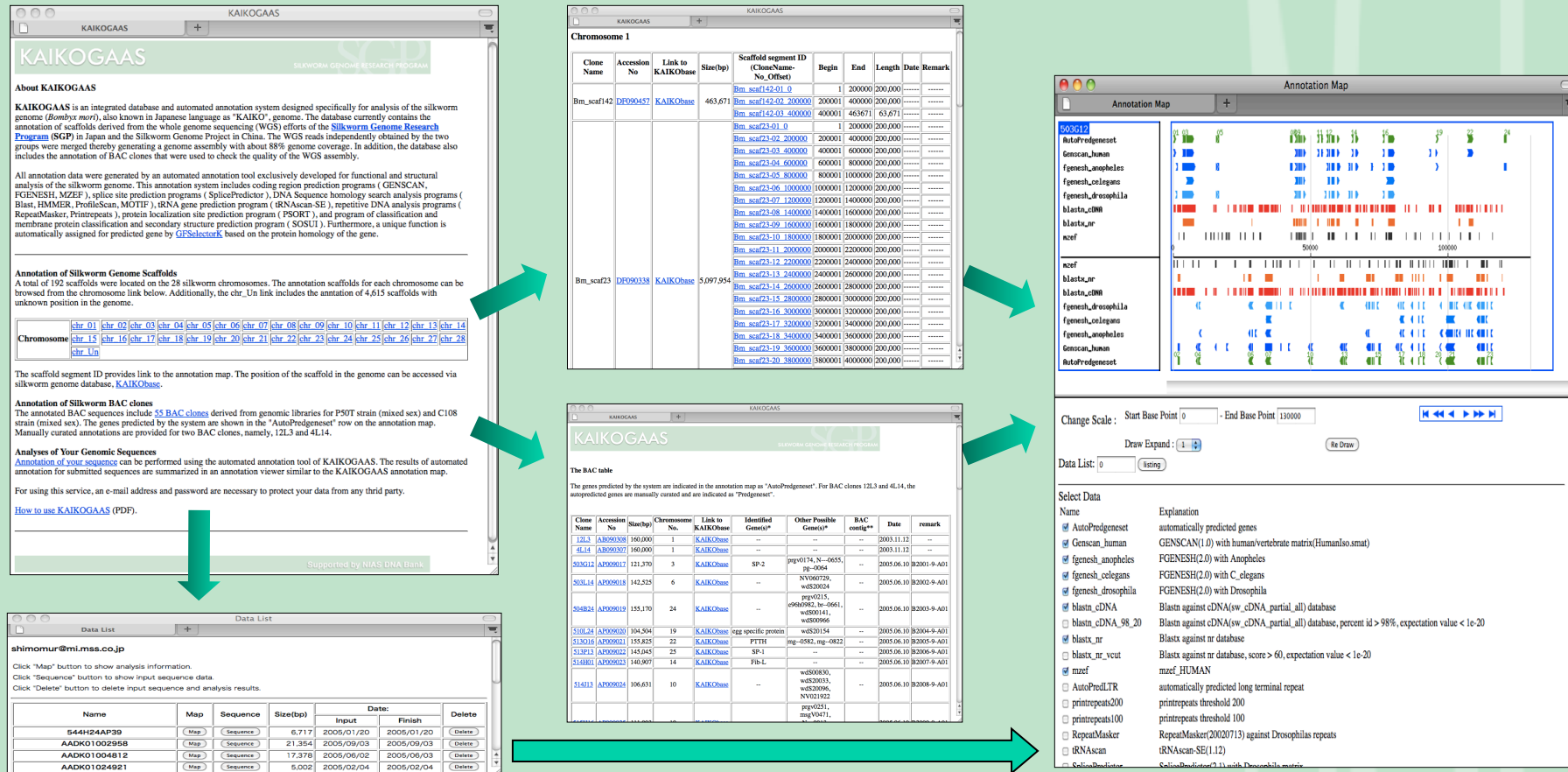


Fig. 1 The 5 main pages of KAIKOOGAAS.

Fig. 2 presents an example of KAKOGAAS result for scaffolds on chromosome 1. KAIKOGAAS has a limitation in size up to 200 kb for processing data, therefore, large scaffolds having more than 200 kb are divided into 200 kb pieces, which are labeled with "Scaffold segment ID". The link to "KAIKObase" provides view to scaffold position on chromosome and transcriptome information, etc. For details, please visit KAIKObase homepage.

Clone Name	Accession No	Link to KAIKObase	Size(bp)	Scaffold segment ID (CloneName-No_Offset)	Begin	End	Length	Date	Remark
Bm_scaf142	DF090457	KAIKObase	463,671	Bm_scaf142-01_0	1	200000	200,000	-----	-----
				Bm_scaf142-02_200000	200001	400000	200,000	-----	-----
				Bm_scaf142-03_400000	400001	463671	63,671	-----	-----
Bm_scaf23	DF090338	KAIKObase	5,097,954	Bm_scaf23-01_0	1	200000	200,000	-----	-----
				Bm_scaf23-02_200000	200001	400000	200,000	-----	-----
				Bm_scaf23-03_400000	400001	600000	200,000	-----	-----
				Bm_scaf23-04_600000	600001	800000	200,000	-----	-----
				Bm_scaf23-05_800000	800001	1000000	200,000	-----	-----
				Bm_scaf23-06_1000000	1000001	1200000	200,000	-----	-----
				Bm_scaf23-07_1200000	1200001	1400000	200,000	-----	-----
				Bm_scaf23-08_1400000	1400001	1600000	200,000	-----	-----
				Bm_scaf23-09_1600000	1600001	1800000	200,000	-----	-----
				Bm_scaf23-10_1800000	1800001	2000000	200,000	-----	-----
				Bm_scaf23-11_2000000	2000001	2200000	200,000	-----	-----
				Bm_scaf23-12_2200000	2200001	2400000	200,000	-----	-----
				Bm_scaf23-13_2400000	2400001	2600000	200,000	-----	-----
				Bm_scaf23-14_2600000	2600001	2800000	200,000	-----	-----
				Bm_scaf23-15_2800000	2800001	3000000	200,000	-----	-----
				Bm_scaf23-16_3000000	3000001	3200000	200,000	-----	-----
				Bm_scaf23-17_3200000	3200001	3400000	200,000	-----	-----
				Bm_scaf23-18_3400000	3400001	3600000	200,000	-----	-----
				Bm_scaf23-19_3600000	3600001	3800000	200,000	-----	-----
Bm_scaf23-20_3800000	3800001	4000000	200,000	-----	-----				

Scaffold in "Clone name" column is described in order on chromosome.

Clicking the Accession No. opens the details of the clone sequence as registered in DDBJ.

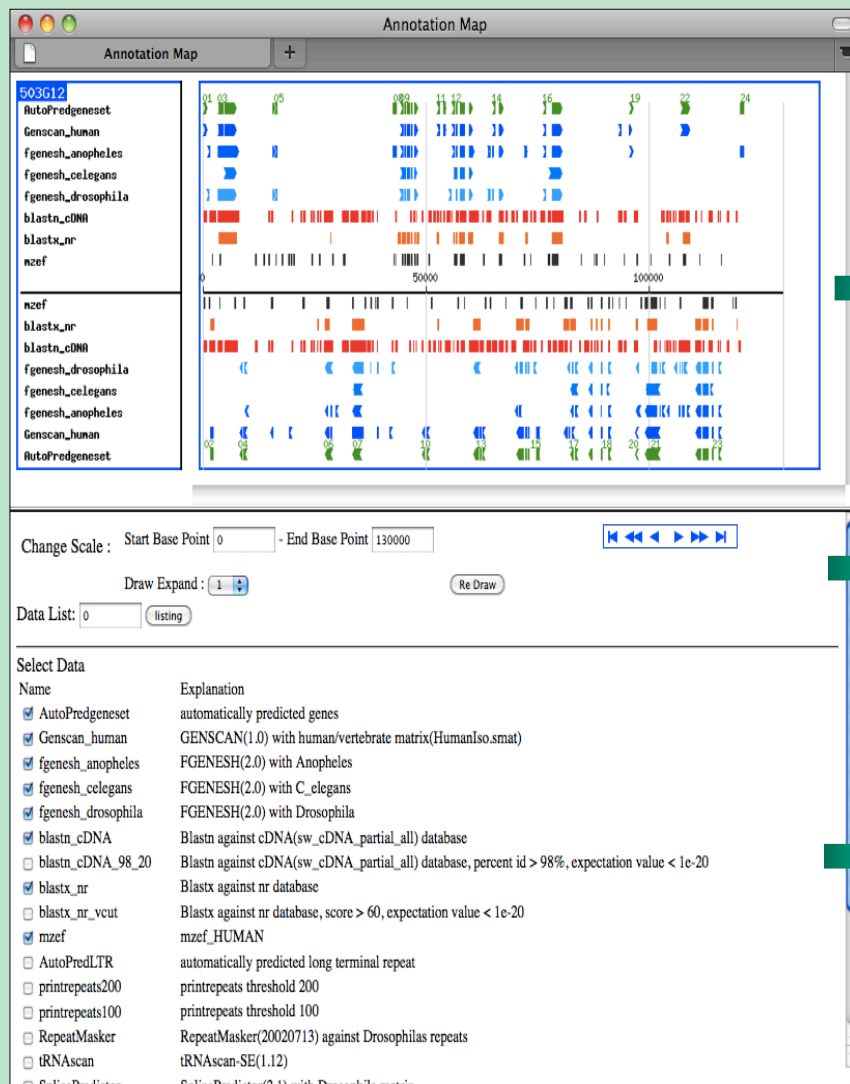
Clicking KAIKObase jump to KAIKObase of keyword result page, user can be viewed scaffold position on chromosome and transcriptome information so on.

Clicking the Divided Name opens the annotation map. See Fig. 3.

Begin, End of Scaffold segment ID positions by reference to scaffold and length of Scaffold segment ID.




Scaffold length with gap.

Fig. 2. scaffold build2 table



The annotation map page consists of three sections.

The upper frame shows a graphical representation of the results of the different prediction programs, homology searches and predicted gene models. See Fig. 4.

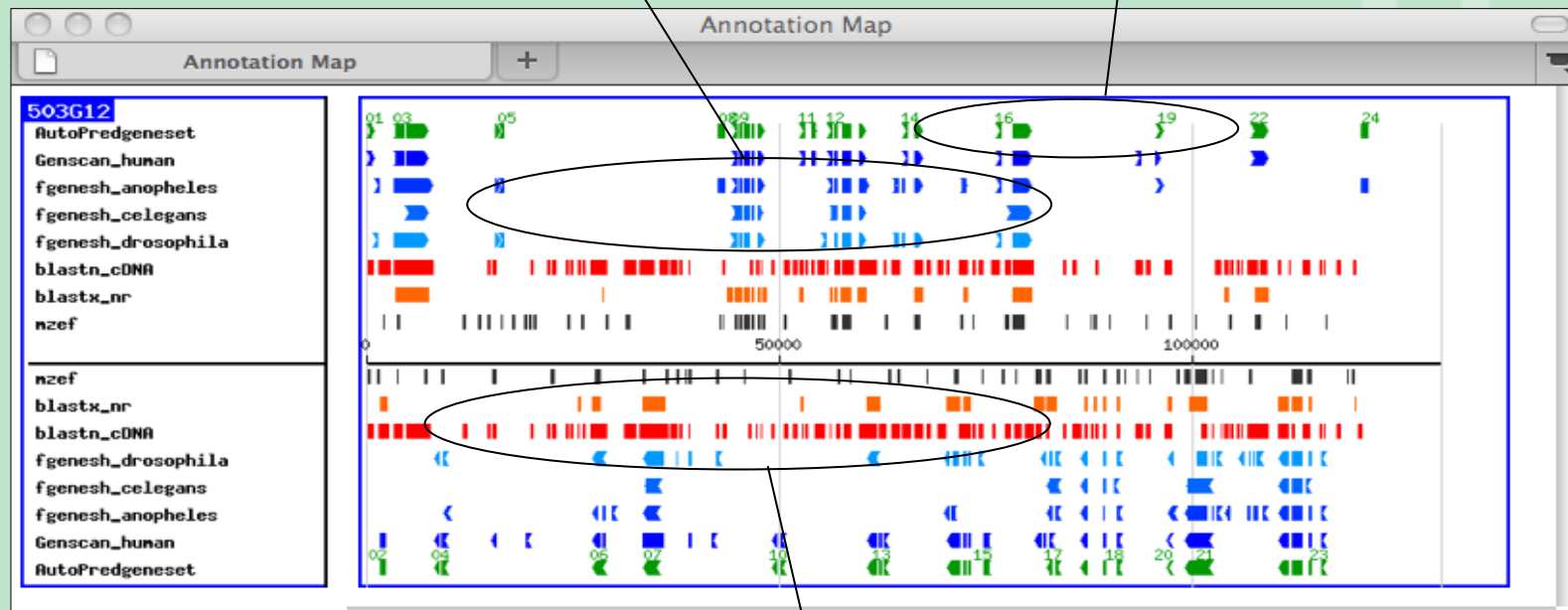
The middle frame allows the user to specify the start and/or end base point of the map viewer and change the magnification (x1-x5). Clicking the "Redraw" button executes the changes. Clicking the blue arrows adjusts the map viewer to the 0 bp position , full-screen scroll , or scroll to the end of clone/scaffold segment ID .

The lower frame provides an option for selecting or clearing specific data in the annotation map by checking or clearing the boxes provided for each analysis program. Clicking the "Redraw" button executes the changes in the annotation map.

Fig. 3 Annotation Results Page

Clicking any region of the autopredgeneset or predgeneset (BAC clone 3L13, 4L14 only) (green bar) shows the detailed information of the predicted gene model. See Fig. 5.

Clicking any region of the gene predicted by any prediction program (blue bar) shows the detailed information of the predicted gene.



Clicking any region of the protein or EST homology shows the detailed results of Blastx (orange bar) or Blastn (red bar).

Fig. 4 Details of annotation map



Result of domain search against Pfam database.

Detailed information of the predicted gene including chromosome number, clone name, position of exons and GC content.

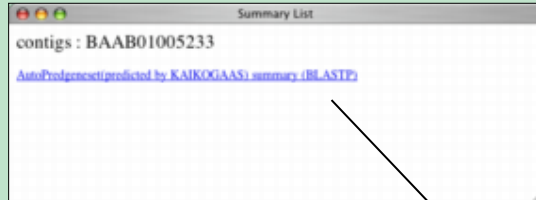
Results of homology search using Blastn (top 3 ESTs), Blastp (top 10 proteins), HMMER and ProfileScan with the corresponding alignments of the sequence.

Display the results of queries to amino acid analysis sever/site such as PSORT, SOSUI and MOTIF.

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

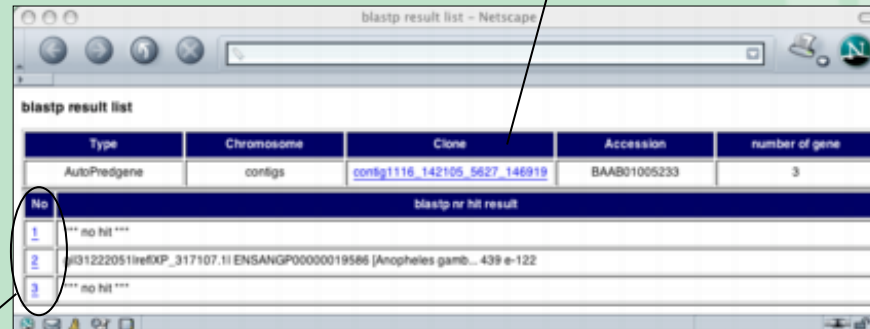
Fig. 5 Details of predicted gene model

Fig. 6 Autopredgeneset summary page



The summary list page

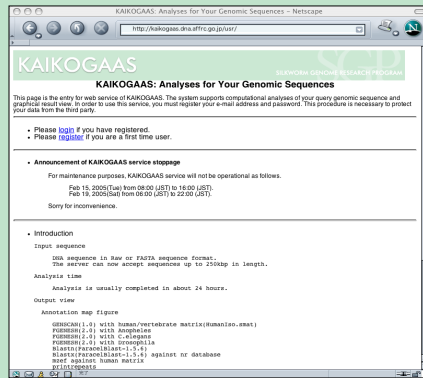
Clicking the clone name opens the annotation of this contig. See Fig. 3.



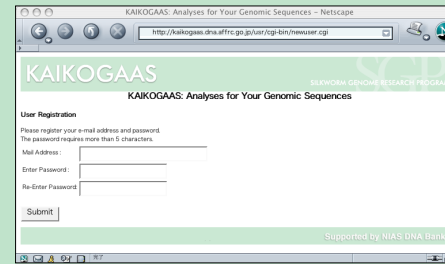
Clicking here opens the details of predicted gene model. See Fig. 5.

Fig. 7 On-line annotation of sequence data

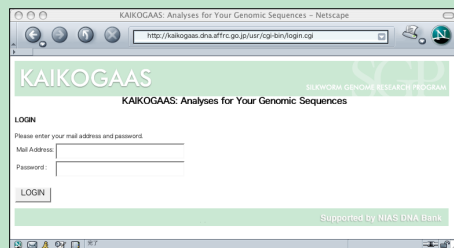
On-line users can submit sequence data for annotation after registering an e-mail address and password from on-line users top page. After being authenticated, the sequence can be submitted directly. The results can be viewed after one day through the data list page.



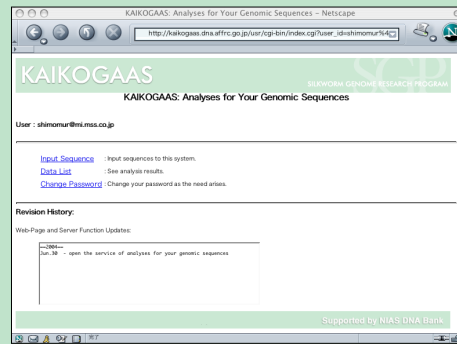
On-line user top page



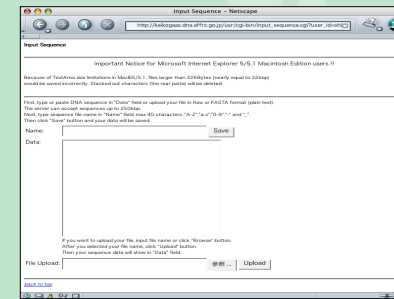
Registration page



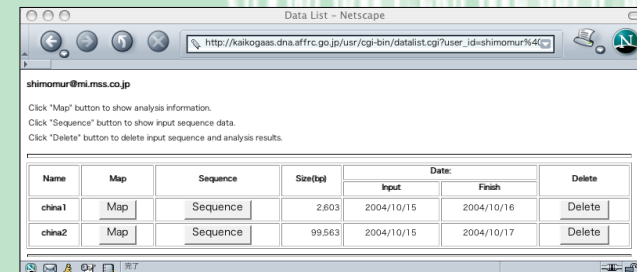
Authentication page



User's page



Data entry page



List of annotated sequence