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IMC GE 1 Month



Brand: in silico biology, inc.
Product Code: IMC-GE-MN

Price: \8,800

Ex Tax: \8,000

Short Description
IMC Genomics Edition

1 Month License

User Registration Required

Pre-order Trial Use Required

Description

General Functions

Window Capture

- Screen capture function of the whole main window or specified region. The captured image is immediately saved in the specified file. The save format is PNG format only.

Toolbox Display and Hide Button

- Toggle button to toggle display and hide of tool box below menu bar. The toolbox can also be docked out from the main window.

Lab Note

- Record IMC operations on a command basis.
- The recorded contents are execution date, command, execution window, reference location of input data, storage location of output data, used database, execution parameters, position on the genome sequence.
- These results can be narrowed down by specifying the time range.
- The list is printable.

Operation History Manager

- This function automatically saves the operation history.
- Items to be saved are the feature key, position, strand, operation command, execution date and time of operation subject.
- History can be sorted by three kinds of sort keys.
- The sort key is the feature key, genome position, operation date and time.
- You can narrow down the list and delete history.
- The list can be output as CSV file.

Checking, Downloading and Installing of the Latest Version.

- Checking, downloading and installing the latest version of IMC installer and help.
- A confirmation dialog is displayed before downloading and installing.

Dock-in and Dock-out

- The dock-in / dock-out panes are Main Directory Tree, Reference Directory Tree, Info Tab, Main Feature Map, Reference Feature Map.
- Toolbox can be removed from the main window in a different way.

Sequence / Feature

Sequence Operations

Auto Sequence Format Checker

- It automatically judges whether the loaded sequence file is a nucleic

acid sequence or an amino acid sequence.
- Besides this, you can also specify sequences as nucleic acids or amino acids and read them.
- Each time you click one exclusive toggle button, the button changes.

Feature Information Tab

- Displays the information content of the feature on the currently loaded current genome sequence.
- The directory tree and the tab are switched and displayed.

Creation of Databases for Blast Search

- Databases for Blast search from nucleic acid sequence file and amino acid sequence file can be created.
- For the array file loaded in the main current directory and the reference current directory, the Blast database is automatically created when it is loaded and it is automatically deleted when the load is canceled.

Zoom and Scroll of the Main Feature Map and Settings

- The main feature map can scroll left and right in base unit and screen unit.
- There is a dedicated button for each.
- Vertical scrolling is controlled with the scroll bar. To zoom, use the toolbox or zoom button on the menu.
- You can zoom in by specifying by mouse drag on the array lane or by right clicking the mouse.
- The speed of zooming and scrolling can be set from the Setting menu.

Display Settings of Sequence Lane

- Items that can be changed on the sequence lane are as follows.
- Change of font size of nucleic acid base and amino acid, display position change of amino acid 1 character code, display color change of nucleotide and amino acid residue, display and display of candidate of start and stop codon and display color setting

Operations of the Sequence Lane

- The operations that can be executed on the sequence lane are as follows.

- Selection of sequence, deselection, insertion of sequence, deletion of sequence, sequence substitution, sequence copy, new feature registration, homology arm design, PCR primer design.

Operations on the Feature

- Operations that can be executed from the feature are as follows.
- Homology search to the reference genome, codon frequency table display, amino acid profile display, copy of sequence and annotation, design of primer to amplify features, activation of annotation window, activation of description window, activation of sequence viewer and start codon candidate Display, Change lane attribute setting.

Qualifier Editing of the Feature

- The features you can set with Qualifier on the right mouse button are as follows.
- Display color setting, document file attachment, molecular structure file attachment, feature map display, genome map display, genetic code table change.
- You can edit all editable qualifiers from the description window and annotation window.

Editing of the Feature

- Feature editing functions are as follows.
- Deletion designation, deletion, duplication, deletion of introns, deletion of exons.

Feature Fusion

- If there are two or more features with the same Feature Key at the same position in the current sequence, it will merge these Qualifiers into one feature.

Feature Operators

- If the features belonging to the same feature-key, and are in a position where they overlap each other, you can create and register new AND / OR / XOR features for those features.
- You can specify the feature key of the newly generated feature.

Feature Map Synchronization with Search Results

- Each result screen of feature key search, keyword search, array pattern search, function classification search, genome statistics display, and feature map are synchronized.

Add Sequential Numbers to Features Hit from Search Functions

- Sequential numbers can be added to features hit from Feature Key Search, Keyword Search, Genome Statistics search results.

Feature and Feature Key Design

Feature Layout Styles Manager

- From the feature layout style manager window, you create, edit, and delete feature feature styles.
- You can import and export styles individually.
- You can save the entire list as a different name.
- You can change the default style.
- This list is displayed as a pull-down menu in the upper indicator area of the main window and can be applied immediately to the currently loaded current sequence.
- When selecting multiple sequence files in the current directory and specifying one style from the pull down menu, it applies to all selected files.

Feature Layout Style Design

- It is the design window of the feature layout style.
- Register, edit, delete, change the display order of the new lane to the style, and save the style with a different name.
- You can also call up existing styles and edit them.
- We describe the editing function of each lane by lane.

Feature Layout Settings

- The following functions can be executed from the feature lane setting dialog.
- Display feature key (s), strand selection, arrangement method (Six Lane, Three Lane, Two Lane, One Lane, Pack), Chain change (Forward, Reverse, Both), Exon display method change, Placement density, Lane

Height change, offset change.

Content Profile Lane Settings

- The items that can be set from the content / profile lane setting dialog are as follows.
- Change the background color, change the parameters of the profile graph, change sliding window parameters, thinning out (6 contents, such as GC Content, GC / AT Skew, Cumulative GC / AT Skew, Import Map Data, Fickett Profile) Function, change graph color.

Navigation Lane Settings

- The items that can be changed from the navigation lane setting dialog are as follows.
- Feature (s) can be selected. Strand selection (Forward, Reverse, Both), placement method selection (Six Lane, Three Lane, Two Lane, One Lane, Pack), thinning setting change.

Restriction Enzyme Lane Settings

- The items that can be changed from the restriction enzyme lane setting dialog are as follows.
- Lane height, set switching, narrowing down of restriction enzyme list (recognition sequence length, palindromicity, terminal shape (Blunt, Sticky), DAM / DCM, number of cleavage sites of target sequence, selection of restriction enzyme.

Local Genome Rearrangement Map Lane Settings

- The changeable parameters from the local genome rearrangement map lane dialog are as follows.
- (Six Lane, Three Lane, Two Lane, One Lane, Pack), Display Chain Change (Forward, Reverse, Both), Display Features (Multiple Designations), Strand Designation (Forward, Reverse, Both) Reverse, Both), exon display method change, placement density

Lane Without Parameter

- Lanes without parameter change are as follows.
- Sequence Lane, Vertical Scroll Bar Lane, Sequence Scale Lane, Map Scale Lane, Frame Lane

Feature Key Registration Dialog

- From the feature key registration dialog, you can register, edit and delete feature keys.
- However, you can not edit or delete required feature keys.
- When registering newly, it is possible to use the already registered feature key as a template.
- You can specify feature key name, shape, background pattern, frame color, fill color, frame size, display area selection, qualifier to be labeled, and multiple qualifiers to use.

Viewers

GenBank File Viewer

- A viewer that can view the currently loaded sequence file in its original format.
- When you click on an sequence or annotation, the main feature map will display a map of that position.
- Conversely, with this viewer open, you can click on a part of the main feature map to display the text at the corresponding position in the file.

Sequence Viewer

- A viewer that displays a sequence of the area currently displayed in the main feature map.
- You can display the display range on the viewer, show / hide the reverse strand, display / not display the amino acid translation, change the display method of the scale, display number of bases displayed. You can output image files in PDF, PNG, EMF format respectively.

Annotation Viewer / Editor

- A tool prepared for genome annotation.
- It is mainly used for annotating CDS.
- The window is divided into three parts, you can enter annotations directly, you can directly edit them, you can link the results of the homology search to the CDS features themselves and display them and post them.
- At the same time existing features can be selectively displayed in the sequence display area.
- You can change the display settings for sequences, features, and tick

marks. Image contents can be output in PDF, PNG, EMF format.
- From this window you can also perform a homology search that queries this feature and the results are linked immediately.

Circular Genome Map Viewer / Editor

- Editing / deleting of profile concentric circles, addition / editing / deletion of profile concentric circles, automatic map creation of multiple genomes, printing · image file output (PDF, PNG, EMF) is possible.
- The designed circular layout can be saved as a layout style and another genome sequence can be created with similar design.
- You can add concentric circles of various styles to the map.
- For one concentric circle, you can display and set multiple features, and you can specify strand designation, color classification, only specified features.
- Also, you can freely set the resolution such as content map such as GC content.
- It is also possible to draw by sequentially switching genomic sequences loaded in the current directory.
- You can change map resolution, diameter, phone size, and map name.

Plasmid Map Viewer / Editor

- It is similar to the circular genome map editor, but draws a relatively small circular genome.
- The annular lanes are arranged concentrically, and you can place multiple feature keys on one concentric circle.
- Strand, frame, feature shape, color designation of fill and frame, thickness of frame, selection of color classification, display / non-display of label, selection of qualifier to be used as a label, font size, two concentric circle overlay functions , You can change the scale interval.
- Designed styles can be saved and applied to other plasmids.
- You can change the order of concentric circles, add / delete, and edit.
- Plasmid maps can be output in three types of image formats: PDF, PNG, and EMF.

Trace File Viewer / Editor

- It is a viewer / editor which is used when reading output file from ABI, SCF capillary sequencer.
- Not only the base sequence, but also its waveform (trace) can be

displayed.
- You can change the base call.

Description Window

- It is a window for editing the feature description.
- It is launched from the feature and consists of genome position, strand, qualifier list and value, and nucleic acid sequence and amino acid sequence display area.
- Each sequence can be copied to the clipboard.

Search Operations

Feature Key Search

- Counts the number of feature keys registered in the main current array and displays a list.
- Several features to be searched can be selected, and the search range can be limited.
- On the search result screen, buttons for feature key number, position on array, base length, gene name, base sequence, button to annotation to descriptions are listed.
- In CDS, it is possible to perform operations such as selection of amino acid sequence, + chain strand only, collective deletion, codon table, serial number addition, Fusion PCR.
- When you click a line, the main feature map shows the location of that feature.
- File output in CSV / FastA / GenBank format is possible.

Keyword Search

- It is a function to search annotations by entering keywords.
- Multiple target feature keys can be selected.
- Multiple keywords can be specified and logical operations between keywords can be selected by AND / OR / NOT.
- Search scope can be limited to CDS area and Inter Genic area separately.
- On the search results screen, buttons for feature key number, position on sequence, base length, gene name, base sequence, button to annotation to descriptions are listed.
- CDS shows amino acid sequence, + chain.
- You can perform operations such as display selection only for chains, delete all at once, display codon table, search and add sequence

number to features, transfer list to FusionPCR function.
- When you click on the row in the results list, the main feature map will display a map of that feature - position.
- You can output files in CSV / FastA / GenBank format. . Qualifier batch deletion is also implemented.

Sequence Pattern Search

- Select multiple registered array patterns and detect patterns existing in the current array.
- It is also possible to search by entering new patterns when searching.
- The search range can be specified and the search target strand can also be specified. Mismatch detection of 1 to 2 letters is possible.
- You can also specify the search region of the CDS region or intergenic region.
- It is possible to search only upstream / downstream designated areas of CDS.
- In addition, multiple arrays can be set as search targets.
- On the search results screen, you can display the detected number, the position on the array, and the genes upstream and downstream for each pattern.
- In addition, results can be automatically registered as new features.
- The result can be output as file in CSV / FastA format.
- When you click on a row in the search result list, the main feature map moves so that the position of the pattern is at the center of the map, and the corresponding pattern array on the array lane is highlighted.

Sequence Pattern Registration

- Registration, editing and deletion of base sequence pattern and amino acid sequence pattern (motif) are possible.
- Sequence pattern conforms to regular expression. Pattern name and pattern regular expression can be registered.
- You can save the list of selected patterns in IMC proprietary format (pattern.dat).
- It is also possible to return to the initial setting.

Gene Function Code Search

- We select multiple genetic function codes (code is optional but COG classification is common) and search for CDS features with those functions.

- Search range can be specified, and multiple arrays can be searched.
- From the search result screen, the CDS number, the position on the sequence, the strand, the explanation of the COG, the locus_tag, the upstream downstream gene, the CDS base sequence, the description window and the link to the annotation window are displayed from the search result screen .
- An amino acid sequence can be output separately.
- Batch delete of hit CDS, Fusion PCR, codon usage frequency table display is possible.
- When you click on the row of the result list, the main feature map shows its position.
- List output in CSV / FastA / GenBank format is also possible.
- There is also the option to display only the searched features on the current map.

Cloning

Restriction Enzyme

Restriction Enzyme Manager

- There are the following as the control functions of restriction enzymes.
- Partial set selection, narrowing down by type (number of recognized bases, palindrome, smoothing / overhang, DAM / DCM, number of cut points).
- Alias names of restriction enzymes list can be saved, list editing is possible.
- You can also register enzymes, edit enzymes, delete enzymes.

Restriction Enzyme Recognition Site Search

- As a search function of restriction enzyme recognition site, there are the following functions.
- Search region selection, recognition site search, recognition site list display, restriction enzyme map display, collective search from multiple sequences.

Operations on the Search Result Window

- The following operations are available from the restriction enzyme search result window.
- Sequence switching, additional enzyme search, digestion

fragmentation, registration of new features at the recognition site, registration of digested fragment files, gel electrophoresis by fragment, list output (CSV, Fast A), synchronization of lists and feature maps.

Operations on Restriction Enzyme Map Window

- Possible operations from the restriction map window include the following:
- Target sequence file switching, feature map display, zoom / scroll, slider, band cutting out, gel electrophoresis window activation.

Operations on Gel Electrophoresis Window

- Operation from the gel electrophoresis window of digested fragment of restriction enzyme has the following.
- Electrophoretic image printing, image file output (PDF, PNG, EMF), band extraction and corresponding sequence file saving.

PCR Primer

Management of PCR Primer

- Imported or designed PCR primers are stored in the primer file and their management operations are possible in the primer management window.
- Attributes of registered primers are as follows.
- Primer ID, Primer sequence, Primer base length, Tm, GC content, registration date, comment, link to the file that executed PCR.
- The primer list can be sorted using Primer ID, Length, Tm, GC (%), Comment as a key.
- From the manager dialog, it is possible to newly register, edit, delete, add restriction enzyme recognition site to the end, insert restriction enzyme recognition site to any part of the primer, copy to the clipboard.
- You can also save the entire list or a part of the list as a different name, read another list, and import it into the list of primers.

PCR Primer Design

- PCR primers can be designed from sequence lanes and feature lanes.
- On the sequence lane, you can drag and select the base sequence and register it as a new one .
- Drag on the feature lane to design the optimal primer within (outside)

the selected region. In the design result window, primer sets matching the conditions are listed in order of score. Item attributes are product (base length, Tm, GC content), F / R Primer (Priming position, Tm, GC content, base sequence).
- There is an option to add A base to the 3'-end. It is also possible to limit with maximum product base length.
- From this window you can select a primer set and execute PCR.
- It is also possible to register the selected primer set as a new feature.
- Additionally, additional registration from the outside is possible on the primer list.
- A file can be output in CSV format for the selected set.

PCR Primer Design Parameters

- It is possible to design primer design inside (or outside) the selection area.
- The designable region width change, minimum product base length, primer (longest and shortest base length, minimum · maximum Tm, minimum · maximum GC content, annealing oligo concentration, salt concentration), 3 'terminal base designation (G, C) Self-complementarity, 3 'stability, 3' self complementarity, score function (selection, Tm coefficient, product coefficient), Priming Parameter (E-value, Percent Identity, Overlap Length), Timer difference between Primers, , Design avoidance area configurable (not designed in designated feature key area).

Batch PCR Primer Design

- PCR primers can be designed to amplify them collectively for features belonging to a specified feature key on the genome.
- Beforehand save the list of the CDS etc. to be PCR amplified on that genome by using Feature Key search etc.
- Entering that file and running this function will automatically design all the primers that will amplify each CDS in the list.
- Regarding areas that could not be designed, it is possible to repeat automatic design by changing parameters.
- The designed primer set can be newly registered as a feature and newly registered in the primer list.
- Also, file output in CSV format is possible.

Whole Genome Covering Primer Design

- Automated primer design function to obtain products covering whole genome with equal length products.
- Regarding areas that could not be designed, you can change the parameters and repeat the design until the whole area succeeds.
- The designed primer list can be newly registered as a feature, and it is newly registered as a primer.
- As for design result, file output in CSV format is possible.

Sequencing Primer Design

- Automatically designs an entire sequencing Primer set for sequencing the current sequence.
- As design parameters, you can set the primer distance in addition to the default Primer design parameters.
- Regarding areas that could not be designed, you can change the parameters and repeat automatic design.
- The design result can be output as a file in CSV format.

in silico PCR Reaction

- Perform in silico PCR.
- There are methods such as selecting Primer Set to use from the primer list, executing from the design list from the feature map, and so on.
- When Amplify is executed, a list of products is displayed, products can be selected and loaded into the current folder, or files in CSV / FastA format can be output.
- It also works in conjunction with the Contig Bridge function.

PCR Reaction for Multiple Templates

- It is a function to perform PCR reaction with the same Primer set for multiple genome sequences.
- You can display the number and position of Priming Site on each template and load selected products into the current folder.
- As for the result, file output in CSV format is possible.

Bridge Contigs

- Enter multiple contig sequences and multiple PCR product sequences to list PCR product sequences that can bridge multiple contig sequences.

Ligation

- It will ligate the two fragments on the current folder. It also self-ligates one fragment on the current folder.
- Ligation is possible when the terminal shapes of the fragments match.
- If both ends of two fragments are of the same shape, two fragments of one fragment generate two ligation products in opposite direction to the other fragment forward and reverse.

Genome Sequence Editing

- It is a function of editing genome sequence in information processing regardless of molecular biological means.
- Deletion of designated area, fragmentation by disconnection at specified (plural) positions, replacement of codon, etc. are possible.

Genome Analysis

Gene Finding

Codon Usage

- Create a codon frequency table of the current genome sequence file and create it.
- For annotated genomic sequences, the total frequency of all CDSs is calculated. CDS number, codon number on CDS, number of bases.
- Notations are mRNA and DNA display, you can switch between codon percentage and frequency.
- Also, amino acid frequency can be displayed.
- It is also possible to output a file in the frequency table in CSV format.

Genome Feature Statistics

- Displays the number of registrations by feature key of all the features existing in the current genome sequence.
- A list of features belonging to the selected feature key is displayed and the display items include genome position, strand, GC content, base number, base composition, GC Skew, number of AT Skew start codon candidates, description window activation button , Annotation window start button, and so on.
- You can also select by strand. There is a sequential number adding function for the selected feature.
- The list can be output as a file in CSV format.

- In conjunction with the selected feature - the main feature map will move and will move to display that feature - in the center.

ORF Extraction

- Extract ORF candidates from the current genome sequence.
- Extraction range designation, gene region limitation, intergenic region length definition, longest extraction from overlapping candidates, selection of starting positions, extraction of candidates with no start codon suitable / inappropriate, comparison of already registered feature keys overlapping Designation, etc. can be specified.
- The extracted candidate can be registered as a new feature.
- Results can be output in CSV / FastA format file.

Translation and Change Feature Key

- Convert the specified feature key into an amino acid sequence with the specified codon table.
- Specifiable feature keys are CDS, ORF. You can choose Prokaryote or Eukaryote.
- The ORF feature will be changed to CDS after translation.

Amino Acid Profiling

- Calculate the following profile for the amino acid sequence of CDS and display it as a graph.
- Hydrophobicity, hydrophilicity, chain flexibility, surface property, molecular weight, alpha helix, beta sheet, beta turn, polarity, bulky nature, total score

Settings of Profe

- The following items can be changed from the amino acid profile setting dialog.
- Sliding window setting, profile color setting, normalization, amino acid motif display, display profile selection, automatic · manual scale, reference line change, weight change,

Mapping

EST Mapping

- Specify a number of single EST sequences and map by homology on the current genome sequence.
- Specify the maximum base length of the intron and exclude it from the mapping target when the adjacent exon distance is far away.
- After execution, a mapping candidate list is displayed, and only selected ones can be registered as new features.

Trace Mapping

- Mapping the sequence file from the ABI / SCF format capillary sequencer onto the current genome sequence.
- After execution, the mapping candidate list is displayed and only the selected one can be registered as a feature -.
- After registration, you can display the waveform profile from the mapped feature.

A.A. Sequence Mapping

- Specify multiple amino acid sequence files and map them on the current genome sequence.
- Fragments mapped from one amino acid sequence are joined and can be registered as one feature consisting of multiple positions because they map only to the exon region.
- If amino acids have annotations they will be posted.

Homology Search

Homology Search by Sequence Entered

- Perform a homology search to the selected sequence in the current directory (main and reference) using the sequence entered by copy-and-paste or sequence specification as a query.
- Possible homology search programs are blastn, blastp, blastx, tblastx, tblastn.
- From the homology search result list, each map of the main reference is shifted so that the hit region is displayed in the center.

Homology Search by Sequence of Selected Features

- Performs homology search for each selected sequence in the current directory and data specified from the generated search database with the selected feature as a query.

- From the homology search result window, items such as Percent Identity, Overlap Length, E - value, and Bit score are displayed, and you can display the alignment and pairwise alignment.
- Multiple selections can be made from the hit sequence, multiple alignment can be outputted, and molecular phylogenetic trees can be drawn.
- Annotation can be added locally by automatically posting the specified Qualifier among the qualifiers of the hit sequence.

Homology Search by Current Sequence

- Perform a homology search on the specified search database using the current sequence as a query.
- Automatic posting of the specified Qualifier out of the qualifiers of the hit sequence.

Repeat Search

- Extract repetitive sequences in the current sequence.
- A result window will be displayed, and clicking on the corresponding line will show the main feature map its location.
- The list shows the sequence base length, the position of the two sequences, and the base sequence.
- The selected iterative sequence can be registered as a new feature.
- The list can be output as a file in CSV format.

Compare Genomes

Search for Unique Region of Genomes

- It searches for a specific (non homologous) region by comparing the current genome sequence with the current loaded genomic sequence of the reference genome as a query.
- When you click an region from the unique region search result window, each map displays its position.
- Results can be output in CSV format.

Dot Plot

- We display homology regions between two genomic sequences in dot matrix.
- Select and compare the current genome sequence and one genomic

sequence loaded in the current reference directory.
- You can set dot color by Overlap base length,% Identigy level.
- In the result display window, zooming, shifting, enlarging an arbitrary region selected by rectangle, dot color setting, navigation window, restriction on the number of display dots, and feature key display (display of annotations with feature - mouseover) are possible.
- A dot image can be output as a file in PDF / PNG / EMF format, and print setting is also possible.
- The dot list can be output as a file in CSV format.

Global Genome Rearrangement Map

- We create and draw genomic rearrangement maps over the entire length between closely related genomes at the feature level.
- Compare the genome full length in pair wise between the current genome sequence and the genomic sequence (s) selected among closely related species genomic sequences loaded in the current reference directory.
- Comparison with nucleic acid sequence and comparison with amino acid sequence are possible.
- Homology determination criteria can be changed. For amino acid sequence comparisons, CDS must be annotated for both genomes.
- From the result window you can zoom vertically and horizontally, scroll, pick up homologous lines, display any feature key, display heterogeneous regions, display navigation window.
- The result image can be output as a file in PDF / PNG / EMF format.
- Homologous lists can be output as CSV files.

Local Genome Rearrangement Map

- We create and draw a local genomic rearrangement map at the nucleotide level throughout the two closely related species.
- Based on the current sequence genome, homology regions with different closely related species genomes loaded in the current reference directory are detected, and a local genomic rearrangement map in which the nucleotide sequences and the features of the respective genomes are aligned is drawn.
- We call it the local genome rearrangement map.
- After execution, a new sequence that incorporates the reference sequence is generated, and that sequence becomes the current sequence.
- Here the lane of the reference genome is automatically added to the

feature lane.
- Also, since the mismatch list and the generated array file are linked, the mismatch list can not be removed.
- Focus on a specific feature key and it can be re-displayed.

Venn Diagram Analysis

- Using GenBank format files of closely related genomic nucleotide sequences for which genes have already been identified, it is judged whether or not they are common genes among all the genes present on each genome, and it is judged whether or not it is a common gene between 3 genomes or 2 genomes Draw Venn Diagram of Venn.
- To determine common genes, use Percent Identity and Overlap Length for amino acid sequence homology search by NCBI Blast.
- Information on genes belonging to each group can be displayed from the result window, and file output is possible.
- Also, each element of the list is linked with a feature map.
- The result image can be output as a file in PDF / PNG / EMF format.

Core Genome Analysis

- Core genome analysis is a function to identify conserved core genes among multiple closely related genomes.
- For the current genome sequence, genome to be analyzed can be selected from the genomic sequence in the current reference directory.
- In the analysis result window, core genes are listed, and when you click on each gene line, the main feature map and reference genome map display their gene regions.
- Multiple alignment display is possible, the function is the same as the function of multiple alignment window.
- The selected core gene can be output as a file in CSV format.
- The analysis result is saved as a dedicated format file and can be read and displayed.

Mutation Search

- Detects mutation sites between closely related genomes in base units.
- Based on the current genome sequence, you can select and compare two or more from the genomic sequence loaded in the current reference directory.
- The genomic sequence must be genetically extracted and the CDS feature must be registered.

- The detection site can be set on CDS or intergenic region.
- For detection criteria, you can change % Identity and Overlap ratio.
- A list of mutated bases is displayed on the analysis result window, and the display items are mutated bases, mutation positions, gene names, ocus-Tags by genome sequence.
- Results can be output in CSV format.

EC Number Compare List

- We will list the status of addition of EC numbers in multiple closely related genomes.
- The analysis results show presence / absence in each genome sequence in order of EC number.
- You can output this list in CSV format.

Multiple Alignment

- Make an alignment between multiple nucleic acid or amino acid sequences.
- Multiple selections are possible from the sequence loaded in the main current directory.
- You can also activate this function from the homology search result window.
- From the result window, you can use the phylogenetic tree drawing function, simple editor function, copy to the clipboard, and print.
- You can change the number of characters displayed on one line.

Phylogenetic Tree

- From the multiple alignment result, draw the molecular phylogenetic tree of the selected feature.
- You can specify horizontal display, vertical display, and rootless tree.
- It is also possible to show / hide the evolution distance.
- You can select the shape of the node from Box, Circle, None.
- A phylogenetic tree diagram can be output as a file in PDF format.
- You can read and display the phylogenetic tree file (dnd format) created externally.

Alignment Editor

- It is an editor for editing consensus sequence from multiple alignment result.

- You can change the match and mismatch symbols and colors.

Gene Cluster Alignment

- We load multiple annotated genomic sequences on the reference genome map, search homologous genes in other genes from one CDS of one genome, and also detect homology between surrounding genes.
- Alignment of the gene cluster can be obtained as a result.

Multiple Aligned Linear Genome Map

- Multiple linear genomic maps are also referred to as reference genomic maps and are parallel feature maps from multiple genomic chromosomes between closely related species.
- All of the genomic sequences loaded into the reference genome map and automatically loaded into the current directory are automatically drawn on the map.

Single Reference Genome Map

- The single reference genome map is loaded and automatically drawn for comparison with the current genome on the main feature map.
- A map of one selected genome sequence is drawn in the genome sequence loaded in the current reference directory.

Annotation

Genome Auto Annotation

- Performs automatic annotation of the specified genomic sequence (s).
- You can select from local, local emulator, external server as execution location.
- It is necessary to create search database in execution place using Create DB beforehand.
- Commands that can be selected depend on the OS of the execution location.
- Multiple genome sequences can be specified at once, and execution is batch processing.
- Commands for searching can be selected from blastp, blastx, tblastx.
- The output file is GenBank format.

Transcriptome Auto Annotation

- Perform automatic annotation of the transcriptome sequence.
- The execution location is local only.
- It is necessary to create a search database beforehand.
- You can specify the feature key of the generated gene.
- You can specify the order from top to include in the annotation from the top hit.

Auto Annotation from Reference Genome Sequence

- Automatically annotate the whole genome sequence loaded in the main current directory using the reference genome sequence as a query.
- After execution, the candidate list is displayed and you can manually select whether or not to register.

Settings of External Server for Annotation

- Set up an external server for auto annotation.
- The commands that can be set are MetaGenomeAnnotator, AUGUSTUS, tRNAScan-SE, RNAmmer.

Finding Overlapped Genes

- Search for overlapping CDS on a genome sequence.
- Search result, its position and strand.
- You can output the result list in CSV format.

Metagenome Analysis

Metagenome Analysis

- Settings of 16SrRNA Variable Regions
- As pre-processing of 16S rRNA metagenomic analysis, Variable regions are assigned to be used as search database.

Metagenome Analysis using 16SrRNA: Preprocessing to Searching Database.

- Preprocess fragment sequence reads of 16S rRNA sequenced with NGS.
- In the case of paired fragments, it will join automatically.
- The number of data to use can be limited. It is necessary to load the 16S rRNA database beforehand.

- Search each fragment read against the database and execute the Taxonomy annotation.

Metagenome Analysis using 16SrRNA: Creation of Summery

- 16 SrRNA Generates graph data by Taxonomy Rank by using search results of metagenome analysis.

Genome Design
Reverse Complement Operation

- Convert the current sequence, including all the features, into an arrangement that uses the reverse complementary strand as it is, and the feature map also turns around with the reverse complementary strand in order and is displayed.
- The reverse complementary strand converted sequence can be output in that state.
- The tool button becomes the toggle display of the reverse complement button, and once it is executed again, it returns to the original chain.

Codon Replacement

- Replace the selected CDS so that it can not be digested and cleaved with the specified restriction enzyme.
- The codon used for substitution is set based on the specified codon frequency table, and frequently used codons are set.
- The original codon that was changed is registered in Qualifier / modified_base = of the corresponding CDS feature.

Gene Replacement based on CAI

- In order to perform heterogenous recombination, convert the gene sequence of the inserted gene into a sequence matched to the CAI of the host.
- Load the genome sequence of the host into the current reference genome, find the CAI from the codon usage frequency analysis result, and replace the gene of the main current sequence based on that.

In-Fusion Cloning: Design and Build

- For In-Fusion cloning, we will automatically design primers for In-Fusion so that several fragments can be inserted into the vector at the same time.
- Load the vector to be used for In-Fusion cloning as the current sequence.
- On the design dialog, the vector sequence is shown in the opened state first.
- If you drop multiple sequences that you wish to clone into the open part from outside the IMC, fragments will be placed in the open part.
- The arrangement of fragments can be moved.
- Parameters for Primer design for In-Fusion include Primer Size, overlap base length of 5 'Junction and 3' Junction, and the like, add name, add base length, Tm
- There is a value addition, automatic naming (serial number) setting, strands. Primers designed are displayed in the list, new registration in the Primer list, loading as a construct is possible.
- The result can be file output in CSV format.

Fusion PCR: Design and Build

- It is a function to recombine many insert sequences into the same vector.
- List the CDSs from the loaded current sequence, connect each to the designated promoter and marker, and design a primer set for Fusion PCR continuously.
- Designed primers can be registered in the primer list, and results can be output in CSV format file.

Homology Arm Design

- Design primers to amplify homology arms for homologous recombination.
- Select regions to be homologous recombination on the genome sequence in the feature lane.
- The product of amplification can be loaded as the current sequence or loaded into the reference genome map.

Homologous Recombination

- Homologously recombine into the main current sequence and replace the recombination region.

- By loading the insert sequence on the current folder of the reference genome map and designating the homologous region in the current genome sequence, homologous recombination is performed and the genomic sequence is replaced with the insert sequence.
- The recombined genome can be loaded as a separate sequence into the current folder.

Gene Cluster Design Checker

- Check that the current sequence is correctly constructed as a gene cluster.
- The presence / absence of start / stop codon, the number of designated restriction enzyme sites, the number of repelling sequences, the presence or absence of an essential sequence within the specified base length from the start codon, detection of rare codon in the host sequence, etc., if the design is incorrect A warning message is displayed.

Tools and others
in silico Assembler

- in silico Assembler is de novo Assembler.
- DNA fragments of 50 bp or more can be assembled.
- Reads from NGS can also be assembled.
- In the preprocessing, limited number of processing, designation of minimum QV, maximum N bases can be limited.

iSpider

- It is a tool to automatically download sequence files specified from the public database.
- Although five types of databases (RefsSeq microbial, COG, KOG, NR, TrEMBL) are registered by default in the download list, the user can register arbitrary sequence database.
- Save download list as a different name.
- Similarly, it is possible to read the list, import the list, and recover to the initial state. It is possible to execute download manually, or automatically execute specified start date and time.
- The downloaded files are stored in the specified folder and the list is recorded, so you can quickly find and use the downloaded sequence.

Taxspider

- It downloads attribute list of microbial genome sequences, stores them locally and places them on each branch of Taxonomy Tree.
- The Taxonomy Tree is divided into two, and from Super Kingdom to Order, the left pane, one Tree belonging to the selected Order is expanded to the middle pane from there.
- If you select mainly Species at the end of Taxonomy, the list of the sequence is displayed in the right pane, and the Nuc sequence, AA sequence distinction, Locus, definition, length etc are displayed.
- Actual sequence data is downloaded from NCBI by referring to the attribute at the terminal node.

ARM: The Pathway Finder / Editor

- ARM is a metabolic pathway search tool, and the following operations are possible.
- Search and display of metabolic pathways from source compounds to target compounds, synthesis of multiple single pass, overlay of enzyme expression level data graphs and maps, mapping and graphical display of compound metabolism data, new reaction registration, new compound registration, Carbon · nitrogen · sulfur atom tracing function.

Search Pathway using ARM

- It is a tool to find a metabolic pathway that connects two compounds by specifying a source compound and a target compound on two CDSs on a feature map.
- ARM is started during execution.
- Atom trace is possible and can be set for carbon, nitrogen and sulfur.

NGS Paired File Converter

- It is a tool to combine NGS's paired fragments into one.

Multiple GenBank File Expander

- It is a tool that expands GenBank format data in which a large number of genome sequence data is stored in one file to a tree tree with reference to its definition information.
- It makes it easier to understand what kind of sequence data is in the file.

Format Checker

- This tool inspects and automatically restores GenBank and EMBL format files.

Specification

Monitors	
Screen size	W1024px x H768px
Environment	
Minimum Memory Size	1.0GB
Licensing	
Version Up	Unlimited during the term
Licensing Term	One Month
Delivery Method	
Download	Downloadable
Package Delivery	Not Available
OS	
JAVA Version	JAVA 8
MACOS	MACOS 10.13, 10.14, 10.15, 11, 12, 13
Windows	Windows 10 11
Input File Format	
BlastDB Creative Sequence Format	FastA, GenBank/EMBL, GenPept
Feature File Format	CSV, Glimmer 1-5, GenScan, Gambler, XanaGenome, tRNAScan 1-2, Blast result, JSNP1-2, GFF, AUGUSTUS, BED, dbSNP, , Seq_gene, IMC Keyword Search, Simple Annotation, InterProScan
Loadable Amino Acid Sequence Format	GenPept, FastA
Loadable Nucleotide Sequence Format	GenBank,EMBL,DDBJ, FastA, Plain Text, ABI, SCF
Output File Format	
Image File Format	PNG, PDF, EMF
Profile File Format	IMC Original Format
Writable Nucleotide Sequence Format	GenBank, EMBL, DDBJ, FastA
Functions: Basic Operations	
Auto Sequence Format	It is automatically determined whether the

Check	**loaded sequence file is a nucleic acid sequence or an amino acid sequence. In addition to this, it also has the function of specifying the sequence as nucleic acid or amino acid and reading it. These three activa**
Check, Download, Install the IMC Latest Version	**Perform release check, download and installation of the latest version of IMC installer and help. A confirmation dialog is output before downloading and installing.**
Creation of Blast Search Dabase	**A database for Blast search is generated from the nucleic acid sequence file and the amino acid sequence file. For the array file loaded in the main current directory and the reference current directory, the Blast database is automatically created at the**
Feature Info Tab	**Display the information content of the feature on the currently loaded genome sequence. Switch to directory tree and displayed.**
Function Search (Beta Version)	**This function is not used.**
Lab Note	**Record IMC operations on a command basis. The recorded contents are the execution date, the command, the execution window, the reference location of the input data, the storage location of the output data, the database used, the execution parameters, the**
Operation History Manager	**A function to automatically save the operation history. Items to be saved are the feature key, position, strand, operation command, execution date and time of operation subject. History can be sorted by three kinds of sort keys. The sort key can output th**
Toggle Button of Toolbox Visibility Change	**Toggle button to toggle display and hide of tool box below menu bar. The toolbox can also be docked out from the main window.**
Window Capture	**Screen capture function of the entire main window or designated area. The captured image is immediately saved in the specified file. Save format is PNG format only.**
Function: Viewer / Editor	

Annotation Viewer/Editor	**A tool prepared for genome annotation. It is mainly used for annotating CDS. The window is divided into three parts, you can enter and edit annotations directly · Descriptions pane, you can link the result of homology search to the CDS feature itself, dis**
Circular Genome Map Viewer / Editor	**Editing / deleting of profile concentric circles, addition / editing / deletion of profile concentric circles, automatic map creation of multiple genomes, printing · image file output (PDF, PNG, WEF) possible. The designed circular layout can be saved as**
Description Window	**Window for editing Feature Description. It is launched from the feature and consists of genomic location, strand, Qualifier list and value, and nucleic acid sequence and amino acid sequence display region. Each array can be copied to the clipboard.**
GenBank/EMBL File Viewer	**A viewer that can view the currently loaded array file in its original format. When you click on an array or annotation, the main feature map will display a map of that position. Conversely, while this viewer is open, clicking a part of the main feature m**
Plasmid Map Viewer / Editor	**It is similar to the circular genome map editor but draws a small circular genome. The annular lanes are arranged concentrically, and a plurality of feature keys can be arranged on one concentric circle. Strand, frame, feature shape, color designation of**
Sequence File Viewer	**Viewer that displays the array of the area currently displayed in the main feature map. You can display the display range on the viewer, show / hide the reverse strand, display / hide the amino acid translation, change the display method of the scale, dis**
Trace File Viewer / Editor	**It is used when reading the output file from the capillary sequencer of ABI, SCF. Not only the base sequence but also its waveform (trace) can be displayed. Also you can change the base call.**
Functions: Feature Map Operations	

Co-movement of Feature Map with a Feature List	**Result screen of feature key search, keyword search, sequence pattern search, function classification search, genome statistics display, and feature map are linked.**
Dock In & Dock Out	**The Main Directory Tree, Reference Direactory Tree, Info Tab, Main Feature Map, Reference Feature Map, Toolbox can be retrieved in another way for dockable / dockable panes.**
Feature Map Zooming Scrolling Parameter Change	**The main feature map can scroll left and right in units of bases and screens. There is a dedicated button. Vertical scrolling is controlled by the scroll bar. To zoom, use the toolbox or zoom button on the menu. Zoom in can be specified by mouse drag on a**
Operations on the Sequence Lane	**Items that can be set on the array lane include font size change of nucleic acid base and amino acid, display position change of amino acid 1 letter code, display color change of nucleobase and amino acid residue, display of start and stop codon candidate**
Settings on the Sequence Lane	**Items that can be set on the array lane include font size change of nucleic acid base and amino acid, display position change of amino acid 1 letter code, display color change of nucleobase and amino acid residue, display of start and stop codon candidate**
Function: Operation on a Feature or Feature Lane	
Edit Qualifiers of the Feature	**Display color setting, attached document file, molecular structure file attachment, feature map display, genome map display, genetic code table change**
Editing of Feature	**Deletion designation, deletion, duplication, deletion of introns, deletion of exons**
Execution from Feature	**Homology search to the reference genome, codon frequency table display, amino acid profile display, copy of sequence and annotation, design of primer to amplify features, activation of annotation window, activation of description window, activation**

	of seq
Functions: Feature Map Layout Design	
Content / Profile Lane	Change the background color, change the parameters of the profile graph, change sliding window parameters, thinning out (6 contents, such as GC Content, GC / AT Skew, Cumulative GC / AT Skew, Import Map Data, Fickett Profile) Function, change graph color.
Enzyme Map Lane	Setting change (lane height, set switching, restriction enzyme list narrowing down (recognition sequence length, palindromic nature, terminal shape (Blunt, Sticky), DAM / DCM, number of cut sites of target sequence, selection of restriction enzyme)
Feature lane	Display feature key (s), strand selection, arrangement method (Six Lane, Three Lane, Two Lane, One Lane, Pack), Chain change (Forward, Reverse, Both), Exon display method change, Placement density, Lane Height change, offset change
Feature Layout Style Designer	Design manager of feature layout style. Register, edit, delete a new lane to a style, change the display order, and save the style as a different name. It is also possible to call and edit an existing style. The editing function of each lane is described
Feature Layout Style Manager	Newly register, edit, and delete feature layout styles. Also import and export styles individually. Save the entire list with a different name. You can change the default style. This list is displayed as a pull-down menu in the upper indicator area of the
Local Genome Rearrangement Map Lane	The parameters that can be changed are lane height, vertical offset, the feature to display (multiple designation possible), strand designation (Forward, Reverse, Both), arrangement method (Six Lane, Three Lane, Two Lane, One Lane, Pack) Change of display
Navigation Lane	Selectable feature (s) can be selected. Strand selection (Forward, Reverser, Both), placement method selection (Six Lane, Three Lane, Two Lane, One Lane, Pack)

No Parameter Lane	Array Lane, Vertical Scroll Bahrain, Array Scale Lane, Map Scale Lane, Frame Lane
Feature and Feature Key Design	
Add Sequential Number to a Feature	Sequential numbers can be added to features hit from each search result of feature - key search, keyword search, genome statistics.
Feature Key New Registration / Editing / Delete	New feature keys can be registered, edited and deleted. However, it is not possible to edit or delete essential feature keys. When newly registered, it is possible to use the already registered feature key as a template. You can specify feature key name,
Function: Reference Map Operatoins	
Multiple Linear Genome Map = Reference Genome Map	A multiple linear genome map is a parallel feature map from multiple genomic chromosomes between closely related species. All of the genome sequences loaded into the reference genome map and automatically loaded into the current directory are automaticall
Function: Search	
Feature Key Search	You can count the number of feature keys in the current array, select multiple features to be searched, limit the search range, on the result screen, the number of each feature key, the position on the array, the base length, the gene name,
Gene Functional Code Search	Select multiple genetic function codes (optional but general COG classification) and search for CDS features with those functions. Search range specification possible. Multiple sequences can be searched. From the search result screen, the CDS number, the
Keyword Search	Enter keywords and search annotations. Multiple target feature keys can be selected. Multiple keywords can be specified. Logical operation between keywords is AND / OR / NOT. Search range can be limited. In the result screen, buttons for feature key
Search Overlapped Genes	Search for arrays with overlapping CDS on the array. Search result, its position and strand. You can output the result list in CSV

	format.
Sequence Pattern Registration	It is possible to register, edit and delete the base sequence pattern and the amino acid sequence pattern (motif). Array pattern conforms to regular expression. Pattern name and pattern regular expression can be registered. You can save the list of select
Sequence Pattern Search	A plurality of registered array patterns are selected, and patterns existing in the current array are detected. It is also possible to search by entering a new pattern when searching. Search range specification possible. Search target strands are possible
Function: Tools	
DNA Assembler	Capillary sequencer fragment assembler. It is currently being improved, so it can not be used.
File Format Checker	Inspect GenBank / EMBL format file and automatically restore it.
iSpider	A tool that automatically downloads the sequence file specified from the public database. Though five types of databases (RefsSeq microbial, COG, KOG, NR, TrEMBL) are registered by default in the download list, the user can register arbitrary sequence
Metabolic Pathway Finder / Viewer	Search and display of metabolic paths from source compounds to target compounds, synthesis of multiple single pass, overlay of enzyme expression level data graphs and maps, mapping and graphical display of compound metabolism data, new reaction registrati
Metabolic Pathway Search between two compounds	A tool to locate a metabolic pathway connecting two compounds, specifying a source compound and a target compound on two CDSs on a feature map. ARM is started during execution. Atomic traces are possible and can be set for carbon, nitrogen and sulfur.
Multiple GenBank Format File Phylogenetic Tree	A tool that develops data in which a large number of genome sequence data is stored in one file to the tree tree shape with

Expansion Tool	reference to the definition information. It is easy to understand what kind of sequence data is available.
NGS Paired File Converter	A tool that combines NGS paired fragments into one.
TaxiSpider	A tool that downloads attribute lists of microbial sequences, stores them locally, and places them on each branch of Taxonomy Tree. Disk space of 47 GB is required locally. The Taxonomy Tree is divided into two, and from Super Kingdom to Order, the left p
Function: Cloning	
Batch PCR Primer Designer	Save the file in advance using a Feature Key search etc. for the list of CDS etc. to be PCR amplified on that genome. When that file is executed, this function is executed and all the primers which amplify each CDS in the list are automatically designed a
Contig Bridge	List PCR product sequences that can bridge multiple contig sequences
DNA Fragment End Modification	Add Restriction Enzyme Recognition Sequence, Add Thymine, Blunting, Phosphorylation/Dephosphorylation
Genome Sequence Editing	Edit genomic sequence in information processing regardless of molecular biological means. Deletion of specified area, fragmentation by disconnection at specified (plural) positions, replacement of codon
Ligation	Ligation of two fragments on the current folder, self-ligation of one fragment on the current folder
Operations on the Gel Electrophoresis Bands by Restriction Enzyme Digestion Fragments	Electrophoretic image printing, image file output (PDF, PNG, EMF), band extraction and corresponding array file save
Operations on the Restriction Enzyme Map	Sequence file switching, feature map display, zoom / scroll, slider, band extraction, gel electrophoresis window activation
Operations on the Restriction Enzyme Recognition Site List	Sequence switching, additional enzyme search, digestion fragmentation, registration of a new feature at the recognition site, registration of digested fragment file, gel

	electrophoresis by fragment, list output (CSV, Fast A), linked list and feature map
PCR Primer Design Parameters	It is possible to design a primer inside (or outside) the selection area. The designable region width change, minimum product base length, primer (longest and shortest base length, minimum · maximum Tm, minimum · maximum GC content, annealing oligo concen
PCR Primer Designer	New sequence can be registered by selecting base sequence of sequence lane. Drag the feature lane to design the optimum primer within (within) the selected area. In the design result screen, the primer sets matching the conditions are listed in order of s
PCR Primer Manager	The registered primer attributes are Primer ID, Primer sequence, Primer base length, Tm, GC content, Registration date, Comment, Link to the file that executed PCR. The list can be sorted using Primer ID, Length, Tm, GC (%), Comment as a key. New registra
PCR Reaction	Perform in silico PCR. Execution includes a method of selecting a Primer Set to be used from a primer list, execution from a design list from a feature map, and the like. When Amplify is executed, a list of products is displayed, a product can be selected
PCR Reaction for Multiple Template Seqeunces	Function to perform PCR reaction with the same Primer set for multiple genome sequences. You can display the number and position of Priming Site on each template, load selected products into the current folder, and output files in CSV format.
Restriction Enzyme List Operations	Set selection, narrowing down (number of recognition bases, palindrome, smoothing / protrusion, DAM / DCM, number of cut points, list saving, list editing, enzyme new registration, enzyme editing,
Restriction Enzyme Recognition Site Search	Search area selection, recognition site search, recognition site list display, restriction enzyme map display, collective search from

	multiple sequences
Sequencing Primer Designer	Automatically design an entire sequencing Primer set for sequencing the current sequence. As the design parameters, in addition to the default Primer design parameters, the primer distance can be set. For areas that could not be designed, change the param
Whole Genome Covering PCR Primer Designer	Automated primer design function to obtain products covering whole genome with equal length products. For areas that could not be designed, the parameters can be changed and the design can be repeated until the entire area succeeds. The designed primer li
Function: Genome Analysis	
16SrRNA Meta Genome Analysis: Pre-processing to Searching	Preprocess fragment sequence of 16S rRNA sequenced with NGS. In the case of paired fragments, they are combined automatically. Limited number of data to use. It is necessary to load the 16S rRNA database beforehand. Search each fragment sequence against t
16SrRNA Variable Regions Setting	As preprocessing of 16S rRNA metagenomic analysis, we set the variable region to be used and generate the database.
Alignment Editor	Edit the consensus sequence from the multiple alignment result. You can change the match and mismatch symbols and colors.
Amino Acid Sequence Mapping	Multiple amino acid sequence files are specified and mapped on the current genome sequence. Since it is mapped only to the exon region, fragments mapped from one amino acid sequence can be combined and registered as one feature consisting of multiple posi
Auto Annotation	Perform automatic annotation of genome sequence. You can select from local, local emulator, external server as execution location. It is necessary to create the search database in advance in the execution place using Create DB in advance. The commands tha
Auto Annotation from	Using the reference genome sequence as a

Reference Sequence	**query, auto annotate to the whole genome sequence loaded in the main current directory. After execution, the candidate list is displayed and you can manually select whether to register.**
Auto Transcriptome Annotation	**Perform automatic annotation of transcriptome sequences. The execution location is local only. It is necessary to create a search database in advance. You can specify the feature key of the generated gene. You can specify the order from top to include in**
Batch Homology Search by Current Sequence	**Perform a homology search on the specified search database using the current sequence as a query. Automatically transfers the specified Qualifier among the qualifiers of the hit sequence.**
Batch Homology Search for Selected Feature Sequences	**Homology search is performed on each sequence data in the current directory and data specified from the generated search database using the selected feature as a query. Automatically transfers the specified Qualifier among the qualifiers of the hit sequen**
Core Genome Analysis	**Core genome analysis is a function to identify conserved core genes among multiple closely related genomes. For the current genome sequence, it is possible to select a genome to be analyzed from the genomic sequence in the current reference directory. Hom**
Display Data Creation from the Results of 16SrRNA Metagenome Analysis	**Using the search result of 16S rRNA metagenome analysis, generate graph data etc. by Taxonomy Rank.**
Draw Phylogenetic Tree	**From the multiple alignment result, draw a phylogenetic tree of the selected feature. You can specify horizontal display, vertical display, and rootless tree. It is also possible to show / hide the evolution distance. The shape of the node can be selected**
EC Number List between Multiple	**List the status of EC number addition in multiple closely related species genomes.**

Genomes	**Analysis results show presence / absence in each genome sequence in order of EC number. You can output this list in CSV format.**
EST Mapping (on Current Feature Map)	**Specify multiple single EST sequences and map them by homology on the current sequence. Specify the maximum base length of the intron, and exclude it from the mapping subject when adjacent exon distances are separated. After execution, a mapping candidate**
Feature Fusion	**If there are two or more features with the same Feature Key at the same position in the current sequence, these Qualifers are inherited and merged into one feature.**
Gene Cluster Alignment	**A plurality of annotated genomic sequences are loaded on the reference genome map, homologous genes in other genes are searched from one CDS of one genome, and homology between the surrounding genes is also detected, and as a result, genes Obtain cluster**
Genome Info: Feature Statistics	**Displays the number of registrations by feature key of all the features existing in the current genome sequence. A list of features belonging to the selected feature key is displayed and the display items include genome position, strand, GC content, base**
Global Genome Rearrangement Map Analysis	**Create and draw a genomic rearrangement map over the entire length between closely related genomes. Compare the genome length in pair wise between the current genomic sequence and the genomic sequence (s) selected among closely related species genomic seq**
Homology Search by Input Sequence	**Homology search is performed on the selected sequence among the sequences in the current directory (main and reference) using the sequence entered by copy and paste or sequence designation as a query. Possible homology search programs are blastn, blastp,**

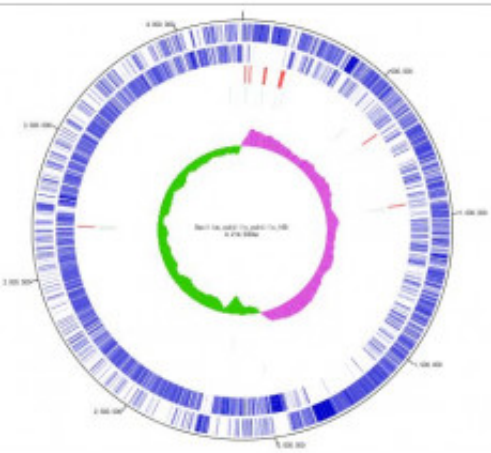
Local Genome Rearrangement Map Analysis	**Generate and draw a local genomic rearrangement map across the whole between two closely related species at the sequence level. Based on the current sequence genome, homologous regions with different closely related species genomes loaded in the current r**
Multiple Alignment	**Make an alignment between multiple nucleic acid or amino acid sequences. Multiple selections are possible from the arrays loaded in the main current directory. This function can also be activated from the homology search result screen. From the result scr**
Mutation Search	**Detects mutation points between closely related species genomes as base units. Based on the current genome sequence, a plurality of genome sequences loaded in the current reference directory are selected and compared. The genomic sequence must be genetica**
ORF Extraction	**Extract ORF candidates from the current genome sequence. Extraction range designation, gene region limitation, intergenic region length definition, longest extraction from overlapping candidates, selection of starting positions, extraction of candidates w**
Overlapped Feature Processing by Feature Operators	**If the features belonging to the same feature - key are in a position where they overlap each other, a new AND / OR / XOR feature of those features is generated and registered. You can specify the feature key of the newly generated feature.**
Repeat Sequence Search	**Extract repetitive sequences in the current sequence. A result window is displayed, and when you click on the corresponding line, the main feature map shows its position. In the list, the sequence base length, the positions of the two sequences, and the b**
Reverse Complement Conversion	**Convert the current sequence including all the features into an arrangement with the reverse complementary strands as the**

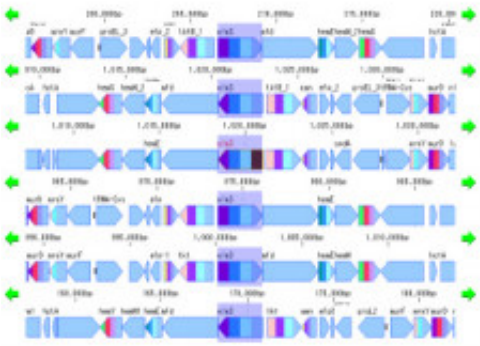
	ordinal chain. Array with reverse complementary strand conversion can output file in that state. Run it again to return to the origin
Settings of External Server for Annotation	Set up an external server for auto annotation. The commands that can be set are MetaGenome Annotator, AUGUSTUS, tRNAScan-SE, RNAmmer.
Show Codon Usage	Create a codon frequency table for the current sequence file. For annotated genomic sequences, the total frequency of all CDSs is calculated. CDS number, codon number on CDS, number of bases are displayed. Notation is mRNA and DNA display possible. The ra
Trace Mapping	Mapping the sequence file from the ABI / SCF format capillary sequencer onto the current array. After execution, the mapping candidate list is displayed, and only the selected one can be registered as a feature -. After registration, you can display its w
Translation	The nucleotide sequence of the specified feature key is converted into the amino acid sequence by the specified codon table. Selectable feature keys are CDS, ORF_XXX, Prokaryote or Eukaryte. The ORF feature is changed to CDS after translation.
Unique Region Search between Genomes	It searches for a specific (non homologous) region by comparing the current genome sequence with the current loaded genomic sequence of the reference genome as a query. When you click an area from the unique area search result screen, each map displays it
Venn Diagram Analysis	Using GenBank format files of closely related genomic nucleotide sequences for which genes have already been identified, it is judged whether or not they are common genes among all the genes present on each genome, and it is judged whether or not it is a
Function: Amino Acid Sequence Analysis	
Profile	Hydrophobicity, hydrophilicity, chain

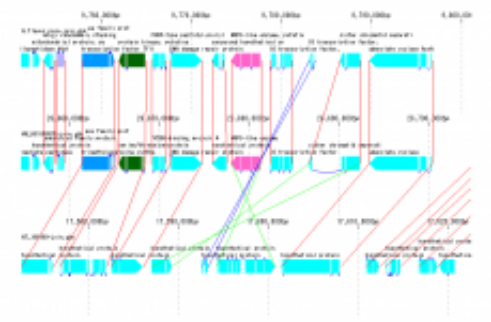
	flexibility, surface property, molecular weight, alpha helix, beta sheet, beta turn, polarity, bulky nature, total score
Settings	Sliding window setting, profile color setting, normalization, amino acid motif display, display profile selection, automatic · manual scale, reference line change, weight change,
Function: Genome Design	
Codon Replacement	Replace the selected CDS so that it can not be digested and cleaved with the designated restriction enzyme. The codon used for substitution is based on the specified codon frequency table and used frequently. The changed original codon is registered in Qu
Fusion PCR: Design and Build	List the CDSs from the current sequence being loaded and connect each to a designated promoter and marker to design a primer set for Fusion PCR continuously. Designed primers can register primer lists and output files in CSV format.
Gene Sequence Design using CAI Analysys	In order to perform heterologous recombination, the gene sequence of the inserted gene is converted into a sequence matched with CAI of the host. Load the host genome sequence into the current reference genome and edit the main current sequence.
Genome Design Checker	Check that the current sequence is correctly constructed as a gene cluster. Presence / absence of start / stop codon, number of designated restriction enzyme sites, number of repeller sequences, presence of essential sequence within the specified base len
Gibson Assembly; Design and Build	
Homologous Recombination	By loading an insert sequence on the current folder of the reference genome map and specifying a homologous region in the current genome sequence, homologous recombination is carried out and the genomic sequence is replaced with the insert sequence. The r
Homology Arm Design	Regions to be homologously recombined on

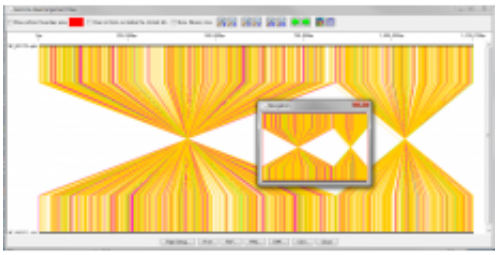
	the genome sequence are selected in the feature lane, and when this is done, primers are designed to amplify the homology arms for homologous recombination. It is possible to load and load products by amplification
In-Fusion Cloning: Design and Build	Load the vector used for In-Fusion cloning as the current sequence. On the design screen, the vector sequence is shown in the opened state at the beginning. When multiple sequences that you wish to clone in the open part are dropped from the outside of th

Product Gallery

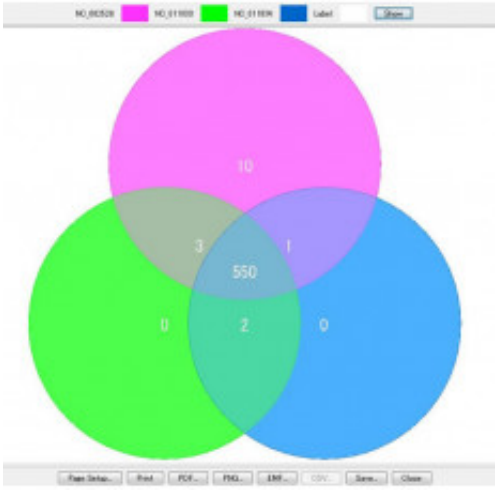











10
3
1
550
0
2
0

