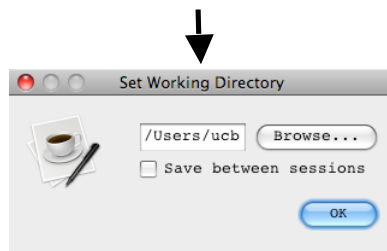
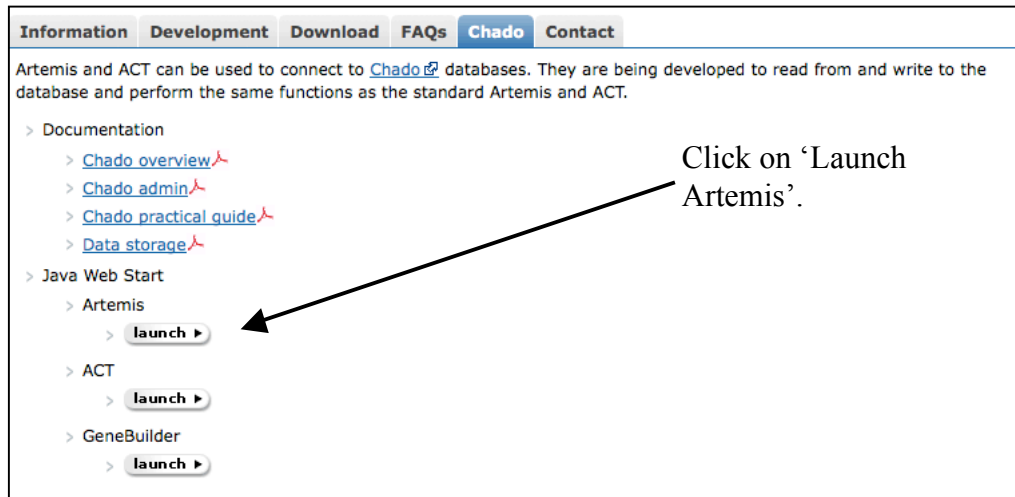


Annotation in the database version of Artemis

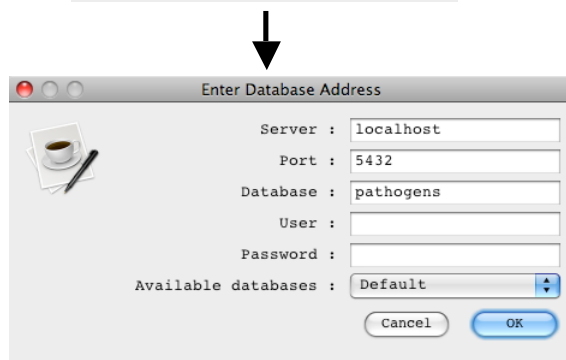
1. Functional annotation

To start up the Artemis software, go to the following website:

http://www.sanger.ac.uk/resources/software/artemis/#t_5



Set your working directory for the backup files and optionally save this setting between sessions.

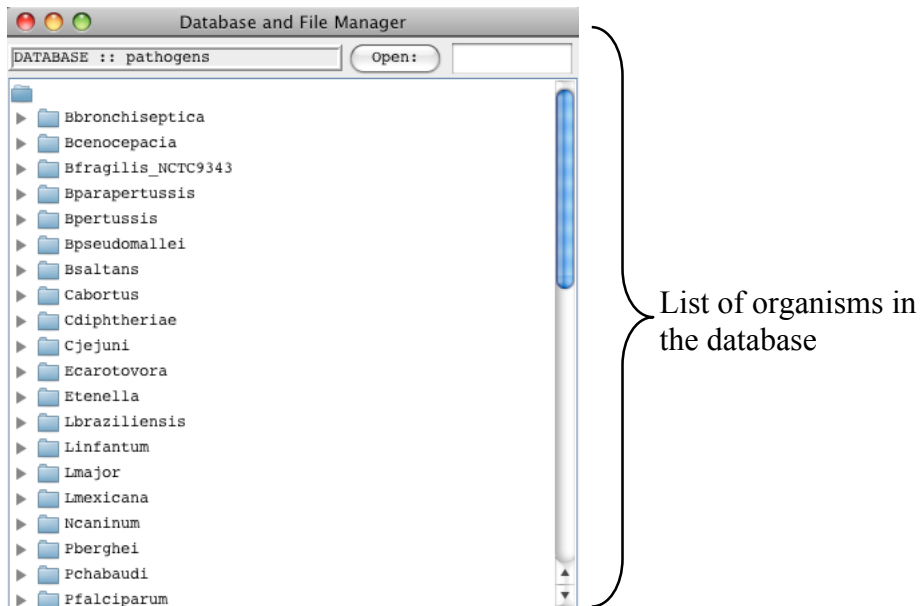


The following window will come up. Enter your user name and password and then click OK.

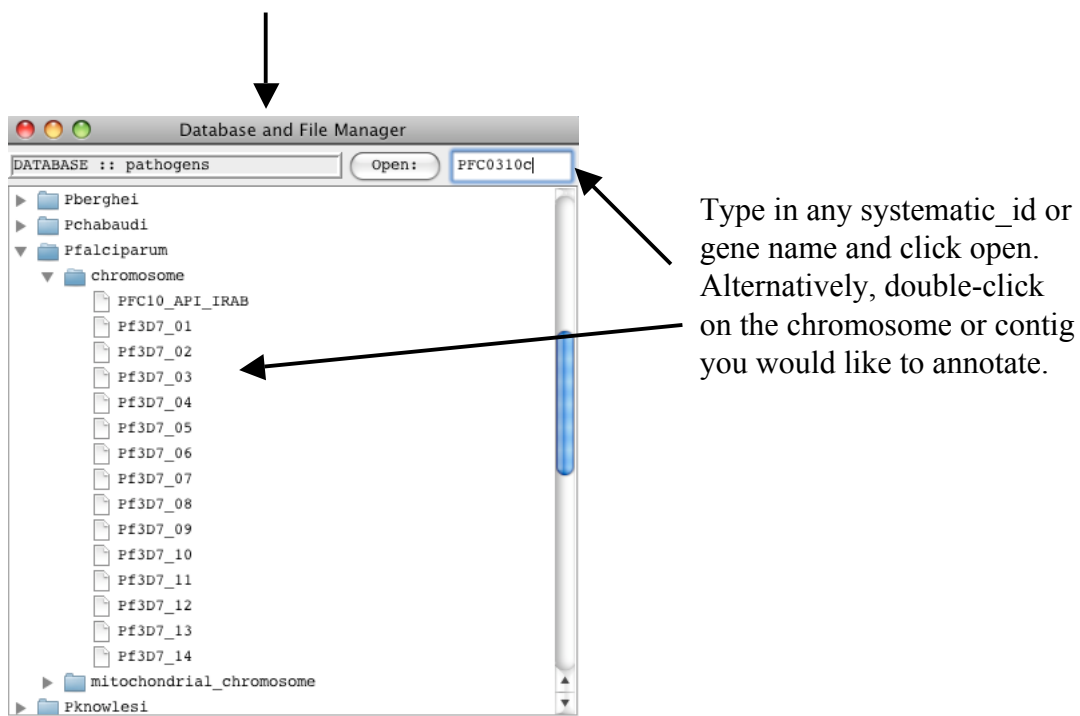
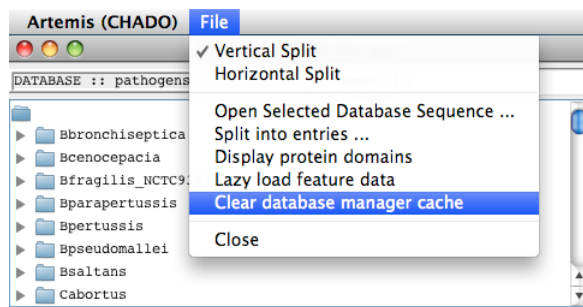


Wait for the 'Database and File Manager' to be loaded.

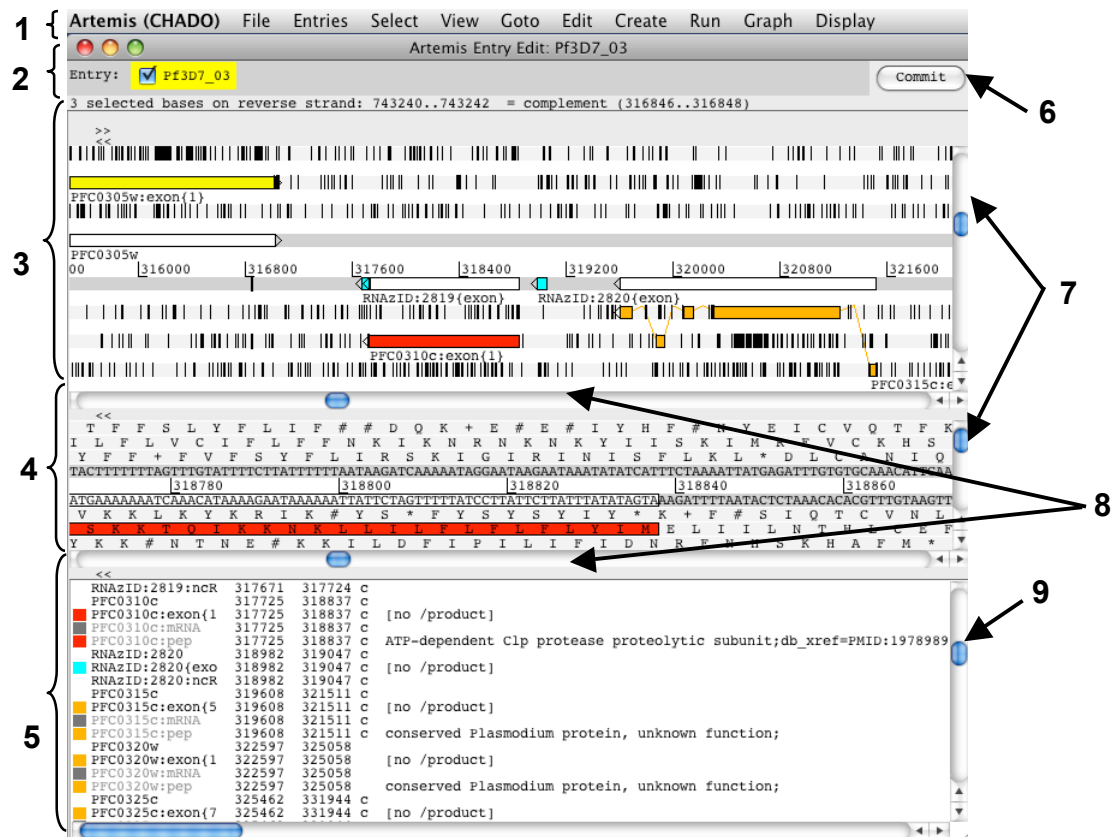
After the loading is done, double-click on the chromosome or contig you want to annotate.



The database manager is cached, so after time you may need to clear this. To see the latest version of the organism list in the database, go to the File menu and select the option to clear the database manager cache. You will then need to re-open Artemis afterwards.



Main Artemis window



1. Drop-down menus.
2. Shows what entries are currently loaded (top line) and gives details regarding the feature selected in the window below (bottom line).
3. This is the main sequence view panel. The central 2 grey lines represent the forward (top) and reverse (bottom) DNA strands. Above and below those are the 3 forward and 3 reverse reading frames. Stop codons are marked as black vertical bars. CDS and other features (eg. Pfam matches) are displayed as coloured boxes.
4. This panel has a similar layout to the main panel but is zoomed in to show nucleotides and amino acids. Double click on a gene in the main view to see the zoomed view of the start of that gene model. Note that both this and the main panel can be scrolled left and right (8, below) zoomed in and out (7, below).
5. This panel lists the various features in the order that they occur on the DNA with the selected CDS highlighted. The list can be scrolled (8, below).
6. Commit button, to commit changes to the database. The button will turn red once a change has been made.
7. Sliders for zooming view panels.
8. Sliders for scrolling along the DNA.
9. Slider for scrolling feature list.

Artemis Entry Edit: Pf3D7_03

Entry: ☒ Pf3D7_03

Selected feature: bases 1113 amino acids 370 PFC0310c:exon(1) (/isObsolete=false /Parent=PFC0310c:mRNA)

>>

<<

PFC0305w:exon(1)

PFC0305w

00 316000 316800 317600 318400 319200 320000 320800 321600

RNAzID:2819(exon)

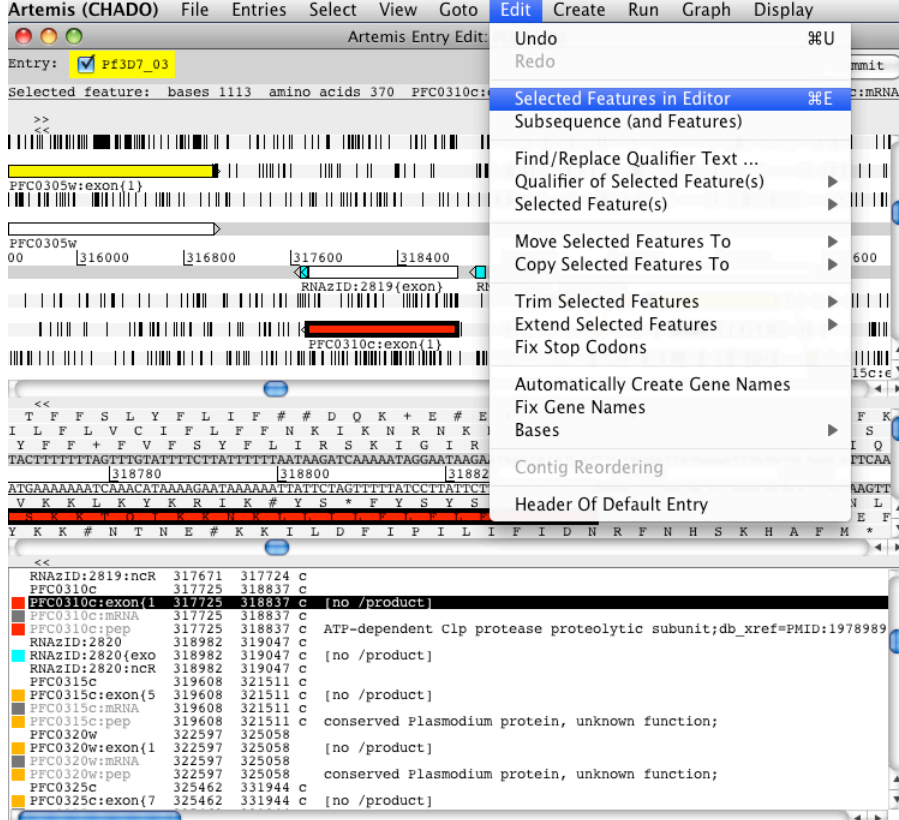
RNAzID:28 PFC0315c

PFC0310c:exon(1)

PFC0315c:exon(1)

T T F F S L Y F L F I F # # D Q K + E # E # I Y H F # N Y E I C V O T F K
I L F L V C I F L F F N K I K N R N K N K Y I I S K I M R F V C K N H S
Y Y F F + F V F S F L I R S K I G I R I N A T I S F L K L * D L C A N I O
T A C T I T T T T A G T T G T T T C T A T T T T T A A G A T C A A A A T A G G A T A A G A A T A T A T C A T T C T A A A T T A G A G A T T G T G T C G A A C A T T C A A
318780 318900 318820 318840 318860
A T G A A A A A A A C A A A T A A A A G A A A A A A T T A T C T A G I T T T A T C C T A T T C T A T T A T A T A G T A A G A T T A A T A C T C T A A A C A C A G G T T G A A G T T
V K K L K Y K R I K # Y S * F Y S Y S Y I Y * K + F # S I O T C V N L
Y K R # N T N E # K K I L D F I P I L I F I D N R F N H S K H A F M *
318880 318900 318920 318940 318960 318980 319000 319020 319040 319060 319080 319100 319120 319140 319160 319180 319200 319220 319240 319260 319280 319300 319320 319340 319360 319380 319400 319420 319440 319460 319480 319500 319520 319540 319560 319580 319600 319620 319640 319660 319680 319700 319720 319740 319760 319780 319800 319820 319840 319860 319880 319900 319920 319940 319960 319980 320000 320020 320040 320060 320080 320100 320120 320140 320160 320180 320200 320220 320240 320260 320280 320300 320320 320340 320360 320380 320400 320420 320440 320460 320480 320500 320520 320540 320560 320580 320600 320620 320640 320660 320680 320700 320720 320740 320760 320780 320800 320820 320840 320860 320880 320900 320920 320940 320960 320980 321000 321020 321040 321060 321080 321100 321120 321140 321160 321180 321200 321220 321240 321260 321280 321300 321320 321340 321360 321380 321400 321420 321440 321460 321480 321500 321520 321540 321560 321580 321600 321620 321640 321660 321680 321700 321720 321740 321760 321780 321800 321820 321840 321860 321880 321900 321920 321940 321960 321980 322000 322020 322040 322060 322080 322100 322120 322140 322160 322180 322200 322220 322240 322260 322280 322300 322320 322340 322360 322380 322400 322420 322440 322460 322480 322500 322520 322540 322560 322580 322600 322620 322640 322660 322680 322700 322720 322740 322760 322780 322800 322820 322840 322860 322880 322900 322920 322940 322960 322980 323000 323020 323040 323060 323080 323100 323120 323140 323160 323180 323200 323220 323240 323260 323280 323300 323320 323340 323360 323380 323400 323420 323440 323460 323480 323500 323520 323540 323560 323580 323600 323620 323640 323660 323680 323700 323720 323740 323760 323780 323800 323820 323840 323860 323880 323900 323920 323940 323960 323980 324000 324020 324040 324060 324080 324100 324120 324140 324160 324180 324200 324220 324240 324260 324280 324300 324320 324340 324360 324380 324400 324420 324440 324460 324480 324500 324520 324540 324560 324580 324600 324620 324640 324660 324680 324700 324720 324740 324760 324780 324800 324820 324840 324860 324880 324900 324920 324940 324960 324980 325000 325020 325040 325060 325080 325100 325120 325140 325160 325180 325200 325220 325240 325260 325280 325300 325320 325340 325360 325380 325400 325420 325440 325460 325480 325500 325520 325540 325560 325580 325600 325620 325640 325660 325680 325700 325720 325740 325760 325780 325800 325820 325840 325860 325880 325900 325920 325940 325960 325980 326000 326020 326040 326060 326080 326100 326120 326140 326160 326180 326200 326220 326240 326260 326280 326300 326320 326340 326360 326380 326400 326420 326440 326460 326480 326500 326520 326540 326560 326580 326600 326620 326640 326660 326680 326700 326720 326740 326760 326780 326800 326820 326840 326860 326880 326900 326920 326940 326960 326980 327000 327020 327040 327060 327080 327100 327120 327140 327160 327180 327200 327220 327240 327260 327280 327300 327320 327340 327360 327380 327400 327420 327440 327460 327480 327500 327520 327540 327560 327580 327600 327620 327640 327660 327680 327700 327720 327740 327760 327780 327800 327820 327840 327860 327880 327900 327920 327940 327960 327980 328000 328020 328040 328060 328080 328100 328120 328140 328160 328180 328200 328220 328240 328260 328280 328300 328320 328340 328360 328380 328400 328420 328440 328460 328480 328500 328520 328540 328560 328580 328600 328620 328640

rtomis (CHADO) File Entries Select View Goto Edit Create Run Graph Display



The Artemis Gene builder will open in a separate window and you can make changes to the annotation.

The screenshot shows the 'Artemis Gene Builder: ClpP' window. The top panel displays the 'Gene Map' with a hierarchy of ClpP, PFC0310c:mRNA, and PFC0310c:pep. The middle panel shows the 'Annotation :: PFC0310c:pep' details, including a list of qualifiers (Dbxref, EC_number, etc.) and a table of GO terms. The bottom panel shows the 'Match' section with a table of orthologs/paralogs. Annotations are entered under the 'polypeptide' key.

Protein annotation needs to go under the key 'polypeptide'

Gene builder showing gene hierarchy, consisting of gene, transcript and CDS.

Adding qualifiers to the core annotation.

Literature and Dbxrefs can be entered here

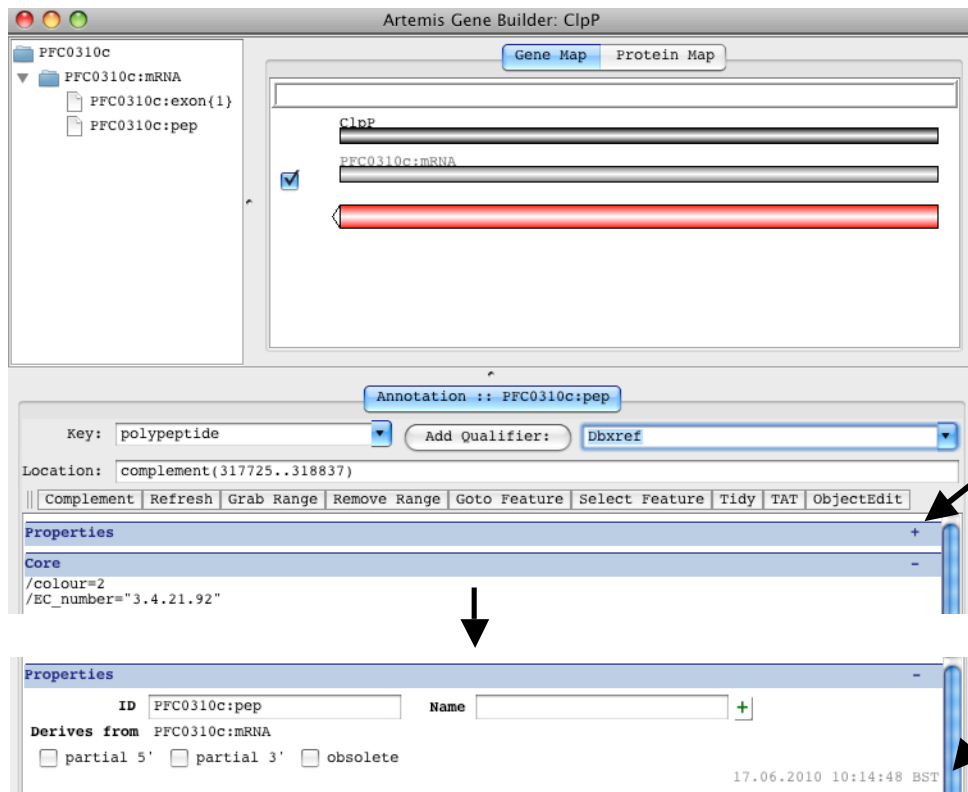
Controlled Vocabulary - Product - GO - controlled curation

Ortholog/Paralog

Alternative view

OK will close the 'Artemis Gene Builder'. If you need to keep the window open, just click 'Apply'.

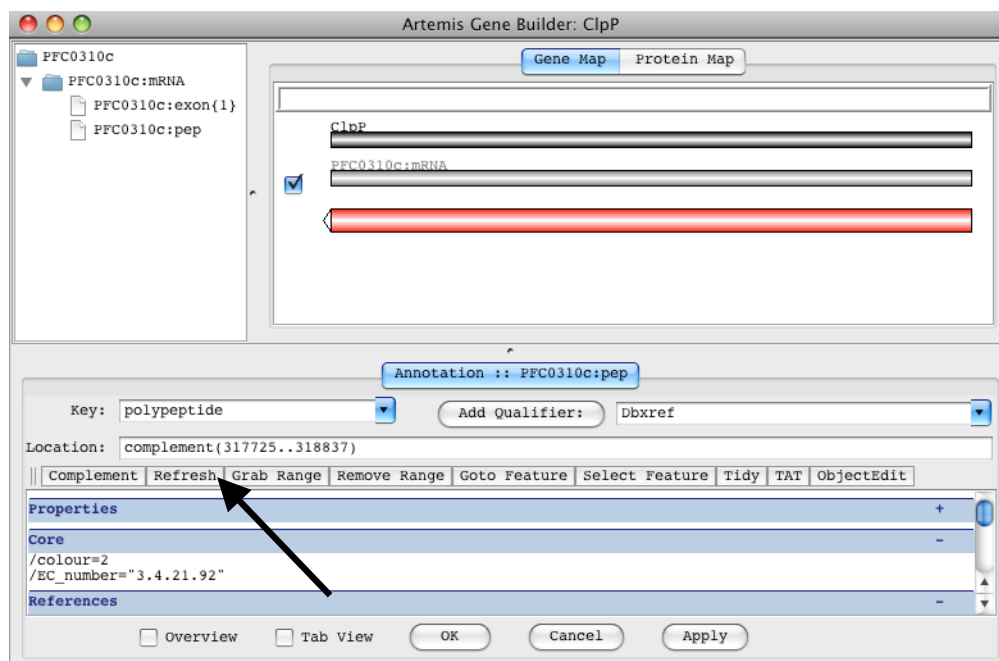
If you would like to check when the annotation has last been changed go to properties.



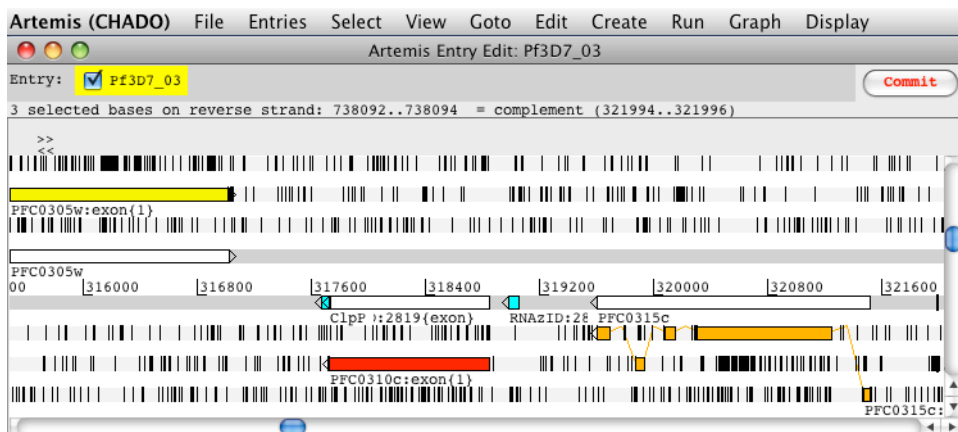
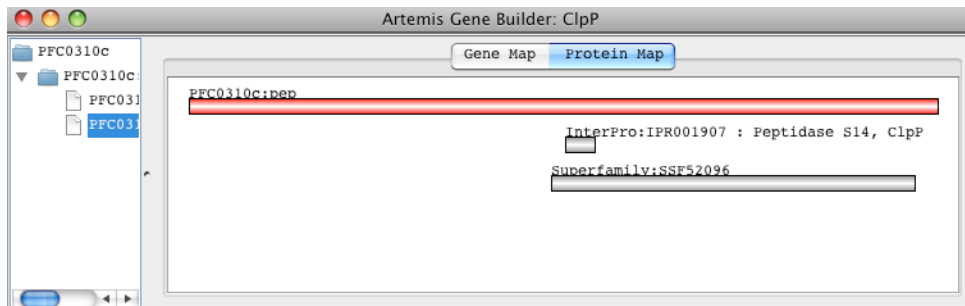
Click on the '+' in order to view 'Properties'

If you would like to check when the annotation has last been changed go to the Properties section in the gene builder.

In case several people work on the same chromosome, click on refresh in order to see recent changes.

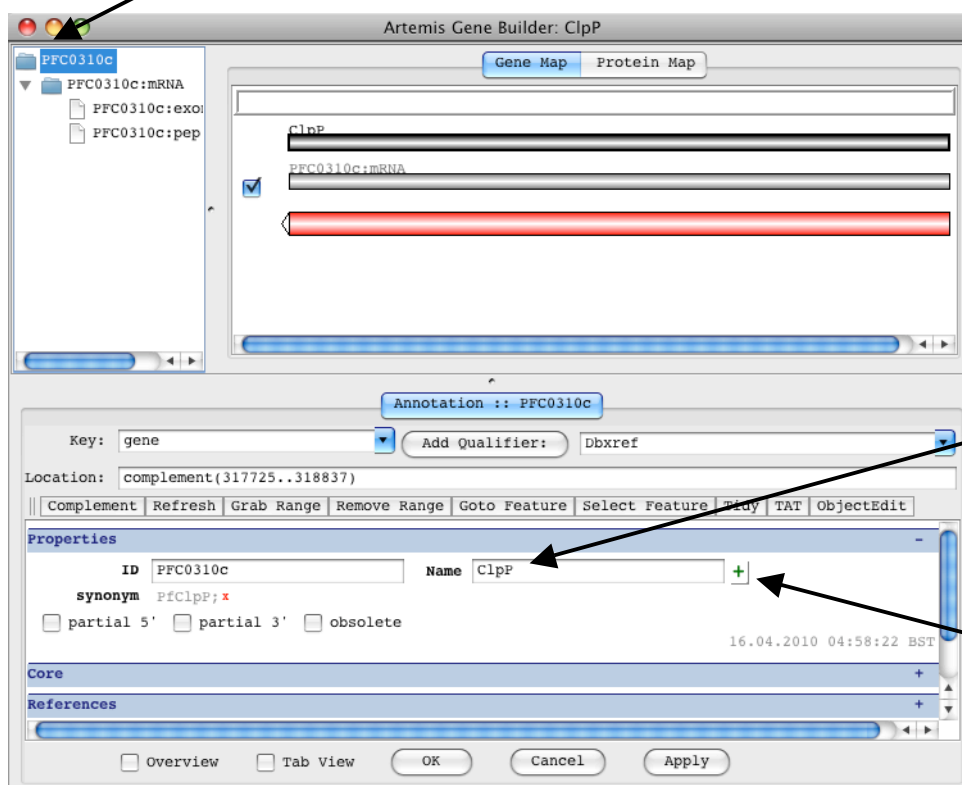


Go to 'Protein Map' to see all the Interpro matches for the gene model. By clicking on the matches the corresponding website will open.



Once you added any changes, the commit button will turn red. Press **commit** to submit all the changes to the database.

In order to add gene annotation, click on gene.

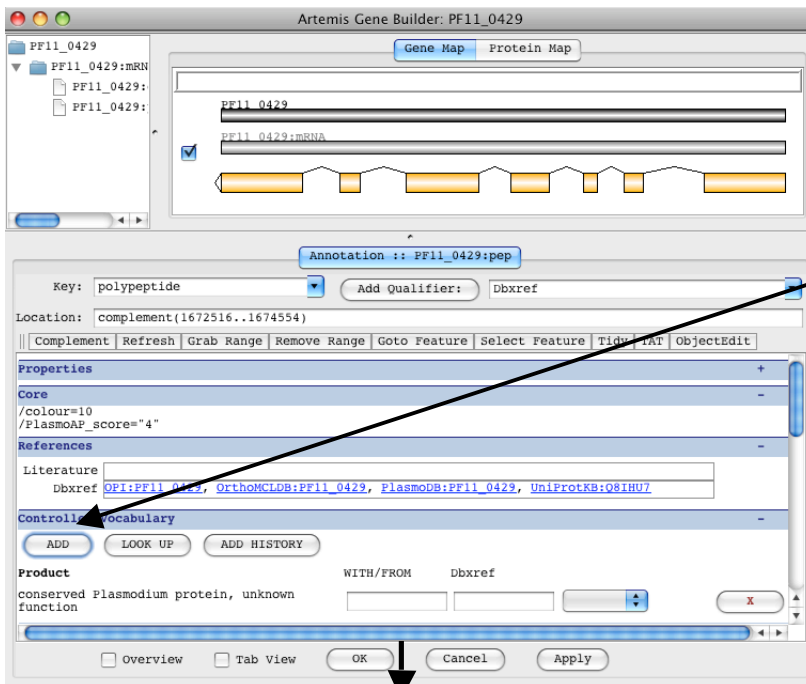


Section to add gene name.

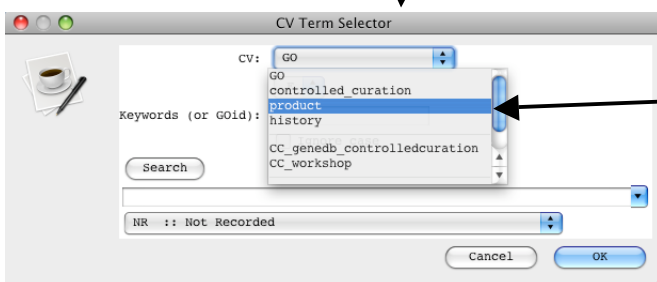
Click on the '+' in order to add gene name synonyms

Changing the product line

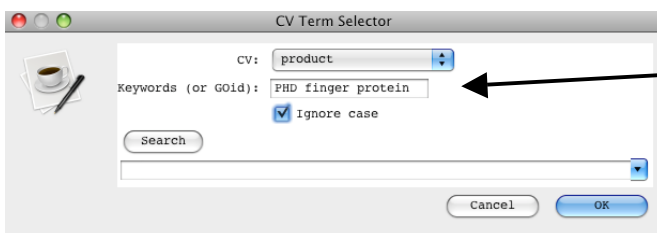
(a) Choosing a product from the product list (if the product already exists)



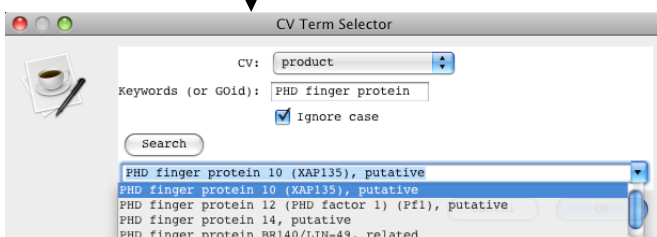
To add a new product name, open the 'Artemis Gene Builder' window -> go to 'Controlled Vocabulary' and click on 'ADD'.



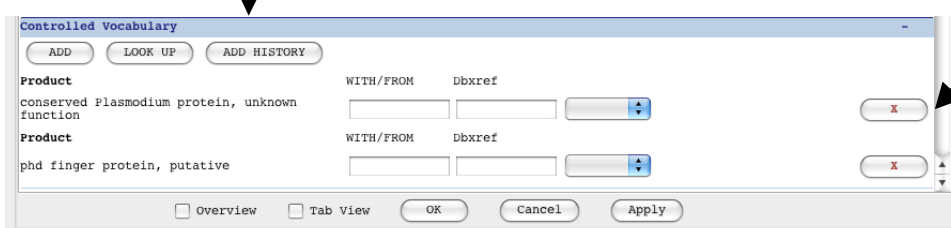
Select product



Type a keyword. The products can be in upper or lower case in the database, so always click on 'ignore case' if you are not completely certain about the product name. Then click 'Search'.



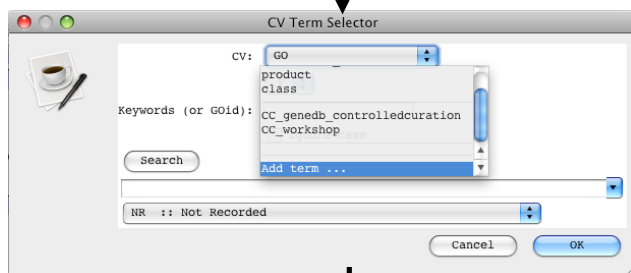
Select a product from the list and click 'OK'



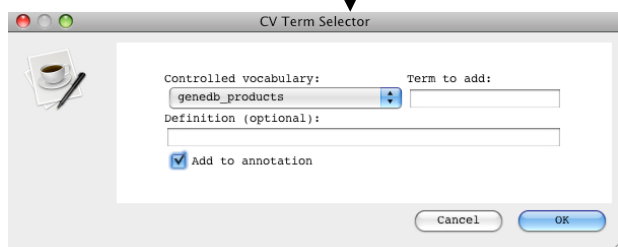
Click to delete the old product.

(b) Adding a new product to the already existing list

In case you don't find the product you are looking for, go to 'Controlled Vocabulary' section and click 'ADD'.

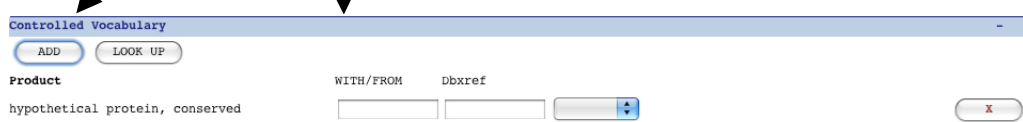
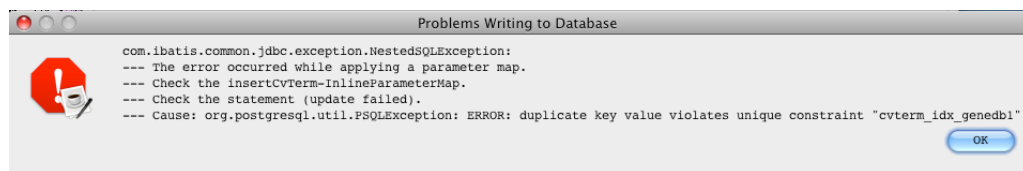


Choose in the scroll down list 'Add term'

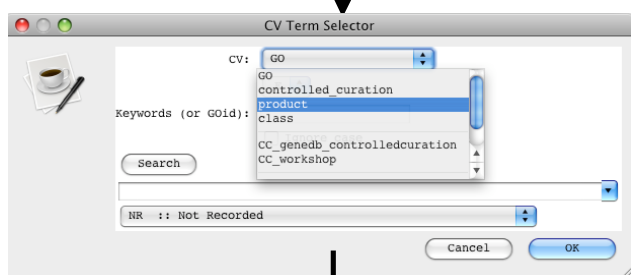


Choose 'genedb_products' and type the new product name. Then click OK. This adds the term to the database. To add this straight into your annotation check the 'Add to Annotation' option.

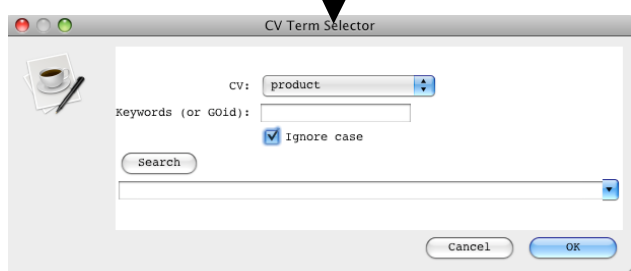
In case the product already exists in the database, the following error message will appear.



If you get the error message go back to the 'Controlled Vocabulary' and click 'ADD'.



Select product -> click 'OK'



Select 'Ignore case' to see if the product you were trying to add is written in a different case.

(c) Adding GO terms

If you would like to add a GO term, go to the Controlled Vocabulary section and click ‘ADD’.

Controlled Vocabulary

ADD LOOK UP

Product

hypothetical protein, conserved

WITH/FROM Dbxref

GO terms

GO terms	WITH/FROM	Dbxref	Evidence	Qualifier	Date
GO:0005575 [C]			ND ...		----/--/--
GO:0003674 [F]			ND ...		----/--/--
GO:0008150 [P]			ND ...		----/--/--

CV Term Selector

CV: GO

F

Keywords (or Goid):

Search

NR :: Not Recorded

Cancel OK

Choose GO and type a Goid or a key word in the GO term. Click ‘Search’

CV Term Selector

CV: GO

F

Keywords (or Goid): 0003842

Search

1-pyrroline-5-carboxylate dehydrogenase activity

NR :: Not Recorded

ISM :: Inferred from Sequence Model

ISO :: Inferred from Sequence Orthology

ISS :: Inferred from Sequence or Structural Similarity

NAS :: Non-traceable Author Statement

ND :: No Biological Data available

RCA :: inferred from Reviewed Computational Analysis

TAS :: Traceable Author Statement

NR :: Not Recorded

OK

Once the search is finished, choose the GO evidence code. Then click ‘OK’.

GO terms

GO terms	WITH/FROM	Dbxref	Evidence	Qualifier	Date
GO:0005575 [C]			ND ...		----/--/--
GO:0003674 [F]			ND ...		----/--/--
GO:0008150 [P]			ND ...		----/--/--
GO:0003842 [F]			ISO...		2009/11/13

You can see the newly added GO term associated with a date.

(d) Recording all the changes made in the history qualifier

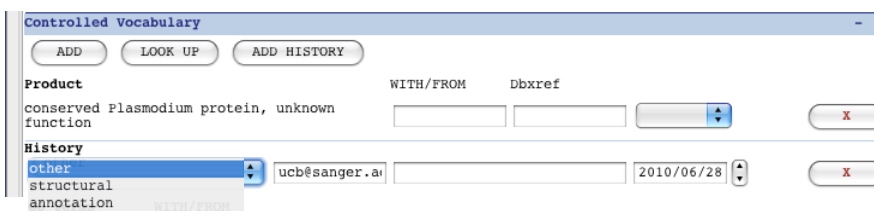
If you would like to record all the changes you've made to a gene model, go to Controlled Vocabulary and click on Add History.



Controlled Vocabulary

ADD LOOK UP ADD HISTORY

Product conserved Plasmodium protein, unknown function WITH/FROM Dbxref



Controlled Vocabulary

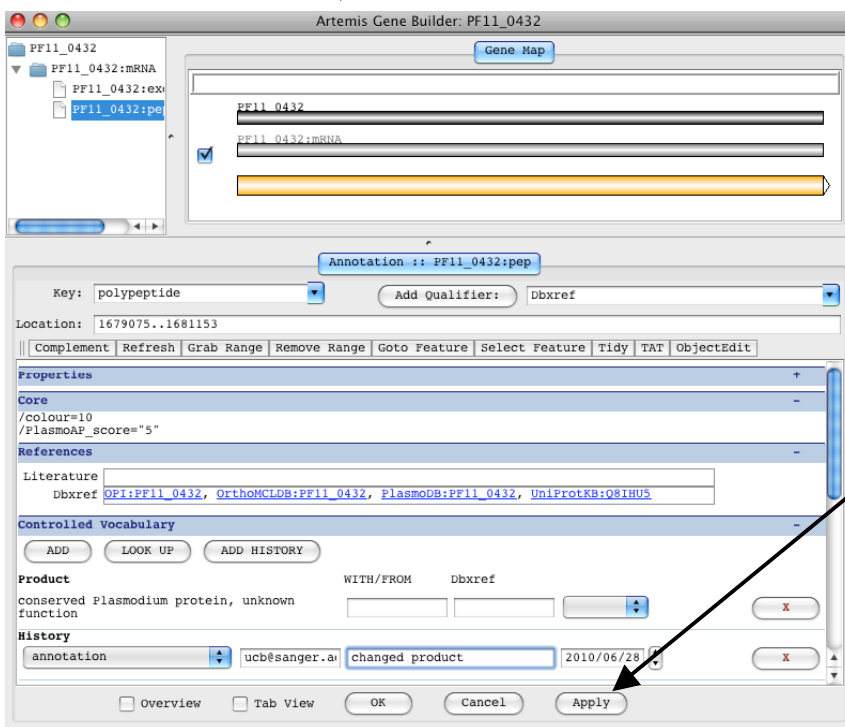
ADD LOOK UP ADD HISTORY

Product conserved Plasmodium protein, unknown function WITH/FROM Dbxref

History other structural annotation

ucb@sanger.ac.uk 2010/06/28

You can choose between structural and functional annotation.



Artemis Gene Builder: PF11_0432

Gene Map

PF11_0432

PF11_0432:mRNA

PF11_0432:exon

PF11_0432:pep

Annotation :: PF11_0432:pep

Key: polypeptide Add Qualifier: Dbxref

Location: 1679075..1681153

Complement Refresh Grab Range Remove Range Goto Feature Select Feature Tidy TAT ObjectEdit

Properties

Core

/colour=10

/PlasmaAP_score="5"

References

Literature

Dbxref

Controlled Vocabulary

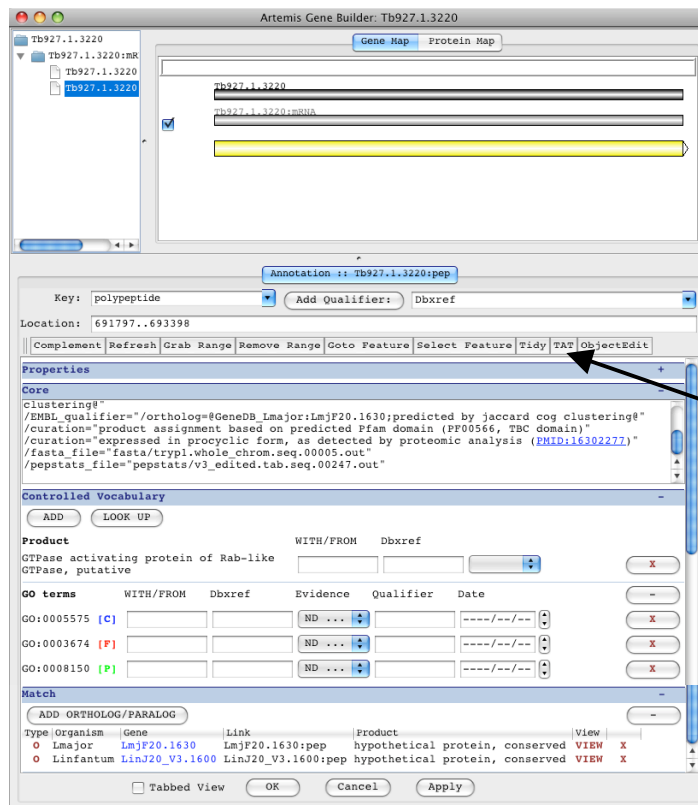
ADD LOOK UP ADD HISTORY

Product conserved Plasmodium protein, unknown function WITH/FROM Dbxref

History annotation ucb@sanger.ac.uk changed product 2010/06/28

Overview Tab View OK Cancel Apply

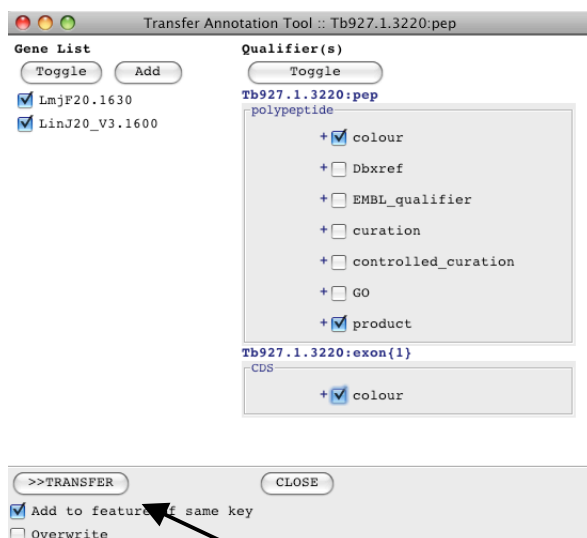
Once you've added history, click apply and OK. Then commit the changes to the database.

(e) Transfer Annotation Tool

The Transfer Annotation Tool (TAT) can be used to transfer annotation between features within an EMBL file or features within the same Chado database.

To use the transfer annotation tool, just click on 'TAT' in the Artemis Gene Builder

Orthologs are automatically added.



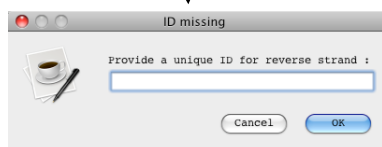
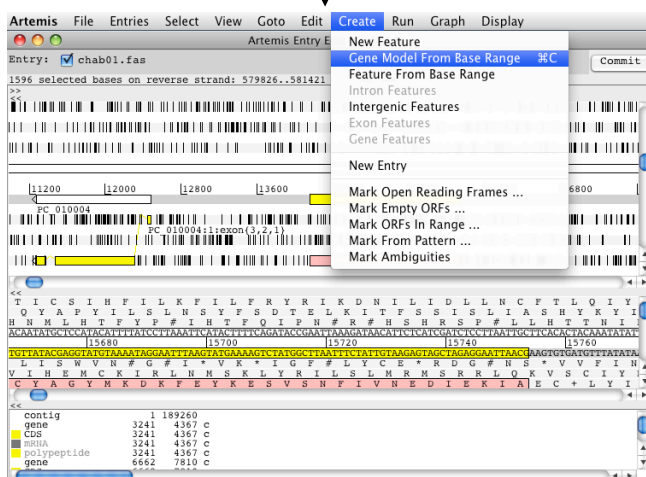
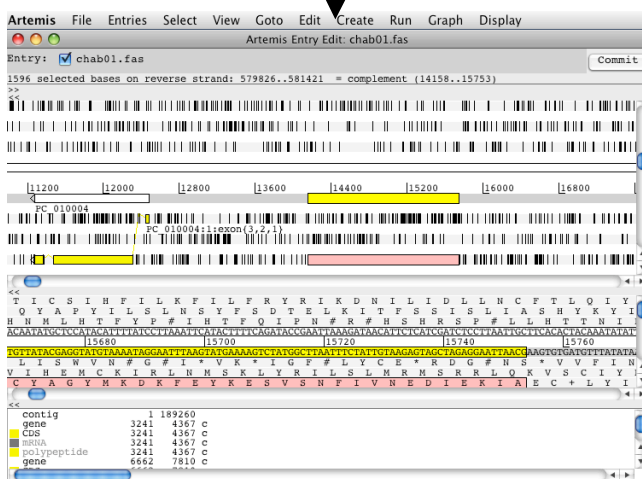
This shows qualifiers for all features in the gene model.

Different qualifiers can be transferred, like product and colour.

To finish the transfer of the qualifiers click on the ">>TRANSFER" button. Caution: be careful as this will automatically transfer the annotation straight to the database and you will not be asked if you want to commit the changes.

2. Structural annotation

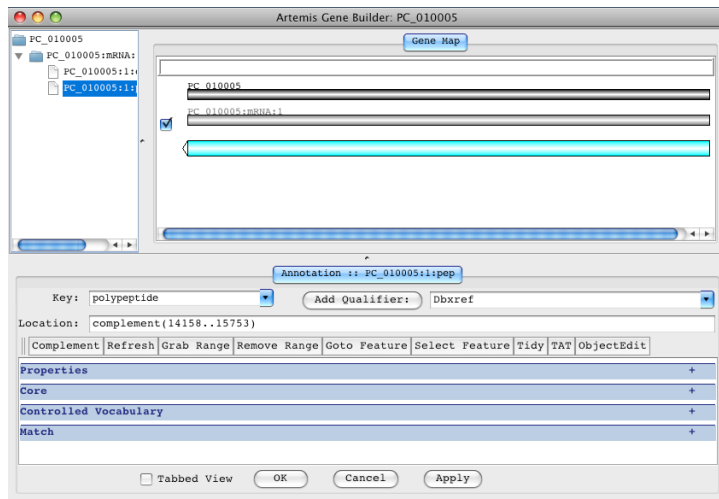
(a) Creating a new gene model



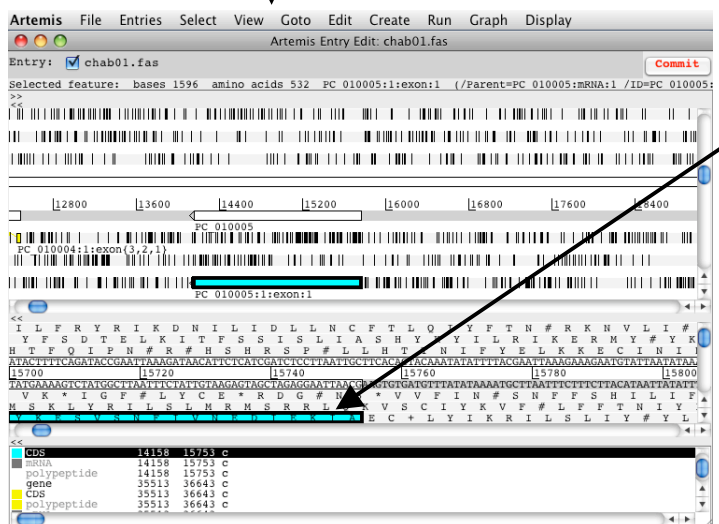
Use the mouse pointer to select the area where the missing gene is (in the appropriate reading frame on a given strand). You can do this by double clicking with the middle button and the range between stop codons will be selected.

Go to 'Create' -> 'Gene model from base range' or simply click 'C'

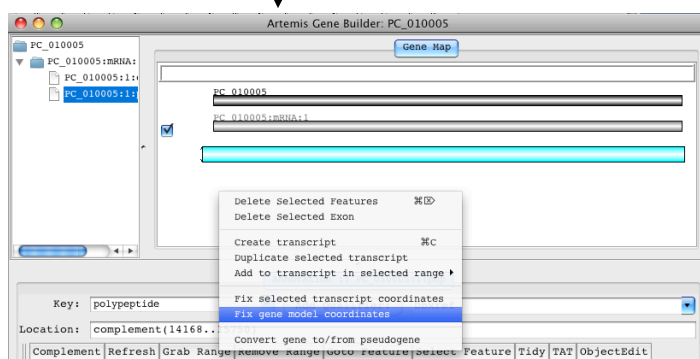
Choose a unique ID, possibly one which is related to the surrounding genes. Then click OK.



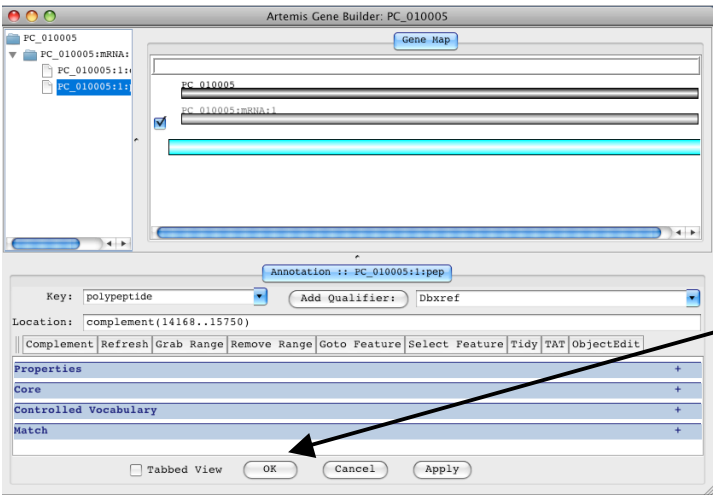
After giving the gene a unique ID, the 'Artemis Gene Builder' will open. Keep this window open.



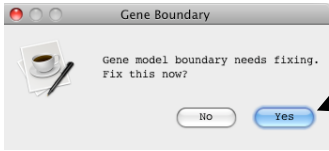
Use the mouse pointer to adjust the gene boundaries by clicking on the end of the feature and dragging it.



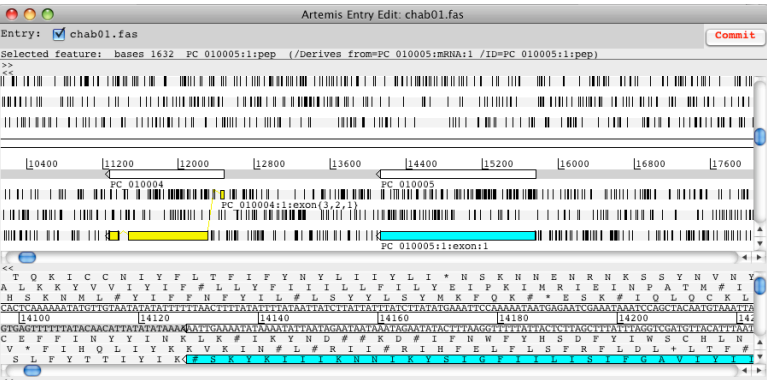
Go to the 'Artemis Gene Builder'. Right-click in the top right-hand box and select 'Fix gene model coordinates'. Click Apply, then 'OK' at the bottom of the window. Then close the 'Artemis Gene Builder'.



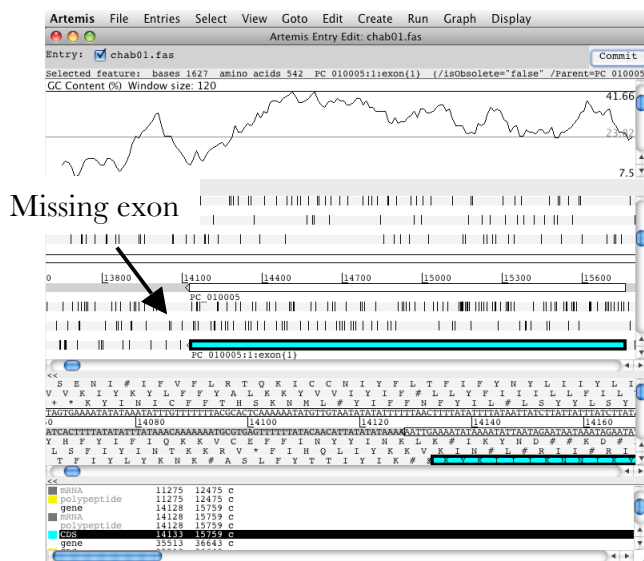
Alternatively, if you forget to fix the gene model coordinates, once you click OK, a window appears prompting you to fix the coordinates.



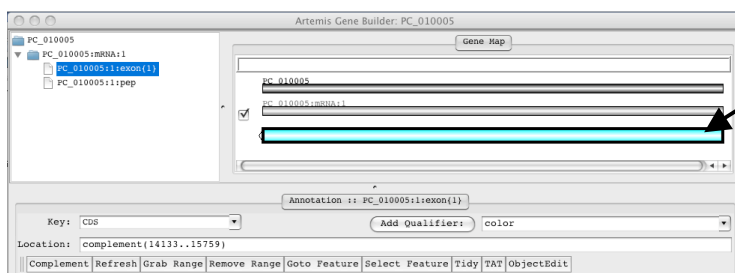
Click OK.



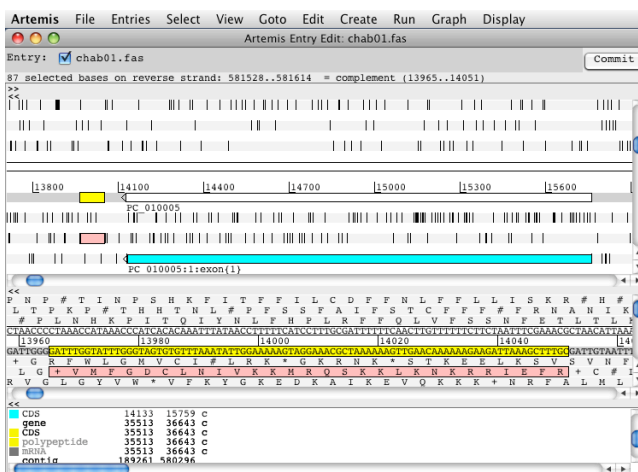
Commit the changes to the database.

(b) Adding an exon to an existing gene by using the grab range option

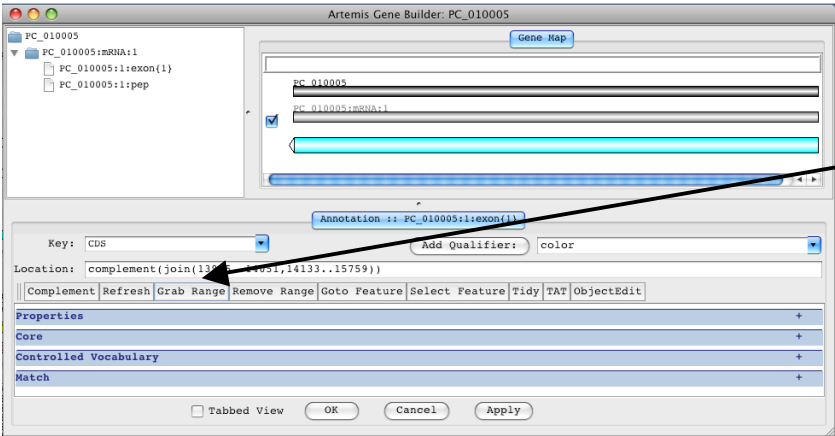
Click on the CDS and open the 'Artemis Gene Builder'.



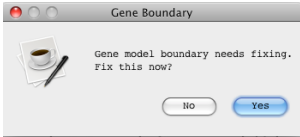
Once the gene builder is open, select the CDS. Leave the 'Artemis Gene Builder' open.



Go back to the 'Artemis Entry Edit' and drag your mouse pointer to mark the exon you would like to add.



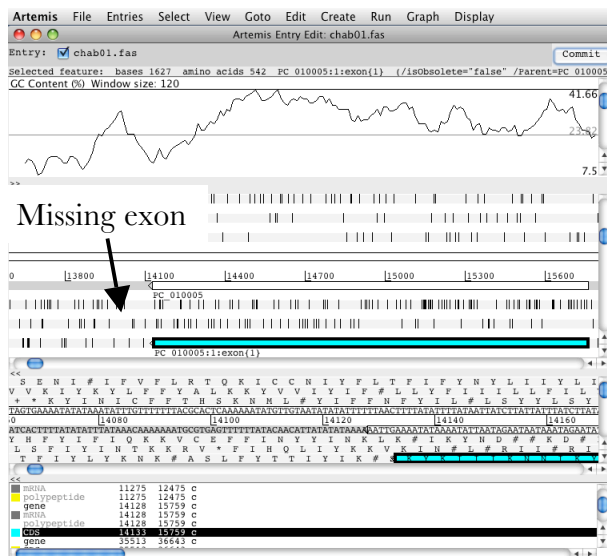
Go back to the Artemis Gene Builder, click 'Grab Range', then click OK. Be careful not to click on the Gene Map section. This will deselect the CDS.



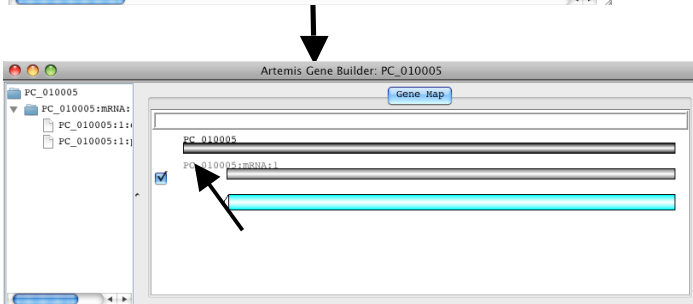
Fix the gene boundaries by selecting yes.



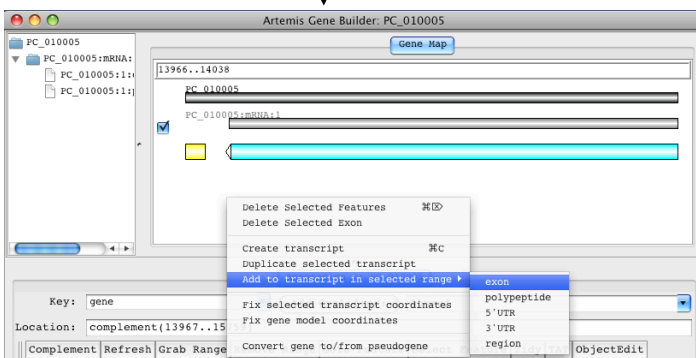
Commit changes to the database

(c) Adding an exon to an existing gene by extending the gene boundaries

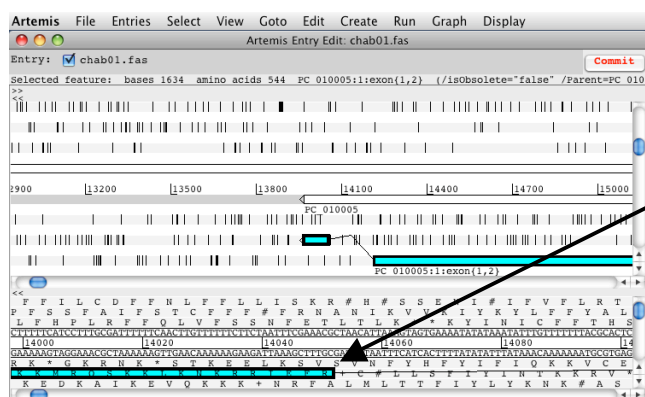
Click on the CDS and open the “Artemis Gene Builder”.



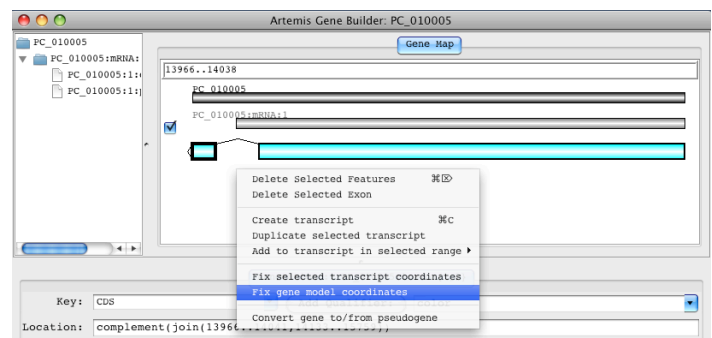
Extend the gene boundaries as required at 3' and 5' ends with your mouse pointer by clicking and dragging.



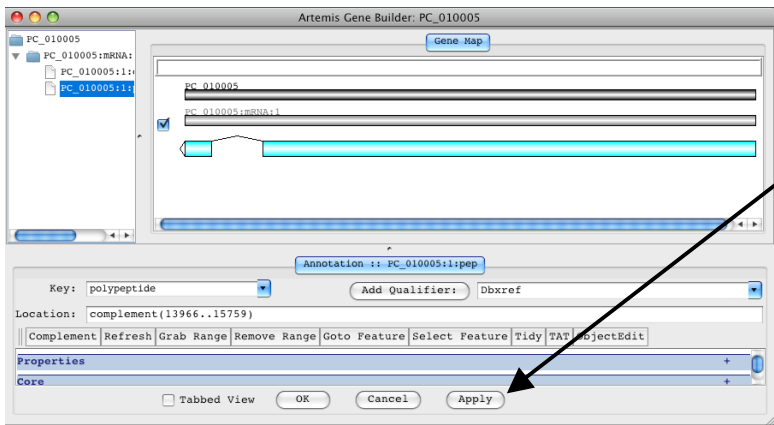
To build a new exon, select a range adjacent to the CDS with your mouse pointer by clicking and dragging. With right-click ‘Add to transcript in selected range’ and select ‘exon’.



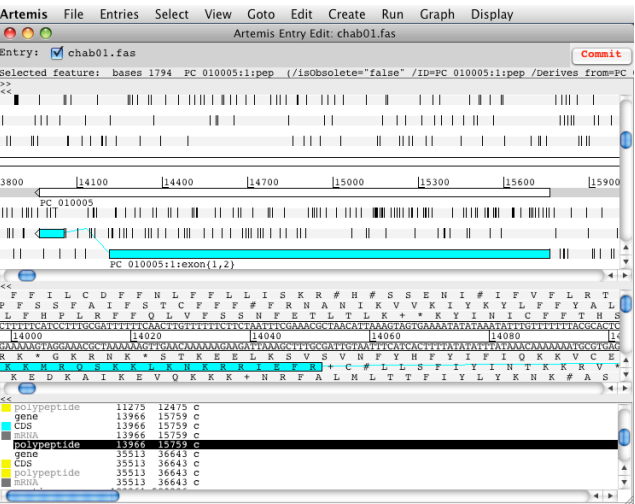
Adjust the exon boundaries in the “Artemis Entry Edit” view. Click and hold at one end of the exon. Move the mouse pointer to change the exon boundaries.



Go back to the “Artemis Gene Builder” and right-click in the top right-hand box select “Adjust gene model coordinates”.

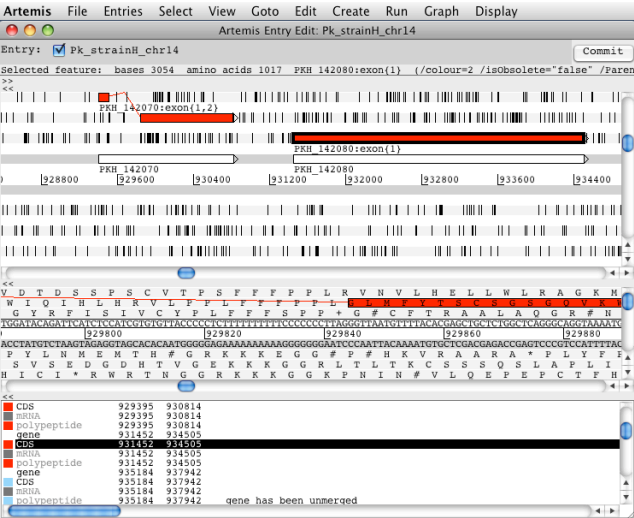


Apply changes, then click OK.

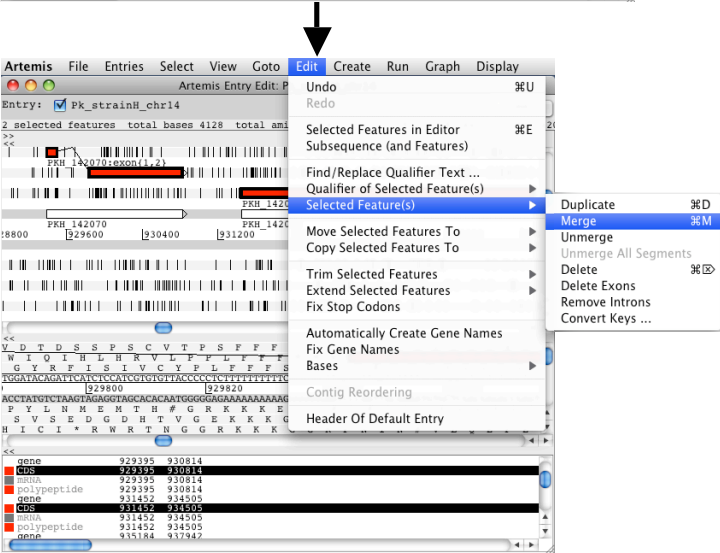


Commit changes to the database

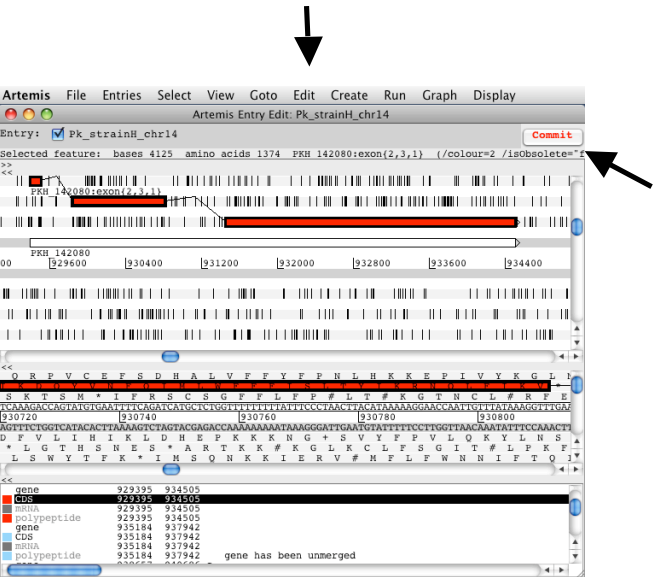
(d) Merging 2 genes



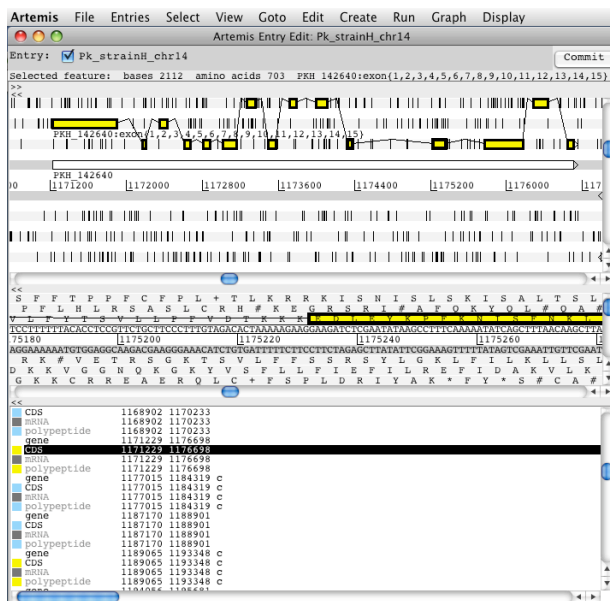
First select the gene that you want to keep the annotation from. Then with the shift key select the second gene you want to merge.



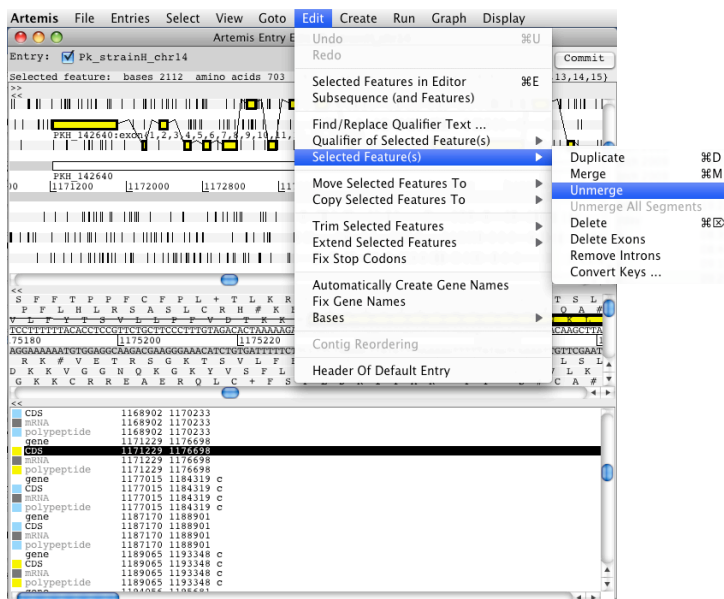
Go to Edit → merge selected features.



Commit changes to the database.

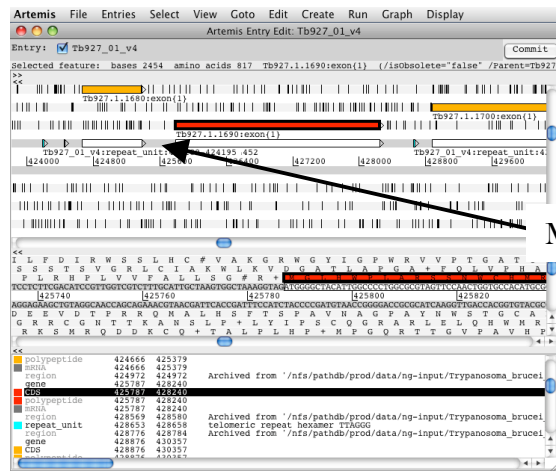
(e) Splitting a gene

Use the shift key to select both exons you would like to separate.

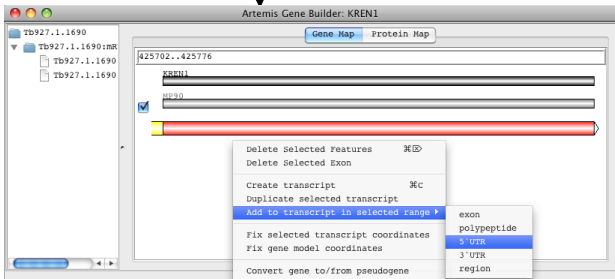


Go to 'Edit' → 'Selected Feature(s)' → 'Unmerge'.
After changing the gene model **commit** to the database.

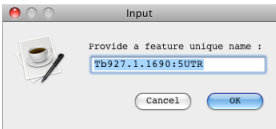
(f) Adding UTRs to an existing gene



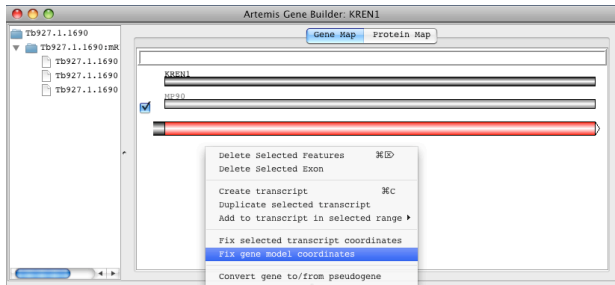
Missing UTR



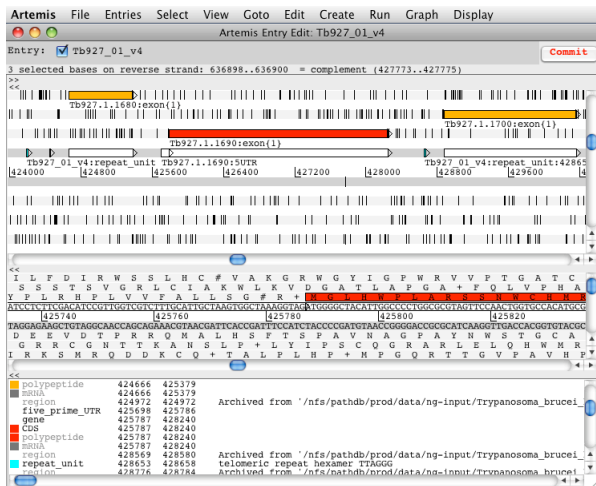
Go to the ‘Artemis Gene Builder’ window and create a box adjacent to the red exon. With right-click go to “Add to transcript in selected range -> 5’UTR.



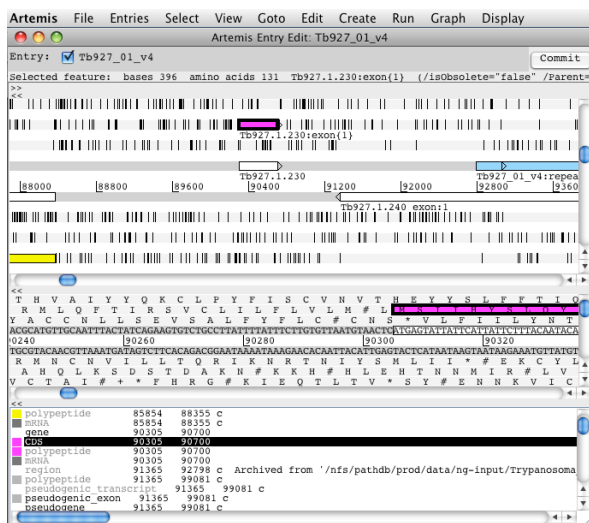
Click OK.



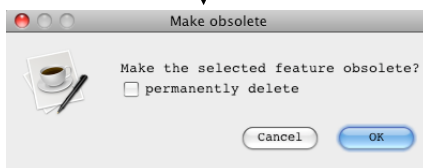
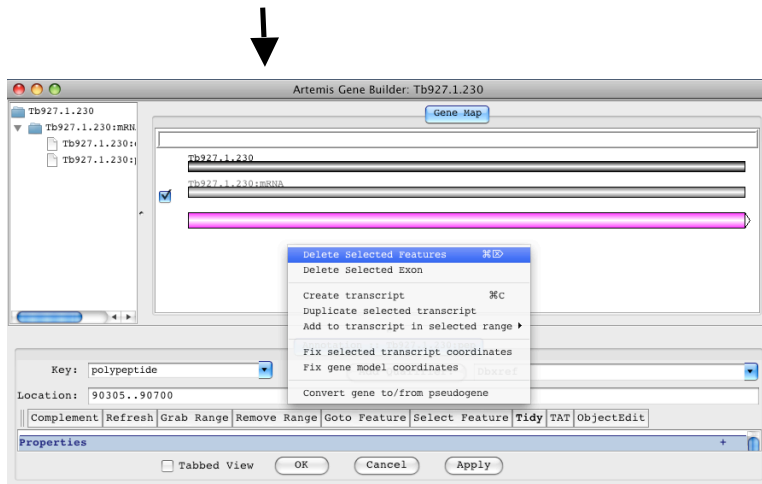
After fixing the UTR boundaries in the main Artemis window, go back to the ‘Artemis Gene Builder’ right-click on the window and ‘Fix gene model coordinates’



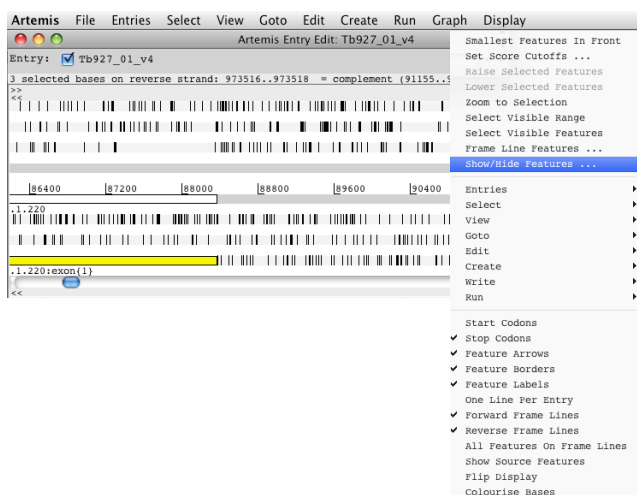
Commit changes to the database

(g) Delete a gene/make a gene obsolete

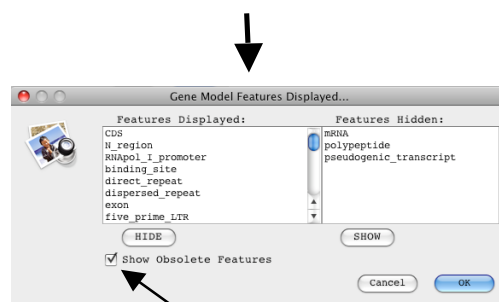
Select the gene model you would like to delete and open the Artemis Gene Builder.



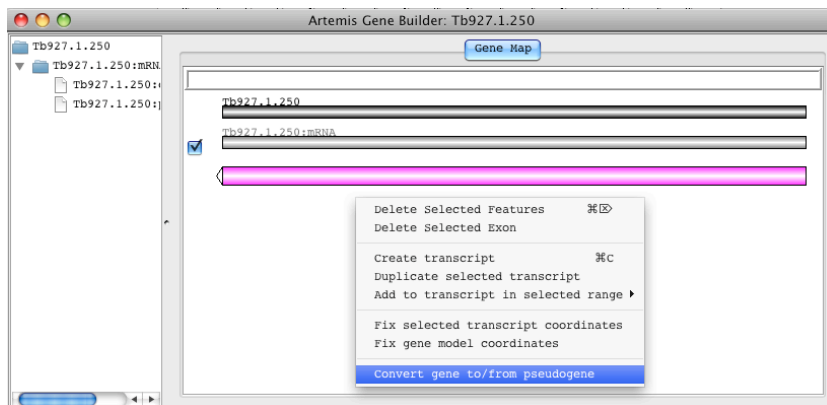
A gene can either be deleted permanently or it can be made obsolete which means they are invisible but still present in the database.



If you want to see all the obsolete genes, right-click on the main sequence view panel and select 'Show/Hide Features'. Click on 'Show Obsolete Features'

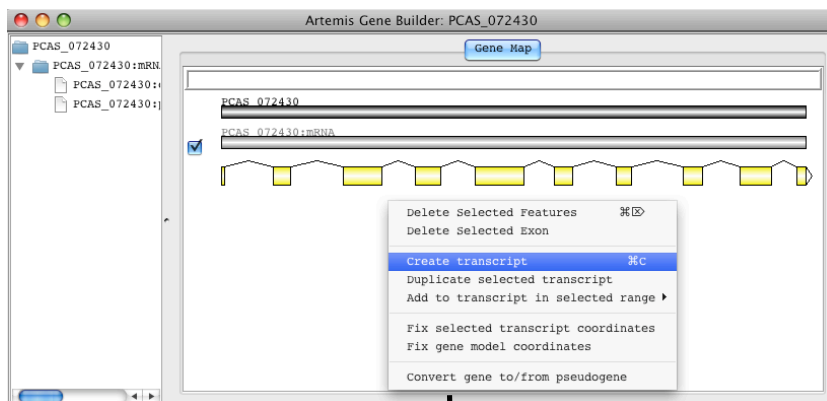


(h) Convert a gene into a pseudogene

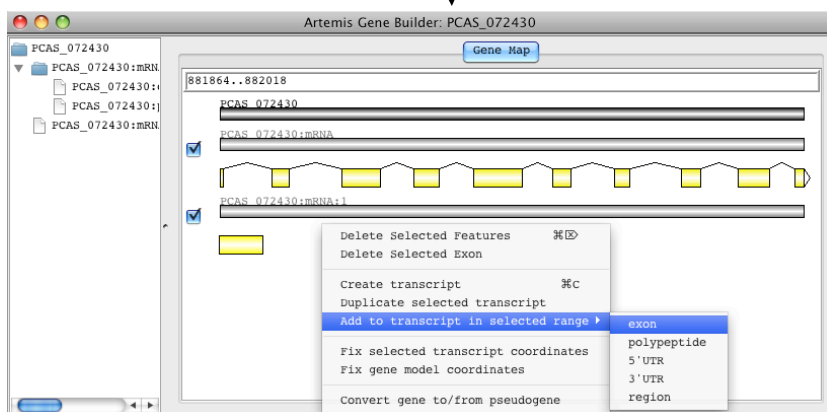


Open the 'Artemis Gene Builder', with right-click go the 'Convert gene to/from pseudogene'

(i) Addition of an alternatively spliced form to a gene model

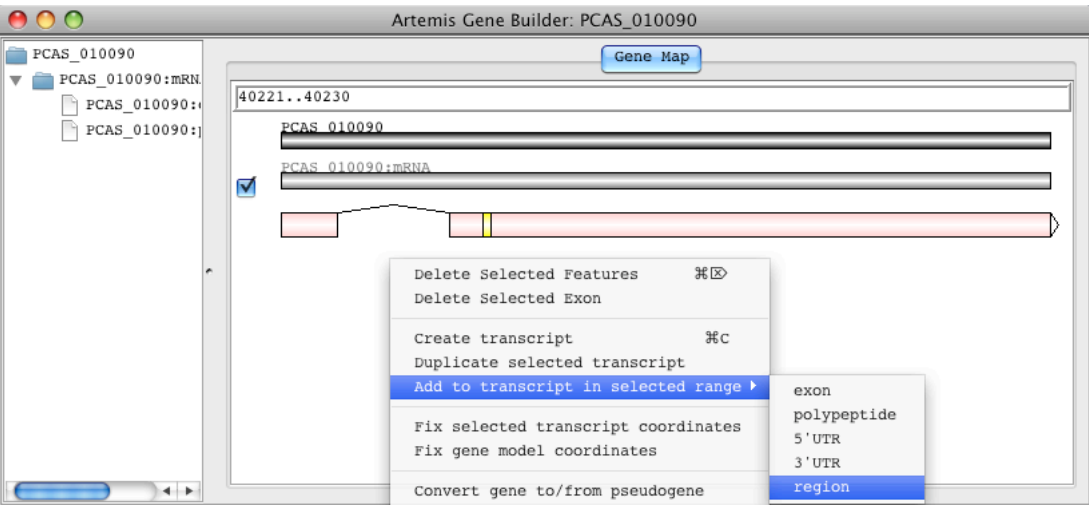


Open the 'Artemis Gene Builder', with right-click go to 'Create transcript'.

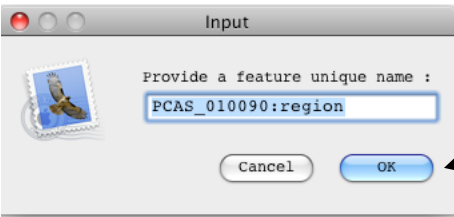


Once the alternative transcript has been created, go with right-click to 'Add to transcript in selected range' and build the gene model (see section (a)).

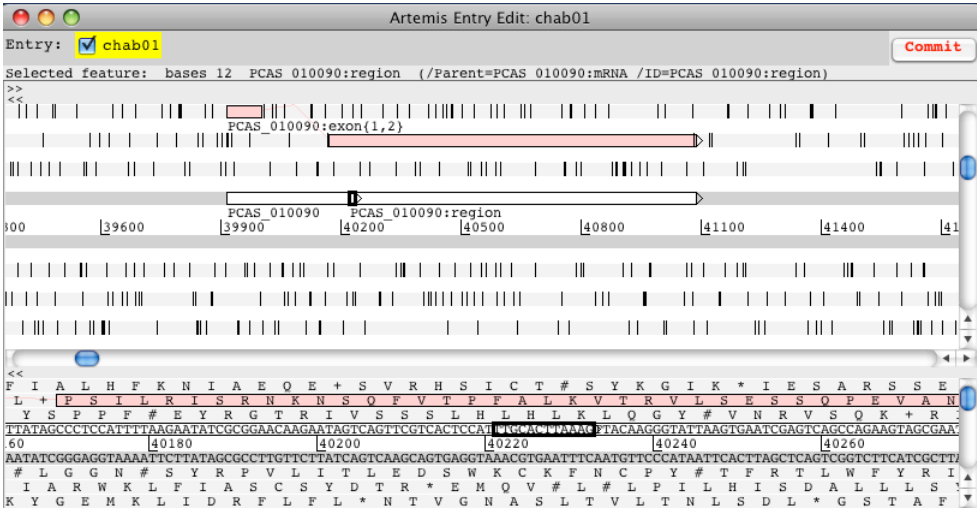
(j) Add regions to a gene in the gene builder (e.g. catalytic residue or other sequence ontology features)



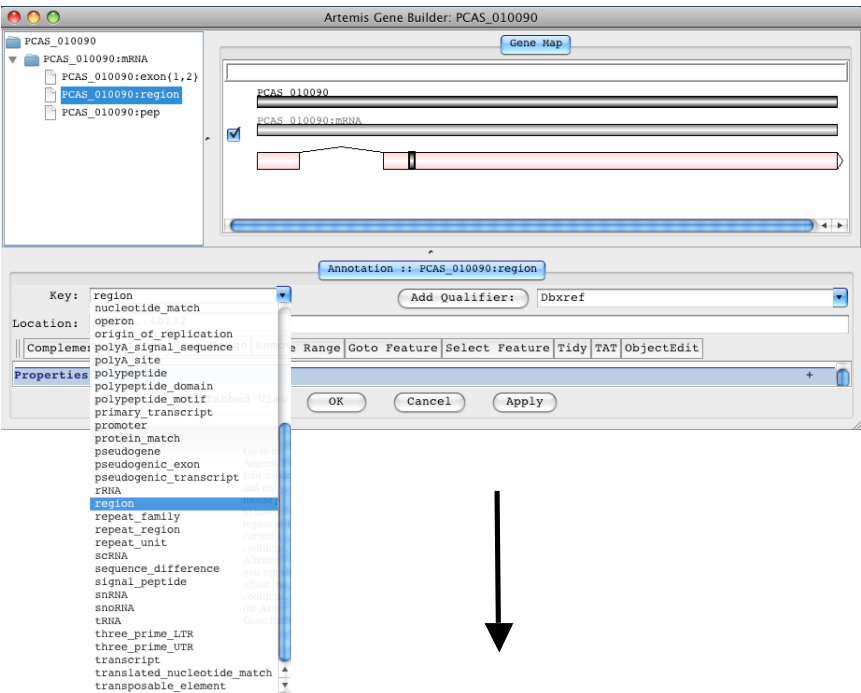
Open the ‘Artemis Gene Builder’. Use your mouse pointer to select a region. Right-click in the top right hand box and select ‘Add to transcript in selected range’ then choose ‘region’.



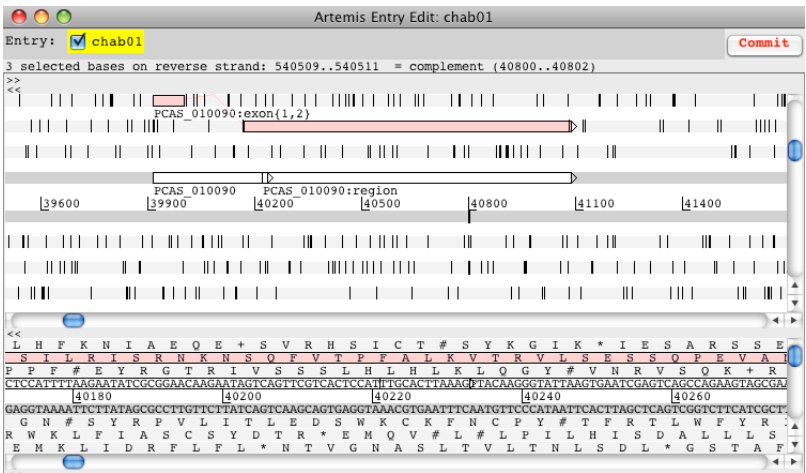
Click OK.



Go to the Artemis main feature display and use the mouse to drag the boundaries of the new feature to the correct coordinates. Alternatively you can adjust the coordinates in the Artemis Gene Builder.



Go back to the Gene Builder and select the new feature. If you would like to choose a different key, go to the drop down menu and choose one of the existing keys. You can also add a new key (from SO), like catalytic_residue. You may get a warning message that asks if you want to add this key. This will only occur the first time you added a new key that is not on the list of keys Artemis is already aware of.



Commit to the database