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Note: The locators with the letters '*f*' and '*t*' refers to figures and tables respectively

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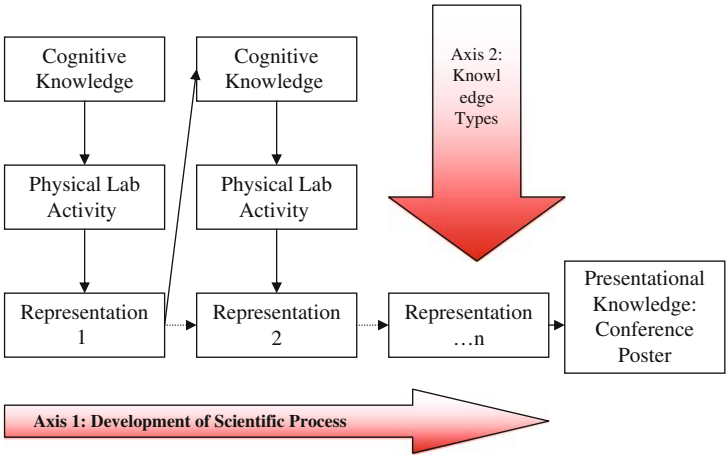

Fig. 2.2 A Schematic Representation of the Scientific Inquiry Process

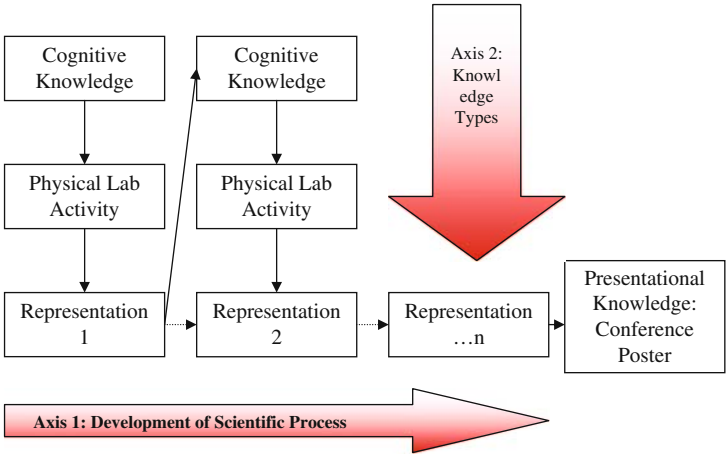

Fig. 5.2 A schematic representation of the scientific inquiry process

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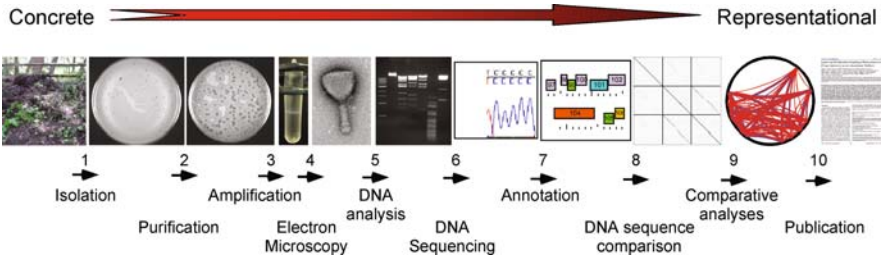

Fig. 6.3 The ten steps of the PHIRE program. Each of the ten steps in the PHIRE program are illustrated with the central arrow showing the transition from concrete to abstract comprehension from step 1 to step 10

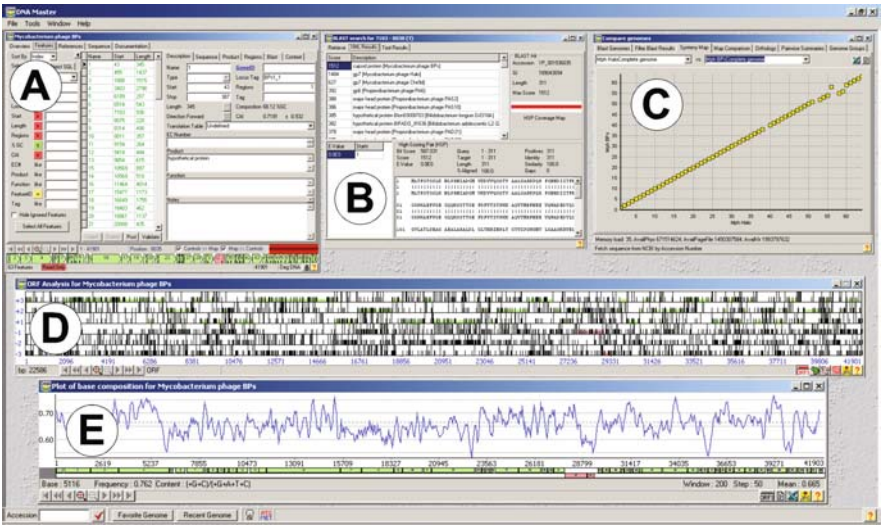

Fig. 6.6 DNAMaster: A program for phage genome annotation. Screen shots are shown from several representative windows of DNAMaster (**A–E**). (**A**) Window presenting features of mycobacteriophage BPs. The "Feature" tab is selected, showing a list of the genes with their coordinates. (**B**) The "Compare Genomes" window showing the results of a BlastP search of phage BPs gp7. (**C**) Comparison of phage BPs and phage Halo genomes, with each yellow box indicating the position of genes that are shared between the two genomes. (**D**) The "Frames" window showing the positions of stop and start codons in all six reading frames. The positions of identified opening reading frames are colored either *green* (forward direction) or *red* (reverse direction). (**E**) Plot of base composition showing the average GC% content across the BPs genome. These represent just a small subset of the available functions with DNAMaster (available as a free download from http://cobamide2.bio.pitt.edu)

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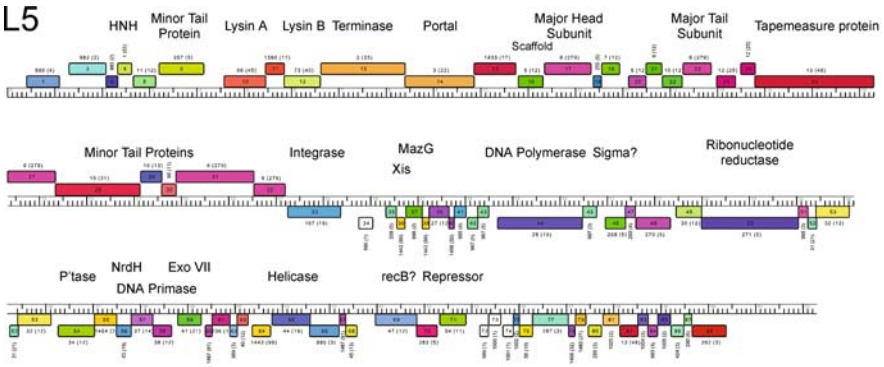

Fig. 6.8 Genome map of mycobacteriophage L5. The L5 genome is represented as a *horizontal bar* with markers spaced at 1 kbp intervals. Each of the predicted genes is shown as a colored box either above or below the genome; those above are transcribed rightward, and those below are transcribed leftward. The map was generated by the program Phamerator, which sorts the predicted genes into phamilies (Phams) as functions of their predicted amino acid sequence relatedness. The Pham number is shown above each gene with the number of Pham members in parentheses, and each gene is colored according to its Pham. Some of the predict gene functions are noted

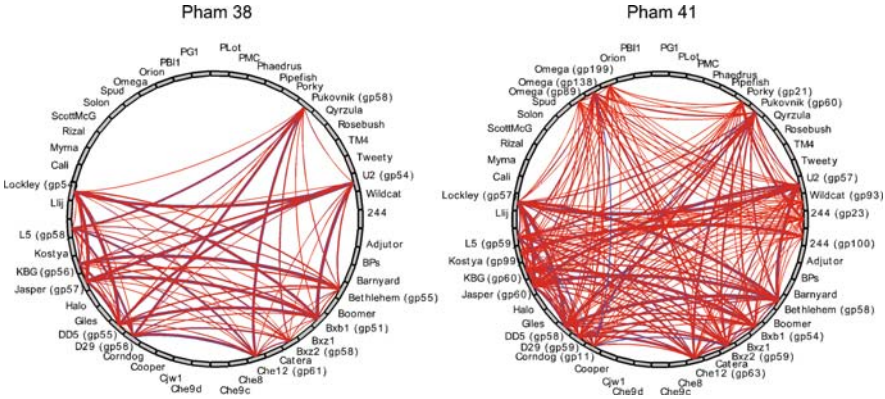

Fig. 6.9 Phamily circles. Phamily circles for Pham38 and Pham41 are shown. In the L5 genome (see Fig. 6.8), genes 58 and 59 are members of these two Phams, respectively, and the phamily circles suggest that they have distinct and different evolutionary histories. Each of the phages is listed around the circumference of each circle and an arc is drawn between members of each phamily with line thickness corresponding to strength of the relationship

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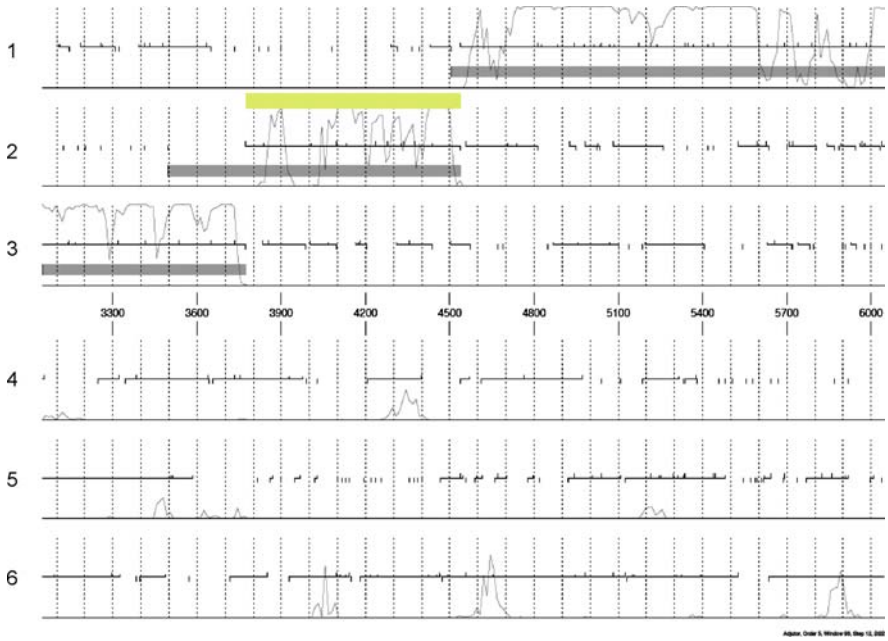

Fig. 7.1 Graphic Output of GeneMark Program. A segment of phage Adjutor genome sequence was analyzed using the program GeneMark, which generates a graph of the coding potential in each of the six possible open reading frames (ORFs) (labeled 1–6; frames 1–3 are expressed in the rightward direction, and 4–6 in the reverse direction). ORFs are identified as *horizontal lines* between translation stop codons (*down ticks*), and potential start codons are shown as *up ticks*. Coding potential is indicated by the line graph. The thick horizontal gray lines (still italicized) are considered areas of interest. One such gene is highlighted in *green*

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GLIMMER (ver. 3.02; iterated) predictions:

orfID	start	end	frame	score
>Adjutor				
orf00001	43	309	+1	5.50
orf00002	421	1524	+1	11.60
orf00003	1568	1762	+2	7.44
orf00004	1772	1936	+2	19.55
orf00005	1946	2125	+2	2.27
orf00006	2136	3776	+3	9.08
orf00008	3773	4543	+2	7.48
orf00010	4540	6306	+1	13.68
orf00011	6328	7914	+1	15.10
orf00012	7925	8137	+2	8.51
orf00013	8134	8586	+1	6.27
orf00014	8555	8734	+2	9.56
orf00015	8822	9067	+2	1.62
orf00016	9235	9636	+1	6.98
orf00017	9669	10376	+3	10.88
orf00019	10392	10811	+3	10.24
orf00020	10848	12032	+3	12.62
orf00022	12029	12397	+2	12.81
orf00023	12400	12732	+1	7.05
orf00024	12729	13136	+3	7.45
orf00025	13129	13491	+1	8.23
orf00026	13488	13907	+3	5.12
orf00027	13944	14300	+3	8.89
orf00028	14312	14512	+2	4.14
orf00029	14541	15344	+3	9.78
orf00030	15426	16079	+3	10.30
orf00032	16102	16320	+1	8.00
orf00034	16322	21094	+2	10.80
orf00036	21084	22604	+3	14.22
orf00038	22601	24256	+2	12.44
orf00039	24256	26526	+1	13.24
orf00040	26526	28574	+3	11.64
orf00043	28574	29440	+2	4.49
orf00044	29450	29770	+2	11.76
orf00046	29773	30201	+1	4.90
orf00048	30210	31193	+3	10.50
orf00049	31190	31444	+2	7.17
orf00051	31715	32254	+2	2.39
orf00053	32238	32693	+3	6.68

Fig. 7.2 Glimmer Program Output. A segment of the phage Adjutor genome sequence was analyzed by Glimmer generating a list of potential ORFs, their start and stop codons, reading frame, and evaluative score. The *red box* designates one specific candidate gene

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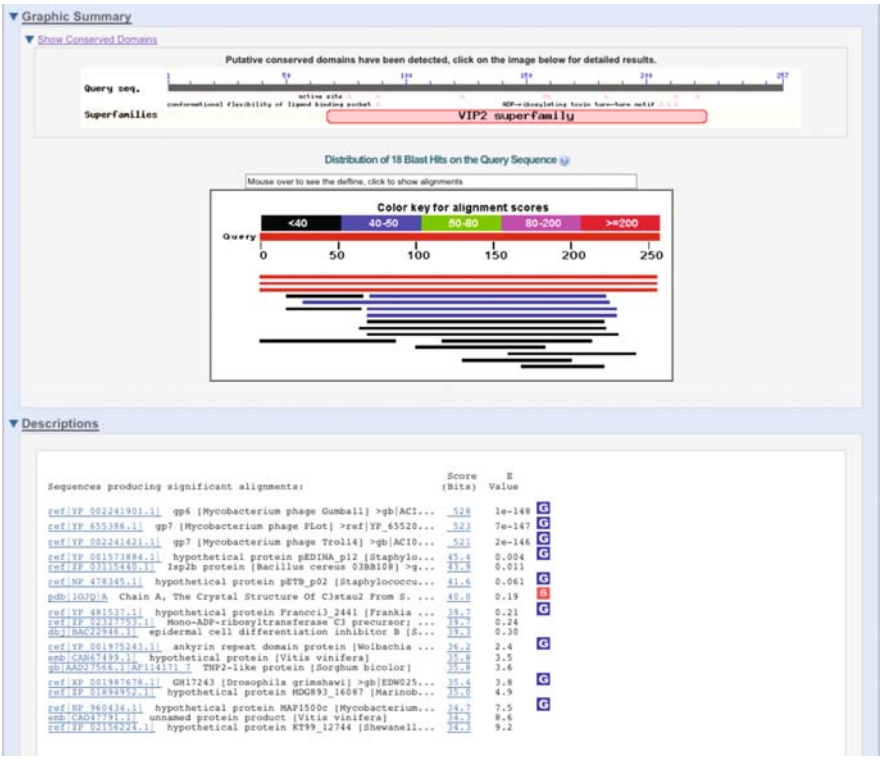

Fig. 7.3 Output of a BLASTP search using the BLAST server at NCBI. The amino acid sequence of a predicted phage protein was submitted as a search query to the server, which returned a summary of the search results; a screen shot of the results window is shown. At the *top*, a diagram shows the correspondence of a putative conserved domain identified in the search with a linear representation of the query sequence. Below that is a diagram of related sequences identified in the search, with the closest matches shown in *red*. The identities of the specific matches and their scores are shown in the *bottom panel*

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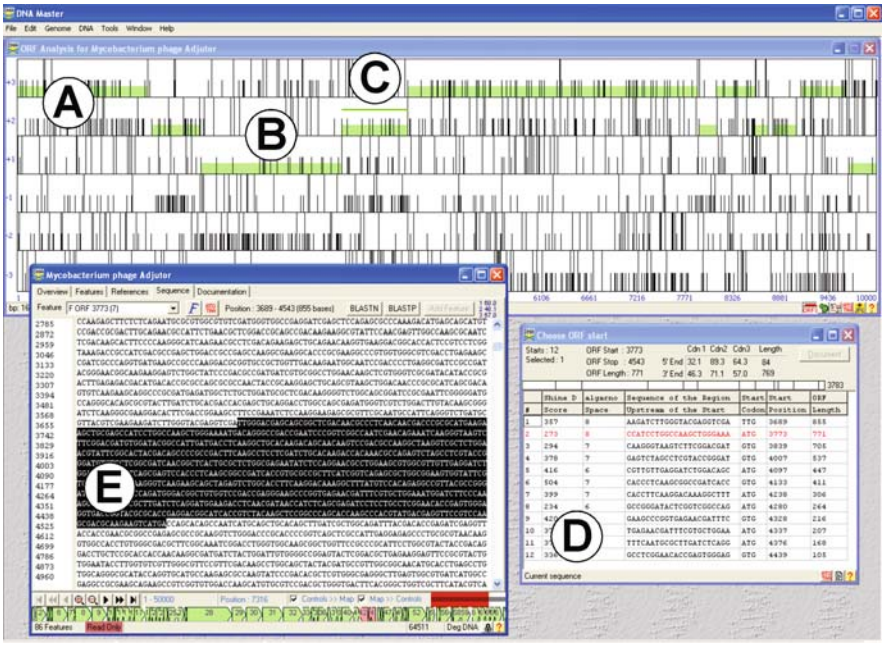

Fig. 7.4 Representations of genome analyses using DNA Master. (**A**) The output from the "Frames" routine in DNA Master showing six reading frames, with start (*short vertical lines*) and stop codons (*full height lines*) indicated. (**B**) ORFs with strong prediction for coding potential predicted by GenMark and Glimmer are designated by a *thick green horizontal line*. (**C**) Clicking on a segment of a frame of interest produces a *thin green* line and also links to the "choose start" routine shown in (**D**) the ORF and start codon corresponding to the frame segment in (**C**) is in *red*. (4). (**E**) The genome segment highlighted in (**C**) is revealed as a selected segment (black background) in the "Sequence" panel of DNA Master, and can be added to the annotation or copied as either a nucleotide or a translated amino acid sequence for BLAST analyses

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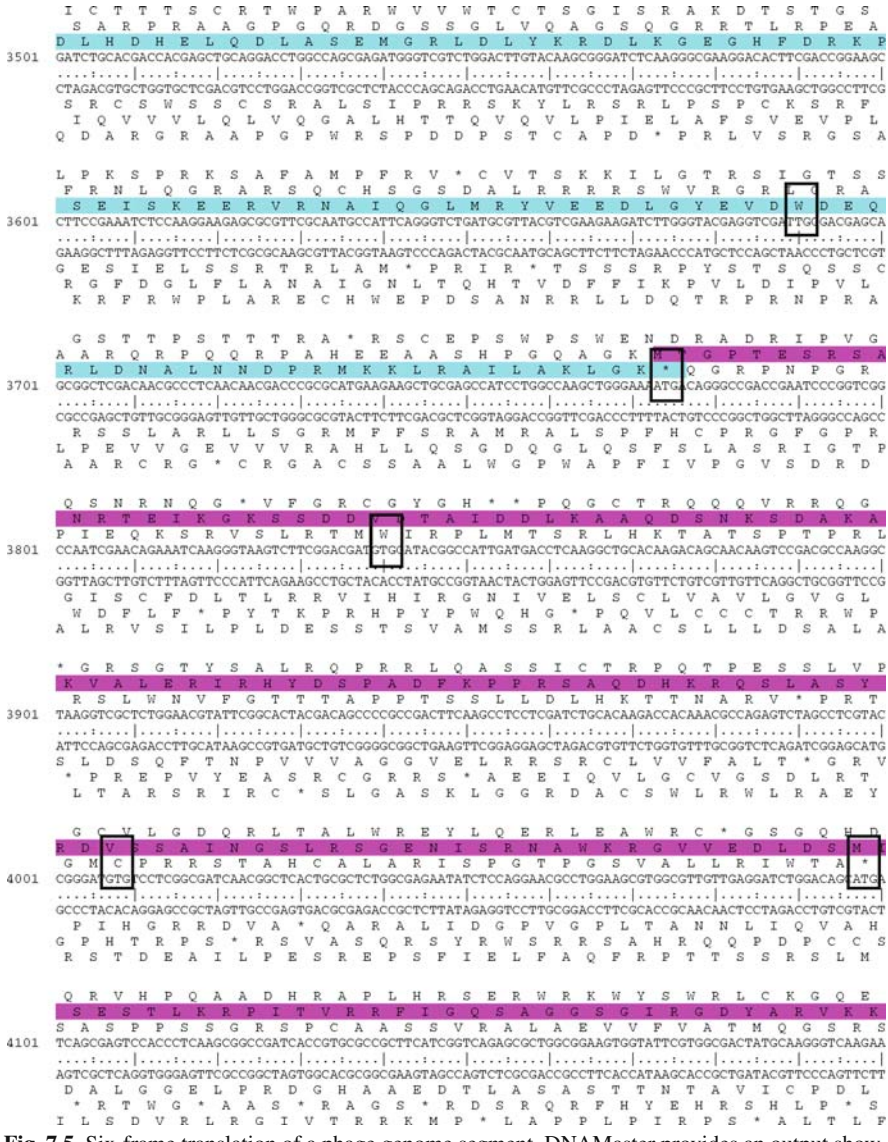

Fig. 7.5 Six-frame translation of a phage genome segment. DNAMaster provides an output showing the DNA sequence of both strands as well the amino acid sequences in each of the potential six reading frames. The amino acid sequences of the potential ORFs predicted by Glimmer and GenMark are colored. Each of the potential start codons shown in Fig. 7.4E (and within this DNA segment) are shown *boxed*