

## CLUSEAN Analysis of Secondary Metabolite Clusters

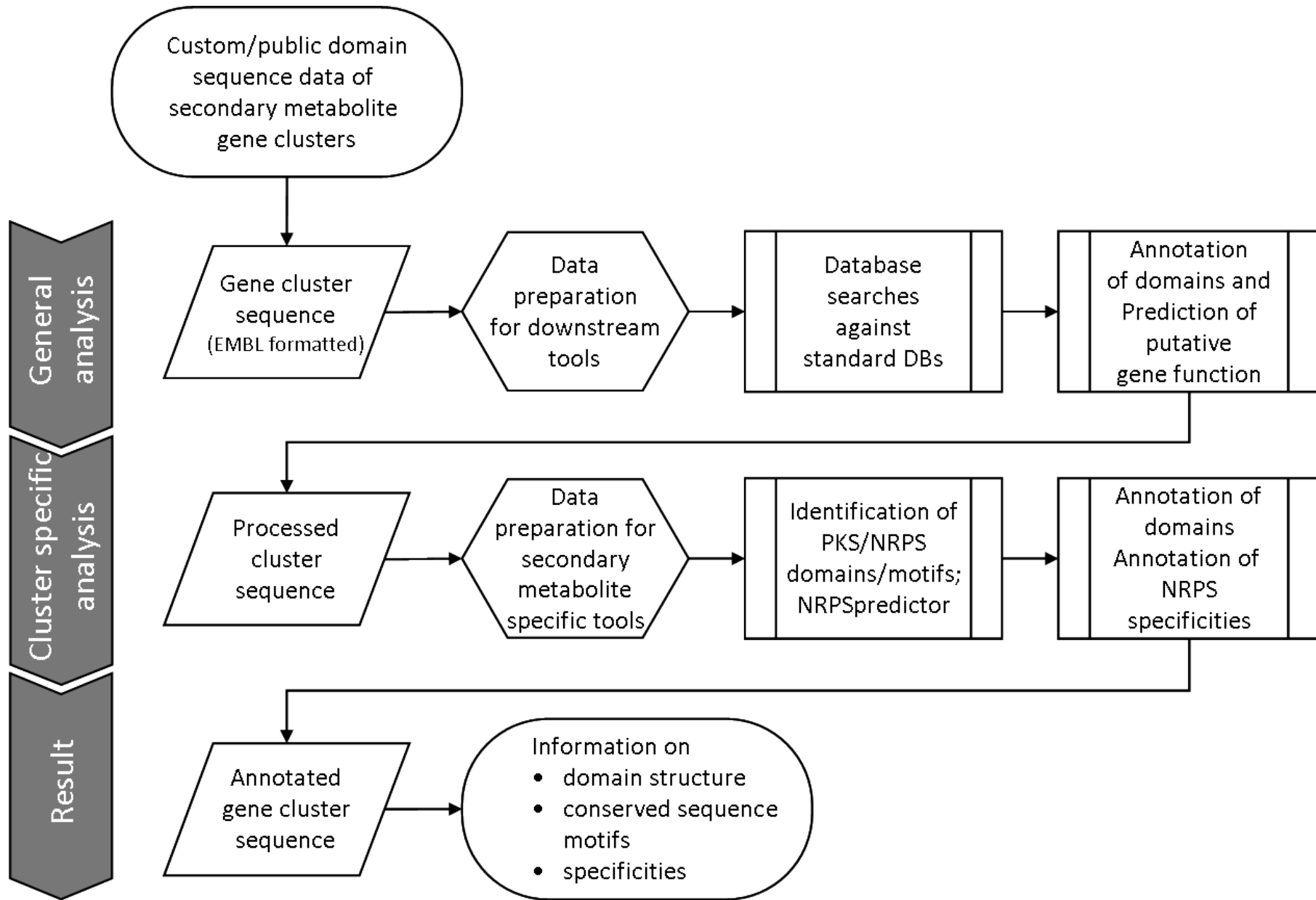
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# Pipeline Steps



# Output

The screenshot shows the Artemis Entry Edit interface for the file `balh.final_fixed.embl`. The top menu includes `File`, `Entries`, `Select`, `View`, `Goto`, `Edit`, `Create`, `Run`, `Graph`, and `Display`. The entry `balh.final_fixed.embl` is selected. The selected feature is `bases 1194 AUTOORF_00007 (/locus tag="AUTOORF_00007" /label=NRPS-A-domain /note="/home/kai/dev/CLUSEAN/lib/`.

The main display shows a genomic map with several features. The `bpsA` feature is highlighted in cyan. Below it, a series of `AUTOORF_00007` features are shown as arrows pointing right, with their start and end coordinates: 7200-8000, 8800-9600, 10400-11200, 12000-12800, and 13600-14400.

The sequence below the map is as follows:

```
L Q Q Q R R R P H H P A D V T G G D D D D T A F L G D R E Q R F D G L F H K Q G Q V
C S S S V A D P T T R L M * P E A M M T T R R F S A I G S S V S M A S S T S R D R S
. A A A A S P T P P P G * C D R R R * * R H G V S R R S G A A F R W P L P Q A G T G
CTGCAGCAGCAGCGTCGCCGACCCACCACCCGGCTGATGTGACCGGAGGCGATGATGACGACACGGCGTTTCTCGGCGATCGGGAGCAGCGTTTCGATGGCCTCTTCCACAAGCAGGGACAGGTC
|20 |40 |60 |80 |100 |120
GACGTCGTGTCGCGAGCGGCTGGGGTGGTGGGCCGACTACACTGGCCTCCGCTACTACTGCTGTGCCGCAAGAGCCGCTAGCCCTCGTCGCAAAGCTACCGGAGAAGGTGTTGTCGTCCTGTCCAC
A A A A D G V G G G P Q H S R L R H H R C P T E R R R D P A A N R H G R G C A P V P F
. C C C R R R G W W G A S T V P P S S S S V A N R P S R S C R K S P R K W L C P C T
Q L L L T A S G V V R S I H G S A I I V V R R K E A I P L L T E I A E E V L L S L D
```





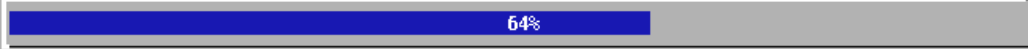
# User Interface Improvements

CLUSEAN development branch

Running Blast against clusean

Processing Y16952.orf30.fasta (64.86 %)

64%

A progress bar with a blue fill and a white border, showing 64% completion. The text '64%' is centered within the bar.

# Output

balh.NRPSP.csv - OpenOffice.org Calc

File Edit View Insert Format Tools Data Window Help

Liberation Sans 10

A1 f(x) Σ = bpsA

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	bpsA	./NRPSPred/Y16952.nrps1.out	7138	16635	1	7627	8043	164	302	LDASFDASLFEMYLLTGGDRNMYGPTTEATMCATW	DAFYLGMMCK	<a href="#">gly=ala=val=leu=ile=abu=iva-like</a> ; Score: 0.810	<a href="#">val=leu=ile=abu=iva-like</a> ; Score: 0.829	Q939Z1_m1_leu Id: 10
2	bpsA	./NRPSPred/Y16952.nrps1.out	7138	16635	1	10702	11109	1189	1324	LAHAFDITVSEMKAVAAGEINAYGPTTETTCATM	DTSKVAAICK	<a href="#">phe=trp=phg=tyr=bht-like</a> ; Score: 0.733	<a href="#">tyr=bht-like</a> ; Score: 0.689	O52819_m2_bht Id: 10
3	bpsA	./NRPSPred/Y16952.nrps1.out	7138	16635	1	15256	15660	2707	2841	YHCSFDLTVTATKALLGGEVNEYGPTTEATVGCVE	DLTKLGEVVK	<a href="#">asp=asn=glu=qln=aad-like</a> ; Score: 1.190	<a href="#">asp=asn-like</a> ; Score: 1.125	O52819_m3_asn Id: 10
4	bpsB	./NRPSPred/Y16952.nrps2.out	16635	28868	1	18474	18890	614	752	LEPAFDISLFEVHLLTGGDRHLYGPTTEATLCATW	DIFHLGLLCK	<a href="#">ser=thr=ser=thr=dht=dhpg=dpg=hpg-like</a> ; Score: 1.189	<a href="#">dhpg=dpg=hpg-like</a> ; Score: 2.175	Q93N87_m2_hpg Id: 10
5	bpsB	./NRPSPred/Y16952.nrps2.out	16635	28868	1	22962	23378	2110	2248	LDPAFDASLVEVHLLTGGDRQLYGPTEITLCATW	DAVHLGLLCK	<a href="#">ser=thr=ser=thr=dht=dhpg=dpg=hpg-like</a> ; Score: 0.975	<a href="#">dhpg=dpg=hpg-like</a> ; Score: 1.703	O52820_m2_hpg Id: 10
6	bpsB	./NRPSPred/Y16952.nrps2.out	16635	28868	1	27513	27920	3627	3762	LAHSFDAIVSEMTVLTGGGEIQAYGPTTETTCSTM	DASTLGAICK	<a href="#">phe=trp=phg=tyr=bht-like</a> ; Score: 0.722	<a href="#">tyr=bht-like</a> ; Score: 0.689	Q939Z0_m3_bht Id: 10
7	bpsC	./NRPSPred/Y16952.nrps3.out	28888	34464	1	30751	31167	622	760	LDAAFDPSLYAVHLGTGGDRNTYGPTEITLTCATW	DPYHGGTLCK	<a href="#">ser=thr=ser=thr=dht=dhpg=dpg=hpg-like</a> ; Score: 0.846	<a href="#">dhpg=dpg=hpg-like</a> ; Score: 1.916	Q70AZ6_m1_dhpg Id: 10
8														
9														
10														
11														

