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#! /usr/local/bin/perl -w -I/home/berger_a/lib/perl5/site_perl/5.8.0

use strict;
use warnings;

use Text::Wrap;
use DBI;
use DBD::SQLite;
use CGI;

$Text::Wrap::columns = 60;

#connect
my $dbh = DBI -> connect
("dbi:SQLite:dbname=/project/rodent/web/bin/fifth.sqlite",'','') or
die DBI -> errstr;

#setup CGI handle
my $cgi = new CGI;

#start HTML
print $cgi->header;

write_search_header();

my $item;
my $clones;my $cloneList;
my @row;my $row;
my $trace_name;my $clone_name;
my $clone;
my $search;my $search_plus = ' ';
my $uniqseq_name;my $cluster;my $traces;
my $annotation1; my $annotation2; my $annotation3;
my $uniqseq_sequence;
my $OFP;my $OFP_new;my $OFP_old;my $OFP_new2;
my $OFP_name_new;my $OFP_name_old;my $OFP_clone_rank;
my $size;
my $neurula_expr;my $neurula_num;
my $gastrula_expr; my $gastrula_num;
my $organogenesis_expr; my $organogenesis_num;
my $ovary_expr; my $ovary_num;
my $Rstat;

my $case = 0;
my $info0; my $info1;my $info2; my $info3;my $info4;my $info5; my
$info6; my $info7;

#####
#web version

#handle any queries that have been sent
$clone = $cgi->param('search_what');
$clone = validate($clone);
$search = $cgi -> param('search_crit');
if ($cgi -> param('search_plus')) {$search_plus = $cgi -> param
('search_plus');}
my $Button1 = $cgi -> param('QueryAbundance');
my $Button2 = $cgi -> param('Query');
my $Button3 = $cgi -> param('QueryBlast');
#####

#####
#test auf abundance profile

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#$search = '';
#my $Button2 = '';
#my $Button1 = 'Search';
#my $Button3 = '';
#$clone = '';
#####
#test auf Klon
#$search = 'Clone_id';
#my $Button2 = 'Search';
#my $Button1 = '';
#my $Button3 = '';
#$clone = '23B21';
#####
#test auf TraceID
#$search = 'Trace_id';
#my $Button2 = 'Search';
#my $Button1 = '';
#my $Button3 = '';
#$clone = '1A09';
#####
#test auf RearrayID
#$search = 'Rearray1_id';
#my $Button2 = 'Search';
#my $Button1 = '';
#my $Button3 = '';
#$clone = '1B11';
#####
#test auf OFP
#$search = 'OFPcluster_idplus';
#my $Button2 = 'Search';
#my $Button1 = '';
#my $Button3 = '';
#$clone = 'OFP857';
#####
#$clone = validate($clone);
#my $ok=1;
#$search = 'OFPcluster_id';
#print "$clone";
#print $search;
#$clone = '1';
#$search_plus='YES';

if ($Button1 eq 'Search'){
#####
#####
#handle AbundanceProfiles
#####
#####

my $search_neurula_expr = $cgi -> param('neurula_expr');
#my $search_neurula_expr = 'nothing';
if ($search_neurula_expr eq 'nothing'){ $neurula_expr = '%';}
else {if ($search_neurula_expr eq 'one'){ $neurula_expr = '1';}
else{ if ($search_neurula_expr eq 'minusone'){ $neurula_expr = '-1';}
else {if ($search_neurula_expr eq 'zero'){ $neurula_expr = '0';}}}}

my $search_gastrula_expr = $cgi -> param('gastrula_expr');
#my $search_gastrula_expr = 'nothing';
if ($search_gastrula_expr eq 'nothing'){ $gastrula_expr = '%';}
else {if ($search_gastrula_expr eq 'one'){ $gastrula_expr = '1';}
else{ if ($search_gastrula_expr eq 'minusone'){ $gastrula_expr = '-1';}
else {if ($search_gastrula_expr eq 'zero'){ $gastrula_expr = '0';}}}}

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my $search_organogenesis_expr = $cgi -> param('organogenesis_expr');
#my $search_organogenesis_expr = 'nothing';
if ($search_organogenesis_expr eq 'nothing'){$organogenesis_expr =
'%';}
else {if ($search_organogenesis_expr eq 'one'){$organogenesis_expr =
'1';}
else{ if ($search_organogenesis_expr eq 'minusone')
{$organogenesis_expr = '-1';}
else {if ($search_organogenesis_expr eq 'zero'){$organogenesis_expr =
'0';}}}}

my $search_ovary_expr = $cgi -> param('ovary_expr');
#my $search_ovary_expr = 'one';
if ($search_ovary_expr eq 'nothing'){$ovary_expr = '%';}
else {if ($search_ovary_expr eq 'one'){$ovary_expr = '1';}
else{ if ($search_ovary_expr eq 'minusone'){$ovary_expr = '-1';}
else {if ($search_ovary_expr eq 'zero'){$ovary_expr = '0';}}}}

$OFP = $dbh->selectall_arrayref(qq{select
OFP_name,size,neurula_num,neurula_expr,gastrula_num,gastrula_expr,o
rganogenesis_num,organogenesis_expr,ovary_num,ovary_expr from OFP
where neurula_expr like '$neurula_expr' and gastrula_expr like
'$gastrula_expr' and organogenesis_expr like '$organogenesis_expr'
and ovary_expr like '$ovary_expr' ORDER BY size DESC});
if ($OFP -> [0]){
print "<p style=\"color:red\"><big>OFP cluster</big><br></p>";
print "<table border=\"1\"><tr><th>cluster name</th><th>cluster size
</th><th>neurula clones</th><th>gastrula clones</th><th>organogenesis
clones</th><th>ovary clones</th></tr>";
  foreach my $item (@$OFP){
    @row=@$item;
    print "<tr><td><small><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&search_crit=OFPcluster_id&search_what=$row[0]
&Query=Search\">$row[0]</a>";
    print "</small></td><td><small>$row[1]</small></td><td><small>
$row[2] ($row[3])</small></td><td><small>$row[4] ($row[5])</small>
</td><td><small>$row[6] ($row[7])</small></td><td><small>$row[8]
($row[9])</small></td></tr>";
  }
print "</table>";
}
else {print "<p><i>No clusters for such a abundance profile found.
</i></p>\n";}
}

#####
#####
# handle Klon- und Clusterinformationen
#####
#####

else{ if ($Button2 eq 'Search'){

  if ($search eq 'Clone_id'){

#Klonliste besteht nur aus Klonen
$cloneList = $dbh->selectall_arrayref(qq{SELECT DISTINCT clone_name
FROM clone WHERE clone_name like '%$clone%' ORDER BY clone_name ASC})
|| die $dbh->errstr;

}#if ($search eq 'Clone_id')

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    if ($search eq 'Trace_id'){

#Klonliste besteht nur aus Klonen, für die traces existieren
$cloneList = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone.clone_name FROM clone,trace_uniqseq WHERE
trace_uniqseq.trace_name = clone.trace_name AND clone.trace_name like
'%'$clone%' ORDER BY clone.clone_name ASC}) || die $dbh->errstr;}

    if ($search eq 'Rearray1_id'){

        $cloneList = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone_name FROM clone WHERE clone.rearray1 like '%'$clone%' ORDER BY
clone_name ASC}) || die $dbh->errstr;}

    if ($search eq 'Rearray2_id'){

        $cloneList = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone_name FROM clone WHERE rearray2 like '%'$clone%' ORDER BY
clone.clone_name ASC}) || die $dbh->errstr;}

if (($search eq 'Rearray2_id') || ($search eq 'Rearray1_id') ||
($search eq 'Clone_id') || ($search eq 'Trace_id') || ($search_plus eq
'YES')){

    print "<br><p style=\"color:red\"><big>Clone information</big>
</p><br>\n";
    print "<table border=\"1\"><tr><th>clone name</th><th>trace name
</th><th>library</th><th>rearray1</th><th>rearray2</th><th>OFP
cluster_id</th><th>EST cluster_id</th><th>clone_sequence</th></tr>
\n";

    my $found = 0;
    if ($cloneList -> [0]){
        foreach my $item (@$cloneList){
            @row = @$item;
            ($info0,$info1,$info2,$info3,$info4,$info5,$info6,$info7,$case)
= find_cloneinfo($row[0]);
            unless ($case == 5){
                write_cloneinfo($info0,$info1,$info2,$info3,$info4,$info5,
$info6,$info7,$case);
                $found = 1;}
            else {unless ($found){$found = 0;}}}}
        else {print "<p><i>No clone information found</i></p>\n";}
        unless ($found){print "<p><i>No clone information found</i></p>
\n";}

    print "</table>";

}#if (($search eq 'Rearray2_id') || ($search eq 'Rearray1_id') ||
($search eq 'Clone_id')...

#####
#####
# Suche nach UniqueSequence_id
#####
#####

if ($search eq 'UniqueSequence_id'){
    $cluster = $dbh->selectall_arrayref(qq{select DISTINCT
uniqseq_name,size,annotation,uniqseq_sequence from uniqseq where
uniqseq_name like '%'$clone%' ORDER BY uniqseq_name ASC});

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    $traces = $dbh->selectall_arrayref(qq{select * from trace_uniqseq
where uniqseq_name like '%$clone%' ORDER BY uniqseq_name ASC});
print "<br><p style=\"color:red\"><big>Sequence cluster information
</big></p>";

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if ($cluster->[0]){
print "<table border=\"1\"><tr><th>Cluster/Singleton name</th><th>
Cluster size</th><th>GO/blastx<br>SPTrembl/TIGR<br>blastx nrprot<br>
blastn TIGR<br>motif search</th><th>sequence</th></tr>";
foreach my $item (@$cluster){
    @row = @$item;
    print "<tr>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=UniqueSequence_id&amp;search_what=$row[0]
&amp;Query=Search\">$row[0]</a></small></td><td valign=\"TOP\">";
        for (my $i=1;$i<(scalar(@row)-1);$i++){
            print "<small>$row[$i]</small></td><td valign=\"TOP\">";
            print "<small><font face=\"courier\">";
            print wrap (' ', '$row[3]);print "</font></small></td></tr>\n";
            print "</table>\n";
        }
    if ($traces -> [0]){
        print "<br><table border=\"1\"><th align=\"LEFT\">Cluster</th>
<th align=\"LEFT\">Clones</th>";
        foreach my $item (@$traces){
            @row = @$item;
            print "<tr><td align=\"LEFT\"><small>$row[1]</small></td>";
            print "<td align=\"LEFT\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Trace_id&amp;search_what=$row[0]&amp;Query=Search\">
$row[0]</small></a></td></tr>";
            print "</table>\n";
        }
    }
    else {print "<br><i>No cluster information found</i>\n";}
}

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```

#####
#####
# Suche nach OFP-Cluster
#####
#####
#my $further = 0;

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#if ($search eq 'OFPcluster_id' || $search eq 'OFPcluster_idplus'){
# print "<br><p style=\"color:red\"><big>Fingerprint cluster
information</big></p>\n";

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#nur Klone mit traces
# $OFP_new = $dbh->selectall_arrayref(qq{select
clone.clone_name,clone.trace_name,clone_OFP.OFP_name_old,clone_OFP.OF
P_name_new,clone_OFP.clone_rank,clone.library from clone_OFP,clone
where clone_OFP.clone_name=clone.clone_name AND
clone_OFP.OFP_name_new like '%$clone%' AND clone.trace_name like
'McF%' ORDER BY clone.clone_name ASC});
#auch Klone ohne traces
# $OFP_new2 = $dbh->selectall_arrayref(qq{select
clone.clone_name,clone.trace_name,clone_OFP.OFP_name_old,clone_OFP.OF
P_name_new,clone_OFP.clone_rank,clone.library from clone_OFP,clone
where clone_OFP.clone_name=clone.clone_name AND
clone_OFP.OFP_name_new like '%$clone%' AND clone.trace_name like
'NA' ORDER BY clone.clone_name ASC});

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# unless (($OFP_new ->[0]) and ($OFP_new2 -> [0])){#alter
OFPcluster, der in anderen Cluster eingegangen ist
# $OFP_old = $dbh->selectall_arrayref(qq{select distinct
OFP_name_new,OFP_name_old from clone_OFP where OFP_name_old like

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'$clone'}});
#   if ($OFP_old -> [0]){
#       $row=$OFP_old -> [0];
#       $OFP_name_new = $row -> [0];
#       $OFP_name_old = $row -> [1];
#       print "$OFP_name_old has been put into <a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&search_crit=OFPcluster_idplus&search_what=
$OFP_name_new&Query=Search&search_plus=$search_plus\">!!<br>
<br>";
#   else {print "No fingerprinting cluster information found.";}

#   else {# unless (($OFP_new ->[0]) and ($OFP_new2 -> [0]))
#   unless ($clone =~ /Med/) {#kein OFP Singleton
#   unless ($OFP_new -> [1]){ unless ($OFP_new2 -> [1]){
#   if ($OFP_new -> [0]){ $row = $OFP_new -> [0]; $OFP_name_new =
$row -> [0];}
#   else { $row = $OFP_new2 -> [0]; $OFP_name_new = $row -> [0];}
#   #nur 1 result and no OFP singl
#   $OFP = $dbh->selectall_arrayref(qq{select
OFP_name,size,R_stat,neurula_expr,neurula_num,gastrula_expr,gastrula
_num,organogenesis_expr,organogenesis_num,ovary_expr,ovary_num
from OFP where OFP_name = '$OFP_name_new'});

#   if ($row = $OFP -> [0]){
#   print "<p>Data for $row->[0] (traces available):<br>";
#   $size = $row -> [2];
#   $Rstat = $row -> [0];
#   $neurula_expr = $row -> [3]; $neurula_num = $row -> [4];
#   $gastrula_expr = $row -> [5]; $gastrula_num = $row -> [6];
#   $organogenesis_expr = $row -> [7]; $organogenesis_num = $row ->
[8];
#   $ovary_expr = $row -> [9]; $ovary_num = $row -> [10];
#   print "<b>$row->[0]</b> contains $size clones (without OL
clones)<br></p>\n";
#   print "<p><big>Abundance profile:</big> (0 - no changes; 1 -
overexpressed; -1 - underexpressed)<br>\n";
#   print "Neurula: $neurula_num clones ($neurula_expr) ";
#   print "Gastrula: $gastrula_num clones ($gastrula_expr) ";
#   print "Organogenesis: $organogenesis_num clones
($organogenesis_expr) ";
#   print "Ovary: $ovary_num clones ($ovary_expr)</p>\n";}
#   }}}

#   print "<table border=\"1\"><tr><th>clone name</th><th>trace name
</th><th>library</th><th>new OFP name</th><th>old OFP name</th><th>
OFP clone rank</th></tr>";
#   foreach my $item (@$OFP_new){
#       @row=@$item;

#       print "<tr><td><small>
#<a href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&search_crit=Clone_id&search_what=$row[0]
&Query=Search&\">$row[0]</a></small></td><td><small>
#<a href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&search_crit=Trace_id&search_what=$row[1]&Query=Search\">
$row[1]</small></a></td>
#<td><small>$row[5]</small></td>
#<td><small><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&search_crit=OFPcluster_id&search_what=$row[3]
&Query=Search&\">$row[3]</small></a></td>
#<td><small><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?

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&amp;search_crit=OFFPcluster_id&amp;search_what=$row[2]
&amp;Query=Search&amp\">$row[2]</small></a></td>
#<td><small>$row[4]</small></td></tr>";
#    }

#    if ($search eq 'OFFPcluster_idplus'){
#        foreach my $item (@$OFFP_new2){
#            @row=@$item;
#            print "<tr><td><small>
#<a href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Clone_id&amp;search_what=$row[0]
&amp;Query=Search&amp\">$row[0]</a></small></td><td><small>
#<a href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Trace_id&amp;search_what=$row[1]&amp;Query=Search\">
$row[1]</small></a></td>
#<td><small>$row[5]</small></td>
#<td><small><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFFPcluster_id&amp;search_what=$row[3]
&amp;Query=Search&amp\">$row[3]</small></a></td>
#<td><small><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFFPcluster_id&amp;search_what=$row[2]
&amp;Query=Search&amp\">$row[2]</small></a></td>
#<td><small>$row[4]</small></td></tr>";}
#}
#print "</table>\n";}}

#unless ($search eq 'OFFPcluster_idplus'){
#    print "<a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFFPcluster_idplus&amp;search_what=
$clone&amp;Query=Search\">Show all clones.</a>";}

my $further = 0;

if ($search eq 'OFFPcluster_id' || $search eq 'OFFPcluster_idplus'){
    print "<br><p style=\"color:red\"><big>Fingerprint cluster
information</big></p>\n";

    if ($search eq 'OFFPcluster_idplus'){
        $OFFP_new = $dbh->selectall_arrayref(qq{select
clone.clone_name,clone.trace_name,clone_OFFP.OFP_name_old,clone_OFFP.OF
P_name_new,clone_OFFP.clone_rank,clone.library from clone_OFFP,clone
where clone_OFFP.clone_name=clone.clone_name AND
clone_OFFP.OFP_name_new like '%$clone' ORDER BY clone.clone_name
ASC});}
        else {
            $OFFP_new = $dbh->selectall_arrayref(qq{select
clone.clone_name,clone.trace_name,clone_OFFP.OFP_name_old,clone_OFFP.OF
P_name_new,clone_OFFP.clone_rank,clone.library from clone_OFFP,clone
where clone_OFFP.clone_name=clone.clone_name AND
clone_OFFP.OFP_name_new like '%$clone' AND clone.trace_name like
'McF%' ORDER BY clone.clone_name ASC});}

        unless ($OFFP_new ->[0]){
            #OFFP cluster ohne traces
            $OFFP_new = $dbh->selectall_arrayref(qq{select
clone.clone_name,clone.trace_name,clone_OFFP.OFP_name_old,clone_OFFP.OF
P_name_new,clone_OFFP.clone_rank,clone.library from clone_OFFP,clone
where clone_OFFP.clone_name=clone.clone_name AND
clone_OFFP.OFP_name_new like '%$clone' ORDER BY clone.clone_name
ASC});}
            unless ($OFFP_new ->[0]){

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#alter OFPcluster, der in anderen Cluster eingegangen ist
$OFP_old = $dbh->selectall_arrayref(qq{select distinct
OFP name_new,OFP_name_old from clone_OFP where OFP_name_old like
'$clone'});
if ($OFP_old -> [0]){
#   $further = 1;
   $row=$OFP_old -> [0];
   $OFP_name_new = $row -> [0];
   $OFP_name_old = $row -> [1];
   print "$OFP_name_old has been put into


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'McF%'}});}
}#if ($OFP_old -> [0]){
else {print "No fingerprinting cluster information found.;"#unless
($OFP_new -> [0])alter OFPcluster
else {$OFP_name_new = $clone;$further = 1;}
}
else{$OFP_name_new = $clone;$further = 1;}

if ($further){
if ($OFP_name_new !~ /Med/){
# unless ($OFP_new ->[1]){
$OFP = $dbh->selectall_arrayref(qq{select * from OFP where
OFP_name = '$OFP_name_new'});

if ($row = $OFP -> [0]){
print "<p>Data for $row->[1]:<br>";
$Rstat = $row -> [0];
$size = $row -> [2];
$neurula_expr = $row -> [3];$neurula_num = $row -> [4];
$gastrula_expr = $row -> [5]; $gastrula_num = $row -> [6];
$organogenesis_expr = $row -> [7]; $organogenesis_num = $row ->
[8];
$ovary_expr = $row -> [9]; $ovary_num = $row -> [10];
print "<b>$row->[1]</b> contains $size clones (without OL clones)
<br></p>\n";
print "<p><big>Abundance profile:</big> (0 - no changes; 1 -
overexpressed; -1 - underexpressed)<br> R statistics: R = $Rstat <br>
\n";
print "Neurula: $neurula_num clones ($neurula_expr) ";
print "Gastrula: $gastrula_num clones ($gastrula_expr) ";
print "Organogenesis: $organogenesis_num clones
($organogenesis_expr) ";
print "Ovary: $ovary_num clones ($ovary_expr)</p>\n";}
#}
}

print "<table border=\"1\"><tr><th>clone name</th><th>trace name
</th><th>library</th><th>old OFP name</th><th>new OFP name</th><th>
OFP clone rank</th></tr>";
foreach my $item (@$OFP_new){
@row=@$item;
if ($row[1] =~ /NA/){$search_plus='YES';}
else {$search_plus=' ';}
print "<tr><td><small>
<a href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Clone_id&amp;search_what=$row[0]
&amp;Query=Search&amp;search_plus=$search_plus\">$row[0]</a>
</small></td><td><small>";
if ($row[1] =~ /NA/){print "$row[1]";}
else {print"<a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Trace_id&amp;search_what=$row[1]&amp;Query=Search\"
$row[1]</a>";}

print "</small></td><td><small>$row[5]</small></td><td><small><a
href=\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFPcluster_id&amp;search_what=$row[2]
&amp;Query=Search&amp;\">$row[2]</small></a></td><td><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFPcluster_id&amp;search_what=$row[3]
&amp;Query=Search&amp;\">$row[3]</small></a></td><td><small>$row[4]
</small></td></tr>";
}
print "</table>\n";

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        unless ($search eq 'OFFcluster_idplus'){
            print "<a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&search_crit=OFFcluster_idplus&search_what=
$OFF_name_new&Query=Search\">Show all clones.</a>";}
        $further = 0;}

#####
#####
# Suche nach Keyword
#####
#####

if ($search eq 'AnnotationKeyword'){
    $cluster = $dbh->selectall_arrayref(qq{select DISTINCT
uniqseq_name,annotation,uniqseq_sequence from uniqseq where
annotation like '%$clone%' ORDER BY uniqseq_name ASC});

print "<br><p style=\"color:red\"><big>Sequence cluster information
</big></p>";
my $uniqseq_sequence;

if ($cluster->[0]){
print "<table border=\"1\"><tr><th>Cluster/Singleton name</th><th>
GO/blastx<br>SPTrembl/TIGR</th><th>blastx nrprot<br>blastn TIGR</th>
<th>motif search</th><th>sequence</th></tr>";
foreach my $item (@$cluster){
    @row = @$item;
    print "<tr>";
    print "<td valign=\"TOP\"><a href=\"http://www.molgen.mpg.de/
~rodent/bin/MedakaDB_new.cgi?
&search_crit=UniqueSequence_id&search_what=$row[0]
&Query=Search\"><small>$row[0]</small></a></td>";
    print "<td valign=\"TOP\">";
        for (my $i=1;$i<(scalar(@row)-1);$i++){
            print "<small>$row[$i]</small></td><td valign=\"TOP\">";
            print "<small><font face=\"courier\">";
            print wrap ('', '$row[4]);print "</font></small></td></tr>\n";
            print "</table>\n";}
else {print "<br><i>No cluster information found</i>\n";}#if
($search eq 'AnnotationKeyword')
}#Button2

else {if ($Button3 eq 'Search'){
#handle blastresults
print "Is not working!";
#    $search = $cgi->param('Input_seq');
#    $search = ">oo";
#    my $blast_input = '/project/rodent/web/blast_temp_input';
#    my $blast_AllHiQualDB = '/project/rodent/web/test_AllHiQualDB';
#    my $blast_AllClustDB =
'/project/rodent/web/test_AnjaMcFinalDB';
#    my $blast_output = '/project/rodent/web/blast_temp_output';
#    if ($search !~ /^>\w*/){print "\n<br>Sequence is not in FASTA
format!\n<br>";}
#    system "nohup nice +30 blastall -p blastn -e 1.0e-10 -o
$blast_output -d $blast_AllClustDB -i $blast_input";
#    print "";
}}

write_footer();

#end HTML
print $cgi->end_html;

```

```

#disconnect from db
$dbh->disconnect();
exit;

#validate user input
sub validate {
    my $string = shift;
    $string =~ s/\s+//g;$string =~ s/\n//g;$string=~s/*//g;
    return $string;
}

#schreibt Max-Planck-Header plus Search Leiste
sub write_search_header {
print "<!DOCTYPE HTML PUBLIC "-//W3C//DTD HTML 4.0 Transitional//EN
\">
<html>
    <head>
        <title>Mouse Medaka MHC - Vertebrate Genomics</title>
        <meta http-equiv=\"Content-Type\" content=
\"text/html; charset=iso-8859-1\">
        <meta http-equiv=\"content-language\" content=\"en\">
        <meta http-equiv=\"Reply-to\" content=\"wwwadm
@molgen.mpg.de\">
        <meta name=\"robots\" content=\"index, follow\">
        <meta name=\"allow-search\" content=\"yes\">
        <meta http-equiv=\"Content-Script-Type\" content=
\"text/javascript\">
        <meta http-equiv=\"Content-Style-Type\" content=
\"text/css\">
        <link rel=STYLESHEET type=\"text/css\" href=
\"ags2001.css\">
        <script language=\"JavaScript\" src=\"mainjs2001.js
\" type=\"text/javascript\">
<!--self.defaultStatus = document.title;// -->
</script>
    </head>

<body bgcolor=\"#FFFFFF\" text=\"#000000\" link=\"#007B70\" alink=\"#
990000\"vlink=\"#2E90B4\" leftmargin=\"0\" topmargin=\"0\"
marginwidth=\"0\"marginheight=\"0\"><cr>
        <table cellpadding=\"0\" cellspacing=\"0\" border=\"0
\" width=\"100%\" height=\"120\">
            <tr valign=\"top\" align=\"left\" height=\"88
\">
                <td rowspan=\"2\" width=\"7%\"
valign=\"middle\"align=\"center\"><img src=\"minerva.jpg\" width=\"84
\" height=\"84\" border=\"0\"></td>
                <td align=\"left\" rowspan=\"2\"
valign=\"middle\" width=\"83%\">
                    <div align=\"left\">
                        <font face=
\"Verdana,Arial,Helvetica,sans-serif\" size=\"+2\">MAX PLANCK
INSTITUTE for MOLECULAR GENETICS</font>
                    </div>
                </td>
                <td align=\"left\" rowspan=\"2\"
valign=\"middle\" width=\"10%\"><a href=\"http://www.molgen.mpg.de/
\"><font size=\"-3\">home</font></a>
                    <p><a href=
\"http://www.molgen.mpg.de/contact.html\"><font size=\"-3\">contact
</font></a></p>
                    <p><a href=
\"http://www.molgen.mpg.de/search.html\"><font size=\"-3\">search

```

```

</font></a></p>
                                </td>
                                </tr>
                                <tr valign=\"top\" align=\"left\"></tr>
                                <tr valign=\"top\" align=\"left\">
                                    <td height=\"36\" colspan=\"2\"
align=\"left\" bgcolor=\"#E3E4E0\" background=\"mhead2001
_brownline_back.gif\">
                                <table cellpadding=\"0\"
cellspacing=\"0\" border=\"0\" height=\"36\">
                                    <tr valign=\"top\"
align=\"left\">
                                        <td width=
\"196\" valign=\"middle\" height=\"36\" nowrap background=\"mhead2001
_titlesmall_blank.gif\"><font class=\"catsmalltitle\" face=
\"Verdana,Arial,Helvetica,sans-serif\" color=\"#FFFFFF\" size=\"-2\">
&nbsp;<a href=\"http://www.molgen.mpg.de/research/lehrach/\"><img
src=\"m2001_ar.gif\" width=\"12\" height=\"12\" alt=\"[back to
Vertebrate Genomics]\" title=\"[back to Vertebrate Genomics]\" align=
\"top\" hspace=\"4\" border=\"0\" vspace=\"1\"></a>Vertebrate
Genomics</font></td>
                                        <td height=
\"36\" valign=\"middle\" nowrap align=\"left\"><font class=
\"catsubtitle\" face=\"Verdana,Arial,Helvetica,sans-serif\" color=\"#
000000\" size=\"+1\">Mouse - Medaka - MHC</font></td>
                                        <td height=
\"36\" valign=\"middle\" nowrap width=\"10\" align=\"left\"></td>
                                        <td height=
\"36\" valign=\"middle\" nowrap align=\"left\"><font size=\"+1
\">/Projects/Medaka transcriptome analysis</font></td>
                                    </tr>
                                </table>
                                </td>
                                <td height=\"36\" align=\"left\"
bgcolor=\"#E3E4E0\" background=\"mhead2001_brownline_back.gif\"
width=\"10%\"></td>
                                </tr>
                                </table>\n
<br>
<table width = \"80%\">
<tr><td align = \"right\"><h3><font size = \"5\">Search in Medaka
ESTdb</font></h3></td>
<td align = \"right\"><a href=\"http://www.molgen.mpg.de/
~rodent/MedakaDB_help.html\"><font color = \"red\" size = \"4\">HELP
</font></a></td></tr>
</table>;
}

sub write_footer{

print "\n";
print "<br>
-----<br>\n";
print "<p><a href=\"http://www.molgen.mpg.de/~rodent/CloneInfo.html
\"><h4>Search for clone or cluster information</h4></a></p>\n";

print "<p><a href=\"http://www.molgen.mpg.de/
~rodent/AbundanceProfile.html\"><h4>Search for abundance profile</h4>
</a></p>\n";

print "<p><a href=\"http://www.molgen.mpg.de/~rodent/BlastEST.html\"
><h4>Blast your sequence</h4></a></p>\n";
}

```

```

#übergeben wird Info und Fall
sub write_cloneinfo {

my ($info0,$info1,$info2,$info3,$info4,$info5,$info6,$info7,$case) =
@_;

if ($case ==1){
    print "<tr>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Clone_id&amp;search_what=$info0&amp;Query=Search\">
$info0</a></small></td>\n";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Trace_id&amp;search_what=$info1&amp;Query=Search\">
$info1</small></a></td>\n";
    print "<td valign=\"TOP\"><small>$info2</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info3</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info4</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFPcluster_id&amp;search_what=$info6
&amp;Query=Search\">$info6</a></small></td>\n";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=UniqueSequence_id&amp;search_what=$info7
&amp;Query=Search\">$info7</a></small></td>\n";
    print "<td valign=\"TOP\">\n";
    print "<small><font face=\"courier\">";
    print wrap (' ', '$info5');print "</font></small></td></tr>\n";
}#if ($case_1 == 1)

if ($case ==2){
    print "<tr>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Clone_id&amp;search_what=$info0
&amp;Query=Search&amp;search_plus=YES\">$info0</a></small></td>";
    print "<td align=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Trace_id&amp;search_what=$info1&amp;Query=Search\">
$info1</small></a></td>\n";
    print "<td valign=\"TOP\"><small>$info2</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info3</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info4</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=OFPcluster_id&amp;search_what=$info6
&amp;Query=Search\">$info6</a></small></td>";
    print "<td valign=\"TOP\"><small>No Cluster info</small></td>";
    print "<td valign=\"TOP\"><small>$info5</small></td>";
    print "</tr>";}

if ($case == 3){
    print "<tr>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?

```

```

&amp;search_crit=Clone_id&amp;search_what=$info0&amp;Query=Search\">
$info0</a></small></td>";
    print "<td valign=\"TOP\"><small>$info2</small></td><small></td
\n";
    print "<td valign=\"TOP\"><small>$info3</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info4</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>No OFF Cluster info</small>
</td>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=UniqueSequence_id&amp;search_what=$info6
&amp;Query=Search\">$info6</a></small></td>";
    print "<td valign=\"TOP\">\n";
    print "<small><font face=\"courier\">";
    print wrap ('', '$info5'); print "</font></small></td></tr>\n";}
#if ($case_3 == 1)

if ($case == 4){
    print "<tr>";
    print "<td valign=\"TOP\"><small><a href=
\"http://www.molgen.mpg.de/~rodent/bin/MedakaDB_new.cgi?
&amp;search_crit=Clone_id&amp;search_what=$info0&amp;Query=Search\">
$info0</a></small></td>";
    print "<td valign=\"TOP\"><small>$info2</small></td><small></td
\n";
    print "<td valign=\"TOP\"><small>$info3</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>$info4</small></td><small></td>
\n";
    print "<td valign=\"TOP\"><small>No OFF Cluster info</small>
</td>";
    print "<td valign=\"TOP\"><small>No Cluster info</small></td>";
    print "<td valign=\"TOP\"><small>$info5</small></td>";
    print "</tr>";}
}

sub find_cloneinfo{

my ($clone) = @_ ;

my $clones;
my @row;

# alle Klone mit Sequenzinfo plus OFF info
    $clones = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone.clone_name, clone.trace_name,clone.library, clone.rearray1,
clone.rearray2,clone.clone_sequence, clone_OFF.OFP_name_new,
trace_uniqseq.uniqseq_name FROM clone,trace_uniqseq,clone_OFF WHERE
clone.clone_name=clone_OFF.clone_name AND trace_uniqseq.trace_name =
clone.trace_name AND clone.clone_name like '%$clone%' ORDER BY
clone.clone_name ASC}) || die $dbh->errstr;

    unless ($clones -> [0]){#nocase_1
        #alle Klone ohne Sequenzinformation, kein EST Cluster info;
fkt. nur für Klone mit OFF Info
        $clones = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone.clone_name, clone.trace_name,clone.library, clone.rearray1,
clone.rearray2,clone.clone_sequence,clone_OFF.OFP_name_new FROM
clone,clone_OFF WHERE clone.clone_name=clone_OFF.clone_name AND
clone.clone_name like '%$clone%' ORDER BY clone.clone_name ASC}) ||
die $dbh->errstr ;

```

```

unless ($clones -> [0]){#nocase_2
    #alle Klone mit Sequenzinfo, also EST info, aber kein OFP info
    $clones = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone.clone_name, clone.trace_name,clone.library, clone.rearray1,
clone.rearray2,clone.clone_sequence, trace_uniqseq.uniqseq_nameFROM
clone,trace_uniqseq WHERE trace_uniqseq.trace_name = clone.trace_name
AND clone.clone_name like '%$clone%' ORDER BY clone.clone_name ASC})
|| die $dbh->errstr;
    unless ($clones -> [0]){#nocase_3
        #alle Klone ohne Sequenzinfo, ohne OFP info
        $clones = $dbh->selectall_arrayref(qq{SELECT DISTINCT
clone.clone_name, clone.trace_name,clone.library, clone.rearray1,
clone.rearray2,clone.clone_sequence FROM clone WHERE clone.clone_name
like '%$clone%' ORDER BY clone.clone_name ASC})|| die $dbh->errstr ;
        unless ($clones -> [0]){#nocase_4
            return(0,0,0,0,0,0,0,0,0,5);}
            else {$row = $clones -> [0];
                return($row->[0],$row->[1],$row->[2],$row->[3],$row->
[4],$row->[5],0,0,4);}
            else {$row = $clones -> [0];
                return($row->[0],$row->[1],$row->[2],$row->[3],$row->
[4],$row->[5],$row->[6],0,3);}
            else {$row = $clones -> [0];
                return($row->[0],$row->[1],$row->[2],$row->[3],$row->[4],
$row->[5],$row->[6],0,2);}
            else {$row = $clones -> [0];
                return($row->[0],$row->[1],$row->[2],$row->[3],$row->[4],
$row->[5],$row->[6],$row->[7],1);}
        }
    }
}

```