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SmallPond™ Operating and User Procedures

1. The SmallPond™ (SM) database will require a username and password that will be assigned by the SM Administrator.



Login



SmallPond is a private, web-based, DNA-Profile matching technology. It maintains a database of STR DNA-Profile information and provides for efficient matching of new DNA-Profile data against the database to assist in the generation of leads and/or identification of individuals.

Unauthorized access to or use of this system is strictly prohibited and may be punishable under federal and state law.

2. Once successfully logged in, you will have access to all of the ponds that have been defined.

Ponds

- 1. In the SmallPond™ system, profiles from a given site can be organized into units called **Ponds**.
- 2. The Ponds used at the DESPP DSS are as follows;
 - a. CT Convicted Offender Profiles
 - b. Unknown Forensic Samples- Single Source
 - c. Staff Elimination Database

Pools

- 1. In the SmallPond™ system, ponds can be grouped together into **Pools**. When ponds are grouped together into a pool, it signifies to the SmallPond™ matching service to cross-match the profile data in each on the ponds against the profile data in all of the other ponds in the same pool.
- 2. The Pools used for the CT RapidHit ID systemare as follows;
 - a. Offender DB vs Unknown (SS)

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b. Unknown (SS) vs Staff

Stringency

1. The following base stringency is followed for match notifications.

Medium – For a given locus, all alleles for one of the matching profiles must exist for the other profile.

- 2. In addition to the above rules being applied at every locus, the following conditions must also be met:
 - a. If, at any locus, there is no allele data for either one of the profiles, then the locus is considered a match. It may be better to think of this as not being excluded.
- 3. The following tables illustrate how SmallPond™ applies in evaluating several different locus matching scenarios. These settings are similar to the CODIS settings at the Division.

Profile 1	Profile 2	High	Medium	Low	Comment
2,3	2,3	Match	Match	Match	Exact match at every allele
7,9	7	Exclude	Match	Match	All alleles in Profile 2 are also in Profile 1
2,3	3,4	Exclude	Exclude	Match	Allele 3 appears in both profiles
2,3	7,8	Exclude	Exclude	Exclude	No alleles match
2,3		Match	Match	Match	No allele data for Profile 2 so not excluded
	3,4	Match	Match	Match	No allele data for Profile 1 so not excluded
		Match	Match	Match	No allele data whatsoever so not excluded

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Match Behavior

Specify the match behavior parameters to control how the match is performed.

Stringency:

Medium 🗸

Minimum Loci matched with data



This setting defines the minimum number of loci, with alleles defined for both profiles, that must match.

Above shows that match behavior used for searching.

Importing Sample

- 1. There are two methods for entering new Profiles into a pond:
 - a. **Manual Entry** Profile information and individual locus allele values for a single profile are entered manually by the user. To add a profile manually, click on the **Profiles | Add Profile** menu item on the function bar at the top of every page.
 - b. **Import from File** Profile information and individual locus allele values for multiple profiles are defined in a CODIS CMF file (or another file format) and are imported as a batch operation. To add profiles from a file, click on the **Profiles | Import Profiles** menu item the function bar at the top of every page.
- 2. Regardless of the method chosen to add a profile, whenever a profile is added to a pond the SmallPond™ system will automatically search it against all of the other Profiles in the pond using the pond's configured match stringency settings as well as the stringency settings defined for any pools of which the pond is a member.

Manually Importing a Sample from RapidHit Software through GeneMarker HID

- 1. Clear call flags (Yellow/Red), by editing/deleting/confirming alleles (See RDNA SOP-02)
- 2. After clearing flags, in GeneMarker, go to Applications → Export CODIS

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± ... Caw Data

Allele Call

✓ LD: Trace_ Trace_LN18

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GeneMarker HID - GM_Analysis.sgf

File View Project Applications Tools Help

Comparison View

GeneMarker HID - GM_Analysis.sgf

Applications Tools Help

Export CODIS

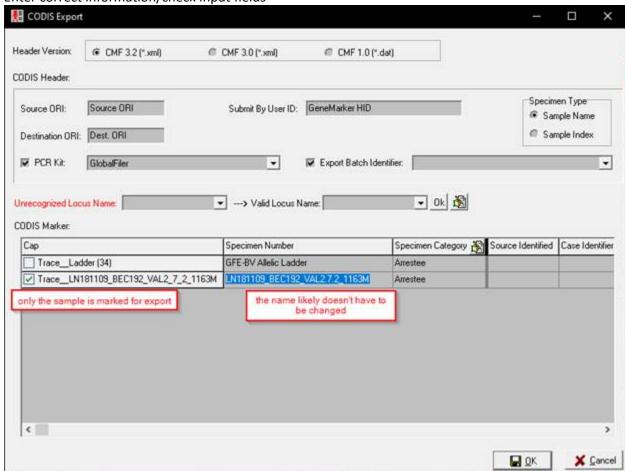
Profile Comparison View

Relationship Testing

Cell Line Authentication

Mixture Analysis

3. Enter correct information/check input fields



4. Navigate to the original runfolder and over-write the GM_Analysis.xml

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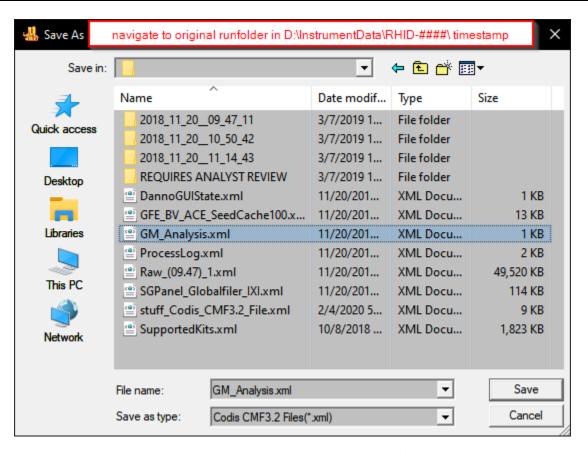
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 Log into Smallpond and navigate to Import Profiles. You can drag/drop the GM_Analysis.xml to upload into appropriate pond which most likely will be the Unknown Forensic Samples- Single Source (Unknown folder).



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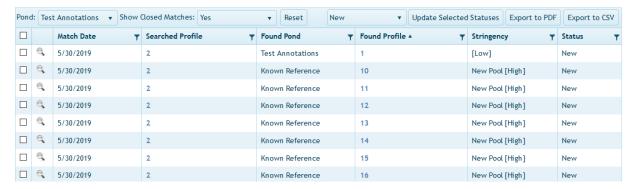
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6. When a match occurs, the system will automatically notify users of the pond based on their individual notification settings. Matches can also be reviewed at any time by going to the **Match History** page.

Matches

You can review all matches that have been found for your Pond on this page.

The system will automatically search for a match whenever a new DNA Profile is added. It uses the Pond's Match Stringency parameters when performing the match. Notifications
are automatically sent when new matches are made.



Match Report

- 1. Navigate to the Match Report page by clicking the **Matching | Match Report** link in the function bar on the top of every page.
- 2. Enter the specimen id of the desired profile.
- 3. Click the Search button.
- 4. The following match report is shown as an example. The match report shows all matches made to the selected profile including the ponds and pools searched as well as the stringencies used in performing the search. A separate page will be generated for each match. This will be maintained by the Rapid Administration.

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Match Date: 4/16/2013 5:02:49 PM

Locus	Target Pond: Clark PD - Knowns Specimen ld: 1234 Unknown	Candidate Pond: Clark PD - Knowns Specimen ld: 1234d579-fcd8- 4a3b-b230-850ac4330992 Unknown	Match Quality
D8S1179	12,14	12,14	Exact
D21S11	27.2,36.3	27.2,36.3	Exact
D7S820	8,11.1	8,11.1	Exact
CSF1PO	6,11	6,11	Exact
D3S1358	14.3,18	14.3,18	Exact
TH01	6,6.1	6,6.1	Exact
D13S317	14,17	14,17	Exact
D16S539	14,14.3	14,14.3	Exact
D2S1338	18,23.3	18,23.3	Exact
D19S433	11,17.2	11,17.2	Exact
vWA	22,23	22,23	Exact
TPOX	5,6	5,6	Exact
D18S51	13.1,15.3	13.1,15.3	Exact
AMELOGENIN	x	x	Exact
D5S818	14,16	14,16	Exact
FGA	27.2,42.1	27.2,42.1	Exact

Source ID:	No	No
Partial Profile:	No	No
Mixture:	No	No

Match Detail:

Search Program: SmallPond Maximum number of candidates to return from search: ALL

Searched Ponds:

Pond	Stringency	Profiles Searched		
Clark PD - Knowns	Must match ALL loci			
	Mixtures included: Yes			
	Exact match required: Yes	520037		
Total		520037		

Searched Pools:

Pool	Stringency	Ponds	Profiles Searched
Clark PD Pool	Must match ALL loci	Clark PD - Unknowns	
	Mixtures included: Yes	Clark PD - Knowns	I
	Exact match required: Yes		531047
Total			531047

Report Sent to Agencies

The below template is similar to what will be sent to the agency Rapid Operator(s) when an association has been made.

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RapidHITTM ID Notification Form

XXX Police Department Case #XXX Date

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Recent RapidHIT ID analyses have generated an association between DNA profiles from XX Case #XX-XX. Please find below the analyses summary and case related information.

This information is provided only as an investigative lead, and any possible connection between samples must be determined by further investigation and conventional DNA testing by submitting samples to the Division of Scientific Services.

Submitting Agency Case/Sample #	Sample Name	Matching Profile
XX	Swab from	
XX	Swab from	
XX*	Swab from	
XX	Swab from	

^{*}Note: The profile assessed was deduced from a mixture.

Standard CMF

SmallPond™ supports the CODIS Interface Specification (CMF 3.2) Revision 9 published by the CODIS Operations and Maintenance Support Services of the Federal Bureau of Investigations.

References

SmallPond™ User's Guide Version 3.0.0

SmallPond Technical Training_CT 2021