

Forensic Biology



Overview

The Forensic Biology unit is staffed by 29 scientists including 2 full-time federally funded grant positions. In 2009, this unit received over 2,000 requests for analysis.

Forensic Biology is divided into three sections – Screening, DNA and CODIS. Screening examines evidence for biological materials and determines its suitability for DNA. The screened evidence is then passed on to the DNA section to generate a DNA profile through a four-step process. Eligible profiles are then uploaded into CODIS for the exchange and comparison of DNA profiles.

Screening

The screening section examines items of evidence for blood, semen and other biological substances to determine the best evidence to pass on for DNA analysis.

Blood

All examinations of items begin with a visual examination.

Any items where the presence of blood is suspected are chemically tested using the Kastle-Meyer test.

Kastle-Meyer (KM) Test:

- KM reagents are applied to sample from stain
- If blood is present a pink color change will occur
- Not a confirmatory test because other substances can produce a false positive reaction
- Animal blood will also test positive

In cases where animals may have been present at a crime scene, a species origin test can be conducted to determine if the source of the biological material is human.

Overview Screening

Blood

Semen

Other

DNA

Extraction

Quantification

Amplification

Characterization

CODIS

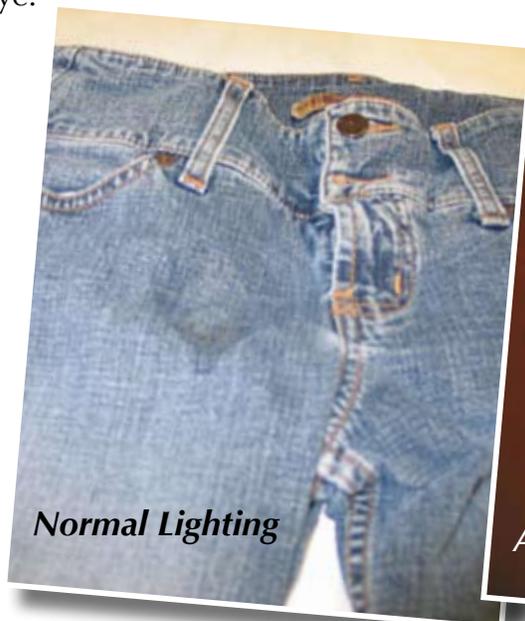
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Semen

Evidence is first inspected using normal lighting. Any non-swab items are then also viewed with an alternate light source (ALS) which allows the analyst to view possible semen stains that are not visible to the unaided eye.



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Suspected areas of semen are then tested using the Acid Phosphatase test and microscopic examination.

Acid Phosphatase (AP) Test:

- Acid phosphatase is an enzyme found in high concentrations in semen
- AP reagent is applied to sample from stain
- If semen is present a purple color change will occur
- Not a confirmatory test because other substances can produce a false positive reaction

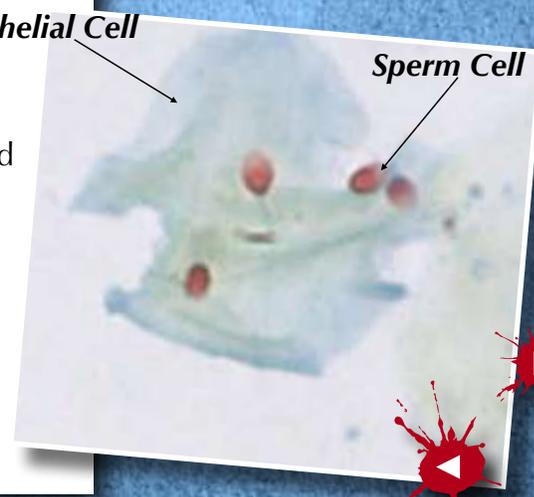


Microscopic Examination for Sperm Cells:

- Sampled stain is used to prepare a microscope slide
- Slides are treated with the Christmas Tree staining method
- When examined under the microscope nuclear material, e.g. sperm heads, is red while other cellular material is green
- Confirmatory test for semen because sperm cells will not be present without semen

Epithelial Cell

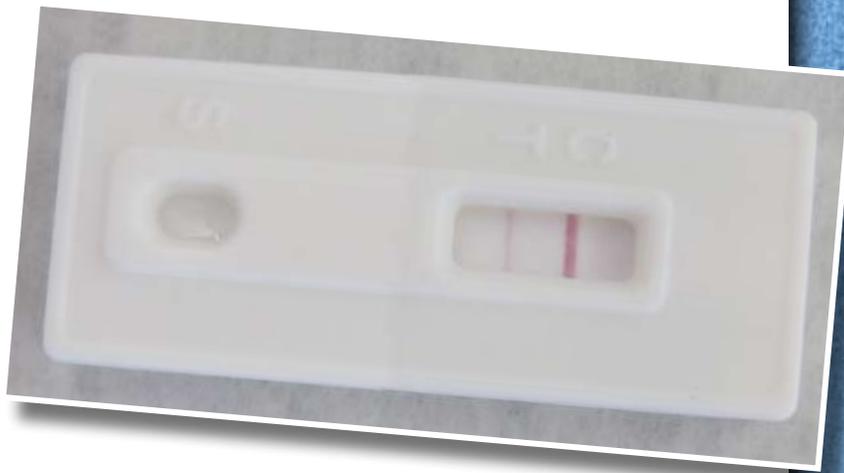
Sperm Cell



Sometimes semen can be present without the presence of sperm. In these situations a p30 test can be conducted.

p30 Test:

- p30 is a protein produced by the prostate gland and is a component of semen
- Sampled stain is extracted in water to separate the p30 from the item
- Part of the fluid is placed on a membrane-based card test
- If semen is present two lines will appear on the card (similar to a pregnancy test)
- Can be used in situations when no sperm is present (i.e. a vasectomized male is the source of the semen)



Other

If stains are not present, biological evidence may still be collected for possible DNA analysis. Evidence collected at a scene can be submitted for "touch DNA" or the presence of skin cells. Some of these items include, but are not limited to, cigarette butts, tools, clothing, bottles and food.



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DNA (Deoxyribonucleic Acid)

DNA is the blueprint of life or the genetic make-up that makes each individual unique. Only identical twins have the same DNA. It is inherited directly from a person's biological parents – half of an individual's DNA comes from the father and half from the mother.

There are some limitations to DNA analysis:

- DNA cannot determine when a person was at the crime scene
- DNA does not determine consent in sexual assault cases
- DNA cannot determine how it was left on the evidence
- Sometimes complex mixtures (generally 3 or more people) are not interpretable
- Limited samples can require possible sample consumption or yield incomplete profiles

There is a four-step process to DNA analysis – extraction, quantification, amplification and characterization of amplified DNA.

Extraction

Various chemicals are used to break apart the cells and isolate the DNA within a liquid buffer. When sperm cells are present different chemicals are added at various times in order to separate out the sperm cells from non-sperm cells.

Quantification

The amount of DNA present is determined for each sample in order to help with the next step. Having the correct amount of DNA to amplify is critical to the final outcome – too little or too much can result in inadequate results.

Amplification

Millions of copies are made of specific locations on the DNA through a process called polymerase chain reaction (PCR). With this process small quantities of DNA can produce results. During PCR fluorescent tags are incorporated within the copies.

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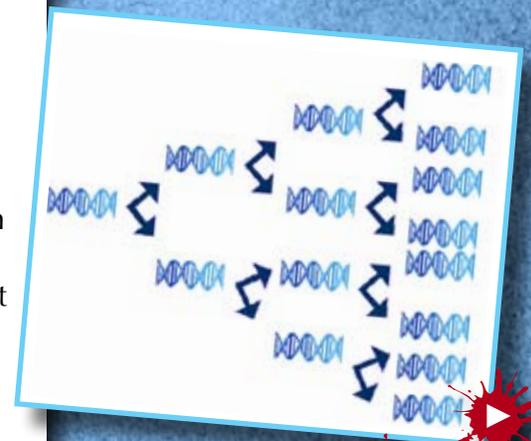
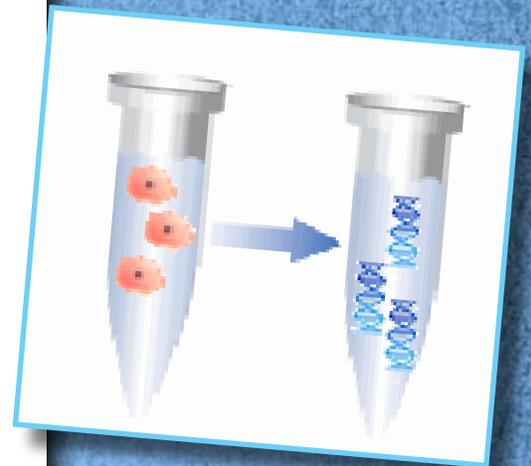
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Characterization

A genetic analyzer is used to detect the fluorescent tags. The data is put into a graph or electropherogram in which the analyst can interpret.

The DNA section uses a process called Short Tandem Repeats (STRs). With STRs analysts are looking at specific areas of DNA that are repeat sequences and do not code for anything (i.e. an analyst cannot determine ethnicity, height, hair color, health risks, etc.). Analysts are able to make comparisons between reference profiles from known samples and profiles developed from unknown evidence samples.

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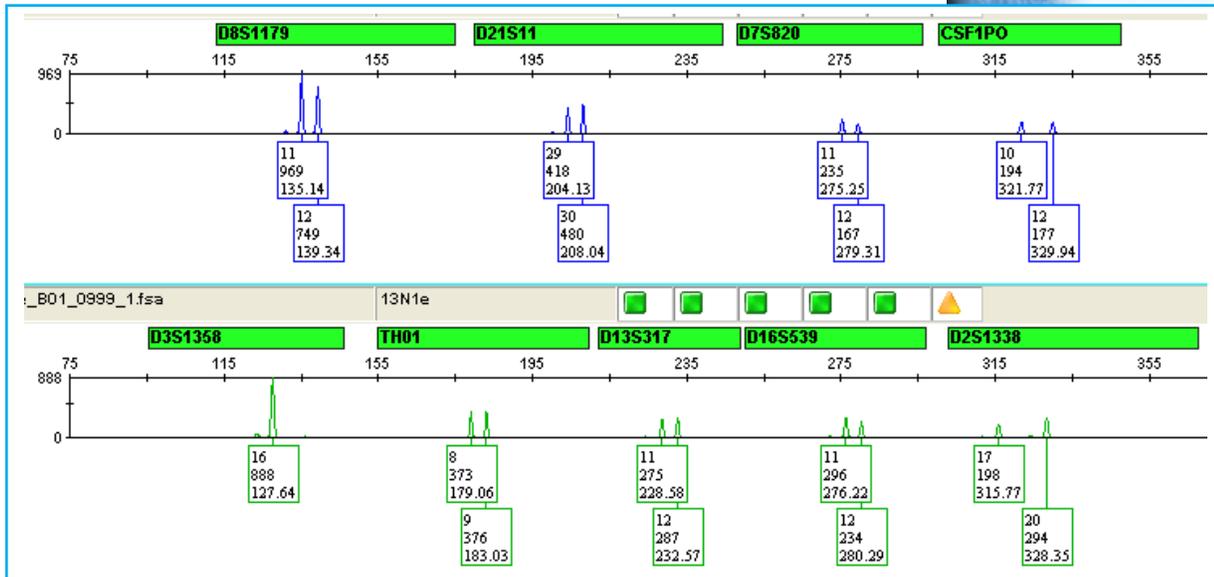
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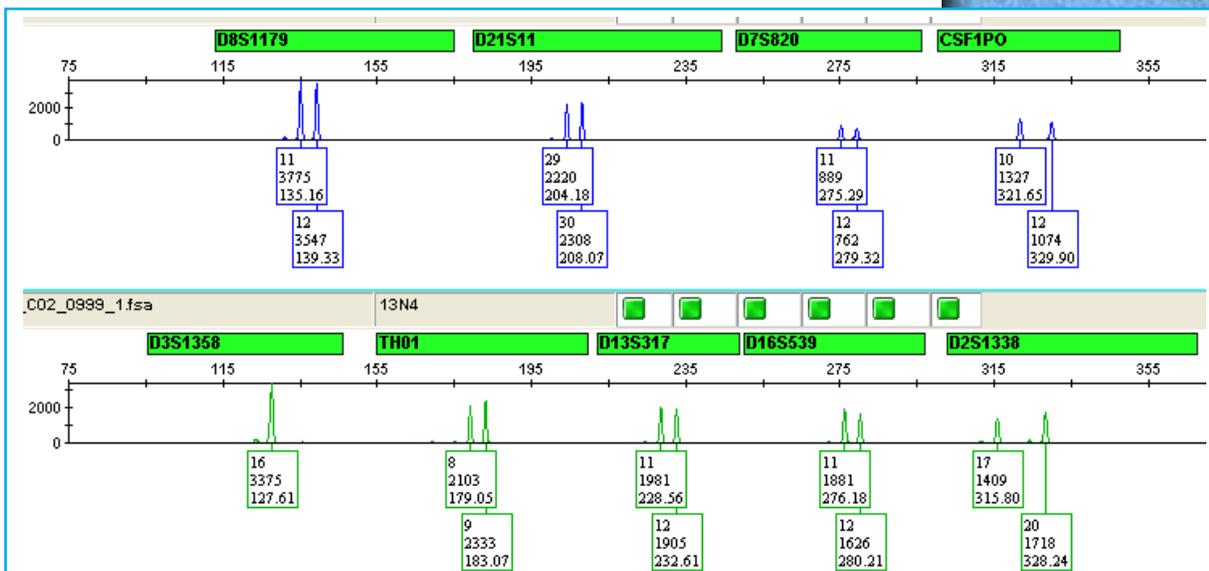
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Unknown Evidence



Known Reference Sample



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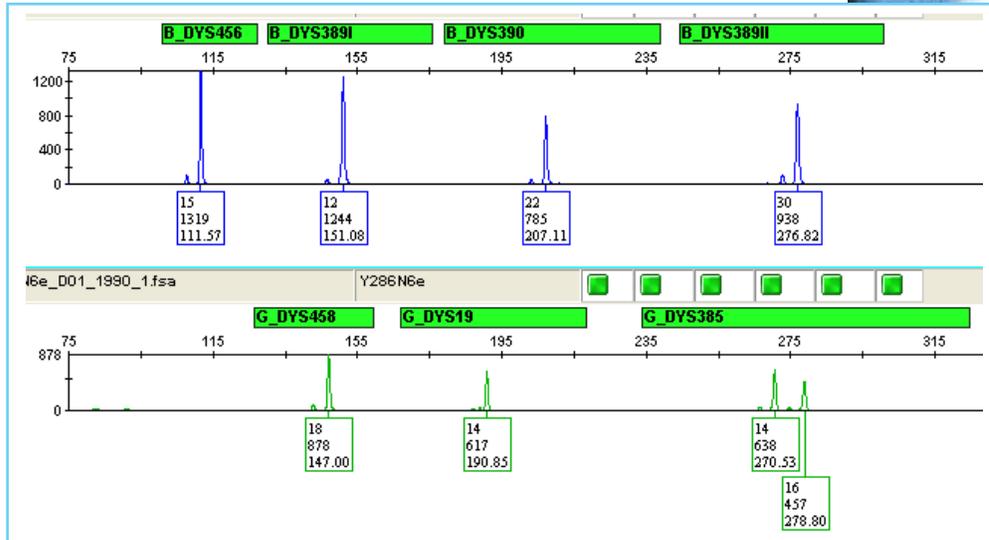
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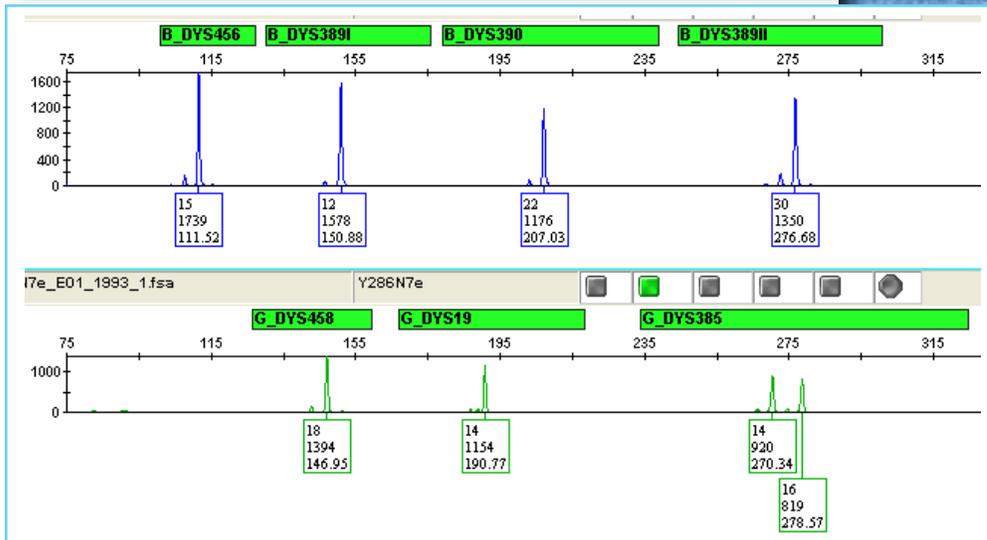
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In addition to STRs, the DNA section also utilizes Y chromosomal testing or Y-STRs. Y-STRs are short tandem repeats on the Y chromosome. Because only males have a Y chromosome, female DNA does not interfere with Y chromosomal testing. Unlike STR testing, Y-STRs are not unique to each individual. Y-STRs are paternally inherited, meaning that all paternally related males will have the same Y-STR profile.

Biological Father

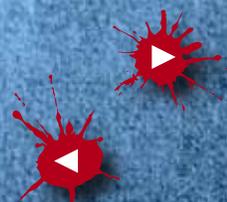


Son



CODIS

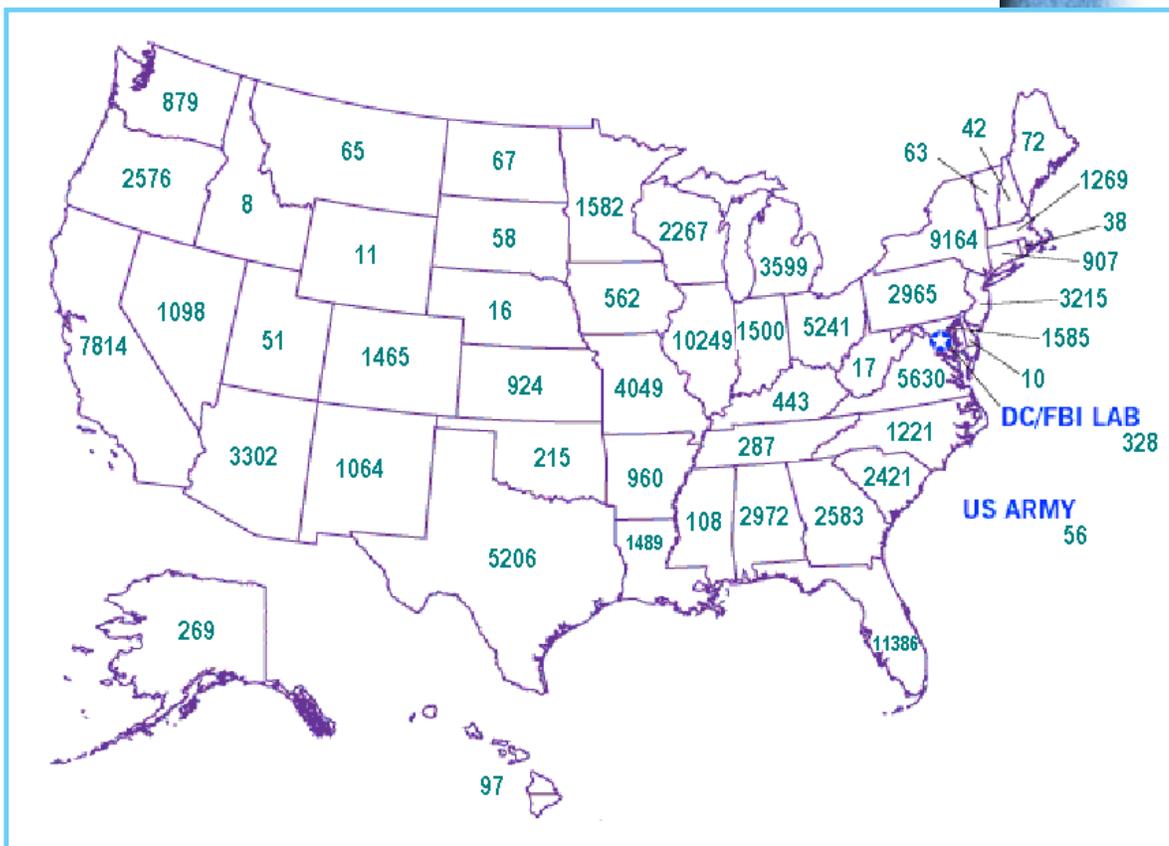
The Combined DNA Index System (CODIS) is a nationwide database administered by the FBI. It is used for linking serial crimes and unsolved cases with repeat offenders. CODIS was launched in October 1998 and now electronically links all 50 states plus 2 federal laboratories and Puerto Rico. Federal guidelines regulate what samples are qualified for entry into CODIS. Forensic unknown samples must be linked to a crime in order to be eligible for CODIS entry.



The following are examples of profiles that are not allowed into CODIS:

- Victim profiles
- Profiles developed from known/reference samples (excluding convicted offender samples)
- Profiles developed from evidence which match the victim, witness, etc.
- Non-probative profiles
- Officer's profiles

INVESTIGATIONS AIDED – January 2010



CODIS allows investigators to exchange information. Several different sample types can generate a “hit” or match. All matches are confirmed by the laboratory. Matches can link:

- Two or more cases and allow investigators to coordinate activities
- A solved case with an unsolved case
- Two or more solved cases

Within Arizona there are seven CODIS laboratories. They include the Phoenix PD Crime Lab, Mesa PD Crime Lab, Tucson PD Crime Lab, Scottsdale PD Crime Lab and three DPS laboratories (Phoenix, Tucson, and Flagstaff).

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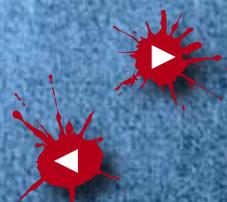
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PHOENIX PD CODIS HITS: January 2008 - February 2010

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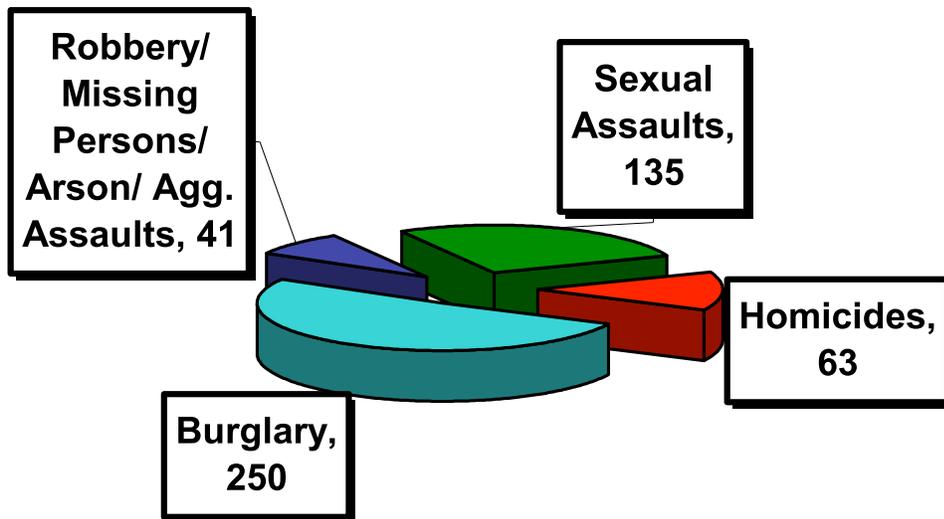
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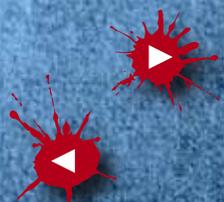
Phoenix PD CODIS Hits



CODIS Success Stories

Sarah Clark Case

On May 16, 1988, the body of 22-year old Sarah Clark was found in her apartment. She had been brutally raped and murdered. Evidence was collected and preserved. Potential suspects were ruled out and the case grew cold over time. In June 2001, the Phoenix Police Department's Cold Case Unit brought Sarah Clark's case to the Crime Lab, with the hope that DNA testing and the CODIS database would shed some light on who may have committed this horrendous crime. A DNA profile was developed from semen taken from Sarah's sexual assault kit. This unidentified male's profile was entered into the CODIS database in August 2001. The profile was continuously searched against other forensic samples as well as convicted offender samples for several years – with no luck. On January 13, 2005, a "hit" happened. The unidentified male profile was matched to a convicted offender's sample that had just been entered into the database. Through a confirmation process, the convicted offender was identified as Mario Pete. Mario Pete was a 16 year old juvenile who lived in Sarah's apartment complex. Further DNA testing was completed on multiple items of evidence that had been collected at the crime scene and sitting silently in the police property facility. A bloody palm print on the wall outside of Sarah's apartment was compared to Mario Pete and found to match. Mario Pete's DNA was also present on other



items as well; including blood trails leading from Sarah's apartment and semen on a towel left near Sarah's body. In March 2007, Mario Pete was put on trial for the rape and murder of Sarah Clark and was convicted within hours. He was sentenced to life in prison in April 2007, coincidentally on his 35th birthday.

Tiffany Botello Case

On the morning of March 26, 1996, the body of 26-year old Tiffany Botello was found in an alley. She was dressed only in a black t-shirt, with trauma to her face, neck, and breast area. She was last seen the previous night at a Circle K store in her neighborhood. The autopsy revealed the cause of death as manual strangulation and was ruled a homicide. Over time the case grew cold. In April 2003, the Cold Case Unit re-investigated the case, requesting the crime scene evidence be examined by the Phoenix Police Crime Lab. Upon examination of the evidence one sperm cell on a vaginal slide was identified and a hair with a root was found on the victim's T-shirt. Those items along with others were forwarded on for DNA analysis. A DNA profile was obtained from a breast swab sample and the hair removed from the T-shirt. The profile was entered into CODIS, and in June 2004 a "hit" was made with a convicted offender sample. Through a confirmation process, the convicted offender was identified as William Mitchell. In 1996, William Mitchell lived in the area where the victim was last seen and her body found, but was never a suspect in the homicide. He was contacted and made statements concerning his activities in 1996. He was a registered sex offender, with a conviction for sexual assault and attempted murder. In August 2004 he was arrested for the murder of Tiffany Botello. He pled guilty to 1st degree murder in August 2005 and was sentenced to life in prison.

More Information

For resources related to the use of DNA technology in solving crimes, protecting the innocent and identifying missing persons:
<http://www.DNA.gov>

For information on the CODIS database:
<http://www.fbi.gov/hq/lab/html/codis1.htm>

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