**A DNA change is identified at position 141972905 on chromosome 7. The following evidence is needed to determine if this DNA change leads to increased sensitivity to the taste of bitter foods like Brussels sprouts.**

**Types of evidence needed**
*The DNA change*:

- *occurs within a gene* **A**
- *alters the sequence of amino acids* **B**
- *alters the function of a protein* **C**
- *alters the amount of protein produced* **D**
- *is somewhat common across the population studied* **E**
- *is present in people who can taste bitter, and absent in people who cannot* **F**
- *other evidence:*

Use the Progress of Science Timeline (timeline.hudsonalpha.org) to explore the "Big Science Projects" listed below. Each contributes to understanding the structure, function, and variation present within the human genome. As you learn about each project, write a brief description. Then review each evidence type above and determine which project likely generated the data associated with that evidence. Write the evidence type on the corresponding project line.

| Big Science Projects (project start - stop) | Dates on Timeline | Project Description | Evidence Obtained from Project |
|---|---|---|---|
| Human Genome Project *(1990-2003)* | 1990, 1992, 1999, 2000, 2003 | | |
| ENCODE (Encyclopedia of DNA Elements) *(2003-ongoing)* | 2003, 2012 | | |
| International HapMap *(2002-2010)* | 2003 | | |
| 1000 Genomes *(2008-2015)* | 2008, 2011 | | |
| TCGA *(2005-2016)* | 2006 | | |
| ClinVar *(2012-ongoing)* | 2013 | | |

# Teacher Key

HudsonAlpha Developed

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| Big Science Projects (project start - stop) | Dates on Timeline | Project Description | Evidence Obtained from Project Data |
|---|---|---|---|
| Human Genome Project *(1990-2003)* | 1990, 1992, 1999, 2000, 2003 | The HGP identified the sequence of the ~3 billion chemical bases in a human genome and mapped the location of ~21,000-23,000 human genes. This project also predicted intron/exon boundaries for each gene and in many cases identified known or predicted amino acid sequence for the corresponding proteins. | A,B |
| ENCODE (Encyclopedia of DNA Elements) *(2003-ongoing)* | 2003, 2012 | ENCODE seeks to identify all of the functional parts of the genome, determining what sequences regulate the transcriptional activity of the genes. It builds upon the findings of the Human Genome Project to develop the operating manual for the human genome. | D |
| International HapMap *(2002-2010)* | 2003 | The International HapMap identified almost 4 million specific variations (SNPs:single nucleotide polymorphisms) in our DNA, where they occur and their frequency across 4 different populations. Genome-wide Association Studies (GWAS) used the SNPS identified by HapMap to find common genetic variants that affect health and disease | E,F |
| 1000 Genomes *(2008-2015)* | 2008, 2011 | This project provided a reference for common human genetic variation at a higher resolution than HapMap. It identified an almost complete set of DNA variants for any region across 26 different populations. This collection serves as a reference when analyzing DNA changes identified in individuals with genetic disorders. | E |
| TCGA *(2005-2016)* | 2006 | TCGA identified genomic changes in over 33 types of human cancer to better understand how DNA mutations caused cells to become cancerous and to determine how that understanding could lead to better prevention, diagnosis and treatment of cancer. | C,D (for cancer causing changes) |
| ClinVar *(2012-ongoing)* | 2013 | ClinVar is a comprehensive database where individuals submit human DNA changes and their assessment of its functional and clinical consequences. | C,F (for clinically relevant changes) |