

ERCC6 Gene & Cockayne Syndrome



by Zachary Beethem

What is Cockayne Syndrome?

A rare, autosomal recessive, neurodegenerative disorder

Invariably fatal

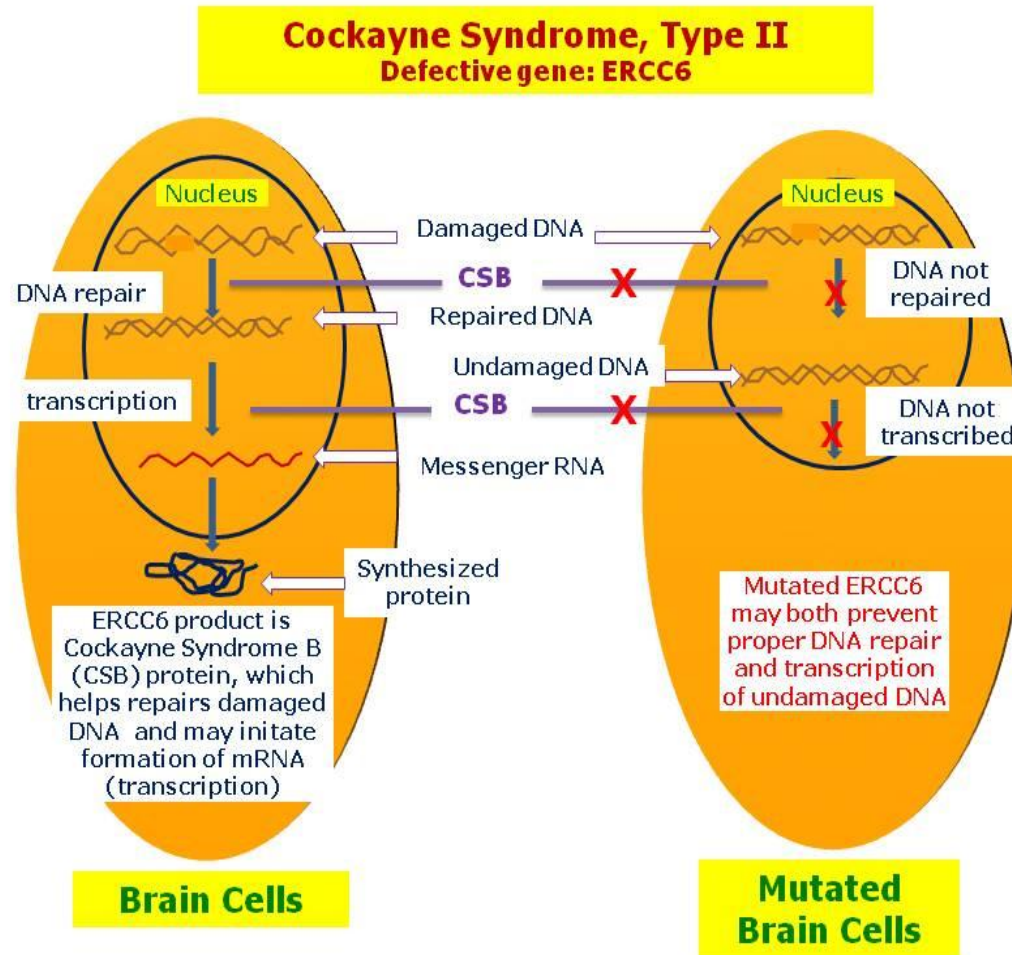
Wide range of symptoms

Four types: I, II, III, and xeroderma pigmentosum (XP-CS)

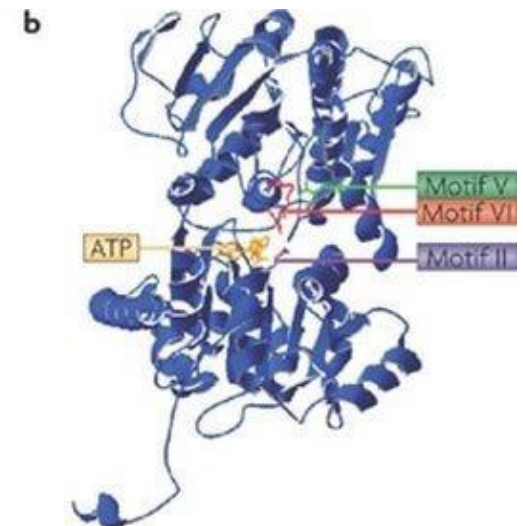
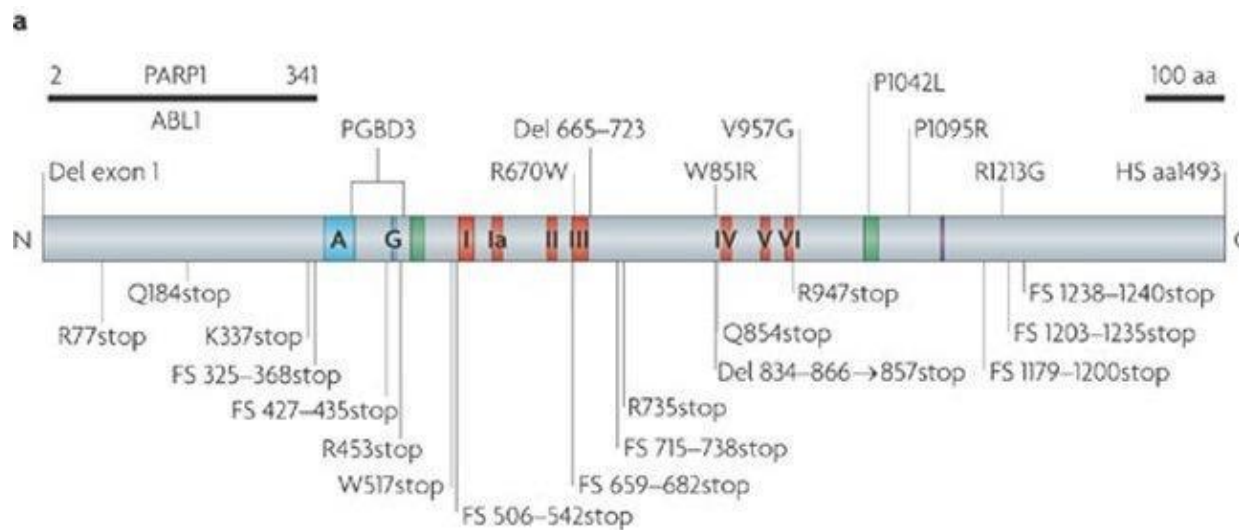
Cockayne Syndrome Type II



What causes CS Type II?

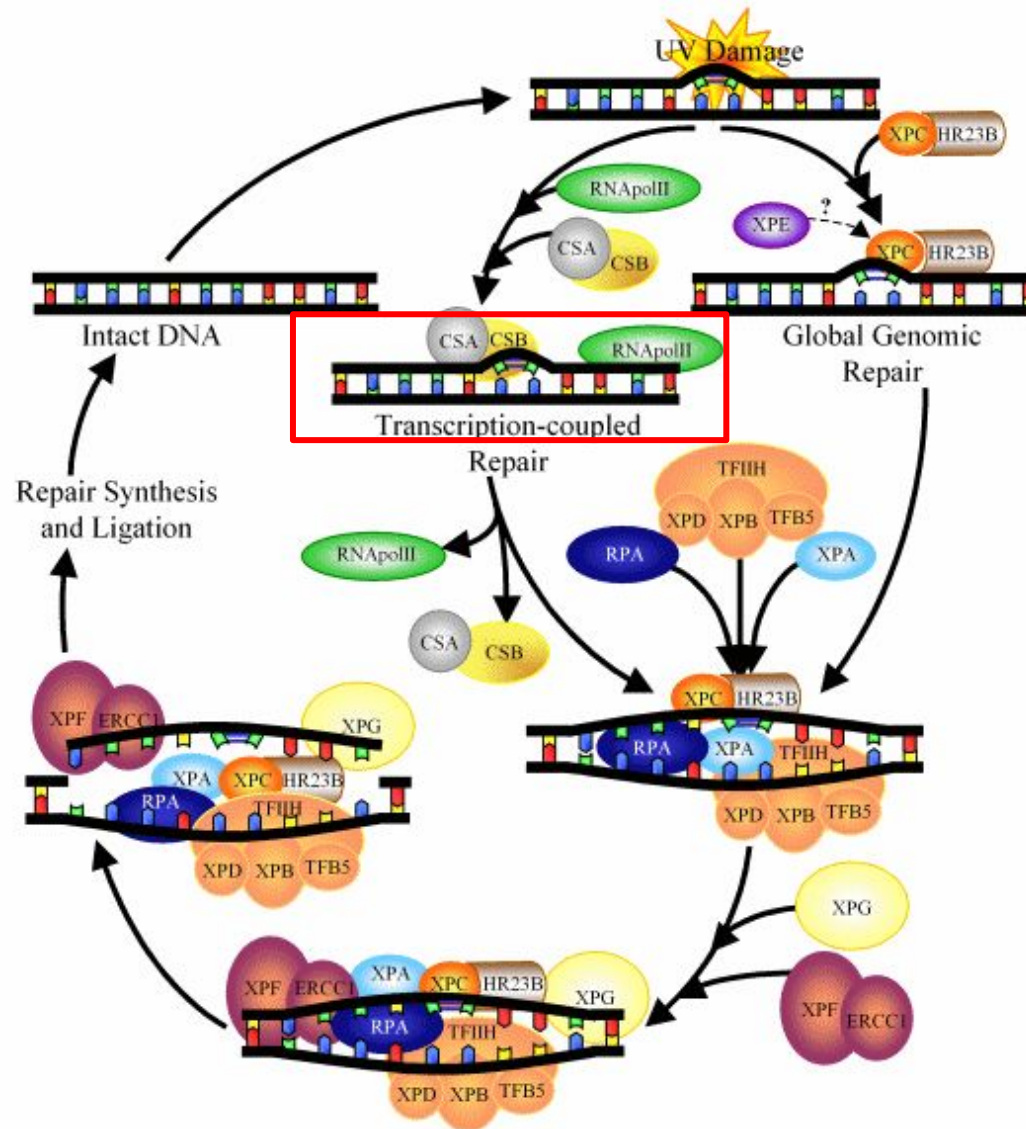


The ERCC6 Gene



Nature Reviews | Genetics

What is ERCC6's role in DNA repair?



What domains does ERCC6 have?



SNF2_N: Molecular function is to bind ATP. Proteins with this domain can disrupt histone-DNA interactions.

HELICc: C-terminal domain helicase. Molecular function is ATP binding and helicase activity.

What do common ERCC6 homologs look like?

Human

SNF2_N (510-812)

HELICc
(869-952)

1493aa

Mouse

SNF2_N (506-808)

HELICc
(865-948)

1481aa

79% Identity

Chimpanzee

SNF2_N (508-810)

HELICc
(867-950)

1491aa

99% Identity

Zebrafish

SNF2_N (487-789)

HELICc
(847-930)

1390aa

60% Identity

Cow

SNF2_N (289-803)

HELICc
(860-943)

1482aa

78% Identity

How similar are the common homologs?

Orangutan, 97.98% identity

Gorilla, 99.13% identity

Chimpanzee, 99.46% identity

Mouse, 79.07% identity

Cow, 78.27% identity

Zebrafish, 59.86% identity

Rat, 78.97% identity

Wild Boar, 84.88% identity

Elephant, 82.19% identity

Panda, 84.61% identity

Sheep, 81.77% identity

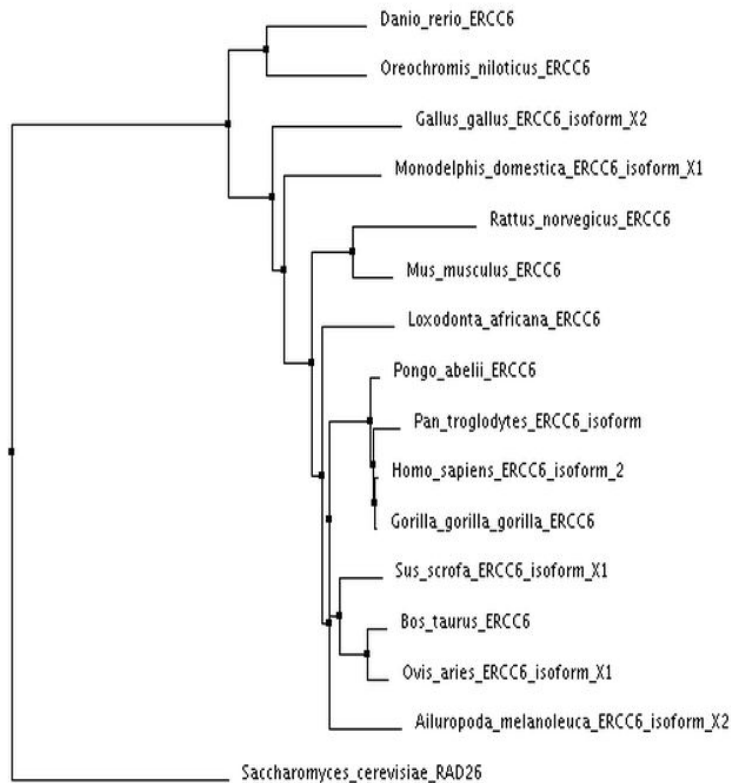
Red Junglefowl, 64.55% identity

Tilapia, 56.65% identity

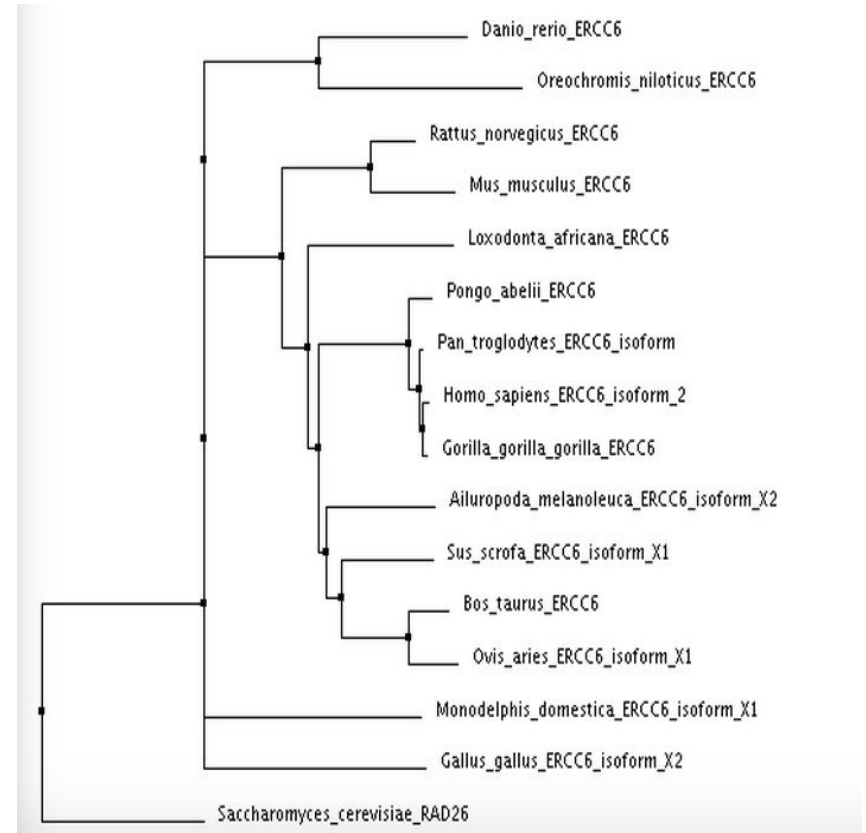
Possum, 69.24% identity

Saccharomyces cerevisiae, 38.52% identity

How are these homologs related? (NJ)

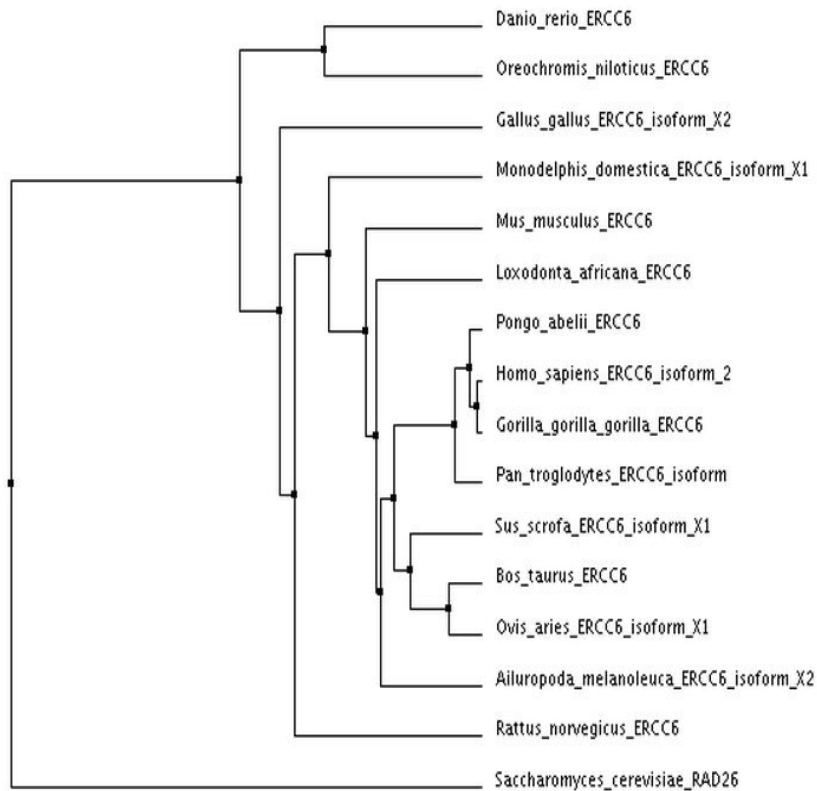


BLOSUM62 NJ

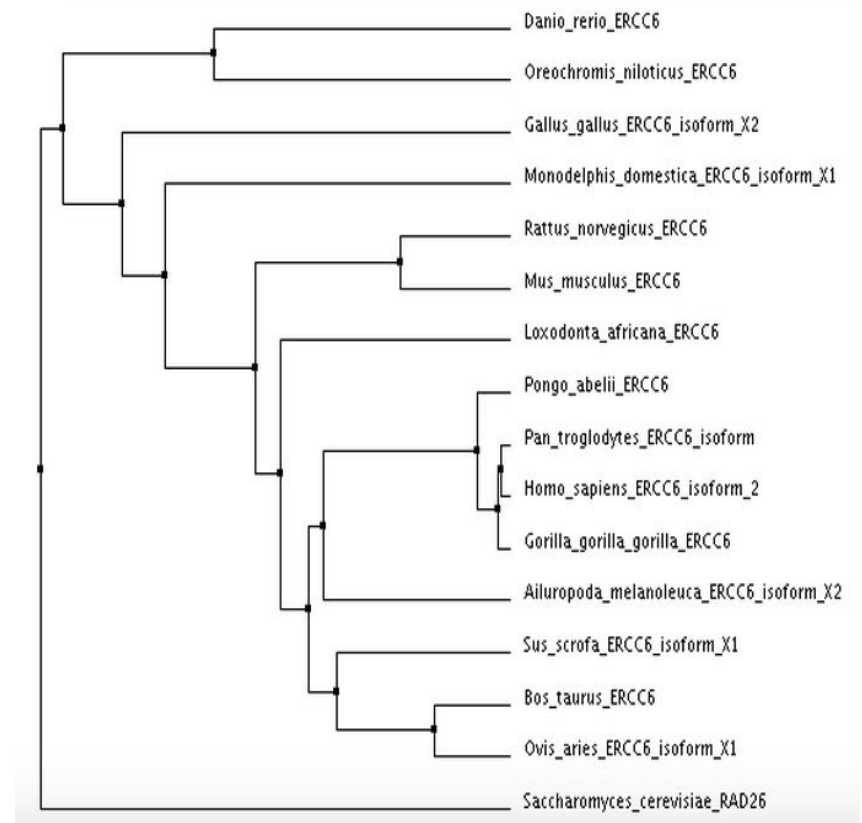


Percent Identity NJ

How are these homologs related? (AD)



BLOSUM62 Average Distance



Percent Identity Average Distance

What is not known?



Gap in Knowledge

A major symptom of CS is progeria, or premature aging. Aging is caused by oxidative damage.

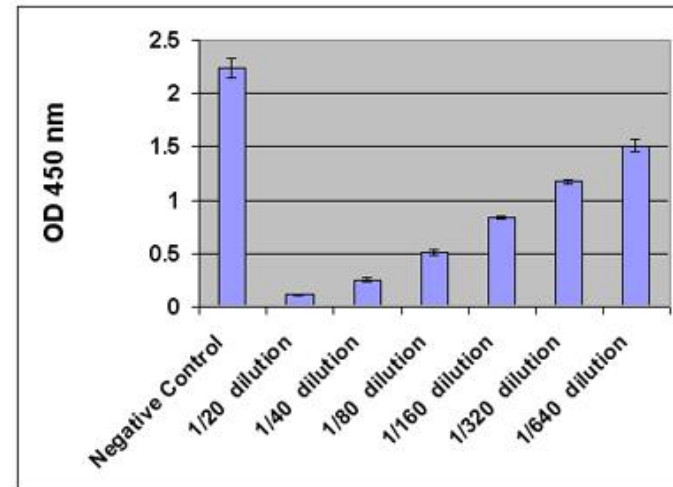
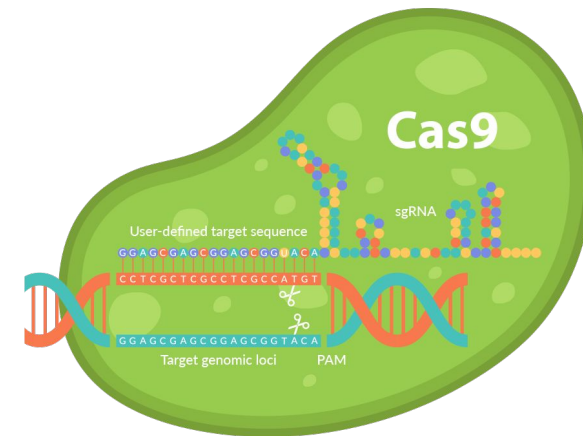
ERCC6 is thought to play a molecular role in processing and possibly fixing oxidative damage.

What is this role?

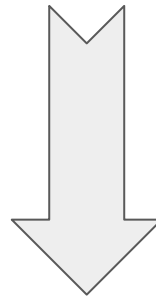
What is the ideal model organism for studying oxidative damage?



Aim 1: Which protein domains are important for managing oxidative stress?

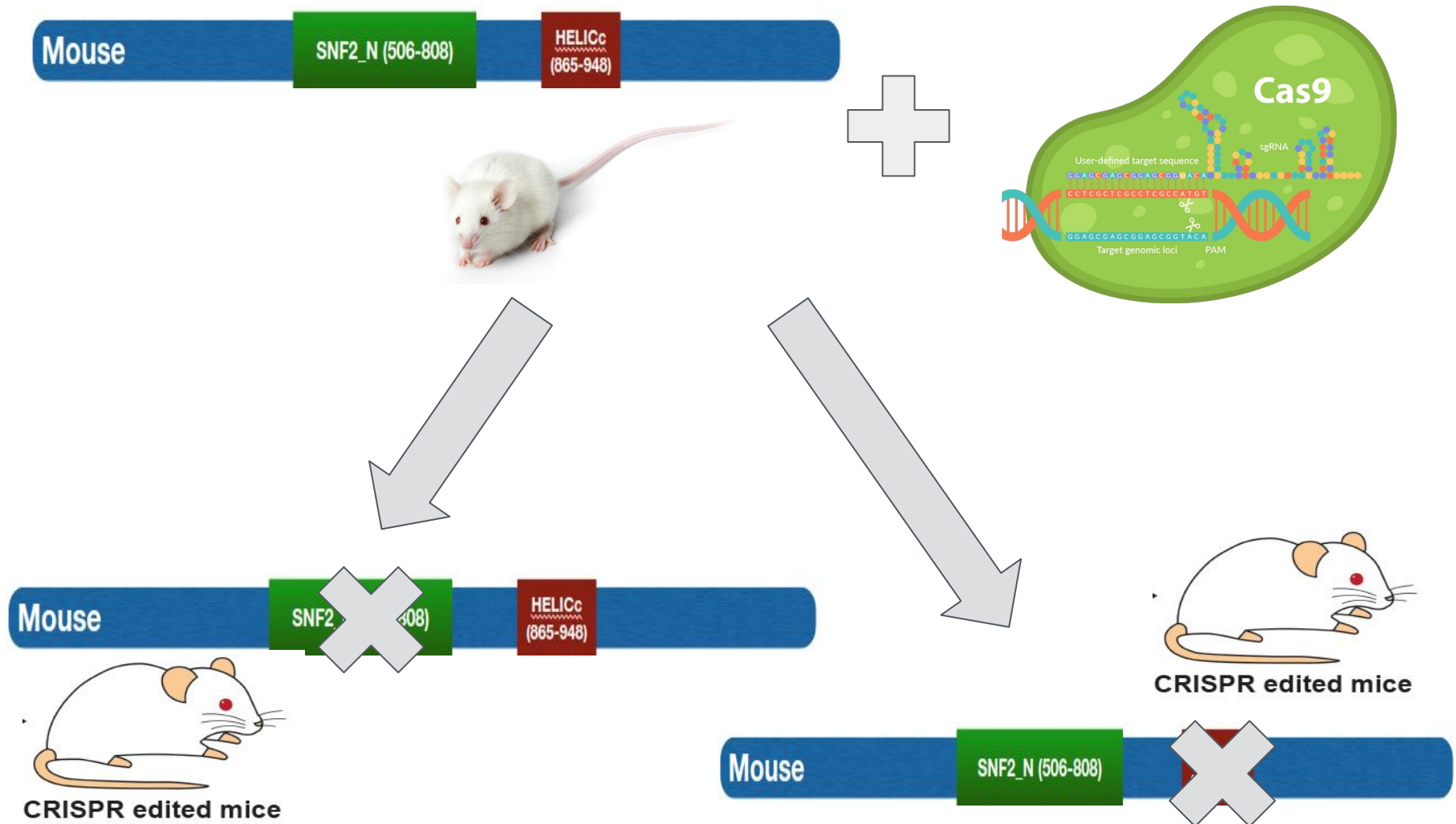


Aim 1, Step 1: Identify



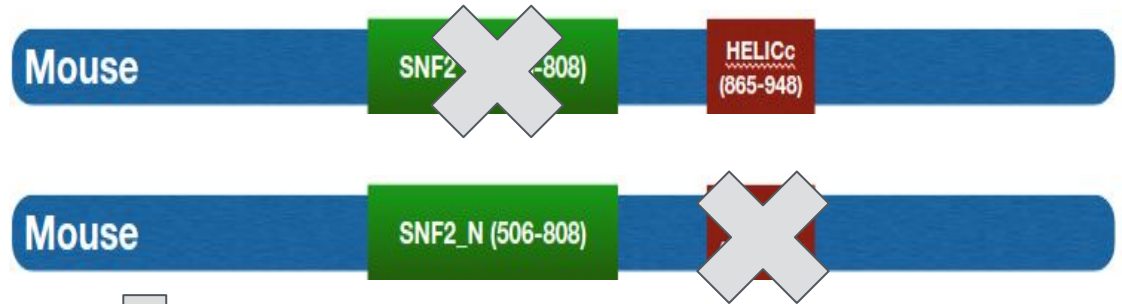
<http://pfam.xfam.org/> , <http://smart.embl-heidelberg.de/>

Aim 1, Step 2: Edit



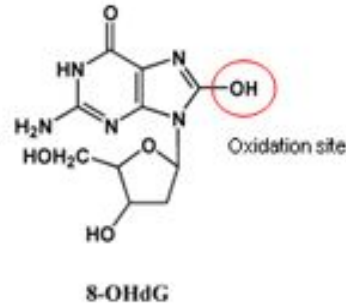
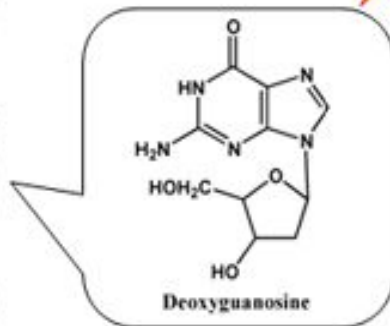
<http://www.thomasgoetz.com/blog/2014/5/20/where-the-white-lab-mouse-came-from> , <https://www.synthego.com/crispr/> ,
<http://news.berkeley.edu/2016/05/27/faster-more-efficient-crispr-editing-in-mice/>

Aim 1, Step 3: Induce Stress



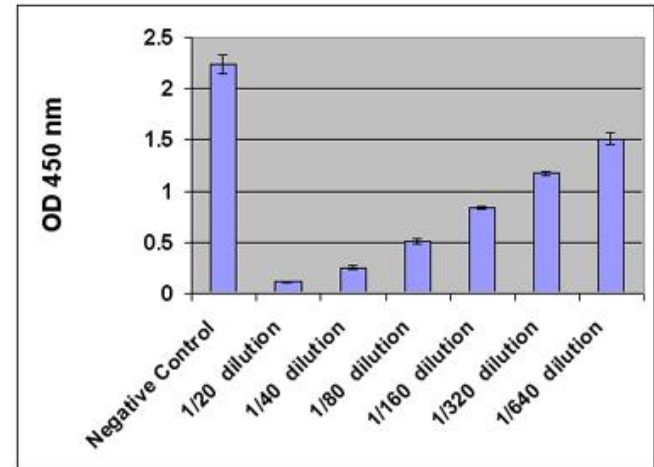
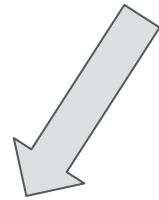
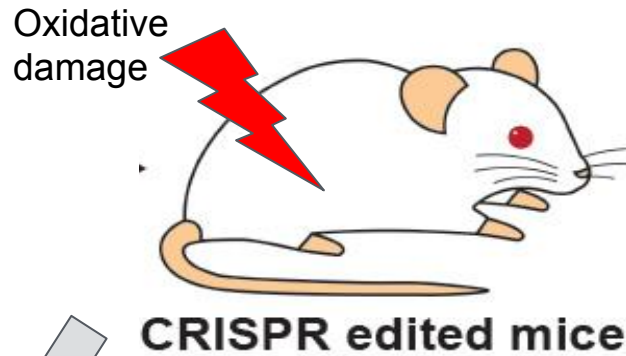
Oxidative Stress

DNA



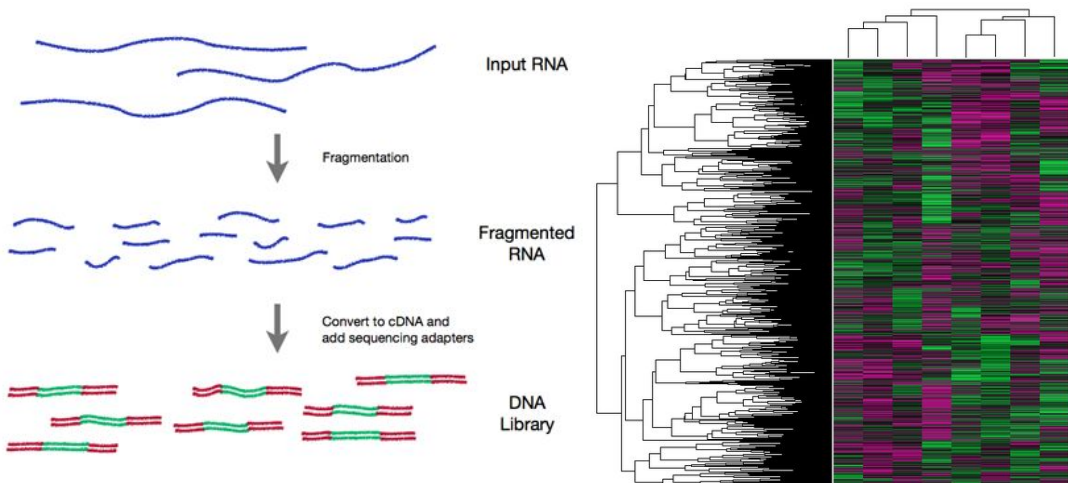
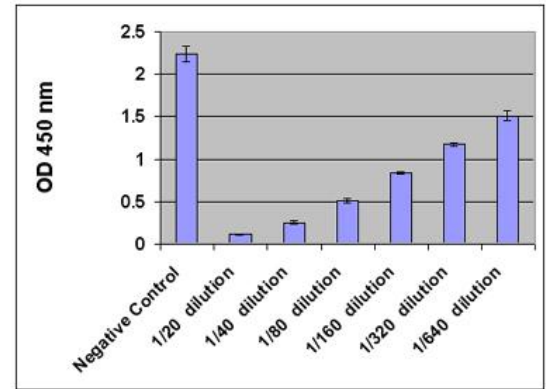
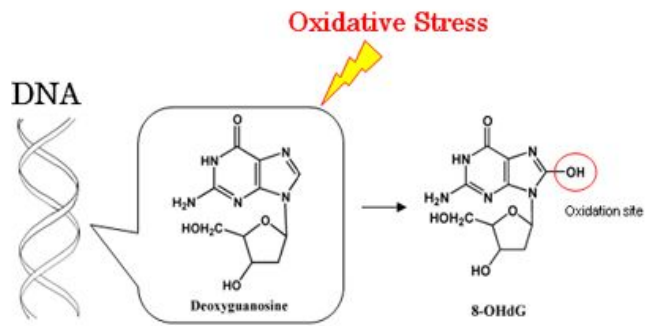
Produces 8-OHdG

Aim 1, Step 4: Measure 8-OHdG in CRISPR mice models



8-OHdG levels in urine. High levels = successful processing of oxidative damage

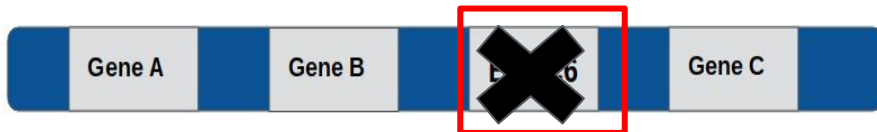
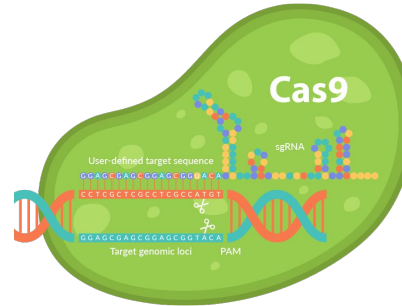
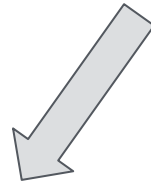
Aim 2: What genes does ERCC6 interact with when fixing oxidative damage, and do certain genes compensate for the loss of ERCC6?



Click to get gene list for a category:

- [biological adhesion \(GO:0022610\)](#)
- [biological regulation \(GO:0065007\)](#)
- [cellular component organization or biogenesis \(GO:0071840\)](#)
- [cellular process \(GO:0009987\)](#)
- [developmental process \(GO:0032502\)](#)
- [immune system process \(GO:0002376\)](#)
- [localization \(GO:0051179\)](#)
- [locomotion \(GO:0040011\)](#)
- [metabolic process \(GO:0008152\)](#)
- [multicellular organismal process \(GO:0032501\)](#)
- [reproduction \(GO:0000003\)](#)
- [response to stimulus \(GO:0050896\)](#)

Aim 2, Step 1: CRISPR & Oxidative Stress



CRISPR edited mice

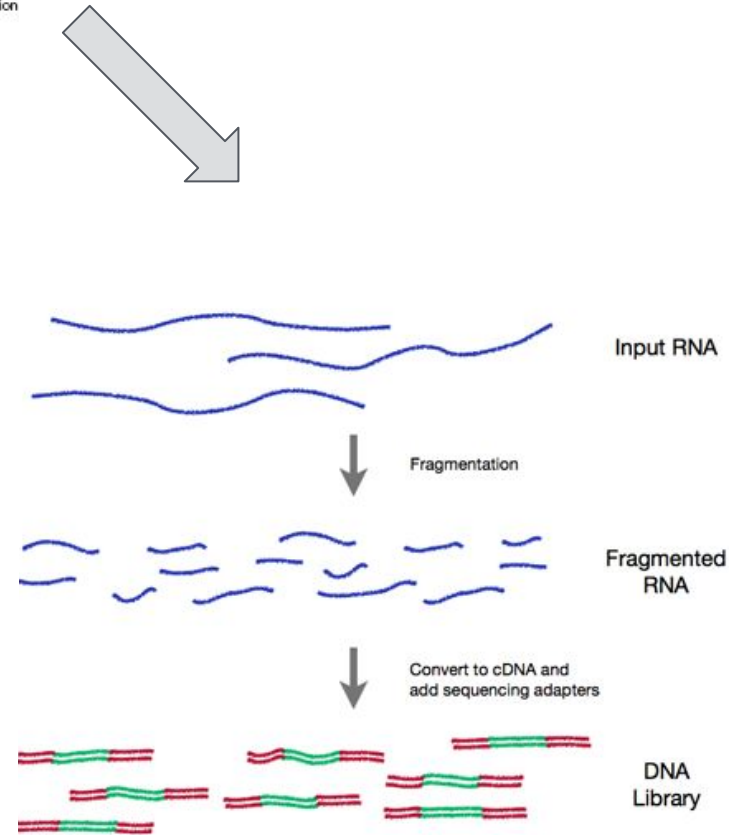
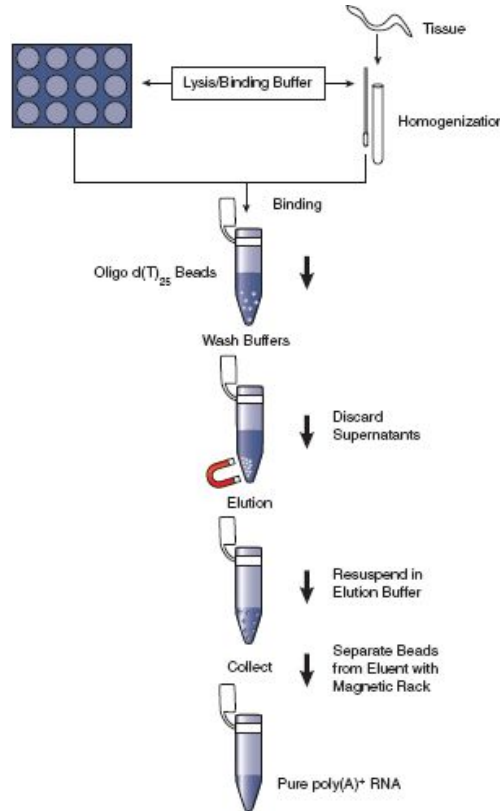
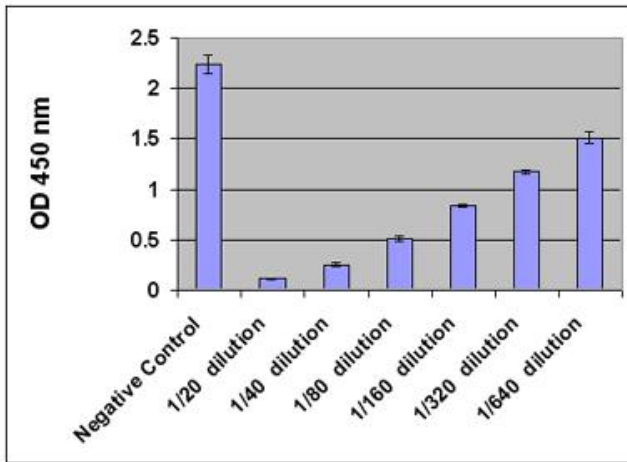
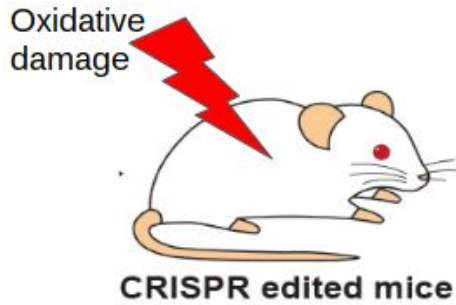


Oxidative damage

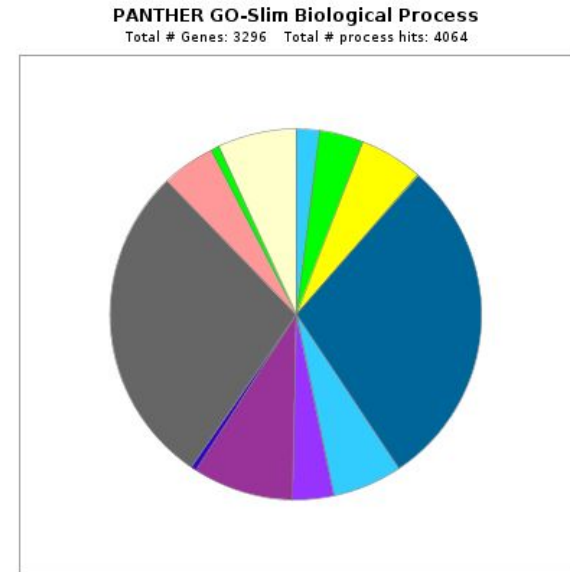
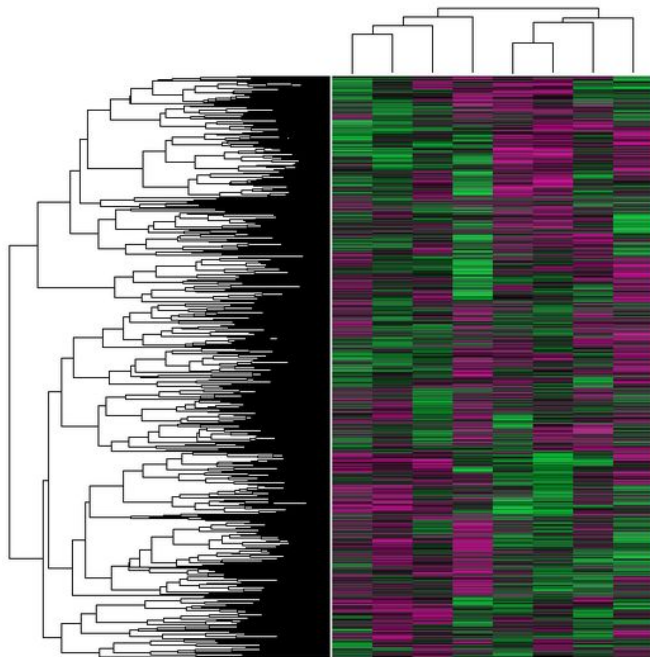


CRISPR edited mice

Aim 2, Step 2: Measure and RNA-Seq



Aim 2, Step 3: Measure expression, identify processes



Click to get gene list for a category:

- [biological adhesion \(GO:0022610\)](#)
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- [cellular process \(GO:0009987\)](#)
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References