Evrin, Cecile, et al. "Histone H2A-H2B Binding by Pol α in the Eukaryotic Replisome Contributes to the Maintenance of Repressive Chromatin." The EMBO Journal, vol. 37, no. 19, 2018, doi:10.15252/embj.201899021.

In the first part of this experiment, DNA Pol α was shown to have a binding motif for histone proteins H2A and H2B that was also conserved in human Pol α. They then showed that mutation of this binding motif does not affect DNA replication, but instead prevented genes from properly being silenced at telomere and mating-type loci. They then showed that histone complexes were bound by cmg Helicase, FACT complex, and DNA POL α (all members of the replisome) at the same time. They conclude that replisome units have many histone-binding responsibilities, and are responsible for the preservation of histone-based gene silencing from parent to daughter cell.

Heins, James N., et al. "Characterization of a Nuclease Produced by Staphylococcus Aureus." Journal of Biological Chemistry, vol. 242, 10 May 1967, pp. 1016 - 1020., doi:10.1515/znb-1969-0820.

This paper describes the characteristics of nucleases produced by *S. aureus*. This nuclease contains both deoxyribonuclease and ribonuclease activity, and the specifics of when it works and the environment it requires were specified in this paper. This paper describes how to use the nuclease to degrade nucleic acids and genetic material, and that nucleic acids must be in their naked form in order to be properly degraded.

Herrmann, Christin, et al. "Differential Salt Fractionation of Nuclei to Analyze Chromatin-Associated Proteins from Cultured Mammalian Cells." Bio-Protocol, vol. 7, no. 6, 2017, doi:10.21769/bioprotoc.2175.

This paper talks about the changes to chromatin structure in response to different environmental stimuli such as stress, and describes different protocols to study the structure of chromatin and its association with various proteins. One process described is Micrococcal Nuclease (MNase) digestion, a process that is used to study chromatin's association with proteins. DNA is digested down to the mononucleosome, as DNA wrapped around histone proteins is protected from MNase digestion. The rate at which the linked DNA is digested is also affected by the accessibility of the DNA.

Huang, Hongda, et al. "A Unique Binding Mode Enables MCM2 to Chaperone Histones H3–H4 at Replication Forks." Nature Structural & Molecular Biology, vol. 22, no. 8, 2015, pp. 618–626., doi:10.1038/nsmb.3055.

In this paper, the MCM2 subunit of CMG helicase was shown to help chaperone H3 and H4 onto nascent DNA. Two binding sites on MCM2 were found to bind H3 and H4. Mutations in these binding sites were shown to impair cell proliferation, and chromatin formation. MCM2 was shown to help chaperon both new and old histones. As Pol α was shown to bind the MCM2 subunit, it is possible that the two of them work in concert to chaperone different histones onto nascent DNA.

Kunkel, Thomas A., and Peter M. J. Burgers. "Arranging Eukaryotic Nuclear DNA Polymerases for Replication." BioEssays, vol. 39, no. 8, 2017, p. 1700070., doi:10.1002/bies.201700070.

This paper gives a good background into the yeast replisome, focusing on the different DNA Polymerases and CMG Helicase's role in coordinating the different polymerases. It describes in detail the structure of this portion of the yeast replisome, and provides insight into the coordination of the different polymerases in the replisome. This paper provided sufficient background knowledge of replisome proteins for my paper.

Martin, Benjamin J. E., et al. "Transcription Promotes the Interaction of the FAcilitates Chromatin Transactions (FACT) Complex with Nucleosomes In S. Cerevisiae." 2018, doi:10.1101/376129.

This paper provides solid background on the FACT complex in yeast cells, a complex in the replisome that is found to be enriched in highly transcribed genes. In this paper, FACT was shown to bind destabilized nucleosomes, and is likely targeted to the chromatin by polymerases. MNase digestions were also used in this experiment to show differences in chromatin structure between FACT-bound and non-FACT-bound chromatin. This paper also briefly reviews FACT's interactions with other replisome components (such as CMG Helicase and different DNA polymerases)

Nobile, C, et al. "Nucleosome Phasing on a DNA Fragment from the Replication Origin of Simian Virus 40 and Rephasing upon Cruciform Formation of the DNA." Molecular and Cellular Biology, vol. 6, no. 8, 1986, pp. 2916–2922., doi:10.1128/mcb.6.8.2916.

This paper studied the simian virus, and although the findings of the paper are somewhat irrelevant to my proposal, the methods employed were adapted for my proposal. The researchers used nuclease digestions to show nucleosome formation, as nucleosomes were protected from digestion. As such, a larger number of nucleosomes resulted in lesser degradation by the nucleases, a core concept used in my experimental design.

Park, Young-Jun, and Karolin Luger. "Histone Chaperones in Nucleosome Eviction and Histone Exchange." Current Opinion in Structural Biology, vol. 18, no. 3, 2008, pp. 282–289., doi:10.1016/j.sbi.2008.04.003.

This paper provides background into who histone chaperones assist in the formation of nucleosomes, and how they may also be involved in the removal of histones for replication. Different histone chaperone variants were shown to affect nucleosome structure, stability, and chromatin condensation. Histone chaperones were shown to be integral to the formation of chromatin structure, and as such, it is inferable that modifying proteins that affect the ability of histones to be placed onto nascent DNA will also affect chromatin architecture.

Winkler Duane D., Luger Karolin. "The histone chaperone FACT: structural insights and mechanisms for nucleosome reorganization." J. Biol. Chem. Vol 286, pp. 18369 - 18374. 2011, doi:10.1074/jbc.R110.180778

This paper provides sufficient background to the FACT complex in the yeast replisome, which is responsible for chromatin remodeling and histone chaperoning. This paper is a review of previous studies that have provided insight into FACT-mediated nucleosome organization, and also discuss newer models for FACT's function.