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The Structure and Functions of Enzyme 42

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Abstract
In the video game *Subnautica*, Enzyme 42 is an enzyme produced by the Sea Emperor Leviathan. It is able to destroy the Kharaa bacterium, a disease-causing pathogen. The structure of an enzyme is often specific to its function. This paper unites the function of Enzyme 42 with a hypothetical structure, based on both its purpose in *Subnautica*, and real enzymes with similar functions.

Keywords: *Computer Game; Biology; Protein Structure; Subnautica*

Introduction
In the video game *Subnautica*, the Kharaa bacterium is a pathogen which causes a lethal disease. The cure for the disease is Enzyme 42, which is able to completely destroy the bacterium. It is produced naturally by a creature known as the Sea Emperor Leviathan [1]. This paper will consider a hypothetical structure of Enzyme 42 that is consistent with its purpose.

Digestive Enzymes
Enzymes are biological molecules which catalyse chemical reactions inside an organism by. They have specific structures which allow them to carry out reactions [2]. In proteins and enzymes, a domain is a region of a protein which serves a specific function, such as chemically binding to another molecule. Enzymes can have domains for binding, and domains which carry out the catalytic activity [3].

Digestive enzymes are enzymes which aid in digestion by breaking down large structures into small molecules. Some of the digestive enzymes present in humans are amylase, lipases and peptidases, which catalyse the breakdown of starch, fats and proteins respectively [4]. The Sea Emperor Leviathan is a filter-feeder, which subsists entirely on microorganisms, including bacteria [1]. Digestive enzymes that facilitate the breakdown of bacteria cells are called lysozymes. The way that lysozymes function is by breaking a linkage between glycopeptides in the bacteria cell wall. This causes the cell to split open, resulting in cell death [5] (see Figure 1).

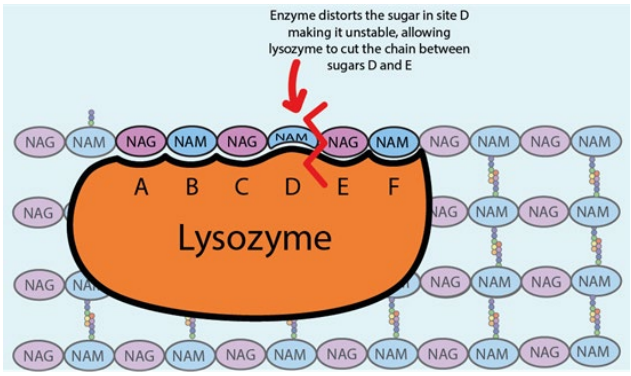

Figure 1 – The shape of the enzyme puts strain on one of the glycopeptide linkages (at point D). This allows the lysozyme to break the chain of molecules in the bacterium's cell wall, which causes the death of the cell [6].

There are a number of different types of lysozymes on Earth. However, they share a similar structure, which is two domains (sections) separated by a deep cleft. One of these domains is a helical structure (an α helix), and the other is a sheet structure (a β pleated sheet) (Figure 2) [7]. Due to its function, we can assume that one possible structure of Enzyme 42 is that of a lysozyme.

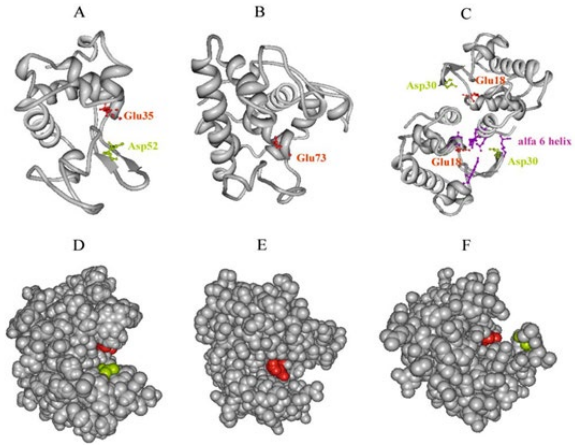

Figure 2 – The structures of various lysozymes. The shapes of these enzymes are very similar, with two domains with a cleft/gap in between [7].

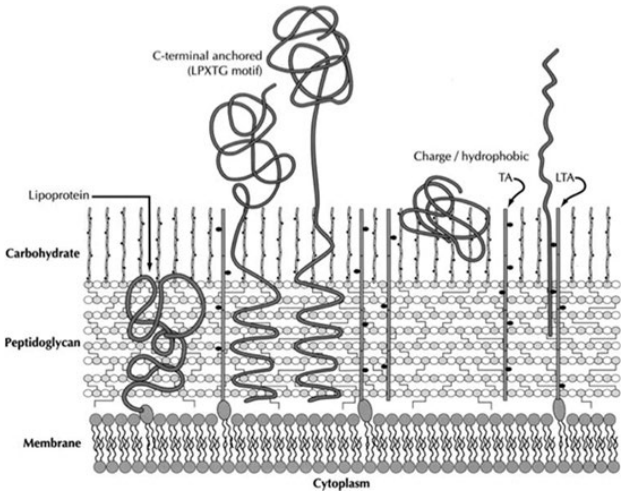

Figure 3 – A diagram of the cell surface of a bacterial cell, with examples of various molecules that protrude out of the cell wall [8]. Note how an enzyme with a specifically shaped domain may be able to attach itself to one of them.

Surface Molecules

Bacterial cells have molecules attached to their cell surface (see Figure 3). These can include various glycoproteins, lipoproteins, and receptors. These are used for a variety of functions that the bacterium requires, such as movement, adherence to surfaces, and transporting molecules in and out of the cell [8].

Since Enzyme 42 is one of the only cures for the Kharaa bacteria, its structure must contain a domain that interacts specifically with the surface of the bacterial cells. The structure of Enzyme 42 may have a domain with a shape complementary to a molecule present on the cell surface of the Kharaa bacterial cell. This would allow Enzyme 42 to bind to the cell via this domain, anchoring the enzyme in place and therefore making it easier for the cell to be destroyed via the lysozyme mechanism described above.

Conclusion

The function of an enzyme depends on its structure. Since Enzyme 42 is capable of destroying the Kharaa bacterium, it may have a general structure similar to that of a lysozyme, a type of enzyme specialised for the breakdown of bacterial cells. Because Enzyme 42 is capable of destroying the bacterium whereas other molecules cannot, it must have a way to bind specifically to the cell, such as through having a domain that anchors it to the bacteria via a cell surface molecule. This would then allow the enzyme to stay anchored while catalysing the breakdown of the bacterial cell wall.

References

[1] Unknown Worlds Entertainment, Gearbox Software, (2014) *Subnautica* [Computer game] San Francisco, USA

[2] Lewis, T. & Stone, W.L. (2022) *Biochemistry, Proteins Enzymes*, in: StatPearls. StatPearls Publishing, Treasure Island (FL).

[3] EMBL-EBI (2020) *What are protein domains? | Protein classification*. [Online] European Molecular Biology Laboratory training. Available at: https://www.ebi.ac.uk/training/online/courses/protein-classification-intro-ebi-resources/protein-classification/what-are-protein-domains/ [Accessed 1st March 2023]

[4] Key, A.P. (2021). *What Are Digestive Enzymes?* [Online] Nourish by WebMD. Available at: https://www.webmd.com/diet/what-are-digestive-enzymes [Accessed 27th February 2023]

[5] Oliver, W.T. & Wells, J.E. (2015) *Lysozyme as an alternative to growth promoting antibiotics in swine production*. Journal of Animal Science and Biotechnology 6, pp. 35. DOI: 10.1186/s40104-015-0034-z

[6] Sebald, A. & Mitchell, D.A. (2019) *Saliva and oral health* [Online] Maxfacts. Available at: https://maxfacts.uk/help/oral-hygiene/saliva-and-teeth-mucosa [Accessed 26th February 2023]

[7] Callewaert, L. & Michiels, C.W. (2010) *Lysozymes in the animal kingdom*. Journal of Biosciences, 35, pp. 127–160. DOI: 10.1007/s12038-010-0015-5

[8] Fischetti, V.A. (2019) *Surface Proteins on Gram-Positive Bacteria*. Microbiology Spectrum, 7. DOI: 10.1128/microbiolspec.GPP3-0012-2018