# Structural Studies of Adhesion Protein P1

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## Introduction

*Streptococcus mutans* is a major etiologic agent of human dental caries, the most prevalent infectious disease worldwide. *S. mutans* is particularly effective at colonizing hard tissues of the human oral cavity and its adherence is mediated by sucrose-dependent and independent mechanisms. In the presence of sucrose, its surface-localized glucosyl- and fructosyltransferases produce sticky glucans and levans allowing adhesion to enamel surfaces and possibly acting as a nutrient reserve. In the absence of sucrose, its wall-associated fibrillar lectin P1, previously known as Antigen I/II or PAc, facilitates attachment to the acquired pellicle on teeth [1]. This multifunctional adhesin mediates interactions with salivary constituents, host cell matrix proteins such as fibronectin, fibrinogen, collagen, and other oral bacteria.

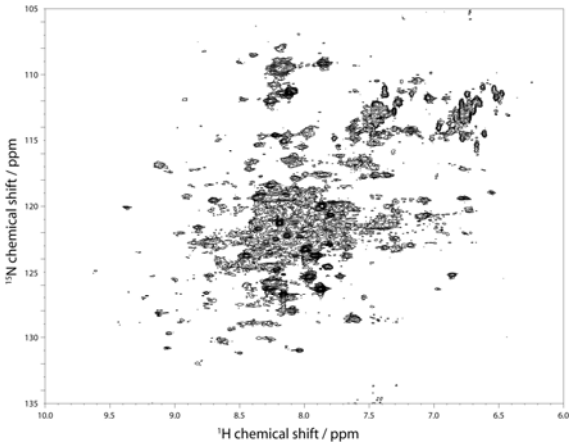
Our previous study [2] has demonstrated that, P1 possesses functional amyloid properties, which contributes to *S. mutans* virulence. Structures of various regions of P1 have been studied by X-ray crystallography [3]. Our plan is to utilize solid state NMR, along with high resolution NMR, spectroscopy to gain further insights into its structure and self-assembly properties. Determining P1 ultrastrucuture is highly likely to reveal critical information regarding the process of amyloidogenesis and biofilm formation by *S. mutans*.

## Experimental

Different regions of P1, namely the A3VP1 segment as well as the C-terminus, have been expressed and purified. Despite their relatively large sizes (55kDa and 60kDa respectively), we have successfully collected some preliminary high resolution NMR data at the AMRIS facility using both the 600-cryo and the 750 MHz magnets.

## Results and Discussion

Shown below is the first $^{1}H$-$^{15}N$ TROSY spectrum of the C-terminus of P1 at pH 7.4.




## Conclusions

Our preliminary NMR data have proven that, despite the relatively large size of our target protein, high resolution NMR is still viable for this study. To further improve the quality of our future spectra, optimization on the NMR conditions (pH and temperature) will be carried out next. From there, we hope to finish the assignment and gather more structural information on the whole assembly via solid state NMR.

## Acknowledgements

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## References

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[2] M. W. Oli, *et al*., Microbiology., **158**, 2903-2916 (2012).
[3] M. R. Larson, *et al*., Proc Natl Acad Sci., **107**, 5983-5988 (2010).