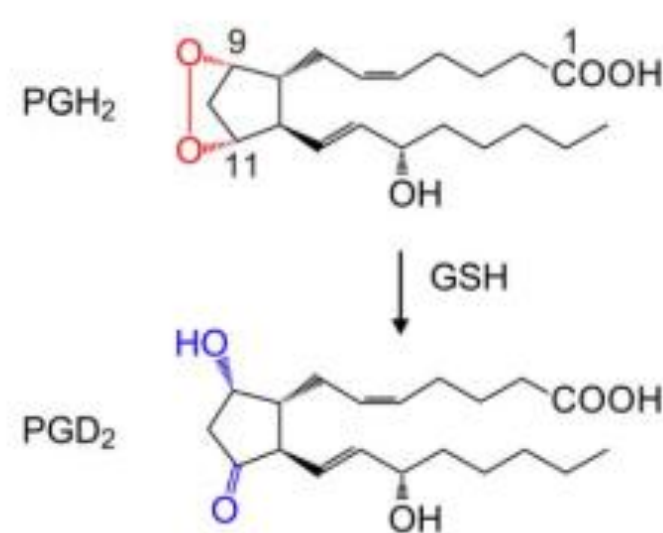


## Purification of Human Hematopoietic Prostaglandin D-Synthase

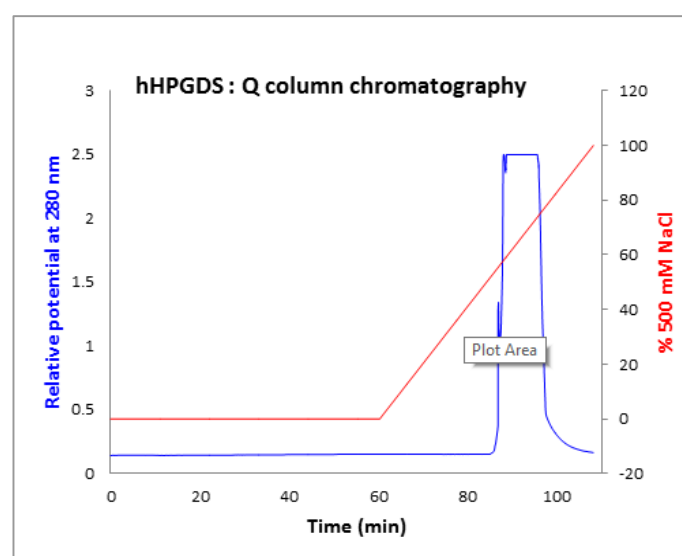
*Katherine Peffen, Department of Chemical Engineering  
RCEU Sponsored by Department of Biological Sciences*

### Introduction

Human Hematopoietic Prostaglandin D2-Synthase (h-HPGDS) **EC.5.3.99.2** is an isomerase that converts  $\text{PGH}_2$  to  $\text{PGD}_2$ . In patients with muscular dystrophy, muscle cells where H-HPGDS is localized undergo necrosis [1]. For the purpose of neutron crystallization, purity of h-HPGDS is critical for the formation of a large crystal. To improve crystal quality, the purification protocol needed to be optimized. Anion-exchange chromatography was focused on specifically in the purification process due to lack of effective separation of the desired protein. A pH and salt gradient was established for more effective separation.



Reaction catalyzed by PGD-synthase [2]



First Q Column Chromatography attempt

### Materials and Methods

#### I. Expression

Recombinant *E. coli* with h-HPGDS expression vector in 10 L large growth batch

#### II. Purification

##### 1. Nickel Column Chromatography

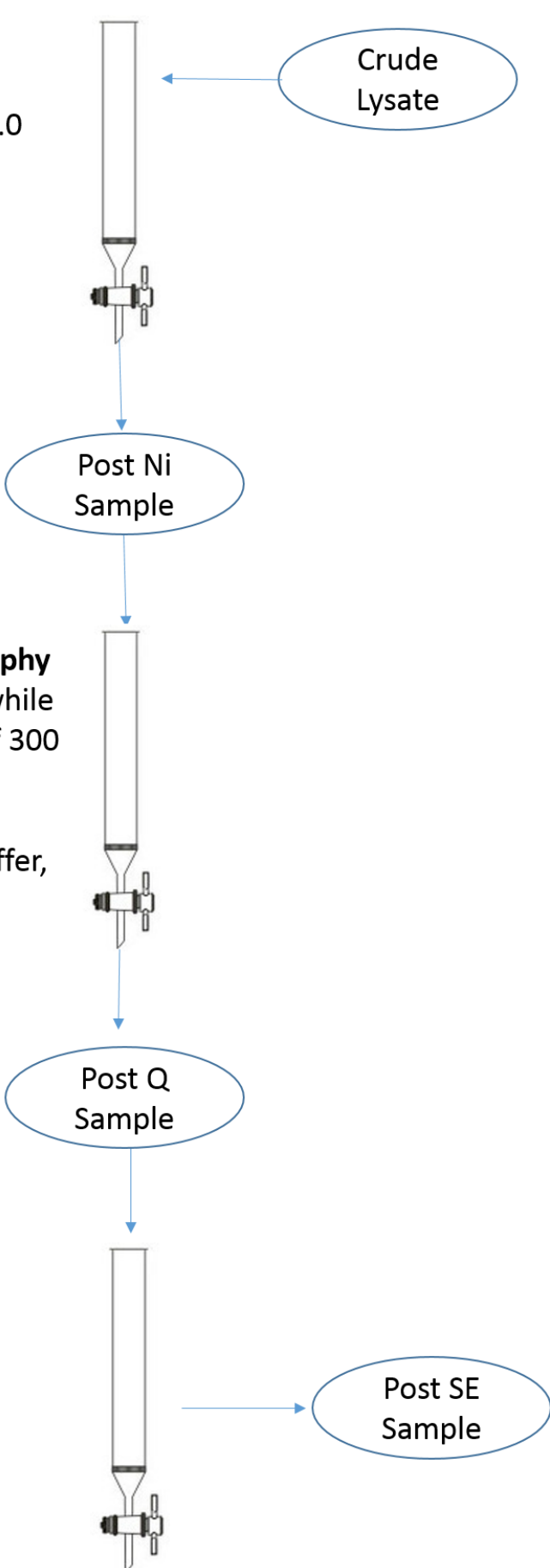
Start buffer: 50 mM sodium phosphate buffer, pH 8.0  
300 mM NaCl  
Elution buffer: SPB Start Buffer  
500 mM imidazole  
Wash buffer: SPB Start Buffer  
10 mM imidazole

##### 2. Quaternary Ammonium (Q) Column Chromatography

Protein bound at pH 7.5 but did not bind at pH 6.8, while unnecessary proteins eluted at salt concentrations of 300 mM or higher. To mitigate this issue, a pH and salt gradient was established.  
Start buffer: 20 mM sodium phosphate buffer, pH 7.5  
0.5 mM EDTA  
0.1 mM DTT  
1 mM PMSF  
Elution buffer: Same as Start Buffer, pH 6.8  
200 mM NaCl

##### 3. Size Exclusion Chromatography

Sephacryl S100 was used for high resolution  
Buffer: 20 mM HEPES-NaOH, pH 7.5  
0.1 mM DTT  
0.1 mM PMSF  
100 mM NaCl



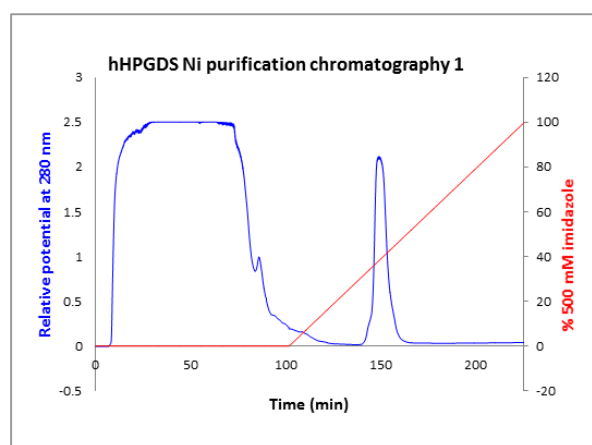
#### III. Activity Assay

- Glutathione S-transferase (GST) Activity Assay
- Assay performed on samples from each post column fraction
- Readings were taken every 30 sec for 30 min at 340 nm

### Data/Results

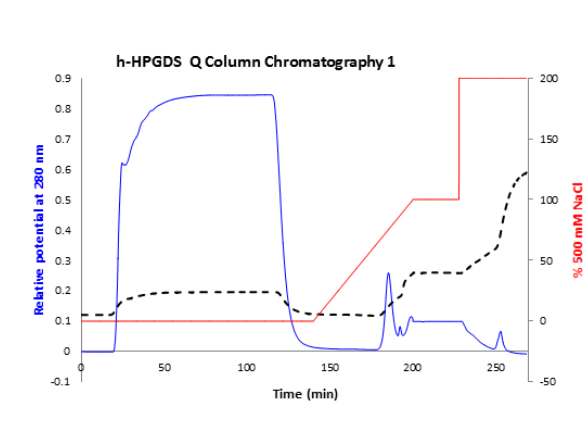
Post Column Fraction	Volume (mL)	Concentration (mg /mL)	Estimated amount (mg)	$A_{280}/A_{260}$	Specific Activity ( $\mu\text{m}/\text{ml}/\text{min}$ )
Crude lysate	200	20.20	4039.48	0.61	10.2
Post Ni	500	0.41	207.03	1.16	20.6
Post Q column	35	3.59	125.51	1.64	38.9
Post Size Exclusion	12	6.32	75.85	1.73	44.12

#### I. Nickel Column

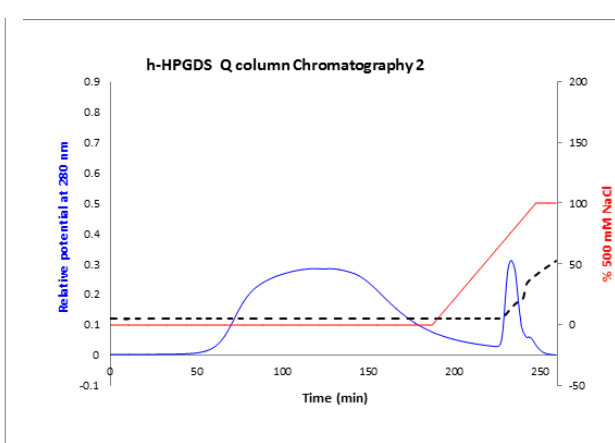


Nickel column purification chart

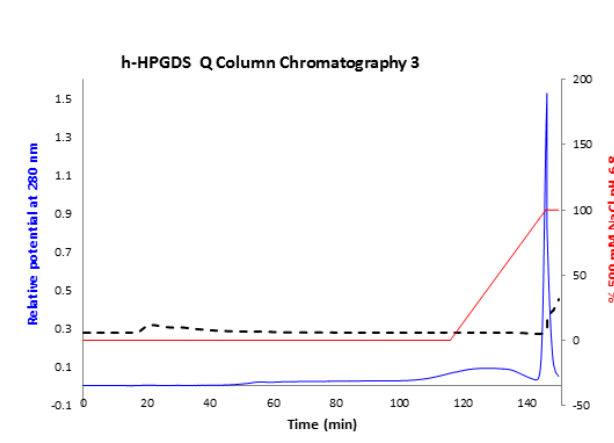
#### I. Q-Column



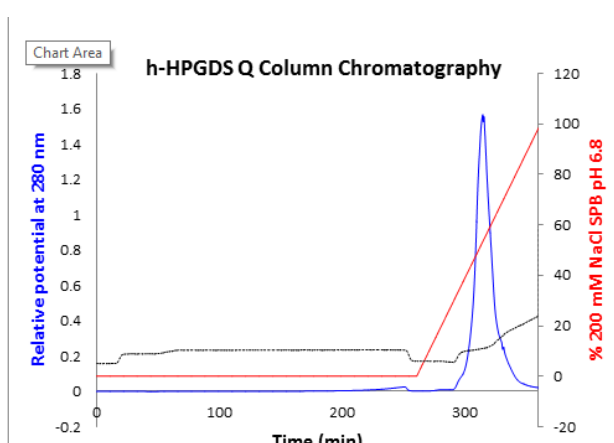
SPB buffer pH 6.8 with high NaCl in charged sample



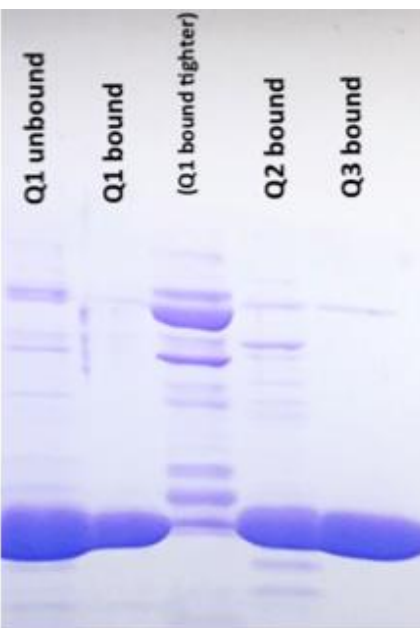
SPB buffer pH 6.8 with low NaCl in charged sample



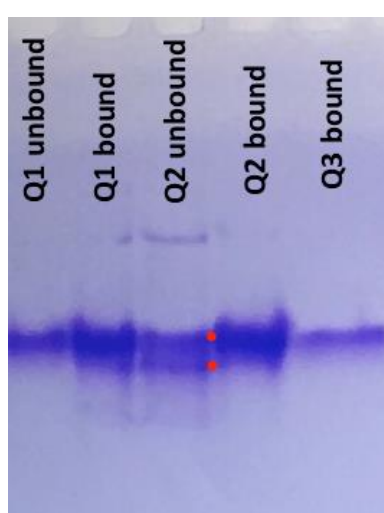
SPB Buffer pH 7.5 with low NaCl in charged sample



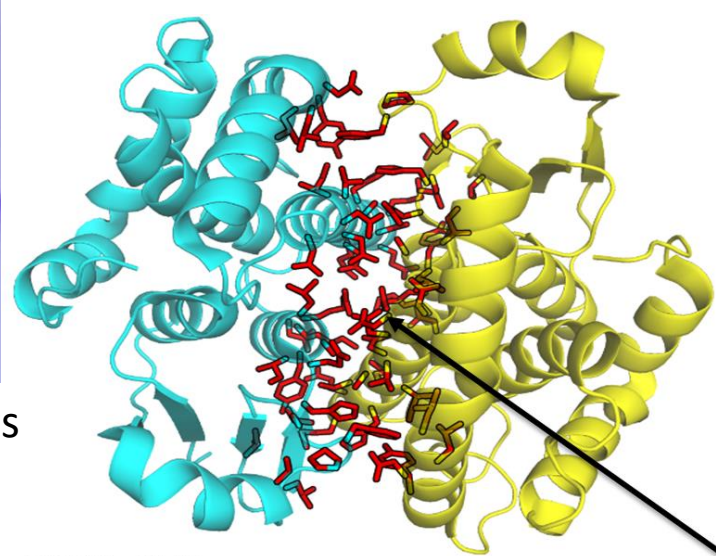
Optimized Q-Column Chromatography



SDS PAGE Results



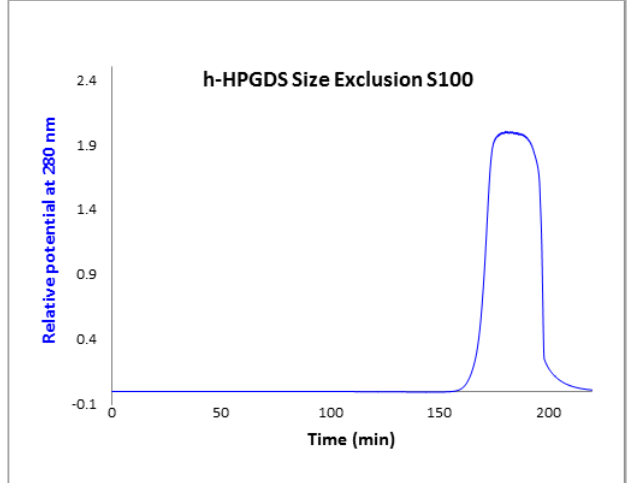
Native PAGE results



PDBID: 1IYH  
X-ray Crystallography Structure

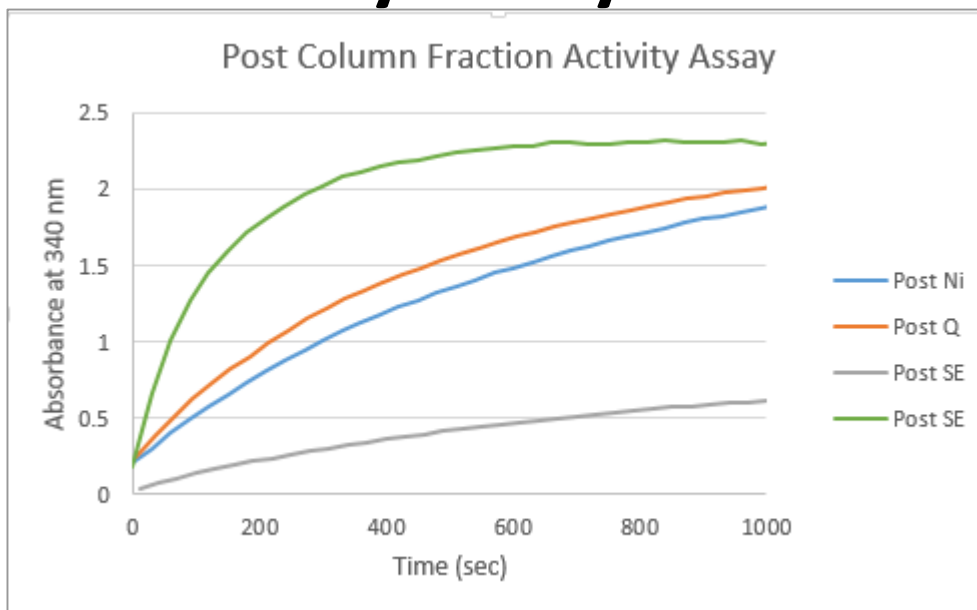
The hypothetical pI was originally determined to be 6.1. Accounting for interfacing residues that would have little effect on the overall surface charge changed, the hypothetical pH to 6.8.

#### III. Size Exclusion



Size Exclusion Chromatography Chart

#### IV. Activity Assay



GST Activity Assay for Post Column Fractions

### Impact/Conclusions

Optimizing the purification protocol removes impurities that may hinder the quality of h-HPGDS crystal for neutron crystallography purposes. Neutron crystallography allows for a higher resolution, and therefore better structure determination, which is critical for determining a more specific inhibitor for h-HPGDS.

### References

- Urade et al. (2012). International Journal of Microgravity Science and Applications. 29 (3) : 125-131
- Irikura et al. (2009). Journal of Biological Chemistry. 284 (12) : 7623-7630.

### Acknowledgements

Acknowledgements go out to Dr. Jospeh Ng, Dr. Noriko Inoguchi, Department of Biological Sciences, Dean of the College of Science, Office of the Provost, and the President, and Vice President of Research.