CALIFORNIA STATE SCIENCE FAIR
2001 PROJECT SUMMARY

Your Name (List all student names if multiple authors.)
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S0314

Project Title (Limit: 120 characters. Those beyond 120 will be ignored. See pg. 9)
Comparison of Protein Gel Electrophoresis and Mutli-Coupling Spectroscopy Through Digestion of HSA and Fibrinogen

Division
S Junior (6-8) S Senior (9-12)

Preferred Category (See page 5 for descriptions.)
3 - Biochemistry / Molecular Biology

Abstract (Include Objective, Methods, Results, Conclusion. See samples on page 14.)
Use no attachments. Only text inside these boxes will be used for category assignment or given to your judges.

Objective: In our project, we attempted to compare a standard method of protein and protein digestion observation (running electrophoresis gels) with a new proprietary method developed by Signature BioScience, multi-coupling spectroscopy, by characterizing digestions of both HSA and fibrinogen using each method.

Materials and Methods: We prepared the protein solutions by buffering our protein samples in phosphate-buffered saline (PBS). We then prepared protease solution by buffering crude protease in hydrochloric acid (HCL). For electrophoresis, we prepared 8 time-lapse protein digestion solutions, stopping digestion after intervals of 0, 1, 2, 5, 10, 30, 60 minutes and overnight using 2-mercaptoethanol. We then ran SDS-PAGE electrophoresis gels with the samples and a lane for a molecular weight ladder. For multi-coupling spectroscopy, we loaded a 200ul "plug" of protein solution over the resonator to establish a baseline, and then mixed 2ul of protease solution with another 200ul of protein solution and loaded that plug over the resonator. We then collected data at 60-second intervals until the digestion had appeared to have stopped.

Results: We obtained successful results for both procedures using both proteins. The time-lapse electrophoresis gels show the protein being digested into smaller and smaller polypeptide fragments over time, while the MCS graphs depict the changing dielectric properties and spectroscopy resonances.

Discussion: While the standard time-lapse electrophoresis gel method provides valuable (if not precise) information regarding the size of the polypeptide fragments, MCS has much more to offer. Not only does it allow for quicker experiments and the use of proteins in their native solutions, but the results are more precise, in the form of spreadsheets with exact numbers that can be manipulated easily after an experiment. Also, different types of measurements are recorded, such as the changing spectroscopy curve and the dielectric properties graph.

Summary Statement (In one sentence, state what your project is about.)
We compared two methods used for observing the changing structure and properties of proteins during digestion, using two different proteins.

Help Received in Doing Project (e.g. Mother helped type report; Neighbor helped wire board; Used lab equipment at university X under the supervision of Dr. Y; Participant in NSF Young Scholars Program) See Display Regulation #8 on page 4.
Used lab equipment at Signature BioScience under the direction of Dr. Bob Chapman.