# Stargazer-2

*DSLS INSTRUMENT FOR THE THERMOSTABILITY ANALYSIS OF PROTEINS*


**LABEL-FREE TECHNOLOGY**

Stargazer-2 measures protein aggregation through the scattering of visible light. No fluorescent probes are used, meaning samples which were previously difficult to screen using DSF are now readily accessible using Stargazer-2's label-free DSLS technique.

**10 - 95°C OPERATION**

384-well microplates, heating rates up to 5°C/minute, and a short cool-off time translates into high-throughput experiments and fast results.

**SAMPLES AS LOW AS 2.5 µL**

Using a standard low-volume 384-well optical bottom microplate, Stargazer-2 is capable of simultaneously collecting data from up to 383 samples per experiment. (Well A24 is reserved for use by the instrument.) To conserve valuable reagents, Stargazer-2 can detect aggregation in sample volumes as low as 2.5 µL/well. Typical protein concentrations used range from 0.05 mg/mL to 1 mg/mL.

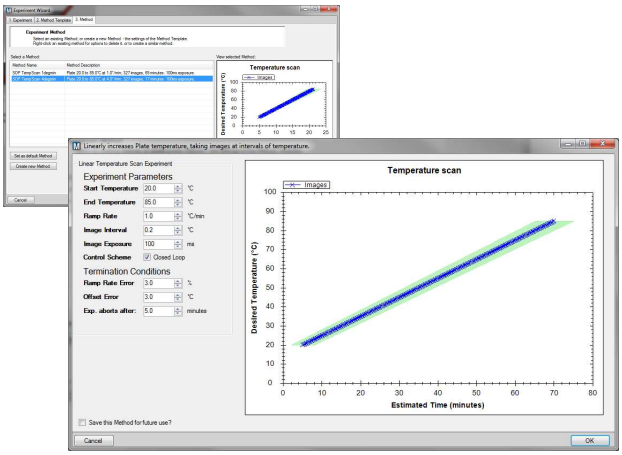
**ADVANCED SOFTWARE**

Method-based experiments in the Magellanic control software allow users to customize the operations of Stargazer-2 to their needs. Automated data processing using Stargazer-AIR lets users quickly analyze data. Export plugins provide Excel, BioActive, and LIMS compatibility. Optional online software updates ensure an up-to-date user experience.

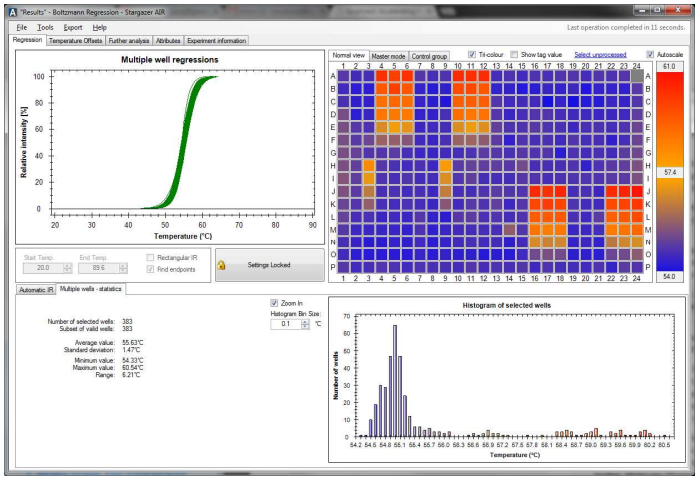
Stargazer-2 Differential Static Light Scattering

**STARGAZER-2** is Epiphyte3's second-generation DSLS instrument, designed to study the thermal stability of proteins. Using the label-free differential static light scattering technique pioneered by our scientists and engineers, Stargazer-2 measures the aggregation of protein in a 384-well microplate under controlled thermal conditions. This thermal aggregation assay can be used for many applications:

- Thermal stability analysis of proteins using temperature scanning & isothermal methods
- Formulation development of therapeutic monoclonal antibodies
- Characterization of membrane proteins
- Comparison of ligand specificity, including substrates, co-factors, inhibitors, etc.
- Validation of HTS hits
- Quality control of protein biologics
- Focused library screening for buffer optimization, protein crystallization, chemical biology
- Comparison of stability of SNP proteins




***The Magellanic instrument control software allows users to create, share, and modify methods.***




***Stargazer-AIR automatically processes experiment data and provides users with powerful data analysis tools.***

## Selected Publications


1. Vedadi M et al. Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. Proc Natl Acad Sci U S A. 2006 Oct 24;103(43):15835-40.
2. Senisterra GA et al. Screening for ligands using a generic and highthroughput light-scattering-based assay. J Biomol Screen. 2006 Dec;11(8):940-8.
3. Hong BS et al. Crystal structures of human pantothenate kinases. Insights into allosteric regulation and mutations linked to a neurodegeneration disorder. J Biol Chem. 2007 Sep 21;282(38):27984-93.
4. Adams M et al. Crystal structure of PhnH: an essential component of carbon-phosphorus lyase in Escherichia coli. J Bacteriol. 2008 Feb;190(3):1072-83.
5. Senisterra et al. Assessing the stability of membrane proteins to detect ligand binding using differential static light scattering. J Biomol Screen. 2010 Mar;15(3):314-20.
6. Zhang et al. Conformational stabilization of ubiquitin yields potent and selective inhibitors of USP7. Nat Chem Biol. 2013 Mar;9(3):192.
7. Goldberg, DS, Bishop, SM, Shah, AU and Sathish, HA (2011), Formulation development of therapeutic monoclonal antibodies using high-throughput fluorescence and static light scattering techniques: Role of conformational and colloidal stability. J. Pharm. Sci., 100: 1306–1315. doi: 10.1002/jps.22371.
8. Samra HS and He F, Advancements in High Throughput Biophysical Technologies: Applications for Characterization and Screening during Early Formulation Development of Monoclonal Antibodies, Molecular Pharmaceutics 2012 9 (4), 696-707.
9. Omar AM, Elfaky MA, Arold ST, Soror SH, Khayat MT, Asfour HZ, Barmane FH and El-Arby ME. 1H-Imidazole-2,5-Dicarboxamides as NS4A Peptidomimetics: Identification of a New Approach to Inhibit HCV-NS3 Protease. Biomolecules 2020, 10(3), 479.
10. El-Araby ME, Omar AM, Soror SH, Arold ST, Khayat MT, Asfour HZ, Bamane F, Elfaky MA. Synthetic bulky NS4A peptide variants bind to and inhibit HCV NS3 protease. Journal of Advanced Research 24 (2020) 251-259.


## Technical Summary

Scattering wavelength: 620nm (other wavelengths, inquire)

Sample temperature range: 10 - 95°C, 0.1 - 5.0°C/minute

Number of samples: 1 - 383 samples (well A24 reserved)

Sample volume: 2.5 - 50µL (average 0.1 mg/mL concentration)

Protein consumption: 100µg / microplate (383 x 2.5µL @ 0.1 mg/mL)

Approved microplates: Corning 3540, Nunc 242764

Physical dimensions: 40 x 43 x 75cm (W x D x H), 50kg

Power: 10A, 100-240VAC, 50-60Hz, 1Φ

Included Software: Stargazer-Magellanic, Stargazer-AIR

Computer: Two USB 2.0 ports available, 3 GB RAM minimum

stargazer™

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