Molecular Dimensions

ACHIEVE MORE.

Durham Osmolyte Screen

Harness the power of intracellular environment-control compounds to improve your results.

The new Durham osmolyte screen allows you to test which of a broad range of cell components help stabilise your protein, improving the results of structural and functional studies.

Osmolytes are uncharged, highly soluble organic molecules that act in cells to balance high external salt concentrations without disturbing intracellular ionic strength. This makes osmolytes the ideal additives for stabilising your protein during structural and functional studies as they are usually present in high concentrations in native cell environments without affecting protein behaviour.

Easily identify which osmolytes are most beneficial to your research with The Durham Osmolyte screen, a 96-well screen that scans more than 50 different osmolytes, exclusively from Molecular Dimensions.

To optimise your protein's complete environment, we recommend using the Osmolyte screen together with the Durham pH and Salt screens. All three screens were developed at Durham University by Ehmke Pohl, Daniel Bruce and Emily Cardew.

Clear presentation of results

Durham screen data can easily be analysed with NAMI. This free-to-download GUI-based software provides an intuitive plate-based colour gradient to enable easy identification of stabilising and denaturing conditions.

Discover the detail

Bruce, D *et al. J. Vis. Exp* 144: e58666 (2019). Video presentation describing the use of stability screens in aiding your protein research. Moldim.com/stability-video.

Osmolytes:

- Often stabilise proteins as a result of their frequent presence in the native protein environment.
- Rarely affect protein function because of their neutral chemical characteristics.
- Uncharged, highly soluble organic molecules which microorganisms accumulate at significant concentrations to balance high salt external environments.
- Include:
  - Sugars
  - Amino-acids
  - Polyols
  - NDSBs

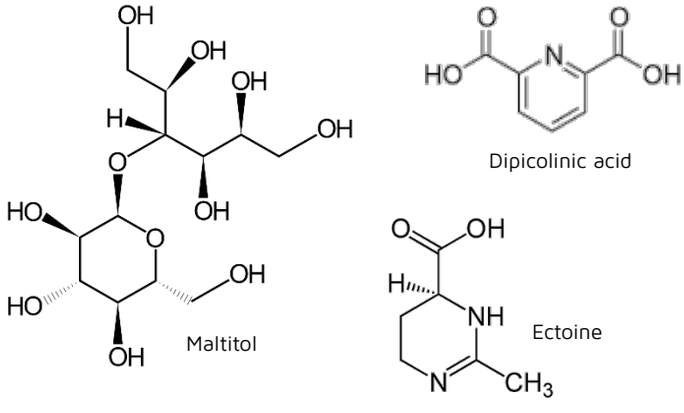

Fig. 1: Examples of some of the osmolytes in the screen.

ORDERING INFORMATION

	Pack Size	Description
MD1-120	96 x 0.5 mL	The Durham Osmolyte Screen
MD1-101	96 x 0.5 mL	The Durham pH Screen
MD1-102	96 X 0.5 mL	The Durham Salt Screen
MD1-103	384 x 0.5 mL	The Protein Stability Combo Kit (The Durham pH and Salt Screens and Rubik Buffer and Additive Screens)

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The Durham Salt and pH Screens

Optimise your protein sample for better results from initial purification to final structure.

How thermal shift assays help your research

By optimising protein stability you can improve your protein's crystallisability and the quality of your final structure. Thermal shift assays provide information on the effect various environmental factors have on the thermal denaturation of a protein, which in turn is related to protein stability. The most common thermal shift assay is ThermoFluor®, which measures increasing fluorescence induced by SYPRO® Orange binding to the exposed protein hydrophobic core.

Steamline structure solution.

Salts are both common precipitating agents and additives in crystallisation conditions. Use the Durham Salt screen to identify which salts interact with your protein, and streamline the process of identifying the optimum crystallisation conditions.

Ideal for fragment-based drug design.

The Durham pH Screen allows you to quickly identify molecular which behave like ligands and bind to specific pockets on the protein, competing with the small molecules in your fragment screen. Like ligands, these buffer molecules (de)stabilise your protein and can be detected by ThermoFluor.

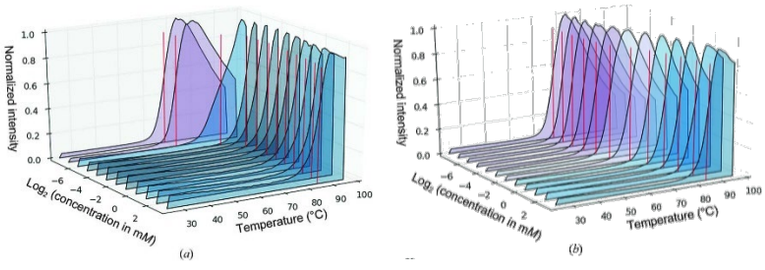
	1	2	3	4	5	6	7	8	9	10	11	12
A	67.3	64.4	65.1	60.7	58.5	63.7	60.1	68.1	68.5	67.3	67.7	66.9
B	65.4	64.8	69.5	68.3	74.1	71.5	70.7	65.5	62.7	64.4	63.6	48.1
C	50.0	59.8	64.7	67.2	68.4	68.2	68.0	68.2	67.7	67.9	67.7	66.7
D	N/S	47.4	59.4	65.8	68.1	68.6	68.1	68.5	68.5	68.6	69.0	68.1
E	56.4	63.6	65.5	66.4	66.5	66.2	66.0	65.6	67.3	65.5	65.4	64.5
F	67.5	67.4	67.3	67.3	67.2	67.1	67.5	67.1	67.3	67.1	67.2	67.3
G	67.9	68.4	70.5	61.6	68.1	69.7	68.1	68.7	69.8	67.1	67.2	68.8
H	57.7	68.3	70.1	60.4	67.7	69.7	64.4	65.5	66.9	63.6	66.0	65.3

Least stable — No change — Most stable

Glucose Isomerase pH dependence

Dependence of melting temperature on concentration of magnesium and cobalt chloride for glucose isomerase. Thermal denaturation curves at a range of concentrations for (a) $CoCl_2$ and (b) $MgCl_2$..

- Identify optimum protein conditions for crystallisation with thermal shift assays.
- Optimize your protein's complete environment using the Durham Osmolyte, Salt and pH screens together.
- Explore the effect of more than 30 salts in your protein with the salt screen:
  - Identify phasing agents with the lanthanide series.
  - Find out if controlling the redox conditions is important with TCEP and DTT.
- Deconvolute the effect on your protein of buffer chemistry and pH with the pH screen:
  - pH range: 4-11.
  - 28 different buffers.



Identify specifically bound metals and anions!

Using NAMI* with the Salt Screen is a powerful tool for assessing the optimum concentration of salt to add to your protein. NAMI can generate waterfall plots of the thermal shift data at multiple salt concentrations or plots of melting temperature against concentration. These differentiate a sudden increase in protein stability indicating a specific interaction and steady increases in stability due to the changing protein environment.

*NAMI is a free to download GUI-based program that aids thermal shift data analysis.

LUBIO SCIENCE
Part of Europa Biosite

Your distributor in Switzerland

LubioScience GmbH
Baumackerstrasse 24
8050 Zurich

+41 41 417 02 80
info@lubio.ch
www.lubio.ch

A: Molecular Dimensions Inc
434 West Dussel Drive
Maumee OH 43537
USA

T: +1 877 479 4339
F: +1 321 972-8896
W: moleculardimensions.com
E: enquiries@moleculardimensions.com