## Accelerate structural elucidation

OptiMSe your workflow for faster sample screening



## Streamline sample-to-structure with optimized sample preparation

Cryo-EM is a revolutionary tool that is increasingly being used to determine the 3D structure of proteins and their complexes. In the last decade, innovation in hardware and software have allowed cryo-EM to achieve atomic resolution at increasingly higher throughput. As ever more challenging proteins and complexes are being studied by cryo-EM, so increases the need for more robust ways to prepare cryo-EM grids through a process called vitrification, wherein the protein is embedded in a thin layer of vitreous ice.

One aspect that is sometimes overlooked when preparing cryo-EM grids is the correlation between the quality of the sample and the vitrification process. A stable and homogeneous protein sample is much less likely to encounter artifacts during vitrification, like aggregation or dissociation of a protein complex. However, to obtain an ideal sample for cryo-EM, there are many different aspects that require optimization such as ionic strength, use of detergents or additives, and sometimes even construct design.

To find the best conditions, samples are typically vitrified and then screened using a transmission electron microscope. If microscope time is not available, a negative stain screening can be used to embed the sample in a thin layer of heavy metal stain. Unfortunately, this process can introduce artifacts like aggregation and a direct correlation to the results in cryo-EM can be difficult to establish.

The Thermo Scientific<sup>™</sup> OptiMSe Workflow is a fast, automated, and intuitive way to eliminate unpromising samples for vitrification and cryo-EM, leveraging the power of native mass spectrometry.



### The OptiMSe Workflow

## The OptiMSe Workflow Automated sample screening powered by native MS

Good protein preparation is critical to downstream success for cryo-EM. Optimizing the biochemistry for your protein sample can reduce artifacts during vitrification, such as denaturation, unfolding or reduced structural resolution. The Thermo Scientific OptiMSe Sample Screening Workflow removes guesswork and provides a fully automated sample screening step that can save you time and resources, helping you to select the best quality samples for your microscopic analysis.

#### Utilize the power of native MS for sample screening

Native mass spectrometry (native MS) is a powerful technique that allows for thorough characterization of proteins and their complexes.<sup>1</sup> Unlike most common structural biology techniques, native MS does not average but rather reveals all proteoforms and conformations at the same time. This requires gentle transfer of the protein from solution to the gas phase through a process called electrospray ionization, which does not perturb the structure of the protein or complex studied, thus revealing the state of the protein in solution. Cryo-EM sample prep issues



Many of the commonly occurring cryo-EM sample preparation challenges can be identified with native MS

#### Structural Biologist (Sample Creator)



Mass Spec Operator (Analyst)

#### How can native MS help with sample screening?

Only a small fraction of samples for cryo-EM will be suitable to yield a structure. Of the seven commonly observed blocking sample preparation issues for cryo-EM success, the OptiMSe Workflow is able to identify five of them and help you move only the most promising samples forward, allowing you to focus on what matters: using your microscopy time to solve structures.

#### Focus on the results, not the process

The OptiMSe Workflow was designed to seamlessly integrate in your process. Even if you are not a native MS expert, the OptiMSe Workflow will assist you by preparing LC queues and tuning the instrument while its automated data deconvolution and report generation give you on-the-fly results.

## The OptiMSe Workflow Automated native MS for cryo-EM sample screen

	Guided Experiment	Design
joes	Buffer Screen 🖌	TABLE & TRAY
LID TEMPLATES	Screening - 54 Well (9x6) - Tray #Buffer Screen 1	ohn.doe@thermofisher.com
CEO DIVIKIS	Studies in job	0/54 sample slots
<b>O</b> BOOMS	Standard Samples	0 samples 🚦
CHICP ZONE	+ ADD STANDARD SAMPLE	
•	DufferScreen	0 sub-samples 🚦
LOGOUT	Study Settings	

Easily add samples for screening using pre-populated buffer conditions from OptiMSe SPOT Software. The Thermo Scientific<sup>™</sup> VitroEase<sup>™</sup> Buffer Kit offers numerous buffer combinations and supports custom conditions as well.



OptiMSe SPOT Software provides electronic screening and visual cues to help you save time and eliminate manual recording.



Fast online buffer exchange with NativePAC OBE-1 columns enable 3-5 minute runs.<sup>2,3</sup> When coupled to high resolution accurate mass Thermo Scientific<sup>™</sup> Orbitrap<sup>™</sup> technology even the most challenging proteins and complexes can be analyzed quickly and easily.



#### Online Buffer Exchange ► Automated Acquisition

#### Automated Processing/Reporting



The OptiMSe Workflow determines the best data analysis parameters without user intervention, based on the sample's target mass.

Novel deconvolution algorithms designed specifically for intact protein and protein complex data analysis are deployed automatically and run on acquired data while the subsequent data are collected.

Easily choose the best samples to send for cryo-EM analysis using the intuitive reports generated by the OptiMSe Workflow.



### **Structural Analysis**



Quickly screen out the least promising samples with the OptiMSe Workflow. Reduce your screening time on the microscope so you can focus on the results.



## Tune your sample prep for optimal stability

#### Optimize sample preparation for structural biology with the OptiMSe Workflow

Poor protein sample preparation can sabotage your structure long before the sample reaches the microscope. Shouldn't there be a better way to know what samples are the best candidates for cryo-EM? What if you could screen dozens of different buffers or sample preparation conditions in a single day? With the VitroEase Buffer Optimization Kit and the combined with OptiMSe Sample Screening Workflow you no longer need

to guess how to best prepare your sample or rely on "good enough." Don't let time constrains prevent you from finding the optimal sample conditions. Break through the backlog and accelerate your structural elucidation with high-throughput sample screening.



Buffer# Content (10x) · Buffer screening: C.H.NaO. (0.5M), NaCl (1.5M), pH 3.6 9 µL protein (1ug/ul) + 1 µL buffer (10×) C2H3NaO2 (0.5M), NaCI (3M), pH 3.6 · Detergent screening: MES (0.5M), NaCl (1.5M), pH 5.5 3 9 µL protein (1ug/ul) + 1 µL buffer (10x) + 1 µL detergent (1 CMC) MES (0.5M), NaCl (3M), pH 5.5 Tris-HCI (0.5M), Mg(CH, COO), (0.1M), NaCI (1.5M), pH 7.2 Tris-HCl (0.5M), MgCl, (0.1), CH, CO, K (1.5M), pH 7.5 Tris-HCI (0.5M), Mg(CH<sub>2</sub>COO)<sub>2</sub> (0.1M), KCI (3M), pH 7.2 VitroEase buffer screening kit (A49856) HEPES (0.5M), NaCl (1.5M), pH 7.4 Detergent # Content (10x) 8 HEPES (0.5M), KCI (3M), pH 7.4 A CTAB (0.3%) 9 1 HEPES (0.5M), Mg(CH<sub>3</sub>COO), (0.1M), CH<sub>3</sub>CO<sub>2</sub>K (1.5M), pH 7.4  $\checkmark$ В CHAPS (4.9%) 10 HEPES (0.5M), MgCl, (50mM), CaC, (50mM), NaCl (1.5M), pH 7.4 OG (2.7%)  $\checkmark$ C 11 12 PBS (1.37M NaCl 270mM KCl, 43mM Na, HPO), pH 7.4 Tween-20 (0.1%) Bicine buffer (0.5M), NaCl (1.5M), pH 8.5 Е DM (1%) 13 1  $\checkmark$ CAPSO (0.5M), KCl (3M), pH 8.9 F FOM (0.7%) 14 Note: The colors in the left column correspond to the colors of the vial caps in the VitroEase kit.

Sample preparation

VitroEase Buffer Screening Kit (P/N A49856)



*I* ... I would even say that to do cryo-electron microscopy without native mass spectrometry ... is like working with not one hand behind your back, but two hands behind your back... *J* 

Prof. Brian Chait, Camille and Henry Dreyfuss Professor, The Rockefeller University







Marchaet     France       • Tops tett • Stragstrams: 21/2022 E28:30 HG     • Stragstrams: 21/2022 E28:30 HG       • Stragstrams: 21/2022 E28:30 HG     • Stragstrams: 21/2022 E28:30 HG       • Tops tett     • Stragstrams: 21/202 E38 HG       • Tops tett     • Stragstrams: 21/202 E38 HG       • Tops tett     • Stragstrams: 21/202 E38 HG       • Tops tett     • Tops tett       • Tops tett	Project TyrunateKinase_UtrofaseScreent       9: gir II       10: gir II       11: gir II       11: gir II       12: gir II       12: gir II       13: gir II       14: gir II       14: gir II       15: gir II       16: gir III       16: gir IIII       16: gir IIII       16: gir IIIII       16: gir IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	etected
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Weil     Sample Name     Target %     Experimental Details       X1     21. Immediani.     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.1     21. Immediani.     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.2     XVM work     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.2     XVM work     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.2     XVM work     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.2     XVM work     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.3     XVM work     23.27     MSIG ML WOOD SIM. Mg/CCCCDD 21.19       X4.6     XVM work     24.27     PSIL 37M ALC 27 MM, MaxPO 21 MM, MG/SIG ML WOOD SIM. Mg/SIG M	Weil     Sample Name     Target %     Experimental bitsails       X1     21.10m/stable.1     22.30     M65.51.61.00115     M65.51.61.00115       X1     21.10m/stable.1     22.30     M65.51.61.00115     M65.51.61.00115     M65.51.61.00115       X4     21.10m/stable.1     22.30     M65.51.61.00115     M65.0101.00116     M65.011.00116       X4     EV/stable.0     37.71     M65.51.51.001.01210     M65.701.00116     M65.701.00116       X4     EV/stable.0     67.22     P61.51.274.61.072 PenH, AbaPPO G1 PM, M62.70116     M65.701.00116     M65.701.00116     M65.701.00116     M65.70116     M65.	steded
XA1     Trivenent     25.20     M655.94, Mol 15.94       XA2     Fritzmann     31.81     Trivenent Microsoft Micros	XA1     Trivenent     25:29     MISS M, MOL SM       XA2     Fritzmann     31:31     Third MSS M, GI JM, Might CODD EI M       XA4     Fritzmann     31:31     Third MSS M, GI JM, Might CODD EI M       XA4     Fritzmann     31:31     Third MSS M, GI JM, Might CODD EI M       XA4     Fritzmann     31:37     RRESS M, Might CODD EI M       XA4     Fritzmann     31:37     RRESS M, Might CODD EI M       XA4     Fritzmann     71:28     Ressolution SM     31:30       XA4     Trivenance     81:34     RESS M, Might CODD EI M     31:31       XA4     Trivenance     81:44     RESS M, Might CODD EI M     31:31       XA4     Trivenance     81:44     RESS M, Might CODD EI M     31:31       XA4     Trivenance     81:44     RESS M, Might CODD EI M     31:31       XA4     Trivenance     81:44     RESS M, Might CODD EI M, Might	
XA     Trivitation2     31-81     The Hoft SS M (AD2 TO M), MgGRCC002 E 114       XA     Trivitation2     32-71     Heft SS M (AD2 TO M), MGSRCC002 E 114       XA     Trivitation2     37-71     Heft SS M (AD2 TO M), MGSRC002 E 114       XA     Trivitation2     27-22     PE13 TM, MC 207 e M), MGSRC01 FM       XA     Trivitation2     27-44     PE13 TM, MC 207 e M), MGSRC01 FM       XA     Trivitation2     27-44     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     27-44     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     27-44     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     10-64     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     10-74     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     10-84     PE13 TM, MC 270 e M), MGRC01 FM, MC 2014       XA     Trivitation2     10-84     PE13 TM, MC 2014     MC 2014       XA     Trivitation2     10-84     PE13 TM, MC 2014     MC 2014       XA     Trivitation2     10-84     PE13 TM, MC 2014 <td>XA     Trivitation:     31.81     TherMOSIM     X0.14     March 2014     X1.44     X1.44<td></td></td>	XA     Trivitation:     31.81     TherMOSIM     X0.14     March 2014     X1.44     X1.44 <td></td>	
XAI     Trivenacci     39:70     HER55.51 (M0215ml) C023 5ml, M0115 MI       AI     Trivenacci     61:22     PE51.51 (M0215ml) C023 5ml, M0115 MI       AI     Trivenacci     71:12     Bione Julie G3 MI, M0115 MI       AI     Trivenacci     71:12     Bione Julie G3 MI, M0115 MI       AI     Trivenacci     71:41     Bione Julie G3 MI, M0115 MI       AI     Trivenacci     71:44     PE11 MI, M012 FMI       AI     Trivenacci     71:44     PE11 JM, M012 FMI       AI     Trivenacci     71:44     PE11 JM, M012 FMI       AI     Trivenacci     104     PE11 JM, M012 FMI, M029 G4ml, Meeso G17:6       AI     Trivenacci     104     PE11 JM, M012 FMI, M029 G4ml, Meeso G17:6       AI     Trivenacci     54:38     PE11 JM, M012 FMI, M029 G4ml, Meeso G4:16       BI     Trivenacci     54:38     PE11 JM, M012 FMI, M029 G4ml, Meeso G4:16	XM     Trivenacci     39:70     HERESS M, MU2215mB, GOL2 Smith, MULT SM       A     Trivenacci     61:22     PESS SM, MU2215mB, GOL2 Smith, MULT SM       A     Trivenacci     70:12     Bione buffer SM, Mult TSM       A     Trivenacci     70:12     Bione buffer SM, Mult TSM       A     Trivenacci     70:41     Bione buffer SM, Mult TSM       A     Trivenacci     81:44     PESI TM, MU270mM, MaxPO Gmit, MUR439       A     Trivenacci     104     PESI TM, MU270mM, Mu2PO Gmit, MUR439       A     Trivenacci     84:0     PESI TM, MU270mM, Mu2PO Gmit, MUR439       A     Trivenacci     84:0     PESI TM, MU270mM, Mu2PO Gmit, MUR439       A     Trivenacci     84:0     PESI TM, MU270mM, Mu2PO Gmit, MUR439       A     Trivenacci     84:0     PESI TM, MU270mM, Mu2PO Gmit, MUR439       A     Trivenacci     84:0     PESI TM, MU270mM, Mu2PO Gmit, MU2013mM, MU2013mM, MU213mM, MU21	
14     Transmission     61.22     PE1.17.M.K1279 eM, MartPo141       14     Transmission     71.22     PE1.17.M.K1279 eM, MartPo141       14     Transmission     71.22     PE1.17.M.K1279 eM, MartPo141       14     Transmission     PE1.17.M.K1279 eM, MartPo141     PE1.17.M.K1279 eM, MartPo141	IA     Kinchester     61-22     PR1 127 KK 0279 mth, NatiPPO 21 mth       AA     Di Vincidenzi     70-12     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     70-24     Diender 2017 Mth     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     89-31     PR1 127 Mth     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     89-31     PR1 127 Mth     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     89-31     PR1 127 Mth     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     88-31     PR1 127 Mth     Diender 2017 Mth     Diender 2017 Mth       AB     Di Vincidenzi     88-33     PR1 127 Mth     Diender 2017 Mth     Diender 2017 Mth	
A/s     Trivincianci     70.12     Biore safer 0.5 M, Mol 1.5 M       A/d     Trivincianci     87.94     Bio TLV M, KC270 and N, NaciPe 0.4 mM, CMB 0.3 %       A/Z     Trivincianci     89.41     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.3 %       A/Z     Trivincianci     100     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.2 %       A/Z     Trivincianci     100     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.2 %       A/Z     Trivincianci     100     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.2 %       A/Z     Trivincianci     101     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.2 %       A/Z     Trivincianci     54.08     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.2 %       A/Z     Trivincianci     54.08     PR1 1.7 M, KC270 and N, NaciPe 0.4 mM, CMB 0.0 %	IA5     EV. Stratutes     70.12     Botte huffer 0.5 N, Not 1.5 M       Adv     FV. Stratutes     87.4 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, CNB.0.3 %       AV     FV. Vittedane7.     89.4 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, CNB.0.3 %       AV     FV. Vittedane7.     89.4 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, CNB.6.2 G, 27 %       AV     FV. Vittedane5.     100.4 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, There3.00.1 %       FA8     FV. Vittedane5.     80.8 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, There3.00.1 %       FA8     FV. Vittedane5.     19.8 M     PR51.27 K, K0270 mM, Na2HP0.4 mM, There3.00.1 %	
A6     EV. Vitrodanc-5     87.94     PR51.37 M, K0 270 mM, No24PO 43 mM, CBA3.3 %       Y A7     ZF. Vitrodanc-1     PS1.137 M, K0 270 mM, No24PO 43 mM, CBA5.4 %       Y A8     ZV. Vitrodanc-2     PS1.137 M, K0 270 mM, No24PO 43 mM, CBA5.4 %       Y A8     ZV. Vitrodanc-2     PS1.137 M, K0 270 mM, No24PO 43 mM, Beta-O6 2.7 %       Y A8     ZV. Vitrodanc-2     PS1.137 M, K0 270 mM, No24PO 43 mM, Beta-O6 2.7 %       Y A9     ZV. Vitrodanc-2     PS1.37 M, K0 270 mM, No24PO 43 mM, Beta-O6 2.7 %       Y A9     ZV. Vitrodanc-2     PS1.37 M, K0 270 mM, No24PO 43 mM, Deta-O6 2.7 %       Y A9     ZV. Vitrodanc-2     PS1.37 M, K0 270 mM, No24PO 43 mM, Deta-O6 2.7 %       Y A9     ZV. Vitrodanc-2     PS1.37 M, K0 270 mM, No24PO 43 mM, Deta-O6 2.7 %	A6 <u>K. Vitersbare_5</u> 87.94     PB51.37 M, K02 270 mM, No2HP0 45 mM, CR0.0.3 %       Y A7 <u>K. Vitersbare_7</u> 89.41     PB51.37 M, K02 270 mM, No2HP0 45 mM, CR0.2 %       VA8 <u>K. Vitersbare_8</u> 100     PB51.37 M, K02 270 mM, No2HP0 45 mM, CR0.2 % OL 2 %       VA8 <u>K. Vitersbare_8</u> 100     PB51.37 M, K02 270 mM, No2HP0 45 mM, CR0.2 % OL 2 %       VA9 <u>K. Vitersbare_8</u> 88.03     PB51.37 M, K02 270 mM, No2HP0 45 mM, Deter 20.1 %       VA9 <u>K. Vitersbare_8</u> 88.03     PB51.37 M, K02 270 mM, No2HP0 45 mM, Deter 20.1 %       VA9 <u>K. Vitersbare_10</u> 9.84     PB51.37 M, K02 270 mM, No2HP0 45 mM, Deter 20.1 %	
A 7     PK VitroSusc.7     89.41     PES 1.37 M, KCI 270 mM, Na2HPO 43 mM, GHAPS 4.9 %       V A 8     PK VitroSusc.61     100     PES 1.37 M, KCI 270 mM, Na2HPO 43 mM, GHAPS 4.9 %       V A 9     PK VitroSusc.61     100     PES 1.37 M, KCI 270 mM, Na2HPO 43 mM, GHAPS 4.9 %       V A 9     PK VitroSusc.61     94.80     PES 1.37 M, KCI 270 mM, Na2HPO 43 mM, Tween 200.1 %       V B     PK VitroSusc.61     94.38     PES 1.37 M, KCI 270 mM, Na2HPO 43 mM, DW 1%	A 7     PK: VttroSare.2     89.41     PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, CHAPS 4.9 %       * A8     FK: VttroSare.3     100     PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, Etca VG.2 %       * A9     PK: VttroSare.9     88.03     PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, Tetera VG.1 %       * A9     PK: VttroSare.10     94.38     PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, Tetera VG.1 %       * B1     PK: VttroSare.10     94.38     PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, Tetera VG.1 %	
✓ B1 PK_VitroEase-10 94.38 PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, DM 1 %	✓ B1 PK. VitroEase-10 94.38 PBS 1.37 M, KCI 270 mM, Na2HPO 43 mM, DM 1 %	
E2 PK VitroEase-11 93.37 PBS 1.37 M. KCI 270 mM. Na2HPO 43 mM. FOM 0.7 %	[ < 12 <u>PL'Vondane 11</u> 93.37 PR51.37 M, KCI 279 mM, Na2HPO 43 mM, FOM 57 %	

# Optimize sample preparation for greater biological insight

The bacterial melibiose transporter, or MelB (54 kDa), catalyzes the transport of small saccharides across membranes. However, the conformational mechanism of saccharide transport remains unclear. In this study researchers were able to utilize nanobody (NB, 14 kDa) binding to stabilize the inward-facing conformation of MelB. This provided an opportunity to better characterize the conformational changes associated with sugar binding and release.

Extensive optimization of the sample preparation was performed. The MelB+NB complex has low binding affinity and is stable only in presence of DDM or UDM detergents and maximum complex formation was detected at NB: MelB ratio of 5:1. The OptiMSe Workflow screening of NB and MelB identified multiple proteoforms and the presence of extra proteins (23.5 kDa). High-resolution structure of MelB-NB725 complex has been obtained with Na<sup>\*</sup>.<sup>4</sup>





Selected 2D classes of hybrid complex MelB<sub>st</sub> NB725m, NBFab, and eNB. Grids were prepared with the Thermo Scientific<sup>™</sup> Vitrobot<sup>™</sup> Mark IV System, and cryo-EM single particles were imaged by Thermo Scientific<sup>™</sup> Titan Krios<sup>™</sup> Cryo-TEM with a K3 detector at S2C2. MelB<sub>st</sub> PDB 7L17





#### Mass and intensity of detected species



2D images of MelB<sub>st</sub> NB725m, NBFab, and eNB as well as MelB and Nanobody samples were provided by Prof. Lan Guan, Texas Tech University Health Sciences Center.

Mass spectrometry, and specifically native techniques, have great potential to provide valuable information on sample quality and stoichiometry which can feed into the cryo-EM structure determination pipeline. This may make cryo-EM sample preparation and subsequent structure determination more efficient, as well as provide additional insight through this integrative structural biology approach.

Dr. Stephen Muench, Lecturer in Membrane Proteins, University of Leeds

## Accelerate your structure elucidation with the OptiMSe Sample Screening Workflow



- Simplify sample screening and purity determination of proteins and complexes
- Reduce time to result and increase flexibility with automated acquisition and processing •
- Enable high-throughput sample screening of hundreds of samples per day
- Confidently select the best sample for downstream analysis from a comprehensive set of sample preparations

2. VanAernum Z.L., et al. Nat Protoc. 2020;15(3):1132-1157

1. Olinares PDB, et al. Structure. 2021 Feb 4;29(2):186-195.e6. 3. Thermo Scientific Technical note #001259. Weijing Liu, et al., (2022) Solutions for high-throughput analysis of large biomolecules by native mass spectrometry 4. Lan G et al. A nanobody-trapped novel conformation of a melibiose transporter MelB by cryo-EM single-particle analysis, COMPA, 2022, NYC

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#### Integrative Structural Biology



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Quadrupole-Orbitrap<sup>™</sup> Mass Spectrometer







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