

### Molecular Glue Degraders:

### From Serendipity to Rational Design

4<sup>th</sup> Annual TPD Summit - October 27, 2021

### **Monte Rosa Therapeutics Overview**

Taking molecular glue degraders (MGDs) to new heights

- Next-generation molecular glue-based targeted protein degradation platform developing breakthrough small molecule drugs that selectively degrade therapeutically-relevant proteins
- Targeting the undruggable proteome via AI-based degron prediction & rational design of highly selective MGDs
- DC selection for lead program in 2021 for GSPT1 degrader targeting Myc-driven cancers
- Multiple identified programs targeting high unmet medical needs in oncology and non-oncology indications

Experienced leadership & SAB with deep drug discovery and development expertise and know-how



### **Molecular Glue Degraders (MGDs)**

A powerful and differentiated approach to eradicate disease-causing proteins



Systematic Chemical Reprogramming of E3 Ligases using MGDs

### Cereblon (CRBN), the G-loop Degron and Beyond

A rational approach to unleash the full potential of MGDs



EXPANDING THE DEGRADABLE PROTEOME BY RATIONAL DESIGN

## QuEEN<sup>™</sup> Discovery Platform: A Transformational Approach to MGDs

Building a unique portfolio of precision medicines addressing high unmet medical needs



### **The Degron Encyclopedia**

A rich, differentiated target space across protein domains and diseases



### **Expanding the Target Space by Identifying More Degrons**

Example of degron-containing proteins in different diseases



>85% of degrons have a unique sequence, providing a unique handle to engage MGD chemical matter

### Expanding the Target Space by Identifying More Degrons

Additional structural loops revealed beyond the G-loop degrome



X-loop degrons further expand the list of proteins potentially amenable to a MGD approach

### New Chemical Space: MGD Anatomy and Evolving MGD Library

Increasing novelty and structural diversity to match the target space



>200 unique scaffolds validated with increasing diversity, confirmed binding and structural insights

### **Glueomics™ Toolbox Accelerates Identification of MGDs** *Matching target space to chemical space*



Multiple screening formats enable rapid identification and validation of MGDs for novel degron containing targets

### **Glueomics™ Toolbox Accelerates Exploration of MGD Space**

Exploring target space through chemoproteomics





Chemoproteomics enables rapid target deconvolution and identification of novel degron containing targets

### **Chemoproteomics Accelerates Prediction-to-Validation**

Experimental validation of targets using MS proximity (TurboID) and degradation assays



### **Multiple Protein Domains Contain Degrons**



#### VAV1-directed MGDs Target the SH3 Domain Vav1-SH3 **Rhapsody**<sup>™</sup> domain model CRBN degron **HTRF Dose Response** 15000-**CRBN-DDB1** ratio 10000-EC<sub>50</sub> = 283 nM + VAV1 SH3 Domain HTRF 5000-0.1 0.001 0.01 10 [MGD], µM

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### **Many Kinases Contain Degrons**

An opportunity to selectively degrade tough-to-selectively inhibit proteins



#### **Kinases with degrons**

- Over 170 human kinases have predicted degrons
- Degrons occur in kinase, SH3 and other domains
- Includes multiple kinases with scaffolding functions

#### Degrons provide a unique selectivity handle

- Typically, degrons occur outside conserved regions
- Sequence homology is more diverse than binding pockets, allowing for more selective engagement

Degrome

Uniqueness

### **Many Kinases Contain Degrons**

An opportunity to selectively degrade tough-to-selectively inhibit proteins



% kinase families with a predicted degron

**TURBO-ID** DEGRADATION 1E-013 1E-013 NEK7 1E-012 1E-012 NEK7 1E-011 1E-011 1E-010 1E-010 1E-009 1E-009 1E-008 1E-008 1E-007 1E-007 1E-006 a 1E-006 1E-005 1E-005 1E-004 1E-004 1E-003 1E-003 1E-002 1E-002 1E-001 1E-001 -1.5 -1 0 0.5 1 1.5 2 2.5 3 3.5 4 4.5 -4.5 -4 -3.5 -3 -2.5 -2 -1.5 -1 -0.5 0 0.5 1 1.5 -0.5 Protein fold-change; (log<sub>2</sub>) Protein fold-change; (log<sub>2</sub>) **TURBO-ID** DEGRADATION 1E-013 KINASE A  $\circ$ 

a

> 30 Kinases identified from Turbo-ID





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### **Many Kinases Contain Degrons**

An opportunity to selectively degrade tough-to-selectively inhibit proteins



### Degron sequence is diverse amongst CDK family members



% kinase families with a predicted degron

### **CDK2-Directed MGDs are Selective over other CDKs**

MGDs identified through biochemical screens induce cellular proximity with CRBN



### **Rationally Designed CDK2-Directed MGDs are Selective Degraders**

Demonstration of selective CDK2 degradation with MGD treated cells



### **Monte Rosa Pipeline**

### Rapidly advancing wholly owned MGD programs







# Thank You