# Initial Clinical Characterization of Novel Proximal Biomarkers for NX-1607, a First-in-Class Oral **CBL-B** Inhibitor, in Patients with Advanced Malignancies

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### NX-1607: Proposed mechanism of action

 CBL-B E3 ligase is a master orchestrator of the immune response: – CBL-B knockout mice show robust T and NK APC cell mediated anti-tumor immunity Our CBL-B inhibitor NX-1607 demonstrates an exciting profile: Enhanced IL-2 and IFN-γ secretion in T cells Signal 1 2. Enhanced T cell function and T cell memory generation . Enhanced NK and dendritic cell function 4. Single agent and combination activity in CBL-B multiple tumor models **NX-1607** is an oral, potent, reversible, and specific small-molecule inhibitor of CBL-B



# Methods

### **Biomarker identification and validation**

- Agnostic screening campaigns were performed to identify multiple proprietary proximal biomarkers of CBL-B inhibition in activated T cells.
- Validation of these biomarkers in non-human primate (NHP) and mouse in vivo models, coupled with allometric scaling of PK profiles, were used to identify the predicted therapeutic range of NX-1607 and inform clinical dose selection.
- Dose projection modeling using non-clinical data was used to determine a minimal anticipated biological effect level (MABEL) predictive of activating proximal biomarkers following oral (PO) administration of NX-1607.

### First-in-human trial: NX-1607-101

- NX-1607-101 is a first-in-human Phase 1 trial evaluating NX-1607 in patients with relapsed or refractory cancers (Figure 1).
- During dose escalation, NX-1607 is given orally once daily at 4 ascending dose levels (5, 15, 25 and 50 mg) using an accelerated modified Fibonacci design that transitions to a standard 3 + 3 design based on protocol-specific criteria.
- Efficacy, safety, PK and PD data are currently being evaluated.

### Figure 1. NX-1607-101: Phase 1 first-in-human clinical trial design

Two-part phase 1 monotherapy trial of NX-1607 in relapsed or refractory tumors



# Results



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### **Biomarker identification and validation**

• Phosphorylated hematopoietic lineage cell-specific protein 1 (pHS1), phospholipase C gamma 2 (pPLCy2), and zeta chain of T cell receptor-associated protein kinase 70 (pZAP70), regulators of T-cell receptor (TCR) signaling, were identified as biologically relevant proximal biomarkers for monitoring pharmacologic inhibition of CBL-B in whole blood (**Figure 2**).

Validation of proximal biomarkers in vivo demonstrated target engagement with dose-dependent increases of phosphorylated biomarkers in CD8+ T cells in both NHP (Figure 3) and mice dosed orally with NX-1607 (**Figure 4**):

– Dose-dependent increases of CBL-B proximal biomarkers observed in NHP dosed orally with NX-1607.

- In vivo efficacy observed with NX-1607 at doses of 10 to 60 mg/kg in mice corresponded to >20% pHS1+/CD8+ T cells, and is consistent with dose-projection model.

Dose-responsive biomarker activity was evident with NX-1607 in human whole blood (Figure 5A). A human dose-projection model suggests that minimum anticipated biological effective level (MABEL) of NX-1607 will be reached starting at 5 mg once daily (i.e. dose level 1 in NX-1607-101) (Figure 5B).

Figure 2. Overview of UbiScan<sup>®</sup> technology, identification of direct CBL-B substrates within the TCR signaling cascade and proximal biomarkers of **CBL** inhibition (Phospho-Screen)

- Anti-di-glycine (K-ε-GG) antibody measures remnants left on ubiguitinated lysine residues after trypsin digestion Decreased signal represents direct
- substrates ubiquitinated by CBL-B ligase activity
- Inhibiting CBL-B decreases ubiquitination of important TCR signaling molecules

To analyze the CBL-B ubiquitinome, we applied UbiScan, a technique that uses a ubiquitin remnant motif (K-ε-GG) antibody-bead conjugate to isolate ubiquitinated peptides. Digestion of proteins with trypsin during mass spectrometry sample preparation cleaves ubiquitin at the C-terminus, leaving a Gly-Gly residue (K-ε-GG) that is still attached to a lysine on the target protein, thus providing evidence of a ubiquitinated protein. T cells were incubated with 10uM CBL-B inhibitors and stimulated with anti-CD3. Direct substrates ubiquinated by CBL-B ligase activity upon stimulation were decreased.



116 Phospho-antibodies from distinct signaling pathways —

Upon CBL-B inhibition, stimulation of FCR results in a substantial increase n phosphorylation of

- A substrate for LYN and essential actin-regulatory adaptor protein at the immune synapse, via VAV1
- pZAP70 Key organizer of downstream TCR signaling.
- pPLCy2 Expressed in both B and T cells Associates with LAT and SLP-76 and becomes phosphorylated upon TCR stimulation<sup>2</sup>



- First-in-human trial
- (5, 15, 25 and 50 mg once daily):

As of June 16, 2022, 10 patients have enrolled at 4 ascending oral dose levels of NX-1607

– Preliminary PK data suggest a half-life of 4 to 10 hours and dose-proportional exposures (Figure 6). – Dose-proportional increases of pHS1-expressing T cells were observed in Cycle 1 (Figure 7A). - Together these data are consistent with preclinical human dose projections and are similar to pHS1 levels associated with anti-tumor activity in mouse models (Figure 7B).

### Figure 5. Dose-response biomarker activity in human whole blood and human dose projection model based on PK/PD/efficacy and allometric scaling





### Figure 6. NX-1607-101: Interim PK results suggest linear PK (Cycle 1 Day 1)



### Figure 7. NX-1607-101: Interim PD results show dose-proportionate increases of proximal biomarker pHS1, which correspond with levels associated with potent anti-tumor activity in mouse models



- Patient cohorts dosed with NX-1607 once daily: 5, 15, 25 and 50 mg. • Blood sampled for exposure and PD longitudinally:
- Cycle 1 day 1: pre, 0.5h, 2h, 4h, 24h trough.

Figure 7A: Pharmacodynamic profiles on Cycle 1 Day 1 in patients treated with 5 to 50 mc of NX-1607 once daily. Whole blood was collected into 2 types of TruCulture tubes (Tubes containing no stimulant, "Null" for aliquot 1; and tubes containing anti-CD3/CD28, "CD3/ CD28" for aliquot 2) at each indicated timepoints pre- and post-dosing on scheduled visits (excluding end of treatment) in cycle 1. Percentage phosphorylated HS1 upon stimulation was quantitated in T cells (CD45+/CD8+) using flow cytometry. Graphs represent the mear SEM) percentage phosphorylated HS1 at each time point. Maximal change in phosphorylated HS1+ CD8+ T cells observed was graphed per dose treatment group. Baseline signal observed at approximately 20%. Graphs represent the mean (± SEM) percentage phosphorylated HS1 at each dose level.

# 777

	B					
	Proposed dose level <sup>a</sup>	NX-1607 dose (mg)	Estimated % HS1+/CD8+ T cells			
Minimum bated biological effect level (MABEL)	-1	2.5	22.2			
	<b>1</b> <sup>b</sup>	5	30.0			
	2	15	49.7			
	3	25	60.6			
	4	50	74.0			
		1007 101				

<sup>a</sup>Dose levels in NX-1607-101. <sup>b</sup>Minimum anticipated biological effect level (MABEL)

Figure 5A: Whole blood from six human donors collected in sodium heparin anti-coagulant was treated with increasing concentrations of NX-1607 for 2 hrs at 37°C Treated blood was incubated with 0.2 ug/mL anti-CD3 & 0.3ug/mL anti-CD28 for 5 mins and subsequently stimulated with crosslinker for 60 minutes. Percentage phosphorvlated HS1 was quantitated in T cells (CD8+) using flow cytometry. Graph represents the mean (± SEM) percentage phosphorylated HS1 at each concentration.

Dose	C <sub>max</sub> (ng/mL)	AUC <sub>last</sub> (ng*h/mL)	T <sub>max</sub> (h)	T <sub>1/2</sub> (h)
5 mg (n=1)	4.35	26.2	2.0	7.72
15 mg (n=1)	13.6	86.8	2.0	6.29
25 mg (n=6)	30.1 (109)	201 (37.9)	1.5 (1.0–3.0)	6.82 (27.5)
50 mg (n=2)	79.2 (134)	502 (113)	2.5 (2.0–3.0)	5.88 (7.7)

 $C_{max}$ , AUC<sub>last</sub> are presented as geometric mean (geometric %CV);  $T_{max}$  is presented as median (range);  $T_{1/2}$  is presented as mean (%CV).

Figure 7B: Percentage phosphorylated HS1 upon stimulation was quantitated in T cells (CD45+/CD8+) using flow cytometry. Graphs represent the mean (± SEM) percentage phosphorylated HS1 at each time point. Maximal change in phosphorylated HS1+ CD8+ T cells observed was graphed per dose treatment group. Baseline signal observed at approximately 20% Graphs represent the mean (± SEM) percentage phosphorylated HS1 at each dose level.

# Conclusions

- NX-1607 is a potent, reversible, and selective CBL-B inhibitor optimized for *in vivo* T cell activation.
- Multiple proprietary proximal biomarkers of CBL-B inhibition were identified in activated T cells.
- Validation of biomarkers in NHP and mouse in vivo models dosed orally with NX-1607 demonstrated target engagement with dose-dependent increases of phosphorylated biomarkers in CD8+ T cells.
- Phosphorylated HS1, a regulator of TCR signaling, was identified as the most robust and reproducible biologically relevant proximal biomarker for monitoring pharmacologic inhibition of CBL-B in whole blood.
- Percentage pHS1 coupled with allometric scaling of PK profiles were used to inform clinical dose selection and to characterize the activity of NX-1607 in a first-in-human clinical trial (NCT05107674):
- 10 patients have enrolled on study as of the data cut-off date (16 June 2022) and received NX-1607 at 4 ascending oral dose levels (5, 15, 25 and 50 mg once daily).
- Dose-dependent increases of pHS1-expressing T cells were observed in Cycle 1.
- Preliminary PK data suggest dose-proportional exposures.
- PK and PD data from non-clinical and clinical studies of NX-1607 have shown remarkable concordance. and biomarker levels observed in the clinic correspond with levels associated with potent antitumor activity in mouse models, suggesting that doses of NX-1607 being tested in the first-in-human trial are within target therapeutic range.

## References

1. Rountree R, et al. Cancer Res 2021;81(13 Suppl): Poster #1595. **2.** Fu G, et al. J Immunol 2012;189:2326–32.

### Glossary

AUC<sub>last</sub>, area under the time-concentration curve to last measurable concentration: CBL-B. Casitas B-lineage lymphoma proto ncogene B: CBL-Bi, CBL-B inhibition: CD8, cluster of differentiation maximum plasma concentration: LAT. linker for activated T cells: LOQ. lower limit of quantification: MABEL. minimum anticipate biological effective level: PBMCs, peripheral blood mononuclear cell PD, pharmacodynamics; PK, pharmacokinetics; NHP, non-human primate; pHS1, phosphorylated hematopoietic lineage cell-specific protein 1; pPLCγ2, phosphorylated phospholipase C gamma 2; pZAP70. phosphorylated zeta chain of T cell receptor-associated protein kinase 70 SLP76, SH2-domain-containing leukocyte protein (76 kDa); T<sub>1/</sub>, elimination half-life; TCR, T-cell receptor; T<sub>max</sub>, time to C<sub>max</sub>.

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### Other NX-1607 posters presented at SITC 2022

10 November 2022

#331 Gallotta M. et al. A novel small molecule inhibitor of CBL-B shows potent antitumor activity in combination with Pmel-1 adoptive cell transfer in an aggressive mouse melanoma model

### **11 November 2022**

#824 Gallotta M. et al. NX-1607: a small molecule inhibitor of the CBL-B E3 ubiguitin ligase, promotes T and NK cell activation and enhances NKmediated ADCC in a mouse lymphoma tumor model



