BLU-222, an investigational, potent, and selective CDK2 inhibitor, demonstrated robust antitumor activity in *CCNE1*-amplified ovarian cancer models

Poster Number 2306

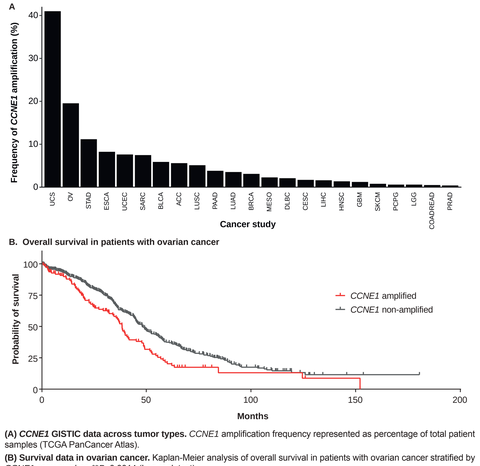
Victoria Brown,[1] Phil Ramsden,[1] Nealia House,[1] Richard Vargas,[1] Jian Guo,[1] Ruduan Wang,[1] Riadh Lobbari,[1] Maxine Chen,[1] Douglas Wilson,[1] Joseph Kim,[1] Neil Bifulco,[1] Michelle Maynard,[1] Emanuele Perola,[1] Dean Zhang,[1] Steve Wenglowsky,[1] Yoon Jong Choi[1]

[1]Blueprint Medicines Corporation, Cambridge, MA, USA

Background

- A broad range of aggressive cancers harbor cyclin E1 (*CCNE1*) gene amplifications[1] (**Figure 1A**)
- *CCNE1* amplification has been associated with poor survival in ovarian cancer, representing an unmet medical need[2,3] (**Figure 1B**)
- Cyclin E1 is the canonical binding partner of cyclin-dependent kinase 2 (CDK2) and the cyclin E1-CDK2 complex drives G1/S progression of the cell cycle[4] (**Figure 2**)
- CDKs are a class of enzymes that, along with their regulatory cyclin binding partners, drive cell cycle progression[4]
- Cell lines harboring *CCNE1* amplification are sensitive to CDK2 knockout or catalytic inhibition with ATP-competitive molecules, suggesting CDK2 may be an attractive therapeutic target for *CCNE1*-amplified cancers[5,6]
- Selectively inhibiting CDK2 for *CCNE1*-amplified tumors may limit off-target CDK-driven toxicities
- BLU-222 is an orally available, selective investigational CDK2 inhibitor[6]
  - The US Food and Drug Administration cleared the investigational new drug application and a phase 1/2 trial (VELA; NCT05252416) of BLU-222 in patients with *CCNE1*-amplified tumors is now enrolling[7]
- We present preclinical validation studies leading to the development of BLU-222 for the treatment of patients with ovarian cancer harboring a *CCNE1* amplification

Figure 1: *CCNE1* amplification is prevalent across various tumor types and correlates with poor overall survival in patients with ovarian cancer[1–3]

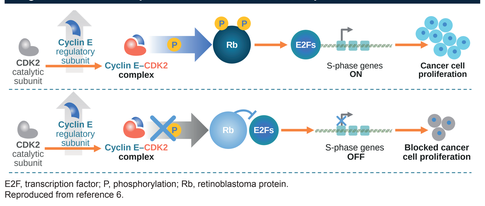


(A) *CCNE1* GISTIC data across tumor types. *CCNE1* amplification frequency represented as percentage of total patient samples (TCGA PanCancer Atlas).

(B) Survival data in ovarian cancer. Kaplan-Meier analysis of overall survival in patients with ovarian cancer stratified by *CCNE1* copy number. ***P*=0.0014 (Log rank test).

ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma; COADREAD, colorectal adenocarcinoma; DLBC, diffuse large B-cell lymphoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; GISTIC, Genomic Identification of Significant Targets in Cancer; LGG, brain lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; HNSC, head and neck squamous cell carcinoma; OV, ovarian serous cystadenocarcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; UCEC, uterine corpus endometrial carcinoma; UCS, uterine carcinoma.

Figure 2: *CCNE1* amplification drives cancer cell proliferation[4]



E2F, transcription factor; P, phosphorylation; Rb, retinoblastoma protein.
Reproduced from reference 6.

Methods

- BLU-222 selectivity was measured by enzyme assays and cellular target engagement assays (NanoBRET)
- Data from Project Achilles[5] and proliferation assays from a panel of cancer cell lines were used to determine CDK2 sensitivity based on *CCNE1* copy number
- *In vitro* cellular potency was assessed by phospho-Rb levels
- Mechanism of action was determined using CRISPR-Cas9 generated Rb knockout cells
- *In vivo* antitumor activity of BLU-222 as a single agent or in combination with standard of care (SOC) agents was measured in the OVCAR-3 cell line-derived xenograft (CDX) tumor model harboring a *CCNE1* amplification

Results

Table 1: BLU-222 is a selective and potent CDK2 inhibitor

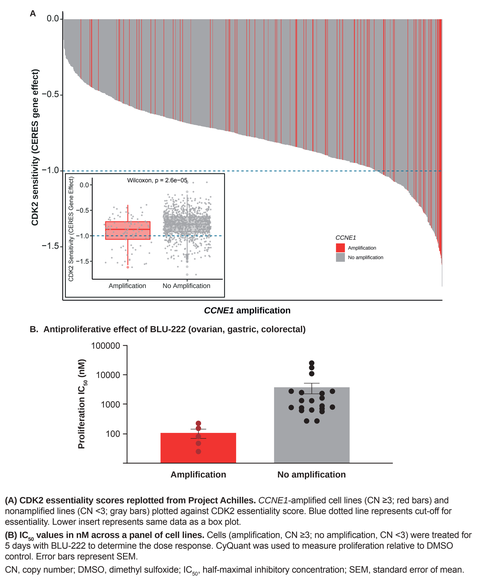
Kinome S (10)[a]	Enzyme activity IC_{50} (nM)[b]						Cellular activity IC_{50} (nM)[d]	
	CDK2	CDK1	CDK4	CDK6	CDK7	CDK9	pRb T821 (CDK2 cell)	pLamin S22 (CDK1 cell)
0.045	2.6	233.6	377.4	275.2	6941.2	6115.1	4.2	380.2

NanoBRET activity IC_{50} (nM)[c]					
CDK2	CDK1	CDK4	CDK6	CDK7	CDK9
17.7	452.3	5104.6	2621.7	6330.4	2697.7

[a]Kinome S(10): fraction of kinases with <10 percentage of control at 3 uM among all the kinases tested, measured by KINOME scan platform against 468 kinases. [b]Enzyme activities IC_{50} were measured at 1 mM ATP using canonical CDK/Cyclin pairs: CDK2/Cyclin E1; CDK1/Cyclin B1; CDK4/Cyclin D1; CDK6/Cyclin D3; CDK7/Cyclin H1/MNAT1; CDK9/Cyclin T1. [c]HEK-293T cells were transfected with canonical CDK/cyclin pairs as in the enzyme assay and treated with compound and a tracer for 2 hours before measurements were taken. [d]pRb T821 protein was assessed in synchronized OVCAR-3 cells to reflect CDK2 cellular potency; pLamin S22 was assessed in asynchronous OVCAR-3 cells to reflect CDK1 cellular potency.
ATP, adenosine triphosphate; IC_{50}, half-maximal inhibitory concentration; pRB, phosphorylated retinoblastoma protein.

- BLU-222 exhibits single-digit nanomolar cellular potency and is selective for CDK2 over other CDK family members

Figure 3: *CCNE1* copy number predicted sensitivity to CDK2 inhibition

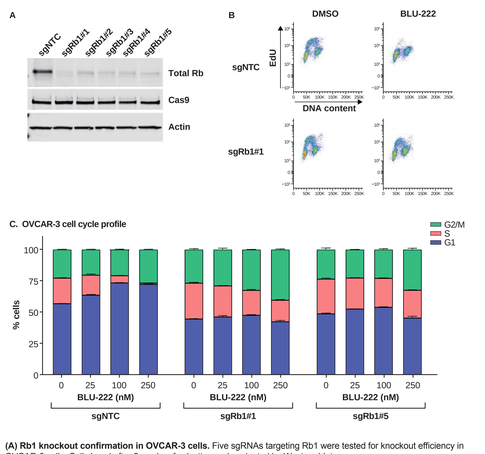


(A) CDK2 essentiality scores replotted from Project Achilles. *CCNE1*-amplified cell lines (CN ≥3; red bars) and nonamplified lines (CN <3; gray bars) plotted against CDK2 essentiality score. Blue dotted line represents cut-off for essentiality. Lower insert represents same data as a box plot.

(B) IC_{50} values in nM across a panel of cell lines. Cells (amplification, CN ≥3; no amplification, CN <3) were treated for 5 days with BLU-222 to determine the dose response. CyQuant was used to measure proliferation relative to DMSO control. Error bars represent SEM.

CN, copy number; DMSO, dimethyl sulfoxide; IC_{50}, half-maximal inhibitory concentration; SEM, standard error of mean.

Figure 4: Treatment with BLU-222 arrested cells at G1/S in an Rb-dependent manner



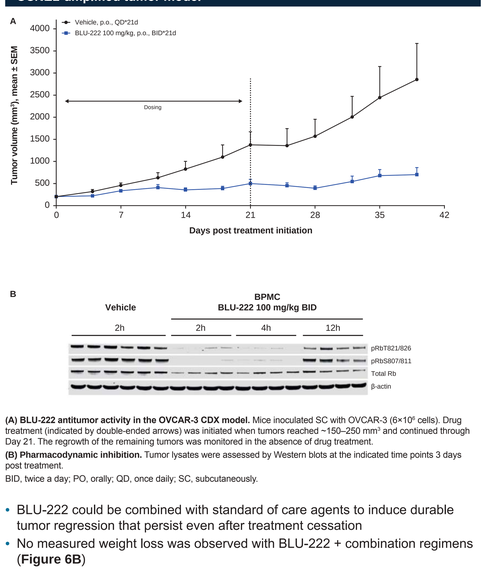
(A) Rb1 knockout confirmation in OVCAR-3 cells. Five sgRNAs targeting Rb1 were tested for knockout efficiency in OVCAR-3 cells. Cells lysed after 2 weeks of selection and evaluated by Western blot.

(B) Representative flow cytometry plots of OVCAR-3 after treatment. OVCAR-3 sgNTC and sgRb1#1 cells were treated with DMSO or BLU-222 (250 nM) for 24 hours. DNA content was measured by FxCycle (X-axis) and S-phase cells were measured by EdU incorporation (Y-axis).

(C) Cell cycle profile of OVCAR-3 cells. OVCAR-3 sgNTC, sgRb1#1, and sgRb1#5 were treated with a dose titration of BLU-222 for 24 hours and the cell cycle profile was determined by FxCycle and EdU incorporation. Error bars represent SEM in two independent experiments.

EdU, 5-ethynyl-2′-deoxyuridine; sgNTC, single-guide RNA against nontargeting control; sgRb, single-guide RNA against Rb.

Figure 5: BLU-222 showed single-agent antitumor activity *in vivo* in a *CCNE1*-amplified tumor model



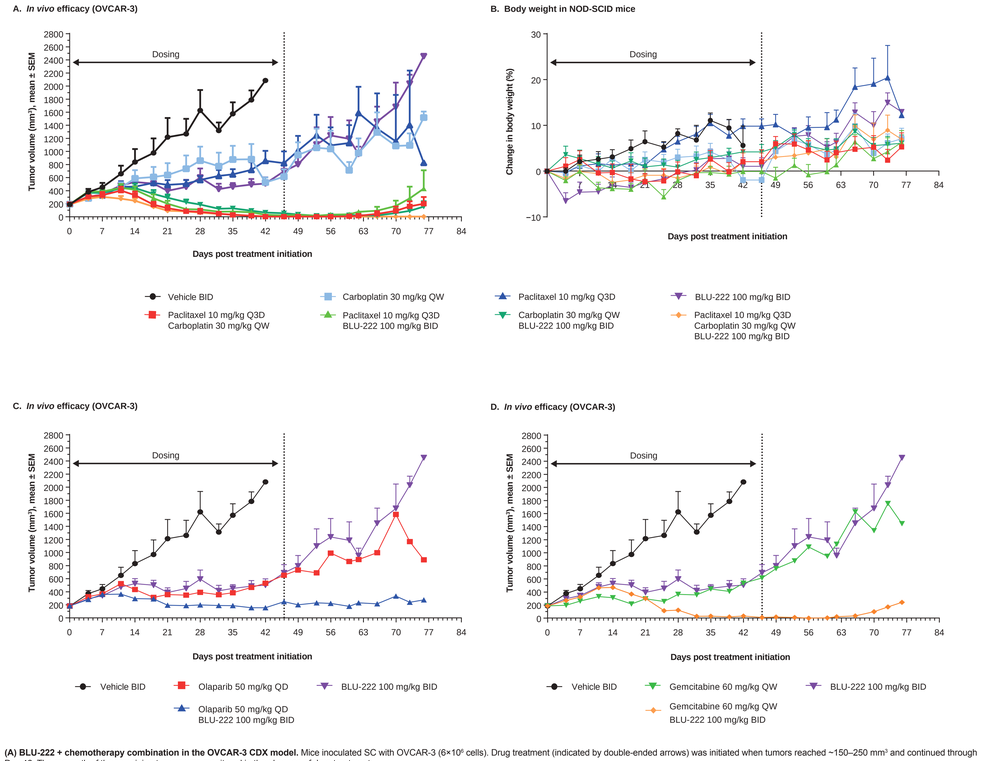
(A) BLU-222 antitumor activity in the OVCAR-3 CDX model. Mice inoculated SC with OVCAR-3 (6×10[6] cells). Drug treatment (indicated by double-ended arrows) was initiated when tumors reached ~150–250 mm^3 and continued through Day 21. The regrowth of the remaining tumors was monitored in the absence of drug treatment.

(B) Pharmacodynamic inhibition. Tumor lysates were assessed by Western blots at the indicated time points 3 days post treatment.

BID, twice a day; PO, orally; QD, once daily; SC, subcutaneously.

- BLU-222 could be combined with standard of care agents to induce durable tumor regression that persist even after treatment cessation
- No measured weight loss was observed with BLU-222 + combination regimens (**Figure 6B**)

Figure 6. Combination treatments with BLU-222 and standard of care therapies induced tumor regression



(A) BLU-222 + chemotherapy combination in the OVCAR-3 CDX model. Mice inoculated SC with OVCAR-3 (6×10[6] cells). Drug treatment (indicated by double-ended arrows) was initiated when tumors reached ~150–250 mm^3 and continued through Day 46. The regrowth of the remaining tumors was monitored in the absence of drug treatment.

(B) Body weight measurement in mice treated with BLU-222 + chemotherapy. Mice were monitored over the course of the study and body weight measurements were taken twice weekly.

(C) BLU-222 + olaparib and (D) BLU-222 + gemcitabine combinations in the OVCAR-3 CDX model. Mice inoculated SC with OVCAR-3 (6×10[6] cells). Drug treatment (indicated by double-ended arrows) was initiated when tumors reached ~150–250 mm^3 and continued through Day 46. The regrowth of the remaining tumors was monitored in the absence of drug treatment.

Q3D, every 3 days; QW, once weekly.

Conclusions and future directions

- *CCNE1* copy number increase was a strong predictor of response to CDK2 inhibition across tumor types in cellular systems
- BLU-222 is a selective and potent CDK2 inhibitor that arrested cells at the G1/S boundary in an Rb-dependent manner
- BLU-222 as monotherapy showed antitumor activity in a *CCNE1*-amplified CDX tumor model
- The combinations of BLU-222 with carboplatin (SOC first-line treatment), BLU-222 with olaparib, and BLU-222 with gemcitabine all induced tumor regression that was sustained even after treatment cessation
- Taken together, this evidence provides scientific rationale for the clinical development of BLU-222 as a monotherapy and in combination with SOC agents in *CCNE1*-amplified cancers

References

1. National Cancer Institute. The Cancer Genome Atlas program. https://www.cancer.gov/tcga. Accessed January 7, 2022.
2. Cerami E et al. *Cancer Discov*. 2012;2(5):401–404.
3. Gao J et al. *Sci Signal*. 2013;6(269):pl1.
4. Malumbres M et al. *Genome Biol*. 2014;15:122.
5. Project Achilles. https://depmap.org/portal/achilles/. Accessed May 10, 2021.
6. Choi YJ et al. AACR 2021. Abstract 1279.
7. (VELA) Study of BLU-222 in Advanced Solid Tumors. NCT05252416. https://clinicaltrials.gov/ct2/show/NCT05252416 Accessed March 2, 2022.

Acknowledgements

The *CCNE1* GISTIC data across tumor types shown here are in whole or part based upon data generated by the TCGA Research Network: https://www.cancer.gov/tcga. The authors would like to thank Karen Ho for her support in the flow cytometry assays; Rob Meissner and Jason Brubaker for their support in the chemistry and oversight of BLU-222 development; Rich Woessner for his support in *in vivo* experimental design; Klaus Hoeflich and Marion Dorsch for their contributions in scientific discussions of CDK2 biology and overall strategy for BLU-222. Editorial support was provided by Maelenge Mdegela, MPhil, and Travis Taylor, BA, all of Paragon, Knutsford, UK, supported by Blueprint Medicines Corporation, Cambridge, MA, according to Good Publication Practice guidelines.

Disclosures

All authors, except R Lobbardi, N Bifulco, M Maynard, S Wenglowsky, and YJ Choi, are current employees and shareholders of Blueprint Medicines Corporation. R Lobbardi, N Bifulco, M Maynard, and S Wenglowsky were former employees of Blueprint Medicines Corporation at the time of the study and do not still receive stock or options.

Poster available for download at: