

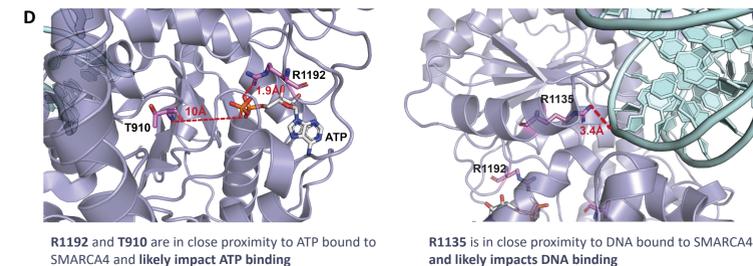
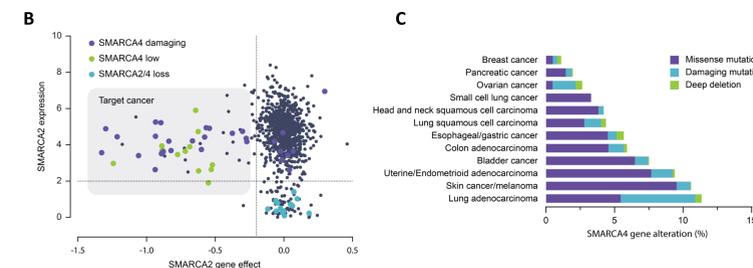
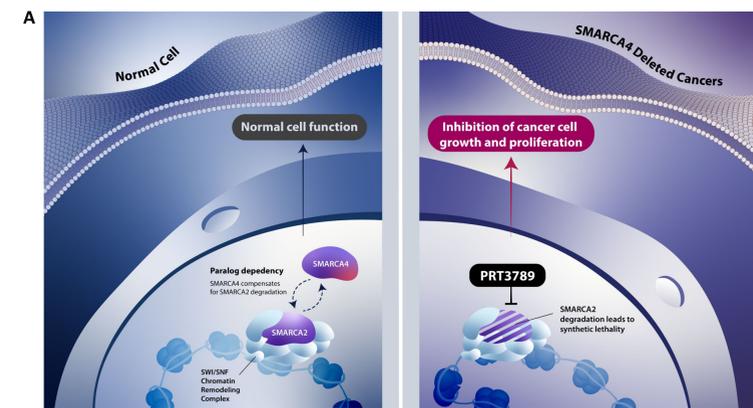
Discovery of PRT3789, a first-in-class potent and selective SMARCA2 degrader in clinical trials for the treatment of patients with SMARCA4 mutated cancers

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Background



(A) SMARCA2 and SMARCA4 are the core catalytic subunits of the SWI/SNF complexes, which play an important role in controlling gene expression by remodeling chromatin. SMARCA4 is mutated in multiple cancers and SMARCA4-deficient cancer cells can become highly dependent on SMARCA2 for their survival. Therefore, targeting SMARCA2 in SMARCA4-deleted cancers using selective SMARCA2 degraders induces synthetic lethality, while sparing SMARCA4 wild-type normal cells; (B) Cell lines with SMARCA4 damaging mutation or low expression show high SMARCA2 gene dependency scores, suggesting the synthetic lethal relationship of targeting SMARCA2 and SMARCA4-deficiency; (C) Percentage of SMARCA4 mutations in different types of cancer. Datasets are from mixed studies (data extracted from cBioPortal in August 2021); (D) In addition to damaging mutation ("loss of SMARCA4 protein"), some tumors express SMARCA4 hotspot missense mutations near its ATP binding site or DNA binding site that likely alters biological function of SMARCA4. The sensitivity of cancer cells expressing such mutations to PRT3789 is under investigation.

Discovery of PRT3789, a Selective SMARCA2 Degradation

Figure 2. Characterization of PRT3789

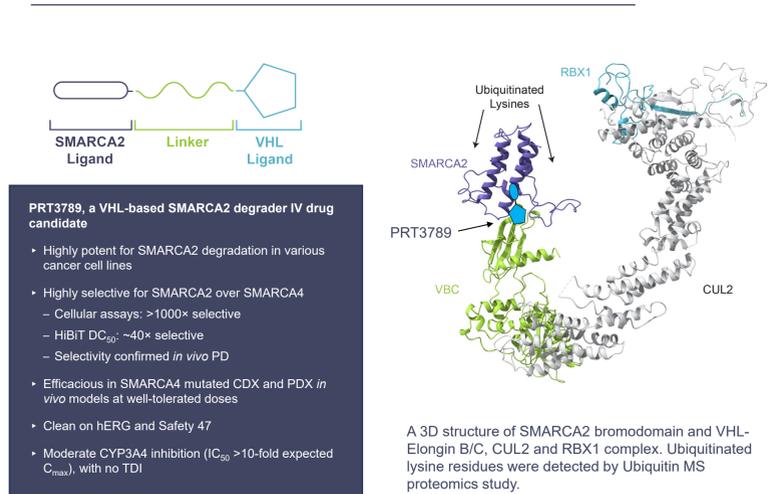
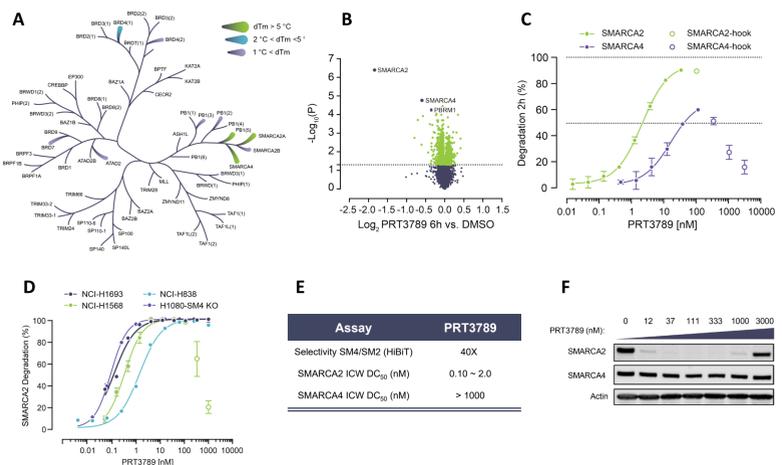


Figure 3. PRT3789 displays excellent SMARCA2 degradation selectivity and potency



(A) DSF shows that PRT3789 is selective for bromodomain subfamily VIII. (B) Global proteomics shows PRT3789 to be highly selective against SMARCA2. (C) SMARCA2 and SMARCA4 HiBIT assays show potent SMARCA2 degradation and selectivity over SMARCA4. (D) SMARCA2 degradation in cancer cell lines analyzed by in-cell Western (ICW). (E) Summary of SMARCA2 degradation selectivity and potency. (F) SMARCA2 and SMARCA4 Western blot with lysates from Calu-6 cells treated with PRT3789.

Figure 4. PRT3789 selectively inhibits growth of SMARCA4 deficient cancer cells in vitro and in vivo

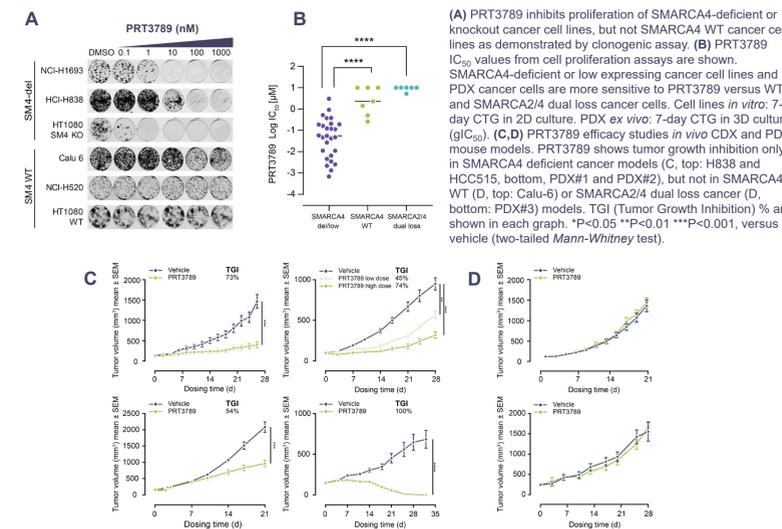


Figure 5. PRT3789 epigenetically regulates gene signatures in SMARCA4 deficient cancer cells, resulting in potential combination strategies

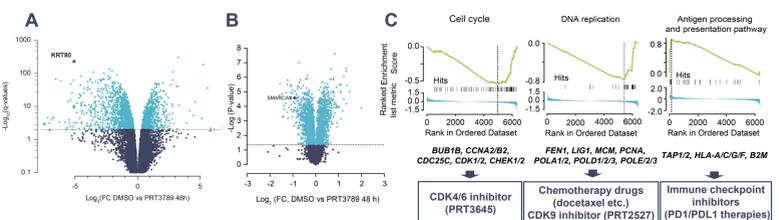
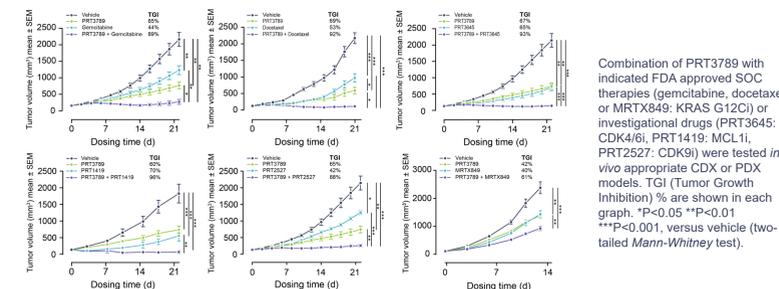


Figure 6. PRT3789 combination effects with FDA approved or investigational drugs



Combination of PRT3789 with indicated FDA approved SOC therapies (gemcitabine, docetaxel or MRTX849: KRAS G12C) or investigational drugs (PRT3645: CDK4/6i, PRT1419: MCL1, PRT2527: CDK9i) were tested in vivo appropriate CDX or PDX models. TGI (Tumor Growth Inhibition) % are shown in each graph. *P<0.05 **P<0.01 ***P<0.001, versus vehicle (two-tailed Mann-Whitney test).

Figure 7. Combination of PRT3789 with pembrolizumab may improve immune response against SMARCA4 deficient cancers

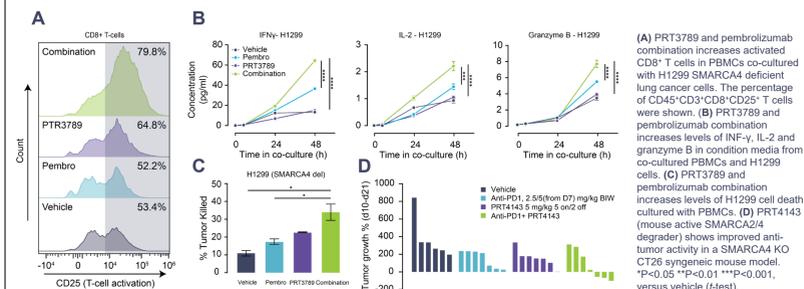
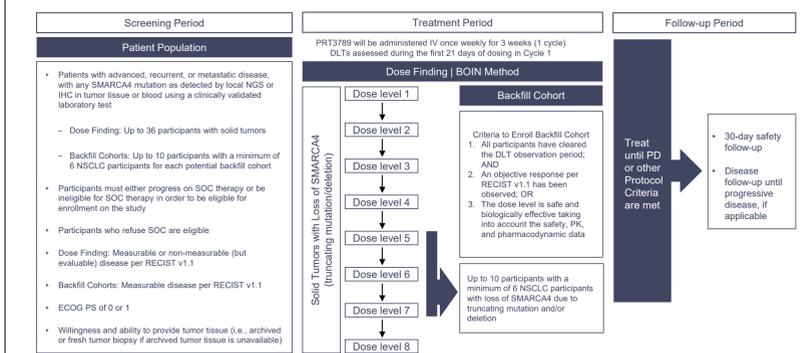


Figure 8. PRT3789-01 Phase 1 Study Design (NCT05639751)



Conclusions

- PRT3789 is a first-in-human potent and selective SMARCA2 degrader
- PRT3789 induces strong synthetic lethality in pre-clinical models of SMARCA4 mutated cancers
- PRT3789 is efficacious in vivo at well-tolerated doses in pre-clinical mouse models
- Evidence-driven potential combination therapies were explored in pre-clinical mouse models
- Currently enrolling patients with SMARCA4 mutated solid tumors in a Phase I dose escalation study in the United States and Europe (NCT05639751)

References:
Hoffman GR et al., Proceedings of the National Academy of Sciences. 2014;111:3128-3133.
Fernando TM et al., Nat Commun. 2020;11:5551.
Tsherniak A et al., Cell. 2017 Jul 27; 170(3): 1130-1143.
Ito K et al., Cancer Res. 2021;81(13): 3451-3461.
Hulse M et al., Can Res. 2022; 82 (12, Supplement): 3263.
Schick S et al., Nat Genet. 2019;51:1399-1410.
Farnaby W et al., Nat Chem Biol. 2019;15:672-680.

Acknowledgments
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Disclosures
1. Authors are or were employees of Prelude Therapeutics, Inc. at the time of research and may own equity in the Company.

