57 FUNCTIONAL BINDING OF PD1 LIGANDS PREDICTS RESPONSE TO ANTI-PD1 TREATMENT IN PATIENTS WITH CANCER

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Background Accurate predictive biomarkers of response to immune checkpoint inhibitors (ICIs) are required for better stratifying patients with cancer to ICI treatments. Here, we present a new concept for a bioassay to predict the response to anti-PD1 therapies, which is based on measuring the binding functionality of PDL1 and PDL2 to their receptor, PD1.[1]
Methods We developed a cell-based reporting system, called the immuno-checkpoint artificial reporter with overexpression of PD1 (IcAR-PD1) and evaluated the functionality of PDL1 and PDL2 binding in tumor cell lines, patient-derived xenografts, and fixed-tissue tumor samples obtained from patients with cancer.
Results In a retrospective clinical study, we found that the functionality of PDL1 and PDL2 predicts response to anti-PD1 and that the functionality of PDL1 binding is a more effective predictor than PDL1 protein expression alone.
Conclusions Our findings suggest that assessing the functionality of ligand binding is superior to staining of protein expression for predicting response to anti-PD1 therapy.
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REFERENCE

1. Bar Kaufman Functional binding of PD1 ligands predicts response to anti-PD1 treatment in patients with cancer. *Sci Adv* 2023:eadg2809. DOI:10.1126/sciadv.adg2809

Ethics Approval The protocol for this study was reviewed and approved by the Soroka Medical Center Institutional Review Board (no. 0156–21-SOR) and the Barzilai Medical Center Institutional Review Board (no. 0048–21-BRZ). s.

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