Chemoproteomics Enabled Discovery of Selective Probes for NuA4 Factor BRD8

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Table S1. Dose response screening of **DN02** using BromoKdELECT (DiscoveRx).

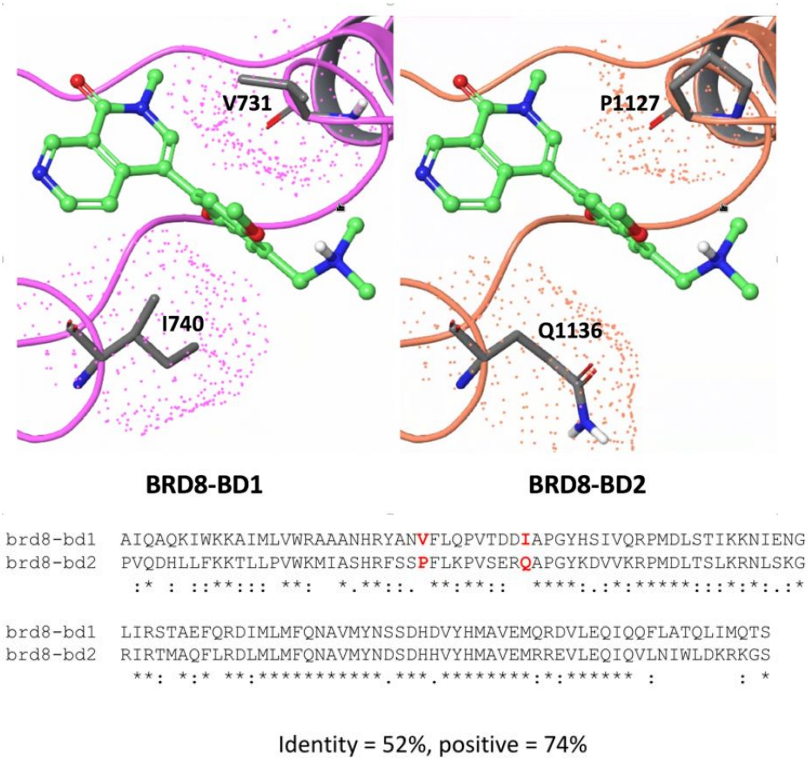
Assay	BRD8(1) (μM)	BRD8(2) (μM)	CBP (μM)	P300 (μM)
BromoKd	0.034	>1.0	>1.0	>1.0

Table S2. Single point screening of **DN02** off targets at 1μM using Bromoscan (DiscoveRx).

Target	DN02
Gene Symbol	% Ctrl (1 μM)
ATAD2A	100
ATAD2B	79
BAZ2A	69
BAZ2B	84
BRD1	89
BRD2(1)	72
BRD2(2)	89
BRD3(1)	76
BRD3(2)	75
BRD4(1)	88
BRD4(2)	94
BRD7	91
BRD9	80
BRDT(1)	88
BRDT(2)	88
BRPF1	65
BRPF3	94
CECR2	74
CREBBP	9.2
EP300	8.4
FALZ	82
GCN5L2	86
PBRM1(2)	85
PBRM1(5)	87
PCAF	69
SMARCA2	74
SMARCA4	71
TAF1(2)	79
TAF1L(2)	91
TRIM24(PHD,Bromo.)	90
Trim33(PHD,Bromo.)	92
WDR9(2)	88

Key:

$0 \leq x < 0.1$	$0.1 \leq x < 1$	$1 \leq x < 10$	$10 \leq x < 35$	$x > 35$

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brd8-bd1  AIQAQKIWKKAIMLVWRAAANHRYANVFLQPVTDDIAPGYHSIVQRPMDLSTIKKNIENG
brd8-bd2  PVQDHLLFKKTLLPVWKMIASHRFSSPFLKPVSERQAPGYKDVVKRPMDLTSLKRNLSKG
           :* : ::**::: **:  *.**::. **:**::  ****:.:*:*****:::*:*:.:*

brd8-bd1  LIRSTAEFQRDIMLMFQNAVMYNSSDHDVYHMAVEMQRDVLEQIQQFLATQLIMQTS
brd8-bd2  RIRTMAQFLRDLMLMFQNAVMYNDSDHHVYHMAVEMRREVLEQIQVLNIWLDKRKGS
           **: *:* **:***********.***.********:*:****** :       : *
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Identity = 52%, positive = 74%

Figure S1. (Top) Comparison of BRD8(1) and BRD8(2) homology model structures with docked ligand (BI-9564). Key proximal residue differences are labeled. (Bottom) BRD8(1) and BRD8(2) sequence alignment.