



# EPIGENEOUS BROMODOMAIN ASSAY: BAZ2B

## TECHNICAL NOTE

**ABSTRACT** Bromodomains (BRDs) are protein interaction modules that specifically recognize epsilon-N-lysine acetylation motifs, a key event in the reading process of epigenetic marks. Bromodomain BAZ2B assay measures the interaction of BAZ2B with [Lys(14)Ac] H3(1-21) peptide and allows interaction inhibitor study.

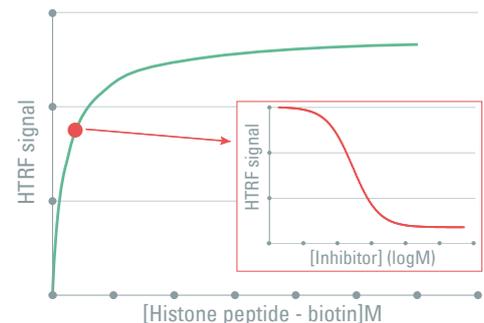
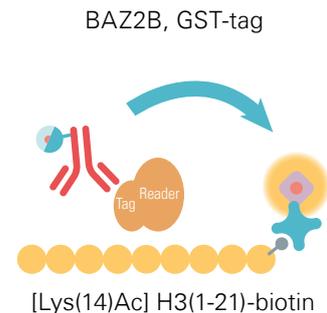
This HTRF assay uses a BAZ2B, GST-tag bromodomain protein, [Lys(14)Ac] H3(1-21) biotinylated peptide, and two HTRF detection reagents: donor cryptate labeled anti GST antibody and red acceptor conjugated streptavidin. HTRF signal is proportional to the amount of BAZ2B, GST-tag / [Lys(14)Ac] H3(1-21)-biotin peptide in interaction.

Bromodomain	BAZ2B, GST-tag [BAZ2B(2041-2168) ; Bromodomain adjacent to zinc finger domain protein 2B ; hWALp4 ; KIAA1476]
Histone peptide	[Lys(14)Ac] H3(1-21)-biotin ARTKQTARKSTGG-K(Ac)-APRKQLA-GGK(Biotin)
Detection reagents	EPIgeneous Binding Domain Kit C

### BAZ2B / HISTONE PEPTIDE INTERACTION ASSAY AND REAGENTS

REAGENT	PROVIDER	REFERENCE
EPIgeneous Binding Domain Kit C	Cisbio Bioassays	# 62BDCPEG
BAZ2B, GST-Tag	EpiCypher	# 15-0042
[Lys(14)Ac] H3(1-21)-biotin	AnaSpec	# 64362

Data shown on this application note has been obtained using Greiner # 784075, 384-well white microplates. For more information on the white plates, please visit [www.cisbio.com/htrf-microplate-recommendations](http://www.cisbio.com/htrf-microplate-recommendations)



## ASSAY PROTOCOL

- Dilute the anti GST-Donor Ab 50-fold with Binding Domain Detection Buffer #2 to obtain the working solution ready to be dispensed.
- The peptide-biotin / streptavidin-acceptor ratio must be equal to 8/1 final in the well (e.g. Peptide-biotin used at 4 nM final in the well, SA-Acceptor must be used at 0.5 nM final in the well). Prepare the SA-Acceptor solution in Binding Domain Detection Buffer #2 to get a 4X working solution depending on the final optimal concentration in the well.

*Prepare working solutions of protein and biotin-peptide in assay buffer just prior to use.*

- We recommend using the GST-tagged binding domain at 5nM final concentration in the well. Prepare the working solution at 5X depending on the final concentration in the well in Binding Domain diluent buffer (here 25 nM).
- Prepare the peptide-biotin at optimal concentration (referenced in table Optimal experimental conditions) in Binding Domain Diluent Buffer to get a 5X working solution depending on the final optimal concentration in the well.
- Prepare supplemented Binding Domain Diluent Buffer with DMSO to get a constant percentage throughout the inhibitor titration. Dilute the compound in this solution to get a 10X working solution depending on final concentration in the well.

*DMSO may act as an inhibitor of GST-binding domain and the biotinylated peptide interaction. This can lead to a decrease of the assay window as DMSO % increases. We recommend the use of compatible DMSO % (See table "Optimal experimental conditions" for DMSO tolerance associated with BAZ2B).*

- Add to a 384-well small volume plate in the following order:
  - 4 µL of BAZ2B, GST-tag (5X)
  - 2 µL of assay buffer (w/ or w/o DMSO)
  - 4 µL of [Lys(14)Ac] H3(1-21)-biotin (5X)
  - 5 µL of SA-Acceptor (4X)
  - 5 µL of anti GST-Donor Ab (4X)
- Cover the plate with a plate sealer and incubate 3h at room temperature.
- *Remark: Signal remains stable after Over Night incubation.*
- Remove plate sealer and read fluorescence emission at 665nm and 620nm wavelengths on an HTRF compatible reader \*.

	PEPTIDE TITRATION		TEST OF INHIBITORS		
	POSITIVE SIGNAL	NEGATIVE CONTROL	INHIBITOR	POSITIVE CONTROL	NEGATIVE CONTROL
<b>BAZ2B, GST-TAG</b>	4 µL	-	4 µL	4 µL	-
<b>INHIBITOR</b>	-	-	2 µL	-	-
<b>BINDING DOMAIN DILUENT BUFFER</b>	2 µL	6 µL	-	2 µL	6 µL
<b>BIOTIN-PEPTIDE</b>	4 µL	4 µL	2 µL	4 µL	4 µL
<b>STREPTAVIDIN-ACCEPTOR</b>	5 µL	5 µL	5 µL	5 µL	5 µL
<b>ANTI GST-DONOR AB</b>	5 µL	5 µL	5 µL	5 µL	5 µL

\* For more information on HTRF compatible reader, please visit [www.cisbio.com/htrf-compatible-readers](http://www.cisbio.com/htrf-compatible-readers).

## OPTIMAL EXPERIMENTAL CONDITIONS

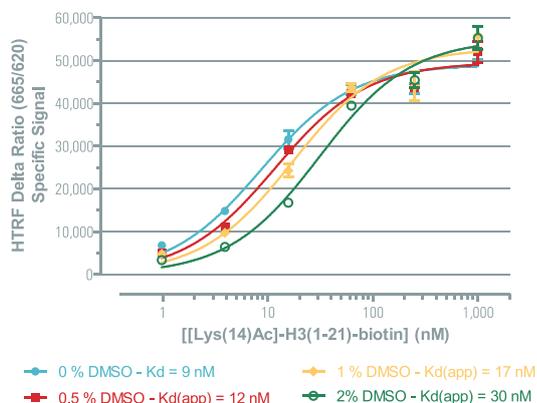
BINDING DOMAIN	RECOMMENDED PEPTIDE CONCENTRATION (FINAL IN THE WELL)	DMSO TOLERANCE
BAZ2B	0 - 1% DMSO: 5 nM - 0 - 2% DMSO: 10 nM	

## DATA REDUCTION

- The TR-FRET signal is treated as HTRF Ratio = Acceptor signal (665nm) / Donor Signal (620nm) x 10<sup>4</sup>
- HTRF Delta Ratio = Ratio (Positive) – Ratio (Negative) where Negative control is performed without reader-protein.
- Assay window = S/B = Ratio (Positive) / Ratio (Negative)

## RESULTS

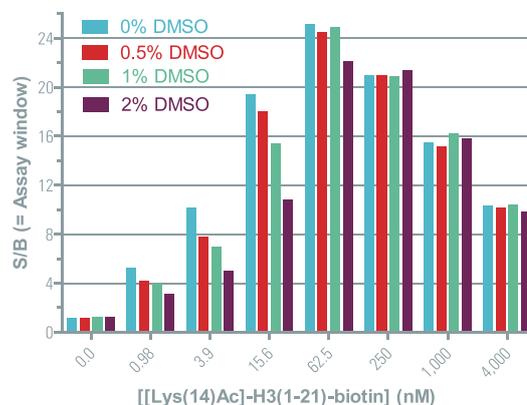
### 1. PEPTIDE-BIOTIN TITRATION



#### Measurement of BAZ2B / histone H3 peptide interaction and DMSO effect

The GST-BAZ2B concentration was fixed at 5 nM while the peptide-biotin was serially diluted. The HTRF Delta Ratio is proportional to the specific interaction measured between GST-BAZ2B and [Lys(14)Ac] H3(1-21)-biotin peptide. The 9nM Kd value is determined from this experiment using a one-site specific binding regression. A shift of apparent Kd is observed while DMSO% increases. This is due to the competitive inhibitor nature of the DMSO on the BAZ2B/H3 peptide interaction.

### 2. DMSO EFFECT ON ASSAY WINDOW



#### Selection of optimal peptide-biotin concentration depending on DMSO % used

Due to the competitive nature of DMSO, the assay window decreases as the DMSO percentage increases. The assay window can then be recovered by increasing the peptide-biotin concentration. The optimal peptide-biotin concentration is selected (between real Kd and EC100 obtained on the titration without DMSO) with a compromise between assay window and assay sensitivity for inhibitor studies. Note that the higher the peptide-biotin concentration, the higher the inhibitor IC50. For further study of inhibitors, 0 to 1% DMSO and 5nM peptide-biotin conditions are recommended.

For more information, please visit us at [www.cisbio.com/epigenetic-binding-domain](http://www.cisbio.com/epigenetic-binding-domain)

## RELATED INFORMATION

Enabling epigenetics studies from HTS to SAR: a novel HTRF® platform to identify and characterize reader domain inhibitors

*Roux T, Badol M, Douayry N, Sergeant L, Trinquet E, Degorce F, Milhas S, Betzi S, Derviaux C, Eydoux C, Letienne J, Lugari A, Collette Y, Guillemot J-C, Morelli X. - Cisbio Bioassays Codolet, France | CRCM, CNRS UMR7258, INSERM U1068, AMU UM105, Institut Paoli-Calmettes, Marseille, France | AFMB, UMR7257, Univ. Aix Marseille-CNRS, Marseille, France*

How do HTRF® epigenetic binding domain assays perform compared to other technologies?

*Thomas Roux, Najim Douayry, Laurent Sergeant, François Degorce and Eric Trinquet. Cisbio Bioassays Codolet, France*

### FOR MORE INFORMATION

Europe and other countries +33(0)466 796 705 U.S. and Canada 1-888-963-4567

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