

# PrimePCR™ Assay Validation Report

## Gene Information

<b>Gene Name</b>	bromodomain PHD finger transcription factor
<b>Gene Symbol</b>	BPTF
<b>Organism</b>	Human
<b>Gene Summary</b>	<p>This gene was identified by the reactivity of its encoded protein to a monoclonal antibody prepared against brain homogenates from patients with Alzheimer's disease. Analysis of the original protein (fetal Alz-50 reactive clone 1 or FAC1) identified as an 810 aa protein containing a DNA-binding domain and a zinc finger motif suggested it might play a role in the regulation of transcription. High levels of FAC1 were detected in fetal brain and in patients with neurodegenerative diseases. The protein encoded by this gene is actually much larger than originally thought and it also contains a C-terminal bromodomain characteristic of proteins that regulate transcription during proliferation. The encoded protein is highly similar to the largest subunit of the Drosophila NURF (nucleosome remodeling factor) complex. In Drosophila the NURF complex which catalyzes nucleosome sliding on DNA and interacts with sequence-specific transcription factors is necessary for the chromatin remodeling required for transcription. Two alternative transcripts encoding different isoforms have been described completely.</p>
<b>Gene Aliases</b>	FAC1, FALZ, NURF301
<b>RefSeq Accession No.</b>	NC_000017.10, NT_010783.15
<b>UniGene ID</b>	Hs.444200
<b>Ensembl Gene ID</b>	ENSG00000171634
<b>Entrez Gene ID</b>	2186

## Assay Information

<b>Unique Assay ID</b>	qHsaCED0046828
<b>Assay Type</b>	SYBR® Green
<b>Detected Coding Transcript(s)</b>	ENST00000278407, ENST00000340687, ENST00000378323, ENST00000378324, ENST00000403558, ENST00000544778, ENST00000306378, ENST00000424123, ENST00000580465, ENST00000342579, ENST00000321892, ENST00000335221, ENST00000573838, ENST00000573834, ENST00000574648, ENST00000579610, ENST00000575874
<b>Amplicon Context Sequence</b>	GCCCCAAGTTGCAGCACAGTCTCAGCCTCAAAGTAATGTCCAAGGACAGTCTCC TGTTTCGTGTCCAAAGTCCATCACAGACTCGAATACGTCCATCAACTCCATCCCAA CTGTCTCCTGGACA
<b>Amplicon Length (bp)</b>	93
<b>Chromosome Location</b>	17:65941790-65941912
<b>Assay Design</b>	Exonic

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## Validation Results

Efficiency (%)	100
R <sup>2</sup>	0.997
cDNA Cq	19.62
cDNA Tm (Celsius)	82
gDNA Cq	24.56
Specificity (%)	100

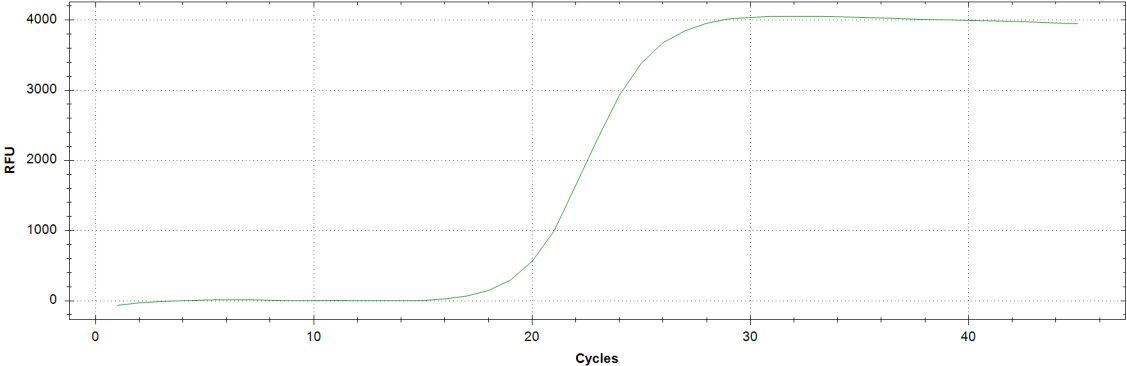
Information to assist with data interpretation is provided at the end of this report.

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BPTF, Human

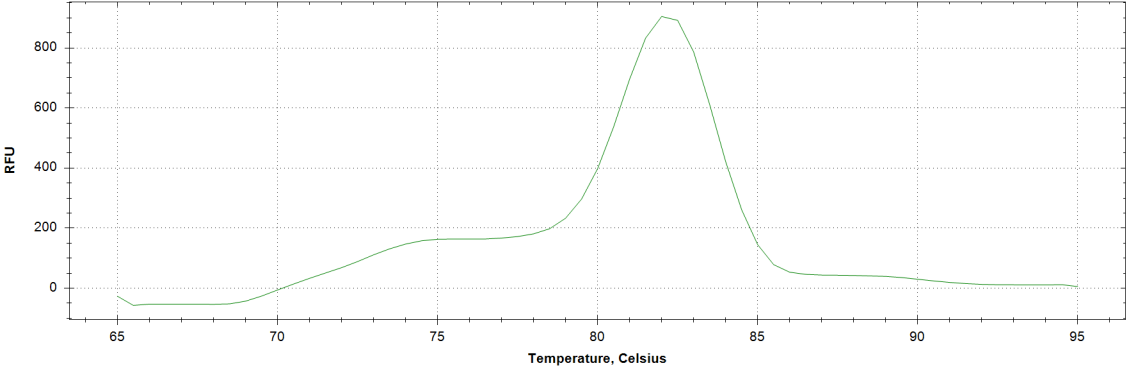
## Amplification Plot

Amplification of cDNA generated from 25 ng of universal reference RNA



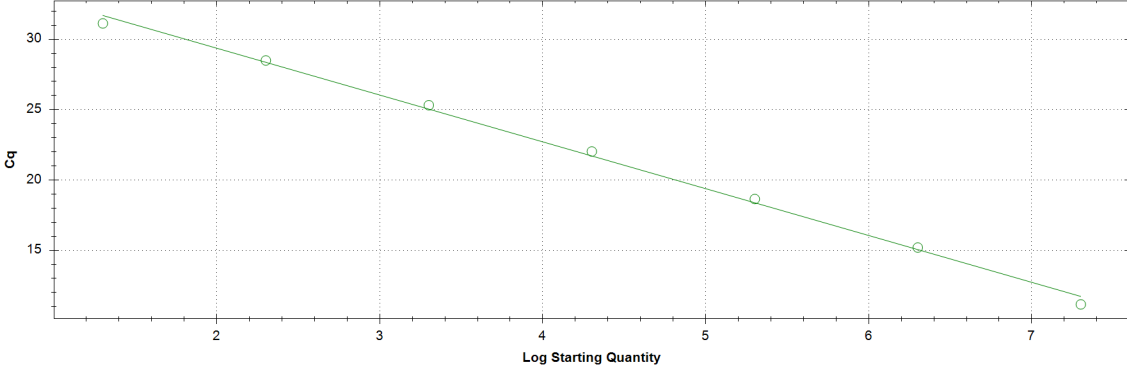
## Melt Peak

Melt curve analysis of above amplification



## Standard Curve

Standard curve generated using 20 million copies of template diluted 10-fold to 20 copies



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## Products used to generate validation data

<b>Real-Time PCR Instrument</b>	CFX384 Real-Time PCR Detection System
<b>Reverse Transcription Reagent</b>	iScript™ Advanced cDNA Synthesis Kit for RT-qPCR
<b>Real-Time PCR Supermix</b>	SsoAdvanced™ SYBR® Green Supermix
<b>Experimental Sample</b>	qPCR Human Reference Total RNA

## Data Interpretation

<b>Unique Assay ID</b>	This is a unique identifier that can be used to identify the assay in the literature and online.
<b>Detected Coding Transcript(s)</b>	This is a list of the Ensembl transcript ID(s) that this assay will detect. Details for each transcript can be found on the Ensembl website at <a href="http://www.ensembl.org">www.ensembl.org</a> .
<b>Amplicon Context Sequence</b>	This is the amplicon sequence with additional base pairs added to the beginning and/or end of the sequence. This is in accordance with the minimum information for the publication of real-time quantitative PCR experiments (MIQE) guidelines. For details, please refer to the following publication, "Primer Sequence Disclosure: A Clarification of the MIQE Guidelines" (Bustin et al 2011).
<b>Chromosome Location</b>	This is the chromosomal location of the amplicon context sequence within the genome.
<b>Assay Design</b>	<p>Exonic: Primers sit within the same exon in the mRNA transcript and can potentially co-amplify genomic DNA. If performing gene expression analysis, it is suggested that the samples be treated with a DNase to eliminate potential unwanted signal from contaminating genomic DNA.</p> <p>Exon-exon junction: One primer sits on an exon-exon junction in mRNA. When performing gene expression analysis, this design approach will prevent unwanted signal from contaminating genomic DNA.</p> <p>Intron-spanning: Primers sit within different exons while spanning a large intron in the mRNA (intron is greater than 750bp). When performing gene expression analysis, this design approach should limit potential unwanted signal from contaminating genomic DNA.</p> <p>Small intron-spanning: Primers sit within different exons with a short intron in between (intron is smaller than 750bp). Small introns may not prevent unwanted signal from contaminating genomic DNA.</p>
<b>Efficiency</b>	Assay efficiency was determined using a seven-point standard curve from 20 copies to 20 million copies. While an efficiency of 100% represents a perfect doubling of template at every cycle and is ideal, typical ranges of good assay efficiency are between 90-110%. For difficult targets, assay efficiency outside of this range are accepted and reported accordingly.
<b>R<sup>2</sup></b>	The R <sup>2</sup> represents the linearity of the standard curve and how well the standard curve data points fit the linear regression line. Acceptable values are >0.98.

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<b>cDNA Cq</b>	<p>Cq value obtained from 25ng of cDNA transcribed from universal RNA when performing wet-lab validation of the assay.</p> <p>Note: Not all genes will be expressed at a detectable level in the universal RNA sample.</p>
<b>cDNA Tm</b>	<p>Melting temperature of the amplicon when running a melt curve analysis.</p>
<b>gDNA Cq</b>	<p>Cq value obtained when running the assay with 2.5ng of genomic DNA. This is more than a moderate level of genomic DNA contamination. Intron-spanning and exon-exon junction assay designs can minimize or eliminate genomic DNA detection.</p> <p>Note: Genomic DNA contamination is often present at variable levels. If concerned about genomic DNA contamination, the genomic DNA contamination control assay is recommended to run with your sample to determine if genomic DNA levels are sufficient to negatively impact results.</p>
<b>Specificity</b>	<p>This value is the percent of specific amplicon reads as measured by next generation sequencing (NGS). While 100% specificity is desirable, small decreases in specificity (&lt;1%) can be due to NGS read errors. More significant reductions are likely due to co-amplification of homologous regions.</p> <p>Note: Since gene expression can be cell type and condition specific, the exact level and impact of co-amplification in a given sample is impossible to predict. If co-amplification is detected, it should be taken into consideration and reported when analyzing gene expression results.</p>