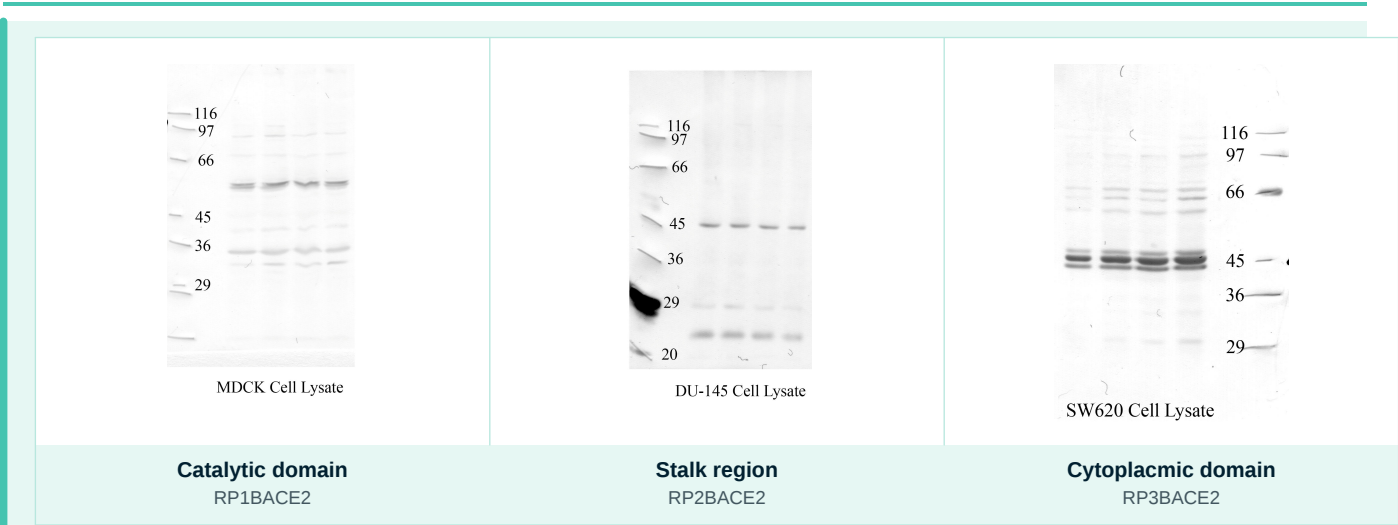


Anti-BACE2 Rabbit Polyclonal Antibody

Beta-secretase 2, EC 3.4.23.45, Aspartic-like protease 56 kDa, Aspartyl protease 1, ASP1, Asp 1, Beta-site amyloid precursor protein cleaving enzyme 2, Beta-site APP cleaving enzyme 2, Down region aspartic protease, DRAP, Memapsin-1, Membrane-associated aspartic protease 1, Theta-secretase,

Gene: BACE2 **UniProt:** Q9Y5Z0 **Host:** Rabbit **Clonality:** Polyclonal (pAb)

Product Image



— Western Blot (3-panel validation across domain-specific antibody clones)

Actual Western blot validation for anti-BACE2 rabbit polyclonal antibody. 3-panel validation across domain-specific antibody clones — each panel labeled with its catalog number and target domain. Reducing conditions; 10–20 µg/lane on 7.5–10% SDS-PAGE.

Key Product Facts

Supplier	Triple Point Biologics, Inc. (Sudbury, Ontario, Canada)
Product Name	Anti-BACE2 Rabbit Polyclonal Antibody
Gene Symbol	BACE2
Alternative Names	Beta-secretase 2, EC 3.4.23.45, Aspartic-like protease 56 kDa, Aspartyl protease 1, ASP1, Asp 1, Beta-site amyloid precursor protein cleaving enzyme 2, Beta-site APP cleaving enzyme 2, Down region aspartic protease, DRAP, Memapsin-1, Membrane-associated aspartic protease 1, Theta-secretase,
UniProt ID	Q9Y5Z0
Host Species	Rabbit
Clonality	Polyclonal (pAb)
Isotype	IgG
Concentration	1mg/ml
Purity	Affinity purified
Pack Size	100ug
Validated Application	WB
Recommended Dilution	WB-1/1000
Species Reactivity	Validated- Human Potential-Mouse, Rat, Pan, Monkey, Dog
Immunogen Type	Synthetic Peptide from Uniprot Sequence
Conjugation	none
Buffer / Preservatives	Sodium Chloride 500 mM, Sodium Phosphate 10 mM, Potassium Phosphate 1.8 mM, Potassium Chloride 2.7 mM, Glycerol 50% (v/v)
Website	triplepointbiologics.com/anti-bace-2-rabbit-polyclonal-antibody

Available Domain-Specific Variants

Triple Point Biologics produces antibodies to defined structural domains of BACE2. Each variant is directed at a specific structural region of the protein. Exact peptide sequences are proprietary; each variant is validated for the applications listed.

Domain / Variant	Epitope Region (approx. residues)	Cat. No.	Availability
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Catalytic domain	92–429 Region spanning the large luminal ectodomain of human BACE2, encompassing both the N-terminal and C-terminal lobes of the bilobed aspartyl-protease fold and the two catalytic DTG/DSG aspartate-bearing loops that constitute the active site cleft; this domain is responsible for substrate recognition and proteolytic activity	RP1BACE2	In catalog
Stalk region	454–473 Region within the membrane-proximal ectodomain stalk of human BACE2, situated between the C-terminal edge of the catalytic ectodomain and the single-pass transmembrane helix; this juxtamembrane segment is thought to position the catalytic domain relative to the membrane surface and contains the primary ectodomain shedding site that releases soluble BACE2 into the extracellular space	RP2BACE2	In catalog
Cytoplasmic domain	495–518 Region corresponding to the short cytoplasmic C-terminal tail of human BACE2, located immediately downstream of the single-pass transmembrane anchor; this segment contains trafficking and retention signals implicated in Golgi/endosomal routing and in regulated recycling of the enzyme through the secretory and endocytic pathways	RP3BACE2	In catalog
—	63–518 Region encompassing multiple structural domains of the full-length human BACE2 ectodomain and transmembrane region, including the catalytic bilobed aspartyl-protease domain, the juxtamembrane stalk, and the transmembrane/cytoplasmic segments; antibodies raised against this broad immunogen are expected to recognize multiple epitopes distributed across the protein's domain architecture	RP-BACE2	In catalog

Applications & Recommended Dilutions

App.	Species	Dilution Range	Notes
WB	Validated-Human Potential-Mouse, Rat, Pan, Monkey, Dog	1:1000	Optimal dilution should be determined per laboratory and lot.

Optimal dilutions should be determined by each laboratory for each application. Triple Point Biologics antibodies include a peptide-neutralized negative control aliquot for specific-signal confirmation.

Storage & Handling

Short-term Storage	+4°C (1–2 weeks)
Long-term Storage	Aliquot and store at -20°C
Shipping Conditions	Shipped in styrofoam cooler on blue ice
Hazard Warning	Product may contain Sodium Azide — POISONOUS AND HAZARDOUS. Handle by trained personnel only.
Shelf Life	12 months from date of receipt under recommended conditions

Target Background

Family & General Biology

BACE2 (Beta-site APP-cleaving enzyme 2; EC 3.4.23.45) is a type I transmembrane aspartic protease belonging to the pepsin family of endopeptidases. It shares approximately 45% amino acid identity with its paralog BACE1 and retains the two canonical DTG/DSG catalytic aspartate motifs characteristic of the family. The mature protein spans 518 amino acids and includes a large luminal ectodomain housing the active site, a single-pass transmembrane anchor, and a short cytoplasmic tail. Unlike BACE1, whose neuronal expression and amyloidogenic role have dominated research attention, BACE2 is recognized as a functionally distinct enzyme with tissue-specific substrates and biological roles.

Expression & Localisation

BACE2 is expressed broadly across human tissues, with particularly high levels detected in the pancreas, kidney, placenta, and intestine. Expression in the brain is comparatively low relative to BACE1, consistent with divergent physiological roles. At the subcellular level, BACE2 localizes principally to the plasma membrane and the trans-Golgi network, with active enzyme oriented toward the extracellular lumen or organelle lumen. In pancreatic beta cells and melanocytes, endogenous BACE2 protein is readily detectable, and the enzyme undergoes regulated trafficking through the secretory pathway. A shed, soluble ectodomain form has also been detected in circulation.

Activation & Zymogen Processing

BACE2 is synthesized as an inactive zymogen bearing a prodomain that occludes the active site cleft. Auto-activation occurs upon acidification in the endosomal/Golgi compartment, or prodomain removal can be facilitated by furin-like proprotein convertases in the secretory pathway. Once the prodomain is cleaved, the mature enzyme adopts an open, bilobed aspartyl-protease fold competent for substrate engagement. Optimal catalytic activity is observed at mildly acidic pH, consistent with its predominant intracellular processing environment. N-glycosylation of the ectodomain contributes to proper folding and trafficking but is not strictly required for catalytic competence.

Key Substrates

BACE2 cleaves amyloid precursor protein (APP) at two sites within the ectodomain: a major site between residues 690–691 (the beta-secretase site) and a second site between residues 671–672. Cleavage releases a soluble APP ectodomain fragment and generates a membrane-tethered C-terminal stub. Premelanosome protein (PMEL/GP100) is cleaved within its M-beta fragment by BACE2, a step required for the regulated amyloid fibril assembly that templates melanosome biogenesis. Collectrin (CLTRN), a regulator of amino acid transport expressed in pancreatic beta cells, is also a validated BACE2 substrate; its ectodomain shedding influences insulin secretion and glucose homeostasis.

Disease Relevance

BACE2 is encoded within the Down syndrome critical region of chromosome 21q22.3, and gene dosage effects arising from trisomy 21 have been proposed to alter BACE2-mediated APP and PMEL processing. In the context of type 2 diabetes, soluble BACE2 levels in plasma are positively correlated with chronic glycemic burden, raising interest in BACE2 as a biomarker of beta cell stress. In melanocytes, aberrant BACE2 activity disrupts melanosome maturation, linking the enzyme to pigmentation disorders. Although BACE2 inhibition has been explored as an adjunct to BACE1-targeted Alzheimer's strategies, selectivity between the two paralogs remains a key challenge in drug development.

Inhibitor Profile

As an aspartic protease, BACE2 is inhibited by classical aspartyl-protease inhibitors including pepstatin A, a broad-spectrum competitive inhibitor that engages the catalytic dyad. Transition-state analogue inhibitors incorporating hydroxyethylamine or statine scaffolds designed for BACE1 frequently cross-inhibit BACE2 given the conserved active site architecture, though potency differences of one to two orders of magnitude are typical. No endogenous protein inhibitor analogous to the TIMP family (relevant to metalloproteinases) has been identified for BACE2. Small-molecule selective BACE2 inhibitors remain an active area of investigation, particularly for metabolic disease indications.

Gene & Protein Reference

Gene Symbol	BACE2
HGNC	HGNC:933
NCBI Gene ID (Human)	25825
NCBI Gene ID (Mouse)	23821
Ensembl	ENSG00000182240
OMIM	605sp605323
UniProt (Human)	Q9Y5Z0
UniProt (Mouse)	Q9WU89
Protein Family	Pepsin family of aspartic endopeptidases (A1 family)
Predicted MW	~56 kDa (mature ectodomain); ~60 kDa full-length
Observed MW	~70–75 kDa (apparent, due to N-glycosylation)
Chromosome	21q22.3
Paralogue	BACE1 (Beta-secretase 1; ~45% amino acid identity)
Key Substrates	APP (amyloid precursor protein), PMEL (premelanosome protein/GP100), CLTRN (collectrin)
Activated by	Acidic pH (endosomal/Golgi); prodomain removal by furin-like proprotein convertases
Inhibited by	Pepstatin A; hydroxyethylamine and statine-based transition-state analogue inhibitors

About Triple Point Biologics

With over 30 years dedicated to antibody production, Triple Point Biologics is a Canadian company and the premier resource for proteinase and proteinase inhibitor research. Products have been cited in thousands of peer-reviewed publications.

The domain-specific antibody strategy — available in standard, ATK, SPA, and GSK kit formats — delivers predefined epitopes, built-in peptide-neutralized negative controls, and superior specificity for Western blot.

Website: www.triplepointbiologics.com

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Product specifications subject to change. Contact Triple Point Biologics for current product and availability information.