UbiQ
targeting the ubiquitin system

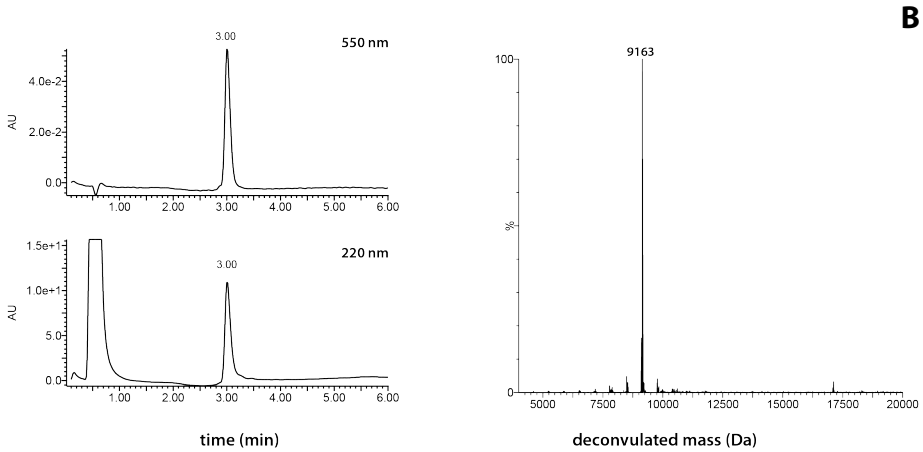
5-TAMRA-Lys(Ub)-Gly-OH *(human sequence, semi-synthetic)*

UbiQ code : UbiQ-012
Batch # : B10102013-001
Amount : bulk, lyophilized powder
Purity : ≥95%
Mol. Weight : 9.16 kDa
Storage : upon arrival, powder at −20°C, solution at −80°C. Protect from light and avoid multiple freeze/thaw cycles.

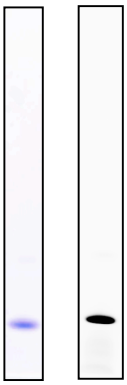
Productsheet

Background. Fluorescence polarization assay reagent which is based on a 5-carboxytetramethylrhodamine (TAMRA) modified Lys-Gly sequence that is linked to ubiquitine via a native isopeptide bond with the lysine side-chain.[1-4] Typical substrate concentrations range from 10–100 nM. DUB concentrations can range from 0.01-10 nM but depend on specific assay conditions and method of detection.

A



B



A: LC-MS analysis. Mobile phase A= 1% CH_3CN, 0.1% formic acid in water (milliQ) and B= 1% water (milliQ) and 0.1% formic acid in CH_3CN. Phenomenex Kinetex C18, (2.1×50 mm), 2.6 µM); flow rate = 0.5 mL/min, runtime = 6 min, column T = 40°C. Gradient: 5%⇨95% B over 3½ min. **B: SDS-PAGE analysis.** 12% Bolt Bis-Tris Plus gel (Life technologies), MES buffer. M= SeeBlue Plus2 Pre-stained Standard (Invitrogen). Left lane= CBB staining, right lane= TAMRA fluorescence scan.

important: sample preparation

- dissolve the powder in DMSO (e.g. 0.92 mg/mL= 100 uM)
- add the DMSO stock to milliQ (please note the order of addition) and mix
- buffer the aq. solution as desired (using 1M HEPES or 1M Tris for example)
- final assay stocks of 100 nM will contain 0.1 vol% DMSO when prepared from a 100 uM DMSO stock, for example.
- all stocks are suitable for storage at −80°C
- full exp. details can be found in open-access reference 5: Geurink et al. *ChemBiochem*, **2012**, *13*, 293.

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General protocol fluorescence polarization assay[5]

FP assays were performed on a PerkinElmer Wallac EnVision 2010 Multilabel Reader with a 531 nm excitation filter and two 579 nm emission filters. Fluorescence intensities were measured in the S (parallel) and P (perpendicular) direction. FP values are given in mP (millipolarization) and calculated using the following formula (1):

$$Polarization\ (mP) = \frac{S\text{-}(G \cdot P)}{S + (G \cdot P)} \cdot 1000 \qquad (1)$$

The confocal optics were adjusted with the average P and S values for TAMRA-Lys-Gly and the grating factor (G) was determined using a polarization value (L) for TAMRA of 50 mP using the following formula (2):

$$G = \frac{average\ S}{average\ P} \cdot \frac{1 - (\frac{L}{1000})}{1 + (\frac{L}{1000})} \qquad (2)$$

The assays were performed in "non-binding surface flat bottom low flange" black 384-well plates (Corning) at room temperature in a buffer containing 20 mM Tris·HCl, pH 7.5, 5 mM DTT, 100 mM NaCl, 1 mg/mL 3-[(3-cholamidopropyl) dimethylammonio] propanesulfonic acid (CHAPS) and 0.5 mg/mL bovine gamma globulin (BGG). Each well had a volume of 20 µL. Buffer and enzyme were predispensed and the reaction was started by the addition of substrate. Kinetic data was collected in intervals of 2.5 or 3 min. From the obtained polarization values (P_t) the amount of processed substrate (S_t) was calculated with to the following formula (3):

$$S_t = S_0\text{-}S_0 \times \left[\frac{P_t\text{-}P_{min}}{P_{max}\text{-}P_{min}}\right] \qquad (3)$$

Where P_t is the polarization measured (in mP); P_{max} is the polarization of 100% unprocessed substrate (determined for every reagent at all used substrate concentrations); P_{min} is the polarization of 100% processed substrate; S_0 is the amount of substrate added to the reaction.

From the obtained P_t values the values for initial velocities (v_i) were calculated. The v_i values are used to determine the Michaelis-Menten constants (K_m, V_{max} and k_{cat}) by fitting the data according to formula (4) (where $k_{cat} = V_{max}/[E]$). All experimental data was processed using Ms Excel and Prism 4.03 (GraphPad Software, Inc.).

$$v_i = \frac{V_{max} \times S_0}{K_m + S_0} \qquad (4)$$

Literature. (1) Tirat et al. *Analyt Biochem* **2005**, *343*, 244-255. (2) Huang et al. *Methods in Molecular Biology* **2009**, *565*, 127. (3) Levine et al. *Analyt Biochem* **1997**, *247*, 83. (4) Faesen et al. *Chem Biol* **2011**, *18*, 1550. (5) Geurink et al. *ChemBiochem*, **2012**, *13*, 293. (6) Bingol et al. *Nature* **2014**, *510*, 370.

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