QL9 TFA

Cat. No.: HY-P0287A

Molecular Formula: $C_{52}H_{74}N_{10}O_{14}.xC_2HF_3O_2$

Sequence: Gln-Leu-Ser-Pro-Phe-Pro-Phe-Asp-Leu

Sequence Shortening: QLSPFPFDL

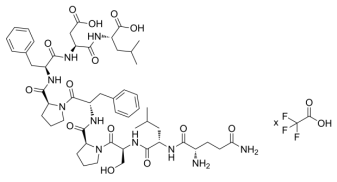
Target: Others

Pathway: Others

Storage: Sealed storage, away from moisture

Powder	-80°C	2 years
	-20°C	1 year

* In solvent : -80°C, 6 months; -20°C, 1 month (sealed storage, away from moisture)



SOLVENT & SOLUBILITY

In Vitro	DMSO : 100 mg/mL (Need ultrasonic)
In Vivo	1. Add each solvent one by one: 10% DMSO >> 40% PEG300 >> 5% Tween-80 >> 45% saline Solubility: ≥ 2.5 mg/mL (Infinity mM); Clear solution 2. Add each solvent one by one: 10% DMSO >> 90% (20% SBE-β-CD in saline) Solubility: ≥ 2.5 mg/mL (Infinity mM); Clear solution 3. Add each solvent one by one: 10% DMSO >> 90% corn oil Solubility: ≥ 2.5 mg/mL (Infinity mM); Clear solution

BIOLOGICAL ACTIVITY

Description	QL9 (QLSPFPFDL) TFA is a high-affinity alloantigen for the 2C T cell receptor (TCR).
In Vitro	Mouse T cell clone 2C recognizes two different major histocompatibility (MHC) ligands, the self MHC K^b and the allogeneic MHC L^d. Two distinct peptides, SIY (SIYRYYGL) and QL9 (QLSPFPFDL), act as strong and specific agonists when bind to K^b and L^d, respectively. QL9 binding to MHC L^d is influenced by the majority of peptide side chains, distributed across the entire length of the peptide. Findings with both systems, but QL9-L^d in particular, suggest that many single-residue substitutions, introduced into peptides to improve their binding to MHC and thus their vaccine potential, could impair T cell reactivity due to their dual impact on TCR binding. T cell activation assays are performed to measure effects of peptide SIY and QL9 residues on T cell function[2]. MCE has not independently confirmed the accuracy of these methods. They are for reference only.

PROTOCOL

Cell Assay [2]	Wild type 2C and high affinity 2C T cell transfectants m67 and m6 are incubated with K^b- or L^d-positive cells and various concentrations of peptide SIY and QL9 alanine variants. T cell activation is measured by assaying for levels of IL-2 release. Briefly, T cell transfectants (7.5×10^4) are incubated with T2-K^b (7.5×10^4) or T2-L^d (7.5×10^4) along with various concentrations

of peptide for 20-24 h at 37 °C and 5% CO_2. Supernatant is harvested, and levels of IL-2 are measured in an enzyme-linked immunosorbent assay type format. Results are plotted as percentage of maximal IL-2 release=(($A_{450\ (sample)}$-$A_{450(no\ peptide)}$)/(Max $A_{450(sample)}$-$A_{450(no\ peptide)}$))×100; signal obtained from no peptide is similar to that obtained for the null peptides MCMV or OVA. Binding curves are generated in GraphPad Prism by plotting the percentage of maximal IL-2 release against peptide concentration. The concentrations of peptide yielding 50% maximal IL-2 release (SD_{50}) are calculated using non-linear regression (sigmoidal fitting; GraphPad Prism) of the activation curves[2].

MCE has not independently confirmed the accuracy of these methods. They are for reference only.

REFERENCES

[1]. Bowerman NA, et al. Different strategies adopted by K(b) and L(d) to generate T cell specificity directed against their respective bound peptides. J Biol Chem. 2009 Nov 20;284(47):32551-61.

[2]. Speir JA, et al. Structural basis of 2C TCR allorecognition of H-2Ld peptide complexes. Immunity. 1998 May;8(5):553-62.

Tel: 609-228-6898 Fax: 609-228-5909 E-mail: tech@MedChemExpress.com

Address: 1 Deer Park Dr, Suite Q, Monmouth Junction, NJ 08852, USA