rigid hydrogel with antibacterial activity. The synthetic peptide MAX1 (H_2N-VKVKVKVK$V^DPPTKVKVKVKV$-$CONH_2$) is composed of 20 amino acid units of alternating valine (V) and lysine (K) molecules with a central D-valine-diproline-threonine sequence (V^DPPT) driving the formation of a type-II β-turn (Schneider et al. 2002). At acidic pH, below the p*K*a of lysine, assembly does not occur due to charge repulsion. At basic pH, above the p*K*a of lysine, a β-hairpin forms due to lack of repulsion driving self-assembly and molecular interactions. The β-hairpin secondary structure motif forms two faces of varying character. An outlying hydrophobic face composed of valines and an internal hydrophilic lysine face. Hydrophobic interactions (van der Waal's, dipole-dipole) and hydrogen bonding (between respective amide/peptide bonds) are responsible for driving intermolecular self-assembly and hydrogel formation.

Modification of MAX1 peptide also allows thermo-responsiveness to be introduced. The potential applications of MAX1 were expanded for use as three dimensional biomineralization scaffolds (Altunbas et al. 2010). Lysine groups provided sufficient cationicity to allow the addition of tetraethoxysilane and silica on the fibril surface forming defined silica shells with increased mechanical properties when compared to MAX1 alone. At increased pH (above pH 7) silicic acid (from tetraethoxysilane) dissociates into its silicate anion, $[SiO(OH)_3]^-$, catalysed by the presence of a polycationic lysine surface. This dissociation increases as the pH is elevated resulting in greater electrostatic interactions between anionic silicate and cationic lysine and an increased density of silicate anions at the peptide fibril surface. The successful production of a silica-peptide hydrogel material holds great promise for future use as tissue engineering scaffolds.

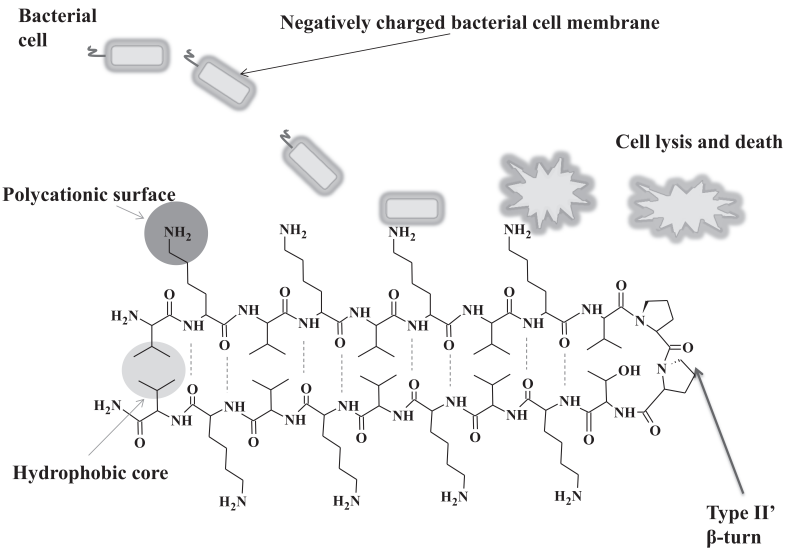

Fig. 2. Primary amino acid sequence and structural organization of MAX1 peptide at basic pH. The presence of cationic lysine molecules endow antimicrobial activity to the peptide. Adapted from (McCloskey et al. 2014).