



## Cryptides: latent peptides everywhere

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## Cryptides: latent peptides everywhere

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## 3 **Cryptides: latent peptides everywhere**

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8 Proteomic surveys with top-down platforms are today revealing thousands of naturally  
9 occurring fragments of bigger proteins. Some of them have not functional meaning because  
10 they derive from pathways responsible for protein degradation, but many have specific  
11 functions, often completely different from that one of the parent proteins. These peptides  
12 encrypted in the protein sequence are nowadays called cryptides. They are frequent in the  
13 animal and plant kingdoms and represent a new interesting -omic field of investigation. To  
14 point out how much widespread is their presence, we describe here the most studied cryptides  
15 from very common sources such as serum albumin, immunoglobulins, hemoglobin, and from  
16 saliva and milk proteins,. Given its vastness, it is unfeasible to cover the topic exhaustively,  
17 therefore only several selected examples of cryptides from other sources are thereafter  
18 reported. Demanding is the development of new -omic platforms for the functional screening  
19 of new cryptides, which could provide suggestion for peptides and peptido-mimetics with  
20 variegate fields of application.

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Keywords: cryptides; encrypted peptides; latent peptides; hidden peptides: albumin;  
immunoglobulins; hemoglobin; hemorphins.

## 1 2 3 4 5 1. Introduction

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The name of cryptides was firstly introduced by Mukai and colleagues after the discovery of bioactive peptides deriving from mitochondria, which were named mitocryptide-1 and mitocryptide-2 (Mukai et al. 2009). They defined cryptides the fragmented peptides generated during maturation or degradation processes of functional proteins showing various biological activities distinct from those of the parent proteins. Later, cryptides were classified by Autelitano and colleagues in three families: type I cryptides were defined as bioactive peptides detectable *in vivo* with a function different from its precursor; type II cryptides were defined as peptides detectable *in vivo* with activities related but not identical to those of the parent protein; type III cryptides were defined as bioactive peptides generated *in vitro* by digestion of a protein that may or not also exist *in vivo* (Autelitano et al. 2006; Samir and Link 2011). It is well known that the discrimination between a peptide and a protein is conventional, limiting the definition of a peptide to the number of the amino acids in the sequence (commonly not more than 50 residues), however some cryptides might be larger. Moreover, not all the peptide fragments generated by the *in vivo* digestion of a protein have a biologic role and not all the biologically active peptides are cryptides because they might not derive from a parent mature protein. For instance, in the last years it was demonstrated that small peptides are originated from the translation of short upstream RNA open reading frames (Andrews and Rothnagel 2014). However, even if the latter peptides show regulatory activities, they cannot be properly considered cryptic peptides because they are not encrypted in a protein sequence (Fig. 1). We limited in this review our description of cryptides to the examples reported in Fig. 1, where their definition is restricted to **functional** sequences encrypted into a **functional** polypeptide of any length which can be released *in vivo* **within a cell** (**intracellular cryptides**) and that can be utilized within the cell and/or outside the cell after their release, as well as to peptides hidden in a **functional** polypeptide sequence of any length generated by proteolytic events occurring **after secretion** (**extracellular cryptides**) regardless they occurred

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2     *in vivo, ex vivo or in vitro* (Fig. 1). It is relevant to remark that all cryptides must have a function  
3     distinct or related, but not similar to that one of the parent polypeptide.  
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7     The first assumption of the existence of these peptides fragments was made around 1960 –'70 by  
8     the observation of not-identified proteolytic products from human and mammals milk with  
9     antibacterial and antiviral activity (Liepke and Zucht 2001; Oddy 2001; Hosea Blewett et al. 2008;).  
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12     The possibility that parent proteins can release peptides with variegate activities has been further  
13     supported in the 1975-'85 decade by the discovery of active fragments of hemoglobin such as  
14     neokyotorphin, a peptide hidden in the  $\alpha$ -globin chain (Gomez et al. 2010), and hemorphins, small  
15     “non-classical” opioid-like peptides generated by specific enzymatic hydrolysis of the  $\beta$ -type chains  
16     of hemoglobin (Zhao et al. 1997; Nyberg et al. 1997). The advent of the modern high throughput  
17     proteomic platforms is to date largely expanding the number of putative cryptides identification.  
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20     The best approach able to characterize with confidence and robustness naturally occurring “latent”  
21     peptides is top-down proteomics, that avoiding any proteolytic pre-treatment allows studying  
22     directly the complex of the peptides deriving from bigger proteins present in the biological sample  
23     (Messana et al. 2013). The aim of this review is to point out the widespread presence of cryptides  
24     underlying their important role in several biological pathways selecting interesting examples  
25     deriving from the most common and well known proteins, such as serum albumin, immunoglobins,  
26     hemoglobin, as well as describing cryptides deriving from bodily fluids as saliva or milk, with  
27     particular emphasis to human cryptides. Because the number of cryptides from other sources is  
28     huge, the last section is devoted to the description of selected examples, apologizing for relevant  
29     omissions.  
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## 50     2. Serum albumin cryptides 51 52

53     Human serum albumin (HSA) is the most abundant protein in blood and cerebrospinal fluid. It  
54     controls the plasma oncotic pressure and it is a relevant carrier for endogenous and exogenous  
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1 compounds, increases the lifetime of hydrophobic compounds, inactivates toxic compounds,  
2 induces chemical modifications of some ligands, and displays antioxidant and enzymatic properties  
3 (Ascenzi et al. 2015). Furthermore, HSA can be a source of various cryptides. For instance, the  
4 subdomain IIIB of HSA acts as gonadotrophin surge-attenuation factor, an ovarian factor that acts  
5 on the pituitary to attenuate the pre-ovulatory LH surge. Tavoulari and colleagues (Tavoulari et al.  
6 2004) have shown that recombinant C-terminal domain of HSA (residues 490-585, subdomain IIIB)  
7 reduces the GnRH-induced LH secretion of primary rat pituitary cultures by 50-80%. Interestingly,  
8 the recombinant full HSA domain III (residues 381-585) or full-length HSA are inactive  
9 demonstrating the specificity of subdomain IIIB. Tryptic and chymotryptic digestion of HSA  
10 generates two peptides with cathepsin B inhibitory properties. These peptides correspond to  
11 fragments 65-70 (SLHTLF; one letter code) and 403-407 (FQNAL) of HSA and were named cabin-  
12 A1 and cabin-A2, respectively (Nakagomi et al. 2002). The trypsin digest of HSA originates  
13 peptides with ACE inhibition activity too. One is acein-1 (Nakagomi et al. 1998), a heptapeptide  
14 (YLYEIAR, fr. 138-144) acting as non-competitive inhibitor with an  $IC_{50}$  value of 16  $\mu$ moles/L  
15 although, as we are aware, its anti-hypertensive activity was not explored *in vivo*. Another non-  
16 competitive ACE-inhibitor is albutensin A (AFKAWAVAR), corresponding to fragment 210-218  
17 of HSA and with an  $IC_{50}$  value of 1.7  $\mu$ moles/L (Nakagomi et al. 2000). It was demonstrated that  
18 albutensin A is able to contract ileum *in vitro* with a contraction profile similar to casoxin C (see  
19 section on casein cryptides) and oryzatensin, a cryptide deriving from rice albumin (Takahashi et al.  
20 1998). All these peptides have homology with the C-terminal sequence of complements C3a and  
21 C5a and it was demonstrated that, as oryzatensin and casoxin C, albutensin A exhibits its ileum-  
22 contracting ability as an agonist for their receptors (Takahashi et al. 1998). Albutensin A is also able  
23 to decrease food intake in mice and the effect is always mediated through the complement C3a  
24 receptor (Ohinata et al. 2002).

25 Serorphin (YGFQNA) is a cryptide derived from fragment 399-404 of bovine serum albumin with  
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2 opioid-like activity (Takahashi et al. 1998). The study on serorphin stimulated the search of other  
3 peptides with opioid-like activity containing the YXF sequence (where X represents a polar amino  
4 acid residue) such as historphin (YGF<sub>n</sub>G, from histone H4), valentorphin (YGF<sub>n</sub>I, from  
5 carboxipeptidases A and B) and kapporphin (YSF<sub>n</sub>G, from immunoglobulin  $\kappa$ -chain) (Takahashi  
6 et al. 1998).  
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9 During proteomic survey by a top-down platform on different samples from bodily fluids, cell and  
10 tissues, various fragments of HSA were detected (Vento et al. 2009). Many of them appeared  
11 specifically related to sample under analysis, while others were consistently found in almost all the  
12 samples analyzed. In particular the fragment 27-50 (DAHKSEVAHRFKDLGEENFALVL) that is  
13 ubiquitous and should be submitted to functional screening to establish potential biological  
14 activities.  
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### 27 3. Immunoglobulins cryptides 28 29

30 The biological role of antibodies (Abs), related to humoral immunity, is exerted by their ability to  
31 recognize and bind with high affinity and specificity antigens (Ags). The structure of the Abs  
32 consists of two identical heavy and light polypeptide chains linked by disulfide bonds characterized  
33 by variable and constant regions. Hypervariable domains of variable regions are defined  
34 complementarity-determining regions (CDRs), and represent the specific Ag binding site, while a  
35 constant part (fragment crystallizable, Fc) acts after the formation of the Ab-Ag complex by  
36 recruiting other immune system cells and molecules, and leading to the elimination of Ag.  
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39 Several studies performed in recent decades have evidenced that Abs may represent an important  
40 source of cryptides not only able to modulate the functions of the immune system, but also exerting  
41 anti-infective and antitumor activity. The tetrapeptide tuftsin generated from the Fc-segment of  
42 IgGs by the action of splenic endocarboxypeptidase and leucokininase was the first phagocytosis-  
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2 stimulating Ab-derived peptide characterized (Najjar and Nishioka 1970), later shown to act also as  
3 neurotrophic, immunostimulatory and antitumor agent both *in vitro* and *in vivo* (Siemion 1999).  
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5 This finding provided the impulse to the search for other bioactive fragments of immunoglobulin  
6 origin and led to the characterization of several fragments of the H-chain of IgG generated by  
7 enzymatic cleavage of IgG, including rigin, immunorphin, immunocortin, peptide p24 and its  
8 fragments, with immunoregulatory properties (Navolotskaya 2014). These peptides have never been  
9 detected *in vivo*. Three Fc-peptides derived from the major classes of IgG, IgM and IgA, and named  
10 H4L, N10K, T11F, showed a significant fungicidal activity at micromolar concentrations also  
11 against resistant strains (Polonelli et al. 2012). Furthermore, N10K displays immune-modulatory  
12 activity toward human monocytes *in vitro* (Gabrielli et al. 2012).  
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15 The *in vivo* potential antifungal activity of peptides generated by the less conserved Ab CDRs can  
16 be considered of relative importance due to the low amount of the fragments that may be delivered.  
17 However, the importance of CDRs as inspiration supplier of potentially bioactive sequences has  
18 been stressed in several studies. Indeed, it has been demonstrated that CDRs-derived peptides may  
19 display antimicrobial, antiviral and antitumor activities regardless of their specificity for a given Ag  
20 (Polonelli et al. 2008). Polonelli and colleagues (Polonelli et al. 2003) were the first to describe an  
21 Ab-derived microbicidal peptide, obtained by the substitution E→A in a very active synthetic CDR-  
22 related peptide, named “killer peptide” (KP). KP was active at micromolar concentrations against  
23 many pathogenic yeasts, even those resistant to conventional antifungal agents. KP also showed  
24 activity against pathogenic bacteria, protozoa, HIV-1 and influenza A viruses (Ciociola et al. 2014),  
25 as well as immunomodulatory effects. The different biological activities of KP have been related to  
26 its dimeric form derived by self-aggregation of  $\beta$ -sheet structures resulting in the formation of  
27 hydrogel-like aggregates (Pertinhez et al. 2009) able to provide protection against proteases.  
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30 PEP3H originated by CDR H3 of RS-348 showed *in vitro* and *in vivo* antiviral activity against RSV  
31 (Bуржоис et al. 1998), and synthetic peptides derived from CDRs of an anti-CD4 monoclonal  
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2 antibody were able to inhibit HIV-1 promoter activation (Monnet et al. 1999). Also a tyrosine  
3 sulfated peptide derived from an HIV-1-neutralizing Ab was demonstrated to be able to inhibit  
4 HIV-1 infections (Dorfam et al. 2006).  
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8 Among the different CDR peptides with antitumor activity, noteworthy is a 16-residue peptide (C7  
9 H2) derived from CDR H2 of KAb mAbC7 able to inhibit both the germination of human umbilical  
10 vein endothelial cells and the lung colonization by melanoma cells in mice (Arruda et al. 2012). A  
11 screening on the antitumor activity of synthetic peptides derived from conserved CDR sequences of  
12 different immunoglobulins against human tumor cell lines and murine B16F10-Nex2 melanoma  
13 evidenced that rather frequent CDR sequences are endowed with specific antitumor properties and  
14 may be candidates to be developed as anti-cancer drugs (Figueiredo et al. 2014).  
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17 **4. Hemoglobin cryptides**  
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20 Hemoglobin (Hb), the milestone of quaternary cooperative protein, beside its fundamental role of  
21 oxygen transport and energy metabolism in vertebrates is a precious source of bioactive peptides  
22 originating from both  $\alpha$ - and  $\beta$ -globin chains (Giardina et al. 1995), that constitute a tissue specific  
23 pool (Ivanov 1997). The latter concept originated from the recognition of different panels of peptide  
24 patterns in diverse tissues, suggesting the occurrence of tissue specific enzymatic cleavages on large  
25 circulating hemoglobin fragments (Ivanov et al. 1997).  
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28 An interesting paper (Zamyatnin 2009) compared the amino acid sequence of natural regulatory  
29 oligopeptides from the EROP-Moscow database with the primary structure of bovine hemoglobin in  
30 order to disclose, by a theoretical structure/function analysis, possible associations between specific  
31 sequences and selected functions. In addition to recognized bioactive hemoglobin peptides, many  
32 natural regulatory oligopeptides in the database resulted to contain sequence traits, at least of five  
33 amino acid residues, of bovine hemoglobin associated to antifreeze, antimicrobial, enzyme  
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2 inhibitor, hormone, neuropeptide, peptide potentiatory activities. More recently, the advances in the  
3 knowledge of endogenous peptides derived from hemoglobin chains have been interestingly  
4 reviewed also discussing about their biological activities and possible origins (Gomez et al. 2010).  
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7 The discovery of hemoglobin peptides begin in the 1980s with the identification of neokytorphin,  
8 a five amino acid residues C-terminal peptide of the  $\alpha$ -globin chain, containing the kytorphin  
9 dipeptide and showing analgesic properties similar to Leu-enkephalin together with other biological  
10 roles (Gomes et al. 2010). Neokytorphin and its des-Arg neokytorphin showed cytolytic activity  
11 towards human erythroid leukemia and murine transformed fibroblast cell lines (Blishchenko et al.  
12 1996). Additionally, hemoglobin fragments related to neokytorphin were reported to have a  
13 proliferative effect on diverse cell cultures (Sazonova et al 2003).  
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16 Corresponding to specific sequences of the  $\beta$ -globin chain, the hemorphins peptides have been  
17 isolated from bovine blood treated with a mixture of gastrointestinal enzymes (Brantl et al. 1986)  
18 and successively isolated from extracts of cortex and subcortex bovine brain (Karelin et al. 1994).  
19 These tissue specific small peptides, all containing the tetrapeptide YPWT in the sequence, belong  
20 to the group of non-classical opioid peptides with affinity towards  $\mu$ - and  $\sigma$ -opioid receptors, and  
21 were additionally reported to exert numerous other biological activities (Nyberg et al. 1997; Zhao et  
22 al. 1997; Gomez et al. 2010). Table 1 describes the diverse hemorphin's subfamilies based on their  
23 N-terminal sequence. Particularly, the LVV-hemorphin-7 and VV-hemorphin-7, head of the LVV-  
24 and VV- hemorphins' subfamilies, are 10 and 9 amino acids peptides, respectively, specific of the  
25 central nervous system (CNS) and corresponding to fragments 32-41 and 33-41 of  $\beta$  (or  $\gamma$ ,  $\delta$  and  $\varepsilon$ )  
26 globin chain (Nyberg et al, 1997). In addition to the opioid like activity, the LVV-hemorphin-7 was  
27 identified as the endogenous ligand of angiotensin IV receptor (Moeller et al. 1999) and showed  
28 inhibitory activity towards angiotensin converting enzyme (ACE) (Lantz et al. 1991) and insulin-  
29 regulated aminopeptidase (IRAP) (Lammerich et al. 2003) together with an important role of in  
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2 homeostasis (Barkhudaryan et al. 2010).  
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5 Hemorphins have been studied in relation to different physio-pathological conditions. LVV-  
6 hemorphin-7 seems to play a role in blood pressure regulation (Cejka et al. 2004), in connection to  
7 their ACE inhibitor capability, and in learning and memory by inhibition of IRAP (Albiston et al.  
8 2004) and was identified in the bronchoalveolar lavage fluid of a non-small cell lung cancer patient  
9 (Duethman et al. 2000). Hemorphins have been also reported as potential drug candidate and  
10 putative biomarkers of breast cancer (Cohen et al. 2003; Song et al. 2012). Hemorphins showed  
11 citotoxicity towards tumor cell lines (Blishchenko et al. 2002a; Blishchenko et al. 2002b) and tumor  
12 growth inhibition capacity (Mikhailova et al. 1996; Blishchenko et al. 2005). A study on a rat  
13 sarcoma model demonstrated the capability of LVV-hemorphin-7 and hemorphin-7 to modulate  
14 calcineurin activity, DNA methylation and to form DNA complexes (Barkhudaryan et al. 2012,  
15 Blishchenko et al. 2005). The top-down proteomic characterization of CSF in relation to posterior cranial  
16 fossa pediatric brain tumors identified the LVV- and VV-hemorphin-7 as candidate biomarkers for  
17 the prognosis of disease (Desiderio et al. 2012). Together with them, a panel of four peptides with  
18 molecular weight around 3 kDa and corresponding to specific sequences of both  $\alpha$ - and  $\beta$ -globin  
19 chains has been also identified. These peptides, whose biological function is still not clear, have  
20 been also characterized in lipoaspirate fluid (Inserra et al. 2016) and craniopharyngioma  
21 adamantinomatous pediatric brain tumor intracystic fluid (Martelli et al. 2014). These peptides have  
22 been previously isolated in lysates of human erythrocytes (Karelin et al. 1995).  
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25 Together with its role in pain by modulation of enkephalin degradation, the LVV-hemorphin-4, also  
26 called spinorphin, was reported as possible anti-inflammatory endogenous regulator (Yamamoto et  
27 al. 2002). In addition to hemorphins, other bioactive fragments of hemoglobin, particularly of  $\alpha$ -  
28 globin, have been identified under the name of hemopressins. Following the first identification of  
29 the  $\alpha$ -globin hemopressin peptide (PVNFKFLSH), with CB1 cannabinoid receptor antagonist  
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2 activity, from rat brain extracts (Rioli et al. 2003), other hemopressins with N-terminal extensions,  
3 namely RVD- and VD-hemopressins, have been also identified in mouse, together with a similar  
4 VD-hemopressin peptide from the hemoglobin beta-chain. Differently from the original peptide, the  
5 N-terminal extended form of hemopressin showed agonist activity towards cannabinoid receptors  
6 (Gomes et al. 2010). Hemopressin additionally showed antinociceptive properties and capacity to  
7 reduce blood pressure (Gelman and Fricker 2010). Other bioactive peptides fragments from  $\alpha$ -  
8 globin, corresponding to fragments 110-125 and 129-134, show bradykinin-potentiating action  
9 (Gelman and Fricker 2010). Another fragment of  $\alpha$ -hemoglobin, isolated from human endometrial  
10 scraping samples, exhibited a potent antibacterial activity (Deng et al. 2010).  
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23 In conclusion hemoglobin still holds many mysteries to clarify. The diverse functions of its peptide  
24 fragments could represent a good recycling strategy of the cells to exert multiple actions in  
25 economy. Initially ascribed to the catabolism of blood hemoglobin at tissue level, the majority of its  
26 derived bioactive neuropeptides seems to origin directly from the hemoglobin expressed in brain  
27 tissues (Gelman et al. 2010). The process of synthesis and the mechanisms of action of the  
28 hemoglobin derived peptides need to be clarified yet making this issue an intriguing field of  
29 investigation.  
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## 39 **5. Cryptides from saliva**

  
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41 In human saliva many putative latent peptides derive from proline-rich proteins (PRPs). Within  
42 whole human saliva PRPs account for more than 30% (w/w) of total protein content and for about  
43 50-60% (w/w) of proteins secreted by parotid (Bennick 1982; Manconi et al. 2016). From this  
44 group of proteins three different families are distinguished, namely acidic PRPs (aPRPs), basic  
45 PRPs (bPRPs), and glycosylated (basic) PRPs (gPRPs) (Oppenheim et al. 2007). bPRPs are  
46 secreted only by parotid glands. On the contrary aPRPs are secreted by both parotid and  
47 submandibular/sublingual glands (in different percentages) and can be detected both as intact and  
48 subunit forms (Oppenheim et al. 2007).  
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1 truncated proteoforms The intact proteoforms are called PRP-1, PRP-2, Pif-s, Db-s, and Pa, the first  
2 two codified by the locus *PRH2* and the last three codified by the locus *PRH1*. A convertase  
3 cleavage at Arg<sub>106</sub>.(Arg<sub>127</sub> for the Db-s proteoform) is responsible for the releasing from four  
4 truncated proteoforms (Pa is not cleaved for the substitution Arg<sub>106</sub>→Cys) named PRP-3, PRP-4,  
5 Pif-f and Db-f and of a common C-terminal peptide of 44 amino acid residues, called P-C peptide.  
6 Differently from aPRPs, bPRPs encoded by *PRB1*, *PRB2* and *PRB4* genes are instead detectable in  
7 saliva only as proteins fragments from the pro-proteins, with a molecular weight ranging from 5 to  
8 27 kDa. Today at least 18 bPRPs have been structurally characterized, namely II-2, P-E, IB-6, Ps-1,  
9 Ps-2, IB-1, P-J, IB-8a, P-F, P-H, P-D, II-1, protein glycosylated A, CD-IIg, and G11-4. Acidic and  
10 basic PRPs, after secretion, are further hydrolyzed in the mouth by endogenous and exogenous  
11 enzymes (Messana et al. 2008; Hemerhorst et al. 2008) in smaller putative cryptides 7-20 residue-  
12 long, mainly originating from cleavages at the XPQ↓G site (with X preferably K, to a lesser extent  
13 S or R (Hemerhorst et al. 2008), as reported in Table 2. From these observations Hemerhorst and  
14 colleagues were able to characterize a new glutamine endoprotease deriving from Rhodia bacteria  
15 (Hemerhorst et al. 2010, Zamakhchari et al. 2013).  
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18 The role of the parent proteins is different from that one of the fragment released. Indeed, aPRPs  
19 interact to hydroxyapatite with high affinity (Hay et al. 1987), can participate to the constitution of  
20 acquired enamel pellicle (Moreno et al. 1982) and are involved in oral calcium homeostasis  
21 inhibiting calcium phosphate precipitation (Bennick et al. 1983). bPRPs functional roles are not  
22 completely clarified. Even though their similar structure, the diverse proteoforms from the same  
23 pro-protein can exert proper biological activities. As an example, II-2 peptide and Ps-1 protein are  
24 involved in the PROP bitter taste responsiveness (Cabras et al. 2012; Melis et al. 2013) while P-E,  
25 IB-6, and Ps-2 together with IB-1, P-H (Lu and Bennick 1998; Cai et al. 2006) and P-D peptides  
26 (Charlton et al. 1996; Canon et al. 2013) can interact to and precipitate the harmful tannins.  
27 Furthermore, IB-6 promotes adhesion of *Candida albicans* on hydroxyapatite surface (O'Sullivan et  
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al. 1997).

6 The cryptides generated from the oral proteolysis have different properties of the parent proteins.  
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8 For instance, six latent peptides from IB-8a (Con1<sup>+</sup>/Con1<sup>-</sup>), one from P-E, one from IB-1, and one  
9 from each PRB1-S, M, L proteins were identified in enamel pellicle (Vitorino et al. 2007). Other  
10 originated from PRB2-L (nine peptides) and from PRB1-S, M, L-related proteoforms (three  
11 peptides) were identified as enamel bounded peptides (Siqueira and Oppenheim 2009). A 20 residue  
12 proline-rich peptide (p1932: GPPPQGGNKPQGPPPGKPQ), commonly present in human saliva  
13 and patented for its antiviral activity, was internalized within primary gingival fibroblast cell line  
14 and squamous cancer cell lines (Radicioni et al. 2015). The cytosolic localization was dependent on  
15 the cell type: p1932 peptide and its retro-inverso form were able to localize within nuclei of tumor  
16 cells, but not in the nuclei of gingival fibroblasts. It acts as an antagonist of the progesterone  
17 induced cytosolic Ca<sup>2+</sup> mobilization in a tongue squamous carcinoma cell line and this dose-  
18 dependent activity is mainly confined in the C-terminal region characterized by a four proline repeat  
19 flanked by a lysine residue. The lack of activity of the retro-inverso form suggested the involvement  
20 of a specific molecular recognition mechanism at the basis of peptide antagonistic effect. The  
21 search for progesterone receptors in this oral cancer cell line, identified in the PRGMC1 the main  
22 expressed form, suggesting a modulation role of the peptide in the transduction signal pathway  
23 mediated by this receptor (Palmerini et al. 2016). The intrinsic propensity of p1932 to adopt a  
24 polyproline-II helix arrangement joined to PxxP motifs is suggestive for the interaction with the  
25 SH3 domain family. Surface plasmon resonance spectroscopy evidenced specific interactions only  
26 with Fyn, Hck and c-Src SH3 domains at nanomolar to micromolar values of dissociation constants.  
27 Interestingly, these interacting domains are all included in the Src kinases family, suggesting that  
28 p1932 can be involved in the signal transduction pathways modulated by these kinases (Righino et  
29 al. 2016). From Table 2 it is evident that p1932 is one of a large series of putative salivary cryptides  
30 waiting for a more detailed study of their functions.

Several peptides detected in human saliva derive from crevicular gingival fluid (CGF) arising from the gingival plexus that contains a diverse population of cells including bacteria from the adjacent plaque mass as well neutrophils, mononuclear cells, lymphocytes and migrating leukocytes and desquamated epithelial cells, which may release several secretory products, and microbial metabolites (Seguier et al. 2000). CGF is also distinctive for a very high concentration of thymosin  $\beta_4$  (T $\beta_4$ ), a ubiquitous peptide with a pivotal role in the cytoskeletal system as G-actin sequestering peptide, activity probably related to its effects on the regulation and differentiation of T lymphocytes (Low et al. 1986). T $\beta_4$  can release a cryptide called seraspenide, i.e. the Ac-SPDK tetrapeptide corresponding to its N-terminal sequence (Grillon et al. 1990), which inhibits the entry of hematopoietic pluripotent stem cells into the S-phase *in vivo* blocking them in the G0-phase of the cell cycle (Lenfant et al. 1989). It was reported that seraspenide is a substrate of ACE (Rousseau et al. 1995) which in turn seems to be involved in its degradation in human plasma (Rieger et al. 1993). The protective effect of T $\beta_4$  in acute myocardial infarction seems essentially due to the cardioprotective properties of seraspenide (Rossdeutscher et al. 2008).

## 6. Milk cryptides

More than 400 proteins are present in very different amounts in human breast milk (Roncada et al. 2012; 2013; D'Alessandro et al. 2010; Molinari et al. 2012), which, further than nutritive properties, exert relaxing, satiating, antimicrobial, immune-modulatory, metal-binding, anti-lipidaemic and anti-cancer activities (Nongonierma and Fitzgerald, 2015). During the digestion process these proteins are cleaved in smaller peptides by the action of endogenous (digestive enzymes) or exogenous proteinases (microbiota) that can modulate different biological pathways as reviewed (Korhonen and Pihlanto, 2003; Park and Nam, 2015; Capriotti et al. 2016; Théolier et al., 2014;). The major proteins present in human milk belong to the whey and casein families, while mucins represent a minor percentage of the total proteins (Lonnerdal 2004). Not all these proteins can

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2 generate cryptides. Some of them may be resistant to digestion and act only in the intact form,  
3 others can generate bioactive peptides of different dimensions formed during digestion and some  
4 are completely digested and utilized as a source of amino acids (Lonnerdal 2014).  
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8 **6.1 Whey proteins deriving cryptides**  
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10 While mucins are confined in the milk fat globule membrane, the proteins detectable in high level  
11 in the whey fraction are lactoferrin,  $\alpha$ -lactalbumin, lactoglobulin, IgS, lysozyme, and serum albumin  
12 (Lonnerdal 2004). Cryptides from serum albumin and immunoglobulins have been described  
13 previously in sections 1 and 2.  
14

15 Lactoferrin (or lactotransferrin) is a protein responsible for the iron transport that can generate, after  
16 proteolysis, peptides with an antimicrobial and antiviral action which was partly attributed to its  
17 fragment called lactoferricin. Human lactoferricin (lactoferricin H) corresponds to the fragment 1-  
18 48 of the parent protein and consists of two subunits (namely fragment 1-11 and 12-48 connected  
19 by a disulfide bridge; Tab.3), while bovine lactoferricin (lactoferricin B; Tab. 3) corresponds to the  
20 fragment 17-41 of the parent protein (Wakabayashi et al. 2003). Lactoferricin binds to the bacterial  
21 surface and plays a relevant role in membrane-mediated activities of lactoferrin and reveals antiviral  
22 activity against papilloma infections (van der Kraan et al. 2004). Shestakov and colleagues  
23 (Shestakov et al. 2012) have shown that lactoferricin, but not lactoferrin, inhibits herpes simplex  
24 virus like 2 infection in mice. The N-terminal region of lactoferricin showed powerful antifungal  
25 activity against *Candida albicans* species (van der Kraan et al. 2004). A second antimicrobial  
26 peptide called lactoferrampin was detected in the N-1 domain of human and bovine lactoferrin  
27 (Tab. 3). Bovine lactoferrampin has high candidacidal activity and it is active against *Bacillus*  
28 *subtilis*, *Escherichia coli* and *Pseudomonas aeruginosa* but not against *Actinomyces naeslundii*,  
29 *Porphyromonas gingivalis*, *Streptococcus mutans* and *Streptococcus sanguis* (van der Kraan et al.  
30 2004). Bovine lactoferrampin, together with human lactoferricin can inhibit nuclear translocation of  
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2 HIV integrase (Wang 2016). Moreover, Eliassen and colleagues (Eliassen et al. 2006) have shown  
3 the cytotoxic effect of lactoferricin B against neuroblastoma cell *in vitro* by rapid destabilization of  
4 the cytoplasmic membrane and formation of membrane blebs. Depolarization of the mitochondria  
5 membranes and irreversible changes in the mitochondria morphology were also evident.  
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8 Lactoferricin can in turn generate shorter peptides, which can be defined cryptides of second  
9 generation (Fig. 1), that are promising candidates with antibacterial activities suggesting the  
10 synthesis of peptidomimetics for the treatment of various infectious diseases (Haug et al. 2007).  
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13 Some examples are represented by the fragment 1-11 deriving from the reduction of lactoferricin H  
14 (GRRRSVQWCAV) with antiviral and high antibacterial activity (Wang 2016, Bruni et al. 2016),  
15 which were confirmed in animal models and in a phase 1 study in human volunteers (Bruni et al.  
16 2016), and a tetrameric peptide deriving from lactoferricin B ((RRWQWR)<sub>4</sub>) exhibiting specific  
17 cytotoxic effects against oral squamous-cell carcinoma cell lines (Solarte et al. 2015). This  
18 antitumor activity was further confirmed by the PFR-peptide (Tab. 3) derived from lactoferricin H  
19 that induced necrotic cell death and G0/G1 cell cycle arrest in MEL and HL-60 leukemia cell-lines  
20 (Lu et al. 2016). In this study, researchers demonstrated that PFR-peptide inhibited leukemia cell  
21 growth *in vivo* in immunocompromised mice transplanted with MEL cells.  
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24 Moreover, the fragment 18-40 of lactoferricin H, another cryptide of second generation called  
25 Lfpep (Tab 3), showed powerful fungicidal activity against *Candida* spp., including fluconazole-  
26 and amphotericin B-resistant clinical isolates. The killing activity of Lfpep is mediated by its  
27 permeabilizing activity on *Candida albicans* membranes (Viejo-Diaz et al. 2005). The candidacidal  
28 activity of Lfpep is higher than that observed for kaliocin-1, another cryptide corresponding to the  
29 fragment 171-201 of human lactoferrin (Tab. 3). The comparison among the structure of various  
30 antifungal cryptides deriving from lactotransferrin may be of interest in the design of new  
31 antifungal drugs.  
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An in vitro peptic digest of human lactoferrin generated three opioid antagonistic cryptides which were called lactoferroxins A-C (Tab 3) (Tani et al. 1990). While lactoferroxin A has antagonistic effect on mu-receptors, lactoferroxin B and C are more specific for kappa-receptors.

Several whey derived cryptides are termed lactokinins, peptides with inhibitory properties against angiotensin-1-converting enzyme (ACE). Among them  $\alpha$ -lactorphin (human or bovine  $\alpha$ -lactalbumin Fr. 50-53),  $\beta$ -lactorphin ( $\beta$ -lactoglobulin bovine Fr. 102-105) and  $\beta$ -lactotensin ( $\beta$ -lactoglobulin bovine Fr. 146-149) can be reported as relevant examples (Tab. 3), the first two with sequence similarity to enkephalins (YGGFM or YGGFL). However, the lactokinin with the highest inhibitory ACE activity *in vitro* is the fragment 142-148 of  $\beta$ -lactoglobulin bovine (ALPMHIR) (FitzGerald and Meisel 1999). A statistically significant hypotensive effect has been demonstrated in humans for a limited number of milk cryptides (FitzGerald et al. 2004). Alpha and beta-lactorphins increase the acetylcholine induced relaxation of mesenteric arterial preparations in spontaneously hypertensive rats, but the effect does not involve the prostanoid pathway, instead it seems related to the nitric oxide pathway (Sipola et al. 2002) Interestingly, despite the very similar structure, the beneficial effect of  $\alpha$ -lactorphin is directed only towards endothelial function, while  $\beta$ -lactorphin enhances also endothelium-independent relaxation. Beta-lactotensin exhibits anxiolytic-like activity as an agonist for neurotensin NTS2 receptor via activation of dopamine D1 receptor (Hou et al. 2011) and rapidly reduces the levels of serum cholesterol (Yamauchi et al, 2003) in mice. The hypo-cholesterolemic activity was blocked by levocabastine showing the involvement of NTS2 receptor and was blocked by raclopride demonstrating an action of the peptide via dopamine D2 receptor too. Further experiments on mice showed that  $\beta$ -lactotensin increased memory consolidation in the step-through-type inhibitory avoidance test in mice. This effect is specifically mediated by the dopamine D2 receptor but not by the dopamine D1 receptor, because the effect is inhibited by raclopride, but not by SCH23390, an antagonist of D1 receptor (Ohinata et al. 2007). Overall  $\beta$ -lactoglobulin derived peptides, although not having the potency of synthetic anxiolytic,

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2 hypo-cholesterolemic or anti-hypertensive drugs, may represent potential natural, non-toxic food  
3 ingredients for prevention of stress, atherosclerosis and high blood pressure.  
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8 **6.2 Caseins deriving cryptides**  
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10 Caseins (CNs) are divided in different types according to their solubility. The best studied are  
11 bovine caseins which are named  $\alpha$ S1,  $\alpha$ S2,  $\beta$  and  $\kappa$ -casein (Nguyen et al. 2015). To date, the  
12 extensive study of  $\beta$ -casein allowed detecting at least 13 variants of this protein, including A1-4, B,  
13 C, D, E, F, H1 and H2, of which A1 and A2 are the most common variants (Kaminski et al. 2007).  
14 Human milk contains  $\alpha$ -,  $\beta$ - and  $\kappa$ -caseins and they account for about 13% w/w of the total protein  
15 content, the lowest casein concentration in the breast milk of any studied mammals (Andreas et al.  
16 2015).  $\kappa$ -Casein stabilizes the insoluble  $\alpha$ - and  $\beta$ -caseins forming a colloidal suspension. During the  
17 digestion process CNs are differently degraded forming numerous fragments whose activity was  
18 only partly investigated.  $\alpha$ - and  $\beta$ -CNs can generate phosphorylated peptides  
19 (caseinophosphopeptides, CPPs), which facilitate metal ion availability (calcium, iron, zinc). The  
20 most studied was the CPP  $\beta$ -CN(1-25)4P (4 phosphates) which exhibits a positive effects on iron  
21 availability (Bouhallab and Bouglé, 2004). By isothermal titration calorimetry carried out under  
22 experimental conditions mimicking those present in the ileum it was established that  $\beta$ -CN(1-25)4P  
23 binds  $\text{Ca}^{2+}$ ,  $\text{Mg}^{2+}$  and  $\text{Zn}^{2+}$ , but not  $\text{Cu}^{2+}$  with 1:2 stoichiometry and low binding affinity constants,  
24 suggestive for the release of metal ions during intestinal absorption (Zidane et al. 2012). A study  
25 performed with three CPPs  $\beta$ -CN(1-25)4P,  $\alpha$ (s1)-CN(64-74)4P and  $\alpha$ (s2)-CN(1-19)4P bovine on  
26 Caco-2 cells established that they increase ferritin synthesis versus iron sulphate alone,  $\beta$ -CN(1-  
27 25)4P being the most effective (Garcia-Nebot et al. 2013). They also increase zinc uptake but in a  
28 way similar to the increase observed in the presence of zinc sulphate alone, suggesting that, for this  
29 ion, the peptide did not exert a specific function. A recent study showed that five CPPs named P1 to  
30 P5, characterized by means of LC-MS/MS, were able to selectively allow  $\text{Mg}^{2+}$  absorption towards  
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2  $\text{Ca}^{2+}$  in Caco-2 cells growing in a medium enriched with  $\text{Ca}^{2+}$  and  $\text{Mg}^{2+}$  (Cao et al. 2017)]. The  
3 fragmentation of  $\alpha$ - and  $\beta$ -CN generates several antimicrobial peptides. The first peptides detected  
4 after chymosin digestion were called casecidins and originated from the C-terminal sequence of  $\beta$ -  
5 CN bovine (Lahov and Regelson, 1996). Casecidins inhibited *in vitro* staphylococci, sarcina,  
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7 *Bacillus Subtilis*, *Diplococcus Pneumoniae* and *Streptococcus pyogenes*. However, the low activity  
8 of casecidins *in vitro*, compared with common antibiotics, induced to explore others CNs fragments  
9 and in particular a non-immunogenic product of chymosin digestion that was called isracidin and  
10 corresponded to the N-terminal fragment 1-23 of  $\alpha(s1)$ -CN bovine, whom activity is comparable to  
11 that of commercial drugs. Casecidin 15, casecidin 17 and isracidin (Tab. 4) have been recently  
12 found naturally in bovine colostrums (Birkemo et al. 2009) where probably contribute to modulate  
13 microbiota in the early calf age. As we are aware these peptides until now have not been detected in  
14 human.

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16  $\beta$ -Casomorphins (BCMs) are a group of peptides with opioid-like activity and, among them, only  
17 casomorphin 7 ( $\beta$ -CN bovine 60-66; BCM7; Tab. 4) has been largely investigated (Nguyen et al.  
18 2015). The release of BCM7 by hydrolysis of  $\beta$ -CN occurs in the presence of  $\beta$ -CN A1, B and C  
19 bovine, which differently from other  $\beta$ -CN variants such as  $\beta$ -CN A2 bovine, show a His residue  
20 instead of Pro at position 67 (Nguyen et al. 2015). Several epidemiological studies suggested a link  
21 between consumption of milk containing the A1 variant and increased risk of type 1 diabetes and  
22 heart diseases (Laugesen and Elliott, 2003). However, the European Food Safety Authority in 2009  
23 concluded that the data were insufficient to establish a causal relationship between BCM7 ingestion  
24 and disease. A recent study showed that BCM7 has a protective effect against glucose-induced renal  
25 oxidative stress both *in vivo* (streptozotocin-induced diabetic rats) and *in vitro* (NRK-52E cells)  
26 (Zhang et al. 2013). Surely the availability of new analytical methods can in the next future help to  
27 elucidate the effective role of BMC7.

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$\beta$ -CN bovine can release casomokinin L (Tab. 4) a derivative of BCM with endothelium-dependent vasorelaxing activity probably mediated by NO. Although casomokinin L has only three residues in common with substance P, it binds to NK<sub>1</sub> receptors, relaxing the artery and exerting an antihypertensive effect (Fujita et al. 1996). Cleavage of  $\beta$ -CN bovine can release two short peptides acting as macrophage activators and with bradikinin-potentiating activity which were named casoparan, and casohypotensin (Tab. 4) and various antioxidant peptides (Lebrun et al. 2004).

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During gastric digestion,  $\kappa$ -CN can release the caseinomacropeptide (CMP) a 7-kDa peptide exhibiting growth-promoting activity for lactobacilli and bifidobacteria. During the digestive process peptides derived from CMP can be detected in the intestinal lumen. Recent studies have shown that pepsin and trypsin treatments of CMP promoted the growth of probiotics and that the pepsin treatment was more effective (Robitaille and Champagne, 2014). Therefore, it appears that some casein derived cryptides could have a relevant role in the modulation of the intestinal microbiota, especially in the pediatric age. Kaye and Jollès (1978) evidenced structural similarity of the peptide fragments of bovine  $\kappa$ -CN (Fr. 106-116) and the  $\gamma$ -chain of human fibrinogen (Fr. 400-411). This finding stimulated the discovery of a class of  $\kappa$ -CN fragments called casoplatelins (Tab. 4) with antithrombotic activity, because they are inhibitors of both the aggregation of ADP-activated platelets and the binding of the human fibrinogen  $\gamma$ -chain to its receptor on the platelet surface (Fiat et al. 1993). Although the potential physiological effects of these antithrombotic peptides have not been determined, they have been detected in physiologically active concentrations in the plasma of newborn infants after ingestion of a cow's milk-based formula or human milk, respectively suggesting that these bioactive peptides are released from milk proteins during digestion (Gobetti et al. 2007).

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The proteolysis of  $\kappa$ -CN by pepsin can generate various opioid antagonistic peptides called casoxins (Chiba et al. 1989). Among them, casoxin C (Tab. 4) evokes contraction of the ileum with a

contractile profile like that of the structurally homologous fragment 70-77 of human complement C3a. Indeed casoxin C had high affinity for C3a receptor and the induced ileum rapid contraction was mediated by histamine release, while the slow contraction was mediated by a prostaglandin E2-like substance (Takahashi et al, 1997). Finally,  $\alpha$ -,  $\beta$ - and  $\kappa$ -caseins can release, as  $\alpha$ -lactalbumin and  $\beta$ -lactoglobulin, more than twelve peptides ACE inhibitors, collectively termed casokinins having significant hypotensive effects (FitzGerald et al, 2004). On the whole this limited reported examples of milk cryptides indicated that an accurate study of their activities can be of great stimulus for the characterization of milk derived nontoxic nutraceuticals with the potential to significantly reduce global healthcare cost.

## 7. Miscellaneous cryptides

It is easily conceivable that many other sources of latent peptides exist: cell organelles, tissue protein matrices may provide a diversity of biologically active molecules. Mitochondria are in this view a rich source of cryptides (Raoof et al. 2010). As an example, cytochromes from porcine neutrophil mitochondria provide important biologically active cryptides. As reported in the introduction, the first discovered were named MCT-1 and MCT-2 (mitochondrial tricopeptide-1 and -2) (Mukai et al. 2009). The sequences of these two peptides coincided with the 23 C-terminal residues of porcine cytochrome c oxidase subunit VIII (LSFLIPAGWVLSHLDHYKRSSAA) and the 15 N-terminal residues of porcine mitochondrial cytochrome b (formyl-MTNIRKSHPLMKIIN), respectively. MCT-1 and MCT-2 are thought to play an important role in the innate immune system, contributing to enhance neutrophil responses to inflammation and traumas, thus to be considered as parts of the damage-associated molecular patterns (DAMPs) molecules produced in mitochondria (MTDs) (Hu et al. 2015). Interestingly, both these peptides present human counterparts (hMTC-1 and hMTC-2) showing identical biological activities (Mukai et al. 2009). Similarly, an octadecapeptide named mitocryptide-CYC (MCT-CYC), isolated from

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2 porcine heart resulted to be identical to the 68-85 sequence of mitochondrial cytochrome C. It was  
3 shown to possess features comparable to those of MCT-1 and MCT-2 enhancing the  $\beta$ -  
4 hexosaminidase release from neutrophilic-differentiated HL-60 cells (Hokari et al. 2012). Bacterial  
5 and mitochondrial proteins are the only source of N-formyl peptides in nature being recognized by  
6 specific N-formyl-peptide receptors (FPRL-1, 2). FPRLs have probably evolved to mediate  
7 phagocyte migration to sites of bacterial invasion. Mitochondrial N-formyl peptides are damage-  
8 associated molecules generated from cytochrome c oxidase (CoxI, CoxII and CoxIII), NADH  
9 dehydrogenase subunits (ND1, 2, 3, 4, 4L, 5 and ND6) and ATP synthase sharing structural  
10 similarity to bacterial N-formylated peptides. Different novel mitochondrial formyl-peptides have  
11 been identified and characterized as agonists for human FPRL-1 and FPRL-2 suggesting that might  
12 play a role in inflammatory or degenerative processes upon their stimulation (Rabiet et al. 2005).  
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16 Collagen was seen to be another source of latent peptides possessing interesting features linked to  
17 wound healing, chemotaxis and antioxidant activities. In particular, a peptide named E1  
18 (GETGPAGPAGPIGPVGARGPAGPQGPRGDKGETGEQ) was purified and structurally  
19 characterized after the treatment of collagen derived from bovine Achilles tendon with bacterial  
20 proteolytic enzymes. Although its sequence does not contain amino acid residues considered typical  
21 antioxidants such as tyrosine, a certain ability to scavenge radical species was observed (Banerjee et  
22 al. 2012). Further, the same peptide was shown to possess also wound healing properties (Banerjee  
23 et al. 2016). Collagen was seen to be a source of bioactive peptides helping in endothelial injury  
24 upon bacterial infection. When capillary-endothelial-derived extracellular matrices were treated  
25 with collagenase derived from *Clostridium histolyticum*, a series of peptides were identified by mass  
26 spectrometry which were demonstrated to possess wound healing properties (Demidova-Rice et al.  
27 2010).  
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30 Autophagy is an important evolutionarily conserved cytoplasm-homeostatic complex of cellular  
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2 mechanisms aimed to eliminate damaged cellular components. During this function p62, a protein  
3 dedicated to this role also known as Sequestosome-1, sequesters cytosolic proteins (ribosomal  
4 protein rpS30 precursor FAU and ubiquitin) into autophagosomes where they are proteolytically  
5 converted into cryptides. In the case of *Mycobacterium tuberculosis* infection, p62 may capture  
6 bacteria in autophagosomes where they are challenged with the peptides originated as above  
7 mentioned that behave as antimicrobial peptides (Ponpuak et al. 2011).  
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11 Plasma proteins linked to coagulation were shown to be another rich source of cryptides. In  
12 particular, a wide range of peptides from C-terminal sequences of serine proteases, mainly from the  
13 coagulation and kallikrein systems, share characteristics common with classical antimicrobial  
14 peptides of innate immunity (Kasetty et al. 2011). A series of peptides were predicted by means of  
15 bioinformatics approaches identifying 68 S1 serine proteases deriving peptides with antimicrobial  
16 activity and sharing the X-[PFY]-X-[AFILV]-[AFY]-[AITV]-X-[ILV]-X(5)-W-[IL]-X sequence  
17 (Papareddy et al. 2010; Kasetty et al. 2011). In a similar fashion, antithrombin III (ATIII) beside its  
18 anticoagulant effect, exerts anti-inflammatory activity and preserves the microvascular leakage  
19 counteracting the bacterial growth in systemic infections. This last property was shown to be linked  
20 with the activity of the bacterial proteases which may release several peptides from the parent  
21 protein. One of these, named FFF21, deriving from the D helix in ATIII, was identified as an  
22 antimicrobial peptide effective against *E. coli* and *P. aeruginosa* through a membranolytic  
23 mechanism of action (Papareddy et al. 2014). Also thrombin releases various active peptides  
24 (Papareddy et al. 2010): it was indeed demonstrated that the thrombin derived host-defence peptide  
25 GKY25 (GKYGFYTHVFRKKWIQKVIDQFGE) deriving from the C-terminus of the protein  
26 inhibits LPS-induced responses of monocytes, macrophages and neutrophils *in vitro*, *ex vivo* and  
27 *in vivo* (Singh et al. 2013; Hansen et al. 2015; Lim et al. 2017). GKY25 have a broad and inhibitory  
28 effect on multiple sepsis pathologies. In a mouse model of *Pseudomonas aeruginosa* sepsis, while  
29 mediating a modest antimicrobial effect, GKY25 is able to significantly inhibit the pro-  
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3 inflammatory response, to decrease fibrin deposition in the lungs and to reduce mortality. It is  
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5 therefore an attractive candidate for the treatment of invasive infections (Kalle et al. 2012).  
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## 8. Conclusions

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11 It is important to remark that cryptides reported in this review are limited examples of a huge  
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13 number of peptides described in a growing and vast literature impossible to cover in its totality.  
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15 Apologizing for many and relevant omissions, the paradigms here described clearly indicate that  
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17 “cryptides” research is only at the beginning and that they represent a wide biological event hitherto  
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19 underestimated. Some of them were detected in bodily fluids (as cryptides from milk and saliva)  
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21 that are in contact with the microbiota. These cryptides are at the most challenging to study, because  
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23 they can be generated by the host proteinases and can exert retro-actions, modulating at-turn the  
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25 colonization of the gastro-intestinal tracts. Therefore, their role has to be established in the complex  
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27 interplay occurring in symbiosis. Other examples, i.e. cryptides either with opioid-like or with  
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29 antimicrobial activity, suggests that their generation is strictly and finely connected to the life-span  
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31 of the parent proteins, which, terminating its role, can release smaller peptides able to modulate  
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33 functions in some way related to the function of the parent protein. The continuous discovery of  
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35 new cryptides induces to postulate that bigger proteins are probably assembled during evolution  
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37 from building blocks of smaller peptides with variegate function, often disconnected from those of  
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39 the parent protein. Cryptides are therefore a strong suggestion for the presence of genomes with  
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41 multiple information inside the exonic polynucleotide sequence. The investigation of the timing of  
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43 cryptides production and of the enzymes responsible for their release is a challenge that enhances  
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45 the complexity of proteomic studies. Nonetheless their knowledge adds new insights in the  
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47 articulated interaction between the genome and the proteome.  
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53 The identification and characterization of many cryptides by *in vitro* experiments will require very  
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55 accurate experimental plans in order to avoid false positive and negative determinations and to  
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1 exactly reproduce the specific proteolytic cascades occurring *in vivo*. Challenging will be the study  
2 of the cryptides role in the cellular pathways and of their interactions in the cellular machinery as  
3 well as the determination of the enzymatic cascade responsible for their generation. Also  
4 challenging will be the development of new –omic platforms for the fast and easy characterization  
5 of their function in complex mixtures. As mentioned, many cryptides are generated by a fine  
6 interplay between the host and his/her microbiota and the comprehension of these interactions will  
7 require the development of new throughput strategies to better understand reciprocal interactions.  
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9 Proteomics, particularly with the use of top-down strategies, can contribute to large surveys for  
10 cryptides detection. However, demanding is the development of new high throughput platforms for  
11 the experimental identification of cryptides with specific functions. In this respect very interesting  
12 are theoretical predictions on the basis of common structural determinants found in cryptides with  
13 similar role. Several successful examples of the application of this strategy have been reported in  
14 the previous section for the theoretical detection of peptides with variegate activities from bovine  
15 hemoglobin (Ivanov et al. 1997) or for the detection of antimicrobial peptides from sequestosome-1  
16 (Papareddy et al. 2010; Kasetty et al. 2011). Recently, Pane and colleagues (Pane et al. 2017)  
17 established that the antimicrobial potency of cationic antimicrobial peptides (CAMPs) linearly  
18 correlates to the product of  $C^mH^nL$ , where C is the net charge of the peptide, H is the measure of its  
19 hydrophobicity and L the length. The m and n exponents are related to the relative contribution of  
20 charge and hydrophobicity and, interestingly, are strain specific. Some strains are more sensitive to  
21 highly charged CAMPs, while others are more susceptible to the peptide hydrophobicity. This  
22 computational analysis represented a strategy to identify CAMPs included inside the structure of  
23 larger proteins and precursors. Among various cryptides, this strategy allowed to postulate the  
24 existence of a new CAMP from 11-hydroxysteroid dehydrogenase-1  $\beta$ -like protein, called GVF27  
25 that demonstrated to be not toxic towards human and murine cell lines and to trigger significant  
26 immune response by attenuating expression levels of pro-inflammatory interleukins and NO-release  
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3 in LPS induced macrophages (Bosso et al. 2017). This approach was designed for the screening of  
4 potential CAMPs in large pools of sequences and the development of further CAMPs surely will  
5 reinforce the predictive power of the therotical model. Indubitably similar platforms could allow in  
6 the future design creative classes of peptide-mimetics with powerful and specific antibacterial  
7 activity.  
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14 In conclusion, cryptide presence in biological systems affords new complexity to the  
15 comprehension of the phenotype expression and implicates superimposition in the information  
16 resident in the gene codifying the parent protein. Cryptide study could be hence of great help to  
17 decipher better the message included in polynucleotide sequences. Without any doubt a better  
18 definition of their presence and role in biological systems will offer to scientists new suggestions  
19 for the synthesis of bioactive peptides and peptido-mimetics characterized by low toxicity in  
20 numerous fields of application.  
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The authors report no conflict of interest.

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Principal pathways for the generation of cryptides. In the present review the term cryptide refers to a bioactive peptide, encrypted inside a bigger functional polypeptide and released by a proteolytic event, with a function distinct or related, but not super-imposable, to that one of the parent polypeptide. The majority of cryptides are extracellular cryptides (right part of the Figure) generated by proteolytic processes occurring on functional polypeptides of any length after secretion (either *in vivo* or *ex vivo* or *in vitro*). According to this definition, the functional peptides generated by the cleavage (usually by convertases) of pre-pro-proteins before the secretion (see for instance the Section on saliva) are not discussed in this review, since they cannot be considered cryptides. Indeed, the cleavage occurring during the Golgi transit allows the maturation of the functional form of the polypeptide, which will exert its activity only after secretion. Anyhow, these functional peptides can hide inside their sequence functional cryptides. On the left part of the Figure the possible production of intracellular cryptides is briefly depicted. They are less studied than the extracellular ones. Their related proteolytic events can follow various pathways, such as lysosomal and proteasomal cleavages. Intracellular cryptides can exert their function either inside or outside the cell, for instance after apoptotic or necrotic events. If devoted to specific functions in tissues they could be generated before the maturation of the functional protein, however to verify this route remains a question mark. Recently, many evidences indicated that functional small peptides are encoded by short open reading frames (ORF) upstream from a downstream coding DNA sequence (CDS) (Andrews and Rothnagel 2014). These peptides are not considered cryptides in this review because they are not encrypted into a bigger functional polypeptide sequence. Any cryptide, in turn, can nest inside their sequence smaller cryptides (cryptides of second generation). The scheme does not include other particular routes for cryptides production, such as that of polypeptides encoded by the DNA of the mitochondrion.

Table 1. Hemorphins' subfamilies.

Hemorphins'	amino acid	name
subfamilies	sequence	
LVV-hemorphins	LVVYPWTQRF	LVV-hemorphin-7
	LVVYPWTQR	LVV-hemorphin-6
	LVVYPWTQ	LVV-hemorphin-5
	LVVYPWT	LVV-hemorphin-4 (spinorphin)
VV-hemorphins	VVYPWTQRF	VV-hemorphin-7
	VVYPWTQR	VV-hemorphin-6
	VVYPWTQ	VV-hemorphin-5 (valorphin)
	VVYPWT	VV-hemorphin-4
V-hemorphins	VYPWTQR	V-hemorphin-7
	VYPWTQ	V-hemorphin-6
	VYPWT	V-hemorphin-5
	VYPW	V-hemorphin-4
hemorphins	YPWTQRF	hemorphin-7
	YPWTQR	hemorphin-6
	YPWTQ	hemorphin-5
	YPWT	hemorphin-4

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2  
3 Table 2. Several fragments of human salivary proline-rich proteins recurrently detected in human  
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5 saliva with potential protective and antibacterial activity.  
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amino acid sequence	Gene
SPPGKPQ	<i>PRB1-PRB2-PRB4</i>
PQGPPPQ	<i>PRB1-PRB2-PRB3-PRB4</i>
PEGPPPQ	<i>PRB3-PRB4</i>
GPPPGKPQ	<i>PRB1-PRB4</i>
GPPPPGKPQ	<i>PRB1</i>
GPPPQGGSKSR	<i>PRB2</i>
RPPPPPGKPQ	<i>PRB4</i>
RPPPPPGKPE	<i>PRB4</i>
GPPPQGGNKPQ	<i>PRB1-PRB2</i>
GPPPQGGNQPQ	<i>PRB1-PRB2</i>
GPPQQEGNNPQ	<i>PRB1-PRB2</i>
GPPPQGDKSRSP	<i>PRB1-PRB2</i>
SPPGKPQGPPPQGGNQPQ	<i>PRB1-PRB2</i>
GPPPQGGNKPQGPPPGKP	<i>PRB1-PRB2</i>
GPPPPGGNPQQPQAPPAGKPQ	<i>PRB4-M,L</i>
GPPPQGGNQPQGPPPPGKPQ	<i>PRB1-PRB2</i>

Table 3. Several cryptides detected in whey from breast milk

Parent polypeptide	Cryptide Sequence (one letter code)			Known function	Reference			
Lactoferrin Human	Lactoferricin H *	GRRRSVQWCA <sup>10</sup> VSQPEATKCF <sup>20</sup> QWQRNMRKVR <sup>30</sup> GPPVSCIKRD <sup>40</sup>	SPIQCIQA	antimicrobial and antiviral activity	Haug et al. 2007			
	Lfpep (from lactoferricin H)	TKCF <sup>20</sup> QWQRNMRKVR <sup>30</sup> GPPVSCIKRD <sup>40</sup>		candidacial activity	Viejo-Diaz et al. 2005			
	PFR-peptide	PFWRIRIRR-NH <sub>2</sub>		antitumoral activity	Lu et al. 2016			
	Kaliocin-1	FFSASCVPGA <sup>10</sup> DKGQFPNLCR <sup>20</sup> LCAGTGENKC <sup>30</sup> A		candidacial activity	Viejo-Diaz et al. 2005			
	Lactoferrampin human	WNLLRQAQEK <sup>10</sup> FGKDKSPK		antimicrobial and antiviral activity	Bruni et al. 2016			
	Lactoferroxin A	YLGSY	Lactoferroxin B	RYYGY	Lactoferroxin C	KYLGPQY	opioid antagonists	Tani et al. 1990
	Lactoferricin B **	FKCRRWQWRM <sup>10</sup> KKLGAPSITC <sup>20</sup> VRRAF		antimicrobial and antiviral activity	Wakabayashi et al. 2003			
Lactoferrin Bovine	Lactoferrampin bovine	DLIWKLLSKA <sup>10</sup> QEKFGKNKSR		antimicrobial and antiviral activity	Wang 2016			
	$\alpha$ -lactalbumin human or bovine	$\alpha$ -lactorphin YGLF		ACE-inhibitory activity	FitzGerald and Meisel 1999			
$\beta$ -lactoglobulin bovine	$\beta$ -lactorphin YLLF			ACE-inhibitory activity	FitzGerald and Meisel 1999			
	$\beta$ -lactotensin HIRL			ACE-inhibitory activity	FitzGerald and Meisel 1999			

\* Lactoferricin H is cleaved between residues V<sub>11</sub> and S<sub>12</sub>. The fragments are connected by a disulfide bridge between C<sub>9</sub> and C<sub>19</sub>.

\*\*Disulfide bridge between C<sub>3</sub> and C<sub>20</sub>.

Table 4. Several cryptides detected in casein from bovine breast milk

Parent polypeptide	Cryptide Sequence (one letter code)	Known function	Ref.
bovine $\beta$ -casein	Casecidin 15 YQEPVLGPVR <sup>10</sup> GPFPPI	antimicrobial activity	Birkemo et al. 2009
	Casecidin 17 YQEPVLGPVR <sup>10</sup> GPFPPIV	antimicrobial activity	Birkemo et al. 2009
	Casomorphin 7 (BMC7) YPFPGPI	opioid-like activity	Nguyen et al. 2015
	Casomokinin L YPFPPL	endothelium-dependent vasorelaxing activity	Fujita et al. 1996
	Casoparan INKKI	macrophage activator, bradikinin-potentiating activity	Lebrun et al. 2004
	Casohypotensin YPVEPFTE	bradikinin-potentiating activity	Lebrun et al. 2004
bovine $\alpha$ (S1)-casein	Isracidin RPKHPIKHQG <sup>10</sup> LPQEVLNENL <sup>20</sup> LRF	antimicrobial activity	Birkemo et al. 2009
bovine $\kappa$ -casein	Casoplatelins MAIPPKNQDK MAIPP MAIPPKK NQDK Casoxin C YIPIQYVLSR	antithrombotic activity opioid antagonistic	Fiat et al. 1993 Takahashi et al, 1997

