Corrigendum

Steroid hormone synthesis by a vaccinia enzyme: a new type of virus virulence factor

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A typographical error was made in the preparation of Figure 1, resulting in the removal of several regions of amino acid sequence. The correct figure is shown below.

Bovine Human SalF7L	MAGWSCLVTGGGGFLGQRIICLLVEEKDLQEIRVLDKVFRPEVREEFSKLQSKIK-LTLLEGDTLDEQCLKGACQGTMTGWSCLVTGAGGFLGQRIIRLLVKEKELKEIRVLDKAFGPELREEFSKLQNKITK-LTVLEGDILDEPFLKRACQDVMAVYAVTGGAGGFLGRYIVKLLISADDVQEIRVIDIVEDPQPITSKVVKVINYIQCDINDFDKVREALDGV	76 76 69
Bovine Human SalF7L	S V V <mark>I H T A S V I D V R N A V P R E T I M N V N V K G T Q L L L E A C V Q A S V P V F I H T S T I E V A G P N S Y R E I I Q D G R E E E H H E S A W S S S V I I H T A C I I D V F G V T H R E S I M N V N V K G T Q L L L E A C V Q A S V P V F I Y T S S I E V A G P N S Y K E I I Q N G H E E E P L E N T W P A N L I I H T A A L V D V F G K Y T D N E I M K V N Y Y G T Q T I L A A C V D L G I K Y L I Y T S S M E A I G P N K H G D P F - I G H E H T L Y D I S P G H</mark>	153 153 145
Bovine Human SalF7L	PYPYSKK LAEK AVL GANG WALKNOG TLYTCALRPM YIYGEG SPFL SAYMH GALNNN GILT NH CKF SRVN P-VYVG NV PYPH SKK LAEK AVLAANG WN LKN GG TLYTCALRPM YIYGEG SRFL SASINE ALNNN GILSSV G KF STVN P-VYVG NV VYAKSKR MAEQ LVM KANNSV I MN GAKLYTC CLRPT GIYGEGD KLTKV FYE Q CKQHG NIJM YR TVDD DAVH SR <u>VYVG NV</u>	229 229 222
Bovine Human SalF7L	A WAHILALRALR DPKK V P NIQGO FYY I SDD TPH QS Y DD LNY TLISKE WGFC LDSRM S LPI S LQ Y W LAF L LE I V S FIL LS A WAHILALRALQ DPKKAP S IRGQ FYY I SDD TPH QS Y D N LNY TLISKEFGLR LDSRW S FPL S LM Y W I G F L LE I V S FIL LRAWMEN V LAAKY I QYP G S EIKGN AYFC Y DY S PS C S Y DM F N L LLMKP LG I E Q G S R IPR W M L K M Y A C K N D M K R I L F R	306 306 295
Bovine Human SalF7L	PIYKYNPCFNRHLVTLS NSVFTFSYKKAQ RDLGYEPLYTWEEAK Q KTKEWIGSLVK QHKETLKTKIH PIYTYRPPFNRHIVTLIS NSVFTFSYKKAQ RDLAYKPLYS WEEAK Q KTVEWVGSLVDRHKETLKSKT Q KPSLLNNYTLKIS NTTFEVRTN NAELDLFNYSEPIFN VD VAAFERTRKWLEESE	373 373 346

Fig. 1. Amino acid alignments of vaccinia SalF7L and bovine and human 3β-HSD sequences. Sequences were aligned using the programme Pileup of the Genetics Computer Group Package [Devereux,J., Haeberli,P. and Smithies,O. (1984) *Nucleic Acids Research*, **12**, 387–395]. Residues conserved in all three sequences are boxed.