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Sequence conservation of linker histones between chicken and mammalian species

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ABSTRACT

The percent identity matrices of two sequence multiple alignments between linker histones from chicken and mammalian species are described. Linker histone protein sequences for chicken, mouse, rat and humans, available on public databases were used. This information is related to the research article entitled "Identification of novel post-translational modifications in linker histones from chicken erythrocytes" published in the Journal of Proteomics [1].

Specifications table

Subject area	Biology
More specific subject area	Molecular evolution
Type of data	Tables
How data was acquired	Multiple sequence alignment using ClustalW running under MEGA 5.2
Data format	Analyzed
Experimental factors	Two multiple sequence alignments were performed corresponding to the H1.1–H1.5 clade and the H1.0/H5 clade [2]. Initial methionine was removed from the protein sequence prior to the multiple sequence alignment.
Experimental features	Percent identity matrix contains the identity score from all of the pairwise comparisons calculated as the number of identities between two sequences divided by the length of the alignment and represented as a percentage.
Data source location	Not applicable
Data accessibility	All the sequences are registered at Uniprot or NCBI protein databases. The specific accession numbers are described below in Section 3.

Value of the data

- Paralogous comparisons show that the six H1 subtypes from chicken (H1.01–H1.03, H1.10, H1.1L and H1.1R) are significantly closer, with an average percent identity of 90%, than mammalian paralogs (H1.1–H1.5) in any of the analyzed species, with an average percent identity of 73% (Table 1). The larger divergence of the mammalian paralogs in comparison with chicken paralogs suggests that the mammalian subtypes have acquired specific functions [3–5].
- Orthologous comparisons show that the H1 subtypes (H1.0–H1.5) from mouse, rat and humans, are highly conserved in interspecies comparison, reinforcing the idea of the functional differentiation of the H1 subtypes (Tables 1 and 2). The most divergent subtype is H1.1 with percentages of identity over 79%, while the more conserved subtypes are H1.0 and H1.4 with percentages of identity over 94% [3,4].
- All six chicken H1 subtypes have higher percentages of identity when compared with H1.4 (more than 65%), suggesting that its function is conserved between avian and mammalian species (Table 1).
- The percentage of identity between H5, an avian specific linker histone associated with terminal differentiation and its mammalian counterpart H1.0 is over 66%, indicating function conservation (Table 2).
- Figs. 1 and 2 show that the globular domain is the most conserved region of the linker histones [3,4].

1. Experimental design, materials and methods [1]

Two separate sequence alignments were performed with chicken linker histones (see Figs. 1 and 2). The first included chicken H5 and H1.0 from mouse, rat and humans (Fig. 1), and the second included the six chicken H1 subtypes and H1 subtypes (H1.1–H1.5) from the above specified species (Fig. 2). In both cases an initial alignment was obtained using ClustalW running under MEGA 5.2. The alignment was then optimized by visual inspection. The pairwise identity score was calculated by the number of identities between two sequences divided by the length of the alignment and represented as a percentage. The accession numbers for the chicken (ch), mouse (m), rat (r) and human (h) sequences were as follows: H5_ch, Uniprot: P02259; H1.01_ch, Uniprot: P08284; H1.02_ch, Uniprot: P09987; H1.03_ch, Uniprot: P08285; H1.10_ch, Uniprot: P08286; H1.1L, Uniprot: P08287; H1.1R, Uniprot: P08288; H1.0_m, Uniprot: P10922; H1.1_m, Uniprot: P43275; H1.2_m, Uniprot: P15864; H1.3_m, Uniprot: P43277; H1.4_m, Uniprot: P43274; H1.5_m, Uniprot: P43276; H1.0_r; Uniprot: P43278; H1.1_r, NCBI Protein: NP_001099583; H1.2_r, NCBI Protein:XP_001071565; H1.3_r, NCBI Protein:XP_001072089; H1.4_r, NCBI Protein: x67320, H1b_r, NCBI Protein: NP_001102887; H1.0_h, Uniprot: P07305; H1.1_h, Uniprot: Q02539; H1.2_h, Uniprot: P16403; H1.3_h, Uniprot: P16402; H1.4_h, Uniprot:P10412; H1.5_h, Uniprot: P16401.

Table 1

Percent identity matrix of the avian and mammalian H1 subtypes.

	H1.01_ch	H1.02_ch	H1.03_ch	H1.10_ch	H1.1L_ch	H1.1R_ch	H1.1_m	H1.2_m	H1.3_m	H1.4_m
H1.01_ch	100.00									
H1.02_ch	91.66	100.00								
H1.03_ch	88.33	86.25	100.00							
H1.10_ch	92.50	90.83	89.16	100.00						
H1.1L_ch	89.16	86.66	89.58	90.00	100.00					
H1.1R_ch	90.00	87.08	89.58	90.41	92.08	100.00				
H1.1_m	60.41	61.66	60.00	59.58	60.41	61.25	100.00			
H1.2_m	62.50	62.91	60.83	63.74	62.08	62.91	63.33	100.00		
H1.3_m	66.66	66.25	64.58	65.83	64.16	66.25	68.75	78.75	100.00	
H1.4_m	70.00	67.91	65.41	68.33	65.00	67.50	68.75	78.75	87.08	100.00
H1.5_m	65.00	64.16	62.91	64.16	61.66	63.74	67.91	69.16	81.25	77.50
H1.1_r	60.41	60.83	58.75	58.75	60.41	60.00	95.00	62.08	66.25	67.91
H1.2_r	62.50	62.91	60.83	63.74	62.08	62.91	64.16	97.91	78.75	79.58
H1.3_r	65.00	65.00	63.33	64.16	62.91	65.00	66.25	75.83	94.58	83.33
H1.4_r	69.16	67.50	65.41	67.50	65.00	67.50	68.75	80.41	88.33	97.08
H1.5_r	63.74	62.50	61.66	62.50	60.00	62.50	66.25	67.08	80.00	76.25
H1.1_h	60.41	60.83	59.16	59.58	60.41	60.83	80.83	64.58	70.83	70.00
H1.2_h	64.58	65.00	62.50	65.00	62.91	63.74	63.74	87.91	80.83	80.00
H1.03_h	65.41	65.00	63.33	64.16	62.08	64.16	66.66	75.00	88.75	84.16
H1.4_h	70.00	69.16	67.08	70.00	67.08	69.58	69.58	81.25	90.00	94.16
H1.5_h	67.50	67.08	64.58	67.08	65.00	67.08	64.58	72.50	81.25	81.66

	H1.5_m	H1.1_r	H1.2_r	H1.3_r	H1.4_r	H1.5_r	H1.1_h	H1.2_h	H1.3_h	H1.4_h	H1.5_h
H1.01_ch											
H1.02_ch											
H1.03_ch											
H1.10_ch											
H1.1L_ch											
H1.1R_ch											
H1.1_m											
H1.2_m											
H1.3_m											
H1.4_m											
H1.5_m	100.00										
H1.1_r	66.25	100.00									
H1.2_r	69.16	62.91	100.00								
H1.3_r	77.91	64.58	75.83	100.00							
H1.4_r	77.91	67.91	81.25	84.58	100.00						
H1.5_r	96.25	65.00	67.08	76.66	76.66	100.00					
H1.1_h	68.75	79.16	65.00	69.16	70.83	67.50	100.00				
H1.2_h	71.25	62.50	87.91	77.50	80.41	69.16	65.00	100.00			
H1.03_h	75.83	65.41	75.00	84.16	84.58	74.58	69.16	78.33	100.00		
H1.4_h	80.00	68.75	81.25	85.83	95.41	78.75	72.50	81.66	85.83	100.00	
H1.5_h	91.25	63.74	72.50	77.91	82.08	89.16	68.33	72.91	77.08	84.16	100.00

The pairwise identity score was calculated by the number of identites between two sequences, divided by the length of the alignment represented as a percentage. Abbreviations: ch, chicken; m, mouse; r, rat and h, humans.

Table 2
Percent identity matrix of avian H5 and mammalian H1.0.

H5_ch	100.00			
H1.0_m	67.01	100.00		
H1.0_r	66.49	97.93	100.00	
H1.0_h	67.01	94.84	94.32	100.00
	H5_ch	H1.0_m	H1.0_r	H1.0_h

The pairwise identity score was calculated by the number of identites between two sequences, divided by the length of the alignment represented as a percentage.
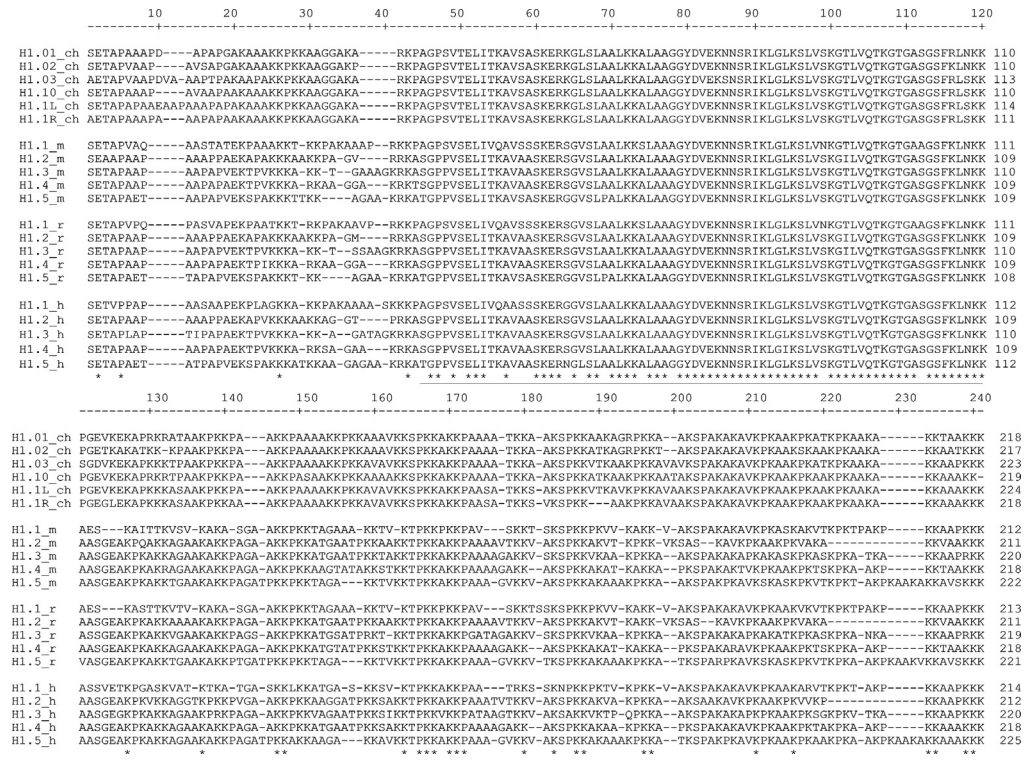Abbreviations: ch, chicken; m, mouse; r, rat and h, humans.

```
                10        20        30        40        50        60        70        80        90       100       110       120
         --------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+

H1.01_ch SETAPAAAPD----APAPGAKAAAKKPKKAAGGAKA-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLNKK 110
H1.02_ch SETAPVAAP----AVSAPGAKAAAKKPKKAAGGAKP-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 110
H1.03_ch AETAPVAAPDVA-AAPTPAKAAPAKKPKKAAGGAKA-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKSNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLSKK 113
H1.10_ch SETAPAAAP----AVAAPAAKAAAKKPKKAAGGAKA-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLSKK 110
H1.1L_ch SETAPAPAAEAAPAAAPAPAKAAAKKPKKAAGGAKA-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLSKK 114
H1.1R_ch AETAPAAAPA---AAPAPAAKAAAKKPKKAAGGAKA-----RKPAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLSKK 111

H1.1_m   SETAPVAQ-----AASTATEKPAAAKKT-KKPAKAAAP--RKKPAGPSVSELIVQAVSSSKERSGVSLAALKKSLAAAGYDVEKNNSRIKLGLKSLVNKGTLVQTKGTGAAGSFKLNKK 111
H1.2_m   SEAAPAAP----AAAPPAEKAPAKKKAAKKPA-GV-----RRKASGPPVSELITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGILVQTKGTGASGSFKLNKK 109
H1.3_m   SETAPAAP----AAPAPVEKTPVKKKA-KK-T--GAAAGKRKASGPPVSELITKAVSASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 110
H1.4_m   SETAPAAP----AAPAPAEKTPVKKKA-RKAA-GGA---KRKTSGPPVSELITKAVSASKERGGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 109
H1.5_m   SETAPAET-----AAPAPVEKSPAKKKTTTKK----AGAA-KRKATGPPVSELITKAVSASKERGGVSLPALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 109

H1.1_r   SETAPVPQ-----PASVAPEKPAATKKT-RKPAKAAVP--RKKPAGPSVSELIVQAVSSSKERSGVSLAALKKSLAAAGYDVEKNNSRIKLGLKSLVNKGTLVQTKGTGAAGSFKLNKK 111
H1.2_r   SETAPAAP----AAAPPAEKAPAKKKAAKKPA-GM-----RRKASGPPVSELITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGILVQTKGTGASGSFKLNKK 109
H1.3_r   SETAPAAP----AAPAPVEKTPVKKKA-KK-T--SSAAGKRKASGPPVSELITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGILVQTKGTGASGSFKLNKK 110
H1.4_r   SETAPAAP----AAPAPAEKTPIKKKA-RKAA-GGA---KRKASGPPVSELITKAVSASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 109
H1.5_r   SETAPAET-----TAPAPVEKSPAKKKT-KK----AGAA-KRKATGPPVSELITKAVSASKERGGVSLPALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 108

H1.1_h   SETVPPAP-----AASAAPEKPLAGKKA-KKPAKAAAA-SKKKPAGPSVSELIVQAASSSKERGGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 112
H1.2_h   SETAPAAP-----AAAPPAEKAPVKKKAAKKAG-GT----PRKASGPPVSELITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 109
H1.3_h   SETAPLAP-----TIPAPAEKTPVKKKA-KK-A--GATAGKRKASGPPVSELITKAVSASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 110
H1.4_h   SETAPAAP-----AAPAPAEKTPVKKKA-RKSA-GAA---KRKASGPPVSELITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIKLGIKSLVSKGTLVQTKGTGASGSFKLNKK 109
H1.5_h   SETAPAET-----ATPAPVEKSPAKKKATKKAA-GAGAA-KRKATGPPVSELITKAVAASKERNGLSAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFKLNKK 112
            *  *                 *                          *  ** **  ***  *  **** ** ** **** ***  ****************  *********** ******** 


                130       140       150       160       170       180       190       200       210       220       230       240
         --------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+

H1.01_ch PGEVKEKAPRKRATAAKPKKPA---AKKPAAAAKKPKKAAAVKKSPKKAKKPAAAA-TKKA-AKSPKKAAKAGRPKKA--AKSPAKAKAVKPKAAKPKATKPKAAKA------KKTAAKKK 218
H1.02_ch PGETKAKATKK-KPAAKPKKPA---AKKPAAAAKKPKKSPKKAKKPAAAA-TKKA-AKSPKKATKAGRPKKT--AKSPAKAKAVKPKAAKSKAAKPKAAKA-------KKAATKKK 217
H1.03_ch SGDVKEKAPKKKTPAAKPKKPA---AKKPAAAAKKPKKAVAVKKSPKKAKKPAAAA-TKKA-AKSPKVTKAAKPKKAVAVKSPAKAKAVKPKAAKPKATKPKAAKA------KKAAPKKK 223
H1.10_ch PGEVKEKAPRKRTPAAKPKKPA---AKKPAAAAKKPKKAAAAAKKSPKKAKKPAAAA-TKKA-AKSPKKAAATAKSPAKAKAVKPKKAATAKSPAKAKAVKPKAAKPKAAKA-----KKAAAKK- 219
H1.1L_ch PGEVKEKAPKKKASAAKPKKPA---AKKPAAAAKKPKKAVAVKKSPKKAKKPAASA-TKKS-AKSPKKVTKAVKPKKAVAAKSPAKAKAVKPKKAAKPKAAKPKAAKA------KKAAAKKK 224
H1.1R_ch PGEGLEKAPKKKASAAKPKKPAA---AKKPAAAAKKPKKAVAVKKSPKKPAASA-TKKS-VKSPKK---AKSPKKAVAAKSPAKAKAVKPKKAAKPKAAKPKAAKA------KKAAAKKK 218

H1.1_m   AES---KAITTKVSV-KAKA-SGA-AKKPKKTAGAAA-KKTV-KTPKKPKKPAV---SKKT-SKSPKKPKVV-KAKK-V-AKSPAKAKAVKPKASKAKVTKPKTPAKP-----KKAAPKKK 212
H1.2_m   AASGEAKPQAKKAGAAKAKKPAGA-AKKPKKATGAATPKKAAKKTPKKAKKPAAAAVTKKV-AKSPKKAKVT-KPKK-VKSAS--KAVKPKAAKPKVAKA-------------KKVAAKKK 211
H1.3_m   AASGEAKPKAKKAGAAKAKKPAGA-AKKPKKATGAATPKKAAKKPGATAGAKKV-SKSPKKVKAA-KPKKA---AKSPAKAKAPKAKATKPKASKPKA-NKA-----KKAAPRKK 220
H1.4_m   AASGEAKPKAKRAGAAKAKKPAGA-AKKPKKAAGTATAKKSTKKTPKKAKKPAAAAGAKK---AKSPKKAKAT-KAKKA---PKSPAKAKTVKPKAAKPKTSKPKA-AKP-----KKTAAKKK 218
H1.5_m   VASGEAKPKAKKTGAAKAKKPAGATPKKPKTAGA---KKTVKKTPKKAKKPAAA-GVKKV-AKSPKKAAAKPKKA--TKSPARPKAVKSKASKPKVTKPKA-AKPKAAKAAKKAVSKKK 222

H1.1_r   AES---KASTTKVTV-KAKA-SGA-AKKPKKTAGAAA-KKTV-KTPKKPKKPAV---SKKTSSKSPKKPKVV-KAKK-V-AKSPAKAKAVKPKAAKVKVTKPKTPAKP-----KKAAPKKK 213
H1.2_r   AASGEAKPKAKKAAAAKAKKPAGA-AKKPKKATGAATPKKAAKKTPKKAKKPAAAAVTKKV-AKSPKKAKVT-KAKK-VKSAS--KAVKPKAAKPKVAKA-------------KKVAAKKK 211
H1.3_r   AASGEAKPKAKKVGAAKAKKPAGS-AKKPKKATGSATPRKT--KKTPKKAKKPGATAGAKKV-SKSPKKVKAA-KPKKA---AKSPAKAKAPKAKATKPKASKPKA-NKA-----KKAAPRKK 219
H1.4_r   AASGEAKPKAKKAGAAKAKKPAGA-AKKPKKATGTATPKKSTKKTPKKAKKPAAAAGAKK---AKSPKKAKAT-KAKKA---PKSPAKAKAPKAAKPKTSKPKA-AKP-----KKTAAKKK 218
H1.5_r   VASGEAKPKAKKTGAAKAKKPTGATPKKPKKTAGA---KKTVKKTPKKAKKPAAA-GVKKV-TKSPKKAAAAKPKKA--TKSPARPKAVKSKASKPKVTKPKA-AKPKAAKVKKAVSKKK 221

H1.1_h   ASSVETKPGASKVAT-KTKA-TGA-SKKLKKATGA-S-KKSV-KTPKKAKKPAA----TRKS-SKNPKKPKTV-KPKK-V-AKSPAKAKAVKPKAAKARVTKPKT-AKP-----KKAAPKKK 214
H1.2_h   AASGEAKPKVKKAGGTKPKKPVGA-AKKPKKAAGGATPKKSAKKTPKKAKKPAAATVTKKV-AKSPKKAKVA-KPKKA---AKSAAKAVKPKAAKPKVVKP-----------KKAAPKKK 212
H1.3_h   AASGEGKPKAKKAGAAKPRKPAGA-AKKPKKVAGAATPKKSIKKTPKKVKKPATAAGTKKV-AKSAKKVKTP-QPKKA---AKSPAKAKAPKAAKPKSGKPKV-TKA-----KKAAPKKK 220
H1.4_h   AASGEAKPKAKKAGAAKAKKPAGA-AKKPKKATGTATPKKSAKKTPKKAAAAGAKK--AKSPAKAKA--PKSPAKAKAVKPKAAKPKTAKPKA-AKP-----KKAAPKKK 218
H1.5_h   AASGEAKPKAKKAGAAKAKKPAGATPKKAKKAAGA---KKAVKKTPKKAKKPAAA-GVKKV-AKSPKKAKAAAKPKKA--TKSPARPKAVKPKAAKPKAAKPKA-AKPKAAKAKKAAAKKK 225
            *           *       **       * *** ***  *   *    **     *     *    **           **        **      **   **   **  ** 
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Fig. 1. Multiple sequence alignment of chicken (ch) H1 subtypes and mammalian subtypes (H1.1–H1.5) from mouse (m), rat (r) and humans (h). The globular domain is underlined. Conserved aminoacids are denoted with an asterisk (*).
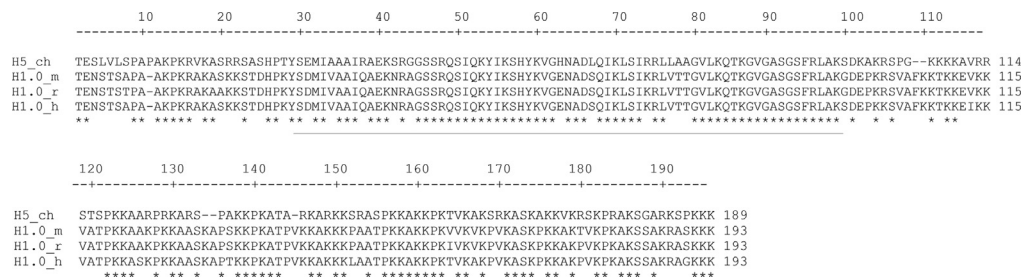
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              10        20        30        40        50        60        70        80        90       100       110
        --------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+------

H5_ch   TESLVLSPAPAKPKRVKASRRSASHPTYSEMIAAAIRAEKSRGGSSRQSIQKYIKSHYKVGHNADLQIKLSIRRLLAAGVLKQTKGVGASGSFRLAKSDKAKRSPG--KKKKAVRR 114
H1.0_m  TENSTSAPA-AKPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSRQSIQKYIKSHYKVGENADSQIKLSIKRLVTTGVLKQTKGVGASGSFRLAKGDEPKRSVAFKKTTKKEVKK 115
H1.0_r  TENSTSTPA-AKPKRAKAAKKSTDHPKYSDMIVAAIQAEKNRAGSSRQSIQKYIKSHYKVGENADSQIKLSIKRLVTTGVLKQTKGVGASGSFRLAKGDEPKRSVAFKKTTKKEVKK 115
H1.0_h  TENSTSAPA-AKPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSRQSIQKYIKSHYKVGENADSQIKLSIKRLVTTGVLKQTKGVGASGSFRLAKGDEPKRSVAFKKTTKKEIKK 115
        **      **  *****  **    *   ** ** **  ***  *** * *  *****************  **  ***** **  ****************    *  *    *  **


             120       130       140       150       160       170       180       190
        --+---------+---------+---------+---------+---------+---------+---------+-----

H5_ch   STSPKKAAARPRKARS--PAKKPKATA-RKARKKSRASPKKAKKPKTVKAKSRKASKAKKVKRSKPRAKSGARKSPKKK 189
H1.0_m  VATPKKAAKPKKAASKAPKKPKATPVKKAKKKPAATPKKAKKPKIVKVKPVKASKPKKAKTVKPKAKSSAKRASKKK 193
H1.0_r  VATPKKAAKPKKAASKAPSKPKPKATPVKKAKKKPAATPKKAKKPKIVKVKPVKASKPKKAKPVKPKAKSSAKRASKKK 193
H1.0_h  VATPKKASKPKKAASKAPTKKPKATPVKKAKKKLAATPKKAKKPKTVKAKPVKASKPKKAKPVKPKAKSSAKRAGKKK 193
        ****  *  *  *  *  ** **  ***  ** ** ** * *  ****  ** ** *** ***  **  **  ***
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Fig. 2. Multiple sequence alignment of chicken (ch) H5 and mammalian H1.0 from mouse (m), rat (r) and humans (h). The globular domain is underlined. Conserved aminoacids are denoted with an asterisk (*).

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