

577.15: [611+594.3]

(, ,).

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glabrata (Homo sapiens). **14** *Biomphalaria*

100

2,8 21 640 98%. 2,5

23 139 95%. 26 000 73%. *Danio rerio* () 1,4

(73-61%), (98,8-80%), (50-26%) [1, 2, 3].

Danio rerio,

[4].

[5, 6].

[7].

[8].

[9].

[10].

3R (Replacement - , Reduction - , Refinement -). « »

(« » () « »

« » . 2004

« », : 626 561 -

[11].

(-) 26
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(*Sus Scrofa*), (*Drosophila melanogaster*), (*Caenorhabditis elegans*), (*Homo sapiens*),
(*Mus musculus*), (*Gallus gallus*), (*Danio rerio*),
(*Saccharomyces cerevisiae*), (*Arabidopsis thaliana*)
(*Biomphalaria glabrata*).

<https://www.ensembl.org>;

<https://www.ncbi.nlm.nih.gov>

BLAST;

<https://www.uniprot.org>;

https://www.ebi.ac.uk/Tools/psa/emboss_needle/.

: →

() —* NS () AAS

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12 : :3.4.16.5 - CathepsinA (CTSA), :3.4.18.1 -
Cathepsin Z (CTSZ), :3.4.21.79 - Granzyme (GZMB), EC:3.4.22.1 - Cathepsin (CTSB),
EC:3.4.22.15 - Pro-cathepsinL (CTSL), EC:3.4.22.16 - Pro-cathepsin H (CTSH), EC:3.4.22.27 - Cathepsin S
(CTSS), EC:3.4.22.34 - Legumain (LGMN), EC:3.4.22.38 - Cathepsin (CTSK), EC:3.4.22.41 - Cathepsin
F (CTSF), EC:3.4.22.42 - Cathepsin O (CTSO), EC:3.4.23.5 - Cathepsin D (CTSD);

14 : :3.4.17.1 - Carboxypeptidase A1 (I);
:3.4.17.2 - Carboxypeptidase (I); :3.4.24.56 - Ptirilysin (PITRMI); EC:3.4.13.19 - Dipeptidase
(DPEPI); EC:3.4.24.B18 - ATP-dependent zincmetalloprotease (YME1L1); EC: 3.4.24.11 - Neprilysin
(MME); EC:3.4.24.106 - Hepsin (HPN); EC:3.4.21.4 - Trypsin (PRSS); EC: 3.4.22.36 - Caspase 1 (CASP1);
EC:3.4.22.56 - Caspase 3 (CASP3); EC:3.4.22.60 - Caspase 7 (CASP7); EC:3.4.22.61 - Caspase 8 (CASP8);
EC:3.4.22.52 - Calpain 1 (CAPN1); EC:3.4.22.53 - Calpain 2 (CAPN2).

. 1.

	%	Sus	Mus	Gallus	Danio	Caenorhabditis	Arabidopsis	Biomphalaria
		Scrofa	musculus	gallus	rerio	elegans	thaliana	glabrata
Cathepsin	QC	95	95	93	93	94	86	98
	Ident	90,20	88,70	68,06	50,55	40,81	36,12	52,59
Cathepsin Z	QC	94	91	91	91	82		84
	Ident	85,66	85,30	75,36	67,74	61,11		67,97
Granzyme	QC	92	93		91			91
	Ident	72,73	69,70		38,53			27,27
Cathepsin	QC	98	95	100	97	97	92	97
	Ident	81,49	80,00	77,06	72,51	47,94	44,62	55,36
Pro-cathepsin L	QC	100	100	62	77	91		96
	Ident	78,74	72,07	28,40	67,56	51,13		52,28
Pro-cathepsin H	QC	100	100	92	91			
	Ident	88,06	82,99	74,43	67,54			
Cathepsin S	QC	100	100	94	94			
	Ident	84,59	73,80	70,29	58,92			
Legumain	QC	100	100	99	98	93		89
	Ident	84,76	82,99	72,92	65,89	42,13		48,09
Cathepsin	QC	100	100	95	86			
	Ident	95,45	86,63	74,52	62,24			
Cathepsin F	QC	100	95		92			
	Ident	80,53	75,43		49,35			
Cathepsin 0	QC	86	90	85	85			86
	Ident	86,28	76,55	70,25	58,27			41,64
Cathepsin D	QC	100	96	93	94			33
	Ident	86,65	82,46	68,99	66,75			53,62

88,70%, 53,09%, 28,40%, 77,06%, 72,73%, 95,45%, 69,70%, 38,53%, 72,51%, 36,12%, 44,62%, 27,27%, 67,97%..

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. 2.

	%	Sus	Mus	Gallus	rmo	Drosophila	Caenorhabditis	Biomphalaria
		Scrofa	musculus	gallus		melanogaster	elegans	glabrata
Carboxypeptidase A1	QC	96	69	95	96			60
	Ident	85,75	82,22	72,95	61,54			37,83
Carboxypeptidase	QC	100	100	96	94			59
	Ident	85,34	84,16	59,17	58,94			36,02
Pitrilysin	QC	95	100	100	99			93
	Ident	80,63	86,60	76,37	67,90			45,72
Dipeptidase	QC	95	95	88	90			88
	Ident	91,33	73,10	68,12	60,11			53,46
ATP-dependent zincmetalloprotease	QC	100	100	99	86		66	78
	Ident	96,65	94,83	84,00	80,15		50,00	44,47
Nepirylisin	QC	100	100	100		92	93	74
	Ident	93,60	94,13	78,80		41,17	36,83	40,41

Hepsin	QC	96	99		90	63		57
	Ident	92,09	88,68		53,83	38,57		37,35
Trypsin	OC	99	93	91	75			90
	Ident	80,43	79,13	68,87	67,54			34,17
Caspase 1	OC	100	100	71	67			45
	Ident	72,52	62,13	47,89	43,21			28,65
Caspase 3	QC	100	100	95	86			87
	Ident	88,45	86,64	66,42	61,41			50,41
Caspase 7	QC	100	22	100	97			85
	Ident	87,38	82,16	70,65	66,01			31,12
Caspase 8	QC	99	96	99	98			92
	Ident	72,78	65,57	57,00	40,24			40,00
Calpain 1	OC	100	100	100	99	94	67	94
	Ident	94,69	89,08	81,82	69,96	44,03	48,69	45,02
Calpain 2	OC	100	100	96	100	95		96
	Ident	94,71	92,44	82,10	66,43	43,84		44,99

94,83%, 38,57%, 47,89%, 72,78%, 96,65%, 62,13%,
28,65%, 53,46%, 44,03%, 84,00%, 36,83%, 50,00%, 40,24%, 80,15%,

(*Gallus gallus*), (*Sus Scrofd*), (*Mus musculus*),
(*Danio rerio*), (*Biomphalaria glabrata*),
(*Drosophila melanogaster*), (*Arabidopsis thaliana*),
(*Saccharomyces cerevisiae*).

(*Biomphalaria glabrata*)
(*Planorbarius corneus*), (*Lymnaea stagnalis*)

[10, 12].

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A.A. CHIRKIN, . . . ALAEVA-TIKHOMIRO VA, I.O. SEMENOV, P.Yu. PINCHUK

SELECTION OF MODEL ORGANISMS FOR BIOMEDICAL STUDIES THROUGH THE STUDY OF THE MOLECULAR-STRUCTURAL HOMOMOLOGY OF PROTEOLYTIC ENZYMES

Vitebsk State University named by P.M. Masherova

Summary

The study of the proteolysis system requires the use of model organisms. Mammals (mice, pigs, monkeys) are usually used in preclinical trials and development of therapeutic technologies. However, due to ethical reasons and high cost, their use is declining. At the same time, experiments on cell cultures do not solve many problems of intercellular interaction in body tissues; they require special equipment, reagents, and morphologists. Purpose of the work: to reveal the percentage of identity (molecular structural homology) of 26 proteolytic enzymes of lysosomal and non-lysosomal localization in 9 model organisms in relation to humans. As a result of the studies, data were obtained on the average level of molecular structural homology of 7 lysosomal proteolytic enzymes and 14 non-lysosomal proteolytic enzymes of the freshwater lung mollusk *Biomphalaria glabrata* in relation to humans (*Homo sapiens*). The results of the study substantiate the expediency of using pulmonary freshwater mollusks as model organisms in the study of the proteolysis system, as well as the use of their proteolytic enzymes in the food industry and medicine.

Key words: model organisms, proteolytic enzymes, nucleotide sequences, amino acid sequences, human, freshwater lung molluscs, house mouse, pig, domestic chicken, *Danio rerio*, fruit drosophila, nematode, baker's yeast, Tal's clover.