

Homo -----METPSQRRATRSGAQASSTPLSPTRITRLQEKEDLQELNDR LAVY  
Mus -----METPSQRRATRSGAQASSTPLSPTRITRLQEKEDLQELNDR LAVY  
Danio -----METPGQKRSSRGGVTN---VLSPTRI SRLQEKEDLSNLNDR LAVY  
Drosophila MSARRVTLNTRVSRASTSTPVGGASTSSRVGATSPTSPTRTSRQQEKEELQHLNDR LACY  
Caenorhabditis MS-SRKGTRSSRIVTLERSANSLSNNGGDDSGSTLLET SRLQEKDHLTSLNSRLATY

Homo IDRVR SLETENAGLRLRIT ESEEVVSREVSIGIKAAYEAE L GDARKTLDSVAKERARLQLE  
Mus IDRVR SLETENAGLRLRIT ESEEVVSREVSIGIKAAYEAE L GDARKTLDSVAKERARLQLE  
Danio IDKVR SLEVENAGLRMRI TESETEISRELSGMKAAYEAE L ADARKTLDSVAKERARLQLE  
Drosophila IDRMRNLENENSRLTQELNLAQDTVNRETSNLKAVYEKELAAARKLLDETAKEKAKLEID  
Caenorhabditis IDKVRQLEQENNR LQVQIRDI EVVEKKEKSNLADRFEAEKARLRALDSAQDELAKYRIE

Homo LSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALSTALSEKRTLEGELHDL  
Mus LSKVREEFKELKARNTKKEGDLIAAQARLKDLEALLNSKEAALSTALSEKRTLEGELHDL  
Danio LSKVREDYKELKARNGKKEADLESALARLKDLESLLNSK DASLSTALGEKRTLEV E VRDL  
Drosophila IKRLWEENDDLKPRLDKKTKEATVAENNARLYENRYNEVNGKYNQSLADRKKFEDQAKEL  
Caenorhabditis YDAAKVEVKLKPQVEKLERELAGAEEQALHAQS IADQSQAKQKT LQARNDKLVV E NDDL

Homo RGQVAKLEAALGEAKKQLQDEMLRRVDAENRLQTMKEELDFQKN IYSEELRETKRRHETR  
Mus RGQVAKLEAALGEAKKQLQDEMLRRVDAENRLQTLKEELDFQKN IYSEELRETKRRHETR  
Danio KAQLAKLEGLSNDAKKQLQDEMLRRVDAENRIQTLKEELEFQKN IYSEELRESKRRYESR  
Drosophila ALENERLRRQLDDLRKQLEAETLARVDLENQNQSLREELAFKDVHTQELTETR SRQIE  
Caenorhabditis KKQNI TLRDTVEGLKKA VEDETLLRTAANNKI KALEEDLAFALQ QHKGEL E EVRHKRQVD

Homo LVEIDNGKQREFESRLADALQELRAQHEDQVEQYKKELEKTYSAKLDNARQSAERN SNLV  
Mus LVEIDNGKQREFESRLADALQELRAQHEDQVEQYKKELEKTYSAKLDNARQSAERN SNLV  
Danio VVEIDSGRQQDYESKLADAL TDLRNQHEEQLRIYKEEIEKTYNSKLENARSSAERN SHLV  
Drosophila ISEIDGRLSRQYEAKLQQLQELRDQYEGQMRINREEIELLYDNEIQNLKAAANRAAQGS  
Caenorhabditis MTTYAKQINDEYQSKLQDQIEEMRAQFKNNLHQNKTA FEDAYKNKLN-----

Homo GAAHEELQSRIRIDSLSAQLSQLQKQLAAKEAKLRDLEDRLAREDTSRRLLAEKEREM  
Mus GAAHEELQSRIRIDSLSAQLSQLQKQLAAKEAKLRDLEDRLAREDTSRRLLAEKEREM  
Danio GAAHEELQTRVRMEGVSSQLSQLQKQLAAREAKIRELEEALSREDILRRRLEDKEKEM  
Drosophila ALATEEVRLMRTKIDGLNAKLQNLDTNAGLNARIRELENLLDTERQRHNQYIASLEAEL  
Caenorhabditis -AARERQEEAVSEAIHLRARVRDLETSSSGNASLIERLRSELDTLKRSEKLDKDKARI

Homo AEMRARMQQQLDEYQELLDIKLALDMEIHAYRKLLEGEERLRLSPSPSQR-----  
Mus AEMRARMQQQLDEYQELLDIKLALDMEIHAYRKLLEGEERLRLSPSPSQR-----  
Danio AEMRQRMQQQLDEYQELLDIKLALDMEISAYRKLLEGEERLRLSPSPPPARGVTVTRSS  
Drosophila QRMREMAHQLEFYQGLMDIKVSLDLEIAAYDKLLCGEERLNIESPGRPTTDSGISSNG  
Caenorhabditis AELNQEIERMMSEFHDLLDVVKIQDLAELKTYQALLEGEERLNLNLTQEAPQNTS-----

Homo -----SRGRASSHSSQTQGGGSVTKKRKLESTESR----SSFSQHARTSGRV  
Mus -----SRGRASSHSSQSQGGGSVTKKRKLESSESER----SSFSQHARTSGRV  
Danio GSGSHTRVVQSSTRTSSGSAKRRRLNDNDSASSVVGTVTR----TRISQQASASGRV  
Drosophila SHLTASASSRSGRVTPSGRRSATPGISGSSAVKRRRTVIDESEDRTLSEYSVNAAAKGD  
Caenorhabditis -----VHHVSFSSGGASAQRGVKRRRVVDVNGEDQDIDYLN--RRSKLNKETVGPV

Homo AVEEVDEEGKFVRLRNKSNEDQSMGNWQIKRQNGDDPLLYRFPFKFTLKAGQVVTIWAA  
Mus AVEEVDEEGKFVRLRNKSNEDQSMGNWQIRRQNGDDPLMTYRFPFKFTLKAGQVVTIWAS  
Danio TVDEVDEEGKFVRLNKNKSDQDQSLGHVQVQRQIGSGTPIVYKFPKFNKAGQVVTIWAA  
Drosophila EIIIEADVEGRFIKLNKGTTEEINLTGWQLTRIAGDE-ELAFKFSRGSKVLGGASVTIWSV  
Caenorhabditis GIDEVDEEGKWVRVANNSEEEQSIGGYKLVVKAGNK-EASFQFSSRMKLA PHASATVWSA

Homo GAGATHSPPTDLVWKAQNTWGCNSLRRTALINSTGEEVAMRKLVRSVTVVED--DEDEDG  
Mus GAGATHSPPTDLVWKAQNTWGCSSLRRTALINSTGEEVAMRKLVRSLTMVEDNEDDEDG  
Danio GAGGTHSPPSDLVWKTQNSWGSGLFQTTLISSSGEEMAMRKVTRTLFQDEE-----  
Drosophila DAGTAHDPPNNLVMKKK--WPVANSRMSVLANADKEDVASYDRVR-----  
Caenorhabditis DAGAVHHPPEVYVMKKQ-WPIGDNPSARLEDSEGDVSS-----

```

Homo      DDL LHHH HGSHC SSSGDPAEYNLRSRTVLCGTCGQPADKASASGSGAQVGGPIS-SGSSA
Mus       EELLHHRGSHCSGSGDPAEYNLRSRTVLCGTCGQPADKAAG-GAGAQVGGGIS-SGSSA
Danio     -----DDEMAAHSTCGDSEYNLRSRTVLCGSCGQPSDRNSSCVSASSGVSSASRSFSSG
Drosophila -----ANVSSHTSRHRSSGTP-----STGFTLGSG
Caenorhabditis -----ITVEFSES

```

```

Homo      SSVTVTRSYRSVGGSGGGSFGDNLVTRS YLLGNSSPRTQSPQNCSIM----
Mus       SSVTVTRSFERSVGGSGGGSFGDNLVTRS YLLGNSSPRSQSSQNCSIM----
Danio     GGGGLTEAFVSPSHFIVSNDKPRQVCTVCVEGTFVCLLNSITLWLVSLFFE
Drosophila AGSTGVRSLFSLLF-----
Caenorhabditis SDPSDPADRCSIM-----

```

**Supplementary Figure 1:** Amino acid sequence alignment of human (*Homo sapiens*; Uniprot ID: P02545) prelamin A and its orthologues in mouse (*Mus musculus*; Uniprot ID: P48678) and zebrafish (*Danio rerio*; Uniprot ID: A0A2R8QPG3), and its paralogues in fruit fly (*Drosophila melanogaster*; Uniprot ID: Q03427) and worm (*Caenorhabditis elegans*; Uniprot ID: Q21443) [142]. Highlighted amino acids (a.a) correspond to affected positions cited in this review. Amino acid in red refers to the lamin C specific variant affecting Arginine [R] (Serine [S] for lamin A) at position 571. Alignment was performed using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) [143].

**Supplementary Table 1:** Percent amino acid sequence identity between the lamin A/C orthologues/paralogues relative to *H. sapiens* prelamin A. Values were obtained following amino acid sequence alignment using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>) [143].

Species	% Sequence Identity
<i>M. musculus</i>	96.4
<i>D. rerio</i>	66.83
<i>D. melanogaster</i>	37.65
<i>C. elegans</i>	30.31

