

## SUPPLEMENTARY TABLES

**Supplementary Table 3. Summary of reduced CpG models: performance metrics under elastic net regularization and post-hoc thresholding.**

| Methods         |           | Alpha regularization                           |              | Alpha regularization                           |              | Post-hoc thresholding                             |             |
|-----------------|-----------|------------------------------------------------|--------------|------------------------------------------------|--------------|---------------------------------------------------|-------------|
| Modeling        |           | Elastic net; alpha = 0.5,<br>ll_ratio = 0.9852 |              | Elastic net; alpha = 0.8,<br>ll_ratio = 0.9852 |              | Elastic net; alpha = 0.0178,<br>ll_ratio = 0.9852 |             |
| <i>n</i> of CpG |           | 8                                              |              | 5                                              |              | 6                                                 |             |
| train           | MAE       | 9.377                                          |              | 11.509                                         |              | 5.052                                             |             |
|                 | RMSE      | 12.0175                                        |              | 14.4748                                        |              | 5.943                                             |             |
|                 | <i>r</i>  | 0.8109                                         |              | 0.7299                                         |              | 0.934                                             |             |
|                 | R-squared | 0.4479                                         |              | 0.1991                                         |              | 0.865                                             |             |
| test            | MAE       | 10.4848                                        |              | 11.9844                                        |              | 7.364                                             |             |
|                 | RMSE      | 12.7364                                        |              | 14.6885                                        |              | 11.3                                              |             |
|                 | <i>r</i>  | 0.7628                                         |              | 0.6897                                         |              | 0.726                                             |             |
|                 | R-squared | 0.3742                                         |              | 0.1677                                         |              | 0.507                                             |             |
| Formula         |           | Position                                       | Coefficient  | Position                                       | Coefficient  | Position                                          | Coefficient |
|                 |           | intercept                                      | 55.5899595   | intercept                                      | 44.53694062  | intercept                                         | 163.3170259 |
|                 |           | chr3:12815297                                  | −6.566861612 | chr19:10636467                                 | −6.493581544 | chr3:44761961                                     | 53.498989   |
|                 |           | chr19:10636467                                 | −15.12568411 | chr9:22005565                                  | 8.777387791  | chr17:29042762                                    | 38.623448   |
|                 |           | chr3:12815285                                  | −9.302902911 | chr9:22005510                                  | 3.293509568  | chr3:12815466                                     | −30.351224  |
|                 |           | chr3:12815282                                  | −2.1355773   | chr9:22005577                                  | 5.634173089  | chr3:44761965                                     | 29.531605   |
|                 |           | chr9:22005565                                  | 13.39037812  | chr7:143316521                                 | −2.470404842 | chr19:57527206                                    | 30.667327   |
|                 |           | chr9:22005510                                  | 6.784154861  |                                                |              | chr3:12815426                                     | −40.055187  |
|                 |           | chr9:22005577                                  | 10.73001316  |                                                |              |                                                   |             |
|                 |           | chr7:143316521                                 | −9.800951957 |                                                |              |                                                   |             |

**Supplementary Table 4. Hallmarks of Aging and functional annotations of the 20 skeletal muscle–specific CpG markers.**

| Marker | CpG_ID     | RefGene         | Hallmark of aging                   | Functional annotation                                                                                                          | Supplementary References |
|--------|------------|-----------------|-------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--------------------------|
| MA_01  | cg06458239 | <i>ZNF549</i>   | Epigenetic Alteration               | Zinc finger transcription factor                                                                                               | [1, 2]                   |
| MA_02  | cg02426178 | <i>SLC44A2</i>  | Mitochondrial Dysfunction           | Choline transporter, Mitochondrial choline transporter regulating ATP production, oxidative stress, and metabolic homeostasis. | [3, 4]                   |
| MA_03  | cg11456906 | <i>CFAP74</i>   | Altered Intercellular Communication | Ciliary and flagellar motility                                                                                                 | [5]                      |
| MA_04  | cg07743451 | <i>TPM3</i>     | Mitochondrial Dysfunction           | Thin filament stabilization (actin-binding)                                                                                    | [6, 7]                   |
| MA_05  | cg14812508 | <i>TWF2</i>     | Cytoskeletal Integrity              | Actin-binding protein involved in cell motility                                                                                | [8]                      |
| MA_06  | cg07188513 | <i>MNX1-AS1</i> | .                                   | .                                                                                                                              | .                        |
| MA_07  | cg07502461 | <i>TWF2</i>     | Cytoskeletal Integrity              | Actin-binding protein involved in cell motility                                                                                | [8]                      |
| MA_08  | cg09926178 | <i>ACTA1</i>    | Cytoskeletal Integrity              | Muscle contraction regulation                                                                                                  | [9, 10]                  |
| MA_09  | cg15730967 | <i>CAND2</i>    | Altered Intercellular Communication | Heart muscle development, cAMP signaling pathway                                                                               | [11]                     |

|       |            |               |                                     |                                                         |          |
|-------|------------|---------------|-------------------------------------|---------------------------------------------------------|----------|
| MA_10 | cg07303143 | <i>KIF15</i>  | Stem Cell Exhaustion                | Mitotic spindle and proliferation regulation            | [12]     |
| MA_11 | cg17722263 | <i>MYCNUT</i> | Proteostasis Loss                   | Ubiquitin-proteasome system and protein degradation     | [13]     |
| MA_12 | cg05543030 | .             | .                                   | .                                                       |          |
| MA_13 | cg08390209 | <i>CDKN2B</i> | Cellular Senescence                 | Cell cycle arrest via INK4 family inhibition            | [14–17]  |
| MA_14 | cg19145398 | <i>FOXS1</i>  | Epigenetic Alteration               | Transcriptional regulation via Forkhead box pathway     | [18]     |
| MA_15 | cg26149678 | <i>IL18BP</i> | Inflammaging                        | Immune signaling modulation, antagonist of IL-18        | [19]     |
| MA_16 | cg12966875 | <i>SLPI</i>   | Inflammaging                        | Protease inhibitor, innate immune response modulator    | [20]     |
| MA_17 | cg06059810 | <i>RUFY3</i>  | Altered Intercellular Communication | Vesicle trafficking and autophagy regulation            | [21, 22] |
| MA_18 | cg17922226 | <i>CLCN1</i>  | Neuromuscular Junction Dysfunction  | Chloride ion channel in skeletal muscle excitability    | [23]     |
| MA_19 | cg06144905 | <i>PIPOX</i>  | Mitochondrial Dysfunction           | Peroxisomal amino acid and redox metabolism             | [24]     |
| MA_20 | cg13985639 | <i>DHDPSL</i> | Mitochondrial Dysfunction           | Amino acid metabolism, mitochondrial enzymatic function | [25]     |

**Supplementary Table 5. Primers for quantitative real-time reverse transcription PCR (qRT-PCR).**

| Related CpG | RefGene         | Forward primer sequence (5'→3') | Reverse primer sequence (5'→3') | Size (bp) |
|-------------|-----------------|---------------------------------|---------------------------------|-----------|
| cg06458239  | <i>ZNF549</i>   | CTTTACCGCCCGCCTTTC              | GGCACCTTTGAGCTTCATCA            | 155       |
| cg02426178  | <i>SLC44A2</i>  | TCATGTTCTTCTGTTGGCC             | ATCTGCACAATGGCCAGGAT            | 199       |
| cg11456906  | <i>CFAP74</i>   | AAGGCCGAGGAACACAGATT            | GCGGCAAACTTGATCTGGTA            | 128       |
| cg07743451  | <i>TPM3</i>     | GAAGTTGAGGGAGAAAGGCG            | CTCCTGAGCACGGTCCAG              | 105       |
| cg14812508  | <i>TWF2</i>     | CCTGGTCGCCTGATAACTCC            | ACAGGACGACAGGTGTTTCT            | 164       |
| cg07188513  | <i>MNX1-ASI</i> | CAAAGCTCTGCAGGTCAAC             | TGCATGTGTTTGGTGGCTAC            | 113       |
| cg09926178  | <i>ACTA1</i>    | GGACAGCGCCAAGTGAAG              | CGTCTTCGTCGCACATTGT             | 111       |
| cg15730967  | <i>CAND2</i>    | AGGATAGTGAATTCAGTGAGCAA         | AGCCTTGACGTTCTCCTCG             | 200       |
| cg07303143  | <i>KIF15</i>    | GGCTGCATTGTTTCGGGAT             | TCTTTCTGCAGGAGGACGAA            | 154       |
| cg17722263  | <i>MYCNUT</i>   | CCGATGTACAGGCAGAACTTG           | GACCACAGAACTCAGCCAGA            | 245       |
| cg08390209  | <i>CDKN2B</i>   | CTGGAACCTAGATCGCCGAT            | GGTGAGAGTGGCAGGGTC              | 140       |
| cg19145398  | <i>FOXS1</i>    | GAAGCTGAGCCTGACCCA              | CTTGGTTGGCTCAGTTGTGG            | 104       |
| cg26149678  | <i>IL18BP</i>   | AAGGAAGGCTCTTCAGGACC            | AGGAGCAGGACCCACAAAG             | 147       |
| cg12966875  | <i>SLPI</i>     | AGAGTCACTCCTGCCTTCAC            | TGGGCAGATTCTTAGGAGGA            | 145       |
| cg06059810  | <i>RUFY3</i>    | CTCACCGCTGCCCTTCCT              | CAGCTTGCCCATGTTTCATGA           | 127       |
| cg17922226  | <i>CLCN1</i>    | GGACTGCCCTCTGAGAATGG            | CCTATGTCCTGCTCCCTGTC            | 130       |
| cg06144905  | <i>PIPOX</i>    | GCCTGTCTTTGCTTGCCCTT            | CCTCGGGAGTGTGGTAGAAA            | 195       |
| cg13985639  | <i>DHDPSL</i>   | GGGAAGAAGGTGGACATTGC            | TGCTGGTCAGGAAAGGAAAC            | 172       |
|             | <i>GAPDH</i>    | CCACTCCTCCACCTTTGACG            | CCACCACCCTGTTGCTGTAG            | 211       |

**Supplementary Table 6. Primers used for PCR with bisulfite-converted DNA as the template.**

| Marker | CpG_ID     | Forward primer sequence (5'→3') | Reverse primer sequence (5'→3') | Size (bp) |
|--------|------------|---------------------------------|---------------------------------|-----------|
| MA_01  | cg06458239 | AGGTGTTTTTTTTTGGGTAATGAT        | CCTCTCTTTCTTAAATTAAATCCTCAC     | 129       |
| MA_02  | cg02426178 | AGGGTTAGTAGTAGGAGGTAAAG         | ACCCTACTAAACCTACAAATCTTCA       | 116       |
| MA_03  | cg11456906 | AGGTATAGAGGAATTTAGGGTAGAA       | CTACACCTCCCTAAACCTAAAAAC        | 308       |
| MA_04  | cg07743451 | GGGAGAGGTAGATAGTTTTT            | CTATACTCACAAATACATTACCC         | 154       |
| MA_05  | cg14812508 | GTTTAAAGTAGGGTGTGGTT            | CCCCTACAAAATAACCTCT             | 208       |
| MA_06  | cg07188513 | AGTTATTTTTGTGTTAGGGGTAAG        | CCCAAACACATTAATCCTATCCTAC       | 181       |
| MA_07  | cg07502461 | TTGTTTTGGGGTAGAGGT              | ACAACCTTATACCTTCCCTTACT         | 197       |
| MA_08  | cg09926178 | GAATTAGGAAAAGGGGTATAGG          | CCCAACAAACAAACAATAC             | 207       |
| MA_09  | cg15730967 | AGTGGTTGGGTAGGTAAAT             | CACTACACCCTAACACCTATAC          | 286       |
| MA_10  | cg07303143 | GGATATTGAAGGAAGGGATGAGTTT       | CCCTATTTTTACCCCCAAATACAAC       | 176       |
| MA_11  | cg17722263 | GAGATTAGGGGAAAGGTT              | CCATCACTATCTTTAATCATTC          | 101       |
| MA_12  | cg05543030 | TGTTGTTTTTGGGAGAGTTATTG         | AAACTTTCAATATCTAAATCCCTATCT     | 222       |
| MA_13  | cg08390209 | GAGTGGGAGAAGGTAGTGATTA          | CCTCCACTTTATCCTCAATCTT          | 142       |
| MA_14  | cg19145398 | TTGGGGAGGGATAGGATGTG            | CTCCCTCTTTCTCCCTCTTATAAT        | 144       |
| MA_15  | cg26149678 | GGTTGGTTTTYGAGTTTGTGTGTTAGT     | CACTAATAATCCCAAACCTCCTACCTA     | 211       |
| MA_16  | cg12966875 | AGGTATAGAATAGGTATTGGGGATA       | ACCAAACACAAACTCCCTACTA          | 214       |
| MA_17  | cg06059810 | GTTGGGATGTTGAGTTTATAGGA         | CTCCCAACATCAACAACATCTATA        | 168       |
| MA_18  | cg17922226 | GTGAAAATGAGGAATTGGGTGAAAAGA     | ACATACTTAAATAAACCCAAACTTTCAA    | 124       |
| MA_19  | cg06144905 | GGAGGTGGGTTTTATTTTGG            | CCTACTAATTTTCCCCTCTTC           | 95        |
| MA_20  | cg13985639 | AGGGGAGATTGGTTTGGAGTTA          | CAACCACATACCTTCACATCTACA        | 211       |

**Supplementary Table 7. Four sets of primers used for single base extension (SBE).**

| Group     | Marker | SBE primer sequence (5'→3')                 | Size (bp) |
|-----------|--------|---------------------------------------------|-----------|
| <b>G1</b> | MA_15  | (T) <sub>50</sub> TCCTCCTTATCTATAAACTCTCAC  | 75        |
|           | MA_07  | (T) <sub>41</sub> AAATAAAAAATCTACAACRAAAAAC | 66        |
|           | MA_17  | (T) <sub>32</sub> TTTTAATCAACACCCTACTTACTAC | 57        |
|           | MA_13  | (T) <sub>23</sub> CTCCTCAACAAACATTAATAATAAC | 48        |
|           | MA_01  | (T) <sub>14</sub> CTTTCTTAAATTAAATCCTCACAAC | 39        |
|           | MA_02  | (T) <sub>5</sub> CATATTCTTCTAATTAACCAACTTC  | 30        |
| <b>G2</b> | MA_09  | (T) <sub>50</sub> ATACTCATCCRCRCTTCAAAAAAC  | 75        |
|           | MA_20  | (T) <sub>41</sub> TAACAAAATTAACAAAAACTTTTAC | 66        |
|           | MA_10  | (T) <sub>32</sub> TATAAAAAAATAACAACCTCRAACC | 57        |
|           | MA_14  | (T) <sub>23</sub> CTCATTTTATTTTATCTCTATCCC  | 48        |
|           | MA_18  | (T) <sub>14</sub> TTTTCATTTTAAACACATCACCAC  | 39        |
|           | MA_19  | (T) <sub>5</sub> TACTTTAAAAATTCTAAAAAACCCC  | 30        |
| <b>G3</b> | MA_06  | (T) <sub>45</sub> AATCTTCRAAACTCATACAATTCC  | 70        |
|           | MA_08  | (T) <sub>35</sub> ACAAAAAAATCTCAATAAAATCTC  | 60        |
|           | MA_05  | (T) <sub>25</sub> TTAATAAATACCAAAAACACCTATC | 50        |
|           | MA_16  | (T) <sub>15</sub> CTTAATTCCTAAAATATTTACACC  | 40        |
|           | MA_12  | (T) <sub>5</sub> CTCAAAAAACTTAAATTAACCC     | 29        |
| <b>G4</b> | MA_11  | (T) <sub>35</sub> TTCAAAATACAACRCATACRCTAC  | 60        |
|           | MA_04  | (T) <sub>20</sub> CAAATACATTACCCAAAAAAATACC | 45        |
|           | MA_03  | (T) <sub>5</sub> TAAATTCTTATTACTACTAAACC    | 29        |

**Supplementary Table 8. Primers for single multiplexes of markers in the highest performance model for SBE.**

| Marker | SBE Primer Sequence (5'→3')                 | Size (bp) |
|--------|---------------------------------------------|-----------|
| MA_19  | (T) <sub>1</sub> TACTTTAAAAATTCTAAAAAACCCC  | 26        |
| MA_13  | (T) <sub>10</sub> CTCCTCAACAAACATTAATAAAC   | 35        |
| MA_04  | (T) <sub>20</sub> CAAATACATTACCCAAAAAATACC  | 45        |
| MA_01  | (T) <sub>30</sub> CTTTCTTAAATTAAATCCTCACAAC | 55        |
| MA_08  | (T) <sub>41</sub> ACAAAAAACTTCTCAATAAAATCTC | 66        |
| MA_18  | (T) <sub>52</sub> TTTCATATTTTAAACACATCACCAC | 77        |
| MA_10  | (T) <sub>62</sub> TATAAAAAAATAACAACCTCRAACC | 87        |

## SUPPLEMENTARY REFERENCES

1. Cassandri M, Smirnov A, Novelli F, Pitolli C, Agostini M, Malewicz M, Melino G, Raschellà G. Zinc-finger proteins in health and disease. *Cell Death Discov.* 2017; 3:17071.  
<https://doi.org/10.1038/cddiscovery.2017.71>  
PMID:[29152378](https://pubmed.ncbi.nlm.nih.gov/29152378/)
2. Kamaliyan Z, Clarke TL. Zinc finger proteins: guardians of genome stability. *Front Cell Dev Biol.* 2024; 12:1448789.  
<https://doi.org/10.3389/fcell.2024.1448789>  
PMID:[39119040](https://pubmed.ncbi.nlm.nih.gov/39119040/)
3. Traiffort E, O'Regan S, Ruat M. The choline transporter-like family SLC44: properties and roles in human diseases. *Mol Aspects Med.* 2013; 34:646–54.  
<https://doi.org/10.1016/j.mam.2012.10.011>  
PMID:[23506897](https://pubmed.ncbi.nlm.nih.gov/23506897/)
4. Bennett JA, Mastrangelo MA, Ture SK, Smith CO, Loelius SG, Berg RA, Shi X, Burke RM, Spinelli SL, Cameron SJ, Carey TE, Brookes PS, Gerszten RE, et al. The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. *Nat Commun.* 2020; 11:3479.  
<https://doi.org/10.1038/s41467-020-17254-w>  
PMID:[32661250](https://pubmed.ncbi.nlm.nih.gov/32661250/)
5. Zhang X, Huang G, Jiang T, Meng L, Li T, Zhang G, Wu N, Chen X, Zhao B, Li N, Wu S, Guo J, Zheng R, et al. CEP112 coordinates translational regulation of essential fertility genes during spermiogenesis through phase separation in humans and mice. *Nat Commun.* 2024; 15:8465.  
<https://doi.org/10.1038/s41467-024-52705-8>  
PMID:[39349455](https://pubmed.ncbi.nlm.nih.gov/39349455/)
6. Matyushenko AM, Nefedova VV, Shchepkin DV, Kopylova GV, Berg VY, Pivovarova AV, Kleymenov SY, Bershtsky SY, Levitsky DI. Mechanisms of disturbance of the contractile function of slow skeletal muscles induced by myopathic mutations in the tropomyosin TPM3 gene. *FASEB J.* 2020; 34:13507–20.  
<https://doi.org/10.1096/fj.202001318R>  
PMID:[32797717](https://pubmed.ncbi.nlm.nih.gov/32797717/)
7. Lambert MR, Gussoni E. Tropomyosin 3 (TPM3) function in skeletal muscle and in myopathy. *Skelet Muscle.* 2023; 13:18.  
<https://doi.org/10.1186/s13395-023-00327-x>  
PMID:[37936227](https://pubmed.ncbi.nlm.nih.gov/37936227/)
8. Nevalainen EM, Skwarek-Maruszcwska A, Braun A, Moser M, Lappalainen P. Two biochemically distinct and tissue-specific twinfilin isoforms are generated from the mouse Twf2 gene by alternative promoter usage. *Biochem J.* 2009; 417:593–600.  
<https://doi.org/10.1042/BJ20080608>  
PMID:[18837697](https://pubmed.ncbi.nlm.nih.gov/18837697/)
9. Labasse C, Brochier G, Taratuto AL, Cadot B, Rendu J, Monges S, Biancalana V, Quijano-Roy S, Bui MT, Chanut A, Madelaine A, Lacène E, Beuvin M, et al. Severe ACTA1-related nemaline myopathy: intranuclear rods, cytoplasmic bodies, and enlarged perinuclear space as characteristic pathological features on muscle biopsies. *Acta Neuropathol Commun.* 2022; 10:101.  
<https://doi.org/10.1186/s40478-022-01400-0>  
PMID:[35810298](https://pubmed.ncbi.nlm.nih.gov/35810298/)
10. Clayton JS, Johari M, Taylor RL, Dofash L, Allan G, Monahan G, Houweling PJ, Ravenscroft G, Laing NG. An Update on Reported Variants in the Skeletal Muscle  $\alpha$ -Actin (ACTA1) Gene. *Hum Mutat.* 2024; 2024:6496088.  
<https://doi.org/10.1155/2024/6496088>  
PMID:[40225930](https://pubmed.ncbi.nlm.nih.gov/40225930/)
11. Górka AA, Sandmann C, Riechert E, Hofmann C, Malovrh E, Varma E, Kmietczyk V, Ölschläger J, Jürgensen L, Kamuf-Schenk V, Stroh C, Furkel J, Konstantin MH, et al. Muscle-specific Cand2 is translationally upregulated by mTORC1 and promotes adverse cardiac remodeling. *EMBO Rep.* 2021; 22:e52170.  
<https://doi.org/10.15252/embr.202052170>  
PMID:[34605609](https://pubmed.ncbi.nlm.nih.gov/34605609/)
12. Yin YX, Ding MQ, Yi Y, Zou YJ, Liao BY, Sun SC. Insufficient KIF15 during porcine oocyte ageing induces HDAC6-based microtubule instability. *Theriogenology.* 2024; 226:49–56.  
<https://doi.org/10.1016/j.theriogenology.2024.05.043>  
PMID:[38838614](https://pubmed.ncbi.nlm.nih.gov/38838614/)
13. Li S, Jiang C, Pan J, Wang X, Jin J, Zhao L, Pan W, Liao G, Cai X, Li X, Xiao J, Jiang J, Wang P. Regulation of c-Myc protein stability by proteasome activator REGγ. *Cell Death Differ.* 2015; 22:1000–11.  
<https://doi.org/10.1038/cdd.2014.188>  
PMID:[25412630](https://pubmed.ncbi.nlm.nih.gov/25412630/)
14. Li Y, Li C, Zhou Q, Liu X, Qiao Y, Xie T, Sun H, Ong MT, Wang H. Multiomics and cellular senescence profiling of aging human skeletal muscle uncovers Maraviroc as a senotherapeutic approach for sarcopenia. *Nat Commun.* 2025; 16:6207.  
<https://doi.org/10.1038/s41467-025-61403-y>  
PMID:[40617829](https://pubmed.ncbi.nlm.nih.gov/40617829/)
15. Tumasian RA 3rd, Harish A, Kundu G, Yang JH, Ubaida-Mohien C, Gonzalez-Freire M, Kaileh M, Zukley LM, Chia CW, Lyashkov A, Wood WH 3rd, Piao Y, Coletta C, et al. Skeletal muscle transcriptome in healthy aging. *Nat Commun.* 2021; 12:2014.  
<https://doi.org/10.1038/s41467-021-22168-2>  
PMID:[33795677](https://pubmed.ncbi.nlm.nih.gov/33795677/)
16. Nanda V, Downing KP, Ye J, Xiao S, Kojima Y, Spin JM, DiRenzo D, Nead KT, Connolly AJ, Dandona S, Perisic

- L, Hedin U, Maegdefessel L, et al. CDKN2B Regulates TGF $\beta$  Signaling and Smooth Muscle Cell Investment of Hypoxic Neovessels. *Circ Res*. 2016; 118:230–40.  
<https://doi.org/10.1161/CIRCRESAHA.115.307906>  
PMID:[26596284](https://pubmed.ncbi.nlm.nih.gov/26596284/)
17. Koch CM, Suschek CV, Lin Q, Bork S, Goergens M, Jousen S, Pallua N, Ho AD, Zenke M, Wagner W. Specific age-associated DNA methylation changes in human dermal fibroblasts. *PLoS One*. 2011; 6:e16679.  
<https://doi.org/10.1371/journal.pone.0016679>  
PMID:[21347436](https://pubmed.ncbi.nlm.nih.gov/21347436/)
  18. Kuang Y, Yu Y, Wang C, Li H, Zhou Y, Pan L, Zhang Y, Cheng X, Jiang Z, Hu X. FOXS1, frequently inactivated by promoter methylation, inhibited colorectal cancer cell growth by promoting TGFBI degradation through autophagy-lysosome pathway. *J Adv Res*. 2025; 77:623–36.  
<https://doi.org/10.1016/j.jare.2025.01.037>  
PMID:[39864590](https://pubmed.ncbi.nlm.nih.gov/39864590/)
  19. Zhang LM, Zhang Y, Fei C, Zhang J, Wang L, Yi ZW, Gao G. Neutralization of IL-18 by IL-18 binding protein ameliorates bleomycin-induced pulmonary fibrosis via inhibition of epithelial-mesenchymal transition. *Biochem Biophys Res Commun*. 2019; 508:660–6.  
<https://doi.org/10.1016/j.bbrc.2018.11.129>  
PMID:[30527805](https://pubmed.ncbi.nlm.nih.gov/30527805/)
  20. Mongkolpathumrat P, Pikwong F, Phutiyothin C, Srisopar O, Chouyatchakarn W, Unnajak S, Nernpermpisooth N, Kumphune S. The secretory leukocyte protease inhibitor (SLPI) in pathophysiology of non-communicable diseases: Evidence from experimental studies to clinical applications. *Heliyon*. 2024; 10:e24550.  
<https://doi.org/10.1016/j.heliyon.2024.e24550>  
PMID:[38312697](https://pubmed.ncbi.nlm.nih.gov/38312697/)
  21. Wei Z, Sun M, Liu X, Zhang J, Jin Y. Rufy3, a protein specifically expressed in neurons, interacts with actin-bundling protein Fascin to control the growth of axons. *J Neurochem*. 2014; 130:678–92.  
<https://doi.org/10.1111/jnc.12740>  
PMID:[24720729](https://pubmed.ncbi.nlm.nih.gov/24720729/)
  22. Char R, Pierre P. The RUFYs, a Family of Effector Proteins Involved in Intracellular Trafficking and Cytoskeleton Dynamics. *Front Cell Dev Biol*. 2020; 8:779.  
<https://doi.org/10.3389/fcell.2020.00779>  
PMID:[32850870](https://pubmed.ncbi.nlm.nih.gov/32850870/)
  23. Vivekanandam V, Jayaseelan D, Hanna MG. Muscle channelopathies. *Handb Clin Neurol*. 2023; 195:521–32.  
<https://doi.org/10.1016/B978-0-323-98818-6.00006-6>  
PMID:[37562884](https://pubmed.ncbi.nlm.nih.gov/37562884/)
  24. Kim J, Bai H. Peroxisomal Stress Response and Inter-Organellar Communication in Cellular Homeostasis and Aging. *Antioxidants (Basel)*. 2022; 11:192.  
<https://doi.org/10.3390/antiox11020192>  
PMID:[35204075](https://pubmed.ncbi.nlm.nih.gov/35204075/)
  25. Belostotsky R, Seboun E, Idelson GH, Milliner DS, Becker-Cohen R, Rinat C, Monico CG, Feinstein S, Ben-Shalom E, Magen D, Weissman I, Charon C, Frishberg Y. Mutations in DHDPSL are responsible for primary hyperoxaluria type III. *Am J Hum Genet*. 2010; 87:392–9.  
<https://doi.org/10.1016/j.ajhg.2010.07.023>  
PMID:[20797690](https://pubmed.ncbi.nlm.nih.gov/20797690/)