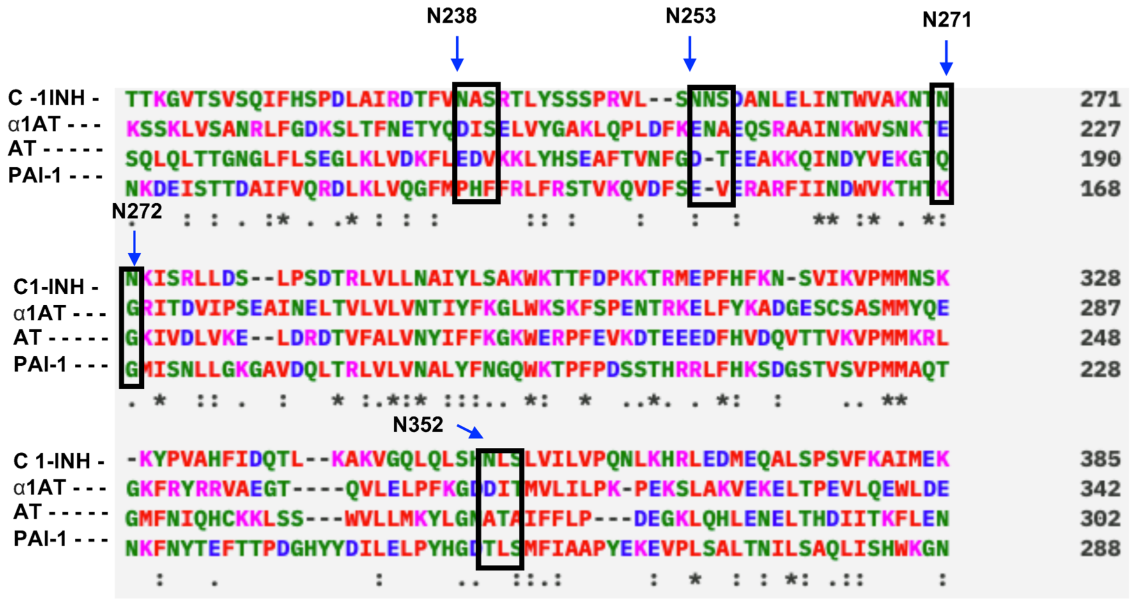

```
C -1INH -      TTKGVTSVSQIFHSPDLAIRDTFVNASRTLYSSSPRVL--SNNSDANLELINTWVAKNTN    271
α1AT - - -     KSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAINKWVSNKTE    227
AT - - - - -   SQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGD-TEEAKKQINDYVEKGTQ    190
PAI-1 - - -    NKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSE-VERARFIINDWVKTHTK    168
               .   : : . :* . .* : : :      :: :    :   :  :     ** :* . *:

C1-INH -       NKISRLLDS--LPSDTRLVLLNAIYLSAKWKTTFDPKKTRMEPFHFKN-SVIKVPMMNSK    328
α1AT - - -     GRITDVIPSEAINELTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSASMMYQE    287
AT - - - - -   GKIVDLVKE--LDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRL    248
PAI-1 - - -    GMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQT    228
               . *  :: .  :   * :.*:* :::.. *:  *  ..*. . *:  :    .. **

C 1-INH -      -KYPVAHFIDQTL--KAKVGQLQLSHNLSLVILVPQNLKHRLEDMEQALSPSVFKAIMEK    385
α1AT - - -     GKFRYRRVAEGT----QVLELPFKGDDITMVLILPK-PEKSLAKVEKELTPEVLQEWLDE    342
AT - - - - -   GMFNIQHCKKLSS---WVLLMKYLGNATAIFFLP---DEGKLQHLENELTHDIITKFLEN    302
PAI-1 - - -    NKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGN    288
                 :   .           :     ..  ::.:      :  *  : : *: .::     :
```

Supplemental Figure 1. Amino acid sequence alignment of selected SERPIN proteins. Sequence alignments were generated with NCBI protein blast software Clustal Omega. Red color presents small and hydrophobic; blue presents acidic; magenta indicates basic; and green shows hydroxyl, sulfhydryl, and amine residues. C1-INH, C1 inhibitor esterase; AT, antithrombin; α1AT, α1-antitrypsin; PAI-1, plasminogen activator inhibitor 1. "*" represents positions with a single, fully conserved residue. ":" represents positions with a conservation between amino acid groups of similar properties. "." Represents positions with conservation between amino acid groups of weakly similar properties.