**Table S2.** **Amino acid changes identified in KP-Pakistan *pfama-1***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Domain | Amino acid change | Frequency(%) | Domain | Amino acid change | Frequency(%) |
| Signal andprosequence | W28G\* | 10.5 | DI | E267Q# | 52.6 |
| H30D\* | 10.5 | I282K# | 100 |
| N34K# | 57.9 | S283L# | 42.1 |
| R39H# | 100 | Q285E# | 10.5 |
| R45S\* | 10.5 | N286S | 10.5 |
| K49T\* | 10.5 | D296H# | 31.6 |
| E52K# | 15.8 | N297T | 5.3 |
| Q57L\* | 5.3 | K300E# | 10.5 |
| S66P\* | 5.3 |  | Q308E# | 57.9 |
| I97N\* | 10.5 | DII | P330S# | 100 |
| M114V\* | 5.3 | I332N# | 100 |
| DI | N162K# | 31.6 | D333E\* | 5.3 |
| T167K# | 47.4 | H393R# | 10.5 |
| G172E# | 31.6 | N401S\* | 5.3 |
| N173K# | 5.3 | T404R# | 100 |
| Y175D# | 100 | E405K# | 89.5 |
| E187N# | 36.8 |  | I435N# | 10.5 |
| E187K# | 21.1 | N439H# | 100 |
| M190I# | 57.9 | DIII | M451K# | 57.9 |
| D196N# | 26.3 | I454T\* | 10.5 |
| E197D# | 52.6 | K485I# | 47.4 |
| E197G# | 26.3 | D493A# | 36.8 |
| E197H# | 21.1 | M496I# | 89.5 |
| H200R# | 21.1 | R503N# | 63.2 |
| H200D# | 79.0 | R503H# | 26.3 |
| D204N# | 57.9 | Trans-membrane and cytoplasmic domain | R512K# | 21.1 |
| K206E# | 100 | K544N# | 47.4 |
| I225N# | 89.5 | K570R\* | 5.3 |
| K230E# | 15.8 | E581Q# | 57.9 |
| D242Y# | 73.7 | D584H# | 52.6 |
| K243E# | 31.6 | N589K# | 47.4 |
| K243N# | 42.1 | P614S\* | 5.3 |

\* Novel amino acid changes identified in KP-Pakistan *pfama-1*

*#* Amino acid changes commonly identified in global *pfama-1*