| Peptide ID | Position | Sequence |
|---|---|---|
| 1 | 1-22 | MTSSRLWFSLLLAAAFAGRATA |
| 2 | 11-30 | LLAAAFAGRATALWPWPQNF |
| 3 | 23-42 | LWPWPQNFQTSDQRYVLYPN |
| 4 | 33-52 | SDQRYVLYPNNFQFQYDVSS |
| 5 | 43-62 | NFQFQYDVSSAAQPGCSVLD |
| 6 | 53-74 | AAQPGCSVLDEAFQRYRDLLFG |
| 7 | 68-83 | EAFQRYRDLLFGSGSWPRPYL |
| 8 | 75-88 | SGSWPRPYLTGKRH |
| 9 | 80-99 | RPYLTGKRHTLEKNVLVVSV |
| 10 | 89-108 | TLEKNVLVVSVVTPGCNQLP |
| 11 | 99-118 | VVTPGCNQLPTLESVENYTL |
| 12 | 109-128 | TLESVENYTLTINDDQCLLL |
| 13 | 119-138 | TINDDQCLLLSETVWGALRG |
| 14 | 129-148 | SETVWGALRGLETFSQLVWK |
| 15 | 139-158 | LETFSQLVWKSAEGTFFINK |
| 16 | 149-168 | SAEGTFFINKTEIEDFPRFP |
| 17 | 159-178 | TEIEDFPRFPHRGLLLDTSR |
| 18 | 169-188 | HRGLLLDTSRHYLPLKSILD |
| 19 | 179-198 | HYLPLKSILDTLDVMAYNKL |
| 20 | 189-208 | TLDVMAYNKLNVFHWHLVDD |
| 21 | 199-218 | NVFHWHLVDDQSFPYESFTF |
| 22 | 209-228 | QSFPYESFTFPELMRKGSYS |
| 23 | 219-238 | PELMRKGSYSLSHIYTAQDV |
| 24 | 229-248 | LSHIYTAQDVKEVIEYARLR |
| 25 | 239-258 | KEVIEYARLRGIRVLAEFDT |
| 26 | 249-268 | GIRVLAEFDTPGHTLSWGPG |
| 27 | 259-278 | PGHTLSWGPGIPGLLTPCYS |
| 28 | 269-288 | IPGLLTPCYSGSEPSGTFGP |
| 29 | 279-298 | GSEPSGTFGPVNPSLNNTYE |
| 30 | 289-308 | VNPSLNNTYEFMSTFFLEVS |
| 31 | 299-318 | FMSTFFLEVSSVFPDFYLHL |
| 32 | 309-328 | SVFPDFYLHLGGDEVDFTCW |
| 33 | 319-338 | GGDEVDFTCWKSNPEIQDFM |
| 34 | 329-348 | KSNPEIQDFMRKKGFGEDFK |
| 35 | 339-358 | RKKGFGEDFKQLESFYIQTL |
| 36 | 349-368 | QLESFYIQTLLDIVSSYGKG |
| 37 | 359-378 | LDIVSSYGKGYVVWQEVFDN |
| 38 | 369-388 | YVVWQEVFDNKVKIQPDTII |
| 39 | 379-398 | KVKIQPDTIIQVWREDIPVN |
| 40 | 389-408 | QVWREDIPVNYMKELELVTK |
| 41 | 399-418 | YMKELELVTKAGFRALLSAP |
| 42 | 409-428 | AGFRALLSAPWYLNRISYGQ |
| 43 | 419-438 | WYLNRISYGQDWRKFYKVEP |

| | | |
|---|---|---|
| 44 | 429-448 | DWRKFYKVEPLAFEGTPEQK |
| 45 | 439-458 | LAFEGTPEQKALVIGGEACM |
| 46 | 449-468 | ALVIGGEACMWGEYVDATNL |
| 47 | 459-478 | WGEYVDATNLVPRLWPRAGA |
| 48 | 469-488 | VPRLWPRAGAVAERLWSNKL |
| 49 | 479-498 | VAERLWSNKLTRDMDDAYDR |
| 50 | 489-508 | TRDMDDAYDRLSHFRCELVR |
| 51 | 499-518 | LSHFRCELVRRGVAAQPLYA |
| 52 | 509-528 | RGVAAQPLYAGYCNQEFEQT |

**Supplementary Table S1. Prospector PEPscreen® Custom Peptide Library for HexM Isoenzyme.**
Blue- Peptide Pool #1 (Peptides unique to μ portion of HexM)
Green- Peptide Pool #2 (Peptides 100% homologous between human and mouse HEXA
Orange- Peptide Pool #3 (Peptides with some homology between human and mouse HEXA)